CGIAR Platform on:

Excellence in Breeding

Tools and services that create synergies and accelerate genetic gains of breeding programs targeting the developing world

Full Proposal 2017-2022

July 2016

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1.0 Platform Narrative

1.0.1 Rationale and scope

Importance of genetic improvement: Over the past decades, genetic improvement has increased agricultural productivity, reduced the pressure on forests, changed the nutritional profile of crops, and made agricultural production more resilient to diseases, pests and droughts. Without genetic improvement, food prices would be substantially higher and more forest land would have been lost to agriculture (Evenson and Gollin, 2003; Stevenson et al., 2013). It is estimated that between 30-60% of the yield increases in farmers' fields can be traced back to breeders changing the genetic make-up of crops, while the rest is due to improved agronomy aligned with better functioning markets and extension systems. Relevant to the developing world, stress tolerance breeding has also resulted in yield increases under conditions that are similar to farmers' real conditions such as drought, low fertility, and waterlogging (Septiningsih et al., 2008; Weber et al., 2013), and averted losses or restored production after the emergence of new devastating diseases (Singh et al., 2011). Research into nutritional traits has resulted in the first bio-fortified crops being released and grown by farmers (Johnson et al., 2015). Examples in livestock include, in the developed world, the myostatin gene (Grobet *et al.,* 1997) and increased milk yields in cattle and, in the developing world, the prolificacy Booroola genes in sheep (Nimbkar *et al.,* 2005).

The challenges ahead: In spite of these successes, the breeding programs targeting the developing world will need to deliver higher rates of genetic gain to cope with the 21st century challenges of 50%-60% greater demands for food commodities, climate change and natural resource constraints. Climate change will reduce crop productivity by about 5% for every degree of warming above historical levels (Challinor et al. 2014). At breeding gains of 1%, this alone will require breeders to speed up current efforts substantially, and even more so considering increasing demands (Fisher et al, 2014). However, the pace of technological modernization in breeding programs targeting the developing world is inadequate and varietal turnover in most countries is slow. Partial modernization of methods and approaches has taken place mostly in the larger CGIAR breeding programs, yet with no formal exchange of methods and approaches across commodities. Mechanization, digitization, or use of DNA markers in forward breeding or quality control are done in proof-of-concept type projects while they urgently need to be mainstreamed. Most breeding programs do not have sufficiently rigorous product profiles, enough quality analysis support or enough multi-location yield testing to confidently select and identify cultivars that can rapidly replace current cultivars. Likewise methods to accelerate genetic gains in livestock, such as better recording of production traits, the use of statistical models to predict genetic merit, the use of genetic marker information in selection programs (Henderson, 1975; Goddard and Hayes, 2007; Clark and van der Werf, 2013) or the use of new reproductive technologies (Kasinathan et al., 2015) have inadequately benefited the developing world.

Increasing both the rate of genetic gain delivered directly by CGIAR breeding programs and improving their ability to support the modernization of national systems is the key scientific challenge facing the system, and the purpose for the proposed Platform. Individually, even the largest CGIAR breeding programs are too small to support rapid modernization by adapting and mainstreaming state-of-the-art breeding technologies such as found in the multinational private sector. Together, coordinated and supported by the Platform, the programs serving smallholders in the developing world can raise the rate of genetic gain they deliver much more effectively.

Scientific concepts and comparative advantage

The relevance of genetic gain: Accelerated genetic gain is a key outcome of the Platform. It is also a generic concept upon which breeding theory is based and breeding methods are designed. Interventions can be targeted and prioritized based on how they influence six factors that influence genetic gain: the genetic diversity that can be accessed (genetic variance); the precision with which a trait can be measured (heritability); the selection intensity applied (population size); the relevance of the trait for the target environment/for the user (selection environments and product concepts); the length of the breeding cycle, including the time required to replace old with new cultivars/breeds; and costs. Many interventions that accelerate genetic gains are, to a significant proportion, generic and can be applied to a range of traits. For example, genome-wide selection, once mastered in a routine breeding process, can be applied to any target trait, including yield potential, drought or heat resilience, nutritional quality or any other complex trait. As a result, interventions that accelerate genetic gains have high leverage for tackling present and future challenges to food and nutrition security, and climate change adaptation.

New opportunities: The quest for accelerating genetic gains is one of the most rapidly evolving science and technology areas given that genomic and marker-assisted selection, bioinformatics, remote sensing and genome editing have great potential for step changes in how breeding is done. More specifically, with the advances in genomics, we are just beginning to understand the wealth of genetic diversity available within crops and animals, which are the building blocks for future cultivars and breeds, and could be much more deliberately deployed to increase the productivity and resilience of agricultural systems (Gorjanc et al., 2016; McCouch et al., 2012; Vikram et al., 2016). New and more cost-effective genotyping and phenotyping technologies allow realizing greater productivity, stress resilience, or nutritional value with greater precision and speed, including through gene editing. Applications of these technologies rely on the ability of breeding programs to process much greater amounts of data, and within a shorter time frame. Capturing and fully integrating genomic and phenotypic data in the breeding process will both accelerate cultivar development and contribute to the genetic analysis of traits and discovery of genes that can be used by other breeders and researchers.

Economies of scale count: Successful R&D investment by the private sector and the larger public sector in crops (maize, rice, wheat) and animal products (milk, meat) accelerated genetic gains through a wide range of interventions, including: clear product conceptualization; improved research management and organization; leveraging diversity; higher quality phenotypic data; genomic selection and more precise marker-assisted selection; predictive analytics and more prescriptive pipelines; faster breeding cycles and seed movement; automation of seed handling, image phenotyping and seed chipping; stewardship practices that ensure greater genetic purity and integrity, improved data tracking and inventory management; and other technologies and operations that reduce costs and allow breeders to turn the wheel faster, with greater precision and at larger scale (Butruille et al., 2016). Many of these changes require specialized support services, including high tech platforms and interdisciplinary teams that are only affordable if they support a substantive number of breeding programs. Achieving higher genetic gains in CGIAR and NARS breeding programs will require the exploitation of economies of scale that can only be achieved by aggregating demand and capacity across programs, centers, and commodities.

Challenges to breeding programs that target the developing world: Progress in the breeding programs of multinational seed companies in the North is in stark contrast to the smaller and independently managed public and private sector breeding programs serving the developing world. Most do not have the necessary investment to translate knowledge- and capital-intensive research insights into streamlined breeding tools. And while publicly accessible academic research provides a vision of what could be achieved with modern tools, there is a huge gap between proof-of-concept research and its practical

application in actual CGIAR and NARS breeding programs. Many breeders *know* that, for example, genome-wide selection or image-based phenotyping would accelerate their breeding gains but *de facto* cannot apply these approaches in their programs due to lack of access to or investment in specialized know-how, tools and support services.

Why public sector investment: Market realities do not support a model wherein a few multinational companies do the breeding for the entire world. Environments are too diverse and returns on investment not high enough for many crop/target environment combinations to be focused on by the multinational breeding sector. This is particularly true in low- and lower-middle-income countries. Of the R&D investments by the private breeding sector, we estimate that less than 5% is invested in programs targeting low- and lower-middle-income countries (derived from Heisey and Fuglie (2011) and expert estimates), yet it is in these countries where 45% of the global area sown to major staples is located, and 48% of the world population and 84% of all poor live (Table 1). Low returns to R&D investments has resulted in a situation where even large, well-resourced companies in Sub-Saharan Africa market obsolete hybrids that are over 20 years old, simply because no competitor is forcing them to change their product line. As a result, farmers have inadequate access to breeding gains. For the animal breeding sector in low and middle income economies, the private sector has mostly concentrated on disseminating improved breeds (especially dairy cattle and chicken) developed in the developed world with almost no investment in R&D. Most of these introductions have met with little success because the introduced breeds are not well adapted to perform cost effectively under the low-input systems that predominate the low and lower middle income economies. The challenge is to enable breeding programs that target these regions with services that allow them to capitalize on cutting-edge technologies and know-how which up to now have only been available in the multinational breeding sector and to incentivize seed systems to deliver new products more quickly, and replace obsolete cultivars.

Vision of success for the Excellence in Breeding Platform: To enable staple crop and animal breeding programs targeting the developing world to make step changes in increasing genetic gains of cultivars and breeds delivered to farmers, for impact on food and nutrition security, climate change adaptation and development at large.

Scope

The Platform agenda will be directed at the needs of public and private sector breeding programs targeting farmers in low-and middle-income countries.

Local public and private sector breeding programs can be divided between those that do pure cultivar selection [i.e., select and release new varieties and hybrids from among varieties and hybrids generated by CGIAR centers or larger NARS ("cultivar selection programs")] and others that make their own crosses and generate their own varieties and hybrids ("cultivar development programs"). There is no statistics available on the number of these programs yet we can make an estimate based on the rationale for public and private sector investments.

In the case of the public sector, breeding investments depend on the agricultural R&D budget and the relative importance of the crop. Public breeding programs are largely (sub-)nationally scoped. Assuming a lower limit of 100,000 (upper-middle-income countries) to 250,000 (lower-middle-income countries) to 1,000,000 hectares (low-income countries) for NARS having adequate funds to initiate a breeding program, we estimate that there may be 250 cultivar development programs conducted by NARS on CGIAR mandate crops (Table 2; yellow highlighted cells). Many crops have too small a target environment to warrant an adequately funded national cultivar development program, resulting in over 500 crop/country combinations that rely mainly on cultivars generated by CGIAR centers or neighboring NARS

(Table 2; green highlighted cells).

In the case of the private sector, many more seed companies produce and sell seed in the developing world than actually breed new cultivars. Initiation of a cultivar development program depends on the size of the target environment, the purchasing frequency and the value of the seed (both higher for hybrid crops) and the costs associated with production, storage and transportation (bulk, phytosanitary concerns with vegetative propagated crops). As a result of the lack of a viable business case for private investment in breeding in most crops, cultivar development programs can only be found in a few regional and national companies focusing on hybrid or cash crops and higher yielding environments. The great majority of local seed companies focus on producing seed bred by the CGIAR or NARS. Overall we estimate that 200-300 local companies are or may be interested in initiating stronger R&D efforts, either by conducting their own trials and selecting cultivars (instead of solely using data from NARS and the CGIAR) or by initiating cultivar development. Equally, the large number of companies found in the developing world livestock sector deal mostly with the supply of semen for dairy breeds, and none undertake activities to develop new breeds.

The CGIAR is the most prominent source of germplasm and breeding know-how to the developing world, providing valuable genetic diversity both in the form of parental lines for use in breeding and as finished cultivars for dissemination. Through agri-food systems (AFS) breeding programs focused on the main commodities[1], 11 CGIAR centers maintain breeding pipelines and/or genebanks, access new technologies and know-how from a wide range of public and private sector partners, and help local public and private sector breeding programs improve their own programs. In the case of crops, the reach is enormous. 94% of all germplasm exchanged internationally by contracting parties of the International Treaty of Plant Genetic Resources for Food and Agriculture (ITPGRFA) are being distributed by the CGIAR (Table 3). Since 2007, 37 % of those samples were sent to recipients in Asia; 20 % to recipients in Africa; 15 % to Latin America and Caribbean, 11 % to Near East, 10 % to Europe and 4 % to North America. Approximately 75% of the materials have been improved by the centers (FAO, 2015). In the case of livestock, breeding is conducted as part of the Dairy and Chicken Genetics Gains Program and the Sheep and Goat Community Based Breeding Programs, undertaken by ILRI and ICARDA, and of fish through Genetically Improved Farmed Tilapia (GIFT) programs run by WorldFish. Between 2007 and 2015 WorldFish distributed 561,000 fry or fingerlings to 137 institutions.

As noted above, many countries and seed companies directly use the cultivars developed by the CGIAR while others both use them directly and adapt them through their own national or privately funded breeding programs. A CGIAR-led initiative will benefit both types of programs, either by NARS and local seed companies getting access to better cultivars and breeds, or by programs being enabled to prioritize, contribute to and adopt the tools and research management approaches adopted or developed within the proposed Platform.

[1] **Crops:** Banana, barley, bean, cassava, chickpea, cocoa, cowpea, forage crops, lentil, maize, millet, pigeonpea, plantain, potato, rice, sorghum, soybean, sweet potato, triticale, wheat and yam. **Animals:** buffalo, camel, cattle, chicken, goats, pigs, sheep.

Table 1. Crop area and population statistics of CGIAR mandate crops (FAOSTAT, 2016 referring to 2012-2014 values; World Bank, 2016) and expert estimates of R&D investments by the private breeding sector.

World Bank country classification	Area		Population		Poor		Private Breeding
	million ha		million		million		R&D
High-income economies	253	55%	1,399	52%	3	16%	> 95%
Upper-middle-income economies	273		2,361		199		
Lower-middle-income economies	324	45%	2,879	48%	798	84%	< 5%
Low-income economies	98		622		277		
Total	**948**	**100%**	**7,261**	**100%**	**1,278**	**100%**	**100%**

Table 2. Number of country/staple crop combinations and their relationship to sustaining public breeding investments in low- and middle-income countries. Green country/crop combinations are likely mostly pure cultivar selection programs; yellow country/crop combinations may sustain one or more national public cultivar development programs.

Number of country/crop combinations	... with a crop area of ... (thousand ha)					
	< 10k	10 - 100	100 - 250	250 - 1,000	> 1,000	Total
Upper-middle-income economies	264	129	42	48	33	516
Lower-middle-income economies	221	138	61	46	51	517
Low-income economies	94	127	45	61	27	354
Grand Total	**579**	**394**	**148**	**155**	**111**	**1387**

Table 3. Germplasm distributed from CGIAR centers and other contracting parties to the ITPGRFA during the 2007-2014 period (Source: FAO, 2015; FAO, 2016; updated with 2007-2014 data from CIAT).

Institution	Plant Genetic Resource for Food and Agriculture (PGRFA)									PGRFA under develop-ment	Total germ-plasm	Ship-ments
	2007	2008	2009	2010	2011	2012	2013	2014	Annual	Annual	Annual	Annual
AfricaRice	364	931	7,538	2,938	2,508	3,355	10,135	8,795	4,571	2,685	7,256	50
Bioversity[1]	421	324	646	680	505	434	997	685	587	69	656	41
CIAT	4,243	7,451	4,809	10,194	8,082	5,471	4,568	5,446	6,283	24,101	30,384	353
CIMMYT	142,695	98,603	139,339	192,278	241,426	256,328	241,247	230,702	192,827	0	192,827	1,877
CIP	877	2,031	2,791	1,052	1,403	1,487	1,357	1,160	1,520	949	2,469	56
ICARDA	8,598	89,999	88,829	98,827	109,645	6,940	20,886	14,783	54,813	0	54,813	
ICRAF[1]					10		25	79	38	0	38	14
ICRISAT			47	21,902	18,637	21,631	16,134	33,412	18,627	3,892	22,519	430
IITA	6,823	1,877	1,477	2,841	2,508	1,391	1,035	3,255	2,651	0	2,651	61
ILRI[1]	1,373	560	516	453	1,195	811	1,680		941	0	941	82
IRRI		55,200	77,598	80,055	95,287	65,971	43,855	63,122	68,727	36,808	105,535	680
Total CGIAR	**165,394**	**256,976**	**323,590**	**411,220**	**481,206**	**363,819**	**341,919**	**361,439**	**351,584**	**68,504**	**420,088**	**3,643**
Other Contr. Parties	4,722	20,384	31,262	27,929	41,568	35,548	33,384	23,093	27,236			
Grand Total	**170,116**	**277,360**	**354,852**	**439,149**	**522,774**	**399,367**	**375,303**	**384,532**	**378,821**			

[1] Genebank only. No breeding program

1.0.2 Platform Structure and Modules

The Excellence in Breeding Platform is to be seen as part of the CGIAR Portfolio of Research Programs and Platforms. It will support the network of partners (CGIAR centers, NARS, local private breeding sector) that are developing new cultivars/breeds and conserving genetic resources within eight Agri-food Systems CGIAR Research Programs (AFS CRPs) and the Genebanks Platform. The Platform will develop international public goods and its know-how and tools will also be accessible to cultivar development programs that work on other commodities (e.g., vegetables) or in non-target (i.e., high-income) countries. Similar to the organization of breeding programs and platforms in multinational, multi-crop companies, the Platform will support the adoption of cutting-edge tools and services that are in demand by multiple commodities and CRPs, exploit economies of scale to reduce costs, and accelerate learning and use of best practices across commodities and CRPs. The Platform will develop, explore and improve access to tools and approaches that are difficult to develop at the commodity level; meanwhile, commodity-specific and cross-cutting research common to a group of crops or animals (e.g., legumes, vegetatively propagated crops, livestock, fish) will be carried out within the respective AFS CRPs (Figure 1).

Agenda and products: At its onset, the Platform's agenda will contain five modules identified as being most in demand by the AFS CRPs and the Genebanks Platform:

1. **Breeding program excellence**: Generic tools and services to support breeding program excellence across CGIAR and NARS breeding programs, based on: (1) common metrics and standards for monitoring performance and indicators of genetic gains in researchers' and farmers' fields; and (2) advice, including from the private sector, on product and breeding program design, tool implementation, and dissemination.
2. **Trait discovery and breeding tools and services:** Drawing on the innovations taking place in breeding and research programs worldwide, lower the transaction costs to identify, access and adopt newly emerging tools that support trait discovery and breeding. This module also provides the web platform where user groups upload successful applications from all modules and feedback from users is captured.
3. **Genotyping/sequencing tools and services:** (1) Procurement and coordination of common genotyping/sequencing services; (2) in collaboration with Module 5, customization of generic tools to support the sampling to data analysis pipeline; and (3) access to advice, including from the private sector, for the effective use of genotypic/sequencing information in breeding programs.
4. **Phenotyping tools and services:** (1) Common approaches, tools, accelerated learning, and advice for using cutting-edge remote sensing, high-throughput precision phenotyping, targeting, mechanization and automation approaches in breeding programs; (2) access to better value-for-cost laboratories for assessing physico-chemical composition and functional properties in plant and animal materials.
5. **Bioinformatics and data management tools and services:** Open-access tools and services linked to core databases to support both complex and integrated data analysis and management of breeding program data, necessary for CGIAR, NARS, and SMEs to increase genetic gains and also as a prerequisite for applying genomic and high-throughput phenotypic information in cultivar/breed development.

Impact on intermediate development outcomes and systems level outcomes will be generated through the use of Platform products by the CGIAR and NARS breeding programs and genebanks and other users, with the ambitious objective of the Platform becoming the one-stop place to go for advice, tested resources and best practices for any breeding program targeting the developing world.

What's new: In the past, breeding programs and projects were only loosely associated and with little accountability on the rate of genetic gain delivered. AFS CRPs strongly endorsed and emphasized the **use of common metrics and standards** for stimulating greater breeding excellence and transparency of breeding programs targeting the developing world. Membership in this community-driven effort and publication of associated metrics will result in a transparent assessment of the success and bottlenecks of breeding programs and may be used to stimulate investments in high-payoff activities, within and across AFS CRPs. The Platform will **foster best practices across the system**, with tools and processes that are effective and adaptable across a broad set of commodities. It will test, adapt and mainstream tools, provide **expert advice** as well as develop a **knowledge base** ("Toolbox") on a broad range of approaches for increasing breeding efficiency**.** Platform interventions should allow lower budget and less advanced CRPs and partners (NARS and SMEs) to capitalize on the bigger budgets of more advanced CRPs and the private sector. The Platform will also **broker access** to cost-effective genotyping/sequencing, laboratory analysis services, and data analysis capacities. Through the networks of the AFS CRPs, it will support **capacity strengthening and knowledge transfer** beyond first users.

Implementation principles: The Platform will execute its agenda through a combination of CoPs, consultancies, and contracted services. Instead of reinventing the wheel through its own staff, the Platform will capitalize on providers of innovation from the public and private sector, including AFS CRPs, and invest in their adaptation, documentation and mainstreaming, with a view to making them available to the greatest number of users, based on priorities set by its members. It will operate both at a strategic level and guide the implementation of best practices. Not every user will need the same service or use the same information. In many instances, tools and approaches should be suitable for resource-constrained breeding programs that often operate far away from service providers. Platform staff and contractors thus need to combine technical expertise with a strong ability to interact with users and understand their needs. As a lesson from the past, it will validate tools and services first with members before making them more widely available. It will need to ensure that data flows connect between Genebanks, the Excellence in Breeding Platform, the AFS CRPs and the Big Data, Information, and Knowledge Platform.

Current focus and future evolution: Focus will be on approaches that are successfully used by champion users within the CGIAR, NARS, ARIs or the private sector in the areas of research management (Module 1), trait discovery and breeding (Module 2), genotyping (Module 3), phenotyping, mechanization, automation (Module 4) and bioinformatics and biometrics (Module 5). This may include: changes in breeding team management; how to increase effective population sizes and reduce breeding cycle times; increasing precision of phenotyping; mechanization approaches; barcodes and electronic data capture; advanced statistical methods; using managed stress environments for biotic and abiotic stresses; using DNA markers for selection and quality control; or pipelines for trait mobilization.

Future evolution: A wider range of cross-commodity synergies may be exploited in the future, both upstream (e.g., on gene editing) and downstream to accelerate cultivar replacement in farmers' fields. In the case of gene editing, it was decided that experiences should first be gained through individual AFS CRPs collaborating with license holders on high return-to-investment and likely-to-succeed traits. Licensing approaches, intellectual property management and other generic insights should be shared as part of Module 2. In the case of activities that exploit synergies of scale for scale-out, possible investments will be assessed and proposed based on insights from Module 1, aligned with the agenda of AFS CRPs.

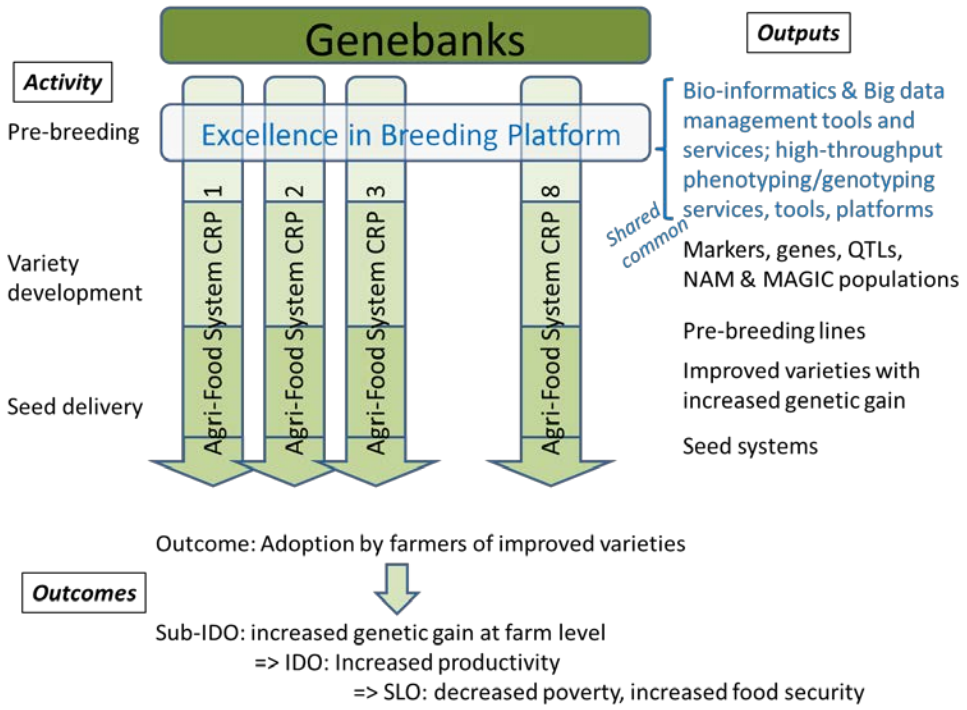

Figure 1. The Excellence in Breeding Platform develops and makes available tools that accelerate breeding gains across multiple CRPs.

1.0.3 Impact pathway and contribution to theory of change of the CGIAR and its programs

Figure 2 and Table 4 describe the Impact pathway and Theory of Change for the Excellence in Breeding Platform. They describe how Platform tools and services are applied by AFS CRPs to contribute to the Intermediate Development Outcomes (IDOs) of the respective CRPs, and thereby to the Systems Level Outcomes (SLOs) of the CGIAR, including reducing poverty (SLO 1), improving food and nutrition security for health (SLO 2), improving natural resources systems and ecosystem services (SLO 3), and enhancing the cross-cutting issues of climate change (A), policies and institutions (C) and capacity development (D). By increasing the effectiveness of breeding programs targeting the developing world, the Platform will thereby contribute to the achievement of eight Sustainable Development Goals outlined by the United Nations (SDGs 1, 2, 3, 8, 12, 13, 15 and 17).

The Platform does not have an independent R&D agenda; rather, it supports the AFS CRPs and external users in generating the sub-IDOs. The Platform tools will be generic and can be applied to a range of traits and species. They will make trait mobilization and breeding more efficient and effective. As a result, cultivars and breeds required by farmers and consumers are better defined and more effectively developed by the AFS CRPs and external users. The Sub-IDOs in Table 4 list the predominant AFS breeding targets. The expectation is that Platform tools will be applied mostly to these Sub-IDOs. Through its work on standardization and metrics in Module 1, the Platform will help align the results-based management (RBM) framework of AFS CRP breeding programs and make investment needs more transparent.

This Theory of Change for the Platform will be the foundation for the monitoring, evaluation and learning plan. It will limit its implementation on monitoring and assessing the research outcomes achieved (green

arrows in Figure 2), associated outputs (see further below Table 7), interventions, assumptions and risks (Table 5 and 10), while each AFS CRP will monitor and assess its own Theory of Change (red arrows in Figure 2) and assess the Platform's contribution to these.

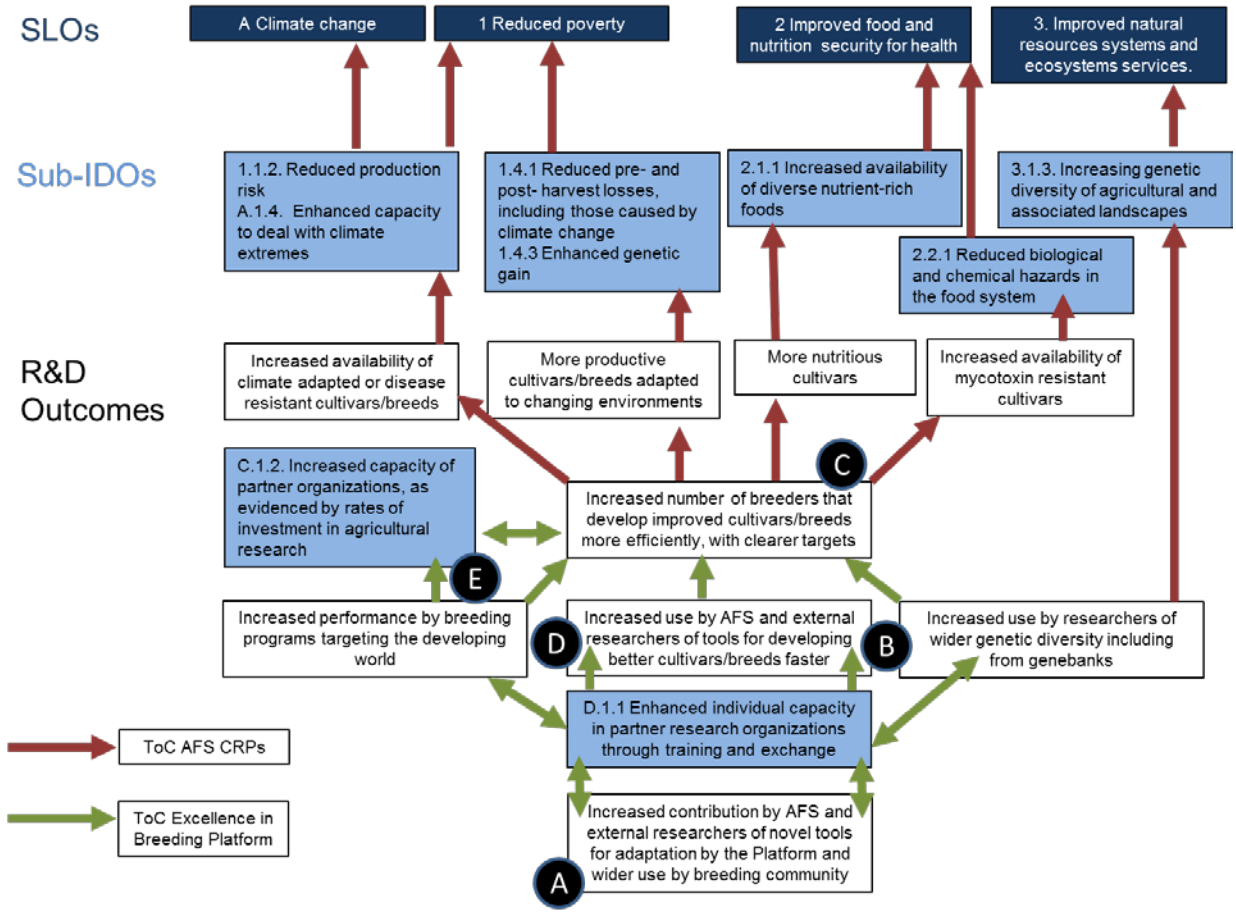

Figure 2. Theory of Change for the Excellence in Breeding Platform in support of the AFS CRPs' Theories of Change.

Table 4. Direct and indirect (through the AFS CRPs and external users) impact of the Platform outcomes on the Sub-IDOs and IDOs of the CGIAR.

Platform Outcomes: Application of Platform tools and services to …	**Impact on Sub-IDO**	**IDO**
Increased availability of climate adapted or disease resistant germplasm/cultivars/breeds (Modules 2-5)	1.1.2 Reduced production risk	1.1 Increased resilience of the poor to climate change and other shocks
	A.1.4 Enhanced capacity to deal with climate extremes	A.1 Mitigation and adaptation achieved
A steady flow of productive cultivars/breeds adapted to changing environments (Modules 2-5)	1.4.1 Reduced pre- and post-harvest losses, including those caused by climate change 1.4.3 Enhanced genetic gains	1.4 Increased productivity
More nutritious cultivars (Module 2-5)	2.1.1 Increased availability of diverse nutrient-rich foods	2.1 Improved diets for poor and vulnerable people
Increased availability of mycotoxin resistant cultivars (Modules 2, 3, 5)	2.2.1 Reduced biological and chemical hazards in the food system	2.2 Improved food safety
Increased use by researchers of wider genetic diversity including alleles derived from genebanks (Modules 2-5)	3.1.3. Increased genetic diversity of agricultural and associated landscapes	3.1. Natural capital enhanced and protected, especially from climate change
Increased number of breeders that develop cultivars and breeds more efficiently, with clearer targets Increased use by AFS and external researchers of tools for developing better new cultivars and breeds faster	Contributes through the AFS CRPs and external users to 1.1.2, 1.4.1, 1.4.3, 2.1.1, 2.2.1, 3.1.3, A.1.4, as listed above this row.	Contributes through the AFS CRPs and external users to 1.1, 1.4, 2.1, 2.2, 3.1, A.1, as listed above this row.
Increased number of breeders that develop cultivars and breeds more efficiently, with clearer targets Increased performance by breeding programs targeting the developing world (Module 1)	C.1.2. Increased capacity of partner organizations, as evidenced by rates of investment in agricultural research	C.1. Enabling environment improved
Increased contribution by AFS and external researchers of novel tools for adaptation by the Platform and wider use by breeding community (Modules 1-5)	D.1.1 Enhanced individual capacity in partner research organizations through training and exchange D.1.2. Increased capacity of partner organizations, as evidenced by rates of investment in agricultural research	D.1. National partner and beneficiaries enabled

Table 5. Assumptions and risks for the Platform's outcomes and associated interventions and outputs.

	Assumptions and Risks	**Interventions and Outputs**
A	• There will be continuous development of new tools • Breeders and associated disciplines are willing to contribute best practices, validate others, and provide feedback • Existence of an enabling environment allowing scientists to take risks, innovate and learn from failures	• Active facilitation of CoPs where everybody learns and shares • User involvement in needs assessment, validation and testing of tools • Proper citation and acknowledgement • Platform funding to AFS CRPs and other members to document best practices • Seek ARI and industry engagement • Incubator to source and ground truth innovations • Fund raising for game-changing solutions Output: Value and volume of documented use cases; best practices, tools and documents as listed in Table 7
B	• Effective assessment of the needs and abilities of users to accelerate genetic gains • There will be continuous demand for new tools • The Platform's toolbox provides an effective communication and information dissemination approach Risks: Intellectual property issues may constrain tool dissemination and use	• Use cases are contributed by AFS CRPs and external users • User involvement in Expert Advisory Committee and Platform Steering Committee • Personnel hired for technical expertise and facilitation skills/service orientation • Results-based management approach; monitoring of use of tools and services Output: Training needs assessment; contracting of expertise and training as listed in Table 7 • Focus on open-access tools • Member and user agreements
C	• Breeders are adequately funded and are willing to learn, adopt and adapt documented tools • Technologies are cost-efficient and can be implemented in resource-constrained environments, away from service providers	• Metrics to make breeding program scope, performance and bottlenecks transparent • User testing of tools • Capitalize on experience from the private sector Output: Brokering of services as listed in Table 7; metrics of the RBM framework.

D	• Availability of resources and capacity for training and backstopping • Conducive environment for CGIAR, ARIs and NARS to participate in capacity building	• Effective toolbox structure aligned with use cases • Virtual platform provides self-explanatory training modules; extensive use of videos • Linkages with AFS CRP and universities for use of and feedback to Platform training modules. • Coordination of face-to-face meetings with major scientific meetings Output: Toolbox and training plan
E	• Metrics and standards are convincing to incentivize implementation of best practices • Metrics and standards are convincing to incentivize non-CGIAR breeding programs to apply the same • Metrics and standards are convincing to guide donor investments Risk: Donors continue funding isolated projects inhibiting joint action or focus on delivery instead of funding germplasm and cultivar development.	• Communicate added value of the Platform to CRP objectives, ToC and IDOs • User involvement in defining standards • Membership agreement • Use of metrics in portfolio report and external reviews; align with AFS CRPs, IEA, ISPC and System Office • Support to both AFS specific and Portfolio fund raising • Seek donor feedback/dialogue Output: Materials, sites and services as listed for Module 1 in Table 7; communication plan

1.0.4 Capacity development

The Excellence in Breeding Platform seeks to ensure that tools and services for accelerating genetic gains are being taken up by a significant number of breeding programs targeting low- and middle-income countries, mostly working through and with the AFS CRPs. The Platform will enhance:

(i) **Science capacity** through CoPs and external consultancies around distinct topics (breeding excellence, trait discovery and breeding, genomics applications, phenotyping, mechanization and automation, bioinformatics and biometrics) which promotes a culture of learning and collaboration. The Platform will invest in members documenting tools, and in Platform personnel and consultants adapting those tools for a wider range of users, as part of a web-based "Toolbox". The Platform will develop a list of internal and external experts for breeding program organization, work flow management, use of genotyping/sequencing and phenotyping tools, biometrics, mechanization and automation. AFS CRPs or external users may also contract them individually for specific consultancies and coaching. In the area of biometrics, with scarce human resources across the CGIAR, emphasis will be placed on expanding the number of biometricians trained in using Platform tools by linking up with universities in CGIAR target countries. Cross-commodity training courses will be organized and aligned with major scientific meetings and focus on train-the-trainer approaches. The Platform will promote an accreditation system for training programs and seek systematic feedback on the value of training programs and experts. Cross-cutting AFS CRPs (FTA, RTB, DCL, Livestock, Fish) will help adapt and broaden applicability to under-invested and challenging commodity groups. Capacity building effectiveness will be measured through tool adoption and demonstrated use.

(ii) **Gender in research design and impact pathways** by ensuring that women farmers and end-users are represented in cultivar/breed design of AFS CRPs, and actively ensuring women are included in communities of practice, expert advisory groups, training events and Platform staffing to accelerate skill development and job opportunities.

(iii) **Results-based management, governance, learning and knowledge sharing** by establishing a CGIAR-wide Breeding Program Assessment system with metric analysis to assess program output, efficiency and effectiveness as part of Module 1. This will support management decisions within and across CRPs to systematically improve breeding programs across the CGIAR and NARS. The approach is to provide an incentive for greater excellence and support such ambitions with capacity building, best practices and targeted investment. The work of the Bioinformatics Module will create greater compatibility and interoperability across breeding-relevant tools at the database, analysis and user interface levels, which is also the basis for meaningful open-access to the large volume of germplasm-related databases within the CGIAR.

(iv) **Stronger capacities in technology dissemination and upscaling** through the web-based knowledge base for best practices ("Toolbox") which will be organized by use cases and user types. The Platform is to enable AFS CRPs and external users globally to use the Platform's training modules and knowledge base for their own training programs, and encourage new users to provide feedback to Platform tools and services. It is expected that a large number of graduate students will become users of Platform tools as they are implementing projects in the areas of trait discovery, molecular breeding, phenotyping or quantitative genetics. They may be linked to the Platform through their supervisors in the AFS CRPs or access the tools as external users.

Annex 5 'Capacity Building' provides further details.

1.0.5 Platform leadership, management and governance

Scientific leadership and management

Scientific leadership will be provided by Platform and Module Leaders to be identified based on competitive processes, once the proposal is approved. They should have crop- and animal-related expertise. Competitive advertisement of these positions needs to be balanced with the ability to interact with each other, members and users, implying that positions and activities should be based in major breeding hubs (centers, ARIs). Module Leaders may be appointed initially on a part-time basis or shared with AFS CRPs or existing projects.

Profile of the Platform Leader

- In-depth understanding of practical breeding applications and logistical constraints relevant to breeding programs targeting the developing world (CGIAR, NARS, local private sector)
- Track record in service provision in areas relevant to the Platform
- Experience developing and implementing a results-based management framework
- Excellent communication, networking and negotiation skills that attract funding, in-kind contributions and ensure alignment with CRPs
- Track record in leading multi-institutional programs or projects, and building consensus among diverse needs of clients

Profile of the Module Leaders

- Specific competence, expertise and track record of delivery
- Enthusiastic about Platform objectives and committed to maximizing value to users; service-orientation that seeks to use and adapt outside solutions before developing in-house solutions
- Track record in building consensus among diverse needs of clients
- Familiar with practical breeding applications and logistical constraints relevant to breeding programs targeting the developing world (CGIAR, NARS, local private sector)

Platform staffing and management: Platform personnel will consist of Platform and Module Leaders and immediate support staff. A large proportion of the activities will be conducted through contracts with members, external experts and through other consultancies. The Platform Leader is to adopt best management practices and approaches from the Genebanks Platform and other CRPs. Collaboration agreements will be established with the leaders of existing projects that are already funded (such as the Integrated Breeding Platform and the Genomic & Open-source Breeding Informatics Initiative) and other potential in-kind contributors (from ARIs, NARS, the private sector) to the Platform whose agendas align with the Platform agenda.

Administrative positions will include one admin/finance support staff. It will contract expertise in M&E and communications. Other services and expertise (legal, human resources, risk management, grants management, monitoring and evaluation, internal audit, open access management) will be provided by the Lead Center, which will also issue and contract external audits.

Governance

Principles: The Platform Leader will report to the Platform Steering Committee (PSC) which is to be kept lean and appropriate to the size of the budget, balanced by: (1) Commodity (major crop, smaller crop, animals); (2) expertise (including those drawn from ARIs, NARSs and the private sector; and (3) the clients the Platform wants to serve in a manner that supports the interrelationship and accountability between

AFS CRPs and the Platform. Governance approaches follow the recommendations of the Governance and Management Review executed by the Independent Evaluation Assessment unit (IEA) of the CGIAR.

PSC membership: The PSC will consist of five regular and two ex-officio members representing: (1) AFS CRP, major crops (CGIAR center or ARI from MAIZE, RICE or WHEAT); (2) AFS CRP, smaller crops (CGIAR center or ARI from DCL or RTB or FTA); (3) AFS CRP, animals (CGIAR center or ARI from Fish or Livestock); (4) NARS; (5) private sector; (6) the Lead Center (ex-officio); and (7) the Platform Leader (ex-officio). Members need to bring expertise relevant to the Platform (breeding program management, breeding, genomics, phenotyping and/or bioinformatics). They need to be familiar with outside opportunities (emerging innovations, tools and services) and the requirements of users, i.e., breeding programs targeting the developing world. Members are appointed for an initial two-year period, after which 1-2 members will be replaced on an annual basis, for terms that are not to exceed five years. While the AFS CRPs will be requested to nominate candidates who could serve as PSC members, the ultimate decision will be taken by the PSC. The PSC relies on the active participation of all of its members and will hence execute annual self-evaluations that may result in the replacement of a member with suboptimal participation.

Meetings: The PSC will meet twice per year, face-to-face or virtually, and more often if the agenda requires. Decisions require the agreement of 70% of members. Meetings will be open to self-sponsored observers representing other AFS CRPs, centers, external members or funders. Once a year, the PSC will organize a virtual interchange with Platform users and other stakeholders where it will account for Platform activities and seek first-hand user feedback.

Terms of Reference: The PSC will provide strategic oversight of the Platform, priority setting and the evaluation of results, and be accountable for the performance of the Platform. It approves Platform specific policies and strategies, including those related to the selection of contractors and consultancies, the conflict of interest management and intellectual asset (IA) management. It oversees workplans and budgets, the results-based management framework, and the systematic collection of user feedback. It will monitor and ensure the effective exercise of expert advisory committees in each module, and the appropriate allocation of resources that benefit "weaker" and "stronger" commodities. It is part of the Reference Committee for external evaluations, evaluates the performance of the Platform Leader, interacts with the Director General (DG) of the Lead Center and, at least once per year, with the Lead Center Board.

Expert Advisory Groups will provide specialized advice at the Module level and ensure ownership and feedback from the wider constituency. Composed of up to 10 AFS members (that could come from CGIAR centers, ARIs or NARS) and external experts, they meet virtually on a regular basis and face-to-face once per year. They provide feedback to the Module workplans and performance, prioritize needs and investments, critically assess proposals and recommend alternative interventions, champion the Platform's activities among their respective constituencies and contribute to the performance assessment of the Module Leader.

Lead Center

The Lead Center will be selected on a competitive basis once the Platform Proposal has passed the review by the Independent Science & Partnership Council (ISPC) and Fund Council in the 2nd quarter of 2016. The Selection Committee will consist of one vote per Center involved in breeding (CIAT, CIMMYT, CIP, ICARDA, ICRAF, ICRISAT, IITA, ILRI, IRRI, WorldFish). Criteria for selecting the Lead Center are:

- Experience in leading multi-center platforms, CRPs or other major initiatives under the supervision of

external Steering Committees.

- A vision and commitment to modernizing breeding approaches for the good of the whole system.
- Manages applied breeding programs, ideally with different breeding systems; expertise and a good track record in modernizing breeding approaches relevant to multiple modules, to serve as an active user committed to implementing Platform solutions including MEL approaches.
- An open culture and a strong track record in collaborating with other CGIAR partners, ARIs, the private sector, NARS and the Global Crop Diversity Trust (GCDT) to develop and implement improved breeding applications including by supporting NARS and local private sector partners.
- Strengths in financial and intellectual property management and implementation of the CGIAR open-access policy; good track record of working internationally and with low costs.

1.1 Platform Budget Narrative

1.1.1 General Information

Platform Name Excellence in Breeding Platform

Platform Lead Center CIMMYT

1.1.2 Summary

Module Name	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
Module 1. Breeding Program Excellence	1,824,627	1,915,858	2,011,651	2,112,234	2,217,846	2,328,738	12,410,954
Module 2. Trait discovery and breeding to	2,146,559	2,253,887	2,366,582	2,484,911	2,609,156	2,739,614	14,600,710
Module 3. Genotyping/sequencing tools	936,116	982,922	1,032,068	1,083,672	1,137,855	1,194,748	6,367,381
Module 4. Phenotyping tools and service	1,534,011	1,610,712	1,691,248	1,775,810	1,864,600	1,957,830	10,434,211
Module 5. Bioinformatics and data manag	3,101,892	3,256,987	3,419,836	3,590,828	3,770,369	3,958,887	21,098,798
Management & Support Cost	456,794	479,634	503,615	528,796	555,236	582,998	3,107,073
Strategic Competitive Research Grant	-	-	-	-	-	-	-
	10,000,000	10,500,000	11,025,000	11,576,250	12,155,062	12,762,816	68,019,128

The Platform proposes an budget from US$ 10 million (Base) to US$ 15 million (Uplift) per annum to execute its agenda which is approximately 5% of the AFS CRPs' overall investments in germplasm development. The outcomes associated with Base and Uplift Budgets are explained in Table 8. Initially, US$ 2 million of W1&W2 funding will be used to initiate Platform activities with the Platform Leader and part time leaders for Modules 1-5, contracted from members for their ability to initiate the CoPs and web-based Platform activities. As donors contribute additional W2, W3 or bilateral funding, leadership and management costs will be equally distributed across all funding sources, resulting in the W1&W2 allocation for the Base scenario. Details for these scenarios are provided in the Section "2.8 Detailed breakdown of the costs", in Tables 12 (Base budget), 13 (Uplift budget), 14 (initial W1&W2 use), and 15 (W1&W2 use as W3 and bilateral support become available). Module-level budgets (Base and Uplift) are presented by work package in the 'Objectives and targets' section of each Module. The level of funding per Module is driven by the workplan. Financial risks are outlined in Table 11, Risks 7.01 to 7.04.

Given that the host institutions for Platform and Module Leaders and external contractors are yet to be determined on a competitive basis, the same cost assumptions were used for all implementers, whether Lead Center, collaborating Center, NARS or ARI, using the actual costs of similar operations at CIMMYT.

They were aligned with the personnel and consultants to be hired by the Platform and the type of activity of the Module. An annual inflation/budget growth of 5% was used. Services contracted by AFS CRPs or external users for individual use are not included in the budget. The Platform would provide those services at cost (e.g., external experts) or users will pay third-party providers directly. No budgetary support will be recovered from members during 2017 - 2022. Such an approach will be assessed in 2021. Any income negotiated earlier, such as from the private sector, would be accounted for as bilateral income.

The main cost drivers are personnel, investments in members (e.g to test use cases and provide Module documentation), consultant time, activities contracted to ARIs, training days, access to server capacity and need for other equipment (genotyping, phenotyping).

AFS members include CGIAR Centers, NARS, the private sector and ARIs, and budgets allocated to AFS members and to training could go to CGIAR Centers, NARS, the private sector and/or ARIs. Funding of contributors is linked to the deliverance of agreed milestones.

Items included in various budget categories

Personnel includes the costs of: Internationally and locally hired staff and students, and their benefits and allowances. Given that the locations of Platform and Module Leaders are yet to be determined, CIMMYT staff costs and personnel policy were used. As a CGIAR-wide survey showed, they are representative of the costs at most other CGIAR centers. International staff benefits and allowances include medical and life Insurance, retirement, costs of children's education (up to high school), housing and utilities, recruitment costs including shipping and transfer, and professional development. Even though a benefit for international staff, costs of car purchase are included in Capital Equipment, and costs of car operation are included in Other Supplies and Services. Local staff benefits include medical and life Insurance, social security, other benefits as per local labor law, retirement, recruitment costs and professional development. Student benefits include medical insurance. Given that some units use research assistants and students interchangeably, an average value was extrapolated from past use in units with similar activities.

Travel includes the costs of: Air fares, subsistence and local transport of Platform personnel and consultants.

Capital Equipment includes the costs of: Platform assets with a value greater than US$ 2,500, including cars, local servers and other ICT infrastructure, software licenses, and equipment associated with phenotyping, genotyping, the web platform and communication specifically acquired or leased for the purpose of executing the Platform's activities.

Other Supplies and Services include the costs of: Publishing, subscriptions, photography, printing, distribution, open access; office services including gas, water, electricity, ICT, postal and courier fees, telecommunication costs, bank charges; insurances; rental (to the extent not owned) of office space and equipment; charges associated with land use; temporary labor; low value project fixed assets including computers, printers, office furniture; vehicle use; repairs and maintenance, 2% Consortium System Costs for bilateral and W3 funded projects. This category also includes the costs of **Training and Workshops,** including participant fares, fees/honoraria, subsistence, local transport, and representation. They exclude self-paying participants.

Collaboration includes the costs of: personnel, travel, training and workshops, capital, other supplies and services of non-CGIAR sub-contractors, and their indirect costs.

Indirect costs include the costs of: Institutional oversight and management, human resources, finance, risk management, audits, institutional systems upgrades, grants and project management, and non-Platform

specific support for legal (e.g. host country agreements, labor law compliance), communication and knowledge management (e.g. basic web platform). The Lead Center rates used are 15% for in-house expenses, 0% for CGIAR members and 5% for collaboration expenses related to other partners.

1.1.3 Platform Funding Plan

Funding Needed	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2	$2,000,000	$2,100,000	$2,205,000	$2,315,250	$2,431,013	$2,552,563	$13,603,826
W3	$4,000,000	$4,200,000	$4,410,000	$4,630,500	$4,862,025	$5,105,126	$27,207,651
Bilateral	$4,000,000	$4,200,000	$4,410,000	$4,630,500	$4,862,025	$5,105,126	$27,207,651
Other Sources	$0	$0	$0	$0	$0	$0	$0
	$10,000,000	$10,500,000	$11,025,000	$11,576,250	$12,155,062	$12,762,816	$68,019,128

Funding Secured	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2(Assumed Secured)	$2,000,000	$2,100,000	$2,205,000	$2,315,250	$2,431,013	$2,552,563	$13,603,826
W3	$0	$0	$0	$0	$0	$0	$0
Bilateral	$1,622,129	$820,000	$300,000	$0	$0	$0	$2,742,129
Other Sources	$0	$0	$0	$0	$0	$0	$0
	$3,622,129	$2,920,000	$2,505,000	$2,315,250	$2,431,013	$2,552,563	$16,345,955

1.1.4 Platform Management and Support Costs

Platform Leader 15% (shared with Module 2, Grade 13; 20% in uplift), Administrator 50% (shared with Module 2, Grade 10), Legal/Open Access 15% (Grade 11), Communication 15% (shared with Module 2, Grade 10 or lower 11; 20% in uplift), M&E 25% (Grade 10 or lower 11), and administrative support (e.g. for design needs), travel including that of the PSC and associated honoraria and meeting costs, lease/purchase of ICT/vehicles, and supplies and services. The gender strategy is externally contracted. Costs were estimated using the actual costs of similar operations at CIMMYT (CRP management, IBP). Platform Management and Support Costs are 5% (Base budget), 4% (Uplift Budget) and 9% (W1&W2 only). Further details are provided in Table 17 in Section 2.8: “Detailed breakdown of the costs”.

1.1.5 Platform Financial management principles

W1&W2 allocation: Initially, US$ 2 million of W1&W2 funding will be used to initiate Platform activities with the Platform Leader and part time leaders for Module 1-5, contracted from among its members for their ability to initiate the CoPs and web-based Platform activities (Table 14). As donors contribute additional W2, W3 or bilateral funding, costs of leadership and management will be equally distributed across all funding sources, resulting in the W1&W2 allocation as shown in (Table 15)

Budget ownership: The Module Leader will be responsible to use the budget to deliver Module outputs and outcomes, aligned with the RBM defined in the first 6 months. Budget use will be discussed in view of the RBM on a quarterly basis. Budgets may be realigned based on the evolution of costs, new projects coming on board, unexpected bottlenecks, user feedback and other external factors.

Annual variations: Budget use is guided by the RBM framework. Significant variations will be explained in the annual reports.

Major capital investments: Server space.

1.1.6 Budgeted Costs for certain Key Activities

	Estimate annual average cost (USD)
Gender	$4,535,000
Youth (only for those who have relevant set of activities in this area)	$7,558,000
Capacity development	$11,337,000
Impact assessment	$75,000
Intellectual asset management	$41,360
Open access and data management	$114,780
Communication	$35,845

1.1.7 Other

Base, Uplift and W1&W2 budget scenarios and further details are provided in "2.8 Detailed breakdown of the costs", and in the individual Module sections.

2. Business case

2.1. Expertise and track record of institutes and key personnel

The Excellence in Breeding Platform is a new Platform. At this stage, several components are being implemented in some AFS CRPs, yet no more than ad-hoc interactions are in place across or among AFS CRPs. Based on favorable consideration of the Proposal by the CGIAR System Council in its meeting in July 2016, a selection committee will be formed with one representative per center involved in breeding. Institutions will be requested to put forward expressions of interest to host the Platform Leader or to host one or several Module Leaders. In the case of the Module Leaders, expressions of interest can also come from ARIs or NARS or the private sector. At the same time, individuals to compose the Platform Steering Committee will be sought. The selection committee will decide on the nomination of the Lead Center (to host the Platform Leader), the host institutes for the Module Leaders, and the Platform Steering Committee membership before the Fund Council meeting in November 2016, following the criteria given in other parts of this document. The process will be facilitated by CIMMYT.

The System Office will establish a contract with the Lead Center. Based on available funding, the Lead Center will give host institutions the go-ahead to appoint the Module Leaders which are typically expected to be affiliated with teams of scientists and specialists with similar expertise at their host institution. The Platform Leader will take an active role in the appointment of Module Leaders by host institutions.

Modules will be supported by Expert Advisory Groups whose initial members are listed in Table 6. Given the current dominance of CGIAR members, efforts will be made to rapidly engage partners from ARIs, NARS and the private sector to complement the skill base of CGIAR researchers. A much larger number of AFS CRP affiliated scientists and external members are expected to take active part in implementing the Platform agenda as members of the CoPs.

Table 6. Members of the Expert Advisory Groups supporting the five Platform Modules. *Curriculum vitae* are provided in the Annex 1 on 'Expertise and Track Record'

CRP or Platform	Module 1: Breeding Excellence	Module 2: Trait Discovery/ Breeding	Module 3: Genotyping	Module 4: Phenotyping	Module 5: Bioinformatics
DCL	Steve Beebe	Michael Baum	Rajeev Varshney	Vincent Vadez	
Fish	John Benzie	John Benzie			
FTA	Ramni Jamnadass	Zacharie Tchoundjeu	Prasad Hendre	Alice Muchugi	Roeland Kindt
Livestock	Raphael Mrode	Olivier Hanotte	Joram Mwacharo	Margaret Worthington	Stephen Kemp
MAIZE	B.M. Prasanna	Sarah Hearne	Mike Olsen	Jill Cairns	Jens Riis
RICE	George Kotch	John Platten	Tobias Kretschmar	William Paul Quick	Mauleon Ramil
RTB	Merideth Bonierbale	Luis Becerra	Michael Abberton	Awais Khan	Andreas Gisel
WHEAT	Hans Braun	Jessica Rutowski	Susanne Dreisigacker	Matthew Reynolds	Kate Dreher
Genebanks		Peter Wenzl	Ruaraidh Sackville Hamilton		
External experts and advisors	To be determined	To be determined	To be determined	To be determined	Kelly Robbins, Jean-Marcel Ribaut, Lukas Mueller

2.2. Access to materials, sites and services

Table 7 provides an overview of materials, services and sites provided or brokered by the Excellence in Breeding Platform and which are described in more detail in the individual Module sections.

Access: Materials, tools and information about services and sites will be accessible through the web platform managed, maintained and backed up by the Lead Center or by the organization responsible for tool development, in which case the access and safeguard obligations will be specified in the subcontract. Databases will be accessible from member institutions, and developed and maintained with AFS CRP funding following CGIAR open-access principles.

Platform support: Materials will be developed or adapted with Platform funding while capitalizing on commodity-specific activities and know-how in AFS CRPs, among external members and experts. The training budget supports virtual workshops, documentation and face-to-face training of personnel within of CGIAR centers and NARS that are key for reaching a wider user community (train-the-trainer approaches).

User support: Users will pay for individualized services including advice from consultants, genotyping and sequencing services, analyses of physico-chemical composition and functional properties, and access to experiment stations and computational infrastructure. AFS CRPs will integrate Platform materials in training targeted at their own partners.

Financial support: The Platform is designed to draw its input from communities of practice, which it actively facilitates, and provide its products as open-access information. The Platform is therefore to be funded for its objectives by pro-bono investors. They may include private sector users in high income countries that may benefit from the Platform's activities. Such benefits are to be assessed on a regular basis and balanced in view of the highly desirable private sector's contribution of tools, information and know-how to the Platform. As a solid user base is being established, the Platform will assess its ability to move towards a membership or user-paid model over several years. Such an assessment will be done in 2021.

Result-based management: Access to materials, sites and services will be documented as part of the Platform's RBM framework which is to ensure: results and user orientation; learning and adaptation through the use of performance information; accountability and transparency for results that are acquired and reported in a transparent manner; and utilization-focused, flexible implementation of RBM tools based on context and needs. For the same purpose, its design engages members and users in governance, management, execution and the provision of feedback. The RBM framework will be documented using a monitoring, evaluation, learning and impact assessment (MELIA) plan to be designed at Platform and Module Level and which is to support the Platform's results-oriented management of strategy, results, people, resources, processes and measurements, aligned with the guidance given by the CoP for MEL at the CGIAR level. Beyond analyzing the performance of the Platform using indicators at the output, outcome and impact levels, the key assumptions of the theories of change, and the critical risks, the monitoring plan will define a set of indicators that quantitatively and qualitatively measure contributions to and use of Platform materials and services. Baseline information will be established in Year 1 aligned with the capacity needs assessment. External evaluations and impact assessments will be implemented in Years 3-6 to assess relevance, efficiency, quality of science, effectiveness, attributable impact and sustainability. The information gained from internal monitoring, external evaluations and impact assessments will be the basis for the Platform's learning as part of its annual planning and reporting cycle, and used to adjust its strategy, agenda, processes, and use of human and financial resources. Table 8 lists the main outcome targets.

Table 7. Materials, services and sites provided or brokered by the Excellence in Breeding Platform.

	Materials		
	Documented use cases and best practices	**Tools**	**Other Documents**
1. Breeding Excellence	Standardized approaches to measure genetic gains Best practice documentation for breeding program management	Breeding excellence assessment process	Commodity-specific adaptation: demand-driven targets, breeding program assessment; breeding program metrics and strategic plan; CGIAR strategic plan
2. Trait discovery and breeding tools and services	For trait discovery and breeding: workflows, components, applications	Practical toolbox for breeders, structured by use cases and type of users Review tool for users	Training needs assessment Training plan RBM metrics
3. Genotyping/ sequencing tools and services	For genotyping and sequencing: workflows, components, applications		Training needs assessment Training plan RBM metrics
4. Phenotyping tools	For phenotyping and environmental analysis, mechanization and automation. ISO 9000 standards for phenotyping and environmental analysis	Tools for capturing and analyzing high-throughput data.	Training needs assessment Training plan Assessment of mechanization and automation in the CGIAR and NARS. RBM metrics
5. Bioinformatics and data management tools and services	For data management and analysis: workflows, components, applications. Core operational guidelines and data standards	Modular and adaptable open-access bioinformatics tools and pipelines to support breeding workflows Breeding API; Databases at member institutions	Sustainability strategy Training needs assessment Training plan RBM metrics
	Services and sites		
	Expertise	**Training**	**Brokering of services at providers' sites**
1. Breeding Excellence	Consultants: breeding program assessment and product concept development	Virtual and face-to-face workshops	
2. Trait discovery and breeding tools and services	Among CoP members and consultants: successful use cases	Virtual and face-to-face workshops	
3. Genotyping/ sequencing tools and services	Among CoP members and consultants: marker conversions and successful use cases	Virtual and face-to-face workshops	Genotyping and sequencing services, CGIAR externally and internally (e.g. at BeCA/ILRI, CIMMYT, ICRISAT, IRRI/GSL)

4. Phenotyping tools	Consultants: mechanization and automation ISO 9000 standards for phenotyping and environmental analysis	Virtual and face-to-face workshops	Lab services for analyses of physico-chemical composition and functional properties Member sites: experiment stations and sites of implementation of best practices
5. Bioinformatics and data management tools and services	Consultants: biometrics	Virtual and face-to-face workshops	Access to computational infrastructure

Table 8: Outcome targets for the Platform, and their scope for Base and Uplift Budget

Module	**2022 Outcomes**	**Scope: Base budget**	**Scope: Uplift budget**
Module 1: Breeding Excellence	Breeding excellence assessment process	Main CGIAR breeding programs, 3-5 NARS	Including sub-units in CGIAR breeding programs, > 10 NARS
	Standardized metrics		
	Genetic gains assessments	4 studies (AFS funding)	> 6 studies (AFS funding)
	Best practices documentation in ToolBox	4 modules/use cases per year	> 10 modules/use cases per year
	Expert consultations	7 per year	> 12 per year
	Investment and ROI increases	20%	> 30%
Module 2: Trait discovery and breeding tools and services	Toolbox (all Modules)	> 5000 users	> 10,000 users
	Best practices documentation for trait discovery and breeding in ToolBox	18 modules/use cases per year	25 modules/use cases per year
	Pipelined analyses approaches tested, adapted and promoted	5	>10
	Training	40 participants per year	125 participants per year
	Expert consultations	> 4 per year	> 6 per year
Module 3: Genotyping/ sequencing tools and services	Common genotyping services	5-10 users	> 15 users
	Marker conversions to SNP-based platforms or best practices documentation for genotyping/ sequencing in ToolBox	8 use cases per year	>12 use cases per year
	Training	16 participants per year	55 participants per year
	Expert consultations or external marker conversions to SNP-based platforms	5 per year	> 7 per year
Module 4: Phenotyping tools	HTP phenotyping	3 successful institutional users reducing phenotyping cost by >25%	> 5 successful institutional users reducing phenotyping cost by >25%
	GxExM analyses	> 5 routine users	> 10 routine users
	Mechanization and automation	> 3 institutional beneficiaries	> 8 institutional beneficiaries
	Best practices documentation for phenotyping/mechanization/ automation in ToolBox	7 modules/use cases per year	>15 modules/use cases per year
	Training	13 participants per year	50 participants per year
	Expert consultations	> 4 per year	> 4 per year

Module 5: Bioinformatics and data management tools and services	Software tools	> 1,000 users	> 2,500 users
	Contributors of BrAPI compatible components	> 5 institutions	> 10 institutions
	Use of computational infrastructure in other institutions	3 users	> 6 users
	Training	75 participants per year	185 participants per year
All	Members	10	> 30

2.3. Interactions of the Platform with users

The Platform is being created based on two pillars: (1) value to be created for users; and (2) an accountability framework between the AFS CRPs and the Excellence in Breeding Platform. During the development of the Platform proposal, AFS CRPs user types (larger crops, smaller crops, fish and livestock) defined the Platform benefits that will compel them to use the Platform's products (Table 9). More details are provided in Annex 2. They also agreed to establish an accountability framework between the AFS CRPs and the Platform which will become part of a membership agreement. External members may join. The AFS CRPs see this inter-relationship as crucial for the Platform's success and different from the independent nature of previous platform-type activities such as the Generation Challenge Program.

Obligations of AFS CRP members viz the Platform: Members develop and implement agreed standards that have been defined to create mutual benefits. They will contribute to and use common Platform metrics to describe breeding excellence; it will be one quality control system the CGIAR designs and implements consistently. AFS CRPs only use the tools that meet their needs. AFS CRPs provide feedback on how Platform standards and products are being used and add value. They report the extent of use and justify why alternative services are being utilized. Using Platform support, AFS members document new approaches they individually develop and contribute or adopt as part of the Platform's knowledge base.

Obligations of the Platform viz AFS CRP members: The Platform uses the PSC and Expert Advisory Groups, both with AFS CRP membership, to prioritize Platform solutions for implementation and to critically assess alternative uses. The Platform will use members' and wider users' feedback to optimize tools and agenda, with a clear focus on cross-commodity opportunities. It will document use and value addition to materials, services and sites provided by members, and ensure due attribution. It will define user requirements for services (timelines, quality). It will publish its MELIA reports including an assessment of Platform performance by users, i.e., how well and often services are being used. When applying for funding, it will demonstrate the value of using/not using Platform recommended solutions.

Value will drive use and orientation of Platform activities. As the Platform evolves, it will expand its membership to include external members.

Members are active contributors to the Platform's products. They may come from CGIAR centers, ARIs, NARS and the private sector. They provide tools and information developed as part of their own mandates and activities, and may receive platform funding to adapt or document such tools and information prioritized in view of meeting Platform objectives. They contribute to testing the products before they are released to the wider public. They have an active interest in the Platform's existence and performance due to the facilitated exchange of best practices, and access to better materials, sites and services. Members have the opportunity to be represented in Expert Advisory Groups and the Platform Steering Committee.

Contractors execute distinct activities prioritized by the Platform's management processes. They may be sourced from members or non-members, based on "best-for-the-job" principles. They also include experts

with private sector experience.

Users access the Platform's products based on license agreements accepted when accessing the Platform's materials and service-related information. They provide feedback through the Platform's user review tool developed as part of Module 2. As part of its communication strategy, the Platform will make a distinct effort to increase interactions with far-from-source users, in particular NARS breeders, so to provide value in proportion and appropriate to their needs.

Table 9. Various AFS CRPs describe the value they want to see generated from the Excellence in Breeding Platform, and which propels them to use Platform products.

General: "*New ideas and approaches to drive improvements in genetic gain; making use of existing data in ways never imagined and implementation of that historical information in novel approaches to add value; high level of support for the breeding programs, similar to the level that is available in private companies; synergy and leveraging across existing pipelines; supports systems thinking about breeding per system to benefit smallholder farmers; allows me to leverage new technologies without needing to become an expert; interdisciplinary data sets; access to brokered cloud computing; access to experts; external appraisals of breeding programs; increase interactions among breeders through formalized communities of practice and access to shared services."*
Larger crops (maize, rice, wheat): "*Platform providing the capacity to analyze and manage molecular data; genotyping services, breeding information management, uniformity of standards; support to improving the breeding programs and the adoption of new technologies like genome-wide selection and high-throughput phenotyping; synergistically sharing and learning best management practices, knowledge, and technologies will drive cultural change in CGIAR breeding programs; exploiting economies of scale, i.e., the ability to access modern tools and technologies at competitive prices that would not be available when working in isolation; ability to exploit new opportunities with less investment in learning how to use them; faster implementation of high quality and/or state-of-the-art tools and resources with advice; supporting not only breeding but also trait discovery.*"
Smaller crops (small grains, legumes, root, tubers and banana, trees, vegetables): "*Opportunities to adopt modern breeding tools and methodologies that would otherwise never be possible for smaller and orphan crops; objective advice on the improvement of breeding programs and access to standards for breeding performance; benefiting from expertise of others in the network; opportunity to be a part of a larger user group and use genomic tools; support to generate resources and funding; capabilities to have a more efficient and effective breeding program; enabling partners to access modern breeding tools and methodologies; access to pipelined tools to integrate molecular and phenotypic data along with information on how best to deploy them; improved speed and capacity to use tools to make decisions and drive genetic gain; group bargaining rates for services, consulting services for mechanization, automation, biometrics and for the analysis of high-throughput data; information on practical scalable approaches, e.g., barcoding for sample tracking; access to resources and negotiated prices for services that are impossible to resource as small programs."*
Fish and livestock: "*Connected data systems will force best practices on everybody; access to skills and visibility; resource use and time efficiency; competitive sequencing prices through economies of scale which may allow livestock to go to the next level in terms of broader application; access to big data storage and computing capacity. Identify better germplasm; genetic improvement of indigenous breeds."*

2.4. Intellectual asset management

Principles and approaches: The Platform is committed to the effective and efficient management of intellectual assets (IA) to maximize impact, in line with the CGIAR Principles on the Management of IA. This will be done by: (i) incorporating IA management into the project lifecycle; (ii) aligning CGIAR IA Principle requirements with local legislation, markets and practices along with private sector interests; (iii) ensuring due diligence to allow for dissemination of outputs, supported by (iv) appropriate intellectual property management expertise. The Platform will take advantage of the Genebanks Platform's policy module for technical backstopping regarding compliance with the ITPGRFA, Nagoya Protocol, and national implementing laws. It will liaise with the Genebanks Platform to make contributions to the governing bodies of those agreements, promoting an enabling environment to share genetic resources and associated data.

Responsibilities: The Lead Center will ensure that the Platform and its contractors and consultants assume their accountability for the appropriate implementation of the CGIAR Principles for the Management of IA and the CGIAR Open Access and Data Management Policy through: IA tracking; negotiation and drafting of agreements; compliance with international treaties including the Convention on Biological Diversity and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGFA); compliance with country laws and regulations on genetic resources; ensuring ethics in research and privacy protection; and contributing to CGIAR and center policy updates.

Assets, dissemination channels, challenges and legal contributions: The Platform will manage several types of IA, including data and information products, know-how, germplasm, new tools, traits. They will be distributed through open-access repositories, information channels adapted to the needs of specific target groups, partnership approaches and capacity development (see Annex 3).

2.5. Open-access management

The Platform will contribute to implementing the CGIAR Open Access and Data Management Policy ("CG OADMP") by: (i) properly designing and putting in place coordination mechanisms among participating centers and/or units for ensuring proper Open Access and Open Data implementation [CG OADMP § 2]; (ii) establishing and implementing procedures and workflows for accomplishing the deadlines for making information products Open Access [CG OADMP § 4.2]; (iii) as part of Module 5 investment, improving interoperability of software, workflows and databases held by CGIAR centers, including appropriate standards for tagging information products with metadata based on controlled vocabularies [CG OADMP § 4.1.3]; (iv) making all its Platform-generated information and software available as open access; (iv) providing incentives and professional expertise in areas of Open Access and Data Management [CG OADMP § 4.1.6]; and (v) translating key documents and other media into pertinent languages, as appropriate given the target audience [CG OADMP § 4.1.7].

Centers under CRP funding are expected to provide for: (i) the implementation, maintenance and improvement of suitable repositories, which includes hardware infrastructure as well as staff for development, maintenance and population [CG OADMP § 4.1.2]; (ii) data storage, format conversion and adequate preservation for future use, which includes costs related to storage volumes, backup storage and disaster recovery plans [CG OADMP § 4.1.4]; and (iii) Incentives and professional expertise in all areas of Open Access and Data Management [CG OADMP § 4.1.6].

A brief Data Management Plan is outlined in the Annex 4 on 'Open Access (OA) and Open Data (OD) Management.

2.6. Communication strategy

Objective: As a service platform, excellent and proactive two-way communication with stakeholders and its implementation team will be crucial to its success (Table 10). External communication will be in support of fostering and discussing joint vision and approaches; assessing needs and priorities of diverse users implementing breeding programs with different levels of sophistication; advertising the Platform's goals and value propositions; providing online tools, data and online help to users; attract investors and providers of innovation, tools, services and advice; receive user feedback and metrics. Internal communication will be in support of executing the Platform agenda efficiently and effectively, fostering joint vision and approaches; developing, implementing and adjusting the workplan based on external feedback; and exchanging Platform documents, data and tools under development.

Stakeholders: External stakeholders include investors; existing and potential users and members and providers of innovations, services, advice and in-kind contributions; and the general public. The internal implementation team includes: Platform Steering Committee, personnel, consultants, contractors, collaborators, members of communities of practice and pilot users.

Means: As a global Platform interacting with a large number of users and a substantive group of implementers, web-based interactions will be the lifeline to many of its operations, next to physical meetings and workshops, publications and news features. Given the Platform's purpose and type of products, the majority of stakeholders – including users – are expected to be internet-savvy and able to make use of web-based approaches. In addition to the public section, the web platform will manage restricted areas accessible to members and the implementation team only. The Lead Center will be responsible for providing or contracting appropriate services that ensure secure and high availability of Platform tools and services.

Table 10. Two-way communication with various types of stakeholders.

Stakeholder	Feedback from stakeholder	Platform communication to stakeholder	Means
The general public, potential investors, potential users, potential providers of innovations, services and advice	Overall goals, needs and priorities; opportunities for joint activities	Relevance to development and partners goals. Value propositions and priorities, aligned with different user needs. Insights from joint work with AFS CRPs	Web platform, publications and news features Communication channels of AFS CRPs with partners (NARS, ARIs, private sector)
Investors, Members, CGIAR	Needs and priorities; opportunities for joint activities. External review feedback	Current and planned value propositions, priorities, MEL results, user feedback, costs. Grant proposals, workplans and reports. Review and audit reports	Web platform, visits, annual reports, annual virtual meeting with PSC
Members: AFS CRPs and external members	Input to standards and MEL framework; members' metrics and standardized M&E information	Process management for standards and MEL framework; circulation of drafts for feedback	Meetings; restricted member platform; online tools; workshops

Global users: existing and potential users	Needs assessment; user feedback	Awareness; measure use and dis-adoption; provide prominent opportunity for systematic feedback on all tools and services	Web platform; online learning tools and other capacity building events
Potential providers of innovations, services and advice	Proposals for tools and services	Advertise Platform priorities and needs; collaboration opportunities on tools and services	Web platform; visits; meetings and conferences
Platform implementers: staff, consultants, contractors, members of communities of practice	Issues and concerns, modification and updates of priorities, workplans, budgets, MEL results, user feedback; draft policies, strategies, agreements (collaboration, consultancy subcontracts)	Issues and concerns, modification and updates of priorities, workplans, budgets, MEL results, user feedback; draft policies, strategies, agreements (collaboration, consultancy subcontracts)	Face-to-face and virtual meetings, emails, restricted collaborator platform
Lead Center	Issues and concerns related to Platform personnel, consultants, contractors, collaborators and administration (HR, Finance, Legal, IP, facilities including IT) and Platform performance (use, user feedback, reputation)	Performance metrics (use, user feedback). Issues and concerns related to Platform personnel, consultants, contractors, collaborators and administration (HR, Finance, Legal, IP, facilities including IT)	Face-to-face and virtual meetings, emails, annual reports
Pilot users from among Members	Adaptation of tools and services to adjust product specifications, investments and timelines for scale-out	Seek systematic pilot user feedback on all tools and services under development; communicate timelines	Restricted collaborator platform; online learning tools; workshops

2.7. Risk management

The PSC and Lead Center Board oversee the implementation of an appropriate risk management framework for the Platform, such as the one shown in Table 11, to manage the main risks. Risks include: loss of physical, information or intellectual assets; non-compliance with CGIAR policies; non-adherence to agreements entered into with the CGIAR, partners, staff, subcontractors and collaborators; inefficiency of operations or failure to deliver valuable products to a significant number of users in time; environmental hazards; change management and finances, and other risks as prioritized by the PSC and Lead Center Board. The framework includes a risk management approach, a risk leader and controls to monitor the implementation of the risk management approach. Risks will be classified on a 1-5 scale for likelihood, impact, risk severity and management effectiveness. The Lead Center will put in place appropriate insurance for staff, assets and legal claims.

Table 11. Management of main Platform risks.

Area	Risk	Risk Management Approach	Risk Leader	Control
1. Assets				
1.01	Loss of physical assets	Lead Center has a Business Continuity Plan in place	Board of Trustees	Business Continuity Plan
1.02	Loss of information assets	Lead Center has appropriate on- and off-site back-up systems and IT security systems and expertise	Head of ICT, Lead Center	Business Continuity Plan
1.03	Loss of intellectual assets: departure/loss of staff, contractors or collaborators	Attractive remuneration and work place; security information during travels	Head of HR and Risk Management, Lead Center	HR policies and procedures
		Attractive vision; responsive management of staff and partners; effective platform document management system in place	Platform Leader; PSC Chair; Lead Center DG	360° input to performance evaluation of Platform Leader
2. Compliance				
2.01	Platform fails to meet contractual obligations with the CGIAR Systems Office	Timing and quality of critical Platform management documents (workplans, reports, budgets, template agreements) are overseen by the Platform Steering Committee, that includes competent members and a committed Chair	Platform Steering Committee	Platform management calendar
2.02	Staff, subcontractors or consultants are not fulfilling their obligations	Workplan, reporting and disbursement schedule in place and monitored for all staff, consultants and contractors. Divergences from schedule brought to attention of Platform Leader, corrective action is taken	Platform Administrator	Milestone-based workplans and contracts
2.03	Legal/compliance issues with CGIAR IA Principles and Policies and Program Implementation Agreement	Internal policies and subcontracts mirror CGIAR Policies and Principles	Focal Point for IP management, Lead Center	BoT certification of the Leader Center report on the management of intellectual assets
2.04	Breach of confidentiality for IA provided by collaborators	Policies and stewardship procedures in place; training of staff	General Counsel, Lead Center	List of personnel with access to confidential information

3. General Management				
3.01	Ineffective team interactions due to decentralized posting	Calendar of physical and virtual meetings in place; clear workplans and milestone driven contracts	Platform Leader	Results-based management framework
3.02	Inability to manage growth	High quality Module Leaders with appropriate project management skills and supports	Platform Leader	Results-based management framework; CV of Module Leaders
3.03	Platform does not deliver value or Platform product fails	Systematic needs assessment and user feedback; testing with pilot users	Platform Leader	Analytical reports of user feedback
3.04	Platform does not deliver quality product in time	Competitive processes for selecting implementers (staff, consultants and contractors); (peer/external) reviews that ensure realistic and pragmatic workplans; PSC expertise	Platform Leader and PSC	Results-based management framework
3.05	Platform delivers value to a few users only	User characterization and needs assessment; focus on pragmatic solutions and incremental value; MEL framework with independent metrics of use; PSC composition	Platform Leader and PSC	Results-based management framework
4. Technology				
4.01	Growing irrelevance; obsolescence of research technologies employed; inadequate technology to deal with changing research requirements	Investment in contracting services over investments in infrastructure; commitment to modular open-access systems with appropriate interoperability; input on technology trends through communities of practice, Platform staff and PSC	Platform Leader and PSC	Results-based management framework
5. Environment				
5.01	Non-compliance with international standards for participating laboratories	Contracted labs provide evidence for appropriate certification	Platform Leader and PSC	Workplan
6. Change Management				
6.01	Risk of inadequate donor investment given political priorities and pressures	Platform elevates performance of breeding programs; common metrics are linked to development goals	Leader of Platform and AFS CRPs	Work products of Module 1: Common metrics and standards for monitoring performance
6.02	Friction between AFS CRPs and Platform	PSC membership and transparency; virtual consultation with CRP Leadership; communities of practice that engage staff of AFS CRPs	PSC; Platform and Module Leaders	PSC minutes; workplan progress; AFS participation

6.03	Bureaucracy and transaction costs, due to unconsolidated CGIAR requirements	Non-redundant roles and responsibilities and aligned workplan of Systems-level units	Fund Council; Center committee	CGIAR website
6.04	Lack of continuity due to changing PSC membership or Platform Leadership	PSC has succession plan in place; Platform and Module Leaders work as team, not in silos; effective platform document management system in place	PSC and Lead Center Board and DG	Succession plan; Platform document management system
7. Financial				
7.01	W1&2 budget is insecure	Operation at realistic income expectations to be defended viz the Lead Center (which carries the risk)	Platform Manager, Lead Center DG	Budgets as uploaded in the Financial System
7.02	Fund transfers are delayed	Prefinancing by Lead Center reserves up to contractually agreed amount	Director of Finance, Lead Center	Cash-flow schedules
7.03	Inappropriate use of funds	Lead Center policies and procedures; internal and external audits; trained personnel; disbursement schedule to contractors based on deliverables	Board of Trustees, Lead Center; Platform Finance Manager	Audit reports; sub-contracts and financial reports
7.04	Compliance and legal claims cause contingent liability	Lead Center policies and procedures; quality of Legal/IP personnel; internal and external audits; insurance	Board of Trustees, Lead Center; General Counsel, Lead Center	Lead Center policies and procedures; internal and external audit reports

2.8. Detailed breakdown of the costs

Sources of funding: The Platform proposes an annual budget of US$ 10 million (Base; Table 12) to US$ 15 million (Uplift; Table 13) to execute its agenda i.e., approximately 5% of the AFS CRPs' investments in germplasm development. The difference between Base and Uplift is explained in Table 8. Initially, US$ 2 million of W1&W2 funding will be used to initiate Platform activities with the Platform Leader and part time leaders for Module 1-5, contracted from among its members for their ability to initiate the CoPs and web-based Platform activities (Table 14). As donors contribute additional W2, W3 or bilateral funding, costs of leadership and management will be equally distributed across all funding sources, resulting in the W1&W2 allocation for the Base scenario as shown in (Table 15).

W3&bilateral projects: In 2017, the Platform counts on W3 and bilaterally funded project activities valued at US$ 4.59 million dollars, of which US$ 1.66 million are managed by CGIAR centers, the rest by independent entities (Integrated Breeding Platform) or ARIs (Table 16). Other activities from external members could likely be linked to the Platform, such as projects funded by the Bill and Melinda Gates Foundation with NARS and the University of Queensland, or the National Science Foundation and United States Department of Agriculture funded investments in root and tuber databases. However ARI and NARS led projects are unlikely to financially report their activities as part of the Platform. The Platform will seek to make collaboration agreements with these projects so to optimally position its agenda.

Budget components of the Platform Management and Support Costs are detailed in Table 17.

Table 12. Base budget for the Excellence in Breeding Platform.

Base Budget	2017	2018	2019	2020	2021	2022
0. Platform Management	$456,794	$479,634	$503,615	$528,796	$555,236	$582,998
1. Breeding Excellence	$1,824,627	$1,915,858	$2,011,651	$2,112,234	$2,217,846	$2,328,738
2. Trait Discovery and Breeding	$2,146,559	$2,253,887	$2,366,582	$2,484,911	$2,609,156	$2,739,614
3. Genotyping Services	$936,116	$982,922	$1,032,068	$1,083,672	$1,137,855	$1,194,748
4. Phenotyping	$1,534,011	$1,610,712	$1,691,248	$1,775,810	$1,864,600	$1,957,830
5. Bioinformatics	$3,101,892	$3,256,987	$3,419,836	$3,590,828	$3,770,369	$3,958,887
Grand Total	**$10,000,000**	**$10,500,000**	**$11,025,000**	**$11,576,250**	**$12,155,062**	**$12,762,816**

Table 13. Uplift budget for the Excellence in Breeding Platform.

Uplift Budget	2017	2018	2019	2020	2021	2022
0. Platform Management	$552,097	$579,702	$608,687	$639,122	$671,078	$704,631
1. Breeding Excellence	$2,588,140	$2,717,547	$2,853,424	$2,996,095	$3,145,900	$3,303,195
2. Trait Discovery and Breeding	$3,219,785	$3,380,774	$3,549,813	$3,727,304	$3,913,669	$4,109,352
3. Genotyping Services	$1,528,296	$1,604,711	$1,684,947	$1,769,194	$1,857,654	$1,950,536
4. Phenotyping	$2,829,413	$2,970,883	$3,119,427	$3,275,399	$3,439,169	$3,611,127
5. Bioinformatics	$4,282,269	$4,496,383	$4,721,202	$4,957,262	$5,205,125	$5,465,381
Grand Total	**$15,000,000**	**$15,750,000**	**$16,537,500**	**$17,364,375**	**$18,232,594**	**$19,144,224**

Table 14. Initial use of the US$ 2 million of W1&W2 funding in the Base budget, before W3 and bilateral funding become available.

W1&W2	2017	2018	2019	2020	2021	2022
0. Platform Management	$175,774	$184,562	$193,791	$203,480	$213,654	$224,337
1. Breeding Excellence	$232,448	$244,070	$256,273	$269,087	$282,542	$296,669
2. Trait Discovery and Breeding	$1,012,296	$1,062,911	$1,116,056	$1,171,859	$1,230,452	$1,291,975
3. Genotyping Services	$99,896	$104,891	$110,135	$115,642	$121,424	$127,495
4. Phenotyping	$99,896	$104,891	$110,135	$115,642	$121,424	$127,495
5. Bioinformatics	$379,691	$398,675	$418,609	$439,540	$461,517	$484,592
Grand Total	**$2,000,000**	**$2,100,000**	**$2,205,000**	**$2,315,250**	**$2,431,013**	**$2,552,563**

Table 15. Use of the US$ 2 million of W1&W2 funding in the Base budget as W3 and bilateral support become available.

W1&W2	2017	2018	2019	2020	2021	2022
0. Platform Management	$91,359	$95,927	$100,723	$105,759	$111,047	$116,600
1. Breeding Excellence	$364,925	$383,172	$402,330	$422,447	$443,569	$465,748

2. Trait Discovery and Breeding	$429,312	$450,777	$473,316	$496,982	$521,831	$547,923
3. Genotyping Services	$187,223	$196,584	$206,414	$216,734	$227,571	$238,950
4. Phenotyping	$306,802	$322,142	$338,250	$355,162	$372,920	$391,566
5. Bioinformatics	$620,378	$651,397	$683,967	$718,166	$754,074	$791,777
Grand Total	**$2,000,000**	**$2,100,000**	**$2,205,000**	**$2,315,250**	**$2,431,012**	**$2,552,563**

Table 16. Valuation of on-going bilateral project activities.

Module	Project	Institution	Donor	2017	2018	2019	2020
3	High throughput genotyping project (HTPG)	ICRISAT	B&MGF	402,129			
3	Integrated Genotyping Support and Service (IGSS)	ILRI	B&MGF	100,000	100,000		
3	Seeds of Discovery (SeeD)	CIMMYT	SAGARPA, Gov of Mexico	160,000	170,000	180,000	
5	Integrated Breeding Platform (IBP) Development	IBP	B&MGF	800,000	700,000	400,000	
5	Integrated Breeding Platform (IBP) Deployment	IBP	B&MGF	600,000	600,000	500,000	
5	Genomic and Open-source Breeding Informatics Initiative (GOBII)	Cornell University	B&MGF	1,500,000	1,500,000	1,600,000	800,000
5	Breeding4Rice (B4R) Transforming Rice Breeding	IRRI	B&MGF	110,000			
5	Genomics for Rice (G4R) Transforming Rice Breeding	IRRI	B&MGF	30,000	30,000		
5	International Rice Improvement Consortium (IRIC) Data and Analysis Portal	IRRI	Membership funds: AGI, CU, CIAT, IRRI, NIAS, TGAC, KAUST, BCS, Syngenta, IRD	120,000	120,000	120,000	
5	Genomic Tools for Sweet Potato Improvement	CIP	B&MGF	700,000	400,000		
5	CassavaBase	Cornell University		Unknown CGIAR external budgets			
5	MusaBase	Cornell University	NSF, USDA CSREES	Unknown CGIAR external budgets			
5	YamBase	Cornell University		Unknown CGIAR external budgets			
5	Reference Ontologies (cROP) of Planteome	Oregon State University & European	US National Science Foundation	65,000			

		Bioinformatics Institute					
5	Global Information System on Plant Genetic Resources for Food and Agriculture	FAO	ITPGRFA	Unknown CGIAR external budgets			
5	DivSeek	GCDT		Unknown CGIAR external budgets			
Total	**W3 & bilaterally funded projects**			**4,587,129**	**3,620,000**	**2,800,000**	**800,000**
		CGIAR		1,662,129	820,000	300,000	0
		Non-CGIAR		2,965,000	2,800,000	2,500,000	800,000

Table 17. Budget components of the Platform Management and Support Costs

COST COMPONENT		AMOUNT BUDGETED						
		2017	2018	2019	2020	2021	2022	6-year Total
A. Basic components as were given in the guidance document	SubTotal:	$397,195	$417,055	$423,267	$444,430	$518,639	$542,778	$2,743,364
A.1 Management fee charged by the Lead Center to handle CRP Finance and Administrative matters (Finance, accounting, reporting, contracts management, legal, HR, IT, communication-if handled by Lead Center)	Amount:	$97,896	$102,791	$107,930	$113,327	$118,993	$124,943	$665,879
A.2 Combines three of the basic components to protect confidentiality of staff salaries – the sum total of these three component should be reported as a single amount: • CRP director including related cost – benefits and on-cost if customary (computer, vehicle lease and office space) based on percentage time allocation • Infrastructure and general and administrative charges if CRP leader is not located at the Lead Center • Financial and administrative support based on time allocation	Amount:	$208,206	$218,617	$229,547	$241,025	$253,076	$265,730	$1,416,200
A.3 Flagship leader and regional coordinators only if a significant percentage time (>50%) is dedicated to managerial activities.	Amount:	$0	$0	$0	$0	$0	$0	$0
A.4 CRP Management Committee and related costs	Amount:	$26,015	$27,315	$28,681	$30,115	$31,621	$33,202	$176,949
A.5 Independent Steering Committee (or Science Committee) and related costs	Amount:	$26,559	$27,887	$14,641	$15,373	$16,142	$16,949	$117,551
A.6 Communication activity related specifically to CRP communication and webpage (not if handled by Lead Center)	Amount:	$31,619	$33,200	$34,860	$36,603	$38,433	$40,355	$215,071

A.7 CRP internal audit by the CGIAR Internal Audit Unit, or its future equivalent in the new System governance structure [1]	Amount:	$6,900	$7,245	$7,607	$7,988	$8,387	$8,806	$46,933
A.8 CRP internal and external reviews (e.g. CCEEs and other evaluations and reviews), as well as impact assessments	Amount:					$51,987	$52,794	$104,781
B. CRP-level cross-cutting components not mentioned in the guidance document	SubTotal:	$42,159	$44,267	$84,588	$87,644	$51,245	$53,807	$363,709
B.1 CRP special events (e.g. CRP-wide program meetings)	Amount:	$0	$0	$0	$0	$0	$0	$0
B.2 CRP leadership meetings (e.g. country coordinators, flagship leaders, cross-cutting coordinators)	Amount:	$0	$0	$0	$0	$0	$0	$0
B.3 CRP M&E coordination and systems (not including external evaluations and impact assessments)	Amount:	$42,159	$44,267	$46,480	$48,804	$51,245	$53,807	$286,762
B.4 CRP communications, open access, IP assets, KMIS (including Lead Centre staff budgeted as direct costs not allowed under A.6 above)	Amount:	$0	$0	$0	$0	$0	$0	$0
B.5 CRP capdev coordination	Amount:	$0	$0	$0	$0	$0	$0	$0
B.6 CRP gender and youth coordination	Amount:	$0	$0	$38,107	$38,840	$0	$0	$76,947
B.7 CRP site integration support	Amount:	$0	$0	$0	$0	$0	$0	$0
B.8 Other: (specify)	Amount:	$0	$0	$0	$0	$0	$0	$0
		AMOUNT BUDGETED						
		2017	**2018**	**2019**	**2020**	**2021**	**2022**	**6-year Total**
C. Funding source: MSC budget is assumed funded from W1/2. Some CRPs have been successful in mobilizing W3/bilateral funding to support CRP-level cross-cutting initiatives. These are listed below: (add rows as needed)	Amount:	$87,871	$92,264	$101,571	$106,415	$113,977	$119,317	$621,415
C.1 Grant: This is a new Platform; W3 and bilateral funding is to be raised and management costs assigned in proportion of funding.	Amount:	$351,483	$369,058	$406,284	$425,659	$455,906	$477,268	$2,485,659

[1] External audits are conducted as part of Lead Center and Members annual external audits, and part of their indirect costs. These funds cover any additional audit needs.

3. MODULES

3.1 Module 1: Breeding Program Excellence

3.1.1 Modules Narrative

3.1.1.1 Rationale and Scope

Breeding is a cyclical product development process that must be integrated from product profile design through to dissemination and cultivar replacement. The purpose of the process is to deliver a stream of improved breeds that raise the productivity, food security, and incomes of farmers and consumers in the developing world. These products must be delivered by breeding organizations with sufficient information to induce governments and seed companies to support them, extension systems to promote them, farmers to adopt them, and end-users to purchase them. Technical and process innovations must be aggressively sought, and their effectiveness rigorously evaluated against these goals.

Many breeding programs serving smallholders in the developing world do not have the capacity to manage this process end-to-end. Indeed, there is surprisingly little standardized information available that would characterize germplasm development or genetic gains across the breeding programs of the CGIAR, NARS and the private sector, making it difficult to invest strategically to improve performance. Project funding fosters proof-of-concept type investments that may be applied in a few breeding populations only and without an overall appreciation of the quantitative impact such an intervention may or may not have on the overall development goals.

The CGIAR proposes to change this. Module 1 proposes to develop a CGIAR-wide breeding program assessment system with metrics to assess program output, efficiency and effectiveness. Once achieved, portfolio management decisions could be implemented within and across CRPs to systematically improve breeding programs across the CGIAR and, hopefully, those managed by NARS. The purpose of the characterization is to provide an incentive for greater excellence, and support such ambitions with capacity building, best practices and targeted investments. Achievement of development goals are quantitative goals. Effective change will not come from individual projects but from the extent to which the CGIAR and NARS are able to mainstream state-of-the-art breeding strategies in a sufficiently large proportion of the breeding programs that will provide the cultivars that farmers will grow in future in the developing world.

While it is most breeders' intent to improve the performance of their programs, the CGIAR could go further by more systematically defining best practices and providing measures that characterize how far public investment reaches and what changes may be needed. Practical evidence comes from the private sector and the genebank community. Given the private sector's abilities for programmatic investments, they use detailed product definitions driven by clients' needs; routinely assess program strengths to determine the likelihood of success and direct resources accordingly; and manage a stage-gate advancement process with defined speed-to-farmer objectives. They also manage the introduction and withdrawal of their products from the market as new generations of cultivars emerge from the pipeline. The framework allows a systematic capture of results to determine if the program meets its objectives (Figure 1.1). These basic management principles are incorporated into a continuous improvement program with an over-arching portfolio strategy. In the case of the CGIAR genebank community, they successfully implemented a best practices discussion and standardized metrics approach across species

in collaboration with the GCDT, which contributed to substantive improvements and clarified investment needs. The Excellence in Breeding Platform aims to do the same for cultivar development.

The CGIAR proposes to establish and follow a common format to set demand-driven targets, drive and accelerate the transparent development of breeding germplasm and cultivars, drive dissemination, and measure program progress, both within the CGIAR system and with NARS partners. Membership in this community-driven effort and publication of associated metrics will result in a transparent assessment of the success and bottlenecks of breeding programs and will lead to a greater ability to direct support to high-payoff investments. The implementation of a common breeding program assessment will also enable a systems perspective of similar technical challenges within and across each CRP which will support internal improvement processes and identify areas of investments for AFS CRPs (commodity-specific) and the Excellence in Breeding Platform (cross-commodity).

Strategically, a common breeding program assessment system will implement higher professional standards and result in better outcomes across CGIAR centers and NARS. It to be community-driven so as to encompass the needs and bottlenecks of the highly diverse commodities. Also, the approach must not promote trade-off decisions between commodities, given that they individually meet critical needs of low income farmers and consumers. Instead, the focus should be on elevating best practices and standards systematically, with tools and processes that are effective and adaptable to smaller and larger breeding programs.

The great majority of CGIAR and NARS breeders chose their careers in order to help alleviate poverty. They strive for excellence. The advantage of a common implementation of best practices will be the ability to compare and improve individual programs, which will be largely driven by breeders striving to get access to the information and services they need to deliver the best results possible. Programs should be able to access advice for aligning their approaches with best practices, while other programs may serve as learning platforms, fostering intra- and inter-CRP collaboration in breeding and breeding support functions. Donors will have the ability to more precisely follow the progress of breeding programs and deliver support where needed, or invest in “game changers”.

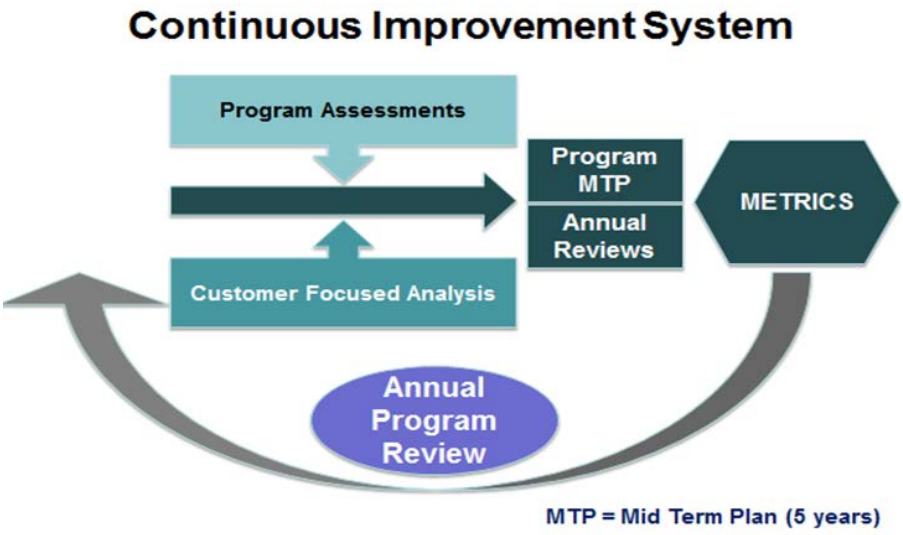

Figure 1.1. Continuous improvement system used in the privates sector.

3.1.1.2 Objectives and targets

The goal of Module 1 is to develop an excellence management and support process for breeding programs that will be broadly appreciated and accepted across the CGIAR and by its donors. Given the diversity of the AFS CRPs, each commodity is expected to adapt the common template to their breeding needs without compromising the ability to successfully compare and contrast across the AFS CRPs. The intent of the Module is not to impose an additional layer of monitoring but to implement best practices in each of the CRPs that will improve genetic gains and accelerate the breeding process. A key element of the Module will be to provide the research leaders of CRPs, Centers, and NARS with a much stronger understanding of how cultivar development pipelines should be managed and assessed. Better understanding, current and potential abilities, and bottlenecks allow breeders, research managers and investors to target investments for program improvements.

The Breeding Program Excellence Module will be organized into five work packages (Table 1.1).

1. Developing a standard template and approaches for monitoring breeding program performance, which includes developing a common set of metrics that will assess genetic gain. The first work package will address three components of a standardized continuous improvement cycle: (i) a standard process to set demand-driven breeding targets and product profiles linked to needs assessments; (ii) components for breeding program assessment (germplasm management and evaluation, phenotyping strategy, trait mobilization, molecular and data analysis, breeding methodology decisions) that can help assess the programs' ability to achieve their breeding targets; and (iii) a standard approach to define breeding program metrics. Genetic gain is a technical term used in breeding theory to describe the change in a quantifiable trait resulting from selection per breeding cycle or unit of time. Given the diversity of needs (trait discovery to cultivar development, traits ranging from stress resilience to productivity to quality and nutrition), CRPs should think carefully when selecting metrics. Poorly designed approaches or metrics could achieve the wrong results. This work package will thus be conducted in collaboration with a CoP of breeding leaders in each AFS CRP, and by Module personnel and contracted experts generating, through crucial site visits, an initial understanding of points of intervention for improvement within the major breeding programs. The CoP will be able to build on private sector experiences and a breeding program assessment tool which is currently being administered and refined by the University of Queensland.

2. Internal breeding program assessment and development of strategic plans to set breeding program direction. Based on the approaches defined in work package 1, AFS breeding programs will execute an internal program assessment and collect the metrics defining breeding program scope and abilities to achieve their breeding targets. The insights will be incorporated into a commodity- and breeding program-specific strategic plan documenting current investments and prioritized improvements. The assessment, metrics and resulting plan will be peer-reviewed to achieve a similar standard across the system. AFS research managers and breeders can use the assessment and plans to prioritize improvements and monitor program success. The same information will be useful to AFS CRP portfolio reviews; they should follow a similar process but the program reviews should be conducted with external reviewers. The Module will summarize commodity-specific insights in a system-wide analysis of current investments and prioritized improvements aligned with the needs of different species. Through the CoP, it will review the usefulness of the standardized system and further improve it.

3. Support breeding programs for needed improvements through consultancies, investments, and/or simulations. Breeding program assessments and strategic plans will identify program gaps. Programs will be able to catch up on best practices through consultancies, workshops and the development of joint funding proposals targeted at highest priority needs. Module personnel will support the documentation of best practices as part of the Module 2 Toolbox, also for use as training material. This may include common approaches to: market research and product profile definition; a stage-gate advancement

system that can be used to assess germplasm advancements as a way to measure program efficiency and effectiveness; and managing product deployment and withdrawal.

4. Extend the assessment to NARS breeding programs. A similar characterizations of NARS breeding programs is highly desirable. Interested NARS will be involved in discussions as tools are being developed. The needs and constraints of CGIAR and NARS breeding programs differ. While CGIAR breeding programs need to address diverse needs, the mandates of NARS extend beyond where the CGIAR typically engages, and trade-off decisions (e.g. investment in personnel *versus* operational resources and capital) may follow different incentives. NARS participation will be voluntary, yet can be promoted if investors decide to support improvement plans with NARS that complete the assessment of their programs.

5. Standardized approaches to measure genetic gains in farmers' fields. There has been much debate about how to reliably measure genetic gains in farmers' fields and be able to link them to development goals. In collaboration with the CoP of work package 1 and socio-economists, current approaches will be reviewed and best practices established at various levels of investment or given different purposes, so that the CGIAR will emerge with a stronger approach for monitoring the reach of improved cultivars and their benefit to farmers, as well as more authoritative statements on germplasm-related impacts on achieving past and future development goals.

Use of Module resources among work packages are projected in Table 1.2. The main cost drivers are explained in Table 1.3.

Table 1.1. Work packages and key milestones to be funded by the Excellence in Breeding Platform.

	Milestones = Output Targets					
Work Packages = Objectives	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1. Developing a standard template and approaches for monitoring breeding program performance, which includes developing a common set of metrics that will assess genetic gains	1. Develop a CoP across the CGIAR system and selected NARS to develop a standardized system for capturing breeding program targets, assessments and metrics	1. Peer review of breeding program assessments, metrics and strategic plans; recommendation for improved approaches		1. Peer review of breeding program assessments, metrics and strategic plans; recommendation for improved approaches		1. Peer review of breeding program assessments, metrics and strategic plans; recommendation for improved approaches
	2. Site visits to discuss and test standardized systems in collaboration with key breeding programs	2. Development of Portfolio plan and investment strategy		2. Development of Portfolio plan and investment strategy		2. Development of Portfolio plan and investment strategy
	3. CRPs to adapt program assessment and collection of metrics to the breeding program's target species	3. Review of Portfolio plan and investment priorities by AFS CRPs	1. Fund-raising and implementation of highest priority interventions (CGIAR)	3. Review of Portfolio plan and investment priorities by AFS CRPs	1. Fund-raising and implementation of highest priority interventions (CGIAR and NARS)	3. Review of Portfolio plan and investment priorities by AFS CRPs
		4. Upload of information on web platform	2. Upload of information on web platform	4. Upload of information on web platform	2. Upload of information on web platform	4. Upload of information on web platform
2. Internal breeding program assessment and development of strategic plans to set breeding program directions	1. First year of internal program assessment and collection of metrics defining breeding program scope and abilities	1. Develop commodity specific strategic plan documenting current investments and prioritized improvements	1. Implementation of prioritized improvements	1. Implementation of prioritized improvements	1. Implementation of prioritized improvements	1. Implementation of prioritized improvements
		2. Annual update of program assessment and metrics	2. Annual update of program assessment and metrics	2. Annual update of program assessment and metrics	2. Annual update of program assessment and metrics	2. Annual update of program assessment and metrics
		3. Use in CRP reports, aligned with increasingly standardized formats and reporting systems forthcoming from the MEL workgroup.				

3. Support breeding programs for needed improvements through consultancies, investments, and/or simulations	1. Breeding programs access advice or visit to best-practices sites on a self-funded basis	1. Breeding programs access advice or visit to best-practices sites on a self-funded basis	1. Breeding programs access advice or visit to best-practices sites on a self-funded basis	1. Breeding programs access advice or visit to best-practices sites on a self-funded basis	1. Breeding programs access advice or visit to best-practices sites on a self-funded basis	1. Breeding programs access advice or visit to best-practices sites on a self-funded basis
		2. Portfolio strategy and gap analysis drives support for program improvements	2. Portfolio strategy and gap analysis drives support for program improvements including by informing the Platform agenda and priorities	2. Portfolio strategy and gap analysis drives support for program improvements including by informing the Platform agenda and priorities	2. Portfolio strategy and gap analysis drives support for program improvements including by informing the Platform agenda and priorities	2. Portfolio strategy and gap analysis drives support for program improvements including by informing the Platform agenda and priorities
4. Establish assessment approaches targeted to the needs of NARS breeding programs	1. Include pilot NARS programs in the CoP to develop a standardized system for capturing breeding program targets, assessments and metrics	1. Assessment of the tools in 2-3 NARS programs.	1. Develop a CoP across the NARS to adapt a standardized system for capturing breeding program targets, assessments and metrics	1. Internal program assessment and collection of metrics defining breeding program scope and abilities of NARS	1. Internal program assessment and collection of metrics defining breeding program scope and abilities of NARS	1. Internal program assessment and collection of metrics defining breeding program scope and abilities of NARS
5. Standardized approaches to measure genetic gains in farmers' fields.	1. Face-to-face workshop among breeders, socio-economists and seed specialists about purpose and approaches for germplasm-related impact assessment	1. Best practices for germplasm impact assessment: draft, review and publication	1. Implementation (and fund-raising) by AFS CRPs for improved impact assessments			

Table 1.2. Use of Base and Uplift budgets among work packages.

Base Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1. Developing a standard template and approaches for monitoring breeding program performances, which includes the development of a common set of metrics that will assess genetic gain	$364,925	$287,379	$60,350	$63,367	$66,535	$69,862
2. Internal breeding program assessment and development of strategic plans to set breeding program directions	$1,003,545	$862,136	$603,495	$316,835	$221,785	$232,874
3. Support breeding programs for needed improvements through consultancies, investments, and/or simulations	$0	$95,793	$543,146	$887,138	$1,042,387	$1,094,507
4. Establish assessment approaches targeted to the needs of NARS breeding programs.	$273,694	$287,379	$402,330	$422,447	$443,569	$465,748
5. Standardized approaches to measure genetic gains in farmers' fields.	$182,463	$383,172	$402,330	$422,447	$443,569	$465,748
Grand Total	**$1,824,627**	**$1,915,858**	**$2,011,651**	**$2,112,234**	**$2,217,846**	**$2,328,738**

Uplift Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1. Developing a standard template and approaches for monitoring breeding program performances, which includes the development of a common set of metrics that will assess genetic gain	$388,221	$326,106	$85,603	$89,883	$94,377	$99,096
2. Internal breeding program assessment and development of strategic plans to set breeding program directions	$1,294,070	$1,087,019	$713,356	$359,531	$314,590	$330,320
3. Support breeding programs for needed improvements through consultancies, investments, and/or simulations	$0	$135,877	$827,493	$1,258,360	$1,478,573	$1,552,502
4. Establish assessment approaches targeted to the needs of NARS breeding programs.	$595,272	$625,036	$656,288	$689,102	$629,180	$660,639
5. Standardized approaches to measure genetic gains in farmers' fields.	$310,577	$543,509	$570,685	$599,219	$629,180	$660,639
Grand Total	**$2,588,140**	**$2,717,547**	**$2,853,424**	**$2,996,095**	**$3,145,900**	**$3,303,195**

Table 1.3. Explanations of the costs in relation to the planned 2022 outcomes.

Module	2022 Outcomes	Scope: Base budget	Scope: Uplift budget	Explanations of the costs in relation to the planned 2022 outcomes
Module 1: Breeding Excellence	Breeding excellence assessment process	Main CGIAR breeding programs, 3-5 NARS	Including sub-units in CGIAR breeding programs, > 10 NARS	Annual budget to members increases from US$ 1,370,000 to US$ 2,056,000
	Standardized metrics			
	Genetic gains assessments	4 studies per year supported (AFS funding)	> 6 studies per year supported (AFS funding)	
	Best practices documentation in ToolBox	4 modules/use cases per year	> 10 modules/use cases per year	
	Expert consultations	> 7 per year	> 12 per year	Annual consultant budget increases from US$ 163,000 to US$ 272,000
	Investment and ROI increases	20%	> 30%	

3.1.1.3 Science quality

It is well established that standardized systems for comparing programs through metrics can upgrade performance (Cooper and Edgett, 2005). Highly productive programs are client-focused, carefully design and target their products, do front-end planning, implement a process of metrics, accountability and continuous learning, use a stage-gate advancement program, take responsibility for clearly identifying products that should be disseminated, have a dissemination plan, and practice transparent and effective portfolio management.

While Module 1 will define metrics for the overall breeding program, CoPs in Modules 2-5 will improve best practices within distinct areas (trait discovery, distinct breeding processes, genotyping, phenotyping, automation, mechanization, design and analysis. Standardization of methodologies will drive comparability, greater data quality and data coherence (e.g., for multi-environmental trials to systematically integrate climate and management data), and allow peer review. Monitoring breeding program performance and metrics can be summarized in CRP reports and used in peer-reviewed articles. Through combined membership and active participation, the Platform is expected to become an authoritative voice for current and prioritized new investments, and actual impact. There is the assumption that breeding program leaders can provide a transparent and critical assessment of their breeding programs. This thesis has yet to be proven and verified through peer review and expert consultancies. The thesis however has its best foundation in members of the AFS CRPs unanimously subscribing to this Module as part of planning the Platform proposal.

There are different reasons and methods for assessing genetic gains, and different ways to ensure progress. Breeding programs measure progress against program objectives, such as critical traits defined in the program strategy. The ability to maintain positive genetic gains in each breeding cycle, and their extent, is a direct measure of a program's success. Different species and different traits advance at different rates, but the measure of the "incremental gain" over unit of time is a standard way to ensure progress. By monitoring the presence or absence of best practices, which can be qualitatively recorded, the potential for enhancing breeding program performance and genetic gains can be assessed.

Enhancing breeding program performance as such will not indicate to what extent new cultivars, a program or project has generated impact in farmers' fields or will contribute to development goals. While germplasm development may be the most impactful activity of the CGIAR, there is no common approach to impact assessment. Different studies may assess adoption, attribution, return to investment and breeding for one trait *versus* improved cultivars. They may also include or exclude farmer-recycled seed, base their information on breeders, informants or farmers' feedback or genotyping, and with different assumptions for establishing baselines, resulting in highly incomparable results. For most traits, genetic gains can be measured by comparing germplasm of different ages under relevant environments and management conditions. The slope of improvement over unit of time is the genetic gain measured. However, several qualitative traits, such as disease resistance or the ability to meet quality standards, are rarely measured as quantitative progress. Also, changing from 2 disease resistant cultivars to 20 in one unit of time is a different kind of achievement. Socio-economic analyses may go beyond and assess cultivar impact on livelihoods, and the reasons for adoption, dis-adoption or non-adoption. By assessing different methodologies and defining their purpose and limits in discussion between breeders and socio-economists and considering formal and informal seed impact pathways, the Module intends to clarify best practices for assessing or measuring ex-ante and ex-post germplasm impacts.

3.1.1.4 System linkages

Investments by AFS CRPs: CGIAR centers and NARS have their own individual ways of defining and organizing breeding programs for highly divergent commodities (seed or vegetatively propagated, crops and animals), with little or substantive investment. Still, different breeding programs can be divided into distinct stages that can be captured with metrics and described by process (e.g., using molecular breeding, or not). Breeders will need to: (i) invest time in designing standardized metrics and descriptions of breeding programs; (ii) implement the agreed template and approaches for monitoring breeding program performance; (iii) contribute to peer review and further improvement of the approach; (vi) provide socio-economists and breeding personnel to discuss current and improved impact assessment approaches, and define best practices; (vii) use best practices to execute impact assessments, aligned with the overall AFS CRP strategy and based on available funding; and (viii) provide opportunities for programs to visit stronger programs or access consultancy services.

Benefits to AFS CRPs include: (i) a common framework to assess the performance of their breeding programs; (ii) systematic use of such information in AFS CRP reports and during external reviews (instead of continuously reinventing the wheel); (iii) greater awareness of best practices and their use in CGIAR and NARS breeding programs; (iv) access to expert advice on how to implement better practices within a given resource framework; (v) more authoritative support to joint and individual project proposals; (vi) more effective use of existing breeding resources; and (vii) exposure to private sector breeding management frameworks.

System level benefits include: (i) breeders becoming part of a performance management framework that allows them to improve their performance based on best practices used in similar circumstances; (ii) research directors and program leaders using best practices for managing and supporting cultivar development pipelines; (iii) accelerated implementation of state-of-the-art breeding and impact assessment practices; (iv) awareness and use of opportunities to share resources and expertise; (v) common metrics in the CGIAR translate into more sharing of information across commodities, environments and programs and extending it to other breeding programs targeting the developing world; (vi) coordinated and more rigorous approaches increase data standardization, cross-system prioritization of investment and medium- and long-term returns on investments in crop research.

Data handling: In collaboration with Module 5, the Platform will manage a centralized repository of information that will also be used by AFS CRPs for reporting purposes.

3.1.1.5 Climate Change

The surge of novel and aggressive pests and diseases, land and water scarcity, desertification, and increased carbon emissions are realities that CGIAR and NARS breeding programs must and have incorporated into their strategic plans. A recent global meta-analysis found that decreases of about 5% in crop productivity are expected for every degree of warming above historical levels (Challinor et al., 2014). Without acceleration of breeding gains, this would require half a decade of breeding investments to simply keep agricultural production at the same level. Given the crucial role of the CGIAR breeding programs, the ability of the AFS CRPs to optimize improvements in genetic gains while climatic conditions change and become less stable is a proxy to determine how well we are able to buffer agricultural production in the developing world. Implementing better breeding practices among CGIAR and NARS in general will contribute to better cultivars reaching more farmers at greater speed. Also, in several instances, the genetic ability or traits associated with mitigation of severe environmental changes are "bottleneck" traits. The breeding programs' ability to develop "bottleneck" trait solutions is critical to initiate a more structured approach to breeding in which disruptive genetic innovations can be better supported when made transparent to investors. Typical examples are genetic gains in less favorable areas that are more vulnerable to climate change, such as coastal deltas being affected by salinity intrusion as a consequence of the rise in sea level, and rainfed areas prone to drought and floods.

3.1.1.6 Capacity development

The Module has an explicit capacity building approach because it improves skills in strategic planning, breeding program management and client focus, and publishes standardized metrics, descriptions of breeding programs and impact assessment approaches, information that is so far lacking. CGIAR and NARS breeding programs will benefit from experts contracted for their private sector expertise and that will provide an outsider view of realistic improvements within individual programs. Private sector expertise and best practices sourced from among centers and NARS will be used to develop the breeding assessment system. Metrics and strategies will inform breeders, research managers and investors how to assess breeding programs and increase the returns of their investments. This is expected to lead to increased capacity of partner organizations, as evidenced by rates of investment in agricultural research.

A scientific workshop will be organized among breeding leaders, socio-economists involved in impact assessment and seed sector specialists to conceptualize various impact assessment approaches and their purposes. The Module will manage a list of best practice sites and external experts that can assist at training venues and for external breeding program assessment.

3.1.1.7 Intellectual asset and open access management

The primary beneficiaries of this Module are farmers in low and middle income countries. Intellectual property will be produced by and for breeders, research managers and investors in breeding programs targeting low- and middle-income countries. The Module will produce, describe and display peer-reviewed information generated by the AFS breeding programs and external members. They may originate from the public or private sector.

If any information or methods are sourced from the private sector, the Module will ensure proper stewardship of their intellectual property as well as intellectual property belonging to other parties for which permission to use has been granted. All parties using third party intellectual property must do so as part as part of any agreement they sign for this Module.

Intellectual assets developed with Platform funding are made available to the public under appropriate licensing conditions. In circumstances where third party intellectual property is utilized, conditions may be added as permitted under Section 6 of the CGIAR Principles on the Management of Intellectual Assets, which establishes the conditions for 'limited exclusivity' or 'restrictive use' agreements.

Research papers, policy briefs, conservation protocols, training materials, written submissions to international policy fora, will be made public through publication on the Platforms' own website and or through publication in journals as open access. Software and web tools will preferably be open source and be made available under suitable open access licenses.

3.1.1.8 Module management

The Module requires a Module Leader, ideally with private sector experience and also familiar with the constraints of CGIAR and NARS breeding programs. The Module Leader will report to the Platform Leader with the Expert Advisory Group contributing to performance assessment. The Module must be close to the clients, ideally client "owned," i.e., housed within an entity that has breeding programs and experience or understanding of different breeding systems relevant to the developing world. Primary candidates to host this Module include CIAT, CIMMYT, CIP, ICRISAT, IITA, ILRI and IRRI.

The Module Leader will work with a CoP of breeding leaders from the various AFS CRPs. This group will meet virtually and occasionally face-to-face to define standardized metrics and descriptions of breeding programs, and will also draw on private sector expertise. One representative for each AFS CRP will become member of the Expert Advisory Group for this Module. They are responsible for managing the process, according to the standards proposed by the CoP. They take critical decisions where opinions differ, ensure completed metrics and breeding program assessments within their AFS CRP, and contribute to further improve the system. As NARS show interest to implement the breeding program assessment, the membership of the Expert Advisory Group will be adjusted accordingly. The Module will contract external experts with private sector expertise that will contribute to developing the breeding assessment system, assist in training and coaching, and can be contracted by members for an external breeding program assessment.

3.1.2 Module Budget Narrative

3.1.2.1 General Information

Platform Lead Center's Name: CIMMYT

Module title: Module 1: Breeding Program Excellence

Center Location of Platform Leader:

3.1.2.2 Summary

Total Module budget summary by sources of funding (USD)

Funding Needed	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2	364925	383172	402330	422447	443569	465748	2482191
W3	729851	766343	804661	844894	887138	931495	4964382
Bilateral	729851	766343	804661	844894	887138	931495	4964382
Other Sources	0	0	0	0	0	0	0
	1,824,627	1,915,858	2,011,651	2,112,234	2,217,846	2,328,738	12,410,954

Funding Secured	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2 (Assumed Secured)	364,925	383,172	402,330	422,447	443,569	465,748	2,482,191
W3	0	0	0	0	0	0	0
Bilateral	0	0	0	0	0	0	0
Other Sources	0	0	0	0	0	0	0
	364,925	383,172	402,330	422,447	443,569	465,748	2,482,191

Total Module budget by Natural Classifications (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
Personnel	843,180	885,339	929,606	976,086	1,024,891	1,076,135	5,735,237
Travel	125,247	131,509	138,085	144,989	152,238	159,850	851,918
Capital Equipment	29,075	30,529	32,055	33,658	35,341	37,108	197,767
Other Supplies and Services	461,628	484,709	508,945	534,392	561,112	589,167	3,139,954
CGIAR collaborations	0	0	0	0	0	0	0
Non CGIAR Collaborations	143,750	150,938	158,484	166,409	174,729	183,465	977,775
Indirect Cost	221,747	232,834	244,476	256,700	269,535	283,011	1,508,303
	1,824,627	1,915,858	2,011,651	2,112,234	2,217,846	2,328,738	12,410,954

Total Module budget by participating partners (signed PPAs) (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
CIMMYT	0	0	0	0	0	0	0
Platform Leader	202,959	213,107	223,763	234,951	246,698	259,033	1,380,511
Module Leader	412,812	433,452	455,125	477,881	501,775	526,864	2,807,908
AFS Members	1,208,856	1,269,299	1,332,764	1,399,402	1,469,372	1,542,841	8,222,535
	1,824,627	1,915,858	2,011,651	2,112,234	2,217,846	2,328,738	12,410,954

3.1.2.3 Additional explanations for certain accounting categories

In the Module budget by natural classification, the budget for Platform Leader, Module Leaders and AFS members is summarized in the line items Personnel, Travel, Capital Equipment, and Other Supplies and Services. The Module budget by participating partner describes who manages (not who uses) the budget. E.g. the Platform Leader manages all subcontracts to AFS members and external contractors and consultants for streamlined issuing of such contracts. The Platform Leader also manages the open access budget.

3.1.2.4 Other Sources of Funding for this Project

As a new Platform, there are currently no other sources of funding.

3.1.2.5 Budgeted Costs for certain Key Activities

	Estimate annual average cost (USD)	Please describe main key activities for the applicable categories below, as described in the guidance for full proposal
Gender	827,397	Increasing to US$ 1,173,620 in the Uplift budget. Outcome expectation: At least 40% of the users will be female.
Youth (only for those who have relevant set of activities in this area)	1,378,995	Increasing to US$ 1,956,033 in the Uplift budget. Outcome expectation: At least 2/3 of the users will be students and young scientists.
Capacity development	2,068,492	Increasing to US$ 2,934,050 in the Uplift budget. The entire Module/Platform is targeted at capacity building (see Theory of Change).
Impact assessment	0	Included in CRP Management costs, not in Module specific costs
Intellectual asset management	0	Included in CRP Management costs, not in Module specific costs
Open access and data management	22,956	Increasing to US$ 45,913 in the Uplift budget

Communication	0	Included in CRP Management costs, not in Module specific costs

3.1.2.6 Other

3.1.3 Module Uplift Budget

Outcome Description	Amount Needed	W1 + W2 (%)	W3 (%)	Bilateral (%)	Other(%)
1. Developing a standard template and approaches for monitoring breeding program performances, which includes the development of a common set of metrics that will assess genetic gain.The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	28,478	20	40	40	0
2. Internal breeding program assessment and development of strategic plans to set breeding program directions. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8..	143,036	20	40	40	0
3. Support breeding programs for needed improvements through consultancies, investments, and/or simulations. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	264,972	20	40	40	0
4. Extend the assessment to NARS breeding programs. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	260,058	20	40	40	0
5. Standardized approaches to measure genetic gains in farmers' fields. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	169,013	20	40	40	0

3.2 Module 2: Trait discovery and breeding tools and services

3.2.1 Module Narrative

3.2.1.1 Rationale, scope

Modules 3-5 are designed to support distinct, user-prioritized improvements in the area of genotyping, phenotyping and bioinformatics, including discovery, decision support and breeding information management tools. Between the 'big picture' priority setting in Module 1 and new tools and opportunities emerging from Modules 3-5, users need to prioritize the components that need to be adapted or developed and interlinked, and the workflows that need to be established for breeding programs to successfully use them for trait discovery, trait mobilization and cultivar development. Also, there are different user needs to consider, given size and sophistication of breeding programs, and the challenges of diverse commodities. Module 2 is designed to support both the breeding programs and the pipelines that provide the ability to mobilize traits through the selection of specific alleles, haplotypes and backgrounds. It acts as a focal point for user discussion, information sharing and collaborative priority setting of high return on investment and essential cross-commodity workflows.

Development of new tools in the multinational trait research and breeding sector typically focuses on the key commodities; these tools are subsequently modified to meet the needs of secondary and tertiary commodities through integrated proprietary systems adapted to the workflows of the organization. In the case of the non-multinational breeding sector (CGIAR, ARIs, NARS, smaller companies), many of the newly emerging tools for trait discovery, mobilization and cultivar development originate in diverse commodity-specific pockets, driven by user demand. Tools developed in one commodity (specific crops, trees or animals) are largely inaccessible to the broader breeding community due to substantive transaction costs, originating from: (i) lack of knowledge of which tools are available; (ii) lack of direct access; (iii) difficulty in application due to data reformatting, pipeline assembly and computational power; (iv) the time required to learn about new tools, their value and application; (v) inability to afford IP; (vi) the tool is not sufficiently adapted to meet user needs; and (vii) lack of understanding of how to best implement tool(s) in a breeding or discovery process. Even for established processes such as a lab information and field trial management, information is not readily available in the pros and cons of off-the-shelf solutions and how to integrate them in commodity-specific discovery and breeding processes.

As a result, many CGIAR, ARI, NARS, smaller company researchers and breeders invest in developing their own commodity-specific solutions rather than adapting and adopting others, thereby reinventing the wheel with varying success, given the need for in-depth understanding of increasingly complex research questions and processes. This diverts resources to the development and maintenance of tools rather than to their application and, what's worse, results in more complex breeding and discovery applications succeeding only at a low rate and with great delay. The most recent and potentially more powerful tools are not adopted as users do not have information on how their application would benefit them, nor the ability to quickly embed the tools in their workflows; they also have no access to training or interpretation expertise, and lack understanding of how to restructure their workflows to optimize the return on investment when using a new approach or tool. Alternatively, a new approach is suggested by enthusiastic researchers as a step change in enhancing genetic gains without associated use case evidence or information on the modifications needed for discovery and breeding programs to fully capitalize on the value of the approach, resulting in erroneous applications and waste of resources.

Module 2 therefore aims to generate a platform where: (i) tools to accelerate and/or strengthen trait characterization, mobilization and cultivar development are identified out of the public and (accessible) private sector; (ii) information on how to restructure workflows and incorporate tools to maximize their benefit is exchanged; (iii) tools are more widely tested, needs and investment/development priorities are set; (iv) accelerated awareness and uptake of the best tools are supported through consultancies, and virtual or face-to-face training. This Module also has cross-cutting function. It develops the "Toolbox" where the knowledge base created in the other modules will be made available and feedback from users will be captured. The feedback will inform the workplans of the other modules. Also, many tools and applications are increasingly data-intensive and need bioinformatics and biometrics support. Therefore, this Module will be crucial to aid the Bioinformatics Module in priority setting. The grand challenge to be addressed is to accelerate effective application of existing and newly emerging tools that support trait identification, mobilization strategies and breeding approaches, reduce the time CGIAR researchers spend in tool identification, testing or development, and increase time and effectiveness of application in actual breeding programs for the delivery of new or improved traits to farmers.

The Module targets breeders and researchers associated with AFP CRPs and any interested external user. We estimate that the Module will initially reach 60 key users from the CGIAR, NARS and ARIs associated with the AFS CRPs. Once established, the Module will maintain a powerful platform for discussing the usefulness of tools in real-life breeding and discovery applications, in particular for the more resource-constrained breeding programs targeting low- and middle-income countries, reaching several thousands of users by the end of 2022. This estimate is based on the download frequency of best practice documentation, software and other documentation already available (in uncoordinated format) from CGIAR centers.

3.2.1.2 Objectives and targets

The Module will accelerate trait discovery, trait mobilization and cultivar development workflows through: (i) the formation of a web-based "one-stop" catalogue ("the Toolbox") of bioinformatics, phenotyping, genotyping, mechanization, automation tools and approaches and their application in a real-life discovery and breeding context (Figure 2.1); (ii) training and documentation of specific tools, workflows and implementation use-cases through webinars; (iii) solicitation and open display of reviews; (iv) development and adaptation of a system to facilitate stand-alone and pipelined data analyses interconnecting multiple in-house and third party reviewed software and database tools. An example is shown in Figure 2.2. It describes how several data-intensive applications (different colors) result in an interconnected workflow of recommended tools (many off-the-shelf) and approaches for discovery (genome-wide selection) and breeding (genomic selection) applications. Though conceived, tried and tested for one species and trait, the documentation both highlights missing pieces ("needed tools") and allows others to contribute and catch up with best practices instead of reinventing a complex wheel. The Module will be organized into three work packages (Table 2.1):

1. Development of a toolbox to support trait discovery, mobilization and breeding. This work package focuses on developing, updating and maintaining a web-based platform to facilitate the description, review and use of tools and workflows relevant to modern and state-of-the-art discovery and breeding applications, resulting in a practical toolbox for researchers and breeders that can be structured by use cases and types of users. Hence, in collaboration with the CoPs in each module, the Toolbox will be populated with a wide range of trait discovery, breeding, phenotyping, genotyping, mechanization, automation and bioinformatics tools, workflows and use cases currently used by the AFS CRPs, the Genebanks Platform and external members, and relevant to various types of users. The Toolbox will be set up through Module 5. The web platform will use an "Amazon" review type approach (such as

AnswerHub) to facilitate reviews and issue reports. The Toolbox will be updated by members adding and reviewing new tools/ approaches/suppliers, and unused or poorly reviewed entities will be removed, to work towards a knowledge base of best practices.

2. Fostering toolbox adoption and its dynamic use. This work package documents and uploads new tools and approaches for trait discovery and breeding, with a strong emphasis on user participation, priority setting and capacity development. The Module Leader will work with a CoP, made up of diversity analysts, trait discovery specialists and breeders from the AFS CRPs and the Genebanks Platform and external members, and the leaders of other modules to document "missing" features, develop use cases relevant to applied trait discovery and breeding programs and prioritize needs for approach and tool development. It includes approaches for pipelined data analysis. Input from Module 1 will be used to assess how ready various CGIAR centers and NARS may be to use new interventions. The Module will be tasked with considering these specific needs in priority setting. User feedback is critical to plan Platform evolution as a whole and, given that many tools increasingly require some sort of bioinformatics support, to give clear guidance to the Bioinformatics Module on what software or database tools to adapt and mainstream within the Platform. The CoPs are key to drive the active participation and feedback from a wide range of users so as to capture a broad range of expertise and opinions in an efficient manner.

The capacity development component of this work package focuses on two main activities: first, the development of better documentation, where required, of extant tools with a strong emphasis on modular “how to” YouTube-type videos and short webinars that can be recorded and linked to tools, workflows and data analysis pipelines within the toolbox. This will include implementation guides on how to restructure a breeding workflow to gain more value from tool and pipeline implementation; this will be linked to specific use case information. This type of information is in strong demand. As an example, a YouTube video released in May 2015 as part of Seeds of Discovery project was viewed 1190 times by January 2016 (Romero, 2015). Second, more intensive face-to-face training of users on implementing specific workflows will be conducted, linked to existing scientific meetings. We anticipate training 40-125 users annually. The work package will also identify internal and external experts that can help trait mobilization and breeding teams to implement fast and low-cost strategies based on their individual needs.

3. Source and ground-truth innovative ideas through an incubator. This work package focuses on brainstorming, discussion and potential ground truthing of blue sky ideas. In association with relevant scientific meetings, forums will be held to discuss physical and virtual cross-disciplinary blue sky ideas. The objective of these forums is to enable researchers within and outside AFS CRP to propose and discuss the application of high-payoff novel approaches to plant and animal trait discovery and breeding targeting the developing world. The forums will promote closer linkages between AFS CRPs and upstream labs and students. Participation of key donors is required to enable potential incubation of project ideas. Instead of testing new ideas in a disconnected manner, coordinated testing and discussion through/by the Platform CoPs could become a powerful approach for directly assessing emerging technologies for genetic gains enhancements in realistic breeding programs. We anticipate that these incubator forums would be held once to twice a year, each with an attendance of 30 to 50 people.

Use of Module resources among work packages are projected in Table 2.2. The main cost drivers are explained in Table 2.3.

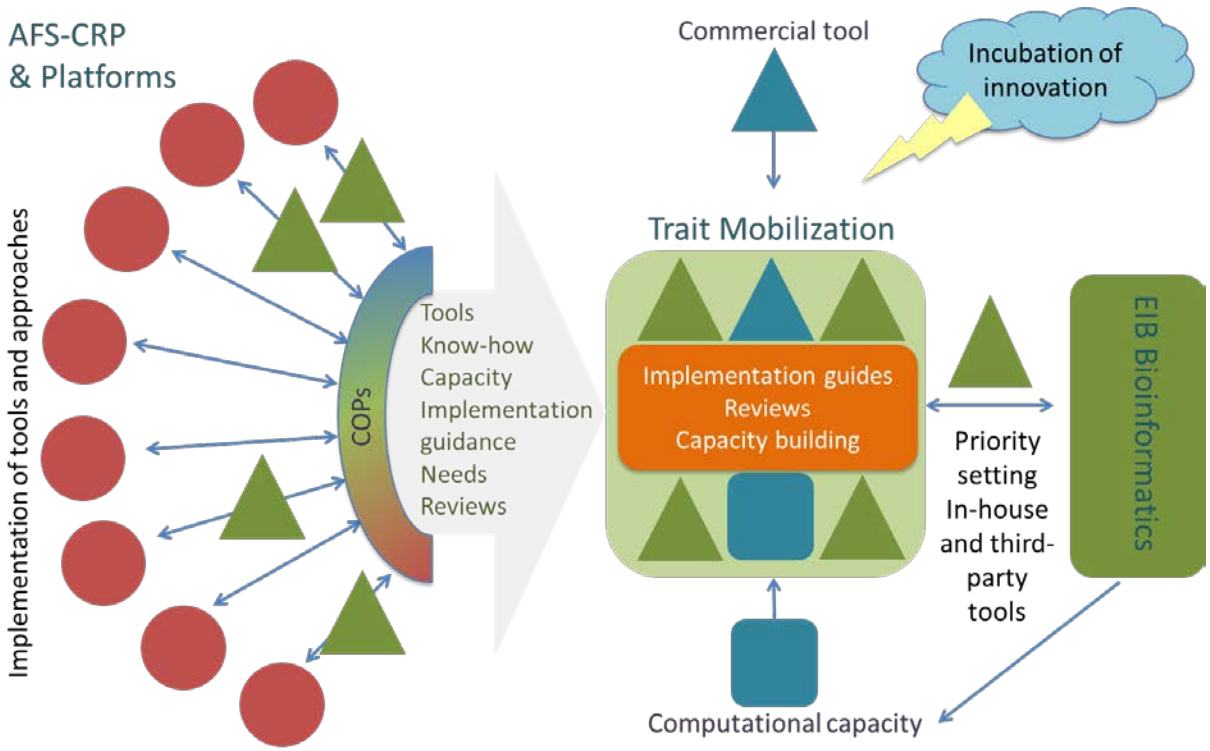

Figure 2.1. Interrelations of the Trait Discovery and Breeding Module with AFS-CRP and the Genebanks Platform, the Bioinformatics Module and external providers of software, know-how and computational capacity.

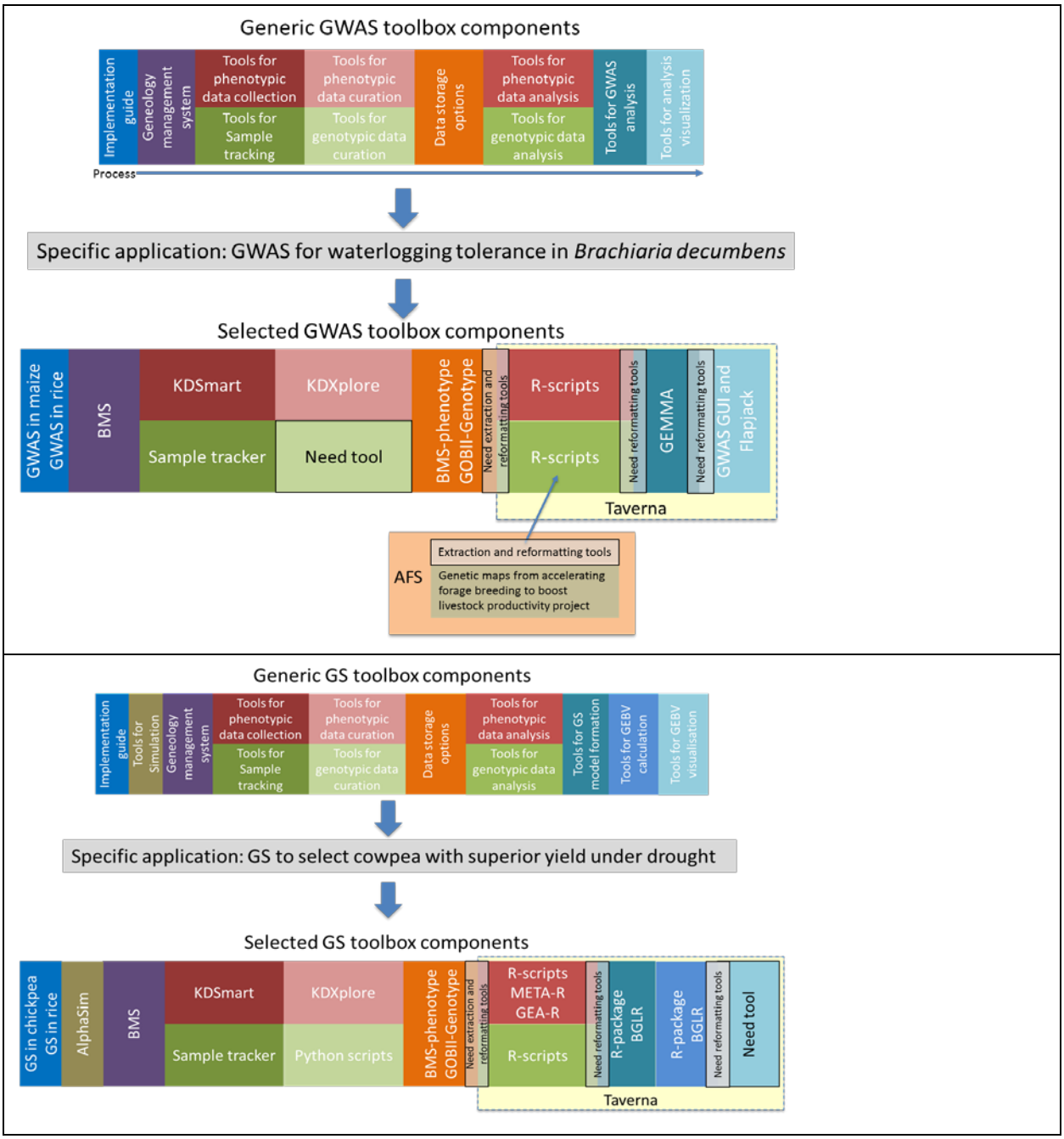

Figure 2.2 Examples of two pipelines of interlaced tools that can support similar use cases – genome-wide selection for complex traits and genomic selection for disease resistance – in other commodities.

Table 2.1. Work packages and key milestones to be funded by the Platform.

	Milestones = Output targets					
Work packages = Objectives	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1 Develop a non-prescriptive toolbox to support trait mobilization and applied breeding.	Develop a web platform (toolbox) to incorporate breeder-relevant tools and workflows used by AFS CRPs and external members. Link to user review system.	1 Incorporate new components, upgrade workflows, remove obsolete components in collaboration with members; engage students in developing such information.				
		2 Existing projects: Tools developed by Seeds of Discovery, GenomeHarvest, GS-RUSE and other projects submitted with documentation to the toolbox and, as applicable, integrated in Galaxy/Taverna.				
2 Foster toolbox adoption and its dynamic use	Formation of / communication with CoPs from relevant members of each module.	1 CoPs document "missing" features in trait discovery, mobilization and precision breeding applications, including prioritization of needs across AFS and CoPs, develop use cases around missing features and work with the Bioinformatics Module to support the formation of technical user requirements for new bioinformatics and/or biometrics tools and approaches. CoPs provide user-based feedback on tools, workflows, suppliers and pipelines, using an Amazon-style review system.				
		1 Training and documentation of end user tools and pipelines through webinars, "YouTube" modules, and implementation guides. (In 2018 & 2019 co-funded with GOBII)				
		3 In-depth training courses/ workshops linked to large meetings.				
3 Source innovative ideas through an incubator	Physical and virtual blue sky discussions associated with scientific meetings, to raise and discuss ideas for high-payoff approaches and discuss and design the incubation of project ideas. Allocation of modest resources to validate technologies in the incubator while jointly seeking additional funding to test more substantive “game changers”.					

Table 2.2. Use of Base and Uplift budgets among work packages.

Base Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1 Develop a non-prescriptive toolbox to support Breeding and precision breeding.	$754,620	$792,351	$831,968	$873,567	$917,245	$963,107
2 Foster toolbox adoption and its dynamic use	$1,236,295	$1,298,110	$1,363,015	$1,431,166	$1,502,724	$1,577,860
3 Source innovative ideas through an incubator	$155,645	$163,427	$171,598	$180,178	$189,187	$198,646
Grand Total	**$2,146,559**	**$2,253,887**	**$2,366,582**	**$2,484,911**	**$2,609,156**	**$2,739,614**

Uplift Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1 Develop a non-prescriptive toolbox to support Breeding and precision breeding.	$943,723	$990,909	$1,040,455	$1,092,478	$1,147,102	$1,204,457
2 Foster toolbox adoption and its dynamic use	$2,039,318	$2,141,284	$2,248,349	$2,360,766	$2,478,804	$2,602,745
3 Source innovative ideas through an incubator	$236,743	$248,580	$261,009	$274,060	$287,763	$302,151
Grand Total	**$3,219,785**	**$3,380,774**	**$3,549,813**	**$3,727,304**	**$3,913,669**	**$4,109,352**

Table 2.3 Explanations of the costs in relation to the planned 2022 outcomes.

Module	2022 Outcomes	Scope: Base budget	Scope: Uplift budget	Explanations of the costs in relation to the planned 2022 outcomes
Module 2: Trait discovery and breeding tools and services	Toolbox (all Modules)	> 5,000 users	> 10,000 users	
	Best practices documentation for trait discovery and breeding in ToolBox	> 18 modules/ use cases per year	> 25 modules/use cases per year	Annual budget to members increases from US$ 923,000 to US$ 1,268,000; a 50% web administrator positions becomes a full-time position; a communication position (shared with Platform Management) becomes a full-time position.
	Pipelined analyses approaches tested, adapted and promoted	5	>10	
	Training	40 participants per year	125 participants per year	Annual training budget triples, from US$ 69,000 to US$ 210,000; an external capacity building position becomes a full-time position
	Expert consultations	> 4 per year	> 6 per year	Annual consultant budget for expert consultations increases from US$ 105,000 to US$ 158,000

3.2.1.3 Science quality

The Trait Discovery and Breeding Module does not aim to force solutions and approaches on members and users; instead, it seeks to work in an interactive and dynamic manner to enable access to information on new phenotyping, genotyping, mechanization and automation tools, bioinformatics components and pipelines, computational capacity, training and implementation that can help increase the rate of genetic gain. Existing tools and know-how from the AFS CRPs will form the initial basis of the "catalogue" of tools and methods (the toolbox; Figure 2.1). This will be complemented by solutions from Modules 3-5 and those available from ARIs and the private sector. Through its systematic landscaping and transparent, non-confrontational discussion of user-driven tools and approaches, the Module is essential for identifying both the "best tool for the job" across the system and step changes in how genetic gains can be achieved. It will ensure that development of new solutions within the Excellence in Breeding Platform, no matter where they come from, stay end-user-driven and address needs of CGIAR and NARS.

The private sector is well known for modifying entire breeding processes and pipelines in order to fully capitalize on the investments and benefits of introducing new tools and approaches into the research and breeding process. Across the AFS CRPs and the public sector in general, similar information remains hidden and unavailable. By providing this information through tools and approaches tested and tried by the various CoPs, the Module ensures that AFS CRPs and external users are able to build on each other's insights, be more successful in applying data-intensive trait discovery and mobilization strategies and breeding approaches, and reduce the time necessary for developing and enhancing the quality of new cultivars. Driven by their individual searches for better tools, the AFS CRPs are linked to the most relevant public and private knowledge and tool providers worldwide, which gives a solid knowledge base to populate the toolbox created.

Incorporation of tools in the platform and the deployment of pipelines will be needed to follow a series of documented requirements. Tools can only be placed on the platform if supported by a CoP member. Also, those submitting the tool will be required to provide evidence supporting successful tool application. Pipelines supporting entire workflows will need to demonstrate repeatability and have implementation protocols.

The ability to seamlessly move between software components will be critical in terms of workflow success, given that users will not want to repeatedly re-format large data sets; furthermore, some users lack the necessary coding skills to do this efficiently. Bioinformatics systems such as Taverna-Galaxy exist to aid this transition. Supported by the Bioinformatics Module in dual functions, they will be used: (i) as a catalogue of analysis scripts, software and visualization tools; and (ii) to enable users to custom-build those analysis platforms that are most relevant to their needs with the assistance of their own AFS CRPs or the Platform Bioinformatics Module. Once tested, these pipelines can be shared (with clear attribution) with others via the catalogue, enabling use by the wider breeding community. The number and location of users of pipeline access and downloads will be monitored to measure adoption.

To most appropriately gauge the value, usefulness and understanding of tools and pipelines, an Amazon-style review system (such as AnswerHub®) will allow users to post reviews and address specific issues. User reviews of tools, workflows and pipelines will provide important feedback to monitor utility and adoption by geographies, and to enable the identification of cross-AFP CRP challenges to be addressed by the Platform. Tools, workflows and pipelines that repeatedly receive poor reviews will be assessed and, if necessary, removed from the system.

3.2.1.4 System linkages

Investments by AFS CRPs, the Genebanks Platform and external members. There is an increasing number of CGIAR-ARI collaborative projects, with collaborators on all continents, that develop tools and assemble pipelines for data-intensive trait discovery and breeding applications, such as the Genomic Open Source Breeding Informatics Initiative (GOBII), Genomic Selection for Resource Use Efficiency (GS-RUSE), GenomeHarvest, Seeds of Discovery (SeeD), Genomic Tools for Sweetpotato Improvement (GT4SP) and others. AFS CRPs and external users will develop specific tools and their documentation, driven by commodity-specific needs. Others, in search of new tools, will access the web platform to use, test and provide feedback on tools, participate in training sessions and meetings and use suitable tools within their breeding programs. Although targeted at upstream users and breeders who rely on data-intensive tools, the Platform, through its generic design, will be able to support other types of applications in high demand by lower-tech users such as laboratory information management systems, bar-coding applications and open-source algorithms for statistical analyses. It is expected that the user base for this Module will diversify in the medium term, based on strengths of the breeding programs, and drive demand and direction for/of the Platform.

Benefits to AFS CRPs, the Genebanks Platform and external users. Based on currently available tools implemented so far only in individual research and breeding programs, the Toolbox will enable users to: (i) accelerate cultivar development; (ii) mobilize traits through breeding integrating advanced breeding technologies (such as breeding design simulation, cross-prediction, use of high-density genomics data for genomic selection, gene-to-phenotype models, and test-to-target environment predictions) with trait pipelines and GxE information; and (iii) quantify genetic diversity and identify and validate useful alleles, haplotypes and genotypes based on genome-to-phenotype information on germplasm groups prior to rapid use in precision breeding. Users will have lower tool self-development and maintenance investment; be able to access a wider range of solutions and innovations; access practical recommendations on use; and benefit from more informed selection and implementation of tools and approaches.

Outcome at the portfolio level. The Module will accelerate the implementation of state-of-the-art trait discovery, mobilization and breeding approaches within CGIAR and NARS genebanks and breeding programs targeting the developing world. Greater use of genetic resources held in CGIAR genebanks, genomic selection, and the integration of genomic, phenotypic and environmental data rely on such tools becoming more widely accessible; otherwise breeders and projects could have the ideas, concepts and ambition to do so, but no access to the tools that would allow them to operationalize the concepts. A greater rate of successful upstream breeding projects and their faster implementation will result in greater use of genetic diversity and faster breeding progress by CGIAR centers and NARS.

Coordination with the Big-Data, Information and Knowledge Platform. As agreed at the portfolio level, the Excellence in Breeding Platform will establish with this Module a unified approach for managing large genetics/bio-informatics data and applications, while the Big-Data, Information and Knowledge Platform will focus on socioeconomic and environmental data and applications. While the breeding process as such is well defined, facilitating clear roles and responsibilities of the two Platforms, there will be use cases that link genetic applications with environmental and socioeconomic data and that will require interaction between the two Platforms, in particular as big picture scenarios and research questions are being tackled to help the CGIAR and other research organizations set their science agendas.

3.2.1.5 Climate Change

This Module assesses and promotes generic tools that accelerate genetic gains for a wide range of traits. A focus on climate change, most prominently heat and drought tolerance, is at the forefront of all AFS CRPs. Abiotic stress tolerance traits are complex and in general not as easy to select for, as, for example, disease resistance. They require genome-wide research and selection approaches to be in place and workflows and data analysis approaches to be combined with improved phenotyping tools. Thus one could say that if the CGIAR does not master efficient workflows for these more complex traits, breeding gains for stress tolerance will stagnate at current rates, making this Module (and the Platform) a crucial component in the overall climate adaptation strategy of the CGIAR and its partners.

3.2.1.6 Capacity development

The web platform structure, associated information and training modules developed through this Module's toolbox follow use cases ("how to" then "what to"), such as "if you want to implement approach X or tool Y in your breeding pipeline, here are specific tools you may want to adopt, and their interconnectivity and database requirements." Given added time requirements, members are encouraged to involve students in documenting use cases for upload.

Capacity building focused on use cases will be enabled through virtual meetings and direct face-to-face training associated with major scientific meetings. It will follow a seminar and online meeting structure. Formation plans for each course/module will be developed and a series of questions posed pre- and post-training in order to assess whether the course achieved the outputs stated in the formation plan. Capacity building impact will be measured in part through tool and pipeline adoption and integration within breeding and research programs. Given that training information requires more than a member uploading a tool or workflow, experts will be hired to review particular use cases and document requirements and suggested uses. They are also resource persons for consultancies. Capacity building activities will be assessed through attendee questionnaires and later through assessment of which approaches have been successfully adopted by breeding/research units.

Primary recipients of capacity building in the first phase of the project are CGIAR, ARI and NARS scientists directly involved in AFS CRP upstream breeding implementation. In a second phase and as use cases evolve and diversify, capacity building activities can be streamlined based on user needs for low- to high-tech applications. Given the extensive involvement of AFS CRPs in capacity building, network analysis should be conducted to identify those individuals and groups that are key to better enabling technology and knowledge dissemination.

3.2.1.7 Intellectual asset and open access management

Intellectual property will be produced by and for breeders and researchers implementing data-intensive trait mobilization and breeding applications, with particular focus on the requirements of users from low- and middle-income countries. The Module will produce, describe and display materials, technologies, and tools ranging from equipment, software, methods, traits, germplasm, and management technologies to information databases and publications. They may originate from the public or private sector.

Members contributing to this Module shall ensure proper stewardship of their intellectual property as well as intellectual property belonging to other parties who have granted and confirmed permission to use. All parties using third party intellectual property must do so as part of any agreement they sign for this Module.

Intellectual assets developed with Platform funding (including tools, germplasm, inventions, improvements, data, processes, technologies, software, trademarks, publications and other information products) will be made available to the public under appropriate licensing conditions. In circumstances where third party intellectual property is utilized, conditions may be added as permitted under Section 6 of the CGIAR Principles on the Management of Intellectual Assets, which establishes the conditions for 'limited exclusivity' or 'restrictive use' agreements. Open-source solutions are preferred to facilitate inter-connectivity and wide adoption of tools.

Management of pay-to-access third-party commercial software, computational infrastructure or expert advice may require cross-member licensing agreements which may benefit providers and could allow for greater use. User feedback on the web platform will demonstrate if tools or services are performing poorly or difficult to connect. The web administrator will need to ensure that user feedback is based on fact and any conflicts of interest will have to be clearly disclosed.

3.2.1.8 Module management

The Module requires a Module Leader which will also be the Platform Leader and a web administrator. Resources are made available to AFS CRPs or external members to contribute to the knowledge base, given that such documentation will require additional time investment, using competitive processes. Drawing on existing collaboration among AFS CRPs, ARIs and the private sector, the Module will seek to collaborate with those with substantive tool development expertise, including the CAAS, CIRAD, CSIRO, the Boyce Thompson Institute, Diversity Arrays Technology, the Genome Analysis Centre, INRA, IRD, the James Hutton Institute, Kansas State University, the Roslin Institute, Wageningen University, USDA, and others. Specific expertise from industry will be requested and may need to be contracted.

The Module must be close to the clients and, ideally, client "owned," i.e., housed within an entity that has both discovery and breeding programs and experience or understanding of different breeding systems relevant to AFS CRPs. Primary candidates to host this Module include CIAT, CIMMYT, CIP, ICRISAT, IITA, ILRI and IRRI. The host institution needs to be able to provide adequate server capacity and connectivity.

The Expert Advisory Group will include members contributing to the CoPs with balanced representation of AFS CRPs, Genebanks and external members. This group will meet virtually to review Toolbox performance with the Module Leader, and will also meet with Module Leaders to review and prioritize needs to be addressed through software improvement projects, documentation and training, and which key tools to move from the test phase to wider scale-out. A minimum of five members of the group representing five AFS is needed to make decisions. Members of the Expert Advisory Group are responsible for sourcing wider feedback from their respective constituencies and promoting the Platform's availability

3.2.2 Module Budget Narrative

3.2.2.1 General Information

Platform Lead Center's Name: CIMMYT

Module title: Module 2: Trait discovery and breeding tools and services

Center Location of Platform Leader:

3.2.2.2 Summary

Total Module budget summary by sources of funding (USD)

Funding Needed	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2	429312	450777	473316	496982	521831	547923	2920142
W3	858624	901555	946633	993964	1043663	1095846	5840284
Bilateral	858624	901555	946633	993964	1043663	1095846	5840284
Other Sources	0	0	0	0	0	0	0
	2,146,559	2,253,887	2,366,582	2,484,911	2,609,156	2,739,614	14,600,710

Funding Secured	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2 (Assumed Secured)	429,312	450,777	473,316	496,982	521,831	547,923	2,920,142
W3	-	-	-	-	-	-	-
Bilateral	-	-	-	-	-	-	-
Other Sources	-	-	-	-	-	-	-
	429,312	450,777	473,316	496,982	521,831	547,923	2,920,142

Total Module budget by Natural Classifications (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
Personnel	992,034	1,041,635	1,093,717	1,148,403	1,205,823	1,266,114	6,747,727
Travel	88,574	93,003	97,653	102,536	107,663	113,046	602,476
Capital Equipment	76,860	80,703	84,738	88,975	93,423	98,094	522,792
Other Supplies and Services	628,867	660,310	693,326	727,992	764,392	802,611	4,277,499
CGIAR collaborations	0	0	0	0	0	0	0
Non CGIAR Collaborations	92,710	97,345	102,212	107,323	112,689	118,324	630,603
Indirect Cost	267,515	280,891	294,935	309,682	325,166	341,425	1,819,614
	2,146,559	2,253,887	2,366,582	2,484,911	2,609,156	2,739,614	14,600,710

Total Module budget by participating partners (signed PPAs) (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
CIMMYT	0	0	0	0	0	0	0
Platform Leader	1,332,060	1,398,663	1,468,596	1,542,026	1,619,127	1,700,083	9,060,554
Module Leader	0	0	0	0	0	0	0
AFS Members	814,500	855,225	897,986	942,885	990,030	1,039,531	5,540,156
	2,146,559	2,253,887	2,366,582	2,484,911	2,609,156	2,739,614	14,600,710

3.2.2.3 Additional explanations for certain accounting categories

In the Module budget by natural classification, the budget for Platform Leader, Module Leaders and AFS members is summarized in the line items Personnel, Travel, Capital Equipment, and Other Supplies and Services. The Module budget by participating partner describes who manages (not who uses) the budget. E.g. the Platform Leader manages all subcontracts to AFS members and external contractors and consultants for streamlined issuing of such contracts. The Platform Leader also manages the open access budget.

3.2.2.4 Other Sources of Funding for this Project

As a new Platform, there are currently no other sources of funding.

3.2.2.5 Budgeted Costs for certain Key Activities

	Estimate annual average cost (USD)	Please describe main key activities for the applicable categories below, as described in the guidance for full proposal
Gender	973,381	Increasing to US$ 1,460,046 in the Uplift budget. Outcome expectation: at least 40% of the users will be female.
Youth (only for those who have relevant set of activities in this area)	1,622,301	Increasing to US$ 2,433,411 in the Uplift budget. Outcome expectation: at least 2/3 of the users will be students and young scientists.
Capacity development	2,433,452	Increasing to US$ 3,650,116 in the Uplift budget. The entire Module/Platform is targeted at capacity building (see Theory of Change).
Impact assessment	-	Included in CRP Management costs, not in Module specific costs
Intellectual asset management	-	Included in CRP Management costs, not in Module specific costs
Open access and data management	22,956	Increasing to US$ 45,913 in the Uplift budget
Communication	-	Included in CRP Management costs, not in Module specific costs

3.2.2.6 Other

3.2.3 Module Uplift Budget

Outcome Description	Amount Needed	W1 + W2 (%)	W3 (%)	Bilateral (%)	Other(%)
1 Develop a non-prescriptive toolbox to support applied breeding. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	214,378	20	40	40	0
2 Foster toolbox adoption and its dynamic use. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	910,349	20	40	40	0
3 Source innovative ideas through an incubator. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	91,938	20	40	40	0
4 Additional Platform management costs (associated with this module - which also is managed by the Platform Leader - given limitations of the budget upload tool). The value is the average difference between the annual Base budget and the annual Uplift budget.	108,041	20	40	40	0

3.3 Module 3: Genotyping/sequencing tools and services

3.3.1 Module Narrative

3.3.1.1 Rationale, scope

Advances in genomics and molecular breeding technologies provide new opportunities to accelerate gene and trait discovery, and enhance breeding outputs. If applied effectively, the correct scale and form of genotyping accelerates the rate of genetic gain and reduces the cost per unit genetic gain. This is evident through the widespread adoption and routine implementation of genotyping by multi-national seed and animal breeding companies (such as Monsanto, DuPont-Pioneer, Syngenta, Alta, Genus, Select Sires and SEMEX).

AFS CRPs applications have so far focused mostly on trait discovery, meanwhile routine implementation as a forward breeding tool is not as advanced. Essentially there are many introgression projects, some proof-of-concept type applications for genomic selection, but almost no application of diagnostic markers in forward selection. Bottlenecks specific to the generation of genomics data include: uncertainty of the suitability of various platforms and technologies and their cost effective use within distinct breeding applications; lack of access to platforms of suitable scale and cost; inadequate turn-around times; complex data formats returned from genotyping providers; lack of knowledge of service providers; inadequate costing of projects' genotyping budgets; difficulty converting costly, low-throughput, gel-based markers into SNP markers.

The Genotyping Module will enable access to appropriate genotyping technologies across the AFS CRPs. This Module aligns closely with the Bioinformatics Module to ensure smooth implementation of the data generated within discovery and breeding applications, and with the Trait Discovery and Breeding Module to ensure adequate capacity building on how to implement genotyping effectively in a workflow. The specific focal areas of the Module include: (i) provision of strategic guidance on the appropriateness of different genotyping technologies for research and breeding applications in different species; (ii) brokering genotyping and DNA isolation services and supplies from providers and aggregation of the sample volumes across programs and crops necessary to support low costs per sample; (iii) prospecting and testing the next genotyping technologies; (iv) formation of a CoP to contribute to developing use cases, reviews and implementation guides for inclusion in the Trait Discovery and Breeding Module toolkit. While there may always be the need for some specific in-house genotyping, the Module will mainstream a shift to flexible and efficient out-source provision across the AFS CRPs, thus enabling broader resource-effective application within breeding and research efforts.

To broadly integrate genomics in discovery and marker-assisted selection in breeding, a number of enabling steps specific to the generation of genotypic data are required, including: (i) lowering the costs of genotyping; (ii) ensuring appropriate data turnaround time; (iii) use the most appropriate technology for the desired application; and (iv) creating an environment of change that drives adoption of more efficient and cost-effective technologies and enables the move from low-throughput to high-throughput systems. These challenges are addressed through the Genotyping Module. Other challenges related to the successful application of genotypic data in research and breeding applications are addressed in the Bioinformatics and Trait Discovery and Breeding Modules with input from bioinformatics, biometrics and application experts.

The strategic rationale for the Genotyping Module lies in exploiting economies of scale and accelerated learning. The cost of genotyping is an issue of economy of scale, as single projects – or, indeed, single AFS CRPs – do not have enough purchasing power to negotiate prices with the private sector. Through aggregation of demand, AFS informed forecasting and streamlining of processes, the Genotyping Module can negotiate better terms and conditions. Also, during application in breeding, sampling, DNA isolation, genotyping and data analysis need to be done within a short period of the life cycle of the species of interest. Independently of pricing, if genotyping cannot be conducted in a time effective manner, it will not be adopted in breeding. Negotiating defined and guaranteed data turnaround times with service suppliers is hence crucial, as is commitment on the part of the breeding programs to forecast sample submission times and volumes, so that service providers can schedule their work. Monitoring client satisfaction and collection of metrics related to genotyping volumes are important features that will be facilitated by the Toolbox in Module 2, which will also manage the knowledge base for the entire Platform.

The choice of optimal technology is not always obvious and made more complex given the rapid evolution of genotyping and associated data analysis approaches. The development and sharing of use cases and implementation guides are critical enabling devices empowering users to be more aware of the suites of technologies and suppliers available. This will benefit all commodities, plants and animals, and particularly those AFS CRPs that have conducted little work in this area. Understanding which technologies have been applied successfully, where and how to best apply technologies in a cost efficient manner is critical to allow smaller commodities to leapfrog many of the testing and evaluation stages larger commodities have gone through. In addition, monitoring the genotyping technology environment to help identify the next technology that may be applied in breeding and discovery enables programs to make decisions regarding application of technologies that may have longer shelf lives.

3.3.1.2 Objectives and targets

The Module will divide its work into three discrete work packages to meet the overall aim of the Genotyping Module (Table 3.1), aligned with three currently funded projects (Table 3.2): (i) The High-ThroughPut Genotyping facility (HTPG), led by ICRISAT, will provide low-cost and fast-turnaround genotyping facilities to CGIAR and partners. It will ensure that SNP markers can be used routinely in forward breeding by reducing genotyping cost to USD 1 per sample, including DNA isolation. (ii) The Integrated Genotyping Support and Service (IGSS) supports the development of a commercial high-density, high-throughput genotyping and information management service in Africa. The service is a public-private partnership between Diversity Arrays Technology (DArT Pty. Ltd.) and the BecA-ILRI hub. It serves plant breeding programs in sub Saharan African including key external programs such as the Program for Africa's Seed Systems of the Alliance for a Green Revolution in Africa (AGRA). (iii) Seeds of Discovery (SeeD), led by CIMMYT, provides support to breeders and other scientists in integrating DNA marker technology and genomic tools in the development and release of new cultivars.

1. Capacity enhancement. This work package will offer experience and guidance on the use of genotyping in different research and breeding applications. Through the development of use cases and implementation guidelines, this objective will help groups optimize and apply genotyping effectively in their work. Researchers working on smaller crops/ livestock/ fishes with minimal genomics exposure will learn from the knowledge and expertise in major crops such as wheat, rice and maize. Knowledge dissemination will be conducted through the online Toolbox developed in Module 2 and through face-to-face or online training. The Platform will maintain a list of internal and external experts to advise individual members on the use of genotyping in different research and breeding applications.

2. Broker access to genotyping supplies and services. This work package will provide support and access

to companies and in-house capacities providing highly competitive, cost-effective genotyping supplies and services. This Module will negotiate with groups and companies for cost, turn-around time and quality of genotyping supplies and services. The objective will be to fund the verification of 10 assays for existing validated trait markers on a new platform (developing an assay for known markers and testing the assay across 94 samples) per AFS, when a new supplier is suggested by an AFS or external user, or approaches the Platform directly. This will enable AFS CRPs to judge the service supplied. Members of the Platform will have access to the best service provider through a common contract. Aggregating the genotyping demand from different AFS CRP is a pre-requisite for obtaining the lowest genotyping cost. It requires strong and well-organized planning and sample aggregation systems on the part of both breeding programs and service providers. Based on demand aggregation and specification of types of genotyping and preferred suppliers, incentive prices (the higher the combined volume, the lower the price; agreed on turn-around times and data formats) for high-throughput, automated genotyping services to AFS CRPs will be finalized. The Module will seek to provide access to both low- and high-density genotyping services. As for low-density genotyping services, a partnership between Intertek Group PLC and CGIAR centers (currently ICRISAT, IRRI, CIMMYT, IITA) is already being developed, led by ICRISAT and supported by the Bill and Melinda Gates Foundation (B&MGF). This collaboration will facilitate access to competitive, quality service for 1-10 markers at a price affordable to the current breeding programs. As for high-density genotyping services (i.e., genotyping-by-sequencing, arrays-based single nucleotide polymorphism (SNP) genotyping; per se sequencing), the Module will explore options with different providers such as Intertek Group PLC, BGI-Shenzhen, Macrogen Inc., DArT Pty. Ltd., Affymetrix Inc. and Illumina Inc. In addition, CIMMYT, ICRISAT, ILRI [BeCA] and IRRI [GSL] have in-house facilities developed either individually or through public-private partnerships which can be considered potential service providers.

This Module's objective will be to work with the Platform's Bioinformatics Module 5 so that the data generated from any low- or high-density genotyping platform may be efficiently curated, analyzed and stored through appropriate tools and databases.

3. Prospect new approaches and customization of new tools. This work package will work in close collaboration with ARIs and the private sector to assess the latest technology improvements and developments for both DNA extraction and genotyping. ARIs are often the earliest adopters of technologies for discovery, whereas the private sector adopts in an industrialized production-oriented manner for breeding. Use cases of collaboration with ARIs from individual AFS CRPs will be examined to provide information on the applicability of the latest technology. The work package will be continuously prospecting technology advances and will advise and guide the AFS programs accordingly. Under an uplift scenario, this objective could explore cross-AFS testing of new technologies and strategic investment in technology access; this could encompass not only new genotyping methods but also sampling technologies such as automated seed chipping.

Use of Module resources among work packages are projected in Table 3.3. The main cost drivers are explained in Table 3.4.

Table 3.1. Work packages and key milestones to be funded by the Platform.

	Milestones = Output targets					
Work packages = Objectives	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1 Capacity enhancement	Yearly: • Develop use cases and develop/contribute to implementation guidelines for genotyping application in discovery and breeding • Update and refine existing documents, remove those no longer appropriate/applicable or when reviews are negative. • Contribute to courses and workshops • Enlist expertise in marker conversion from SSRs/INDELS to SNP-based platforms					
2 Broker access to shared services and supplies	Yearly: • Obtain and aggregate AFS demand for supplies and services o Determine cross-AFS ▪ Genotyping platform preferences ▪ Minimum genotyping quality criteria ▪ Maximum permissible turnaround time for genotyping applications ▪ Minimum number of samples required (at defined unit costs) ▪ Minimum number/volume of supplies required ▪ Minimum marker conversion rate ▪ Number of markers for marker conversion ▪ Etc. • Use collated demand information to broker potential arrangements with service providers and solicit pricing feedback from AFS • Finalize brokering of supplies and services and obtain minimum order commitments from AFS • Obtain feedback from service providers and AFS clients and document issues, concerns and positive feedback collating to form a review for the Trait Discovery and Breeding Toolbox.					
3 Technology prospecting	Prospect newer methods/approaches for sampling/genotyping; use inputs from participating AFS, ARIs, private sector partners and technology developers/providers; evaluate costs and constraints for application in discovery and breeding. Prepare annual review paper for posting in the Trait Discovery and Breeding Toolbox.					

Table 3.2. Key milestones funded by existing bilateral projects.

Project	Work package	2017	2018	2019	2020	2021	2022
1 High-throughput genotyping project (HTPG)	Broker access to shared services and supplies	Services to AFS implemented for single-plex genotyping and DNA extraction	Services to AFS implemented for single-plex genotyping and DNA extraction				
2. Integrated Genotyping Support and Service (IGSS)	Capacity enhancement	Provide support to breeders and other scientists in integrating DNA marker technology and genomic tools in the development and release of new cultivars	Provide support to breeders and other scientists in integrating DNA marker technology and genomic tools in the development and release of new cultivars				
3. Seeds of Discovery (SeeD)	Capacity enhancement	Provide support to breeders and other scientists in integrating DNA marker technology and genomic tools in the development and release of new cultivars	Provide support to breeders and other scientists in integrating DNA marker technology and genomic tools in the development and release of new cultivars				

Table 3.3. Use of Base and Uplift budgets among work packages.

Base Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1 Capacity enhancement	$562,775	$590,913	$620,459	$651,482	$684,056	$718,259
2 Broker access to shared services and supplies	$302,952	$318,100	$334,005	$350,705	$368,240	$386,652
3 Technology prospecting	$70,389	$73,909	$77,604	$81,485	$85,559	$89,837
Grand Total	**$936,116**	**$982,922**	**$1,032,068**	**$1,083,672**	**$1,137,855**	**$1,194,748**

Uplift Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1 Capacity enhancement	$783,265	$822,429	$863,550	$906,728	$952,064	$999,667
2 Broker access to shared services and supplies	$464,072	$487,276	$511,640	$537,222	$564,083	$592,287
3 Technology prospecting	$280,959	$295,006	$309,757	$325,245	$341,507	$358,582
Grand Total	**$1,528,296**	**$1,604,711**	**$1,684,947**	**$1,769,194**	**$1,857,654**	**$1,950,536**

Table 3.4. Explanations of the costs in relation to the planned 2022 outcomes.

Module	2022 Outcomes	Scope: Base budget	Scope: Uplift budget	Explanations of the costs in relation to the planned 2022 outcomes
Module 3: Genotyping/ sequencing tools and services	Common genotyping services	5-10 users	> 15 users	
	Marker conversions to SNP-based platforms or best practices documentation for genotyping/sequencing in ToolBox	8 use cases per year	> 12 use cases per year	Annual budget to members increases from US4 410,000 to US$ 594,000
	Training	16 participants per year	55 participants per year	Annual training budget increases, from US$ 27,000 to US$ 94,000
	Expert consultations or external marker conversions to SNP-based platforms	5 per year	> 7 per year	Annual consultant budget increases from US$ 80,000 to US$ 114,000

3.3.1.3 Science quality

Multi-national companies have fine-tuned the estimation of demand volumes and timing and have optimized systems to meet the genotyping and sequencing needs of their major commodities. They generate large efficiencies and keep costs down by spreading them across many individual breeding units. Genotyping is typically implemented in-house with focus on a few genotyping technologies. While effective for the private sector, this may not be an optimal method for the CGIAR, which deals with a wider range of commodities and use cases, and overall substantially lower investments. Therefore, the Platform's predominant choice will be flexible, out-outsourced approaches that can be selected based on use cases and readily changed as technologies evolve. In-house options will be considered as Platform-promoted solutions where competitive in terms of price and turn-around time.

The aim of this Module is not to be prescriptive but to broker access to supplies and services demanded by multiple AFS CRPs and to negotiate guaranteed best pricing and service standards (data quality, turn-around time) from suppliers, based on volumes submitted and with prices decreasing as the combined volume increases. Initial interactions with new service providers will require test genotyping to assess and compare outputs of different platforms. Clients of selected platforms and service providers will be required to provide feedback on service metrics and perceptions of quality against a client-defined list of minimum quality criteria. These customer and service provider satisfaction surveys will be used to formulate reviews which will be made public through the web platform developed in Module 2.

AFS clients will be supported through the provision of recommendations regarding the inclusion of blind replicates and controls as part of a user guide of recommended best practices compiled by AFS, service providers and other experts. Service providers who fail to meet quality metrics will be removed as suppliers from the Genotyping Module. AFS groups who fail to supply tissue or DNA of adequate quality to service providers will be offered training in collaboration with service providers.

The array of technologies available for genotyping range from single-plex markers to sequence-based applications such as genotyping-by-sequencing. The choice of a specific technology depends on the specific application (e.g., selection for a few markers *versus* genomic selection), genomic complexity of the species of interest, trait complexity and the availability of resources such as reference genomes. The current focus when genotyping for both discovery and breeding is on SNP and presence/absence variation. Technologies range from single-plex, single-marker assays to genotyping-by-sequencing. Currently, re-sequencing and whole genome sequencing are used for SNP discovery applications but not for genotyping. The current focus will be on technologies specifically generating genotypic data rather than sequence data as such.

The current panel of technologies available offers a somewhat bewildering array of potential methods and applications. Even within commodities where genotyping application is more routine, the selection of methods is not always obvious. To better enable selection of technologies across ASF CRP projects, the Genotyping Module will serve two functions. The first is to develop and provide use case and implementation documentation to better enable technology selection, and link AFS CRPs with external experts. The second is to monitor and, through discussions with early adopters in ARIs and the private sector, to evaluate the technological advances in genotyping and provide feedback on trends to the AFS community through the Toolbox described in Module 2.

3.3.1.4 System linkages

Investments by AFS CRPs and external users. Users of the genotyping brokering service are expected to invest time in the generation of accurate forecasting data for their genotyping and supply needs. Accountability for the forecast data will lie with each member and when services are brokered. Members will have to guarantee their minimum order volume to obtain the lowest possible pricing. Given that the number of samples are contingent on funding of (often short term) projects, such forecasts will never be very precise. Contracts will seek to broker incentives systems which will further lower prices if greater volumes are being achieved. Still, the AFS need to provide projected demand in real time and have much stronger forecasting accountability, which may need to be tied to members' contractual obligations. Users of genotyping services will be responsible for meeting quality standards for sample submission and for providing feedback. Attempts to consolidate requirements and broker access to improved genotyping pricing have been made previously through the Generation Challenge Program (GCP). Issues (price, data turnaround) were sometimes not shared with the GCP to enable clearer resolution of common issues. It is hence essential that the Module Leader receives clear feedback on any issues and concerns to facilitate empowered actions.

The costs of converting existing high-demand, gel-based markers to SNP-based markers and proper validation of the latter are borne by the individual AFS supported by expertise provided by the Genotyping Module. Covering the costs of genotyping materials and supplies is the responsibility of the individual AFS CRPs or genebanks, as are associated costs for sampling and DNA isolation, quantification and quality assessment and for sending samples to service providers. The AFS will provide use case and implementation information to the Genotyping Module and will work with the Module to document and periodically review these in a clear and consistent manner. Knowledge of new technologies and suppliers developed/discovered within individual AFS will be shared with the genotyping platform enabling cross-AFS access and opportunity for exploration.

Benefits to AFS CRPs and external users. The Genotyping Module will provide individual AFS with access to lower cost, timely, quality guaranteed, state-of-the-art genotyping services. More effective and cost efficient services will enable breeders to adopt genotyping technologies within their breeding programs and, at the same time, offer opportunities to broaden discovery and application. Enhanced use of genotyping has strongly benefited the larger multinational companies by improving quality control and accelerating genetic gains through faster selection of superior germplasm/individuals. Dynamic application of genotyping within the AFS offers opportunities to broaden the genetic diversity of breeding by initiating many more crosses and using genotypic selection to rapidly and cost effectively lower population size and advance only those entities of higher genetic merit.

Outcome at the portfolio level. Adoption of the most appropriate low cost, efficient and effective genotyping technologies will enable and enhance the application of genomics-assisted breeding and discovery across AFS CRPs and support the characterization of CGIAR genebank holdings. Greater understanding of genetic diversity and tracking of desirable genomes during the selection process in a cost-efficient and streamlined manner are essential for breeders in the AFS CRPs to be able to enhance rates of genetic gain and develop more diverse breeding products, including by more proactive understanding and use of diversity, applying greater precision and intensities during selection, rapidly and repeatedly recombining the best alleles, saving on phenotyping and nursery costs, or ensuring better quality control and fewer errors in the breeding or seed production process.

3.3.1.5 Climate Change

Selection of relevant traits and markers and broadening the genetic basis for climate change-related traits are at the core of most AFS breeding programs and need support from suitable high-throughput genotyping platforms. Drought, heat and waterlogging tolerance are complex traits whose breeding gains can be accelerated with genome-wide selection approaches (Beyene et al., 2015; Rouf Mir et al., 2012). With the unpredictability of weather conditions increasing and new pest and diseases emerging, strategies for establishing greater resilience in agricultural systems need to introduce more genetic variability and polygenic resistance in crops and animals, both of which can be facilitated with genomic information (Chakraborty and Newton, 2011). These are well-known concepts, shown and tested in proof-of-concept type projects, yet investments have been lacking to mainstream suitable approaches in major breeding programs targeting climate change-affected regions in the developing world. It is not an individual research project but the overall volume of breeding germplasm developed by CGIAR, NARS and private sector partners that needs to benefit from best practices in order to result in effective climate change adaptation of agricultural commodities grown by farmers in the next decades. The Excellence in Breeding Platform intends to change this by enabling access to user-tested tools and approaches that support streamlined genotyping (Modules 3 and 5) and phenotyping (Modules 4 and 5) for climate change-relevant traits within an actual breeding context (Module 2).

3.3.1.6 Capacity development

Capacity building in the first two years of the project will focus on those scientists directly involved in the Genotyping Module, including: (i) relevant platform upstream genomics implementation staff; and (ii) CGIAR and NARS breeders in the AFS CRPs. Training will focus on building capacity in forecasting, and in defining and implementing quality sampling and tracking procedures for effective service implementation. In addition, specific expertise and training on marker conversion will be sought to be able to convert currently used gel-based markers to more efficient SNP-based markers.

In a parallel program phase, capacity building activities will be expanded to focus on upgrading the skills of CGIAR and NARS breeders. This will be done using both virtual and face-to-face meetings and aligned with training done in Module 2. The CoP associated with the Genotyping Module will work on specific use case implementation guides. The use cases will provide specific focus on the genetic complexity of the trait or species, and the desired discovery or breeding outcome. Implementation guide contributions will focus on practicalities of implementation and will provide recommendations on critical junctures such as sample tracking, inclusion of quality control measures and breeding program modifications to maximize the value from genotyping applications. The adoption of new genotyping or sequencing technologies in breeding programs is a significant undertaking. In some cases, a major change in the structure and size of the breeding populations may be needed. Breeders may need to suspend ongoing activities while they begin to implement a new strategy, or they may run the two strategies in parallel, slowly reallocating resources from one to the other; the latter option would require significant additional resources for breeding programs. Breeders will hence need to consider these issues when designing their implementation strategy.

3.3.1.7 Intellectual asset and open access management

The Platform will serve as a broker of genotyping services. Products submitted to and data generated by genotyping service providers will remain the intellectual property of the users with neither the Platform nor the service provider gaining any rights to the germplasm or data. Members of this Module will need to sign an agreement that contains the requirements for Platform service use and supply provisions. Platform staff will negotiate services with input from finance and legal experts. Pricing agreements reached with service providers will, if required by service providers, remain confidential.

Members contributing to this Module shall ensure proper stewardship of their intellectual property as well as intellectual property belonging to other parties who have granted and confirmed permission to use. All parties using third party intellectual property must do so as part of any agreement they sign for this Module.

Intellectual assets developed with Platform funding (including tools, germplasm, inventions, improvements, data, processes, technologies, software, trademarks, publications and other information products) will be made available to the public under appropriate licensing conditions. In circumstances where third party intellectual property is utilized, conditions may be added as permitted under Section 6 of the CGIAR Principles on the Management of Intellectual Assets, which establishes the conditions for 'limited exclusivity' or 'restrictive use' agreements. Open-source solutions are preferred to facilitate inter-connectivity of tools and wide adoption.

Management of pay-to-access third-party commercial software, computational infrastructure or expert advice may require cross-member licensing agreements which may be beneficial to providers and could allow for greater use. User feedback on the web platform will demonstrate if tools or services are performing poorly. The web administrator will need to ensure that user feedback is based on fact.

3.3.1.8 Module management

A Module Leader will be recruited from among the executing partners with substantive genotyping activities linked to an active breeding program (CIAT, CIMMYT, CIP, ICRISAT, IITA, ILRI, IRRI). This person must have experience with: application of different genotyping methods in breeding, medium- to high-throughput genotyping, liaison with service providers, and the complexities of different breeding systems and legalities of relevant AFS members and their host countries. Specific expertise of genotyping applications in breeding from the industry will be requested and paid for as needed to better inform the approaches in this Module. Three other part-time positions are required to consolidate logistics and forecasting in Asia, Africa and Latin America. These positions can be recruited from within existing AFS.

The Module Leader will report to the Platform Leader with the Expert Advisory Group contributing to the performance assessment. An Expert Advisory Group will be formed composed of members contributing to the CoP, with no more than one member per AFS CRP plus genebanks. This group will meet virtually to discuss applications and request specific input from experts, take accountability for forecasting information, define quality criteria for respective applications, discuss and agree on the brokering of specific services, document progress and issues, and define which needs should be addressed through training in collaboration with Module 2. A quorum of five group members representing five AFS is needed to make decisions. Each AFS CRP has to agree to be part of a brokered contract. AFS CRPs who do not commit may still solicit services from providers but they are not guaranteed the same negotiated terms. Members of the Expert Advisory Group are responsible for sourcing wider feedback from their relevant constituencies and to promote the availability of the services.

3.3.2 Module Budget Narrative

3.3.2.1 General Information

Platform Lead Center's Name: CIMMYT

Module title: Module 3: Genotyping/sequencing tools and services

Center Location of Platform Leader:

3.3.2.2 Summary

Total Module budget summary by sources of funding (USD)

Funding Needed	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2	187,223	196,584	206,414	216,734	227,571	238,950	1,273,476
W3	374,447	393,169	412,827	433,469	455,142	477,899	2,546,952
Bilateral	374,447	393,169	412,827	433,469	455,142	477,899	2,546,952
Other Sources	-	-	-	-	-	-	-
	936,116	982,922	1,032,068	1,083,672	1,137,855	1,194,748	6,367,381

Funding Secured	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2 (Assumed Secured)	187,223	196,584	206,414	216,734	227,571	238,950	1,273,476
W3	-	-	-	-	-	-	-
Bilateral	662,129	270,000	180,000	-	-	-	1,112,129
Other Sources	-	-	-	-	-	-	-
	849,352	466,584	386,414	216,734	227,571	238,950	2,385,605

Total Module budget by Natural Classifications (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
Personnel	412,566	433,194	454,854	477,597	501,477	526,550	2,806,238
Travel	51,571	54,149	56,857	59,700	62,685	65,819	350,780
Capital Equipment	29,469	30,942	32,490	34,114	35,820	37,611	200,446
Other Supplies and Services	258,019	270,920	284,466	298,689	313,623	329,305	1,755,021
CGIAR collaborations	0	0	0	0	0	0	0
Non CGIAR Collaborations	70,438	73,959	77,657	81,540	85,617	89,898	479,110
Indirect Cost	114,054	119,757	125,745	132,032	138,634	145,565	775,787
	936,116	982,922	1,032,068	1,083,672	1,137,855	1,194,748	6,367,381

Total Module budget by participating partners (signed PPAs) (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
CIMMYT	0	0	0	0	0	0	0
Platform Leader	111,989	117,588	123,468	129,641	136,123	142,929	761,738
Module Leader	462,128	485,234	509,496	534,970	561,719	589,805	3,143,351
AFS Members	362,000	380,100	399,105	419,060	440,013	462,014	2,462,292
	936,116	982,922	1,032,068	1,083,672	1,137,855	1,194,748	6,367,381

3.3.2.3 Additional explanations for certain accounting categories

In the Module budget by natural classification, the budget for Platform Leader, Module Leaders and AFS members is summarized in the line items Personnel, Travel, Capital Equipment, and Other Supplies and Services. The Module budget by participating partner describes who manages (not who uses) the budget. E.g. the Platform Leader manages all subcontracts to AFS members and external contractors and consultants for streamlined issuing of such contracts. The Platform Leader also manages the open access budget.

3.3.2.4 Other Sources of Funding for this Project

Other sources of funding are described in Table 16.

3.3.2.5 Budgeted Costs for certain Key Activities

	Estimate annual average cost (USD)	Please describe main key activities for the applicable categories below, as described in the guidance for full proposal
Gender	424,492	Increasing to US$ 693,023 in the Uplift budget. Outcome expectation: At least 40% of the users will be female.
Youth (only for those who have relevant set of activities in this area)	707,487	Increasing to US$ 1,155,038 in the Uplift budget. Outcome expectation: At least 2/3 of the users will be students and young scientists.
Capacity development	1,061,230	Increasing to US$ 1,732,556 in the Uplift budget. The entire Module/Platform is targeted at capacity building (see Theory of Change).
Impact assessment	-	Included in CRP Management costs, not in Module specific costs
Intellectual asset management	-	Included in CRP Management costs, not in Module specific costs
Open access and data management	22,956	Increasing to US$ 45,913 in the Uplift budget
Communication	-	Included in CRP Management costs, not in Module specific costs

3.3.2.6 Other

3.3.3 Module Uplift Budget

Outcome Description	Amount Needed	W1 + W2 (%)	W3 (%)	Bilateral (%)	Other(%)
1) Establishment of best practices for phenotyping and environmental analysis through a community of practice. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	249,960	20	40	40	0
2 Broker acc 2) Support services from ARIs for A. experimental design and analysis of precision and high- throughput phenoty+A10:A19	182,654	20	40	40	0
3 Technology prospecting. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	238,712	20	40	40	0

3.4 Module 4: Phenotyping tools and services

3.4.1 Module Narrative

3.4.1.1 Rationale, scope

Although the cost of genotyping has rapidly decreased over the past two decades, phenotyping costs have remained relatively static (Fiorani and Schurr, 2013; Furbank and Tester, 2011; Rahaman et al., 2015). Phenotyping remains by far the most expensive and time-consuming activity for breeding programs. It is hence essential to implement improvements that lead to greater genetic gains including: precision and high-throughput remote or ground sensing technologies such as tractor or airborne sensors (Araus and Cairns, 2014) or 3-D laser scanning (Vadez et al., 2015); improved analyses of genotype-by-environment-by-management (GxExM) interactions; increased efficiency in routine physico-chemical analyses; and mechanization and automation of seed preparation, field and greenhouse trials. These advances increase genetic gains by: (i) minimizing environmental variability in field trials and increasing the precision of measured traits (Araus and Cairns, 2014); (ii) increasing the relevance of selections or the choice of appropriate parents; (iii) enabling breeders to measure traits at greater speed, in particular those associated with abiotic stress tolerance, disease resistance, biomass production, bulking of underground storage organs, or rooting patterns (Khan et al., 2016; Villordon et al., 2012; Zaman-Allah et al., 2015); (iv) supporting the collection of greater quantities of non-destructive data at lower cost to increase population sizes (Cooper et al., 2014); (v) when used in combination with genomic selection training populations, supporting a better understanding of the genetic architecture of traits (Cobb et al., 2013; Hammer et al., 2006); and (vi) reducing human error in the management of breeding programs.

Mechanization, automation, precision and high-throughput phenotyping have attracted huge investments in high-income countries. This Platform intends to exploit high leverage investments and quick wins that can be implemented in CGIAR and NARS breeding programs. We propose to develop a CGIAR-wide community of practice and a hub for phenotyping support services to facilitate mechanization and automation, reduce the cost of routine phenotyping for selection, and increase adoption of high-throughput phenotyping tools and GxExM analysis tools across the AFS CRPs and external users. CGIAR breeding programs have the capability to simultaneously and repeatedly generate massive amounts of phenotype data through the use of remote sensing applications that result in improved and more rapid assessments of yield, biomass, flowering, stress tolerance or disease resistance (Araus and Cairns, 2014; Fahlgren et al., 2015; Ghanem et al., 2014). The current bottleneck is caused by having to convert such data to real-time “breeding values” for a large number of plots and progenies that are simultaneously being measured, and link this information with genotype information to routinely feed into gene discovery and cultivar development programs. Joining efforts among CGIAR programs and with public and private sector capacities in high-income countries will greatly accelerate the identification and extension of best practices among CGIAR breeding programs and NARS partners.

The private sector and ARIs have made substantial investments and advances in the development of tools and strategies to capture and analyze phenotypic information (Furbank and Tester, 2011). As a result, this Module will focus on vetting, promoting and understanding existing technologies across CGIAR and NARS breeding programs to improve operational excellence rather than the development of novel phenotyping tools within the CGIAR.

The grand challenge is to drastically increase the quantities of high quality phenotype data in order to

accelerate genetic gains in breeding programs of the CGIAR and NARS partners. Although some phenotyping challenges are specific to a single commodity or AFS CRP, many phenotyping traits and methods are generic (e.g., field-based remote sensing, routine physico-chemical laboratory analysis, approaches to mechanization and automation). Expertise in this area, however, is scarce, often requires interdisciplinary insights (physiology, quantitative genetics, biometrics, data analytics and management), and should be shared for more rapid progress. In addition, phenotype data represent, by definition, interaction with an environment. GxExM interactions are a major challenge for selection, especially for complex traits such as yield, and need to be addressed as a top priority, particularly in the context of genomic selection and gene-to-phenotype predictions. This Module would help foster exchange between teams dealing with similar issues as a means of progressing toward best practices (e.g., Kholova et al., 2013; 2014; Vadez et al., 2012).

Likewise, breeding programs face common challenges to mechanize and automate routine phenotyping, access reliable low-cost physico-chemical laboratory analyses, and reduce environmental variability in field trials while under budget constraints and while using outdated research station infrastructure. Baseline metadata, weather data, the equipment used, and the way that data are stored and managed are largely out of date, not systematically collected, or not available at CGIAR-wide level. CGIAR and NARS breeding programs will be analyzed as part of Module 1. These data, augmented with other lines of inquiry regarding routine physico-chemical analysis capacities and their costs, mechanization and automation in breeding programs, and management and infrastructure in research stations, will be used to establish a baseline for Platform members from which recommendations for "quick wins" can be made including inexpensive service providers and low-cost/state-of-the-art phenotyping equipment. The results of this baseline assessment will help the CGIAR as a whole, as well as individual centers, NARS, CRPs and investors, to identify strategic priorities for high leverage capital investments.

3.4.1.2 Objectives and targets

The Phenotyping Module will be organized into four work packages (Table 4.1).

1. Establishment of best practices for phenotyping and environmental analysis through a community of practice. This work package assesses the types of phenotype data collected, adoption of high-throughput tools and methods, and barriers to adoption of modern phenotyping strategies among members for accelerating the development and implementation of best practices among a wider range of users. In addition to this community of practice being open to ARIs, NARS and the private sector, Module staff will link with existing plant phenotyping networks (e.g., European Plant Phenotyping Network), the private sector and advanced research institutes (ARIs) to assess current state-of-the-art approaches, develop online learning tools and videos in collaboration with members (to be featured in the Module 2 Toolbox), organize joint capacity building workshops and facilitate access to existing phenotyping platforms for training or use. Members' benefit will consist of accelerated adoption of best practices and faster adoption of recent advances in the capture and analysis of image-based phenotyping.

Members will also share best practices in GxExM analysis and gene-to-phenotype models for improving selections and predicting target environments and management practices for new cultivars, building on on-going work in certain crops (e.g., Kholova et al., 2013) and external teams (e.g., Hammer et al., 2006). The specific targets are to assess the commonality of this challenge, develop data standards to support generic GxExM analysis and gene-to-phenotype predictions, and test and adapt generic tools to breeding programs targeting the developing world.

2. Support services from ARIs for A. experimental design, data management, and analysis of precision and high-throughput phenotype data, and B. GxExM analysis and genotype-to-phenotype predictions. This work package is to ensure that CGIAR and NARS breeding programs receive the support and capacity needed

to design well-conceived high-throughput phenotyping and GxExM analysis protocols. The core idea would be to give them access to existing expertise, technology, know-how available particularly in ARIs. For example, in the past few years the capacity to image plants/crops has increased tremendously. Spectral imaging enables researchers to "see" plants/crops from a multitude of spectral signatures. Unfortunately, scientists still need to carry out a lot of basic work to turn these extremely rich data into information that makes biological sense. Several ARIs and centers work on linking spectral indices to critical phenotypes. Once they take this critical step, breeding programs can increase the number of traits and plots they can evaluate, thereby increasing selection intensity and providing data that can be used to understand genetic trait architecture. This work package will also help facilitate the integration of available tools for GxExM analysis and gene-to-phenotype predictions. It will establish the necessary linkages with the management concepts and standards developed for environmental data by the Platform on Big-Data, Information and Knowledge.

3. Coordination and procurement of phenotyping services for routine analyses of physico-chemical composition and functional properties in plant and animal materials in support of breeding. Breeding programs can increase their operational efficiency by identifying and using dedicated service laboratories within and outside the CGIAR system to generate routine phenotype data (e.g., physico-chemical composition and functional properties) rather than attempting to generate all information "in-house." This work package will increase the phenotyping capacity of CGIAR and NARS programs by identifying reliable laboratories for assessing these properties in plant and animal materials, making sure such information is available to users and negotiating group rates. Specific targets include a survey of laboratories, capacities and costs in coordination with the assessment of breeding programs in Module 1, quality audits of proposed service laboratories within and outside the CGIAR, and a list of vetted service labs with negotiated costs for generic physico-chemical and plant functionality phenotyping services which can be updated annually.

4. Needs assessment and consultancy services to improve mechanization and automation across CGIAR and NARS breeding programs, as well as infrastructure and management of research stations. Many CGIAR and NARS breeding programs are poorly mechanized and still rely on planting and harvesting by hand. Likewise, decades-old research station infrastructure is in decline and requires updating. In order to increase breeding program efficiency, CGIAR and NARS must mechanize, automate, and invest in research station upgrades, including modern planting equipment, fully automated combine harvesting (for grain crops), and precision irrigation. The 2017 targets are a series of coordinated assessments of the current state of mechanization and automation across the CGIAR and NARS, suitable equipment and mechanization tools available for each commodity, and current state of research station infrastructure. Based on this information, we will recommend "quick wins" to participating breeding programs (e.g., sample tracking and laboratory workflows which increase operational efficiency and reduce errors with relatively little financial investment) and generate an inventory of robust and easy-to-service mechanization and automation approaches suitable for developing world conditions. Given that quite a range of CGIAR and NARS breeding programs are co-located, the information will also be used to develop recommendations for high-priority investment needs that Centers and AFS CRPs should strategically invest in and to design and implement training courses for experiment station managers.

Use of Module resources among work packages are projected in Table 4.2. The main cost drivers are explained in Table 4.3.

Table 4.1. Work packages and key milestones to be funded by the Platform.

	Milestones formulated as output targets					
Work packages = Objectives	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1) Establishment of best practices for phenotyping and environmental analysis through a community of practice	Survey to assess phenotype and environmental data collected, adoption of high-through-put tools, GxExM and gene-to-phenotype methods, and barriers to adoption in coordination with BPAT Workshop on existing practices, with ARI and private sector participation; identification of quick wins Join and participate in existing plant phenotyping networks	Prioritization and investment in Platform interventions including online learning tools and videos Liaise with private sector and ARIs to access current state-of-the-art technology (Phenotyping)	Workshop to exchange best practices and challenges Test and adapt alternative approaches in members' breeding programs; user feedback (Phenotyping) Discuss the development of ISO 9000 standards (Phenotyping)	Prioritization and investment in Platform interventions including online learning tools and videos Liaise with private sector and ARIs to access current state-of-the-art technology (GxExM and gene-to-phenotype methods) Develop information in support of ISO 9000 standards (Phenotyping)	Workshop to exchange best practices and challenges Test and adapt alternative approaches in members' breeding programs; user feedback (GxExM and gene-to-phenotype methods) Discuss the development of ISO 9000 standards (GxExM and gene-to-phenotype methods)	Finalize information in support of ISO 9000 standards Survey of best practices among member breeding programs
2A) Support services from ARIs for experimental design and analysis of precision and high-throughput phenotype data	Consult with breeders and ARIs to identify tools for capture and analysis of high-throughput data – Priority setting	Testing and adaptation of best generic tools in interaction with distinct members – Trait set I	Testing and adaptation of best generic tools in interaction with distinct members – Trait set I Integration in bioinformatics platform – Launch of Trait set I	Testing and adaptation of best generic tools in interaction with distinct members – Trait set II User survey and trouble-shooting	Testing and adaptation of best generic tools in interaction with distinct members – Trait set II Integration in bioinformatics platform – Launch of Trait set II	User survey and trouble-shooting Impact assessment of new tools and practices

2B) Support services from ARIs for GxExM analysis and Genotype-to-Phenotype predictions	Consult with breeders and ARIs to identify approaches for GxE analysis – Priority setting	Testing and adaptation of best generic tools in interaction with distinct members – GxE	Testing with members Integration in bioinformatics platform User survey and trouble-shooting	Consult with breeders and ARIs to identify approaches for Genotype-to-Phenotype predictions	Testing and adaptation of best generic tools in interaction with distinct members – Genotype-to-Phenotype predictions	Testing with members Integration in bioinformatics platform User survey and trouble-shooting
3) Coordination and procurement of phenotyping services for routine analyses of physico-chemical composition and functional properties in plant and animal materials in support of breeding	Survey of laboratories, capacities and costs in coordination with BPAT	Quality audit	Generate a list of vetted service labs and costs for generic physico-chemical phenotyping services	Update recommended service provider list as needed	Update recommended service provider list as needed	Follow-up survey of laboratories, capacities and costs
4) Needs assessment and consultancy services to improve mechanization and automation across CGIAR and NARS breeding programs as well as infrastructure and management of research stations	Generate an inventory of the current state of mechanization and automation across the CGIAR and NARS in coordination with Module 1 Assess current state of research station infrastructure	Exchange of quick wins (e.g., sample tracking and laboratory workflows) Inventory of mechanization and automation approaches suitable for developing world conditions (robust, easy-to-service)	Joint training for experiment station managers Analysis of recommended high-priority investments for Centers and Agri-Food CRPs (e.g., research station infrastructure in disrepair, key equipment for mechanization)	Documentation of scale-specific approaches to mechanization and automation Members (AFS CRPs, external) consultations and support to investments in high priority upgrades	Documentation of scale-specific approaches to mechanization and automation Members (AFS CRPs, external) consultations and support to investments in high priority upgrades	Follow-up assessment of mechanization and automation among members Follow-up assessment of research station infrastructure

Table 4.2. Use of Base and Uplift budgets among work packages.

Base Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1) Establishment of best practices for phenotyping and environmental analysis through a community of practice	$526,881	$553,225	$580,886	$609,930	$640,427	$672,448
2) Support services from ARIs for A. experimental design and analysis of precision and high- throughput phenotype data; B. GxExM analysis and Genotype-to-Phenotype predictions	$740,804	$777,844	$816,736	$857,573	$900,452	$945,474
3) Coordination and procurement of phenotyping services for routine analyses of physico-chemical composition and functional properties in plant and animal materials in support of breeding	$63,495	$66,670	$70,004	$73,504	$77,179	$81,038
4) Needs assessment and consultancy services to improve mechanization and automation across CGIAR and NARS breeding programs as well as infrastructure and management of research stations	$202,832	$212,973	$223,622	$234,803	$246,543	$258,870
Grand Total	**$1,534,011**	**$1,610,712**	**$1,691,248**	**$1,775,810**	**$1,864,600**	**$1,957,830**

Uplift Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1) Establishment of best practices for phenotyping and environmental analysis through a community of practice	$767,711	$806,097	$846,402	$888,722	$933,158	$979,816
2) Support services from ARIs for A. experimental design and analysis of precision and high- throughput phenotype data; B. GxExM analysis and Genotype-to-Phenotype predictions	$1,436,682	$1,508,516	$1,583,942	$1,663,139	$1,746,296	$1,833,611
3) Coordination and procurement of phenotyping services for routine analyses of physico-chemical composition and functional properties in plant and animal materials in support of breeding	$105,420	$110,691	$116,225	$122,037	$128,139	$134,546

4) Needs assessment and consultancy services to improve mechanization and automation across CGIAR and NARS breeding programs as well as infrastructure and management of research stations	$519,599	$545,579	$572,858	$601,501	$631,576	$663,155
Grand Total	**$2,829,413**	**$2,970,883**	**$3,119,427**	**$3,275,399**	**$3,439,169**	**$3,611,127**

Table 4.3. Explanations of the costs in relation to the planned 2022 outcomes.

Module	**2022 Outcomes**	**Scope: Base budget**	**Scope: Uplift budget**	**Explanations of the costs in relation to the planned 2022 outcomes**
Module 4: Phenotyping tools	HTP phenotyping	3 successful institutional users reducing phenotyping cost by >25%	> 5 successful institutional users reducing phenotyping cost by >25%	Annual budget to members increases from US$ 616,000 to US$ 1,005,000; ARI collaboration increases from US$ 427,000 to US$ 963,000
	GxExM analyses	> 5 routine users	> 10 routine users	
	Mechanization and automation	> 3 institutional beneficiaries	> 8 institutional beneficiaries	
	Best practices documentation for phenotyping/mechanization/automation in ToolBox	7 modules/use cases per year	>15 modules/use cases per year	
	Training	13 participants per year	50 participants per year	Annual training budget increases, from US$ 23,000 to US$ 84,000
	Expert consultations	> 4 per year	> 4 per year	Annual consultant budget decreases from US$ 88,000 to US$ 66,000; consultancy position is converted into a staff position.

3.4.1.3 Science quality

The rapid technological progress in certain fields such as imaging is opening tremendous opportunities for the phenotyping community, but also poses a number of challenges. One of these challenges is to be carried away by the capacity to generate scores of phenotyping data – for instance, terabytes of dense image data (3-D, hyperspectral data cubes) – that have little immediate biological relevance and use in breeding. The scientific quality of this Module will be ensured in part based on its capacity to organize a community of practice that involves relevant partners (CGIAR, ARI, private sector, NARS) and that is capable of harnessing recent technological advances and applying modern tools and strategies to generate relevant phenotypic information which contributes to improved efficiency in cultivar development. There are several international groups who are working in this area. The focus will be on building from the achievements of those groups and ensuring the adaptation of approaches that can be implemented in the context of breeding programs in the developing world.

Science quality will also arise from the increased quality of the data that are generated. However, it is not sufficient to consider quality only from the standpoint of the techniques that are used to measure a number of plant traits, or the number of repeated measurements that are taken. Documenting datasets with rich metadata on experimental conditions is often overlooked and is an equally important target of this community of practice (minimum datasets), especially with regard to GxExM interactions that sink so many breeding efforts. Therefore, the community of practice will need to work toward developing an ISO 9000 quality management approach.

Overall, the aim of this Module is to increase the rate of genetic gain in CGIAR and NARS breeding programs by improving targeted phenotyping, minimizing environmental variability in field trials, and generating more precise phenotyping information (improved experiment station infrastructure and precision phenotyping of targeted traits). Therefore, the scientific quality of this Module should be demonstrated by increased selection efficiency across CGIAR and NARS breeding programs. The relevance of various datasets can be assessed ex-ante using selection indices that are based on heritabilities and genetic correlations with target traits (Richard et al., 2015), through association mapping studies (Pauli et al., 2016), or ex-post through actual selection experiments (Rutkoski et al., 2015).

In collaboration with the phenotyping efforts within each of the AFS CRPs, science quality can be monitored through:

- Publications on phenotyping in the AFS CRPs (methods, data, genetic analysis of key traits, etc.)
- Evidence of increased utilization of precision phenotyping and best practices in CGIAR and NARS breeding programs
- ISO data standards (metadata, weather, etc.)
- Increased selection efficiency in CGIAR and NARS breeding programs

In the area of mechanization and automation, substantive experience exists in the private sector, yet approaches need to be selected that are cost-effective in view of the size of breeding programs and robust and suitable given environmental conditions and available local technical support. As cross-systems data from work package 1 become available, the question is whether technological options could be developed in collaboration with low-tech savvy countries, such as China or India, that are more aligned with the needs and nature of breeding programs in lower-income countries (smaller-scale, decentralized, multi-purpose, easy-to-repair).

3.4.1.4 System linkages

Investments by AFS CRPs and external users: Within the CGIAR alone, there are a substantive number of projects that advance crop-specific learning in cassava (root biomass estimation through ground penetrating radar), chickpea (climate change resilient chickpea), maize (drought, nitrogen use efficiency, heat, virulent diseases), rice (drought, nitrogen use efficiency), sorghum (climate change resilient sorghum) and wheat (heat, drought, yield potential, virulent diseases). Together with experiences from ARIs and the private sector, they provide the basis for individual experiences of members contributing to the Module's best practices. AFS CRPs and external users will: (i) share feedback on phenotyping experiences and validated protocols; (ii) test and provide feedback on new tools and approaches, including negative feedback related to technologies, protocols, approaches; (iii) share a community of practice in terms of standardizing phenotyping approaches including experimental treatments and measurement protocols; (iv) implement data standards and support of open-access databases; (v) support laboratory services where competitive; (vi) participate in training as information providers/users; (vii) invest in crop- and location-specific mechanization; (viii) provide consultants with requisite expertise to help develop phenotyping capacity in CG client countries; and (ix) provide laboratory and field facilities, equipment, and staff with linkages to NGOs, NARS, and the private sector to promote synergism.

Benefits to AFS CRPs and external users include: (i) website with up-to-date information on relevant and tested phenotyping tools and approaches; (ii) accelerated learning of best phenotyping practices; (iii) investments in safe-bet equipment (versus those that may soon become obsolete or do not warrant the investment); (iv) access to a pool of consultants to help set up phenotyping platforms and resolve technical problems; (v) access to labs that provide high quality physico-chemical composition and functional properties assessments at best prices and with appropriate turn-around times; (vi) freeing up of resources through mechanization/automation and for expensive in-house lab analyses; and (vii) linkages to existing phenotyping entities in high-income countries (International Plant Phenotyping Network; European Plant Phenotyping Network), the private sector or specific CGIAR crops (such as the Expert Working Group on Wheat Phenotyping).

System-level benefits include: (i) scientists find needed information readily, reducing transaction time and the risk of costly mistakes; (ii) accelerated implementation of high-throughput or other best phenotyping practices; (iii) faster turn-around, more precise selection and greater selection intensities; (iv) faster genetic gains by incorporating more information into selection indices; (v) CGIAR scientists and external users move towards greater coordination of research protocols resulting in greater translatability of information across labs, environments, and crops; (vi) coordinated and more rigorous phenotyping approaches increase the application of shared data, increasing the medium- and long-term returns on investment in crop research; and (v) increased scope and better standardization of data provide more reliable inputs for crop simulation models that can be used to predict big picture scenarios, helping the CGIAR and other organizations to set science agendas.

Data handling: In collaboration with Module 5, the platform will manage a centralized repository of information about emerging and applied technologies, suppliers and users, experiences, rating of their application, cost and reliability, suppliers of technologies and information, cumulating experiences that are currently mostly found at crop-specific level (e.g., Pérez-Harguindeguy et al., 2013), so as to become a focal point for proposing and disseminating standards based on precedent and approval rating.

3.4.1.5 Climate Change

To maintain global food security, with the added challenge of climate change, crop research needs to adopt an integrated approach for best leverage of technology, expertise and infrastructure (Reynolds et al., 2016). The development of improved cultivars that can cope with the stresses of climate change is a major challenge with unified efforts across the AFS CRPs, implying that the methodological discussions in this Module will predominantly focus on "phenotyping for climate change." General circulation models do not accurately predict future rainfall but all consensually predict increases in temperature. Therefore, the focus will be on phenotyping approaches that allow estimating temperature impacts on the length of phenological stages, reproductive biology or evaporative demand and plant water status.

Phenological stages such as flowering and maturity are usually evaluated by doing simple but tedious measurements. The development of remote sensing techniques to measure flowering can increase breeding program efficiency. For instance, legume flowers have a specific spectral index that can be used to pinpoint flowering time. An inventory of methods and approaches will help to compare the effects of temperature on reproductive biology across crops and to account for confounding temperature effects on both phenology and reproductive biology (e.g., Prasad et al., 2006). Studies on the effect of high temperatures on evaporative demand and plant water status are ongoing in a range of crops. Transpiration response to increased vapor pressure deficit is being measured and mapped in several crops (e.g., pearl millet, Kholova et al., 2010, 2012; sorghum, Gholipoor et al., 2011; maize, Yhang et al., 2012; cowpea, Belko et al., 2013; chickpea, Zaman-Allah et al., 2011; peanut, Devi et al., 2009). High-throughput methods for measuring transpiration have recently been developed (Vadez et al., 2015 - https://youtu.be/M1bMpYvpcRc) and will be promoted through this Module.

3.4.1.6 Capacity development

Human capacity for phenotyping will be developed by making information available through the web platform, virtual meetings, exchange visits and biannual meetings among members, linked to relevant conferences. As part of the Toolbox in Module 2, a phenotyping website with updated resources, new literature, training materials and phenotyping protocols will be maintained as a resource base that AFS CRPs can use in training courses or workshops, particularly with NARS. Much of the material will be developed through the community of practice with a particular focus on easy-to-use, low-tech, standardized phenotyping protocols. Existing trait evaluation protocols and training materials from centers and ARIs will be complemented with videos that show and explain the phenotyping cycle, from conceiving the experiment to data capture and analysis, or detail aspects such as calibration of equipment, use of sensors, experimental design guidelines to allow high-throughput phenotyping with large numbers of genotypes, as well as best practices for storing and labeling planting materials to avoid mistakes and collect efficient metadata.

Coordinated assessments of the current state of needs, infrastructure, mechanization and automation will be used to develop recommendations for high-priority investments with greatest systems pay-off. In collaboration with Module 1, experts will be hired (from centers, ARIs or the private sector) to review existing capacities (station management, scope of operations, work flow mechanization/automation, environmental characterization, physico-chemical analyses and trait phenotyping capacities, phenotypic data storage, and processing capacity) and advise on high leverage investments that support best practices for medium to high-through phenotyping. New data processing pipelines will be made available through the Module 2 Toolbox in collaboration with Modules 2 and 5.

3.4.1.7 Intellectual asset and open access management

The primary beneficiary of this Module are farmers in low and middle income countries wherein the tools to be created will benefit the wider scientific research community around the world. The Module will produce, describe and display materials, technologies, and tools ranging from equipment, software, methods, traits, germplasm, and management technologies to information databases and publications. They may originate from the public or private sector.

Members contributing to this Module shall ensure proper stewardship of their intellectual property as well as intellectual property belonging to other parties who have granted and confirmed permission to use. All parties using third party intellectual property must do so as part of any agreement they sign for this Module.

Intellectual assets developed with Platform funding (including tools, germplasm, inventions, improvements, data, processes, technologies, software, trademarks, and publications) are made available to the public under appropriate licensing conditions. In circumstances where third party intellectual property is utilized, conditions may be added as permitted under Section 6 of the CGIAR Principles on the Management of Intellectual Assets, which establishes the conditions for 'limited exclusivity' or 'restrictive use' agreements. Open-source solutions are preferred to facilitate inter-connectivity of tools and wide adoption.

Management of pay-to-access, third-party, commercial software, computational infrastructure or expert advice may require cross member licensing agreements which may be beneficial to providers due to greater use. User feedback to the web platform will demonstrate if tools or services are poorly performing. The web administrator will need to ensure that user feedback stays fact based.

3.4.1.8 Module management

Two scientists/experts will be hired or contracted to manage this Module, in collaboration with members participating in the community of practice. The first position will manage work packages 1 and 2, in interactions with Modules 2 and 5, and the Big Data Platform. The second position (a consultancy in the Base budget) will manage work packages 3 and 4. The position(s) can be posted at either the Lead Center or another member that has (an) applied breeding program(s) targeting the developing world. Using a widely advertised competitive process, 1-3 ARIs will be selected to provide support services the analysis of precision and high-throughput phenotype data, GxExM analyses and gene-to-phenotype predictions. Options are CEPLAS, CSIRO, JIRCAS, Kansas State University, Rothamsted Research, the University of Arizona, the University of Barcelona, the University of Cordova, the University of Talca and others. Resources will be made available to AFS CRPs to contribute to the Platform's knowledge base, given that such documentation will require additional time investment. Temporary contractors and/or graduate students may be brought in to conduct baseline surveys.

An Expert Advisory Group will be formed with designated representatives from DLC, FTA, Livestock; MAIZE, RICE, RTB, WHEAT and the Genebank Platform. This group will meet virtually and provide feedback on the Module's workplan and performance and the performance of contributors; map phenotyping platforms and initiatives inside and outside the CGIAR; encourage interactions between phenotyping platforms; propose co-investments, for example, in a global network of managed-stress sites; coordinate testing; and advise on suitable troubleshooters to solve technical problems. AFS CRP members will receive a set amount of support services for each commodity/center. Additional services/time will need to be paid based on costs. Lists of recommended/trained contractors will be compiled by the scientists employed by the Module.

3.4.2 Module Budget Narrative

3.4.2.1 General Information

Platform Lead Center's Name: CIMMYT

Module title: Module 4: Phenotyping tools and services

Center Location of Platform Leader:

3.4.2.2 Summary

Total Module budget summary by sources of funding (USD)

Funding Needed	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2	306,802	322,142	338,250	355,162	372,920	391,566	2,086,842
W3	613,605	644,285	676,499	710,324	745,840	783,132	4,173,685
Bilateral	613,605	644,285	676,499	710,324	745,840	783,132	4,173,685
Other Sources	-	-	-	-	-	-	-
	1,534,011	1,610,712	1,691,248	1,775,810	1,864,600	1,957,830	10,434,211

Funding Secured	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2 (Assumed Secured)	306,802	322,142	338,250	355,162	372,920	391,566	2,086,842
W3	-	-	-	-	-	-	-
Bilateral	-	-	-	-	-	-	-
Other Sources	-	-	-	-	-	-	-
	306,802	322,142	338,250	355,162	372,920	391,566	2,086,842

Total Module budget by Natural Classifications (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
Personnel	506,331	531,648	558,230	586,141	615,449	646,221	3,444,019
Travel	75,347	79,114	83,070	87,223	91,585	96,164	512,503
Capital Equipment	36,167	37,975	39,874	41,867	43,961	46,159	246,001
Other Supplies and Services	304,606	319,836	335,828	352,619	370,250	388,762	2,071,900
CGIAR collaborations	0	0	0	0	0	0	0
Non CGIAR Collaborations	454,112	476,818	500,658	525,691	551,976	579,575	3,088,830
Indirect Cost	157,449	165,322	173,588	182,267	191,381	200,950	1,070,957
	1,534,011	1,610,712	1,691,248	1,775,810	1,864,600	1,957,830	10,434,211

Total Module budget by participating partners (signed PPAs) (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
CIMMYT	0	0	0	0	0	0	0
Platform Leader	524,263	550,476	578,000	606,900	637,245	669,107	3,565,990
Module Leader	466,749	490,086	514,591	540,320	567,336	595,703	3,174,784
AFS Members	543,000	570,150	598,657	628,590	660,020	693,021	3,693,437
	1,534,011	1,610,712	1,691,248	1,775,810	1,864,600	1,957,830	10,434,211

3.4.2.3 Additional explanations for certain accounting categories

In the Module budget by natural classification, the budget for Platform Leader, Module Leaders and AFS members is summarized in the line items Personnel, Travel, Capital Equipment, and Other Supplies and Services. The Module budget by participating partner describes who manages (not who uses) the budget. E.g. the Platform Leader manages all subcontracts to AFS members and external contractors and consultants for streamlined issuing of such contracts. The Platform Leader also manages the open access budget

3.4.2.4 Other Sources of Funding for this Project

As a new Platform, there are currently no other sources of funding.

3.4.2.5 Budgeted Costs for certain Key Activities

	Estimate annual average cost (USD)	Please describe main key activities for the applicable categories below, as described in the guidance for full proposal
Gender	695,614	Increasing to US$ 1,283,028 in the Uplift budget. Outcome expectation: At least 40% of the users will be female.
Youth (only for those who have relevant set of activities in this area)	1,159,357	Increasing to US$ 2,138,380 in the Uplift budget. Outcome expectation: At least 2/3 of the users will be students and young scientists.
Capacity development	1,739,035	Increasing to US$ 3,207,570 in the Uplift budget. The entire Module/Platform is targeted at capacity building (see Theory of Change).
Impact assessment	-	Included in CRP Management costs, not in Module specific costs
Intellectual asset management	-	Included in CRP Management costs, not in Module specific costs
Open access and data management	22,956	Increasing to US$ 45,913 in the Uplift budget
Communication	0	Included in CRP Management costs, not in Module specific costs

3.4.2.6 Other

3.4.3 Module Uplift Budget

Outcome Description	Amount Needed	W1 + W2 (%)	W3 (%)	Bilateral (%)	Other(%)
1) Establishment of best practices for phenotyping and environmental analysis through a community of practice. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	320,547	20	40	40	0
2) Support services from ARIs for A. experimental design and analysis of precision and high- throughput phenotype data B. GxExM analysis and Genotype-to-Phenotype predictions. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	788,884	20	40	40	0
3) Coordination and procurement of phenotyping services for routine analyses of physico-chemical composition and functional properties in plant and animal materials in support of breeding. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	47,528	20	40	40	0
4) Needs assessment and consultancy services to improve mechanization and automation across CGIAR and NARS breeding programs as well as infrastructure and management of research stations. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	359,104	20	40	40	0

3.5 Module 5: Bioinformatics and data management tools and services

3.5.1 Module Narrative

3.5.3.1 Rationale, scope

Modern breeding programs rely on information infrastructure that transforms increasingly large and diverse data into valuable information and place it in the hands of researchers and breeders at critical decision points. Advances in phenotyping, remote sensing, and genomic technologies enable the collection of vast quantities of valuable breeding data. In their raw form, and without standardized protocols and nomenclature, these data are difficult to store, manage and utilize. However, when coupled with effective data collection, data management, analysis pipelines and decision support tools, these data can be transformed into coherent information that leads to new insights, more effective breeding decisions and greater rates of genetic gain.

The benefits of integrated data and bioinformatics tools in breeding are clear. Leading breeding companies have shown that it is practically possible to harness them, both through substantive investments and by supporting informed decision-making with defined stage-gate criteria. CGIAR partner institutions as well as many small- and medium-sized breeding programs have not quite succeeded in realizing this potential. Most prominent challenges to reciprocate "a one software approach" for public users has been: the diversity of needs and sizes of breeding programs; the development of software independently from institutions that could ensure future maintenance and upgrades; insufficient user engagement to prioritize, test and provide feedback; and governance dissociated from use.

At the same time, software tools, computer processing and storage capacity, as well as practical experience with integrated breeding workflows, have become more accessible. The development and implementation of application programming interfaces (APIs) enable coherent, interoperable, adaptable data management and analysis workflows ("pipelines") from available, tested and individually evolving bioinformatics components developed by ARIs, CGIAR centers and the private sector. Today, a range of components are available that allow collecting, curating and storing data in a rapid manner to enable turn-key analysis, breeding decisions and client interfaces, both from the private and public sectors (such as GrinGlobal, GeneSys, the Breeding Management System [BMS], Breeding4Rice (B4R), and others). APIs allow these systems to be integrated in a coherent manner and assemble data from multiple sources in support of both genetic resources and breeding programs.

The grand challenge for the CGIAR and this Platform is to enable access by CGIAR, NARS and SME breeding programs to up-to-date, robust bioinformatics and biometrics tools and services that support trait discovery and selection decisions. With Module 2 (i.e., users) prioritizing tool and pipeline development needs aligned with well-defined breeding and trait discovery strategies, the Bioinformatics Module will coordinate the technical implementation of software and pre-packaged software pipelines with multiple partners. It will identify, document and, when necessary, develop informatics and biometrics tools to support data management capabilities, data curation and annotation workflows, analysis pipelines, and decision support. It will incorporate practical trial and sample management tools with genealogy, phenotypic, genomic and environmental information, support testing and backstop implementation. Module interventions should (i) lead to better documented and more robust bioinformatics and biometrics tools that are useful to a wider range of users; and (ii) encourage the collaborative development and implementation of a transparent and cohesive system-wide strategy that will make current and future bioinformatics and biometrics investments

more impactful.

Applying lessons learned from earlier initiatives, the Module will: (i) pursue well defined, frequently applied breeding and trait discovery strategies rather than attempting to provide a generic approach for breeding programs of all sizes; (ii) take actual breeding and research workflows as the point of departure and develop practical solutions that will be tested in specific programs; generalization will only be attempted after progressive adoption beyond the case studies has proven that the solutions work; (iii) identify and adapt existing tools that can be integrated via the nascent Breeding Application Programming Interface (BrAPI) into a modular and integrated pipeline to suit trait discovery, current and advanced breeding needs and workflows; and (iv) only invest in and link up with tools that are backed by reputable institutions as part of their core mandate, so as to ensure a reasonable guarantee of future maintenance and upgrades.

The Module will allow AFS CRPs, the Genebanks Platform and external users to save time and resources when acquiring bioinformatics tools and reduce the considerable risk involved in tool acquisition, development and implementation. This cost reduction and experience-sharing will be valuable for all breeding and trait discovery programs, but particularly so for smaller programs that might otherwise not be able to adopt more comprehensive, integrated breeding approaches.

Based on current bilateral investments, the initial focus will be on improved management and use of phenotypic, genealogical and genomic data in crop breeding and research. Tools and workflows for animal and fish breeding and trait discovery will be considered in an opportunistic way, exploiting synergies where breeding or discovery processes more closely align and where user prioritization indicates high return on investment. Success will open up the possibility of more advanced options, for example, incorporating remote-sensing data to link breeding applications with more detailed target environment characterization or supporting the use of gene editing. As such, this Module will be critical for the technological and methodological advancement of breeding programs.

3.5.1.2 Objectives and targets

The Module will provide modular and integrated pipelines to support specific trait discovery and breeding workflows and support services for CGIAR, NARS and local breeding companies to implement advanced breeding strategies. It will focus on six work packages (Table 5.1) integrating with existing bilaterally funded projects (Table 5.2).

1. Analyze pipelines and tools to clarify user and technical requirements related to selected trait discovery and breeding case studies. This work package will define and document prioritized case studies with distinct user groups as part of Module 2 to ensure practical relevance and ownership by users, whose involvement in Agile Software Development, Iteration Planning and User Acceptance Testing is critical to the success of the outputs of the Module.

2. Develop modular and adaptable pipelines to support breeding workflows for the selected case studies and implement a common BrAPI. Configurable data management, analysis and decision support pipelines will be defined and implemented for the case studies. The current landscape of available tools will be mapped and grouped logically into pipelines, with common BrAPI, developed based on an analysis of existing APIs, and building on established standards and mechanisms to ensure compatibility and interoperability across tools at the database, analysis and user interface levels. The implementation of the case study workflows will incentivize a joint strategy for data access and exchange across application softwares and development of inbuilt commonly-used, routine statistical analyses. The pipelines should be flexible so they can evolve as knowledge, methodologies, technologies and needs change.

3. Support the development of databases and tools to complement and expand the usefulness of existing

bioinformatics initiatives. Several CGIAR and external projects develop fundamental bioinformatics resources, systems and tools that are beneficial to all crop and livestock breeders and researchers, such as for: new alleles discovery from genebanks (Seeds of Discovery), genome-wide association (Seeds of Discovery), genealogical and phenotypic data management (BMS, B4R, CassavaBase); the design of field trials (Agricolae, KDXplore); phenotypic data capture and curation (KSU Fieldbook, KDSmart, KDXplore); genotypic data management and display (GOBII, KDXplore, G4R, GDMS, Flapjack, South Green) high density genotyping data and allele mining (IRIC tools); and data warehousing (Germinate). Case study breeding workflows will reveal gaps in terms of tools, user interfaces and desirable links between tools and with external databases. This work package will develop and adapt new databases and/or tools to address such gaps. Platform co-investment will be conditional on compliance with the BrAPI and associated data standards. In cases where a commercial software option would offer the best value, the Platform provides an avenue to collectively negotiate preferential prices.

4. Define and implement metadata and data standards to facilitate data flows between tools and data sharing. Defining data standards and defining and capturing a suitable amount of metadata in ontologies is a "must have" to ensure linkage across and within workflows and data sets, most prominently passport information, pedigree, global/permanent unique germplasm IDs (GUIDs/PUIDs/DOIs), trait and agronomy ontologies, genetic information and environment conditions, among others. Metadata and data standards will be operationalized through the BrAPI. They will be aligned with standards developed by the Global Information System of the International Treaty on Plant Genetic Resources, and build on the work of the existing Crop and Agronomy Ontology Community of Practice and other initiatives (Planteome, Agroportal, NDEx, QTLNetMiner).

5. Establish a community of practice (CoP) and provide access to bioinformatics and biometrics advice, services and resources. A CoP will be formed among the bioinformatics and biometrics teams of AFS CRPs NARS and ARIs to: develop relevant component tools; facilitate collaboration for large-scale work; establish core operational guidelines; generate and share knowledge on tools and best practices; assess and plan for the sustainability of supported tools; and address capacity development needs. Software developers will be encouraged to adhere to guidelines/best practices, verified through automated checks. As bioinformatics and biometrics technologies and methodologies will continue to evolve, the Module will manage a distinct amount of resources to test, compare and validate emerging methodologies prioritized by Module 2 in collaboration with users. The CoP will seek to train biometricians at universities in CGIAR target countries to use Platform tools and data analysis approaches, and maintain a list of trained resource persons. The work package will invest in brokering access to computational infrastructure. Opportunities will first be sourced from within AFS CRP networks to gain access to free or very low cost facilities at CGIAR centers or ARIs while working with commercial providers on pay-per-use solutions.

6. Advance sustainable deployment and maintenance of tools and applications. The tools used in the modular pipeline to support selected breeding and research workflows will need to continually evolve; therefore, sustainability of software development and maintenance will be an important selection criterion for choosing a tool. Although a number of the bioinformatics software development projects cited in Objective 3 have donor support for the next several years (Table 5.2), funding for continuing support and development is uncertain. It is therefore imperative to plan ahead for resources to support post-deployment maintenance and improvement of tools supporting the developed pipelines.

Use of Module resources among work packages are projected in Table 5.3. The main cost drivers are explained in Table 5.4.

Table 5.1. Work packages and key milestones to be funded by the Platform.

	Milestones = Output targets					
Work packages = Objectives	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1 **Analyze pipelines and tools to clarify user and technical requirements related to selected breeding case studies**	1) Establish overall strategy and prioritize pipeline case studies and related tools		1) Establish overall strategy and prioritize pipeline case studies and related tools		1) Establish overall strategy and prioritize pipeline case studies and related tools	
2 **Develop tools to facilitate modular and adaptable breeding pipelines and coordinate the development and implementation of a common BrAPI**	1) Strategy to implement the Year 1-2 case studies developed 2) Implementation of BrAPI and local APIs for different systems	1) Workflow implemented for the case studies identified in Year 1 2) Implementation of connectivity across the different tools/systems	1) Strategy to implement the Year 3-4 case studies defined 2) Implementation of BrAPI and local APIs for different systems	1) Workflow implemented for the case studies identified in Year 3 2) Implementation of connectivity across the different tools/systems	1) Strategy to implement the Year 5-6 case studies defined 2) Implementation of BrAPI and local APIs for different systems	1) Workflow implemented for the case studies identified in Year 5 2) Implementation of connectivity across the different tools/systems
3 **Support the development of databases and tools to complement and expand the usefulness of existing bioinformatics initiatives**	1) Documented gap analysis for the Year 1-2 case studies 2) Development or acquisition of new database and tools	1) Existing databases and tools assessed and updated 2) Implement strategic sustainability support	1) Documented gap analysis for the Year 3-4 case studies 2) Development or acquisition of new database and tools	1) Existing databases and tools assessed and updated 2) Implement strategic sustainability support	1) Documented gap analysis for the Year 5-6 case studies 2) Development or acquisition of new database and tools	1) Existing databases and tools assessed and updated 2) Implement strategic sustainability support
4 Define and implement metadata and data standards to facilitate data flows between tools and data sharing	1) Crop and Agronomy Ontology CoP incorporates reps from AFS CRPs 2) Strategy to manage and integrate meta-data 3) Crop ontology documented for Tier 1 crops 4) Strategy for GUIDs defined	1) Crop ontology documented for Tier 2 crops 2) Climate data incorporated into breeding workflows 3) Strategy for GUIDs implemented	1) Crop agronomy ontology defined 2) Strategy to manage and integrate meta-data updated		1) Strategy to manage and integrate meta-data updated	

5 Establish a community of practice and provide access to bioinformatics and biometrics advice, services and resources	1) CoP for statisticians and bioinformatics staff established 2) Core operational guidelines for bioinformatics and biometrics defined 3) Common BrAPI defined 4) Capacity development strategy for bioinformatics and software adoption developed 5) Support capacity building and the evaluation of new bioinformatics and biometrics tools and approaches in collaboration with distinct user groups and use cases prioritized in Modules 2-4 6) Training workshops for biometricians in CGIAR target countries to expand the number of resource persons 7) Broker access to proprietary software and computational capacity on a pay-per-use basis	1) Core operational guidelines updated as necessary 2) Common BrAPI updated as necessary 3) Capacity development strategy updated as necessary 4) Review sustainability issues of selected tools 5) Support capacity building and the evaluation of new bioinformatics and biometrics tools and approaches in collaboration with distinct user groups and use cases prioritized in Modules 2-4 6) Training workshops for biometricians in CGIAR target countries to expand the number of resource persons 7) Broker access to proprietary software and computational capacity on a pay-per-use basis	1) Review of CoP effectiveness and modifications made as necessary 2) Software development rules updated as necessary 3) Common BrAPI updated as necessary 4) Capacity development strategy updated as necessary 5) Support capacity building and the evaluation of new bioinformatics and biometrics tools and approaches in collaboration with distinct user groups and use cases prioritized in Modules 2-4 6) Training workshops for biometricians in CGIAR target countries to expand the number of resource persons 7) Broker access to proprietary software and computational capacity on a pay-per-use basis	1) Core operational guidelines updated as necessary 2) Common BrAPI updated as necessary 3) Capacity development strategy updated as necessary 4) Review sustainability issues of selected tools 5) Support capacity building and the evaluation of new bioinformatics and biometrics tools and approaches in collaboration with distinct user groups and use cases prioritized in Modules 2-4 6) Training workshops for biometricians in CGIAR target countries to expand the number of resource persons 7) Broker access to proprietary software and computational capacity on a pay-per-use basis	1) Review of CoP effectiveness and modifications made as necessary 2) Core operational guidelines updated as necessary 3) Common BrAPI updated as necessary 4) Capacity development strategy updated as necessary 5) Support capacity building and the evaluation of new bioinformatics and biometrics tools and approaches in collaboration with distinct user groups and use cases prioritized in Modules 2-4 6) Training workshops for biometricians in CGIAR target countries to expand the number of resource persons 7) Broker access to proprietary software and computational capacity on a pay-per-use basis	1) Core operational guidelines updated as necessary 2) Common BrAPI updated as necessary 3) Capacity development strategy updated as necessary 4) Review sustainability issues of selected tools 5) Support capacity building and the evaluation of new bioinformatics and biometrics tools and approaches in collaboration with distinct user groups and use cases prioritized in Modules 2-4 6) Training workshops for biometricians in CGIAR target countries to expand the number of resource persons 7) Broker access to proprietary software and computational capacity on a pay-per-use basis

6. Advance sustainable deployment and maintenance of tools and applications	1) Sustainable deployment plans documented	1) Deployment plans implemented for Tier 1 crops 2) Support services for Tier 1 crops in place	1) Deployment plans implemented for Tier 2 crops 2) Support services for Tier 2 crops in place			

Table 5.2. Key milestones funded by existing bilateral projects.

Project	Work package, stated as output	2017	2018	2019	2020
1 Integrated Breeding Platform (IBP)	1) BMS development 2) BMS deployment	1) Improved BMS 2) 15 Institutions have adopted the BMS	1) Improved BMS 2) 18 Institutions have adopted the BMS	1) Improved BMS 2) 21 Institutions have adopted the BMS	
2 Genomic and Open-source Breeding Informatics Initiative (GOBII)	1) Genomic Data Warehouse 2)ETL & API 3) Genomic Breeding Tools	1) Data Warehouse Optimization 2) ETL & API	1) Data Warehouse Optimization 2) ETL & API Optimization 3) Genomic Breeding Tools	1) ETL & API Optimization 2) Genomic Breeding Tools 3) Tool Integration in Breeding Workflows	1) Genomic Breeding Tools 2) Tool Integration in Breeding Workflows
3 Breeding4Rice (B4R)	1) Master data management¨ 2) Study creation 3) Data production 4) Processes & services	1) Improved web apps 2) Treaty GLIS compliant 3) API compliant to BrAPI, linked to G4R 4) Deployed to an early adopter institute	1) Improved web apps 2) Embedded GOBII tools 4) Deployed to partner institutes		
4 CassavaBase	1) Genotyping and Phenotyping trial data warehouse 2) Crossing and Evaluation study creation and data collection tools 3) Genomic prediction interface and analysis 4) Server mirror at IITA				

5 Genomic Tools for Sweet Potato Improvement	1) Development of tools for polyploid genomic and genetics analysis 2) Database for sweet potato (Sweet Potato base)	1) Pipeline for SNP identification from polyploid GBS/DArTseq data 2) Sweet potato ontology updated 3) Improved sweet potato base 4) Adopted by sweet potato breeders at CIP and NCSU	1) Software for Genetic map construction, GWAS and for clonally propagated polyploids 2) Software for GWAS and GS for clonally propagated polyploids 3) Adopted by sweet potato breeders at NARs partners		
6 MusaBase	1) Genotyping and Phenotyping trial data warehouse 2) Crossing and Evaluation study creation and data collection tools 3) Genomic prediction interface and analysis 4) Server mirror at IITA				
7 YamBase	1) Genotyping and Phenotyping trial data warehouse 2) Crossing and Evaluation study creation and data collection tools 3) Genomic prediction interface and analysis 4) Server mirror at IITA				

8 Reference Ontologies (cROP) of Planteome	Reference ontologies integrate links to the Crop and Agronomy Ontology	1) All traits available in the crop and agronomy ontologies are integrated into relevant references such as Trait Ontology, Plant Disease Ontology 2) Data of priority crops are annotated with the ontologies and annotations published on the Planteome web site	1) Ontologies extended to additional crops and plant research domains such as phenomics 2) Data on Tier 2 crops are annotated and available on the Planteoeme web site 3) Two ontology curator tools available		
9 IRIC Data and Analysis Portal	1) High density genotype data 2) Visualization tools 3) Phenotypic /Passport/ GWAS results	Large structural variations in rice genomes identified GWAS module implemented Curated data on trait-loci association	Comparative genome analysis tools Tools for trait-loci association analysis	Gene network discovery tools	
10 Genomics for Rice (G4R)	1) Genomic Data Warehouse 2) API 3) Genotype management system	Operational database linked to B4R Develop APIs compliant to BrAPI & GOBII	Integrate Genomic Breeding Tools from GOBII		
11 Global Information System on Plant Genetic Resources for Food and Agriculture	1) Provide germplasm-tracking system	DOI - GID association Develop APIs compliant to BrAPI			

Table 5.3. Use of Base and Uplift budgets among work packages.

Base Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1 Analyze pipelines and tools to clarify users and technical requirements related to the selected breeding case studies	$205,498	$215,773	$226,561	$237,889	$249,784	$262,273
2 Develop tools to facilitate modular and adaptable breeding pipelines and coordinate the development and implementation of a common BrAPI	$785,257	$824,520	$865,746	$909,034	$954,485	$1,002,210
3 Support the development of databases and tools to complement and expand the usefulness of existing bioinformatics initiatives	$1,250,811	$1,313,351	$1,379,019	$1,447,970	$1,520,368	$1,596,387
4 Define and implement metadata and data standards to facilitate data flows between tools and data sharing	$143,847	$151,040	$158,592	$166,521	$174,847	$183,590
5 Establish a community of practice and provide access to bioinformatics and biometrics advice, services and resources	$327,235	$343,596	$360,776	$378,815	$397,756	$417,643
6. Advance sustainable deployment and maintenance of tools and applications	$389,244	$408,706	$429,142	$450,599	$473,129	$496,785
Grand Total	**$3,101,892**	**$3,256,987**	**$3,419,836**	**$3,590,828**	**$3,770,369**	**$3,958,887**

Uplift Budget	**2017**	**2018**	**2019**	**2020**	**2021**	**2022**
1 Analyze pipelines and tools to clarify users and technical requirements related to the selected breeding case studies	$260,726	$273,763	$287,451	$301,823	$316,915	$332,760
2 Develop tools to facilitate modular and adaptable breeding pipelines and coordinate the development and implementation of a common BrAPI	$1,014,549	$1,065,276	$1,118,540	$1,174,467	$1,233,191	$1,294,850
3 Support the development of databases and tools to complement and expand the usefulness of existing bioinformatics initiatives	$1,767,040	$1,855,392	$1,948,162	$2,045,570	$2,147,849	$2,255,241
4 Define and implement metadata and data standards to facilitate data flows between tools and data sharing	$169,262	$177,725	$186,611	$195,942	$205,739	$216,026
5 Establish a community of practice and provide access to bioinformatics and biometrics advice, services and resources	$498,241	$523,153	$549,310	$576,776	$605,615	$635,895
6. Advance sustainable deployment and maintenance of tools and applications	$572,451	$601,074	$631,127	$662,684	$695,818	$730,609
Grand Total	**$4,282,269**	**$4,496,383**	**$4,721,202**	**$4,957,262**	**$5,205,125**	**$5,465,381**

Table 5.4. Explanations of the costs in relation to the planned 2022 outcomes.

Module	2022 Outcomes	Scope: Base budget	Scope: Uplift budget	Explanations of the costs in relation to the planned 2022 outcomes
Module 5: Bioinformatics and data management tools and services	Software tools	> 1,000 users	> 2,500 users	Software investment increases from US$ 3.5 million to US$ 4.8 million; note that software support is needed by all other modules
	Contributors of BrAPI compatible components	> 5 institutions	> 10 institutions	
	Use of computational infrastructure in other institutions	3 users	> 6 users	
	Training	75 participants per year	185 participants per year	Annual training budget increases, from US$ 124,000 to US$ 314,000; special focus: biometricians
All	Members	10	> 30	

3.5.1.3 Science quality

In contrast to a multinational breeding company, this Module deals with a wide range of researchers and breeders that work in different (CGIAR, NARS, ARI) institutions on a much larger range of commodities and with breeding applications ranging from upstream research to downstream, field-based implementation. Science quality will be ensured by a clear definition of the challenges and problems to be addressed. Based on lessons learned from the past, investments must be user-driven, and prioritization will be defined under Module 2.

Investments to support the development of software, biometrics methods and information pipelines need to follow clear rules of engagement: (i) it needs to respond to frequent/highly repeated demand across CRPs; (ii) investment is not readily available from another provider; (iii) it has user time commitment for Agile Software Development Iteration Planning and User Acceptance Testing; (iv) it is compliant with community APIs and associated data standards, and (v) it will be executed by internal and external CGIAR implementers who adhere to agreed guidelines/best practices. Developers will need to have a track record of delivering quality results at reasonable cost within agreed timeframes; have requisite skills to meet expectations; and share a long-term commitment to the work of the Excellence in Breeding Platform. Finally, scale-out is only to be attempted after progressive adoption, beyond the case studies, has proven that the solutions work.

The CGIAR, through the Excellence in Breeding Platform's very active role in further developing and implementing the BrAPI, will be crucial in making it the standard across a range of applications and generating a critical mass of users and uses. This will be achieved by defining a practical and useful breeding API and by making BrAPI compliance a condition for investment in data generation, storage or analytical tools.

An open-source approach will bring indisputable benefits, particularly lower costs and potentially a larger and more diverse community of developers. It will also come with significant challenges. An open-source community will not simply coalesce around these projects and undertake maintenance and continuing development. There may be a loss of coordination with development happening at geographically dispersed locations, each keen on addressing highly nuanced needs. Therefore, an open-access approach will only be successful if the Platform is able to aggregate and credibly respond to user needs through the investment of substantial resources.

The Platform, its Steering Committee and Module Leader will have important roles to play in overseeing that these principles are followed and that user feedback is systematically monitored, analyzed and transparently reported, and management decisions are made accordingly. This will be tracked through the MEL plan of the Platform. Improvements in selection efficiency that are attributable to the use of the tools and attendant services would be the ultimate proof of quality, and efforts will be made to track them.

There are many developers that could develop software tools. However, software tools will need to be maintained and updated. The Platform will only invest in and link up with tools whose developers have an inherent interest in maintaining them as part of their core mandate. Investments focused on improving and linking established components guided by user demand will prevent the Platform from becoming responsible for an increasing amount of software tools. Instead, they increase the value and use of existing tools (also by interconnecting them), which gives the originating CGIAR center or ARI greater incentive to maintain and update them.

3.5.1.4 System linkages

This Module will provide tools and services to support trait discovery and breeding activities, with priorities set by users and a governance approach that incudes users. As the Module and Platform provide true value to users, the number of users and, as a result, internal and external in kind or financial investments are expected to increase.

Investments by AFS CRPs and external users: This Module represents an opportunity for users to acquire tools for data management, analysis and decision support, provided they are prioritized by several CRPs. The breeding programs in AFS CRPs and those of external users will need to allocate resources to use cases that may apply to one CRP only, other specific adaptations and configurations, IT infrastructure and services, and the data management and biometrics capacity required for their work. When asking for bioinformatics investments from the Platform, AFS CRPs and external members will need to identify users who will need to allocate time to clearly define the prioritized use cases with developers, actively test new software and provide timely feedback. In return, they will have access to tools pioneered and tested in collaboration with other users. Once scaled-out, the wider range of users is encouraged to provide feedback and highlight related needs and issues, as this will guide future bioinformatics investments. Given that AFS CRPs will select the case studies, they have an incentive to deploy tools and technologies to their partners through established structures and mechanisms, thereby ensuring sustainable adoption of the tools and breeding pipelines.

Benefits to AFS CRPs and external users: The Bioinformatics Module will deliver tools and technologies that will support modernization of breeding and trait discovery in the AFS CRPs and other stakeholders, increase the speed with which better varieties can be developed and attendant economic benefits of can be generated (Alpuerto et al., 2010). Given similar challenges, the Module will reduce redundant investments across the centers and CRPs, thus allowing each member to progress further. This implies joint priority setting and standards that often require larger users with their own bioinformatics and biometrics investments to make some compromises, adjust workflows and redirect their own bioinformatics support. To smaller breeding programs that cannot afford to make significant investments in their own bioinformatics and biometrics, it will give access to otherwise inaccessible tools and approaches, and to bioinformatics and biometrics capacities within the system.

Outcome at the Portfolio level: The Bioinformatics Module will facilitate the pooling of resources for costly and specialized activities that presently can only be individually pursued by each institution and AFS CRP; and provide a framework for more formalized collaboration for the diverse initiatives in this area. Through mapping the software landscape and common user interest, it will bring coherence to the various efforts, which will result in improved interoperability and compatibility, enabling customization to meet unique needs while staying within defined parameters that enable individual breeding efforts to benefit from tools, knowledge, methodologies and technologies generated by others. The economies of scale gained will accelerate the development of tools and pipelines. Users, together with the Platform, will for the first time establish an overview of bioinformatics system use, user feedback and future priorities, which will hopefully be used by investors.

Coordination with the Big-Data, Information and Knowledge Platform. Use cases that link genetic applications with environmental and socioeconomic data will require and rely on alignment with the standards, approaches and bioinformatics systems coordinated by the Big-Data, Information and Knowledge Platform. The two platforms will also coordinate access to computing capacity.

3.5.1.5 Climate Change

Climate change implies that breeding has to catch up on productivity lost due to higher temperatures and greater frequency of abiotic stresses in the developing world. The data management, analysis and decision support tools, applications and pipelines done by the Platform will enable faster and more accurate selection of alleles contributing to enhanced climate challenge adaptation and climate resilient breeds that mitigate the adverse effects of climate change. Genetic improvements are not based on easy and simple fixes but require improved genotypic and phenotypic information for which bioinformatics tools are absolutely fundamental to expedite the process of collecting data, analyzing and assessing traits and advancing breeding generations to meet the pace set by climate change.

As local environments become more unstable, extreme variability of localized weather conditions and the increased incidence of unpredictable extreme weather events pose a challenge beyond long-term climate shifts. The establishment in this Module of pipelines and APIs to transfer primary breeding data between different systems using standard ontologies will facilitate crop simulation modelling. This will in turn accelerate ideotype design and provide tools that help interpret phenotypic data on breeding populations in multiple changing environments.

3.5.1.6 Capacity development

The Bioinformatics Module will augment the knowledge and skills of crop improvement scientists with a view to improving their access to and use of information, analytical tools, and associated methodologies and technologies. In collaboration with Module 2, the substance of the capacity building efforts will focus on transferring vital skills in using suitable tools and resources related to experimental design; data collection, management and analysis; molecular markers; and breeding decision-making, using actual use cases described by the CoPs in Modules 2-4 for which bioinformatics tools have been developed.

While Module 2 will facilitate joint training opportunities, both virtually and face-to-face, the CoPs of bioinformatics and biometrics specialists will provide trainers, mentors and technical backstopping to partners of AFS CRPs. Train-the-trainer approaches (breeders, biometricians, bioinformatics personnel) will be used for face-to-face sharing of knowledge with the large number of NARS and SME partners and collaborators. Capacity building will be crucial to create a critical mass of appropriately skilled NARS scientists who will hasten the adoption and application of modern breeding approaches in their respective regions and countries.

Biometrics and bioinformatics personnel with a good understanding of the breeding process and quantitative genetics are incredibly scarce. The Module will seek to link up with biometrics personnel at universities and bioinformatics staff in private companies to improve access to competent personnel and widen the knowledge base within an extended CoP. Other capacity building efforts (such as supporting post-graduate students and upgrading crucial ICT equipment) will be beyond the Platform's immediate scope and will have to be undertaken by the individual AFS CRPs, bilateral and multilateral initiatives.

3.5.1.7 Intellectual asset and open access management

The Module will predominantly build on and promote open-access components (bioinformatics resources, systems and tools) from the CGIAR and ARIs for the benefit of the wider scientific research community, with particular focus on low and middle income countries. Contributors shall ensure proper stewardship of their intellectual property as well as that belonging to other parties who have granted and confirmed permission. Users will access the Platform's open-access components under standard licensing conditions that will ensure that the tools remain available for use by the wider scientific community, as well as derivative products when possible. The Platform will distinguish between testing environment (access by members only) and tools that are being promoted for wider use. Responsibility for use of tools will remain with the user.

The Module will promote the data dissemination by helping to identify the best public data warehouses and/or repositories for sharing the data types covered by the Platform, such as Germinate, and supporting their further cross-cutting development as necessary. Supported bioinformatics resources are to provide adequate permission control to manage public/private access to data from a single source and/or to provide tools for transferring data from internal systems to public systems via web services or data output formats that can be readily deposited in the recommended repositories.

In some instances, users will be able to link Platform components with proprietary software from the private sector. At this stage, the latter contributes a relatively small proportion of the components. It will be an expression of the success of the Platform if private sector contributions increase. Management of pay-to-access third-party commercial software, computational infrastructure or expert advice may require cross-member licensing agreements which may be beneficial to providers due to greater use.

3.5.1.8 Module management

The Module Leader will need to be able to link with (and indeed should be co-hosted together with) one of the main CGIAR bioinformatics projects (Table 5.2). The person needs to bring technical and management skills to manage a large, multi-institutional, cross-cutting bioinformatics program and be able to quickly develop an in-depth understanding of the current initiatives, their relevance in an applied breeding context and user feedback, in order to develop an overall strategy for the Module's investment. This needs to take place in a constructively consultative manner with both users and leaders of the existing initiatives.

Within the overall CoP for bioinformatics and biometrics, the leaders of the existing initiatives form the Expert Advisory Group for this Module. They will define mutually acceptable guidelines/best practices and ensure that milestones are met and delivery targets achieved. Execution of the Module's agenda will be done preferably through these members, i.e., by expanding the capacities of bioinformatics teams of existing, well performing projects, or through other external providers of software components that become linked to the BrAPI. Access to Platform funding and the users' voice from Module 2 will give existing project teams an incentive to grow together, follow standards and seek future funding jointly, and aligned with user priorities.

The contracting of implementers is to be open and transparent. The delivery of outputs has to be service-oriented. Selection of tools will have to respond to demand across various stakeholders. The CoP will require proactive moderation by the Module Leader for a clear process, decisions and results. Several of the existing projects have separate management and/or advisory bodies. In interaction with individual donors, Platform members should seek to reduce redundant investments in independent advice and instead increase investments in the commonly agreed agenda.

3.5.2 Module Budget Narrative

3.5.2.1 General Information

Platform Lead Center's Name: CIMMYT

Module title: Module 5: Bioinformatics and data management tools and services

Center Location of Platform Leader:

3.5.2.2 Summary

Total Module budget summary by sources of funding (USD)

Funding Needed	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2	620,378	651,397	683,967	718,166	754,074	791,777	4,219,760
W3	1,240,757	1,302,795	1,367,934	1,436,331	1,508,148	1,583,555	8,439,519
Bilateral	1,240,757	1,302,795	1,367,934	1,436,331	1,508,148	1,583,555	8,439,519
Other Sources	-	-	-	-	-	-	-
	3,101,892	3,256,987	3,419,836	3,590,828	3,770,369	3,958,887	21,098,798

Funding Secured	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
W1+W2 (Assumed Secured)	620,378	651,397	683,967	718,166	754,074	791,777	4,219,760
W3	-	-	-	-	-	-	-
Bilateral	960,000	550,000	120,000	-	-	-	1,630,000
Other Sources	-	-	-	-	-	-	-
	1,580,378	1,201,397	803,967	718,166	754,074	791,777	5,849,760

Total Module budget by Natural Classifications (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
Personnel	1,428,236	1,499,648	1,574,630	1,653,362	1,736,030	1,822,831	9,714,737
Travel	98,499	103,424	108,595	114,025	119,726	125,713	669,982
Capital Equipment	172,373	180,992	190,042	199,544	209,521	219,997	1,172,468
Other Supplies and Services	622,522	653,648	686,331	720,647	756,679	794,513	4,234,341
CGIAR collaborations	0	0	0	0	0	0	0
Non CGIAR Collaborations	418,423	439,344	461,311	484,377	508,596	534,026	2,846,077
Indirect Cost	361,838	379,930	398,927	418,873	439,817	461,808	2,461,193
	3,101,892	3,256,987	3,419,836	3,590,828	3,770,369	3,958,887	21,098,798

Total Module budget by participating partners (signed PPAs) (USD)

	Period 1	Period 2	Period 3	Period 4	Period 5	Period 6	Total
CIMMYT	0	0	0	0	0	0	0
Platform Leader	511,480	537,054	563,907	592,103	621,708	652,793	3,479,045
Module Leader	1,891,377	1,985,946	2,085,243	2,189,506	2,298,981	2,413,930	12,864,983
AFS Members	699,034	733,986	770,685	809,220	849,680	892,165	4,754,770
	3,101,892	3,256,986	3,419,836	3,590,828	3,770,369	3,958,887	21,098,798

3.5.2.3 Additional explanations for certain accounting categories

In the Module budget by natural classification, the budget for Platform Leader, Module Leaders and AFS members is summarized in the line items Personnel, Travel, Capital Equipment, and Other Supplies and Services. The Module budget by participating partner describes who manages (not who uses) the budget. E.g. the Platform Leader manages all subcontracts to AFS members and external contractors and consultants for streamlined issuing of such contracts. The Platform Leader also manages the open access budget.

3.5.2.4 Other Sources of Funding for this Project

Other sources of funding are described in Table 16.

3.5.2.5 Budgeted Costs for certain Key Activities

	Estimate annual average cost (USD)	Please describe main key activities for the applicable categories below, as described in the guidance for full proposal
Gender	1,406,587	Increasing to US$ 1,941,841 in the Uplift budget. Outcome expectation: At least 40% of the users will be female.
Youth (only for those who have relevant set of activities in this area)	2,344,311	Increasing to US$ 3,236,402 in the Uplift budget. Outcome expectation: At least 2/3 of the users will be students and young scientists.
Capacity development	3,516,466	Increasing to US$ 4,854,604 in the Uplift budget. The entire Module/Platform is targeted at capacity building (see Theory of Change).
Impact assessment	-	Included in CRP Management costs, not in Module specific costs
Intellectual asset management	-	Included in CRP Management costs, not in Module specific costs
Open access and data management	22,956	Increasing to US$ 45,913 in the Uplift budget
Communication	-	Included in CRP Management costs, not in Module specific costs

3.5.2.6 Other

3.5.3 Module Uplift Budget

Outcome Description	Amount Needed	W1 + W2 (%)	W3 (%)	Bilateral (%)	Other(%)
1 Analyze pipelines and tools to clarify users and technical requirements related to the selected breeding case studies. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	62,610	20	40	40	0
2 Develop tools to facilitate modular and adaptable breeding pipelines and coordinate the development and implementation of a common Breeding API (BrAPI). The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	259,937	20	40	40	0
3 Support the development of databases and tools to complement and expand the usefulness of existing bioinformatics initiatives. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	585,225	20	40	40	0
4 Define and implement metadata and data standards to facilitate data flows between tools and data sharing. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	28,811				
5 Establish a community of practice and provide access to bioinformatics and biometrics advice, services and resources. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	193,861	20	40	40	0
6. Advance sustainable deployment and maintenance of tools and applications. The value is the average difference between the annual Base budget and the annual Uplift budget. Further explanations are provided in Table 8.	207,693	20	40	40	0

4 Annex

4.1 Annex 1. Expertise and Track Record

The Excellence in Breeding Platform is a new Platform. Staff are yet to be hired based on approval of the proposal by the CGIAR Fund Council. The five Modules will be supported by Expert Advisory Groups whose members come from AFS CRPs or external members. Expert Advisory Groups are the crucial link between Platform and AFS CRPs. They advise Module Leaders on prioritization, assess member and user engagement, and are the one-stop contact for each AFS. Expert Advisory Groups meet virtually four times per year, face-to-face once per year. Membership can change but must be with a senior person that has relevant expertise for the particular Module and is influential within the AFS CRP or otherwise a substantive contributor in an external institution.

Members of the Expert Advisory Groups supporting the five Platform Modules.

CRP or Platform	Module 1: Breeding Excellence	Module 2: Trait Discovery/Breeding	Module 3: Genotyping	Module 4: Phenotyping	Module 5: Bioinformatics
DCL	Steve Beebe	Michael Baum	Rajeev Varshney	Vincent Vadez	
Fish	John Benzie	John Benzie			
FTA	Ramni Jamnadass	Zacharie Tchoundjeu	Prasad Hendre	Alice Muchugi	Roeland Kindt
Livestock	Raphael Mrode	Olivier Hanotte	Appolinaire Djikeng	Margaret Worthington	Stephen Kemp
MAIZE	B.M. Prasanna	Sarah Hearne	Mike Olsen	Jill Cairns	Jens Riis
RICE	George Kotch	John Platten	Tobias Kretschmar	William Paul Quick	Mauleon Ramil
RTB	Merideth Bonierbale	Luis Becerra	Michael Abberton	Awais Khan	Andreas Gisel
WHEAT	Hans Braun	Jessica Rutowski	Susanne Dreisigacker	Matthew Reynolds	Kate Dreher
Genebanks		Peter Wenzl	Ruaraidh Sackville Hamilton		
External experts and advisors	To be determined	To be determined	To be determined	To be determined	Kelly Robbins, Jean-Marcel Ribaut, Lukas Mueller

MARIANNE BÄNZIGER

Current position and affiliation: Deputy Director General, Research and Partnerships, CIMMYT

Profile: Marianne Bänziger has been CIMMYT Deputy Director General for Research and Partnership since October 2009, with background in stress physiology and plant breeding. CIMMYT has over 200 internationally recruited scientists posted in 17 countries and with activities in approximately 70 countries. It routinely collaborates with over 600 institutions - NARS, ARIs, the private seed sector and regional organizations – world-wide.

Employment:
2009-Present: Deputy Director General, Research and Partnerships, CIMMYT, Mexico
2006-2009: Director CIMMYT's Global Maize Program, Kenya
2004-2005: Director of CIMMYT's African Livelihoods Program, Kenya
1996-2004: Scientist and senior scientist for maize stress breeding at CIMMYT, Zimbabwe.

Education
1992: PhD, Natural Sciences, Nitrogen efficiency of spring wheat genotypes, Swiss Federal Institute of Technology (ETH), Zürich, Switzerland.
1988: MSc, Crop Sciences, Swiss Federal Institute of Technology (ETH), Zürich, Switzerland.

Selected Recent Peer-reviewed publications:

- Beyene Y, Semagn K, Crossa J, Mugo S, Atlin GN, Tarekegne A, Meisel B, Sehabiague P, Vivek BS, Oikeh S, Alvarado G, Machida L, Olsen M, Prasanna BM, Bänziger M (2015) Improving maize grain yield under drought Stress and non-stress environments in Sub-Saharan Africa using marker-assisted recurrent selection. Crop Sci. 56:1–10 (2016). doi: 10.2135/cropsci2015.02.0135
- Beyene Y, Semagn K, Mugo S, Tarekegne A, Babu R, Meisel B, Sehabiague P, Makumbi D, Magorokoscho C, Oikeh S, Gakunga J, Vargas M, Olsen M, Prasanna BM, Bänziger M Crossa J (2014) Genetic gains in grain yield through genomic selection in eight bi-parental maize populations under drought stress. doi: 10.2135/cropsci2014.07.0460; Posted online 9 Sept. 2014.
- Almeida GD, Makumbi D, Magorokosho C, Nair S, Borém A, Ribaut JM., Bänziger M, Prasanna BM, Crossa J, Babu R (2013) QTL mapping in three tropical maize populations reveals a set of constitutive and adaptive genomic regions for drought tolerance. Theoretical and Applied Genetics: 126, 583-600.
- Weber VS, Melchinger AE, Magorokosho C, Makumbi D, Bänziger M, Atlin GN (2012) Efficiency of managed-stress screening of elite maize hybrids under drought and low nitrogen for yield under rainfed conditions in southern Africa. 52:1–10.
- Lobell DB, Bänziger M, Magorokosho C, Vivek B (2011) Nonlinear heat effects on African maize as evidenced by historical yield trials. Nature climate change1: 1-4. DOI: 10.1038/NCLIMATE1043.
- Shiferaw B, Prasanna BM, Hellin J, Bänziger M. (2011) Crops that feed the world 6. Past successes and future challenges to the role played by maize in global food security. Food Sec. (2011) 3:307–327. DOI 10.1007/s12571-011-0140-5.

Other Evidence of Leadership, large-program management and delivery:

- 2011 – 2015: Chair person of the MAIZE and WHEAT management committee; oversight of the Management Units for MAIZE and WHEAT
- 2007 to date: Member of the Scientific and Technical Advisory Board of Syngenta.
- 1996 – 2004 Leadership of CIMMYT's drought tolerance breeding program in southern Africa

Role in [this CRP/platform]: Senior author and overall facilitator of the Excellence in Breeding Platform proposal development.

MICHAEL ABBERTON

Current position and affiliation: Head, Genetic Resources Centre, IITA

Profile: Plant breeding, genetic resources, climate change

Employment:
2012-Present: Head of Genetic Resources Centre, International Institute of Tropical Agriculture (IITA), Nigeria
2010-2012: Director of International Development IBERS
2008-2010: Head, Crop Breeding and Genomics IBERS & Genome Diversity and Plant Breeding, Aberystwyth University, UK
2007-2008: Programme Leader, Plant Breeding and Genetics, Institute of Grassland and Environmental Research, UK

Education
1988: PhD, Chromosome specific behaviour in an autopolyploid series, University of Manchester, UK
1984: BSc, Botany, University of Manchester, UK

Selected Recent Peer-reviewed publications:

- Istvan Nagy, Susanne Barth, Jeanne Mehenni-Ciz, Michael T Abberton, Dan Milbourne. A hybrid next generation transcript sequencing-based approach to identify allelic and homeolog-specific single nucleotide polymorphisms in allotetraploid white clover (2013)BMC Genomics 02/2013; 14(1):100.
- Yates, S. , Swain, M. , Hegarty, M. , Chernukin, I. , Lowe, M. , Allison, G. , Ruttink, T. , Abberton, M. , Jenkins, G. , Skot, L. (2014). De novo assembly of red clover transcriptome based on RNA-Seq data provides insight into drought response, gene discovery and marker identification. BMC Genomics, 15, 453,1 - 33 , ISSN 1471-2164 , 2014
- Shitta, N. S. Abberton, M. , Adesoye, A. I. , Adewale, D. B. , Oyatomi, O. (2015) Analysis of genetic diversity of African yam bean using SSR markers derived from cowpea. Plant Genetic Resources: Characterization and Utilization, pages 1 - 7, ISSN 1479-2621, 2015.
- Abberton et al (2015) Global agricultural intensification during climate change: a role for genomics. *Plant Biotechnology Journal.* 2015. 1— 4.
- Kole, C. . et al (2015) *Frontiers in Plant Science*. 6(563) 1— 16

Other Evidence of Leadership, large-program management and delivery:

- Delivery of plant breeding programs, large multinational projects and large UK funded projects including public-private partnerships
- 2010-2012: Chair in Public Good Plant Breeding, Aberystwyth University

Role in [this CRP/platform]: Representing RTB on the Expert Advisory Group for Module 3: Genotyping. Contributor to Module 3 of the Excellence in Breeding Platform Proposal.

MICHAEL BAUM

Current position and affiliation: Director, Biodiversity and Integrated Gene Management Program (BIGM) and Morocco Platform, International Center for Agricultural Research in the Dry Areas (ICARDA)

Profile: plant breeding and cytogenetics; molecular marker application in plant breeding; doubled haploid breeding in wheat and barley; genetic transformation in cereals and legumes.

Employment:
2010-Present: Director, BIGM, ICARDA, Amman- Rabat, Morocco
1992-2010: Biotechnologist, BIGM, ICARDA, Syria
1989-1991: Post-doctoral Fellow, CSIRO, Canberra, Australia
1985-1988: PhD student, Göttingen, University, Germany

Education:
1988: PhD in plant breeding and cytogenetics, University of Göttingen, Germany
1985: Diploma in Agriculture, University of Göttingen, Germany

Selected Recent Peer-reviewed publications:

- W. Tadesse, F. C. Ogbonnaya, A. Jighly, M. Sanchez-Garcia, Q. Sohail, S. Rajaram, and M. Baum (2015) Genome-wide Association Mapping of Yield and Grain Quality Traits in Elite Winter Wheat Genotypes Targeted to the CWANA region. PLOS ONE DOI:10.1371/journal.pone.0141339.
- W. Tadesse, F.C. Ogbonnaya, A. Jighly, K. Nazari, S. Rajaram, and M. Baum. 2015. Association Mapping of Resistance to Yellow Rust in Winter Wheat Cultivars and Elite Genotypes Crop Sci. doi: 10.2135/cropsci2013.05.0289
- S.K. Agarwal, K. Rajendran, J. Kumar, A. Hamwieh, M. Baum (2015). Current knowledge in lentil genomics and its application for crop improvement. Frontiers in Plant science, 6: 78, 1-13.
- Lopes, M., M.Reynolds, L. McIntyre, K. Mathews, J. Kamali, M. Mousaad, F. Yousef, T. Izzat, R. Chatrath, F. Ogbonnaya, M. Baum (2013). QTLs for yield and associated traits in the Seri/Babax population grown across several environments in Mexico, in the West Asia, North Africa and South Asia regions. Theor. Appl. Genet. (2011) 126 (4): 971-984.
- Varshney, R.K., Paulo, M.J., Grando, S., van Eeuwijk, F.A., Keizer, L.C.P., Guo, P., Ceccarelli, S., Killian, A., Baum, M., and A Graner, 2011. Genome wide association analyses for drought tolerance related traits in barley (*Hordeum vulgare*). Field Crops Research 126 (2012) 171–180.
- Khatib f, A. Makris, K. Yamaguchi-Shinozaki, S. Kumar, A. Sarker, W. Erskine and M. Baum (2011). Expression of DREB1A gene in lentil (Lens culinaris Medik. ssp. culinaris) transformed with the Agrobacterium system. *Crop & Pasture Science*, 2011, 62, 488–495.

Other Evidence of Leadership, large-program management and delivery: As director my task is to coordinate the work of up to 40 international scientists (barley, durum and bread wheat, chickpea, lentil, faba bean breeding, cereal and legume pathology, virology, biotechnology, international nurseries, seed health, cereal and legume quality, and more than 50 technical staff in the West Asia and North Africa region with major hubs in Rabat, Morocco, Terbol, Lebanon, Izmir, Turkey, Cairo, Egypt.

Role in [this CRP/platform]: Representing DCL on the Expert Advisory Group for Module 2: Trait Discovery/Breeding. Contributor to Module 1 of the Excellence in Breeding Platform Proposal.

LUIS AUGUSTO BECERRA LOPEZ-LAVALLE

Current position and affiliation: Principal Research Scientist – Group Leader – Genetics and Genomics - International Centre for Tropical Agriculture (CIAT) – Cassava program.

Profile: Breeder

Employment:

- 2015-present: Principal Research Scientist – Group Leader – Genetics and Genomics - International Centre for Tropical Agriculture (CIAT) – Cassava program.
- 2012-2014: RTB Global Theme Leader – Accelerating the development and selection of varieties with higher, more stable yield and added value (Theme 2) - CGIAR Research Program on Root, Tubers and Bananas.
- 2009-2015 Senior Research Scientist – Group Leader – Genetics and Genomics - International Centre for Tropical Agriculture (CIAT) – Cassava program.
- 2004-09/2009: Research Scientist/Engineer – Team Leader-Commonwealth Scientific and Industrial Research Organization (CSIRO) – Division of Plant Industry.

Education

- 2000: PhD in Plant Molecular Genetics, School of Biological Sciences, The University of Sydney (USYD)
- 1995: MSc in Plant Cytogenetics, Cayetano Heredia University, Lima-Peru.

Publications

- SOTO, J. C., ORTIZ, J. F., PERLAZA-JIMÉNEZ, L., VÁSQUEZ, A. X., BECERRA LOPEZ-LAVALLE, L. A., MATHEW, B., LÉON, J., BERNAL, A. J., BALLVORA, A. & LÓPEZ, C. E. 2015. A genetic map of cassava (*Manihot esculenta* Crantz) with integrated physical mapping of immunity-related genes. BMC Genomics, 16, 190.
- AGRE, A. P., DANSI, A., RABBI, I. Y., BATTACHARGEE, R., DANSI, M., GEDIL, M., BECERRA LOPEZ-LAVALLE, L. A., SANNI, A., AKOUEGNINOU, A. & AKPAGANA, K. 2015. Agromorphological Characterization of Elite Cassava (*Manihot esculenta* Crantz) Cultivars Collected in Benin. Int. J. Curr. Res. Biosci. Plant Biol. 2, 1-14.
- PEÑA-VENEGAS, C., STOMPH, T., VERSCHOOR, G., BECERRA LOPEZ-LAVALLE, L. A. & STRUIK, P. 2014. Differences in Manioc Diversity Among Five Ethnic Groups of the Colombian Amazon. Diversity, 6, 792-826.
- WANG, W., FENG, B., XIAO, J., XIA, Z., ZHOU, X., LI, P., ZHANG, W., WANG, Y., MØLLER, B. L., ZHANG, P., LUO, M.-C., XIAO, G., LIU, J., YANG, J., CHEN, S., RABINOWICZ, P. D., CHEN, X., ZHANG, H.-B., CEBALLOS, H., LOU, Q., ZOU, M., CARVALHO, L. J. C. B., ZENG, C., XIA, J., SUN, S., FU, Y., WANG, H., LU, C., RUAN, M., ZHOU, S., WU, Z., LIU, H., KANNANGARA, R. M., JØRGENSEN, K., NEALE, R. L., BONDE, M., HEINZ, N., ZHU, W., WANG, S., ZHANG, Y., PAN, K., WEN, M., MA, P.-A., LI, Z., HU, M., LIAO, W., HU, W., ZHANG, S., PEI, J., GUO, A., GUO, J., ZHANG, J., ZHANG, Z., YE, J., OU, W., MA, Y., LIU, X., TALLON, L. J., GALENS, K., OTT, S., HUANG, J., XUE, J., AN, F., YAO, Q., LU, X., FREGENE, M., BECERRA LOPEZ-LAVALLE, L. A., WU, J., YOU, F. M., CHEN, M., HU, S., WU, G., ZHONG, S., LING, P., CHEN, Y., WANG, Q., LIU, G., LIU, B., LI, K. & PENG, M. 2014. Cassava genome from a wild ancestor to cultivated varieties. Nature Communications, 5, 1-5.

Other Evidence of Leadership, large-program management and delivery: **Luis Augusto** manages a professional research team of up to 30 researchers. In 2012, his achievements earned him the distinctive designation of Global Leader for Development of Varieties for the CGIAR Research Program on Root, Tubers and Bananas. In 2014, he was appointed as Editorial Board Members of the Universidad Nacional de Colombia.

Role in [this CRP/platform]: Representing RTB on the Expert Advisory Group for Module 2: Trait Discovery/Breeding. Contributor to the Excellence in Breeding Platform Proposal.

STEPHEN BEEBE

Current position and affiliation: Bean Program Leader, Centro Internacional de Agricultura Tropical

Profile: Bean breeder responsible for breeding of small seeded common bean of the Mesoamerican gene pool, for resistance to biotic (viral, bacterial and fungal pathogens) and abiotic (drought and soil constraints) stresses. Has developed varieties adopted in more than 10 countries.

Employment
2002 to Present: Project manager, Bean Improvement Project, CIAT, Colombia
1998 to Present: Bean breeder in Bean Improvement Project, CIAT, Colombia
1996-1998: Project manager, Bean Improvement Project, CIAT, Colombia
1992-1998: Germplasm specialist, CIA, Colombia

Education:
1978: Ph.D Plant breeding-plant genetics, University of Wisconsin, USA
1976: M.Sc. Plant breeding-plant genetics, University of Wisconsin, USA

Selected Recent Peer-reviewed publications:

- Assefa, T., S. E. Beebe, I.M. Rao, J.B. Cuasquer, M.C. Duque, M. Rivera, A. Battisti, M. Lucchin. 2013. Pod harvest index as a selection criterion to improve drought resistance in white pea bean. Field Crops Res. 148:24-33.
- Beebe, S. 2012. Common Bean Breeding in the Tropics. In: Plant Breeding Reviews. Ed. J. Janick. 36:357-426.
- Beebe, S., J. Ramirez, A. Jarvis, I. M. Rao, G. Mosquera, J. M. Bueno, and M. W. Blair. 2011. Genetic improvement of common beans and the challenges of climate change. p. 356-369. In: S. Singh Yadav, R. Redden, J. L. Hatfield, H. Lotze-Campen, and A. Hall (eds). Crop adaptation to climate change. Wiley-Blackwell, Ames, IA.
- Beebe, S.E., I.M. Rao, C. Cajiao, and M. Grajales. 2008. Selection for drought resistance in common bean also improves yield in phosphorus limited and favorable environments. Crop Sci. 48:582-592.
- Butare, L., I. M Rao, P. Lepoivre, C. Cajiao, J. Polania, J. Cuasquer, and S. Beebe. 2012. Phenotypic evaluation of interspecific recombinant inbred lines (RILs) of Phaseolus species for aluminium resistance and shoot and root growth response to aluminium–toxic acid soil. Euphytica 186(3): 715-730. DOI: 10.1007/s10681-011-0564-1
- Klaedtke, S.M., C. Cajiao, M.Grajales1, J. Polanía, G. Borrero, A. Guerrero, M. Rivera, I. Rao, S. E. Beebe, J. Léon. 2012. Photosynthate remobilization capacity from drought-adapted common bean (Phaseolus vulgaris) lines can improve yield potential of interspecific populations within the secondary gene pool. Journal of Plant Breeding and Crop Science 4(4):49-61

Awards:

- Technical Management Advisory Committee (TMAC) lifetime achievement award for his contribution to bean research over the last 40 years.
- Scopus award- Elsevier 2011
- Crop Science Society of America. Outstanding Paper on Plant Genetic Resources in the year 2000, for: Beebe, S., P. W. Skroch, J. Tohme, M.C. Duque, F. Pedraza, and J. Nienhuis. 2000. Structure of genetic diversity among common bean landraces of Mesoamerican origin based on Correspondence Analysis of RAPD. Crop Sci. 40(1): 264-273.

Role in [this CRP/platform]: Representing DCL on the Expert Advisory Group for Module 1: Breeding Excellence. Contributor to the Excellence in Breeding Platform Proposal.

JOHN BENZIE

Current position and affiliation: Principal scientist and Leader of WorldFish Genetics

Profile:

- More than 30 years' experience in Aquaculture and Natural Resource Management in marine and freshwater systems working in Government, University and Private Sectors
- Leading multidisciplinary national and international research groups for more than 25 years on aquaculture and biotechnology development in Australia, Europe, America, Asia and Africa.
- Research includes quantitative, population and molecular genetics and their application to ecological, natural resource management and biotechnology developments in aquaculture. Leading breeding programs in aquatic organisms including shrimp, fish and molluscs. More than 140 peer reviewed publications.

Employment:

2013-to date *Principal Scientist, Leader of the Genetics Group WorldFish, Malaysia*
2008-to date *Professor of Marine Molecular Biodiversity / Marine Molecular Ecology, University College Cork, Ireland*
2003-2008 *Head of R&D, Moana Technologies, Hong Kong*
2000-2003 *Professor and Director, Centre for Marine and Coastal Studies, University of New South Wales, Australia*

Education:

1986: PhD Genetics, Australian National University, Canberra, Australia.
1978: BSc (Hon) First class, Zoology, Aberdeen University, Aberdeen, UK.

Selected Recent Peer-reviewed publications:

- Ma, T.H.T., Benzie, J.A.H., He, J-G., Sun, C-B., Chan, S-M (2014) PmPPAF is a pro-phenoloxidase activating factor involved in innate immunity response of the shrimp Penaeus monodon. Developmental and Comparative Immunology 44: 163-172.
- Korres, N.E., O'Kiely, P., Benzie, J.A.H., West J.S. (eds) (2013). Bioenergy Production by Anaerobic Digestion: Using Agricultural Biomass and Organic Wastes. Earthscan / Routledge, Taylor & Francis Publishing Group. 442pp.
- O'Farrell, B., Benzie, J.A.H., McGinnity, P., de Eyto, E., et al. (2013) Selection and phylogenetics of salmonid MHC class I: wild brown trout (Salmo trutta) differ from a non-native introduced strain PLoS ONE PONE-D-12-34666R2.
- Bourlat, S.J., Borja, A., Gilbert, J., Taylor, M.I., Davies, N.,[Benzie, J.] et al. (2013) Genomics in marine monitoring: New opportunities for assessing marine health status. Marine Pollution Bulletin 74: 19-31.
- Benzie, J.A.H., Nguyen, T.T.T., Hulata, G., Bartley, D.M., et al. (2012). Promoting responsible use and conservation of aquatic biodiversity for sustainable aquaculture development. In R.P. Subasinghe, et al., eds. Farming the Waters for People and Food. Proc. Global Conf. on Aquaculture 2010, Phuket, Thailand. Sept. 2010. Pp 337–383. FAO, Rome and NACA, Bangkok.

Other Evidence of Leadership, large-program management and delivery:

More than 168 publications including 3 books, editor for leading journals: Aquaculture, Molecular Ecology.
Development of improved black tiger strain now fully commercialized. More than AUD20M in grants in Australia in genetics of marine systems and aquaculture, 1990-2003; Belgian Dept. Sci. &Tech. €2.1M sex determination in shrimp, 2005-7; EUFP7 Knowledge transfer in marine genomics to industry and government €0.99M 2011-13.

Role in platform: Representing the AFS CRP on Fish on the Expert Advisory Group for Module 1: Breeding Excellence and Module 2 Trait Discovery/Breeding. Contributor to the Excellence in Breeding Platform Proposal

MERIDETH BONIERBALE

Current position and affiliation: Science Leader and Senior Scientist at International Potato Center (CIP)

Profile:
Plant Breeder with over 20 years of experience in germplasm enhancement and crop improvement. Research focus on tools, stocks and approaches for genetic analysis and interploid breeding, comparative molecular genetics, trait transfer from crop wild relatives, valorization and use of landrace diversity, population improvement and selection schemes in clonal crops. Committed to team work and improving processes and capacities for individual and shared results.

Employment:
2013-Present: Science Leader, Genetics, Genomics & Crop Improvement, CIP, Peru
2003-2012: Project Leader Gene Discovery and Division Leader, Germplasm Enhancement & Crop Improvement CIP, Peru.
1997-2002: Senior Scientist and Head, Breeding and Genetics Department , CIP, Peru
1992-1996: Cassava Geneticist, CIAT, Colombia

Education:
1990: PhD, Plant Breeding, Cornell University, USA
1987: MSc, Plant Breeding and Plant Pathology, Cornell University, USA

Selected Recent Peer-reviewed publications:
- Andre C., Evers D., Ziebel J., Guignard C., Hausman J., **Bonierbale M**., Zum Felde T., and Burgos G. 2015. In Vitro Bioaccessibility and Bioavailability of Iron from Potatoes with Varying Vitamin C, Carotenoid, and Phenolic Concentrations. Journal of Agricultural and Food Chemistry, 63 (941): 9012–9021.
- Mihovilovich E., Sanetomo R., Hosaka K., Ordoñez B., Aponte M., & **Bonierbale M.** (2015). Cytoplasmic diversity in potato breeding: case study from the International Potato Center Molecular Breeding, 35: 1- 10.
- Lindqvist-Kreuze H., Gastelo M., Perez W., Forbes G., De Koeyer D., **Bonierbale, M.** (2014) Phenotypic Stability and Genome-Wide Association Study of Late Blight Resistance in Potato Genotypes Adapted to the Tropical Highlands. Phytopathology. 104: 624-633.
- Paget M., Amoros W., Salas E., Eyzaguirre R., Alspach P., Apiolaza L., Noble A., **Bonierbale, M.** (2014). Genetic Evaluation of Micronutrient Traits in Diploid Potato from a Base Population of Andean Landrace Cultivars. Crop Science. 54: 1949-1959.
- Sharma S.K., **et al.** (2013) Construction of Reference Chromosome-Scale Pseudomolecules for Potato: Integrating the Potato Genome with Genetic and Physical Maps. G3-Genes Genomes Genetics 3: 2031-2047.
- Xu, X.; **et al.** (2001). Genome sequence and analysis of the tuber crop potato. Nature. (USA). 475(7355):189-195.

Other Evidence of Leadership, large-program management and delivery:
- PI and Science Leader at CIP (annual budget $6 M to $7 M, 1997- 2016).
- PI of Advancing Achievements in Breeding for Early, Resilient and Nutritious Potato and Sweetpotato, USAID, $5 M 2016-17
- PI of Enhancing Micronutrient Content of Potato (HarvestPlus) realizing first significant genetic gains for iron and zinc concentrations in this crop with international team over 10 years.

Role in platform: Representing RTB on the Expert Advisory Group for Module 1: Breeding Excellence. Contributor and reviewer of the Excellence in Breeding Platform Proposal

HANS-JOACHIM BRAUN

Current position and affiliation: WHEAT and Global Wheat Program Director, CIMMYT

Profile: Hans-Joachim Braun is a native of Germany with background in wheat breeding based in Mexico, has led CIMMYT's Global Wheat Program since 2004 and CRP WHEAT since 2015. Responsible for technical direction and implementation of the program, he leads and manages 40 internationally recruited scientists, who develop wheat germplasm that is distributed to around 200 cooperators in more than 100 countries. He is board member of the Wheat Initiative, the International Wheat Yield Partnership and serves on the stakeholder advisory committee of the Canadian Wheat Alliance. In his 32 years with CIMMYT, he became familiar with all major wheat based cropping systems in the developing and developed world.

Employment:
2015-Present: Director CRP WHEAT, CIMMYT, Mexico
2006-Present: Director Global Wheat Program, CIMMYT, Mexico
2004-2005: Director Rainfed Wheat Systems, CIMMYT, Mexico
1990-2003: Head, CIMMYT/ICARDA International Winter Wheat Improvement Program, Turkey

Education:
1983: Ph.D. Dr. agrar., University of Hohenheim, Germany
1980: M.A. agrar. Ing., University of Hohenheim Diplom, Germany

Selected Recent Peer-reviewed publications:

- Arief, V.N., I. H. DeLacy, J. Crossa, T. Payne, R. Singh, H-J. Braun, T. Tian, K. E. Basford, and M. J. Dieters. 2014. Evaluating testing strategies for plant breeding field trials: redesigning a CIMMYT international wheat nursery to provide extra genotype connection across cycles. Crop Science 55: 164-177.
- Li, Huihui, R. P. Singh, H.-J. Braun, W. H. Pfeiffer, and Jiankang Wang. 2013. Doubled Haploids versus Conventional Breeding in CIMMYT Wheat Breeding Programs. Crop Science 53, 74-83.
- Reynolds MP, Hellin J, Govaerts B, Kosina P, Sonder K, Hobbs P, Braun B, 2012. Global crop improvement networks to bridge technology gaps. *J. Exp. Botany* 63: 1-12
- Braun, HJ., Atlin, G. and Payne, T. (2010) Multi-location testing as a tool to identify plant response to global climate change. In: Reynolds, MP. (Ed.) Climate change and crop production, CABI Climate Change Series, London, UK. 115:138.
- Dixon, J.; Braun, H.-J.; Crouch, J.H. 2009. Overview: Transitioning wheat research to serve the future needs of the developing world. In: Wheat Facts and Futures 2009. Dixon, J.; Braun, H.J.; Kosina, P.; Crouch, J.H. Mexico, DF (Mexico): CIMMYT, p. 1-25.

Other Evidence of Leadership, large-program management and delivery:

- Contributed to the development of more than 40 winter wheat varieties released mainly in West and Central Asia, which are grown on more than 1.5 million ha.
- Instrumental in recognizing Zn deficiency and soil borne diseases as a major constraint for winter wheat production in the dryland areas of West Asia.
- Received the Friendship Award of China for his contribution to develop disease resistant wheat lines for Gansu province.

Role in platform: Representing WHEAT on the Expert Advisory Group for Module 1: Breeding Excellence. Contributor to Module 1 of the Excellence in Breeding Platform Proposal.

JILL CAIRNS

Current position and affiliation: Senior Maize Physiologist, CIMMYT

Profile: Jill Cairns is Senior Maize Physiologist in the CIMMYT Global Maize Program, based at Harare, Zimbabwe. She is leading the efforts for incorporating heat stress tolerance into the CIMMYT and IITA maize breeding pipelines in sub-Saharan Africa (SSA). Cairns has also established remote sensing capacity within the national maize breeding program of Zimbabwe, and facilitated linkages between advanced research institutes and the Crop Breeding Institute (Zimbabwe).

Employment including current position

- 02/2013 to date: Senior scientist, Global Maize Program, CIMMYT, Zimbabwe.
- 07/2009 to 01/2013: Scientist, Global Maize Program, CIMMYT
- 03/2006 to 06/2009: International Research Fellow, IRRI
- 06/2003 to 02/2006: Postdoctoral Fellow, IRRI.

Education

- Ph.D. in Plant Science, University of Aberdeen, UK, 2003

Selected Recent Peer-reviewed publications:

- Zaman‐Allah M, Vergara O, Araus JL, Tarekegne A, Magorokosho C, Zarco‐Tejada PJ, Hornero A, Albà AH, Das B, Craufurd P, Olsen M, Prasanna BM, Cairns J (2015) Unmanned aerial platform‐based multi‐spectral imaging for field phenotyping of maize. Plant Methods 11:35
- Araus JL, Cairns JE (2014) Field high-throughput phenotyping: the new crop breeding frontier. Trends in Plant Sci. 19: 52-61.
- Cairns, J.E., J. Hellin, K. Sonder, J.L. Araus, J.F. MacRobert, C. Thierfelder, and B.M. Prasanna (2013) Adapting maize production to climate change in sub-Saharan Africa. Food Sec. 5: 345-360
- Cairns, J.E., J. Crossa, P.H. Zaidi, P. Grudloyma, C. Sanchez, J.L. Araus, S. Thaitad, D. Makumbi, C. Magorokosho, M. Bänziger, A. Menkir, S. Hearne, and G.N. Atlin (2013) Identification of drought, heat, and combined drought and heat tolerant donors in maize. Crop Sci. 53: 1335-1346.

Other Evidence of Leadership, large-program management and delivery:

- Identified key drought tolerant and heat tolerant donors for maize breeding through systematic screening of inbred lines within CIMMYT and IITA maize breeding programs.
- Quantified genetic gains within the maize breeding pipeline in eastern and southern Africa, providing the baseline for measuring future success of the maize breeding pipeline through the addition of new tools and techniques.
- The publication of Jill's results have been widely incorporated into international and national breeding programs in sub-Saharan Africa, Mexico and Asia.

Role in platform: Representing MAIZE on the Expert Advisory Group for Module 4: Phenotyping

APPOLINAIRE DJIKENG

Current position and affiliation: Director, BecA-ILRI Hub, ILRI

Profile: Appolinaire Djikeng was appointed as Director of the BecA-ILRI Hub in June 2013. Djikeng ensures the implementation of the BecA-ILRI Hub Business Plan and realization of the Hub's mission of improving the livelihoods of resource-poor people in Africa through the development and use of new technologies and strategies for sustaining agricultural production, improving human health, and conserving the environment.

Employment:
2012 – Present: Director, BecA-ILRI Hub, ILRI, Kenya
2009 – 2012: Technology Manager, BecA-ILRI Hub, ILRI, Kenya
2004 – 2009: Genomics Scientist, TIGR and J Craig Center Institute (JCVI), USA
1999 – 2004: Post doctorate and Associate Research Scientist, Yale University, USA

Education:
1999: PhD, Molecular Biology, Brunel University, UK
1994: MSC, Biology, University of Yaoundé I, Cameroon

Selected Recent Peer-reviewed publications:

- Ndunguru J, Sseruwagi P, Tairo F, Stomeo F, Maina S, **Djikeng A**, Kehoe M, Boykin LM. (2015). Analyses of Twelve New Whole Genome Sequences of Cassava Brown Streak Viruses and Ugandan Cassava Brown Streak Viruses from East Africa: Diversity, Supercomputing and Evidence for Further Speciation. ***PLoS One. 2015 Oct 28;10(10):e0141939***.
- Keambou TC, Hako BA, Ommeh S, Bembide C Ngono EP, Manjeli Y, Wamonje FO, Nzuki I, Wanjala B, Wamalwa M, Cho CY, Skilton RA and **Djikeng A** (2014). Genetic Diversity of the Cameroon Indigenous Chicken Ecotypes. ***International Journal of Poultry Science*** 13: 279-291.
- Lang J, Langlois P, Nguyen M, Purdie L, Holton T, **Djikeng A**, Vera Cruz CM, Verdier V and Leach J (2014) Sensitive detection of Xanthomonas oryzae pv. oryzae and X. oryzae pv. oryzicola by Loop Mediated Isothermal Amplification. ***Appl Environ Microbiol.*** 80: 4519-30.
- Kappmeyer LS, Thiagarajan M, Herndon DR, Ramsay JD, Caler E, **Djikeng A**, Gillespie JJ, Lau AOT, Roalson EH, Silva JC, Silva MG, Suarez CE, Ueti MW, Nene V, Mealey RH, Knowles DP, Brayton KA (2012). Comparative genomic analysis and phylogenetic position of *Theileria equi*. ***BMC Genomics*** 13:603. [Epub ahead of print]
- Guerrero FD, Moolhuijzen P, Peterson DG, Bidwell S, Caler E, Appels R, Bellgard M, Nene V and **Djikeng A** (2010). Reassociation kinetics analysis-based approach for partial genome sequencing of the cattle tick *Rhipicephalus (Boophilus) microplus*. ***BMC Genomics*** 11:374.

Other Evidence of Leadership, large-program management and delivery:

- Leader of the BecA-ILRI Hub (55 staff members) with an annual turnover of USD 12 million:
- BMGF & DFID joint award (US$ 12.5 million; 2015 - 2019): To support capacity building of African NARS scientists and institutes; Role: PI; BMGF (US$ 9.75 million; 2015 - 2019): To support CGIAR and African NARS breeding program through an integrated genotyping service and support; Role: PI
- Sida (US$ 20 million; 2012 - 2016): To support a mix portfolio of R4D programs (including the Brachiaria flagship program) and capacity building; Role: PI
- DFAT (AU$ 3 million; 2015 – 2016): To support the BecA-CSIRO partnership, the African Agricultural Productivity Program focusing on core BecA activities (ABCF program Food safety); Role: Partnership co-Manager

Role in platform: Representing AFS CRP on Livestock on the Expert Advisory Group for Module 3: Genotyping. Contributor to the Excellence in Breeding Platform Proposal.

KATE DREHER

Current position and affiliation: Germplasm Data Coordinator, CIMMYT

Profile: After graduating from college, Kate Dreher worked for one year at CIMMYT before going on to carry out her doctoral studies in plant biology at the University of California, Davis, USA. She transitioned from her lab-based research in plant molecular biology to work in biological curation and data management at the Carnegie Institution for Science in the Department of Plant Biology. There she worked to help make data available to the international scientific community through The Arabidopsis Information Resource (TAIR) and the Plant Metabolic Network. She has been working as a Germplasm Data Coordinator at CIMMYT since 2013. She helps to coordinate efforts to implement institutional databases and tools for storing and utilizing maize and wheat phenotypic, genotypic, and genealogical data. Her responsibilities include helping CIMMYT to further develop its Open Access policies, resources, and implementation plans in conjunction with other CGIAR centers.

Employment:
2007-2013: Biocurator, Carnegie Institution for Science, United States of America
2007-2007: Molecular Biology Consultant, CIMMYT, México
2001-2007: Graduate Research Assistant, University of California, Davis, United States of America
1999-2000: Consultant, CIMMYT, México

Education:
2007: Ph.D., Plant Biology , University of California, Davis, USA
1999: B.A. , Biology and Economics, Williams College, USA

Selected Recent Peer-reviewed publications:

- Kim T, **Dreher K**, Nilo-Poyanco R, Lee I, Fiehn O, Lange BM, Nikolau BJ, Sumner L, Welti R, Wurtele ES, Rhee SY. (2015) Patterns of metabolite changes identified from large-scale gene perturbations in Arabidopsis using a genome-scale metabolic network. Plant Physiology. 167(4):1685-98. doi: 10.1104/pp.114.252361.
- Lamesch P, Berardini TZ, Li D, Swarbreck D, Wilks C, Sasidharan R, Muller R, **Dreher K**, Alexander DL, Garcia-Hernandez M, Karthikeyan AS, Lee CH, Nelson WD, Ploetz L, Singh S, Wensel A, Huala E. (2012). The Arabidopsis Information Resource (TAIR): improved gene annotation and new tools. Nucleic Acids Research. 40(Database issue):D1202-10.
- Zhang P., **Dreher K.,** Karthikeyan A., Chi A., Pujar A., Caspi R., Karp P., Kirkup V., Latendresse M., Lee C., Mueller L.A., Muller R., and Rhee SY. (2010). Creation of a genome-wide metabolic pathway database for *Populus trichocarpa* using a new approach for reconstruction and curation of metabolic pathways for plants. Plant Physiology. 153(4):1479-1491.
- **Dreher, K.A.** and Callis, J. (2007) Ubiquitin, Hormones, and Biotic Stress in Plants. Annals of Botany. 99(5):787-822.
- **Dreher, K.**, Khairallah, M., Ribaut, J-M., and Morris, M. (2003) Money matters (I): costs of field and laboratory procedures associated with conventional and marker-assisted maize breeding at CIMMYT. Molecular Breeding. 11 (3): 221-234.

Other Evidence of Leadership, large-program management and delivery:

- 2015-2016: Organizer of the CGIAR Dataverse Community of Practice

Role in platform: Representing WHEAT on the Expert Advisory Group for Module 5: Bioinformatics

SUSANNE DREISIGACKER

Current position and affiliation: Germplasm Data Coordinator, CIMMYT

Profile: Combining genomic tools and quantitative genetic theory for new approaches in crop improvement; understanding the genetic basis of biotic (rust, septoria, tan spot, fusarium) and abiotic (drought, heat) stress responses in wheat; application of selection strategies in wheat breeding (MAS, MARS and GS) to improve biotic stress resistance and abiotic stress tolerance via molecular markers; genetic diversity and its use in crop improvement.

Employment:
2013 – present Senior Scientist, Global Wheat Program, Strategic lead: Wheat Molecular Breeding, CIMMYT, Mexico.
2005 – 2012 Associate Scientist and Scientist, Global Wheat Program, Strategic lead: Wheat Molecular Breeding, CIMMYT, Mexico.

Education:
2000: M.S. Agriculture Biology, University of Hohenheim, Stuttgart, Germany
2004: Ph.D. Plant breeding and Genetics, University of Hohenheim, Stuttgart, Germany

Selected Recent Peer-reviewed publications:

- Dreisigacker, S., Wang, X., Cisneros, B. A. M., Jing, R., & Singh, P. K. 2015. Adult-plant resistance to Septoria tritici blotch in hexaploid spring wheat. Theoretical and Applied Genetics, 1-13.
- Royo C., Dreisigacker, S., Alfaro, C., Ammar, K., and Villegas, D. 2015. Effect of Ppd-1 genes on durum wheat flowering time and grain filling duration in a wide range of latitudes. Journal of Agricultural Science. In press.
- Lopez-Cruz, M., Crossa, J., Bonnett, D., Dreisigacker, S,, Poland, J., Jannink, J-L., Singh, RP., Autrique, E., and de los Campos, G. 2015. Increased Prediction Accuracy in Wheat Breeding Trials Using a Marker× Environment Interaction Genomic Selection Model. G3: g3-114.
- Lopes, M. S., Dreisigacker, S., Peña, R. J., Sukumaran, S., and Reynolds, M. P. 2014. Genetic characterization of the Wheat Association Mapping Initiative (WAMI) panel for dissection of complex traits in spring wheat. Theoretical and Applied Genetics, 128(3): 453-464.
- Hickey, J.M., Dreisigacker, S., Crossa, J., Hearne, S., Babu, R., Prasanna, B.M., Grondona, M., Zambelli. A., Windhausen, V.S., Mathews, K.L., and Gorjanc, G. 2014. Evaluation of genomic selection training population designs and genotyping strategies in plant breeding programs using simulation. Crop Science 54 :1476-1488.

Other Evidence of Leadership, large-program management and delivery:

- Genomic & Open-source Breeding Informatics Initiative (GOBII), 2015-2020, Technology development initiative aims to facilitate the routine use of genomic data.
- Feed the Future Innovation Lab for Applied Wheat Genomics, 2013-2017, Genomic selection to boost genetic gains in wheat targeted to future warmer climates.
- BMZ-large grant, 2013-1015. Increasing the productivity of the wheat crop under conditions of rising temperatures and water scarcity in South Asia.
- BMZ-small grant, 2015-2016. Understanding cross pollination ability to improved seed production for future hybrid wheat.

Role in platform: Representing WHEAT on the Expert Advisory Group for Module 3: Genotyping

ANDREAS GISEL

Current position and affiliation: Bioinformatician, International Institute of Tropical Agriculture (IITA)

Profile:
NGS data analysis specialized on RNA-seq, non-coding RNA and GBS, specialized databases, genome annotation

Employment:
2015-Present: Bioinformatician, International Institute of Tropical Agriculture (IITA), Nigeria
2003-2014: Senior Researcher (Bioinformatics), Institute for Biomedical Technologies, CNR, Bari, Italy
2002-2003: Computational Biologist, Novartis SA, Basel, Switzerland
2001-2002: Bioinformatician, Friedrich Miescher Institute (Novartis Foundation), Basel, Switzerland

Education:
1995: PhD, Plant Sciences,ETH Zurich, Switzerland
1989: Diploma, Natural Sciences with specialization in Molecular Biology, ETH Zurich, Switzerland

Selected Recent Peer-reviewed publications:

- R Flores, S Minoia, A Carbonell, A Gisel, S Delgado, A López-Carrasco, B Navarro, F Di Serio; Viroids, the simplest RNA replicons: How they manipulate their hosts for being propagated and how their hosts react for containing the infection. Virus Research 3(1) 2015
- Sofia Minoia, Alberto Carbonell, Francesco Di Serio, **Andreas Gisel**, James C Carrington, Beatriz Navarro, Ricardo Flores; Specific Argonautes Selectively Bind Small RNAs Derived from Potato Spindle Tuber Viroid and Attenuate Viroid Accumulation In Vivo. Journal of Virology 88(20) 11933-11945
- **Andreas Gisel**, Mirna Valvano, Imane Ghafir El Idrissi, Patrizia Nardulli, Amalia Azzariti, Antonio Carrieri, Marialessandra Contino, Nicola Antonio Colabufo; miRNAs for the detection of multidrug resistance: overview and perspectives. Molecules 2014, 19(5), 5611-5623
- David Gomez-Cabrero, Imad Abugessaisa, Dieter Maier, Andrew Teschendorff, Matthias Merkenschlager, **Andreas Gisel**, Esteban Ballestar, Erik Bongcam-Rudloff, Ana Conesa, Jesper Tegnér; Data integration in the era of omics: current and future challenges. BMC Systems Biology 2014, 8(Suppl 2):I1
- Navarro B, **Gisel A**, Rodio ME, Delgado S, Flores R, Di Serio F.; Viroids: how to infect a host and cause disease without encoding proteins. Biochimie. 2012 Jul;94(7):1474-80.
- Navarro, B **Gisel, A** Rodio, ME Degado, S Flores, R Di Serio, F; RNAs containing the pathogenic determinant of a chloroplast-replicating viroid guide degradation of a host mRNA as predicted by RNA silencing. Small; Plant J Feb 14 2012
- Attwood, T.K **Gisel, A** Eriksson, N-E and Bongcam-Rudloff, E; Concepts, Historical Milestones and the Central Place of Bioinformatics in Modern Biology: A European Perspective. Bioinformatics, edited by: Dr. Mahmood Akhavan Mahdavi, INTECH

Other Evidence of Leadership, large-program management and delivery:

- 2008 – 2014 Executive Board Member of EMBnet
- 2011 – 2014 Coordinator of WP5 (Validation and Training) FP7 Project ALLBIO:
- 2011-2015 Coordinator of WP2 (Action plan for NGS bioinformatics) of the COST Action BM1006

Role in platform: Representing RTB on the Expert Advisory Group for Module 5: Bioinformatics

RUARAIDH SACKVILLE HAMILTON

Current position and affiliation: Principal Scientist, Evolutionary Biology and Head, T.T. Chang Genetic Resources Center, International Rice Research Institute.

Profile: Over 40 years' experience in the conservation and use of crop genetic resources including best practices and workflow management systems for genebank management, database design and data management, statistics, genetics and genomics, crop wild relatives, pre-breeding, plant breeding, plant ecology, GM biosafety, and international policy on access and benefit-sharing.

Employment:
2002-Present: Head, T.T. Chang Genetic Resources Center, IRRI, Los Baños, Laguna, Philippines
1991-2002: Head, Biodiversity Group and Genetic Resources Unit, IGER, Aberystwyth, UK
1986-1991: Senior Research Fellow, University of Wales at Bangor, Bangor, UK
1984-1986: Senior Research Fellow, CIAT, Cali, Colombia

Education:
1980: PhD Plant Genetic Resources, University of Cambridge, UK
1977: MA Applied Biology, University of Cambridge, UK

Selected publications:

- Zhao X; Daygon VD; McNally KL; Sackville Hamilton NR; Xie F; Reinke RF; Fitzgerald MA. 2016. Identification of stable QTLs causing chalk in rice grains in nine environments. Theoretical and Applied Genetics, 129:141-153.
- Hay FR; de Guzman F; Sackville Hamilton NR. 2015. Viability monitoring intervals for genebank samples of *Oryza sativa*. Seed Science and Technology. 43: 218-237
- Leung H; Raghavan C; Zhou B; Oliva R; Choi IR; Lacorte V; Jubay ML; Cruz CV; Gregorio G; Singh RK; Sackville Hamilton, NR. 2015. Allele mining and enhanced genetic recombination for rice breeding. Rice, 8: 1-11
- Alexandrov N; Tai S; Wang W; Mansueto L; Palis K; Fuentes RR; Ulat VJ; Chebotarov D; Zhang G; Li Z; Sackville Hamilton NR. 2015. SNP-Seek database of SNPs derived from 3000 rice genomes. Nucleic acids research. 43: D1023-D1027
- Banaticla-Hilario MCN; McNally KL; van den Berg RG; Sackville Hamilton NR. 2013. Crossability patterns within and among *Oryza* series *Sativae* species from Asia and Australia. Genetic resources and crop evolution. 60: 1899-1914
- Halewood M; Sood R; Sackville Hamilton NR; Amri A; Van den Houwe I; Roux N; Dumet D; Hanson J; Upadhyaya HD; Jorge A. 2013. Changing Rates of Acquisition of Plant Genetic Resources by International Gene Banks. Crop Genetic Resources as a Global Commons.

Other Evidence of Leadership, large-program management and delivery: Major past successes include the GPG1 and GPG2 genebank upgrading projects, establishing a new conservation research program at IRRI, and the 3000 rice genomes project. Member of steering / advisory / executive committees of Svalbard Global Seed Vault, Divseek, Genesys, A15G.

Role in platform: Representing the Platform on Genebanks on the Expert Advisory Group for Module 3: Genotyping. Contributor to Module 3 of the Excellence in Breeding Platform Proposal.

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OLIVIER HANOTTE

Current position and affiliation: Principal Scientist, International Livestock Research Institute (ILRI) and Professor of Population and Conservation Genetics, University of Nottingham

Profile: Hanotte has led a series of ground-breaking research programs examining fundamental aspects of livestock origin, diversity and adaptation both in Africa and Asia. The central theme of his research is the understanding at the genome level of the genetic adaptations of "tropical'' livestock to their production environments and their use in breeding improvement programs. He studies both livestock population selected intensively by human (productivity traits) as well as indigenous population under natural selection using genome-wide approaches. A major baseline element of his work is the understanding of the origin and history of livestock species and animal genetics resources diversity characterization is an important component of this work.

Employment:
2016-Present: Principal Scientist, International Livestock Research Institute (ILRI), Ethiopia
2009-Present: Professor of Population and Conservation Genetics, University of Nottingham, UK
2009-2010: Director, Frozen Ark, UK
1995-2008: Senior Scientist, ILRI, Ethiopia

Education:
1991: PhD Zoology, Université de Mons-Hainaut, Belgium and University of Leicester, UK
1984: Licence en Zoologie, Université de Libre de Bruxelles, Belgium

Selected Recent Peer-reviewed publications:

- Hussain Bahbahani, Harry Clifford, David Wragg, Mary N Mbole-Kariuki, Curtis Van Tassell, Tad Sonstegard, Mark Woolhouse and Olivier Hanotte. 2015. Signatures of positive selection in East African Shorthorn Zebu: A genome-wide SNP analysis. Scientific Reports 5: 11729. http://dx.doi.org/10.1038/srep11729
- Mwacharo, J.M., Nomura, K., Hanada, H., Han, J.L., Amano, T. and Hanotte, O. 2013. Reconstructing dispersal patterns of village chickens across East Africa: insights from autosomal markers. Molecular Ecology 22: 2683-2697.
- Hanotte, O., Dessie, T. and Kemp, S. 2010. Time to tap Africa's livestock genomes. Science 328: 1640-1641.
- Hanotte O., Bradley D. G., Ochieng J., Verjee Y., Hill E.W. and Rege J.E.O. 2002. African pastoralism: genetic imprints of origins and migrations. Science 296: 336-339.
- Hanotte O., Y. Ronin, Agaba M., Nilsson P., Gelhaus A., Horstmann R., Sugimoto Y., Kemp S., Gibson J., Korol A., Soller M. and Teale A. 2003. Mapping of QTL controlling resistance to trypanosomosis in African indigenous cattle. PNAS 100: 7443-7448.

Other Evidence of Leadership, large-program management and delivery: Conducts on-going active scientific collaborations with following institutions inlcude: the International Center for Agricultural Research in the Dry Area (ICARDA, Ethiopia), University of Edinburgh Roslin Institute (Scotland), Universidade Estadual Paulista – UNESP, Brazil.

Role in platform: Representing the AFS CRP on Livestock on the Expert Advisory Group for Module 2: Trait Discovery/Breeding. Contributor to Module 1 of the Excellence in Breeding Platform Proposal.

SARAH JANE HEARNE

Current position and affiliation: Senior Scientist, CIMMYT

Profile: Assessment of the genomic and phenotypic diversity of the CIMMYT genebank collection of maize and other publically accessible maize genetic resources. GWAS for high priority traits using landrace panels. Selection sweep evaluation for key abiotic, biotic and anthropogenic characteristics of maize landraces. Modelling training population formation, selection techniques and breeding methods for GS advancement to optimise landrace based pre-breeding approaches for oligo and polygenic traits. Pre breeding using genomic selection and forward breeding. Development of new analytical approaches to explore and understand maize genetic diversity. Work with bioinformaticians and programmers to develop integrated systems and specific tools for genetic research, breeding application and knowledge dissemination. Leadership, oversight, coordination, planning and monitoring of activities within the maize and informatics components of the SeeD initiative. Fundraising and research strategy development.

Employment:
2011-Present: Senior scientist and molecular geneticist and pre-breeder, CIMMYT, Mexico.
2008-2011: Plant Molecular Geneticist/Physiologist, IITA Ibadan & IITA, Kenya
2005-2008: Plant Molecular Geneticist/Physiologist, IITA, Kenya
2001-2003: Postdoctoral Fellow - Molecular Geneticist / Physiologist, CIMMYT, Mexico

Education:
2001: Ph.D. "Morphological, physiological and molecular interactions between maize and the parasitic angiosperm *Striga hermonthica*," The University of Sheffield, UK
1997: B.Sc., Applied Plant Science, The University of Manchester, UK

Select Publications:

- Gorjanc, G., Jenko, J., Hearne, S.J., Hickey, J.M. Initiating maize pre-breeding programs using genomic selection to harness polygenic variation from landrace populations. (2016) BMC Genomics, 17, DOI:10.1186/s12864-015-2345-z
- Adebayo, M.A., Menkir, A., Blay, E., Gracen, V., Danquah, E., Hearne, S. Genetic analysis of drought tolerance in adapted × exotic crosses of maize inbred lines under managed stress conditions. (2014) Euphytica, 196 (2), pp. 261-270.
- Semagn, K., Babu, R., Hearne, S., Olsen, M. Single nucleotide polymorphism genotyping using Kompetitive Allele Specific PCR (KASP): Overview of the technology and its application in crop improvement. (2014) Mol Breeding, 33 (1), pp. 1-14.
- Swarts K., Li H., Alberto Romero Navarro J., An D., Romay M.C., Hearne S., Acharya C., Glaubitz J.C., Mitchell S., Elshire R.J., Buckler E.S., Bradbury P.J. Novel methods to optimize genotypic imputation for low-coverage, next-generation sequence data in crop plants. (2014) Plant Genome, 7 (3)
- Mir, C., Zerjal, T., Combes, V., Dumas, F., Madur, D., Bedoya, C., Dreisigacker, S., Franco, J., Grudloyma, P., Hao, P.X., Hearne, S., Jampatong, C., Laloë, D., Muthamia, Z., Nguyen, T., Prasanna, B.M., Taba, S., Xie, C.X., Yunus, M., Zhang, S., Warburton, M.L., Charcosset, A. Out of America: Tracing the genetic footprints of the global diffusion of maize. (2013) TAG, 126 (11), pp. 2671-2682.
- Muchero, W., Diop, N.N., Bhat, P.R., Fenton, R.D., Wanamaker, S., Pottorff, M., Hearne, S., Cisse, N., Fatokun, C., Ehlers, J.D., Roberts, P.A., Close, T.J. A consensus genetic map of cowpea [Vigna unguiculata (L) Walp.] and synteny based on EST-derived SNPs. (2009) PNAS, 106 (43), pp. 18159-18164.

Role in platform: Representing MAIZE on the Expert Advisory Group for Module 2: Trait Discovery/Breeding. Author and Co-author of Modules 2 and 3 of the Excellence in Breeding Platform Proposal.

PRASAD S. HENDRE

Current position and affiliation: Genomics Scientist-AOCC genomics lab, World Agroforestry Centre (ICRAF)

Profile: Prasad is appointed as genomics scientist to lead the African Orphan Crops Consortium (AOCC) genomics laboratory at ICRAF, Nairobi, Kenya. His main experience is in the area of genomics and molecular breeding of tree crops.

Employment:
2015-Present: Genomics scientist, ICRAF, Kenya
2012-2014: Research Scientist, ITC-LSTC, India
2007- 2012: Associate Scientist, ITC-LSTC, India

Education:
2007: Ph.D., Life Science, Jawaharlal Nehru University, India
1998: M.Sc. (Agri.) in Genetics and Plant breeding, Mahatma Phule Agric. University, India

Selected Recent Peer-reviewed publications:

- Hendre P.S., A. Muchugi, R. Jamnadass, S. Bo, X. Xu, S. Cheng, X. Liu, J. Featherstone, C. Hefer, J. Rees, A. van Deynze and H-Y Shapiro (2016) African Orphan Crops Consortium: a Global Partnership to Address Food and Nutritional Requirements in Africa through Genomics Applications. Poster presented during Plant and Animal Genome conference-2016.
- Hendre, P.S., Kamalakannan, R. and Mohan Varghese (2012) High throughput and parallel SNP discovery in selected candidate genes in *Eucalyptus camaldulensis* using Illumina NGS platform. Plant Biotechnology Journal, 10, 646-656, doi: 10.1111/j.1467-7652.2012.00699.x.
- Hendre, P.S., Bhat, P.R., Krishnakaumar, V., Ramesh Aggarwal (2011) Isolation and characterization of resistance gene analogues from *Psilanthus* species that represent wild relatives of cultivated coffee endemic to India. Genome, 54, 377-390.
- Hendre, P.S., R. Phanindranath, V. Annapurna, Lalremreuta, A. and R.K. Aggarwal (2008) Development of new genomic microsatellite markers from robusta coffee (*Coffea canephora* Pierre ex A. Froehner) showing broad cross-species transferability and utility in genetic studies. BMC Plant Biology, 8: 51; doi: 10.1186/1471-2229-8-51.
- Aggarwal, R.K., Prasad S. Hendre, Rajeev K. Varshney, Prasanna R. Bhat, V. Krishnakumar and L. Singh (2007) Identification, characterization and utilization of EST-derived genic microsatellite markers for genome analyses of coffee and related species. Theoretical and Applied Genetics, 114: 359-372; doi: 10.1007/s00122-006-0440-x.

Other Evidence of Leadership, large-program management and delivery:

- Coordinated a large association mapping study in *Eucalyptus camaldulensis* under his earlier employment which involved CSIRO (Australia) and his group from ITC-LSTC, Bangalore, India.
- Led an *in-house* genome sequencing and methylome mapping project for *Eucalyptus camaldulensis* under complete private ownership by ITC-LSTC using outsourcing model.
- Awarded NSF-BREAD-2016 grant as a co-applicant from ICRAF along with UNH (Dr. Iago Hale- PI), University of Ghana (WACCI) and CRIG, Ghana.

Role in platform: Representing FTA on the Expert Advisory Group for Module 3: Genotyping. Contributor to Module 3 of the Excellence in Breeding Platform Proposal.

RAMNI H. JAMNADASS

Current position and affiliation: ICRAF Science Domain Leader and ICRAF Leader for African Orphan Crops Genomics Laboratory

Profile:
Main area of expertise: Tree domestication, molecular biology, conservation genetics, tree foods for nutrition and health. >10 years' of experience of science team management.

Employment:
2013-Present: Leader for African Orphan Crops Genomics Laboratory, ICRAF, Kenya
2012-Present: Science Domain Leader (Diversity, Domestication and Delivery), ICRAF, Kenya
2007-2011: Global Research Program Leader, ICRAF, Kenya
2005-2007: Head of Genetics Resources Unit (Global Unit), ICRAF, Kenya

Education:
1997-2003: Post-doctoral fellowship, Genetic Diversity and Conservation of Genetic, University of Nairobi, Kenya
1994: Ph.D. Molecular biology / Biochemistry, International Livestock Research Institute (ILRI) and Brunel University, UK

Most Relevant Publications:

- Dawson I, Harwood C, **Jamnadass R**, Beniest J (eds.) (2012) Agroforestry tree domestication: a primer. The World Agroforestry Centre, Nairobi, Kenya. 148 pp
- Public Private Partnerships in Agroforestry (2014) **Jamnadass**, R. Langford, K. Anjarwalla, P. Mithöfer, D. In van Alfen, N. (ed.) Encyclopaedia of Agriculture and Food Systems Vol.4 San Diego: Elsevier p544-564
- **Jamnadass**, R. McMullin, S. Iiyama, M. Dawson, I.K. Powell, B. Termote, C. Ickowitz, A. Kehlenbeck, K. Vinceti, B. van Vliet, N. Keding, G. Stadlmayr, B. Van Damme, P. Carsan, S. Sunderland, T. Njenga, M. Gyau, A. Cerutti, P. Schure, J. Kouame, C. Obiri, B.D. Ofori, D. Agarwal, B. Neufeldt, H. Degrande, A. Serban, A. **2015** Understanding the roles of forests and tree-based systems in food provision *IUFRO World Series vol. 33 In: Vira, B., Wildburger, C., Mansourian, S. 2015. Forests, Trees and Landscapes for Food Security and Nutrition: a global assessment report* p25-49 2015062 http://bit.ly/1K1Ub8Y
- Utilization and transfer of forest genetic resources: A global review (2014) Jarkko Koskela, Barbara Vinceti, William Dvorak, David Bush, Ian K Dawson, Judy Loo, Ramni **Jamnadass**, Forest Ecology and Management 333, 22-34
- Innovation in input supply systems insmallholder agroforestry: seed sources, supply chains and support systems (2011), Lilles, JBL, Graudal, L, Jamnadass, R. Agroforestry Systems, 83(2) 347-359
- Allanblackia, a new tree crop in Africa for the global food industry: market development, smallholder cultivation and biodiversity management (2010): R Jamnadass, IK Dawson, P Anegbeh, E Asaah, A Atangana, Forests, Trees and livelihoods 19 (3), 251---268
- Colfer C J P, Elias M, **Jamnadass** R, **2015** Women and men in tropical dry forests: a preliminary review *International Forestry Review 17(S2)*

Role in platform: Representing FTA on the Expert Advisory Group for Module 1: Breeding Excellence.

AWAIS KHAN

Current position and affiliation: Senior Scientist at International Potato Center (CIP)

Profile:
Plant Geneticist with over 10 years of experience in genetics, genomics, and molecular breeding with multiple crops of agricultural importance. Research focus on modern genomic, genetic, bioinformatics & breeding tools to understand and improve abiotic stress tolerance and disease resistance in crops at multiple levels. Proven ability to bring together diverse scientific disciplines and stakeholders such as breeders, international research organizations, universities, students, farmers, and donors to conceive and implement innovative projects for crop improvement.

Employment:
2015-Current: Senior Scientist, Genetics of Adaptation & Abiotic Stress Tolerance of Potato & Sweetpotato and database management, at International Potato Center (CIP), Peru
2012-2015: Scientist, Genetics of Adaptation & Abiotic Stress Tolerance of Potato & Sweetpotato and Database Management, International Potato Center (CIP), Peru
2010-2012: Postdoctoral Research Scientist, Department of NRES, University of Illinois, Urbana-Champaign, USA
2008-2010: Postdoctoral Research Associate, CNAP, Department of Biology, University of York, UK

Education:
2007: Ph.D., Molecular Plant Breeding and Quantitative Genetics, Swiss Federal Institute of Technology Zürich (ETH), Switzerland
2003: M.Sc., Plant Breeding and Genetics/Tropical & International Agriculture, Georg-August University Göttingen, Germany

Selected Recent Peer-reviewed publications:

- **Khan MA**, Sovero V, Gemenet D .2016. Genome-assisted Breeding For Drought Resistance. **Curr. Genomics**. 17:1-13. doi: 10.2174/1389202917999160211101417
- Lindqvist Kreuze H, **Khan MA**, Salas E, Meiyalaghan S, Thomson S, Gomez R, Bonierbale M. 2015. Tuber shape and eye depth variation in a diploid family of Andean potatoes. **BMC Genetics**.
- **Khan MA**, Saravia D, Munive S, Lozano F, Farfan E, Eyzaguirre R, Bonierbale M. 2014. Multiple QTLs Linked to Agro-Morphological and Physiological Traits Related to Drought Tolerance in Potato. **Plant Molecular Biology Reporter**, 1-13.
- **Khan MA**, Olsen KM, Sovero V, Kushad MM, Korban SS. 2014. Fruit quality traits might have played crucial role in domestication of apple. **The Plant Genome**
- Cabello R, Monneveux P, Bonierbale M, **MA Khan**. 2014. Heritability of yield components under irrigated and drought conditions in Andigenum potatoes. **American Journal of Potato Research**.
- Wu J, Wang Z, Shi Z, Zhang S, Ming R, Z Shilin, **Khan MA**, et al. 2012. The genome of pear (*Pyrus bretschneideri* Rehd.). **Genome Research**. 23 (2), 396-408.

Other Evidence of Leadership, large-program management and delivery:
1. CIP's PI for Rapid and targeted introgression of traits via genome elimination. National Science Foundation (NSF), Plant Genome Research Program (PGRP); CIP and UC Davis ($1.5 M, 2015-2017).
2. CIP's PI for Genomic and Bioinformatic tools for Sweetpotato Improvement: BMGF; Collaborators, NCSU, BTI, MSU, NaCRRI in Uganda, CSIR in Ghana, University of Queensland, Australia ($12.5 M, 2015-2018).
3. Member of core writing teams for CIP's strategic objectives, Agile Potato for Asia and Game-Changing Solutions and RTB NextGen and breeding community of practice clusters for Discovery flagship of 2nd phase proposal.

Role in platform: Representing RTB on the Expert Advisory Group for Module 4: Phenotyping. Contributor to Module 3 of the Excellence in Breeding Platform Proposal.

STEPHEN KEMP

Current position and affiliation: Program Leader, Animal Biosciences, International Livestock Research Institute (ILRI) and Professor of tropical livestock genetics and health at the Roslin Institute, University of Edinburgh

Profile: Kemp led a series of important research programs, which established novel approaches for investigating the genomics of tropical adaptation, notably disease resistance. He leads a group concerned with genetics, genomics and conservation of livestock diversity and has established a unique structure – physical, human and informatics – to support this work. He has expertise in the genomics of tropical adaptation, particularly host-pathogen interactions and mechanisms of tolerance and resistance as well as informatics systems. He leads ILRI's cross-cutting LiveGene initiative.

Employment:
2005-2012: Senior Scientist and Genomics Team Leader, International Livestock Research Institute
2000-2014: Professor of Molecular Genetics, University of Liverpool
1995-2000: Lecturer, University of Liverpool
1991-1995: Project Leader, Ruminant Genetics, International Laboratory for Research on Animal Diseases

Education:
1985: PhD, Immunogenetics, University of Edinburgh, UK
1979: BSc (Hons) Zoology, University of Wales, UK

Selected Recent Peer-reviewed publications:

- Noyes, H., Githiori, J., Bradley, J., Kemp, S., and Behnke, M. 2014. Evidence for genes controlling resistance to Heligmosomoides bakeri on mouse chromosome 1. Parasitology 7: 1-10.
- Roex N., Noyes, H., Brass, A., Bradley, D., Kemp, S., and Kay S. 2014. Novel SNP Discovery in African Buffalo, Syncerus caffer, using High-Throughput Sequencing. PLOS ONE 7: 11
- Norling, M., Kihara, A. and Kemp S.J., 2013. Web-Based Biobank System Infrastructure Monitoring Using Python, Perl, and PHP Biopreservation and Biobanking. 11: 355-358.
- Silva, M.V.B., Sonstegard, T.S., Hanotte, O., Mugambi, J.M., Garcia, J.F., Nagda, S., Gibson, J.P., Iraqi, F.A., McClintock, A.E., Kemp, S.J., Boettcher, P.J., Malek, M., Tassell, C.P. Van, Baker, R.L. 2012. Identification of quantitative trait loci affecting resistance to gastrointestinal parasites in a double backcross population of Red Maasai and Dorper sheep. Animal Genetics 43:63-71.
- Noyes, H., Brass, A., Obara, I., Anderson, S., Archibald, A.L., Bradley, D.G., Fisher, P., Freeman, A., Gibson, J., Gicheru, M., Hall, L., Hanotte, O., Hulme, H., McKeever, D., Murray, C., Oh, S.J., Tate, C., Smith, K., Tapio, M., Wambugu, J., Williams, D.J., Agaba, M., and Kemp, S.J. 2011.Genetic and expression analysis of cattle identifies candidate genes in pathways responding to Trypanosoma congolense infection. PNAS 108: 9304-9.
- Hanotte, O., Dessie, T. and Kemp S.J. 2010. Time to Tap Africa's Livestock Genomes. Science 328:1640-1641.

Scientific management and leadership: His research group at ILRI comprises some 35 scientists, post-docs, students and technicians. He played a key role in the establishment of the Joint Centre for Tropical Livestock Genetics and Health. Total funding for the group is approximately $5m/year. Current and recent major funders include DFID, BMGF, BBSRC, Wellcome Trust, National Science Foundation.

Role in platform: Representing the AFS CRP on Livestock on the Expert Advisory Group for Module 5: Bioinformatics. Contributor to the Excellence in Breeding Platform Proposal.

ROELAND KINDT

Current position and affiliation: Senior Ecologist, Science Domain 3, World Agroforestry Centre (ICRAF)

Profile:
Roeland Kindt's research is focused on tree species suitability modelling and mapping, combining ensemble suitability modelling algorithms with information on distribution and species assemblages of potential natural vegetation types, using skills in R and KML programming and scripting, GIS, database design and website development. Similar skills were used to develop online decision support tools such as the Agroforestry Species Switchboard and the Useful Tree Species for Eastern Africa. As coordinator of a project on 'Testing options and training partners in participatory tree domestication and marketing in East Africa', various training materials and tools were developed and tested with representative national users such as the Tree Diversity Analysis manual and the Tree Seeds for Farmers toolkit.

Employment:
2013-2016: Senior ecologist, World Agroforestry Centre, Kenya
2008-2013: Ecologist, World Agroforestry Centre, Kenya
2003-2007: Project Coordinator, VVOB, Kenya
1994-2002: Associate scientist, World Agroforestry Centre, Kenya

Education:
2012: PhD degree in Applied Biological Sciences, Gent University, Belgium
1992: MSc degree in Agricultural and Applied Biological Sciences, Gent University, Belgium

Selected Recent Peer-reviewed publications:

- Kindt R. 2016. BiodiversityR: Package for Community Ecology and Suitability Analysis (current version 2.6-1). URL https://cran.r-project.org/web/packages/BiodiversityR
- Oksanen J, Blanchet FG, Kindt R, Legendre P, Minchin PR, O'Hara RB, et al. 2015 Vegan: community ecology package (current version 2.3-3). URL http://cran.r-project.org/web/packages/vegan
- Kindt R, van Breugel P, Orwa C, Lillesø J-PB, Jamnadass R, Graudal L. 2015. Useful Tree Species for Eastern Africa. URL http://www.vegetationmap4africa.org/3_Species/Species_selection_tool.html
- van Breugel P, Kindt R, Lillesø J-PB, van Breugel M. 2015. Environmental Gap Analysis to Prioritize Conservation Efforts in Eastern Africa. PLoS ONE 10:4 DOI: 10.1371/journal.pone.0121444
- Kindt R et al. 2014.Correspondence in forest species composition between the Vegetation Map of Africa and higher resolution maps for seven African countries. Applied Vegetation Science 17: 162-171
- Luedeling E, Kindt R, Huth NI, Koenig K. 2014. Agroforestry systems in a changing climate – challenges in projecting future performance Current Opinion in Environmental Sustainability 6: 1-7
- Ranjitkar S, Kindt R, et al. 2014. Separation of the bioclimatic spaces of Himalayan tree Rhododendron species predicted by ensemble suitability models. Global Ecology and Conservation 1: 2-12.

Other Evidence of Leadership, large-program management and delivery: Roeland is the ICRAF focal point for CRP-FTA flagship 2 and sometimes acts as ICRAF science domain leader (and on occasion as ICRAF deputy director general). He coordinates various projects or work packages, leads the database team of the science domain and genebank, supervises several PhD and MSc students, co-supervises programmers of ICRAF's geospatial lab, is a member of the Forests, Trees and Agroforestry sentinel landscapes methods group and participates in proposal development, training activities, seminars and panel interviews.

Role in platform: Representing FTA on the Expert Advisory Group for Module 5: Bioinformatics.

GEORGE KOTCH

Current position and affiliation: Head of Plant Breeding at IRRI

Profile: R&D Management, Strategic Planning, Portfolio and Talent Management, Change Management

Employment:
January-October 2015: PresentPresident and Owner, George Kotch and Associates Consulting, USA
2013-2015: VP of R&D (Americas/Pacific Rim) HM. Clause, Limagrain, USA
2012-2013: Visiting Industry Scientist, U.C. Davis, USA
2011-2012: Head of Global Vegetable R&D, Syngenta, Switzerland

Education:
1987: Ph.D in Plant Breeding and Genetics, University of Wisconsin-Madison, USA
1983: M.S. in Genetics, Pennsylvania State University, USA

Selected Recent Peer-reviewed publications:

Other Evidence of Leadership, large-program management and delivery: Board of Directors for GenZ Corporation

Role in platform: Representing RICE on the Expert Advisory Group for Module 1: Breeding Excellence. Author of Module 1 of the Excellence in Breeding Platform Proposal.

TOBIAS KRETZSCHMAR

Current position and affiliation: Scientist I – Molecular Biology; Head of Genotyping Services Laboratory (GSL); Plant Breeding Division, IRRI

Profile: Molecular Biology, Molecular Genetics, Molecular Physiology

Employment:
2013-2016: Scientist I-Molecular Biology, Gene Discovery, IRRI, Philippines
2011-2013: Collaborative Research Scientist, Trait Development –Submergence, IRRI, Philippines
2009-2010: Postdoctoral Fellow, Molecular Plant Physiology, University of Zurich, Switzerland

Education:
2009: Doctorate of Philosophy (PhD); Molecular Plant Physiology; University of Zürich; Switzerland
2004: Diploma Thesis (Master Thesis equivalent); Plant Physiology; TU Kaiserslautern; Germany

Selected Recent Peer-reviewed publications:

- Wang F, Rose T, Jeong K, **Kretzschmar T**, Wissuwa M **(2015)** The knowns and unknowns of phosphorus loading into grains, and implications for phosphorus efficiency in cropping systems. **J Exp Bot.** [Epub ahead of print]
- **Kretzschmar T**, Pelayo MAF, Trijatmiko KR, Gabunada LF, Alam R, Jimenez R, Mendioro MS, Slamet-Loedin IH, Sreenivasulu N, Bailey-Serres J, Ismail AM, Mackill DJ, Septiningsih EM **(2015)** A trehalose-6-phosphate phosphatase enhances anaerobic germination tolerance in rice. **Nature Plants 1,** 15124
- Wissuwa M, Kondo K, Fukuda T, Mori A, Rose MT, Pariasca-Tanaka J, **Kretzschmar T**, Haefele S and Rose TJ **(2015)** Unmasking novel loci for internal phosphorus utilization efficiency in rice germplasm through Genome-Wide Association Analysis. **PLOS One**, DOI: 10.1371/journal.pone.0124215
- **Kretzschmar T**, Kohlen W, Sasse J, Borghi L, Schlegel M, Bachelier JB, Reinhardt D, Bours R, Bouwmeester HJ, Martinoia E **(2012)** A petunia ABC protein controls strigolactone-dependent symbiotic signalling and branching. **Nature 483**,341-344.
- **Kretzschmar T**, Burla B, Lee Y, Martinoia E, Nagy R **(2011)** Functions of ABC transporters in plants. **Essays in Biochemistry 50**,145-160.

Other Evidence of Leadership, large-program management and delivery:

- IRRI Principal Investigator of the Genomics Open Source Breeding Informatics Initiative (GOBII)

Role in platform: Representing RICE on the Expert Advisory Group for Module 3: Genotyping. Contributor to Module 3 of the Excellence in Breeding Platform Proposal.

RAMIL P. MAULEON

Current position and affiliation: Scientist II – Bioinformatics Specialist, IRRI

Profile: Bioinformatic analysis for molecular genetics & "-omics" data; Implementing/designing re-usable analysis workflows & computing resources for high throughput datasets with high computing demand

Employment:
2009-Present: Scientist - Bioinformatics specialist, IRRI, Philippines
2006-2009: Post doctoral fellow, Data Analysis Support to Genomics and Transcriptomics, Generation Challenge Program, IRRI, Philippines
2001-2006: Assistant Professor, Institute of Biological Sciences, College of Arts and Sciences, University of the Philippines Los Baños, Philippines
1999-2001: Crop manager for rice business, Syngenta Philippines Inc. Metro Manila, Philippines

Education:
2006: Ph.D. Genetics, University of the Philippines Los Baños, Philippines
1996: M.Sc. Genetics, University of the Philippines Los Baños, Philippines

Selected Recent Peer-reviewed publications:

- 3K R.G.P. The 3,000 rice genomes project. (2014). Gigascience3:7.
- Alexandrov, N., S Tai, W Wang, L Mansueto, K Palis, R Fuentes, VJ Ulat, D Chebotarov, G Zhang, Z Li, R Mauleon, R Sackville Hamilton & KL McNally. (2014). SNP-Seek database of SNPs derived from 3000 rice genomes. Nucl. Acids Res. 43 (D1): D1023-D1027. doi:10.1093/nar/gku1039
- Swamy B P M, HU Ahmed, A Henry, R Mauleon, S Dixit, P Vikram, et al.(2013). Genetic, Physiological, and Gene Expression Analyses Reveal That Multiple QTL Enhance Yield of Rice Mega-Variety IR64 under Drought. PLoS ONE 8(5):e62795. DOI:10.1371/journal.pone.0062795
- Jahn CE, Mckay JK, Mauleon R, Stephens J, McNally KL, Bush DR, Leung H, Leach JE. 2011. Genetic variation in biomass traits among 20 diverse rice varieties. Plant Physiol. 155(1):157-168
- Thomson MJ., K Zhao, M Wright, KL. McNally ,J Rey , CW Tung , A Reynolds , B Scheffler , G Eizenga , A McClung , H Kim , AM. Ismail , M de Ocampo , C Mojica , MY Reveche , CJ. Dilla-Ermita , R Mauleon , H Leung , C Bustamante , SR. McCouch. (2011). High-throughput single nucleotide polymorphism genotyping for breeding applications in rice using the BeadXpress platform. Mol Breeding.DOI 10.1007/s11032-011-9663-x

Other Evidence of Leadership, large-program management and delivery:

- Led IRRI-AWS Public Data Sets initiative for the 3,000 Rice Genomes collaborative project

Role in platform: Representing RICE on the Expert Advisory Group for Module 5: Bioinformatics. Contributor to Module 5 of the Excellence in Breeding Platform Proposal

LUKAS A. MUELLER

Current position and affiliation: Associate Professor, Boyce Thompson Institute, Cornell University

Profile: Mueller leads a 12-member group that designs and implements databases that assist scientists in their research and plant breeders in more efficient crop improvement. The databases and software make transcriptomic, genotypic and phenotypic data from thousands of experiments accessible to the public, often focusing on under-researched staple crops from food-insecure regions. The Mueller laboratory collaborates on a variety of different projects. (i) the Cassavabase; (ii) the Solanaceae Genomics Network—a compilation of all the genetic information known about solanaceous plants; (iii) Breeding databases for yam, sweet potato and the cooking banana; Mueller also collaborates on the Genomic and Open-source Breeding Informatics Initiative (GOBII) to streamline crop breeding for five staple crops—wheat, rice, maize, sorghum and chickpea. Finally, the Mueller group is involved in multiple genome sequencing projects, including tomato, coffee, petunia and Nicotania benthamiana.

Employment:
2014-present, Associate Professor, Boyce Thompson Institute Cornell University, U.S.
2008-2014, Assistant Professor, Boyce Thompson Institute, Cornell University, U.S.
2003-2008, Senior Research Associate, Solanaceae Genomics Network Facility, Cornell University, U.S.
2000-2003, Curator, Arabidopsis Information Resource (TAIR), Carnegie Institution at Stanford, U.S.

Education
1997, PhD in Biochemistry, University of Lausanne, Switzerland
1991, Diploma Natural Sciences, Swiss Federal Institute of Technology (ETH), Zurich Switzerland

Selected Recent Peer-reviewed publications:

- The Tomato Genome Sequencing Consortium (2012) The tomato genome sequence provides insights into fleshy fruit evolution. Nature 485:635-641.
- Bombarely, A, Menda, N, Tecle, IY, Buels, RM, Strickler, S, Fischer-York, T, Pujar, A, Leto, J, Gosselin, J, and Mueller, LA (2011) The Sol Genomics Network (solgenomics.net): growing tomatoes using Perl. Nucleic Acids Res, 39: D1149-D1155
- Tecle, IY, Menda, N, Buels, RM, van der Knaap, E, and Mueller, LA (2010) solQTL: a tool for QTL analysis, visualization and linking to genomes at SGN database. BMC Bioinformatics, 21(11): 525
- Menda, N, Buels, RM, Tecle, I, and Mueller, LA (2008) A community-based annotation framework for linking solanaceae genomes with phenomes. Plant Physiol, 147: 1788-1799
- Mueller, LA, Mills, AA, Skwarecki, B, Buels, RM, Menda, N, and Tanksley, SD (2008) The SGN comparative map viewer. Bioinformatics, 24: 422-423

Role in platform: External member on the Expert Advisory Group for Module 5: Bioinformatics.

RAPHAEL MRODE

Current position and affiliation: Principal scientist in quantitative dairy cattle genetics at the International Livestock Research Institute (ILRI) and professor in Quantitative Animal genetics and genomics at the Scottish Rural College (SRUC).

Profile: Mrode has undertaken outstanding research in the application of linear models for data analyses, methods to reduce the dimensions of multi-trait analyses and genetic evaluation of new or novel traits at the national and international level. Recent work has been focused on the incorporation of molecular information in genetic evaluation procedures for traits of economic importance in livestock. This encompasses the use SNPs in computation of genomic breeding values and genomic selection on a within and across breeds basis.

Employment:
1991 – 2004, Senior Geneticist in MDC Evaluations Limited, United Kingdom.
1989 – 1991, Post-doctoral Fellow in the Department of Animal and Poultry science, University of Guelph
1988 – 1989, Post-doctoral Fellow in AFRC Institute of Animal Physiology and Genetic Research, Edinburgh
1984 – 1985, Assistant Lecturer, University of Ife, Nigeria

Education
1988, PhD, University of Edinburgh, UK
1984, MPhil, University of Ife, Nigeria

Selected Recent Peer-reviewed publications:

- Mucha, S., Mrode, R., I. MacLaren-Lee, M. Coffey, J. Conington. 2015. Estimation of genomic breeding values for milk yield in the UK dairy goats. *Journal of Dairy Science*
- Pickering, N., Chagunda, M., Banos, G., Mrode, R., and McEwan, J., Walls, E. 2015. Genetic parameters for predicted methane production and laser methane detector measurements. *Journal of Animal Science* 93:11-20
- Mucha, S., Mrode, R., Coffey, M., and Conington, J. 2014. Estimation of genetic parameters for milk yield across lactations in mixed breed dairy goats. *Journal of Dairy Science* 99: 2455-2461
- Mrode R.A. 2014. Linear models for the prediction of animal breeding values. Wallingford: CAB International.
- Abdullahpour, R., Shahrbabak, M. M., Nejati-Javaremi, A., Torshizi, R.V and **Mrode, R** (2013) Genetic analysis of milk yield, fat and protein content in Holstein dairy cows in Iran: Legendre polynomials random regression model applied. Archiv Tierzucht (Archives Animal Breeding) 56:48

Scientific management and leadership*:*

- Author of a widely used text book on the use of linear models and genomic selection on the prediction of the genetic merit of animals**.**
- Active and on-going research collaborations include the University of Edinburgh and China Agricultural University

Role in platform: Representing the AFS CRP on Livestock on the Expert Advisory Group for Module 1: Breeding Excellence.

ALICE MUCHUGI

Current position and affiliation: Genetic Resource Unit Manager, World Agroforestry Centre (ICRAF) Nairobi

Profile:
Has over 15 years' experience in research on sustainable utilization and conservation of indigenous plant genetic resources. Research mainly on morphological, biochemical and genetic characterization of plant germplasm

Employment History:
2014-Present: Genetic Resource Unit Manager, World Agroforestry Centre (ICRAF), Kenya
2007-2013: Consultant, Genetic Resource Unit Manager, World Agroforestry Centre (ICRAF), Kenya
2002-2013: Senior Lecturer, Dept of Biochemistry and Biotechnology, Kenyatta University, Kenya
2001-2002: Lecturer, Nairobi Technical Training Institute, Kenya

Education:
2007: PhD in Population Genetics, Kenyatta University, Kenya
2001: M.Sc. in Biotechnology, Kenyatta University, Kenya

Selected peer Publications:

- Josephine Therese Makueti, Gordon Otieno, Zac Tchoundjeu, **Alice Muchugi**, Alain Tsobeng, Ebenezer Asaah and Robert Kariba (2015). Genetic diversity of *Dacryodes edulis* provenances used in controlled breeding trials, Journal of Plant Breeding and Crop Science; 7(12), pp. 327-339. DOI: 10.5897/JPBCS2015.0511
- Samson Gwali, Alexandre Vaillant, Grace Nakabonge, John Bosco Lamoris Okullo,
- Gerald Eilu, **Alice Muchugi** and Jean-Marc Bouvet (2014) Genetic diversity in shea tree (*Vitellaria paradoxa* subspecies *nilotica*) ethno-varieties in Uganda assessed with microsatellite markers. *Forests, Trees and Livelihoods* http://dx.doi.org/10.1080/14728028.2014.
- Macharia MW, Run S, **Muchugi A** and Palapala V. Genetic structure and Diversity of East African taro (*Colocasia esculenta* L Schott (2014). African Journal of Biotechnology 13 (29):2950-2955
- Russell JR, Hedley PE, Cardle L, Dancey S, Morris J, Booth A, Odee D, Mwaura L, Omondi W, Angaine P, Machua J, **Muchugi A**, Milne I, Kindt R, Jamnadass R, Dawson IK et al. (2014) tropiTree: An NGS-Based EST-SSR Resource for 24 Tropical Tree Species. PLoS ONE 9(7):e102502. doi:10.1371/journal.pone.0102502
- Wanjala BW, Obonyo M, Wachira FN, **Muchugi A**, Mulaa M, Harvey J, Skilton RA, Proud J, Hanson J. 2013. Genetic diversity inNapier grass (Pennisetum purpureum) cultivars: implications for breeding and conservation. AoB PLANTS 5: plt022; doi:10.1093/aobpla/plt022
- **Muchugi A**, Muluvi GM, Kindt R, Kadu CAC, Simons AJ and Jamnadass RH (2008). Genetic structuring of important medicinal species of genus *Warburgia* as revealed by AFLP analysis. *Trees Genetics and Genome* 4: 787-795

Leadership /large program management

- ICRAF Focal person- CRP Genebanks; Genebank in Nairobi and field genebanks in six regions.
- Project PI Lake Victoria Research (*VicRes*) Grant (2008-2011) implement in Kenya, Unganda and Tanzania

Role in platform: Representing FTA on the Expert Advisory Group for Module 4: Phenotyping.

MIKE OLSEN

Current position and affiliation: Trait Pipeline and Upstream Research Coordinator, CIMMYT

Profile: Mike has 14 years of private sector experience in conventional and molecular maize breeding as part of Syngenta and Monsanto North America breeding teams. He has two years of public sector experience leading the molecular breeding team of the CIMMYT Global Maize Program and providing strategic direction for upstream research efforts. He is currently serving as Project lead for Improved Maize for African Soils (IMAS), a multi-institutional public-private partnership to develop maize varieties with improved performance under low fertility conditions common in Sub-Saharan Africa. He is also Principal Investigator for the Genomics and Open source Breeding and Informatics Initiative (GOBII), a partnership between Cornell University, ICRISAT, IRRI, and CIMMYT to enable routine use of genomic data in applied CGIAR breeding programs through integration of appropriate infrastructure, databases, analysis pipelines, and user interfaces.

Employment:
2013-Present: Trait Pipeline and Upstream Research Coordinator, CIMMYT, Mexico
2002-2013: Line Development Breeder, Monsanto, USA
1999-2002: Corn Breeder, Wilson Genetics LLC, USA

Education:
1999: PhD Agronomy and Plant Genetics/ Breeding, University of Minnesota – Twin Cities, USA
1992: B.A. Life Science Sedondary Ed. Bethel University, USA

Selected Recent Peer-reviewed publications:

- Beyene Y, Semagn K, Mugo S, Tarekegne A, Babu R, Meisel B, Sehabiague P, Makumbi D, Magorokosho C, Oikeh S, Gakunga J, Vargas M, Olsen M, Prasanna BM, Banziger M, Crossa J. 2014. Genetic gains in grain yield through genomic selection in eight bi-parental maize populations under drought stress. Crop Science 55, 154-163.
- Gowda M, Das B, Makumbi D, Babu R, Seman K, Mahuku G, Olsen MS, Bright JM, Beyene Y, Prasanna BM. 2015. Genome-wide association and genomic prediction of resistance to maize lethal necrosis disease in tropical maize germplasm. Theoretical and Applied Genetics
- Nair SK, Babu R, Magorokosho C, Mahuku G, Semagn K, Beyene Y, Das B, Makumbi D, Kumar PL, Olsen M, Prasanna B. 2015. Fine mapping of Msv1, a major QTL for resistance to Maize Streak Virus leads to development of production markers for breeding pipelines. Theoretical and Applied Genetics
- Semagn K, Beyene Y, Babu R, Nair S, Gowda M, Das B, Tarekegne A, Mugo S, Mahuku G, Worku M, Warburton ML, Olsen M, Prasanna M. 2015. Quantitative trait loci mapping and molecular breeding for developing stress resilient maize for sub-Saharan Africa. Crop Science 55, 1-11.

Other Evidence of Leadership, large-program management and delivery:

- Co-inventor of 23 commercially utilized maize inbred lines and 8 hybrid varieties with US patents issued between 2009 and 2015
- Recognized as Monsanto Fellow in 2012

Role in platform: Representing MAIZE on the Expert Advisory Group for Module 3: Genotyping. Contributor to Module 3 of the Excellence in Breeding Platform Proposal.

JOHN PLATTEN

Current position and affiliation: Plant Breeder, International Rice Research Institute

Profile:

- Molecular biology, gene cloning and validation
- Comparative genomics for candidate gene identification
- Marker design and validation

Employment:

2016-Present: Scientist II, Genomics Applications and Molecular Biologist, International Rice Research Institute, Philippines
2013-2015: Scientist I, Genomics Applications and Molecular Biologist, International Rice Research Institute, Philippines
2009-2012: PDF – Salinity genomics, International Rice Research Institute, Philippines
2004-2009: PDF – Salinity genomics, CSIRO Plant Industry, Australia

Education:

2004: Doctor of Philosophy, Plant developmental genetics, University of Tasmania, Australia
2000: Bachelor of Science, Plant developmental genetics, University of Tasmania, Australia

Selected Recent Peer-reviewed publications:

- Platten JD, Egdane JA, Ismail AM (2013) Salinity tolerance, Na^+ exclusion and allele mining of *HKT1;5* in *Oryza sativa* and *O. glaberrima*: many sources, many genes, one mechanism? BMC Plant Biology 13:32.
- Platten JD, Thomson MJ, Ismail AM (2012) Genomics applications to salinity tolerance breeding in rice. *In: R. Tuberosa and R. Varshney (eds) Genomics Applications in Plant Breeding*, Wiley-Blackwell USA.
- Luo M, Platten JD, Chaudhury A, Peacock WJ, Dennis EJ (2009) Expression, imprinting and evolution of rice homologs of the polycomb group genes. Molecular Plant 2: 711-723
- Byrt CS, Platten JD, Spielmeyer W, James RA, Lagudah ES, Dennis ES, Tester M, Munns R (2007) HKT1;5-like Cation Transporters Linked to Na^+ Exclusion Loci in Wheat, *Nax2* and *Kna1*. Plant Physiol. 143: 1918-1928
- Platten JD, Cotsaftis O, *et al.* (2006) Nomenclature for *HKT* transporters, key determinants of plant salinity tolerance. Trends Plant Sci. 11: 372-374

Other Evidence of Leadership, large-program management and delivery:

- Leader – QTL Deployment Group, IRRI
- Co-leader – Gene Discovery Group, IRRI
- Contributor in ACI-IRRI partnership (Bangladesh)
- Contributed to milestone development in STRASA phase II and III, and achieving of these milestones

Role in platform: Representing RICE on the Expert Advisory Group for Module 2: Trait Discovery/Breeding.

B.M. PRASANNA

Current position and affiliation: MAIZE and Global Maize Program Director, CIMMYT

Profile: B.M. Prasanna is the Director of CIMMYT's Global Maize Program and of the CGIAR Research Program on MAIZE. Based in Nairobi, Kenya, Prasanna leads a multi-disciplinary CIMMYT-Global Maize Program team of 45 scientists located in sub-Saharan Africa, Latin America and Asia. Prior to joining CIMMYT, Prasanna served as a faculty member and maize geneticist at the Division of Genetics, Indian Agricultural Research Institute (IARI), New Delhi, under ICAR, for nearly two decades.

Employment:
2015-Present: MAIZE CRP Director, CIMMYT, Kenya
2010-Present: Global Maize Program Director, CIMMYT, Kenya
2005-2010: National Fellow, ICAR, India
1998-2005: Asian Maize Biotechnology Network (AMBIONET) India team leader, IARI, India

Education:
1991: Ph.D. in Genetics, ICAR-Indian Agricultural Research Institute, India
1987: M.Sc. in Genetics, ICAR-Indian Agricultural Research Institute, India

Selected Recent Peer-reviewed publications:
- Mahuku G, Lockhart BE, Wanjala B, Jones MW, Kimunye JN, Stewart LR, Cassone BJ, Sevgan S, Johnson N, Kusia E, Lava Kumar P, Niblett CL, Wangai A, Kiggundu A, Asea G, Pappu H, Prasanna BM, Redinbaugh MG (2015) Maize lethal necrosis (MLN), an emerging threat to maize-based food security in sub-Saharan Africa. Phytopathology
- Tesfaye K, Gbegbelegbe S, Cairns JE, Shiferaw B, Prasanna BM, Sonder K,. Boote KJ, Makumbi D, Robertson R (2015) Maize systems under climate change in sub-Saharan Africa: potential impacts on production and food security. Int. J. Climate Change Strategies and Management 7
- Prasanna BM, Araus JL, Crossa J, Cairns JE, Palacios N, Das B, Magorokosho C (2013) High-throughput and precision phenotyping for cereal breeding programs. In: Cereal Genomics-II (eds. PK Gupta, RK Varshney). Springer-Verlag, Dordrecht, pp. 341-374.
- Prasanna BM, Chaikam V, Mahuku G (2012) Doubled Haploid Technology in Maize Breeding: Theory and Practice. Mexico D.F.: CIMMYT. 50 pp.
- Cairns JE, Sonder K, Zaidi PH, Verhulst N, Mahuku G, Babu R, Nair SK, Das B, Govaerts B, Vinayan MT, Rashid Z, Noor JJ, Devi P, San Vicente F, Prasanna BM (2012). Maize production in a changing climate: impacts, adaptation and mitigation strategies. Advances in Agronomy 114: 1-58.

Other Evidence of Leadership, large-program management and delivery:
- Led multi-institutional efforts to effectively tackle Maize Lethal Necrosis (MLN) in eastern Africa, overseen the establishment of state-of-the-art Maize Doubled Haploid (DH) Facility in Kenya and the development of several successful public-private partnership projects.
- Guided 14 Ph.D. and 6 M.Sc. students.
- Published more than 100 research/review papers in journals of repute, besides (co)authoring one book, 7 edited volumes, 45 book chapters, and 7 technical manuals.
- Recognized with several awards and honors in India for his contributions to maize research, post-graduate teaching and human resource development.

Role in platform: Representing MAIZE on the Expert Advisory Group for Module 1: Breeding Excellence.

WILLIAM PAUL QUICK

Current position and affiliation: Principal Scientist and Head of C4 Rice Project, IRRI

Profile:
My scientific expertise includes Photosynthesis, Plant Physiology and Biochemistry, Plant Functional Genomics, High-throughput Plant Phenotyping, Systems Biology. Currently, I am the leader of the C4 rice project based at the International Rice Research Institute (IRRI) in the Philippines. The C4 rice project uses cutting edge science to discover the genes that will supercharge photosynthesis to boost food production. I am also Professor of Plant Physiology at the University of Sheffield's Department of Plant and Animal Sciences (1991-2014). I have over 100 publications in peer-reviewed journals; five of which have been cited greater than 200 times and I have an average citation over 30 for all publications. I have written five major book chapters and edited one book. I pioneered the use of transgenic plants for functional analysis of plant metabolism. I also led one of the first groups to establish sugars as regulators of gene expression in plants and produced the first papers that demonstrated the functional significance of sucrose transporter genes in plants.

Employment:
2009-Present: Principal Scientist and Head of C4 Rice Project, International Rice Research Institute, Philippines
2003-Present: Professor – Department Animal & Plant Sciences, University of Sheffield, UK
2001-2003: Reader, University of Sheffield, UK
1995-2001: Senior Lecturer, University of Sheffield, UK

Education:
1984: Ph.D., Department of Botany, University of Sheffield, UK
1981: BSc., Department of Biological Sciences, University of Essex

Publications:

- Furbank R, Quick WP, Sirault XR (2015) Improving photosynthesis and yield potential in cereal crops by targeted genetic manipulation: Prospects progress and challenges. Field Crops Research ISSN 0378-4290, http://dx.doi.org/10.1016/j.fcr.2015.04.009.
- Rizal G, Karki S, Garcia R, Larazo N, Alcasid M, Quick WP (2015) The Use of Maleic Hydrazide for Effective Hybridization of *Setaria viridis*. PLoS ONE 10(4): e0125092. doi:10.1371/journal.pone.0125092.
- Feldman AB, Murchie EH, Leung H, Baraoidan M, Coe R, Yu S-M, et al. (2014) Increasing Leaf Vein Density by Mutagenesis: Laying the Foundations for C_4Rice. PLoS ONE 9(4): e94947. doi:10.1371/journal.pone.0094947.
- Rizal G, Karki S, Alcasid M, Montecillo F, Acebron K, Larazo N, Garcia R, Slamet-Loedin I, Quick WP (2014) Shortening the Breeding Cycle of Sorghum, a Model Crop for Research. Crop Science 54 (2):520-529.
- Karki S, Rizal G , Quick WP (2013) Improvement of photosynthesis in rice (Oryza sativa L.) by inserting the C4 pathway. Rice **6**:28.
- Rizal G, Acebron K, Mogul R, Karki S, Larazo N, Quick WP (2013) Study of Flowering Pattern in Setaria viridis, a Proposed Model Species for C4 Photosynthesis Research
- Journal of Botany Volume 2013, Article ID 592429, 7 pages http://dx.doi.org/10.1155/2013/592429.

Other Evidence of Leadership, large-program management and delivery: I coordinate an international consortium of 20 international scientists to work on developing a C4 rice. I coordinate a plant breeding program to combine diversity in wild rice (BBSRC, Uk, $1.2m). I am lead Pi for a project working on improving drought resistance in rice (BBSRC, UK, $1.1m) in collaboration with China, Thailand and UK. I am a member of an EU photosynthesis program ($8.2m) and have a joint program to develop plant phenomics with Australia (AusAid $0.6m).

Role in platform: Representing RICE on the Expert Advisory Group for Module 4: Phenotyping.

MATTHEW REYNOLDS

Current position and affiliation: Distinguished scientist, principal scientist and head of wheat physiology, CIMMYT

Profile: Germplasm development and improvement of breeding methodology ; understanding genetic and physiological bases of crop adaptation; strategy development, external fundraising and project management.

Employment including current position:
2014-Present: Expert Consultant, Bayer, Mexico
1996-Present: Distinguished scientist, principal scientist and head of wheat physiology, CIMMYT, Mexico
1989-1995: Scientist & Post-Doctoral Fellow, CIMMYT, Mexico
1984-1989: Research Assistant, Cornell University, USA

Education
1989: PH.D., Horticulture Science, Cornell University, USA
1984: M.SC., Crop Physiology, Reading University, UK

Selected Peer-reviewed publications:

- Reynolds et al., An Integrated Approach to Maintaining Cereal Productivity under Climate Change. (2016) Glob. Food Sec. In press.
- Rutkoski J, Poland J, Mondal S, Autrique E, González Pérez L, Crossa J, Reynolds MP, Singh RP: Predictor traits from high-throughput phenotyping improve accuracy of pedigree and genomic selection for yield in wheat. Genet. 2016
- Prins A, Douglas J, Orr P, Andralojc PJ, Reynolds MP, Carmo-Silva E, Parry MAJ (2016). Rubisco catalytic properties of wild and domesticated relatives provide scope for improving wheat photosynthesis. J. Exp. Bot. doi: 10.1093/jxb/erv574
- Lopes MS, Dreisigacker S, Peña RJ, Sukumaran S, Reynolds MP (2015) Genetic characterization of the Wheat Association Mapping Initiative (WAMI) panel for dissection of complex traits in spring wheat. TAG: Theorectial and Applied Genetics 128: 453-464
- Reynolds MP, Tattaris M, Cossani CM, Ellis M, Yamaguchi-Shinozaki K, Saint Pierre C: Exploring genetic resources to increase adaptation of wheat to climate change.(2015) In Advances in Wheat Genetics: From Genome to Field. Edited by Ogihara Y, Takumi S, Handa H. Springer Japan.
- Stirling, C., Hellin, J., Cairns, J., Silverblatt-Buser, E., Tefera, T., Ngugi, H., Gbegbelegbe, S., Tesfaye, K., Chung, U., Pinto RS, Reynolds MP (2015) Common genetic basis for canopy temperature depression under heat and drought stress associated with optimized root distribution in bread wheat. (2015) Theor. Appl. Genet. 128:575–585.
- Sonder, K., Cox, R.A., Verhulst, N., Govaerts, B., Alderman, P., Reynolds, M. (2014). Shaping sustainable intensive production systems: improved crops and cropping systems in the developing world CABI Climate Change Series No.5 (pp. 186-203). Wallingford: CABI.

Other evidence of leadership:

- Initiated Wheat Yield Consortium in 2009 -which became International Wheat Yield Partnership (IWYP) in 2014- to raise genetic yield potential of wheat to its biological limit
- Established the Heat and Drought Wheat Improvement Consortium (HeDWIC), an international partnership involving hundreds of plant abiotic stress experts; target budget of $50m+, endorsed by the Wheat Initiative as a research priority for the wheat community.
- Assists wheat NARS worldwide prepare for challenges associated with climate change

Role in platform: Representing WHEAT on the Expert Advisory Group for Module 4: Phenotyping. Contributor to Module 4 of the Excellence in Breeding Platform Proposal

JEAN-MARCEL RIBAUT

Current Position: Director, Integrated Breeding Platform

Profile
My scientific background is in plant physiology and genetics. As Director of the Generation Challenge Programme I led and coordinating a large network of partners in modern crop breeding and have cumulative experience in agriculture biotechnology and plant science, as well as leadership skills for dispersed global R&D teams. I have a particular interest in promoting modern breeding methods to hasten crop improvement in the developing world, bridging the gap between basic and applied agricultural science.

Employment
2005-2014: Director, Generation Challenge Programme, CIMMYT, Mexico
2003-2005: Deputy Director Genetic Resources Programme, CIMMYT, Mexico
2001-2003: Deputy Director Applied Biotechnology Center, CIMMYT, Mexico
1999-2005: Senior Scientist, CIMMYT, Mexico

Education
1991: PhD, Plant Physiology, University of Lausanne, Switzerland
1984: MS, Biology, University of Lausanne, Switzerland

Selected Publications

- Varshney R, V.K. Singh, J. Hickey, X. Xun, D.F. Marshall, J. Wang, David Edwards and **J.-M. Ribaut** (2015) Analytical and decision support tools for genomics-assisted breeding. *Trends in Plant Science*: http://dx.doi.org/10.1016/j.tplants.2015.10.018
- Varshney R, **J-M Ribaut**, E. S. Buckler, R. Tuberosa, J. A. Rafalski and P. Langridge (2012) Can genomics boost productivity of orphan crops. *Nature Biotech.* 30: 1172-1176
- **Ribaut J.-M.,** M.C. de Vicente and X. Delannay (2010) Molecular breeding in developing countries: challenges and perspectives. *Current Opinion in plant Biology*, 13:1–6
- Varshney R.K., J.C. Glaszmann, H. Leung and **J.-M. Ribaut** (2010) More genomic resources for less studied crops. *Trends in biotechnology*, 28:452-460
- **Ribaut J.-M.** and D.A. Hoisington (1998) Marker-assisted selection: new tools and strategies. *Trends in Plant Science* 3: 236-239

Role in CRP/platform: Member for IBP on the Expert Advisory Group for Module 5: Bioinformatics. Co-author of Module 5 of the Excellence in Breeding Platform Proposal.

JENS RIIS-JACOBSEN

Current position and affiliation: Director of IT, CIMMYT

Profile: Broad experience with promoting use of IT for agricultural research and development purposes including development of germplasm informatics tools for maize, wheat, sweet potato, and potato breeding. 20+ years of international work in 10 different countries, and experience with managing complex multi-institutional projects.

Employment:
2011 – Present: Director of IT, CIMMYT, Mexico
2010 – 2011: Data Manager, CIP-SSA, Kenya
2006 – 2010: Chief Technical Advisor, CTA, Nicaragua
2002 – 2006: Crop Information System Specialist, CIMMYT, Mexico

Education:
2001: Master of Technology Management (MTM) University of Aalborg, Denmark
1991: M.Sc. Forestry and its relation to land use, University of Oxford, England

Other Evidence of Leadership, large-program management and delivery:

- Upgraded CIMMYT's IT infrastructure, procurement of HPC, and data integration across all administrative systems. Contributed to successful fund raising with BMGF (IBP, GOBII), BBRSC (TGAC supercomputing), and GCDT (GrinGlobal), and has more than doubled the annual CIMMYT investment in IT.
- Upgraded IT infrastructure in 20 CTA institutions, implementation of web presence for 32, and implementation of administrative systems in 26 institutions. Attracted further USD 3 million from private company to invest in cellular phone network expansion.
- Lead a USD 3 million dollar rural development project with 4 participating institutions at CTA.

Role in platform: Representing MAIZE on the Expert Advisory Group for Module 5: Bioinformatics. Co-author of Module 5 of the Excellence in Breeding Platform Proposal.

KELLY ROBBINS

Current Position: Director, Genomic Open-source Breeding Informatics Initiative (GOBII), Cornell University

Profile
My background is in quantitative genetics and statistical genomics with a focus on developing advanced statistical and machine learning methodologies to maximize genetic gains in important livestock/crop species. Research areas include: random regression/reaction Norm models, genotype by environmental interactions, genome wide selection, mixed models, Bayesian methodologies, association mapping, and network modeling

Employment
2010-Present: Adjunct Professor, Purdue University, USA
2011-2015: Quantitative Genetics Group Leader, Dow AgroSciences LLC, USA
2008 – 2011: Quantitative Geneticist, Dow AgroSciences LLC, USA

Education
2007: PhD, Animal Science *Statistical Genetics*, University of Georgia, USA
2005: MS, Animal Science *Breeding Genetics,* University of Georgia, USA

Selected Publications

- Rousselle, Y., Jones, E., Charcosset, A., Moreau, P., **Robbins, K.**, Stich, B., Knaak, C., Flament, P., Karaman, Z., Martinant, J., Fourneau, M., Taillardat, A., Romestant, M., Tabel, C., Bertran. J., Ranc, N., Lespinasse, D., Blanchard, P., Kahler, A., Chen, J., Kahler, J., Dobrin, S., Warner, T., Ferris, R., and S. Smith. 2015. Study on Essential Derivation in Maize: III. Selection and Evaluation of a Panel of Single Nucleotide Polymorphism Loci for Use in European and North American Germplasm. Crop Sci. 55.
- Herman, R. A., and **Robbins, K. R.** 2013. Use of hypergeometric distribution for estimating adventitious presence of GM traits in small seed lots may be misleading. Seed Science Research 1-2.
- **Robbins, K. R**., Backlund, J. E., and K.D. Schnelle. 2012. Spatial corrections of unreplicated trials using a two-dimensional spline. Crop Sci. 52.
- Wang, Y. **Robbins, K. R.**, and R. Rekaya. 2010. Comparison of computational models for assessing conservation of gene expression across species. PLos ONE. 5(10)
- Boyd, N. L., **Robbins, K. R.,** Dhara, S. K., West, F. D., and S. L. Stice. 2009. Human Embryonic Stem Cell Derived Mesoderm-like Epithelium Transitions to Mesenchymal Progenitor Cells. Tissue Engineering Part A. 15(8): 1897-1907.
- **Robbins, K. R**., Zhang, W., R. Rekaya, and J. K. Bertrand. 2007. Ant colony optimization for feature selection in high dimensionality data sets. Math. Med. Biol. 24(4):413-26.
- **Robbins, K. R.**, I. Misztal, and J. K. Bertrand. 2005. A practical longitudinal model for evaluating growth in Gelbvieh cattle. J. Anim. Sci. 83:29 -33.

Role in CRP/platform: Member for GOBII on the Expert Advisory Group for Module 5: Bioinformatics. Co-author of Module 5 of the Excellence in Breeding Platform Proposal.

JESSICA RUTKOSKI

Current Position: Cornell assistant professor/CIMMYT adjunct wheat breeder and quantitative geneticist

Profile: Expert in gain from selection theory and implementation of genomic selection in applied breeding programs

Employment
2014-Present: Assistant Professor, Cornell University, USA
2014-Present: Adjunct Assistant Professor, Cornell, USA
2014-Present: Adjunct Associate Scientist, CIMMYT, Mexico

Education
2014: PhD, Plant Breeding and Genetics, Cornell University, USA
2009: BS, Genetics, University of Wisconsin Madison, USA

SELECTED PUBLICATIONS

- **Rutkoski** J. E., J. Poland, R.P. Singh, J. Huerta-Espino, S. Bhavani, J-L. Jannink, M. E. Sorrells. Genetic gain from phenotypic and genomic selection for quantitative resistance to stem rust of wheat. 2015. *The Plant Genome Journal* 8:.
- **Rutkoski** J. E., J. Poland, R.P. Singh, J. Huerta-Espino, S. Bhavani, J-L. Jannink, M. E. Sorrells. Efficient use of historical data for genomic selection: a case study of stem rust resistance in wheat. 2015. *The Plant Genome Journal* 8:.
- **Rutkoski** J. E., J. Poland, R.P. Singh, J. Huerta-Espino, S. Bhavani, M. Rouse, H. Barbier, J-L. Jannink, M. E. Sorrells. Genomic selection for quantitative adult plant stem rust resistance in wheat. 2014. *The Plant Genome Journal* 7:.
- Heslot N., J. **Rutkoski**, J. Poland · J-L. Jannink, M. E. Sorrells. 2013. Impact of marker ascertainment bias on genomic selection accuracy and estimates of genetic diversity. *PLOS ONE* 8(9):e74612.
- **Rutkoski** J.E., J. Poland, J.-L. Jannink, M.E. Sorrells. Imputation of unordered markers and the impact on genomic selection accuracy. 2013. *G3 (Bethesda, Md.)* 3(3): 427–439.
- Poland J., J. Endelman, J. Dawson, J. **Rutkoski,** W. Shuangye, Y. Manes, S. Dreisigacker, J. Crossa, H. Sanchez-Villeda, M. Sorrells, J.-L., Jannink. 2012. Genomic selection in wheat breeding using genotyping-by-sequencing. *The Plant Genome Journal* 5(3):103-113.
- **Rutkoski** J.E., J. Benson,Y. Jia, G. Brown-Guedira, J-L. Jannink, M.E. Sorrells. 2012. Evaluation of genomic prediction methods for Fusarium head blight resistance in wheat. *The Plant Genome Journal* 5(2):51-61.

Leadership

- Genomic selection and high-throughput phenotyping objective lead under the Delivering Genetic Gains in Wheat project. 'Innovate and integrate technologies to accelerate genetic gain' cluster of activity lead under WHEAT CRP FP2

Role in platform: Representing WHEAT on the Expert Advisory Group for Module 2: Trait Discovery/Breeding. Contributor to Module 2 of the Excellence in Breeding Platform Proposal.

ZACHARIE TCHOUNDJEU

Current position and affiliation: ICRAF Regional Coordinator for West and Central Africa Region

Profile: Principal Scientist (Forester specialized in Tree Improvement). Agroforestry, Improvement of livelihoods of small scale farmers, Domestication of high-value but lesser known indigenous fruit trees of tropical forests; sustainable management of tropical forests.

Employment: Regional Coordinator for West and Central Africa, World Agroforestry Centre, Overseeing ICRAF research activities in Sahel and Humid tropics Nodes.

Education:
1989: PhD Natural Resources,University of Edinburgh Scotland, UK
1980: M.Sc. Forestry, ENEF Cap Esterias, Gabon

Selected Recent Peer-reviewed publications:

- Makueti JT, Otieno G, **Tchoundjeu Z,** Muchugi A, Tsobeng A, Asaah E, Kariba R (2015) Genetic diversity of *Dacryodes edulis* provenances used in controlled breeding trials. *Journal of Plant Breeding and Crop Science* 7(12): 327-339
- Makueti JT, **Tchoundjeu Z**, Van Damme P, Kalinganire A, Asaah E, Tsobeng A (2015) Methodological approach to indigenous fruit trees breeding: case of *Dacryodes edulis* (G. Don.) H. J. Lam. (Burseraceae) in Cameroon. *Int. J. Agr. Agri. Res.* 7(2), 142-162.
- Makuti JT, **Tchoundjeu Z**, Tsobeng A, Numbissi F, Tsafack S (2015) Local communities' perception and willingness on sustainable management of a natural threatened resource: case study of *Baillonella toxisperma* Pierre in Eastern Cameroon. *Journal of Biodiversity and Environmental Sciences (JBES)* 6 (5): 74-94.
- Tchatchoua TD, **Tchoundjeu Z**, Asaah E, Tsobeng A, Weber J, Kalinganire A (2012) Methodological approaches for the selection of genotypes in a progeny trial of *Dacryodes edulis* (G. Don) H. J. Lam in Cameroon. *Int. J. Biol. Chem. Sci.* 6(4): 1480-1491.
- **Tchoundjeu Z** , Degrande A, Leakey RRB, Nimino G, Kemajou E; Asaah E, Facheux C, Mbile P, Mbosso C, Sado T, Tsobeng A (2010) Impacts of participatory tree domestication on farmer livelihoods in West and Central Africa. *Forest, Trees and Livelihoods* 19: 217-234.
- **Tchoundjeu Z,** Asaah EK, Anegbeh P, Degrande D, Mbile P, Facheux C, Tsobeng A, Atangana A, Ngo-Mpeck ML, Simons AJ (2006) Putting participatory domestication into practice in West and Central Africa. *Forests, Trees and Livelihoods*. 16: 53–69

Other Evidence of Leadership, large-program management and delivery: Coordinating the World Agroforestry research activities in West and Central Africa Region. A total of 175 staffs based in 8 countries of the region

Role in platform: Representing FTA on the Expert Advisory Group for Module 2: Trait Discovery/Breeding.

VINCENT VADEZ

Current position and affiliation: Principal Scientist, Theme Leader "System Analysis for Climate Smart Agriculture" – ICRISAT

Profile: Crop Physiology, modelling, phenotyping, Agronomy

Employment:
2008-Present: Principal Scientist, ICRISAT, India
2004-2008: Senior Scientist, ICRISAT, India
2000-2003: Project Manager, Brandeis University, Bolivia
1996-2000: Post-doctoral Scientist, University of Florida, USA

Education:
1996: PhD in Plant Physiology, Supagro Montpellier, France
1990: Agronomy and plant production, Supagro Montpellier, France

Selected Recent Peer-reviewed publications:

- Vadez V, Kholova J, Hummel G, Zhokhavets U, Gupta SK, Hash CT 2015. L*easyScan: a novel concept combining 3D imaging and lysimetry for high-throughput phenotyping of traits controlling plant water budget* Journal of Experimental Botany 66(18), 5581-5593 doi: 10.1093/jxb/erv251
- Kholová J, Tharanya M, Kaliamoorthy S, Malayee S, Baddam R, Hammer GL, McLean G, Deshpande S, Hash CT, Craufurd PQ and Vadez V. 2014. Modelling the effect of plant water use traits on yield and stay-green expression in sorghum. Functional Plant Biology 41 (10-11), 1019–1034
- Vadez V 2014. Root hydraulics: the forgotten side of root in drought adaptation. Field Crops Research 165, 15-24 DOI: 10.1016/j.fcr.2014.03.017
- Vadez V, Kholova J, Medina S, Aparna K, Anderberg H 2014. Transpiration efficiency: New insights into an old story. Journal of Experimental Botany 64: 6141–6153 doi:10.1093/jxb/eru040
- Vadez V and Kholová, J 2013. *Coping with drought: Resilience versus risk. Targeting the most suitable G*E*M options by crop simulation modeling* - Secheresse 24: 274-81. doi: 10.1684/sec.2013.0399
- Vadez V, Soltani A, Krishnamurthy L, Sinclair TR 2012. Modelling possible benefit of root related traits to enhance terminal drought adaption of chickpea. Field Crops Research. 10.1016/j.fcr.2012.07.022
- Kholová J, McLean G, Hammer GL, Vadez V, Craufurd PQ 2013. Drought stress characterization of post-rainy sorghum (rabi) in India. Field Crops Research 141, 38-46 http://dx.doi.org/10.1016/j.fcr.2012.10.020

Other Evidence of Leadership, large-program management and delivery:

- Served three interims as Research Program director of Biotechnology – then Dryland Cereals – Department for ICRISAT
- Principal investigator and Co-principal investigator in a substantial number of grants

Role in platform: Representing DCL on the Expert Advisory Group for Module 4: Phenotyping. Contributor to Module 4 of the Excellence in Breeding Platform Proposal.

RAJEEV K. VARSHNEY

Current position and affiliation: Research Program Director – Genetic Gains, ICRISAT

Profile: Strategic direction and supervision and execution of research activities on different disciplines under the Research Program- Genetic Gains including genomics and trait discovery, computational genomics, forward breeding, genebank, pre-breeding, genetic engineering, and seed system.

Employment:
2016-Present: Research Program Director – Genetic Gains, ICRISAT, India
2013-2016: Research Program Director – Grain Legumes, ICRISAT, India
2012-2016: Director, Centre of Excellence in Genomics, ICRISAT, India
2007-2013: Leader, SubProgramme 2, CGIAR- GCP, Mexico

Education:
2001: PhD., Agricultural Botany (Molecular Biology), CCS University, India
1995: MsC, Botany (Genetics, Plant Breeding & Molecular Biology), AMU, India

Selected Recent Peer-reviewed publications:

- Bertioli DJ et al. (2016) The genome sequences of *Arachis duranensis* and *Arachis ipaensis*, the diploid ancestors of cultivated peanut. Nat Genet doi: 10.1038/ng.3517
- Varshney RK et al. (2013) Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. Nat Biotechnol 31 :240-6
- Varshney RK et al. (2011) Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. Nat Biotechnol 30 :83-9
- Varshney RK et al. (2012) Can genomics boost productivity of orphan crops? Nat Biotechnol. 30(12):1172-6
- Varshney RK (2015) Exciting journey of 10 years from genomes to fields and markets: Some success stories of genomics-assisted breeding in chickpea, pigeonpea and groundnut. Plant Sci 242:98-107
- Varshney RK et al. (2013) Fast-track introgression of for root traits and other drought tolerance traits in JG 11, an elite and leading variety of chickpea. Plant Genome 6(3)

Other Evidence of Leadership, large-program management and delivery:

- Established Centre of Excellence in Genomics (CEG), ICRISAT that has provided access to Scientist to next generation sequencing, high-throughput SSR genotyping, SNP genotyping and trained 287 scientists from India and different countries of Asia and Africa
- Coordinator for Tropical Legumes III project having global objective for enhancing the legume productivity with a budget of >US$ 24
- Led several multi-disciplinary, multi-national and multi-crop grants/projects with an amount of >US$ 67 million in last 10 years including Tropical Legume III (ca. US$ 25 M), HTPG (US$ 4 M), GOBII (US$ 4 M)
- Elected fellow of several National and International committees including Crop Science Society of America (CSSA), Indian National Science Academy (INSA), The National Academy of Sciences, India (NASI), National Academy of Agricultural Sciences, India (NAAS)

Role in platform: Representing DCL on the Expert Advisory Group for Module 3: Genotyping. Co-author of Module 3 of the Excellence in Breeding Platform Proposal.

PETER WENZL

Current position and affiliation: Incoming Genetic Resources Program Leader, CIAT

Profile:

- Characterization of genetic resources to identify and mobilize novel variation that accelerates genetic gains in breeding programs
- Genotyping service provision; configuration of genotyping assays for a variety of purposes
- Information management at the interface between genebanks and breeding programs

Employment:

2015-2016: DivSeek Liaison, Global Crop Diversity Trust, Germany
2010-2014: Leader, Seeds of Discovery (SeeD) Project, CIMMYT, Mexico
2009-2010: Manager, Crop Informatics Team, CIMMYT, Mexico
2002-2009: Principal Scientist, Diversity Arrays Technology (DArT) Pty. Ltd., Australia

Education:

2000 PhD, Plant Physiology & Genetics, University of Vienna, Austria
1993 MSc, Biochemistry and Biophysics, University of Vienna, Austria

Selected Recent Peer-reviewed publications:

- Sehgal D, Vikram P, Sansaloni CP, Ortiz C, Pierre CS, Payne T, Ellis M, Amri A, Petroli CD, Wenzl P, Singh S (2015) Exploring and mobilizing the gene bank biodiversity for wheat improvement. *PLoS ONE* 10: e0132112
- McCouch S, et al. (2013) *Feeding the future*. *Nature* 499: 23-24
- Bedo J, Wenzl P, Kowalczyk A, Kilian A (2008) Precision-mapping and statistical validation of quantitative trait loci by machine learning. *BMC Genetics* 9, 35
- Wenzl P, Raman H, Wang J, Zhou M, Huttner E, Kilian A (2007) A DArT platform for quantitative bulked segregant analysis. *BMC Genomics* 8, 196
- Wenzl P, Carling J, Kudrna D, Jaccoud D, Huttner E, Kleinhofs A, Kilian A (2004) Diversity arrays technology (DArT) for whole- genome profiling of barley. *PNAS* 101, 9915–9920

Other Evidence of Leadership, large-program management and delivery:

- Led CIMMYT's SeeD project team of 15 IRS and ca. 70 staff overall; SeeD systematically identifies and mobilizes useful genetic variation in genebanks into maize and wheat breeding programs
- Substantially contributed to the start-up and success of a biotech company that provides high-throughput genotyping and informatics services to plant breeders and researchers
- Completed the Emerging Leaders Training Program, Thunderbird School of Global Management, Arizona State University, Phoenix

Role in platform: Representing the Genebanks Platform on the Expert Advisory Group for Module 2: Trait discovery/Breeding. Contributor to Module 2 of the Excellence in Breeding Platform Proposal.

MARGARET WORTHINGTON

Current position and affiliation: Tropical forage breeder, CIAT

Profile: Applied forage breeder with expertise in marker assisted selection, quantitative genetics, polyploid genomics, QTL mapping, breeding clonally propagated crops, and genetic resistance to pests and diseases.

Employment:
2010-2013: Graduate Research Assistant, North Carolina State University, USA
2008-2010: Graduate Research Assistant, University of California, Davis, USA
2006-2007: US Student Fulbright Fellow, Institute of International Education, India

Education:
2014: Ph.D. in Crop Science, North Carolina State University, Raleigh, NC, USA
2010: M.Sc. in International Agricultural Development, University of California, Davis, CA, USA

Selected Recent Peer-reviewed publications:

- **Worthington, M.L.** and J.W. Miles. 2015. Reciprocal full-sib recurrent selection and tools for accelerating genetic gain in apomictic *Brachiaria*. In: Budak, H. and G. Spangenberg (eds) Molecular Breeding of Forage and Turf: The Proceedings of the 8th International Symposium of Molecular Breeding of Forage and Turf. Springer International Publishing. pp 19-30. doi:10.1007/978-3-319-08714-6_3
- Subbarao G.V., T. Yoshihashi, **M. Worthington**, K. Nakahara, Y. Ando, K.L. Sahrawat, I.M. Rao, J.C. Lata, M. Kishii, and H.J. Braun. 2015. Suppression of soil nitrification by plants. Plant Science. 233:155-164. doi:10.1016/j.plantsci.2015.01.012
- Petersen S., J.H. Lyerly, **M.L. Worthington**, W.R. Parks, C. Cowger, S. Leath, G. Brown-Guedira, and J.P. Murphy. 2015. Mapping of powdery mildew resistance gene *Pm53* introgressed from *Aegilops speltoides* into soft red winter wheat. Theoretical and Applied Genetics. 128:303-312. doi:10.1007/s00122-014-2430-8.
- **Worthington, M.**, S.C. Reberg-Horton, G. Brown-Guedira, D. Jordan, R. Weisz, and J.P. Murphy. 2015. Relative contributions of allelopathy and competitive traits to the weed suppressive ability of winter wheat lines against Italian ryegrass. Crop Science. 55:57-64. doi:10.2135/cropsci2014.02.0150
- **Worthington, M.**, J. Lyerly, S. Petersen, G. Brown-Guedira, D. Marshall, C. Cowger, R. Parks, and J.P. Murphy. 2014. Genetic mapping of *MlUM15*: an *Aegilops neglecta*-derived powdery mildew resistance gene in common wheat. Crop Science. 54:1397-1406. doi:10.2135/cropsci2013.09.0634.
- **Worthington, M.** and S.C. Reberg-Horton. 2013. Breeding cereal crops for enhanced weed suppression: optimizing allelopathy and competitive ability. Journal of Chemical Ecology. 39:213-231. doi:10.1007/s10886-013-0247-6
- **Worthington, M.**, D. Soleri, F. Aragón-Cuevas, and P. Gepts. 2012. Genetic composition and spatial distribution of farmer-managed *Phaseolus* bean plantings: an example from a village in Oaxaca, Mexico. Crop Science. 52:1721-1735. doi:10.2135/cropsci2011.09.0518

Role in platform: Representing the AFS CRP on Livestock on the Expert Advisory Group for Module 4: Phenotyping. Author of Module 4 of the Excellence in Breeding Platform Proposal.

4.2 Annex 2. Interactions between the Platform and Users

The Table below shows interactions with other CRPs and Platforms, in terms of what the Platform receives and provides to distinct Flagships (FP) and Modules (M), respectively. External institutions - i.e., those not affiliated with AFS CRPs or other Platforms (which each include CGIAR centers, NARS, ARI, and local seed companies) - may become members to the Platform. Products will become available as international public goods to the largest extent possible.

Excellence in Breeding Platform			AFS CRPs								GI CRPs		Platforms	
Module	**Receives from CRPs, other Platforms and external members**	**Provides to CRPs, other Platforms, external members and users**	**DCL**	**Fish**	**FTA**	**Livestock**	**MAIZE**	**RICE**	**RTB**	**WHEAT**	**A4N&H**	**PIM**	**Genebanks**	**Big Data**
All	Participation in PSC, expert advisory groups and communities of practice of the Excellence in Breeding Platform and Modules	Joint planning and priority setting Access to RBM results and user feedback	FP2 FP3	FP1	FP1	FP1 FP3	FP2 FP3	FP4 FP5	FP1 FP2	FP2 FP3			M2	
All	Capacity building needs	Virtual training modules; face-to-face capacity building for trainers and other multipliers.	FP2 FP3	FP1	FP1	FP1 FP3	FP2 FP3	FP4 FP5	FP1 FP2	FP2 FP3	FP1		M2	
M1	Breeding program assessment and metrics for target species	Standardized breeding program assessment tool and metrics framework; access to private sector expertise	FP3	FP1	FP1	FP1 FP3	FP3	FP5	FP2	FP3				
M1	Approaches for assessing genetic gain	Standardized approaches for assessing genetic gain	FP3	FP1	FP1	FP1 FP3	FP3	FP5	FP2	FP3				

M1	Approaches for assessing germplasm impact	Standardized approaches for assessing germplasm impact	FP1	FP1	FP1 FP2	FP4	FP1	FP1	FP5	FP1	FP1	FP1	M3	
M1	Commodity-specific adaptation: demand-driven targets, breeding program assessment; breeding program metrics and strategic plan	Strategic plan of current breeding program investments and prioritized improvements across CGIAR and NARS members	FP3	FP1	FP2	FP1 FP3	FP3	FP5	FP2	FP3				
M2	Successful use cases for breeding and trait mobilization	Workflows and pipelined data analyses for trait mobilization	FP2	FP1	FP1 FP2	FP1 FP3	FP2	FP4	FP1	FP2			M2	
M2	User feedback	Practical toolbox for breeders, structured by use cases and type of users	FP2	FP1	FP1 FP2	FP1 FP3	FP2	FP4	FP1	FP2			M2	
M3	Successful use cases for using genotyping and sequencing in applied breeding and quality control of target species	Documented use cases and best practices for using genotyping and sequencing in applied breeding; access to expertise in ARIs and the private sector	FP2 FP3	FP1	FP1	FP1 FP3	FP2 FP3	FP4 FP5	FP1 FP2	FP2 FP3			M2	
M3	Marker conversions, sample forecasting and sample submission	Genotyping and sequencing services, CGIAR externally and internally (e.g. at BeCA/ILRI, CIMMYT, ICRISAT, IRRI/GSL); Workflows, components, applications for genotyping and sequencing	FP2	FP1	FP1 FP2	FP1 FP3	FP2	FP4	FP1	FP2			M2	

M4	Approaches for phenotyping and GxExM analysis in target species	Tools, best practices and ISO 9000 standards for phenotyping and GxExM analysis, mechanization and automation; access to expertise from ARIs and the private sector; access to experiment stations and sites of implementation of best practices	FP2 FP3		FP1	FP3	FP2 FP3	FP4 FP5	FP1 FP2	FP2 FP3				
M4	Successful use cases for high-throughput phenotyping in target species	Tools for capturing and analyzing high-throughput data.	FP2 FP3		FP1	FP3	FP2 FP3	FP4 FP5	FP1 FP2	FP2 FP3				
M4	Information about cost, quality, turn-around of laboratories used	Access to cost-effective lab services for the analyses of physico-chemical composition and functional properties	FP2 FP3		FP1 FP2	FP1 FP3	FP2 FP3	FP4 FP5	FP1 FP2	FP2 FP3				
M4	Information about current mechanization and automation	Assessment of mechanization and automation in the CGIAR and NARS.	FP2 FP3			FP3	FP2 FP3	FP4 FP5	FP1 FP2	FP2 FP3				
M5	Databases at member institutions related to target germplasm	Interconnectivity with tools and other databases through the Breeding API; access to high performance computing capacities	FP2 FP3	FP1	FP1 FP2	FP1 FP3	FP2 FP3	FP4 FP5	FP1 FP2	FP2 FP3			M2	

M5	Information about, or code for bioinformatics tools for making available germplasm and associated information	Core operational guidelines and data standards for members; tested and interconnected bioinformatics and biometrics tools and pipelines to support breeding workflows; documented use cases and best practices (workflows, tools, applications) for data management and analysis; Access to trained biometricians and computational infrastructure; Sustainability strategy for bioinformatics in the CGIAR	FP3	FP1	FP1	FP1 FP3	FP3	FP5	FP2	FP3	FP1		M2	
M5	Information about, or code for bioinformatics tools for trait discovery and mobilization, genotyping, genotype-to-phenotype models used or developed for target crops		FP2	FP1	FP2	FP1 FP3	FP2	FP4	FP1	FP2				
M5	Information about, or code for bioinformatics tools for cultivar development, phenotyping, GxExM analyses used or developed for target crops		FP3		FP1		FP3	FP5	FP2	FP3				
M5	Databases for biophysical and socio-economic data; management concepts	Interoperable databases for genomic, phenotypic and environmental data; management concepts												All

All	Standards for biophysical and socio-economic data	Standards for genetics, genomics and phenotype data												All
All	System-wide consideration and technical contributions to germplasm policy developments, and capacity building for full compliance.	Breeding-related insights and contributions relevant to germplasm policy developments											M3	
Management	Participation in communities of practices for CRP/Platform Management, MELIA, Capacity Development, IA Management, Open Data Access, Gender and Youth		Management units											

4.3 Annex 3. Intellectual Asset Management

Relevance of IA management

All Platform members, as well as external implementers, to the extent that those are able to align, will treat research results and products developed under the Excellence in Breeding Platform following the CGIAR Principles for the Management of Intellectual Assets and the CGIAR Open Access and Data Management Policy as described below.

Critical issues to address in the Excellence in Breeding Platform implementation from IA perspective

Barriers to Full Adoption	Actions implemented to address critical issues	Envisioned improvements
Ensuring CGIAR IA Principles, Center policies, and Center contracts are in compliance with local legislation, local markets, and local practices.	Preparing agreements to align with CGIAR Principles for the Management of Intellectual Assets and with Limited Exclusivity Agreement (LEA) and Restricted Use Agreement (RUA) requirements when local laws and practices differ. Revising internal policies to address critical issues, as well as to align them with local legislation standards and when possible, with local markets and practices.	Monitoring and training of partners in local laws and revise internal and CGIAR policies in view of local laws. Focusing on local seed laws and regulations that affect dissemination of research outputs, as well as management and dissemination of sensitive data (according to local laws).
Lack of incorporation of IA management principles into the project lifecycle.	Including tools in the project management lifecycle to assist with tracking of intellectual assets.	Standardizing such practices in the Excellence in Breeding Platform.
	Preparing freedom to operate analysis for dissemination of the Excellence in Breeding Platform outputs.	
	Formulating flow down obligations and standards from internal and CGIAR policies to Participant Center(s) and other partners, according to their capacities.	Monitoring and training of partners.
Aligning CGIAR IA Principle with private sector partner interests.	Drafting and negotiating agreements with private partners, in light of CGIAR Principles, and if necessary drafting exceptions while ensuring appropriate justification for appropriate dissemination along with the appropriate research and emergency exceptions.	Continue revising internal policies and extending such policies within the CGIAR.

Challenges for Excellence in Breeding Platform implementation as they relate to IA management

1. CGIAR policy requirements are at odds with private sector interests and some private sector stewardship practices. This applies for both outputs created through use of private sector technology or outputs created solely by a Center.
2. There are concerns about confidentiality obligations in order to maintain trade secrets and delay disclosure of information to provide ample time for enablement of patentable inventions in view of the CGIAR IA Principles.
3. Ensuring that the Excellence in Breeding Platform has adequate human resources, funding and capacity development to timely implement all actions needed for a proper IA management.
4. Lack of knowledge among NARS of IA practices from Centers.
5. Non-existence of IP policies within the various NARS.
6. Collecting, Exporting and Licensing seed in view of the International Treaty on Plant Genetic Resources for Food and Agriculture and the Nagoya Protocol.
7. Data dissemination in accordance with CGIAR policies, local legislation and the Nagoya Protocol.

Project planning and implementation

The Lead Center IP & Legal will intervene in the following parts of the project management lifecycle:

Project phase	Intervention from IP & Legal
Planning	Direct and/or participate in drafting of documents for work plan, data management, knowledge management, and dissemination of results. IP & Legal will handle contractual obligations including subgrants to ensure appropriate planning. If appropriate prepare preliminary FTO assessment for dissemination of results.
Implementation, monitoring and evaluation	Draft and negotiate agreements, including material transfer agreements. As needed, monitor work scope, risk issues and legal issues in moving forward with project. Draft commercial licenses, if necessary, for dissemination of outputs. Assist with any audits, if necessary. If appropriate prepare preliminary FTO assessment for dissemination of results. Assist in implement methods and tools such as legal documents and legal language to be incorporated into documents used in the project lifecycle
End of the project	Administrative closeout, ensure sharing of information and/or materials and closing out contract and tracking finalization of any confidentiality clauses.

1. Accountability for the appropriate implementation of the CGIAR policies will be provided through contractual obligations with partners. CGIAR Centers will apply CGIAR policies along with their internal policies and procedures. To the extent possible, non-CGIAR partners will be encouraged to apply CGIAR policies; alternatively, IA management aligned with those policies will be secured through IA management plans and contractual obligations.
2. Implementation is subject to available budget; capacity building for incorporation of CGIAR policies into project planning & implementation will be developed and provided through guidelines, trainings, etc.

Key dissemination pathways for maximizing global impact

Type of Intellectual Asset	Dissemination pathway	IP + Legal contributions
Data & Information Products (databases, publications, multimedia, reports, training materials, software, algorithms, maps)	- Multi-lingual Open Access repositories - Adapted information dissemination channels to specific target groups e.g. farmers - Licensing	• Development of global licenses for dissemination as 'International Public Goods' • Legal advice on: - Access to third party technologies/ data/ software/information; - Management of sensitive/regulated data to comply with local legislation, when applicable; - Agreements to publish information products Through publishers and/or scientific journals; - Freedom to operate opinions; and - Development of IA management strategies to achieve a higher impact.
Know how (protocols, how to guides, best practices)	- OA repositories, - Partnership approaches and capacity development - NARS - Extension specialists - Partners & collaborators	Legal advice on: - Development of IA management strategies to achieve a higher impact; - Dissemination strategies & global licenses for that purpose; - Access to third party know how; and - Management of confidential/ proprietary information;
Germplasm (physical, dissemination)	- As International Public Goods/through NARS / - Public and Private Partnerships - Networks - Participatory development	• Preparation of licenses and other kind of applicable agreements to access and give access to germplasm, including SMTA/MTAs; • Legal advice on: - Collection of germplasm and exportation of germplasm; - Transfer of germplasm; - Contract negotiation for PPP; - Freedom to operate opinions; - Dissemination strategies for scaling up and out; and - Dissemination of data.
New tools such as newly discovered DNA, RNA, enzymatic and analytical methods and processes for use in biotechnology discovery and/or trait development, including but not limited to transformation tools and methods, promoters, introns, enhancers, DNA and RNA modification tools, etc.	- Licensing - Partnerships	Legal advice on: - Contract negotiation and drafting, including access to third party technologies and data sharing; - Freedom to operate opinions; - Use of patents; and - Dissemination strategies that ensure rights for research by all, yet use country-specific laws and regulations to foster competitive commercialization of different products by different providers, resulting in faster access to seed by farmers and lower seed prices.
Traits	- Licensing - Partnerships	Legal advice on : - Contract negotiation and drafting, including access to third party technologies; - Freedom to operate opinions; - Use of patents; and - Dissemination strategies that ensure access to native traits by all. Access to transgenic traits is subject to country-specific legislation being in place and the user having the capacity to meet

		country specific laws and regulations, requirements for stewardship and potential liabilities.
Agronomic technologies/ machinery	- Licensing - Partnerships	Legal advice on : - Contract negotiation and drafting, including access to third party technologies; - Freedom to operate opinions; - Use of patents; and - Dissemination strategies that keep IP rights in the public domain and ensure access and use by any competent provider.

Operations (technical infrastructure, planned activities)

IA/IP operations category	Policy, procedure, work process status	Policy, procedure, process owner
Incorporation into Leader Center project cycle	CG Center Project Management lifecycle	Project Managers + IP & Legal
Incorporation into project cycle	In accordance with policies and decisions taken by each CG Center; Subgrant policies	Participating Centers/ non-CGIAR partners
IA/IP tracking	CG Center Project Management lifecycle	Project Leader + IP & Legal
Negotiation of partner agreements	CG Center IP Policies & IP Manuals	Project Leader + IP & Legal
Convention on Biological Diversity/Farmer's Rights/Nagoya Protocol/ITPGRFA	CG Center Germplasm Policies	Project Leader + IP & Legal
Ethics in Research & Privacy Protection	CG Center Ethics in Research Policies	Project Leader + IP & Legal
Policy development, update of existing	IP policies, guidelines and manuals; CG Center Publications- related policies; CG Center Germplasm policies; CG Center Ethics in Research policies; Project management lifecycle;	IP + Legal
CGIAR Coordination	Overall management	Project Managers

Coordination and decision making (i.e. Policies, procedures, committee, task force)

Topic that triggers coordination with IP + Legal for decision making	Coordination /decision making procedure	Applicable Policy & Status
Development of an IP policy framework to guide implementing partners of the Platform	IP Management Committee composed of selected members of the Expert Advisory Groups	CG Center Intellectual Property Policy & Manual; CGIAR Principles for the Management of IA
Accessing technology that have or may have restrictions for results dissemination	Technical, management and legal advice during the project through participation in management meetings / application of polices in documents produced	CG Center Intellectual Property Policy & Manual
Granting limited exclusivity agreements for commercialization, whether as part of a partnership or a dissemination strategy	Legal advice during the project through participation in management meetings / application of polices in	CG Center Intellectual Property Policy & Manual; CGIAR Principles for the Management of IA
Partnership or strategies that include		CG Center Intellectual Property Policy &

the possibility of registering IPRs	documents produced	Manual; CGIAR Principles for the Management of IA CG Center Germplasm Policies;
Planning direct/specific research activities, particularly if they involve: Collection and transfer of germplasm; Licensing of Tools and Traits; Interaction with Human Subjects/ communities; Collection and/or dissemination or sensitive/ regulated data; Scaling up and out; Dissemination of Data through non-standard platforms.		Policies applicable to all matters: CG Center Intellectual Property Policy & Manual; CGIAR Principles for the Management of IA; For specific topics: Collection of Germplasm: CG Center Germplasm Policies; Interaction with Human Subject/ Communities: CG Center Ethics in Research Policies; Dissemination of Data: CG Center Research Data & Information Management Policies & CGIAR Open Access Policy.

* Additional decisions made will be in accordance with the CGIAR and Centers relevant policies.

4.4 Annex 4. Open Access (OA) and Open Data (OD) Management

Types of information products: The Excellence in Breeding Platform may produce the following types of information products: annual reports, books, monographs, brochures, databases, datasets, fact sheets/flyers, financial management documents, financial statements, guidelines and manuals, gray literature, journal articles, newsletters/bulletins, non-conventional literature, photographs, posters, presentations, proceedings, reports, reprints, research highlights, research plans, research reports, software, special publications, speeches, presentations, technical bulletins, theses, trip reports, videos/film.

Formats: Information products are to be created in digital formats so they can be immediately stored in proper repositories for "into perpetuity" archiving, using commonly used and highly compatible digital file formats, such as PDF, CSV, JPG and MP4. It is premature to define the detailed list of repositories or platforms housing information products from the Platform now. They will be identified during the program implementation based on a comprehensive survey of such information in CGIAR centers, ARIs and the Secretariat of the ITPGRFA. The Excellence in Breeding Platform may invest in transforming relevant legacy information products into digital formats, as a way to preserve institutional knowledge.

Storage and preservation of information products, as state-of-the-art digital repositories: As part of the Excellence in Breeding Toolbox, the Lead Center will need to implement and maintain an institutional multimedia publications repository. Lead Center and partner institutions will need to implement institutional research data and software repositories to ensure preservation, backup and openness of research outputs according to FAIR principles.

Licensing: The Lead Center of the Excellence in Breeding Platform will need to put in place licenses for all its information products that are made publicly available. Those licenses have to be approved by its Legal Unit and shown to the users of the repositories before they can download any information product. This licensing system will apply to all information products of the Platform. Preference is for the least restrictive licensing possible.

Procedures, workflows and embargo periods: All procedures, workflows and embargo periods regarding information products must be in compliance with the regulations given in the CG OADMP. Modules will be asked to develop specific inventories and plans for the implementation of OA and OD, for review and consolidation by the Platform Leader. The Platform intends to capitalize on resources developed by other Centers or CRPs to promote Open Access such as those available from CIP (http://cipotato.org/open-access/) and through the CG Open Access and Open Data Support Pack (https://sites.google.com/a/cgxchange.org/oad-support-pack/oa-od-advocacy-and-guidance-materials).

Technical considerations: It is essential that the information products stored in the repositories cited in the Data Management Plan can be detected by search engines, and their contents indexed via standard protocols. The Excellence in Breeding Platform's repositories need to provide syntactic and semantic interoperability by means of internationally used standards such as OAI-PMH, Agrovoc and Dublin Core, and need to be hosted in first-class cloud servers so the content is properly backed-up and archived "into perpetuity." The Platform plans to implement CGIAR Core metadata in the repositories that it uses to share data with the public. Two of the major repositories, DSpace and Dataverse, already contain the majority of elements required to capture CG Core metadata. Other repositories will be developed as part of Module 5. Use of CG Core metadata and other study-level metadata will improve the discoverability of datasets and other information products. A meta-search functionality, already under development, will allow different datasets to be interconnected at this level. As far as possible, publications will be linked to

their related datasets by means of persistent identifiers. Use of ontologies and controlled vocabulary to map units, traits, environmental conditions, etc., will be required to facilitate the data integration across scales and studies. The Platform will work with the Big Data Platform and the AFS CRPs, to explore emerging software designed to automate or semi-automate data annotation processes, such as the Agrotagger tool (http://aims.fao.org/vest-registry/tools/agrotagger-1).

Operations: Budgets for personnel and infrastructure will be allocated to ensure the following routine and on-demand operations are properly carried out, both as part of the Platform and Module Leaders' budgets and those of members:

- Implementation of suitable repositories and tools (on demand). [CG OADMP § 4.1.2]
- Maintenance and improvement of suitable repositories and tools (routine). [CG OADMP § 4.1.2]
- Implementation of interoperability (on demand). [CG OADMP § 4.1.3]
- Maintenance and improvement of interoperability (routine). [CG OADMP § 4.1.3]
- Implementation of hardware infrastructure, storage volumes, backup storage, and disaster recovery plans (on demand). [CG OADMP § 4.1.4]
- Maintenance and improvement of hardware infrastructure, storage volumes, backup storage, and disaster recovery plans (routine). [CG OADMP § 4.1.4]
- Translation of key documents and other media into pertinent languages (on demand). [CG OADMP § 4.1.7]
- Data curation, metadata tagging, and data quality control (routine). [CG OADMP § 4.1.3 and § 4.1.4]
- Periodic evidence-based review of the implementation of relevant regulations in force (routine). [CG OADMP § 5]
- Continuous coordination among participating centers to ensure proper Open Access and Open Data implementation (routine). [CG OADMP § 2]
- Training activities covering relevant topics to ensure proper staff knowledge and engagement to accomplish envisaged Open Access and Open Data objectives (on demand).

Coordination and decision-making (e.g., workflows/procedures, capacity, governance). Based on OA and OD inventory and plans developed at Module level, procedures and governance recommendations that should be followed CRP-wide will be made by the Module Leader and Expert Advisory Group of Module 5, reviewed by the other modules and approved by the Platform Leader and Platform Steering Committee.

Narrative for required resources (e.g., human and financial). The following Table shows the minimum additional resources estimated for OA/OD activities of the Excellence in Breeding Platform. Additional resources may need to be allocated at Module level once OA and OD plans are elaborated in more detail and member's contributions and capacities are defined.

Annual resource requirements for OA/OD activities of the Excellence in Breeding Platform.

Item	Lead Center	AFS CRPs
Staff for data curation, data quality assurance prior to final publication, metadata tagging, data storage, coordination with other centers and units and implementation of procedures and workflows related to information product management.		Included in budgets of AFS CRPs
Staff for license management, data storage, counseling on information product management and coordination with other centers and units (10%).	USD 14,000	
Server rental and maintenance, storage volumes, backup storage and server disaster recovery set-up.	USD 26,000	
Implementation of suitable publicly accessible repositories (outsourcing).	USD 12,500	
Improvement of suitable publicly accessible repositories, mainly regarding interoperability and dissemination features and channels/pipelines (outsourcing).	USD 50,000	
Translation of key documents and other media into pertinent languages.	USD 10,000	
Fees for publishing in Open Access (see tables below).	USD 90,000	
	USD 202,500	

4.5 Annex 5. Capacity Building

Two capacity-related sub-IDOs were identified to be essential to the Theory of Change and Impact Pathway of the Excellence in Breeding Platform: (i) C.1.2. Increased capacity of partner organizations, as evidenced by rates of investment in agricultural research; and (ii) D.1.2 Enhanced individual capacity in partner research organizations through training and exchange. Through D.1.2 and in combination with the use of new tools, the Platform is expected to also contribute to D.1.1 "Enhanced institutional capacity of partner research organizations" and D.1.3 "Increased capacity for innovation in partner research organizations." Relevant high-level indicators at the CRPII Portfolio level include:

Capacity Development sub-IDO 1: Increased institutional capacity of partner research organizations

- Number of partner research organizations who use CGIAR learning materials and approaches developed by the Platform

Capacity Development sub-IDO 2: Enhanced individual capacity in partner research organizations through training and exchange

- Number, quality and targeting of short-term training
- Number, duration and quality of mentoring and exchange in research partnership agreements

Capacity Development sub-IDO 4: Increased capacity for innovation in partner development organizations, and in poor and vulnerable communities

- Adaptation, adoption and spread of innovations linked to Platform participatory research results

Like other CRPs and Platform, the Excellence in Breeding Platform will be implementing a results-based management framework. Use of tools is at the core of the Platform's success. Monitoring of capacity development indicators will hence be crucial to have early leads on assessing bottlenecks and success.

The Platform will invest specifically in five areas of capacity development: (i) needs assessment and intervention strategy; (ii) learning materials and approaches; (iii) monitoring and evaluation; (iv) organizational development; and (v) capacity to innovate. It will be able to monitor the following outputs and outcomes:

Capacity building element	**Output**	**Outcome**
Needs assessment and intervention strategy	Capacity needs assessment methodology developed for CGIAR and NARS Capacity needs of CGIAR and NARS research partners assessed	Capacity building needs of partner organizations met
Learning materials and approaches	Guidelines on content development published Learning materials designed according to context and audience Learning materials pilot tested with target audience	Learning materials accessible to targeted users Knowledge and skills of training/workshop participants increase after training Users implement the lessons / take decisions based on the training
Monitoring and evaluation	Engagement through participatory discussions to ensure use of best practices for monitoring and	Detailed reporting on a range of capacity development indicators is

	evaluation Guidelines and check lists for monitoring and evaluating capacity strengthening activities developed Regular monitoring and evaluation of capacity strengthening activities by Module	available
Organizational development	Engagement with research partners throughout the research planning and implementation cycle Strengthen research partner skills related to research cycle	Stronger skills of individual and organizations in research planning and management
Capacity to innovate		Increased and better quality experimentation Increased access to novelty: new technology, ideas, innovation Adoption of technology: technical and institutional

4.6 Annex 6. List of References

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4.7 Annex 7. List and Web Links of Projects and Software Tools

Agricolae	Statistical Procedures for Agricultural Research; https://cran.r-project.org/web/packages/agricolae/index.html
Agroportal	http://agroportal.lirmm.fr/
B4R	Breeding for Rice; https://sites.google.com/a/irri.org/breeding4rice/
BMS	Breeding Management System; https://www.integratedbreeding.net/breeding-management-system
BrAPI	Breeding Application Programming Interface https://www.researchgate.net/publication/268116821_Application_Programming_Interface_API_for_Plant_Breeding_Data_and_Software_Tools
CassavaBase	https://www.cassavabase.org/
Flapjack	https://ics.hutton.ac.uk/flapjack/
G4R	Genomics for Rice; https://sites.google.com/a/irri.org/g4r/
GDMS	Genotyping Data Management System; http://mbp.generationcp.org/confluence/display/MBP/Application+2.2.1+Tool+2.10+-+Database+++++2.10.3+IBDB+Genotyping+Data+Management+System+(GDMS)+Schema+v1.0
GeneSys	https://www.genesys-pgr.org/welcome
Germinate	https://ics.hutton.ac.uk/germinate/
GLIS	Global Information System on Plant Genetic Resources for Food and Agriculture; http://www.planttreaty.org/content/gis
GOBII	Genomic & Opensource Breeding Informatics Initiative; http://cbsugobii05.tc.cornell.edu/wordpress/
GrinGlobal	Germplasm Resource Information Network; http://www.ars-grin.gov/npgs/gringlobal/webpages/publicwebsite.html
GS-RUSE	Genomic Selection for Resources Use Efficiency in Rice; http://www.first-gsruse.net/
GT4SP	Genomic Tools for Sweetpotato Improvement; https://cgspace.cgiar.org/handle/10568/69211
IBP	Integrated Breeding Platform; https://www.integratedbreeding.net/
IRIC	International Rice Informatics Consortium; http://iric.irri.org/
KDSmart	https://play.google.com/store/apps/details?id=com.diversityarrays.kdsmart&hl=en
KDXplore	http://software.kddart.com/KDXplore/
KSU Fieldbook	http://www.wheatgenetics.org/field-book
MusaBase	https://musabase.org/
NDEx	http://www.ndexbio.org/

Planteome	http://planteome.org/
QTLNetMiner	https://ondex.rothamsted.ac.uk/QTLNetMiner/
SeeD	Seeds of Discovery; http://seedsofdiscovery.org/
South Green	http://www.cirad.fr/en/research-operations/research-results/2011/south-green-bioinformatics-platform
YamBase	https://yambase.org/

4.8 Annex 8. List of Abbreviations

A4NH	CGIAR Research Program on Agriculture for Nutrition and Health
AFS	Agri-Food Systems
ARI	Advanced Research Institute
B&MGF	Bill & Melinda Gates Foundation
BecA	Biosciences eastern and central Africa
BoT	Board of Trustee
CAAS	Chinese Academy of Agricultural Sciences
CEPLAS	Cluster of Excellence on Plant Sciences
CG OADMP	CGIAR Open Access and Data Management Policy
CIAT	International Center for Tropical Agriculture
CIMMYT	International Maize and Wheat Improvement Center
CIP	International Potato Center
CIRAD	Centre de coopération Internationale en Recherche Agronomique pour le Développement (France)
CoP	Community of Practice
CRP	CGIAR Research Programs
CSIRO	Commonwealth Scientific and Industrial Research Organisation (Australia)
DCL	CGIAR Research Program on Dryland Cereals and Legumes
DG	Director General
FAO	Food and Agriculture Organization of the United Nations
Fish	CGIAR Research Program on Fish
FTA	CGIAR Research Program on Forests Trees and Agriculture
GCDT	Global Crop Diversity Trust
GCP	Generation Challenge Program
Genebanks	CGIAR Platform on Genebanks
GS	Genomic Selection
GWAS	Genome-Wide Association Study
HR	Human Resources
IA	Intellectual Asset
IBP	Integrated Breeding Platform
ICARDA	International Center for Agricultural Research in the Dry Areas

ICRAF	World Agroforestry Centre
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
ICT	Information and Communications Technology
IDO	Intermediate Development Outcome
IEA	Independent Evaluation Assessment Unit of the CGIAR
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
INRA	Institut National de la Recherche Agronomique (France)
IP	Intellectual Property
IPG	International Public Good
IRD	L'Institut de recherche pour le développement (France)
IRRI	International Rice Research Institute
ISO	International Standards Organization
ISPC	Independent Science and Partnership Council
ITPGRFA	International Treaty of Plant Genetic Resources for Food and Agriculture
JIRCAS	Japan International Research Center for Agricultural Sciences
Livestock	CGIAR Research Program on Livestock
MAIZE	CGIAR Research Program on Maize
MEL	Monitoring, Evaluation and Learning
MELIA	Monitoring, Evaluation, Learning and Impact Assessment
NARS	National Agricultural Research Systems
PIM	CGIAR Research Program on Policy, Institutions and Markets
PSC	Platform Steering Committee
R&D	Research and Development
RICE	CGIAR Research Program on Rice
RBM	Results-Based Management
RTB	CGIAR Research Program on Roots Tubers and Banana
SLO	Systems Level Objective
SME	Small and Medium Enterprise
SNP	Single Nucleotide Polymorphism
SRF	Strategic Results Framework
USDA	United States Department of Agriculture
W1	Funding Window 1 of the CGIAR; contributions to the CGIAR

W2	Funding Window 2 of the CGIAR; contributions to a specific CRP
W3	Funding Window 3 of the CGIAR; contributions to a specific CGIAR Center
WHEAT	CGIAR Research Program on Wheat