






























Platform Annual Plan of Work and Budget (POWB) for 2017

COVER PAGE

	Excellence in Breeding Platform (EiB)	CIMMYT
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A substantive range of partners are or have indicated strong interest in getting involved in the Excellence in Breeding Platform during 2017. The list of partners is expected to grow.

List of participating Centers and other key partners	Logo
AfricaRice	
Bioversity International	
International Center for Tropical Agriculture (CIAT)	
International Maize and Wheat Improvement Center (CIMMYT)	
International Potato Center (CIP)	
Cornell University	
Commonwealth Scientific and Industrial Research Organisation (CSIRO)	
Diversity Arrays Technology	
DuPont Pioneer	
Global Crop Diversity Trust (GCDDT)	
Food and Agriculture Organization of the United Nations (FAO)	
International Center for Agricultural Research in the Dry Areas (ICARDA)	

Institut national de la recherche agronomique (INRA)	
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	
International Institute of Tropical Agriculture (IITA)	
International Livestock Research Institute (ILRI)	
Integrated Breeding Platform (IBP)	
International Rice Research Institute (IRRI)	
James Hutton Institute	
John Innes Centre	
Nottingham University	
Oregon State University	
Queensland University	
Swedish University of Agricultural Sciences (SLU)	
Syngenta	
United States Department of Agriculture (USDA)	
Wageningen University	
World Agroforestry Centre (ICRAF)	
WorldFish	

A. Excellence in Breeding Platform

A1. Delivery

A1.1 Adjustments/ changes to your Theories of Change

Even though the Platform is initiated with a partial budget, the overall Theory of Change (ToC) as described in the proposal continues to apply (annex 2).

A1.2 Highlight expected Outputs and Outcomes

The Excellence in Breeding Platform is a new Platform. Meetings with close to 100 Agri-food Systems (AFS) and Genebank scientists in December 2016 and January 2017 confirmed that the proposal defined a solid workplan and priority setting that should be followed. The AFS CRPs and the Genebank Platform assigned 43 Expert Advisory Group (EAG) members that will form the core of strategy definition and the delivery of outputs and outcomes in the Excellence in Breeding Platform. In 2017, a standardized system will be developed to assess strengths and weaknesses of current AFS breeding programs and develop strategic plans that define prioritized improvements. The same framework will be used to make breeding targets more transparent and monitor improvements across different species. This community driven effort entails a significant change to 40-50 years of close-to-independent breeding operations within the CGIAR. Breeding program assessments will be complemented by topic-specific baseline surveys to establish: best practices and actual use of genotyping/sequencing applications; the status of phenotypic and environmental characterization; the landscape of bioinformatics and biometrics tools and services; and the use, quality and costs of internal and external service platforms/providers. A web platform will be developed to host a non-prescriptive toolbox which will be populated with existing best-practice tools and approaches, support community interactions and the Platform's learning management system. The Platform will enable AFS-related breeding programs and germplasm banks to jointly link up with external providers to contract high-throughput genotyping or sequencing applications, and to work with selected ARIs to adapt, test and mainstream state-of-the-art phenotyping and environmental analysis approaches. It will support currently fragmented bioinformatics initiatives to develop and pursue a joint strategy aligned with prioritized breeding and trait discovery processes, leading to greater access to inter-compatible software tools and databases, within AFS CRPs and beyond. The entirety of the Platform's interventions is directed at capacity development. Next to established scientists, young scientists and students are expected to become prominent contributors and users of the Platform. The training strategy and needs assessment will assess the role of gender in men and women getting involved and professionally advancing in plant and animal breeding and related fields.

A.1.3 Use of Different Funding Sources

With a W1-2 budget of US\$ 2 million, the Platform capitalizes on existing CGIAR-linked initiatives, whether funded from within the CGIAR or by ARIs. It will develop W3 and bilateral funding aligned with the proposal to support more rapid improvements of AFS-related breeding programs, ensure contributions by a wider number of organizations, and implement the Platform's training strategy in pursuit of increasing the capacity of partner organizations, greater genetic gains and greater returns on investments (see Table 1).

Table 1: Platform planned budget by module for 2017

Module Name	Planned Budget 2017 (USD)		
	W1/W2	W3/bilateral	Total
(one row per Module)			
Module 1	414,100	1,573,500	1,987,600
Module 2	372,800	1,120,300	1,493,100
Module 3	183,600	826,400	1,010,000
Module 4	183,700	1,417,300	1,601,000
Module 5	670,100	2,781,400	3,451,500
Management & Support Cost	175,700	281,100	456,800
Total	2,000,000	8,000,000	10,000,000

A1.4 Planned revisions to your Program of Work

The Program of Work was revised to adjust to that W3 and bilateral funding will be raised during 2017, as shown in Table 2 and 3, and is not yet available at its onset. Even though donors will only allocate W1-2 funding later in the year, the Platform will count on the full W1-2 budget (US\$ 2 million) and implement activities accordingly, implying that implementers absorb a substantial risk. The Platform will capitalize on in-kind support from ARIs and the private sector. This includes existing ARI-led, CGIAR-linked initiatives such as: the Breeding Program Assessment Tool project (BPAT) implemented by Queensland University; the Genomic & Opensource Breeding Informatics Initiative (GOBII) and the CassavaBase, MusaBase and YamBase initiatives, all led by Cornell University; the Planteome project that establishes Common Reference Ontologies and Applications for Plant Biology (cROP); led by Oregon State University; and the Global Information System on Plant Genetic Resources established by the Food and Agriculture Organization of the United Nations (FAO).

A2. Collaboration and Integration

A2.1 Contribution to and from CRPs

The entire Platform agenda is designed to support the AFS CRPs and the Genebank Platform. AFS CRPs and the Genebank Platform in return provide EAG members; contribute to the overall and Module specific strategies, priority setting and documentation of existing tools, metadata and standards; implement AFS specific breeding program assessments to set breeding program directions; contribute to baseline surveys; implement new tools and applications; increase the development of inter-compatible software tools and databases; provide partner linkages; and contribute to project proposals. Platform investments will be targeted at funding the additional efforts needed to strengthen Platform activities while capitalizing as much as possible on existing in-kind contributions by AFS CRPs and the Genebank community.

A2.2 Cross-Platform interactions

Genebank Platform

The Excellence in Breeding (EIB) Platform provides a unique forum for discussion and sharing of tools and approaches between the genebanks and breeding programs. Genebank Platform representatives have been identified to participate in the EAGs of Modules 2 to 5. While the Genebank Platform will develop data resources and query mechanisms, user germplasm sets and traits related to germplasm bank activities, the Excellence in Breeding Platform will develop means of interoperability with systems and data resources used in the breeding domain, support shared ontologies and the implementation of Digital Object Identifiers (DOI).

Big Data Platform

Through its web platform and associated Toolbox and learning management system, the Excellence in Breeding Platform will become the main vehicle for Open Access/Open Data of germplasm data, information and know-how, aligned with the CGIAR's Open Access and Data Management Policy. It will go beyond the CGIAR community and involve the promotion of Open Access/Open Data from ARIs, NARS and also the private sector. It will capitalize on relevant center support and cloud computing access provided by the Big Data Platform. The Excellence in Breeding and Big Data community will jointly assess critical data gaps in developing germplasm-related international public goods and interoperability between germplasm-related data resources and systems and those managed by the Big Data Platform (economic data, crop modelling, data-driven agronomy and geospatial data).

A2.3 Expected Efforts on Country Coordination

In 2017, the Platform will use CGIAR country coordination mechanisms (meetings) to promote awareness about the Excellence in Breeding Platform and for needs assessments (e.g. training, genotyping etc.). This will be done through local AFS members. The IBP will use country-coordinated trainings to support the use of its Breeding Management System by NARS.

A3. Management, Governance and Monitoring, Evaluation, Learning

A3.1 Relevant Changes

No changes compared to the proposal are expected. Members for the Platform Steering Committee and EAGs will be chosen jointly with AFS CRPs and the Genebank Platform to govern and champion the Platform's activities. Platform and Module Leaders, and personnel for Platform administration, communication and to support the web platform will be appointed using competitive processes.

A3.2 Monitoring, Evaluation, Impact Assessment and Learning Plans

All Modules will invest in establishing baselines, document current best practices and refining strategies and workplans for the Platform's engagement. Details are provided in Section B. To frame the milestones and associated outcomes described in this workplan, the Platform will develop a results-based management framework, which will include the ToC (see annex 2) and indicators to monitor progress. This results-based management framework will be in line with the emerging and increasingly comprehensive CGIAR performance management framework (annex 4) developed by System Management Office and the Monitoring, Evaluation and Learning Community of Practice in collaboration with the ISCP, IEA and donor representatives. The Platform will contribute and provide feedback to the development of the CGIAR performance management framework, including the Taskforce on Indicators, which is finalizing a set of indicators to demonstrate the CGIAR portfolio's progress against the System-Level Outcomes. - Module 1 will conceptualize for the first time a performance management system that can be applied across AFS breeding programs. While assisting in targeting, monitoring and the prioritization of interventions, it will enable more standardized and systematic reporting of AFS breeding programs which will contribute to greater transparency and improved recognition of bottlenecks to increasing breeding program scope and efficiency.

B. Module 1 Excellence in Breeding

B.1 Delivery

B.1.1 Expected Annual Milestones towards Outcomes 2022

Expert Advisory Group members of Module 1, from all AFS CRPs, will work with Queensland University to revise the Breeding Program Assessment Tool (BPAT) in view of developing a standardized system for capturing breeding program targets, assessments and metrics which will reveal bottlenecks and opportunities, and support priority setting within and across breeding programs. The Module Leader will document and upload the resulting standard templates and approaches for monitoring breeding program performance in the Platform's toolbox for wider accessibility. The Module Leader and experts contracted by the Queensland University backstop AFS CRPs in executing the assessment in their own breeding programs in support of (i) the development of program-specific strategic plans for implementing improvements and (ii) more standardized reporting of breeding program performance. The Platform Leader and the Module 1 Leader will invest time to develop co-funding by W3 and bilateral donors to enable (i) the implementation of prioritized improvements in AFS breeding programs, (ii) wider involvement of CGIAR and NARS breeding programs, and (iii) standardized genetic gain assessments in 2018 – 2022.

B.1.2 Output towards Outcomes 2022

Standardized systems for capturing breeding program targets, assessments and metrics and AFS-specific breeding program assessments will contribute to increasing the focus and performance of CGIAR and NARS breeding programs, and result in increased capacity of partner organizations as evidenced by rates of investment in agricultural research (Sub-IDO C.1.2. and D.1.2. – see ToC in annex 2). While the entirety of the Platform's interventions is directed at capacity development, new breeding approaches will inspire and accelerate the professional development of young scientists in particular. The relevance of gender in setting breeding targets will be part of the breeding program assessments and the setting of breeding program targets.

B.1.3 Contribution of W1-2 Funds

W1-2 funds will be used to revise the Breeding Program Assessment Tool (BPAT) currently used by Queensland University for wider use by AFS breeding programs. W1-2 resources will be allocated to AFS CRPs to pay for the additional costs of executing the assessment and formulating breeding program specific plans which will guide future priority setting and investments, and be reflected in AFS CRP reports. W3 and Bilateral fundraising will be directed at supporting prioritized improvements, involving a wider range of breeding programs in the assessment, and enabling the standardization of genetic gain assessments.

B. Module 2 Trait discovery and breeding tools and services

B.2 Delivery

B.2.1 Expected Annual Milestones towards Outcomes 2022

In 2017, a web platform will be developed to incorporate breeder-relevant tools and workflows used by AFS CRPs, the Genebank Platform and external members into a common “Toolbox” which is linked to a user review system. A consultancy company (common sense eLearning and training consultants, Austria) has been contracted to develop the learning management system within the Web Platform. The AFS CRPs and Genebank Platform assign members to the EAG of Module 2 to oversee the Toolbox strategy and link with the Communities of Practice (CoP) from relevant members of each module. The web platform will be tested with EAG members. The focus in the first year will be on aggregating and uploading existing content from all modules into the Toolbox. The EAG will also develop the training strategy and specifications for the training needs assessment. The Platform Leader will invest time to develop co-funding by W3 and bilateral donors to (i) document and incorporate new components, upgrade workflows and develop use cases; (ii) establish linkages with tools from ARIs, universities and the private sector, (iii) implement the training strategy aligned with AFS CRPs and the Genebank Platform; and (iv) source innovative ideas for trait mobilization and breeding through incubators.

B.2.2 Output towards Outcomes 2022

A common web platform with a non-prescriptive toolbox will enable the wider breeding community to upload and exchange tools and best practices (documented breeding processes, databases, information about equipment, manuals, software, videos), and access expertise and services from all modules. It will provide a one-stop shop to facilitate learning, by (i) more widely announcing training events from all partners, and (ii) aggregating e-content from AFS CRPs and universities. This will reduce the transaction costs and redundant investments of CGIAR and NARS when implementing cutting-edge tools and approaches while augmenting the quality of training activities. It will enhance the individual capacity of professionals in partner research organizations and the overall capacity of partner organizations (Sub-IDO C.1.2., D.1.1. and D.1.2 – see ToC in annex 2). While the entirety of the Platform’s interventions is directed at capacity development, young scientists and students will likely become prominent contributors and users of the Platform. The training strategy and needs assessment will assess the role of gender in men and women getting involved and professionally advancing in plant and animal breeding and related fields.

B.2.3 Contribution of W1-2 Funds

W1-2 funds will be used to develop the web platform and Toolbox, and discuss with the EAG the overall strategy and contributions from the AFS CRPs, germplasm banks and external members. It will fund the learning management system (consultancy), the training strategy (EAG) and training needs assessment (consultancy). W1-2 resources will pay for the additional costs of documenting tools and approaches, available expertise and services from all modules. W3 and bilateral fundraising will be directed at involving a wider range of contributors and ensure rapid implementation of the training strategy.

B. Module 3 Genotyping/sequencing tools and services

B.1 Delivery

B.3.1 Expected Annual Milestones towards Outcomes 2022

A schedule of virtual and face-to-face meetings is established among members of the EAG and with other modules to assure progress, share experiences and discuss emerging issues. The EAG develops a baseline survey to establish the current status of each AFS species, genotyping/sequencing volumes and the use of service providers. Module Leader and AFS CRPs develop: (i) current use cases; (ii) operational guidelines to standardize tissue sampling and logistics; and (iii) best practices and protocols for marker conversion to be shared through the Platform's Toolbox. In collaboration with the High throughput genotyping project (HTPG) and the Integrated Genotyping Support and Service (IGSS), CGIAR and NARS breeding programs are enabled to implement industrial-scale low-density SNP genotyping. WebEx seminars for training purposes are being scheduled and linked with the HTPG, IGSS and GOBII training strategies. The focus will be on the promotion of high-throughput applications in species where it is currently ready. As a result of the survey, updated needs and a list of suppliers are being developed and agreements with service providers pursued following EAG advice. Co-support by W3 and bilateral donors is being pursued to mainstream high-throughput applications for higher density genotyping and sequencing applications in support of trait mobilization and forward breeding.

B.3.2 Output towards Outcomes 2022

Establishing current status and needs based on a joint strategy, documenting best practices, developing training material, providing expert advice and increasing access to cost-effective genotyping/sequencing services enable CGIAR and NARS to increase the use of genotyping and sequencing applications in trait discovery and breeding. Increased use by AFS and other researchers of tools for developing better cultivars and breeds faster builds the capacity of members and contributes through the AFS CRPs and external users to Sub IDOs 1.1.2, 1.4.1, 1.4.3, 2.1.1, 2.2.1, 3.1.3, A.1.4 (see ToC in annex 2). The module's activity will inspire young scientists to use genotyping and sequencing applications more readily and strengthen the role of women who traditionally are more represented in laboratory-based jobs.

B.3.3 Contribution of W1-2 Funds

W1-2 funds will enable the EAG to develop the baseline survey and support the Module Leader and selected EAG members in visiting stakeholders to discuss baseline information and provide advice on the feasibility of marker conversion and forward breeding in various species. It will support the Module Leader and AFS CRPs to develop best practice material and training materials for the Platform's Toolbox and widen the reach of already planned training activities. W1-2 also supports interactions with potential service providers. W3 and bilateral funding will verify production markers by Intertek, execute polymorphism screening of parents, and support training. Additional W3 or bilateral funding is being pursued to support (i) expert visits and face-to-face training; (ii) conversion to SNP markers; and (iii) the mainstreaming of a wider range of genotyping/sequencing applications in breeding programs.

B. Module 4 Phenotyping tools and services

B.4 Delivery

B.4.1 Expected Annual Milestones towards Outcomes 2022

Module 4 will conduct surveys among AFS CRPs to assess phenotype and environmental data collected, adoption of high-throughput tools, GxExM and gene-to-phenotype methods, and barriers to adoption, in coordination with Module 1. Support will be provided to document best use cases, those that are already (close to being) mainstreamed in applied breeding programs. Relevant linkages to existing plant phenotyping networks will be established to identify partners involved in developing praxis relevant breeding applications, assess sharing of training modules and organizing joint training events. Proposals will be developed with priority partners for joint support of CGIAR phenotyping and environmental analysis by leading ARIs. An initial survey established a range of desirable partners: CSIRO, Queensland University, and Diversity Arrays in Australia; Jülich Plant Phenotyping Center and IPK Gatersleben in Germany; Kansas State and Purdue Universities, USDA and Quanta Laboratories in the US; INRA in France; and the private sector. Breeding programs within and beyond the AFS CRPs will also be surveyed to assess use of laboratories, capacities and costs for determining physico-chemical and functional characteristics in plant and animal materials. Funding is being developed to assess and implement greater mechanization and automation in CGIAR and NARS breeding programs to increase returns to investment

B.4.2 Output towards Outcomes 2022

Establishing current status, documenting best practices, developing training material and organizing the input of leading ARIs to AFS breeding programs enable CGIAR and NARS to implement best practices for phenotyping and environmental analysis to increase breeding efficiency and returns to investment. Increased use by AFS and other researchers of tools for developing better cultivars and breeds faster contributes through the AFS CRPs and external users to Sub IDOs 1.1.2, 1.4.1, 1.4.3, 2.1.1, 2.2.1, 3.1.3, A.1.4 (see ToC in annex 2). While the entire Platform's intervention is directed at capacity development, new phenotyping and environmental analyses approaches will inspire and accelerate the professional development of young scientists in particular. Women seem to take an increasing interest in new phenotyping applications and the Platform will seek to enhance their involvement.

B.4.3 Contribution of W1-2 Funds

W1&W2 funding will be used to execute surveys among AFS CRPs, document use cases, conduct workshops to develop proposals for joint support of CGIAR phenotyping and environmental analysis by leading ARIs and the private sector. W3 and bilateral fundraising will be targeted at (i) enabling systematic cutting-edge support to AFS CRPs in the area of precision and high-throughput phenotyping, GxExM analyses and Genotype-to-Phenotype predictions; and (ii) expanding the Module's activity to improve mechanization and automation across CGIAR and NARS breeding programs.

B. Module 5 Bioinformatics and data management tools and services

B.5 Delivery

B.5.1 Expected Annual Milestones towards Outcomes 2022

The EAG of Module 2 and 5 will jointly identify key workflows/gaps to establish the overall strategy and priorities for breeding case studies that are to be supported or inter-connected with improved bioinformatics tools. Jointly with the other Platforms, critical data gaps in germplasm related international public goods and interoperability among data resources are established. Selected pipelines and tools are analyzed and documented in the Platform's Toolbox for fit/gap analyses by the wider community. Linkages with existing communities of practice for crop and agronomy ontologies are established. Unique germplasm identifiers (GUIDs) are linked with or conceptualized viz. existing efforts, and recommendable ontologies documented in the Platform's Toolbox. The Module's EAG, in collaboration with key bioinformatics initiatives, will survey and conceptualize the CGIAR linked landscape of bioinformatics tools and services, and develop a support model to implement the Breeding Applied Programming Interface (BrAPI).

B.5.2 Output towards Outcomes 2022

The Module will develop the overall strategy and prioritization of breeding processes that are to be better supported by bioinformatics and biometrics tools, develop the support model to implement the Breeding API (BrAPI) for different systems, co-invest in the development of inter-compatible software tools and databases targeted at the needs of breeding programs in the developing world, and document the current landscapes of metadata standards, ontologies and bioinformatics tools and services. Funding will be developed to expand the scope and relevance of developing and using inter-compatible software tools and databases within the CGIAR/germplasm community. Increased use of tools for developing better cultivars and breeds faster contributes through the AFS CRPs and external users to Sub IDOs 1.1.2, 1.4.1, 1.4.3, 2.1.1, 2.2.1, 3.1.3, A.1.4 (see ToC in annex 2). Appropriate software is at the core of increasing the capacity of breeding programs and will inspire and engage young scientists in particular.

B.5.3 Contribution of W1-2 Funds

W1&2 funds will support the communities of practice that (i) establish overall strategies and priorities for breeding case studies and analyze and document related user and technical requirements; (ii) conceptualize and document the landscapes of ontologies, metadata standards and bioinformatics tools and services; and (iii) design the support model to implement BrAPI and local APIs for different systems. Existing support by the Integrated Breeding Platform allows the optimization of the Breeding Management System for small- to medium-sized field-oriented breeding programs, and initiate the implementation of a collaborative strategy for supporting data intensive applications (e.g. supporting genome-wide selection) for more complex breeding programs. Co-support by W3 and bilateral donors will be developed to (i) develop tools to facilitate modular and adaptable breeding pipelines; (ii) coordinate the development and implementation of a common BrAPI; (iii) support the development of databases and tools to complement and expand the usefulness of existing bioinformatics initiatives; and (iv) advance the sustainable deployment and maintenance of tools and applications.

Table 2: Expected Annual Milestones (progress markers) towards Outcomes 2022

Module No.	Module Outcome 2022	Milestone 2017 Max. of 3 milestones per module outcome 2022	Mapped budget request for 2017	
			W1/ W2 USD	W3/ bilateral USD
Module 1	1.1 Existence of a CGIAR agreement on standard template and approaches for monitoring breeding program performance	1.1.1 AFS CRPs assign members to the EAG of Module 1 to develop a standardized system for capturing breeding program targets, assessments and metrics.	167,700	0
		1.1.2 Revision of Breeding Program Assessment Tool with the EAG		
		1.1.3 Standard template and approaches documented and uploaded on common toolbox		
	1.2 Existence of standardized breeding program assessments & strategic plans to set breeding program direction in the CGIAR.	1.2.1 AFS CRPs executing breeding program assessment	236,400	1,573,500
		1.2.2 AFS CRPs use standard assessment in CRP reporting		
	1.3 Existence breeding program assessments & strategic plans to set breeding program directions with NARS	1.3.1 Attracting co-support by W3 and bilateral donors	10,000	
1.4 CGIAR and NARS implementing prioritized improvements				
1.5 Existence of standardized genetic gain assessments in AFS breeding programs				
Module 2	2.1 Existence of a common web platform to interchange best practices by the trait discovery and breeding community	2.1.1 Web platform developed to incorporate breeder-relevant tools and workflows used by AFS CRPs and external members into a common "Toolbox" which is linked to a user review system.	184,800	0
		2.1.2 AFS CRPs and the Genebank Platform assign members to the EAG of Module 2 to oversee the Toolbox strategy and link with the CoPs from relevant members of each module; initial content developed and uploaded into the Toolbox (all Modules).	178,000	0
		2.1.3 Training strategy and specs for training needs assessment developed; learning management system within the web platform developed.		
	2.2 Wider range of partners contribute to Toolbox (ARIs, CGIAR, NARS, private sector)	2.2.1 Attracting co-support by W3 or bilateral donors	10,000	1,120,300
	2.3 Increased benefits by CGIAR and NARS from virtual/face-to-face training strategy			

Module 3	3.1 Existence of a joint strategy to increase use of genotyping and sequencing applications in trait discovery and breeding	3.1.1 Communication strategy established among EAG members and with other Modules to assure progress and share experiences.	69,500	0
		3.1.2 Baseline survey conducted to describe current status in each AFS specie, genotyping/ sequencing volumes and use of service providers.		
		3.1.3 Core team of Module Leader and selected EAG members visit stakeholders to discuss baseline and establish the feasibility of marker conversion and forward breeding.		
	3.2 Increased use of genotyping and sequencing applications in discovery and breeding	3.2.1 Module Leader and AFS CRPs develop: (i) current use cases; (ii) operational guidelines for standardizing tissue sampling and logistics; (iii) best practices and protocols for marker conversion; for sharing through the Platform's Toolbox.	86,700	388,000
		3.2.2 Shared industrial-scale low-density SNP genotyping for CGIAR and NARS breeding programs implemented		
		3.2.3 WebEx training seminars scheduled and linked with the HTPG, IGSS and GOBII training strategy.		
3.3 Greater access by AFS CRPs and the Genebank Platform to cost-effective genotyping /sequencing services	3.3.1 Needs updated and list of suppliers documented.	17,400	0	
3.4 Increased mainstreaming of genotyping/sequencing applications in a larger number of breeding programs.	3.4.1 Attracting co-support by additional W3&bilateral donors	10,000	438,400	
3.5 Existence of support of CGIAR and NARS to implement a wider range of genotyping/sequencing applications				
Module 4	4.1 Existence of best practice documentation for phenotyping and environmental analysis within the CGIAR	4.1.1 Survey among AFS CRPs conducted 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	130,600	0
		4.1.2 Documentation by AFS CRPs of mainstreamed use cases.		
		4.1.3 Relevant linkages to existing plant phenotyping networks established		
	4.2 Increased use of state-of-the art precision and high-throughput phenotyping, GxExM analyses and Genotype-to-Phenotype predictions applied in AFS breeding programs	4.2.1 Workshop on existing practices, with ARI and private sector participation; identification of quick wins.	34,800	695,600
		4.2.2 Proposals developed for joint support of CGIAR phenotyping and environmental analysis by leading ARIs (CSIRO, Queensland University, Diversity Arrays, Australia; IPK Gatersleben and Jülich University, Germany; Kansas State University, Purdue University, USDA, Quanta lab, USA; INRA/ARVALIS, France; Private sector)		
4.3 Greater access by CGIAR and NARS to cost-	4.3.1 Survey of laboratories, capacities and costs within and beyond AFS CRPs.	8,300	0	

	effective laboratory services for physico-chemical composition and functional properties			
	4.4 Greater mechanization, automation and return to investment of CGIAR and NARS breeding programs	4.4.1 Attracting co-support by additional W3&bilateral donors	10,000	721,700
Module 5	5.1 Existence of a CGIAR strategy for inter-compatible software tools and databases	5.1.1 The EAG liaises with Module 2 to identify key workflows/gaps to establish overall strategy and priorities for breeding case studies. Critical data gaps are assessed in developing germplasm related international public goods and interoperability between data resources.	199,500	136,900
		5.1.2 Selected pipelines and tools are analyzed and documented in the Platform's Toolbox to clarify user and technical requirements related to selected breeding case studies		
		5.1.3 Attracting co-support by W3 and bilateral donors		
	5.2 Greater development of inter-compatible software by the wider bioinformatics community that is facilitated by a common BrAPI and supports modular and adaptable breeding pipelines	5.2.1 Support model to implement BrAPI and local APIs for different systems	252,400	276,500
		5.2.2 Attracting co-support by W3 and bilateral donors		
	5.3 Existence of inter-compatible software tools and databases that complement and expand the usefulness of existing bioinformatics initiatives and are used by the CGIAR/Germplasm community	5.3.1 Breeding Management System for small to medium sized field-oriented breeding programs optimized, providing modern pedigree, phenotype and inventory data management, data collection and decision support tools for cultivar development in particular for the developing world.	50,000	1,929,800
		5.3.2 Collaborative development of a Breeding Management System for more data intensive applications (e.g. supporting genome-wide selection) initiated		
		5.3.3 Attracting co-support by W3 and bilateral donors		
	5.4 Existence of CGIAR recommended metadata and data standards	5.3.1 Crop and Agronomy Ontology CoP incorporates reps from AFS CRPs	83,100	92,600
		5.3.2 Unique Germplasm Identifiers (GUIDs) linked with existing efforts		
5.3.3 Ontologies established and documented in the Platform's Toolbox				
5.5 Greater access to prioritized biometrics and bioinformatics advice, services and resources	5.4.1 Community of practice conceptualizes the CGIAR linked landscape of bioinformatics tools and services;	75,100	114,000	
	5.4.2 Survey executed to assess the wider landscape of bioinformatics tools and services			
	5.4.3 Attracting co-support by W3 and bilateral donors			
5.6 Sustainable access to inter-compatible software tools and databases	5.5.1 Co-support by W3 and bilateral donors	10,000	231,600	

Disclaimer:

- 1) Budget amounts are mapped to outcomes from costing outputs and activities that are required to enable changes that we expect to happen.
- 2) It is important to acknowledge that the budget amounts are most likely not directly correlated to the work proposed for this year, but building on investment and outputs from the past.

Table 3: Expected Output 2017 towards Outcomes 2022

G = Gender, Y = Youth, CD = Capacity Development; 0 = not targeted, 1 = significant, 2 = principal

Module No.	Module Outcome 2022	Expected key outputs 2017	Tagging of expected outputs 2017		
			G	Y	CD
Module 1	1.1 Existence of a CGIAR agreement on standard template and approaches for monitoring breeding program performance	1.1 Standardized system for capturing breeding program targets, assessments and metrics	1	1	2
	1.2 Existence of standardized breeding program assessments & strategic plans to set breeding program direction in the CGIAR.	1.2 AFS specific breeding program assessment to set breeding program directions.	1	1	2
	1.3 Existence breeding program assessments & strategic plans to set breeding program directions with NARS	1.3 Funding developed to implement strategies that improve breeding program performance with the CGIAR and NARS	1	1	2
	1.4 CGIAR and NARS implementing prioritized improvements				
	1.5 Existence of standardized genetic gain assessments in AFS breeding programs				
Module 2	2.1 Existence of a common web platform to interchange best practices by the trait discovery and breeding community	2.1a A non-prescriptive toolbox to support trait mobilization and applied breeding.	1	2	2
		2.1b Best practices documentation for trait discovery and breeding from all Modules in ToolBox	1	2	2
	2.2 Wider range of partners contribute to Toolbox (ARIs, CGIAR, NARS, private sector)	2.2 Funding developed to ensure contributions of tools, approaches and training modules by a wide number organizations and implement training strategy targeted at breeding programs in the developing world	1	2	2
	2.3 Increased benefits by CGIAR and NARS from virtual/face-to-face training strategy				
Module 3	3.1 Existence of a joint strategy to increase use of genotyping and sequencing applications in trait discovery and breeding	3.1 Community of practice and baseline established	1	1	2
		3.2a. Best practices documentation for genotyping/ sequencing in ToolBox	1	2	2

	3.2 Increased use of genotyping and sequencing applications in discovery and breeding	3.2b Use of high-throughput applications for low density SNP genotyping	1	1	2
	3.3 Greater access by AFS CRPs and the Genebank Platform to cost-effective genotyping /sequencing services	3.3 Increasing number of cost-effective genotyping/sequencing services	0	1	2
	3.4 Increased mainstreaming of genotyping/sequencing applications in a larger number of breeding programs.	3.4 Funding developed to mainstream high-throughput applications for higher density genotyping and sequencing applications in support of trait mobilization and forward breeding	1	1	2
	3.5 Existence of support of CGIAR and NARS to implement a wider range of genotyping/sequencing applications				
Module 4	4.1 Existence of best practice documentation for phenotyping and environmental analysis within the CGIAR	4.1 Best practices documentation for existing high-through-put tools, GxExM and gene-to-phenotype methods in ToolBox	1	2	2
	4.2 Increased use of state-of-the art precision and high-throughput phenotyping, GxExM analyses and Genotype-to-Phenotype predictions applied in AFS breeding programs	4.2 Collaboration with ARI(s) funded that support CGIAR & NARS to adapt, test and mainstream precision and high-throughput phenotyping, GxExM analyses and Genotype-to-Phenotype predictions	1	2	2
	4.3 Greater access by CGIAR and NARS to cost-effective laboratory services for physico-chemical composition and functional properties	4.3 Survey of laboratories, capacities and costs	0	0	2
	4.4 Greater mechanization, automation and return to investment of CGIAR and NARS breeding programs	4.4 Funding developed to assess and implement greater mechanization and automation in CGIAR and NARS breeding programs to increase returns to investment	1	2	2
Module 5	5.1 Existence of a CGIAR strategy for inter-compatible software tools and databases	5.1 Overall strategy and prioritization of pipeline case studies and related tools	0	1	2
	5.2 Greater development of inter-compatible software by the wider bioinformatics community that is facilitated by a common BrAPI and supports modular and adaptable breeding pipelines	5.2 Support model to implement BrAPI and local APIs for different systems	0	1	2
	5.3 Existence of inter-compatible software tools and databases that complement and expand the usefulness of existing bioinformatics initiatives and are used by the CGIAR/Germplasm community	5.3 Inter-compatible software tools and databases targeted at the needs of breeding programs in the developing world	0	1	2
	5.4 Existence of a CGIAR recommended metadata and data standards	5.4 Documentation of current metadata standards and ontologies across various initiatives	0	1	2
	5.5 Greater access to prioritized biometrics and bioinformatics advice, services and resources	5.5 Documentation of the wider landscape of bioinformatics tools and services	0	1	2
	5.6 Sustainable access to inter-compatible software tools and databases	5.6 Funding developed to expand the scope and relevance of developing and using inter-compatible software tools and databases within the CGIAR/germplasm community	0	1	2

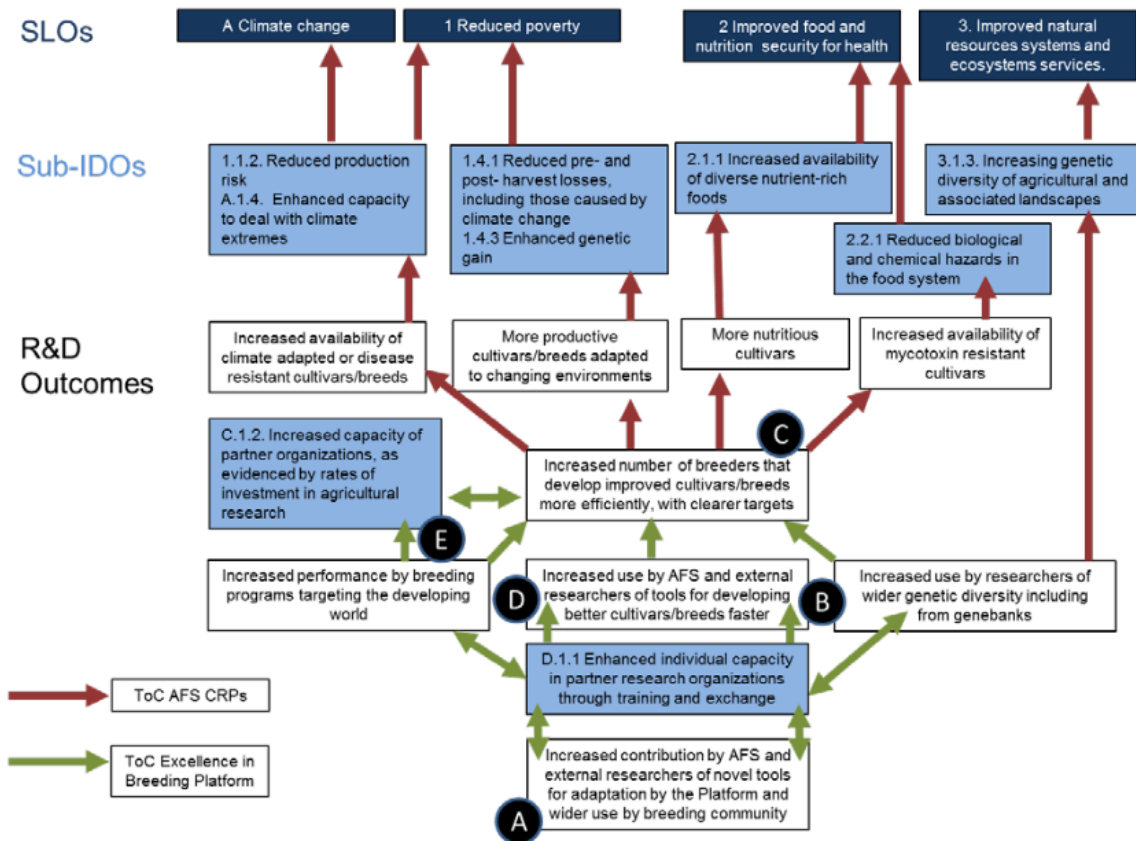
Annex 1: Glossary

- **Impacts:** Positive and negative, primary and secondary long-term effects resulting from a chain of events to which research has contributed, directly or indirectly, intended or unintended. These effects can be economic, socio-cultural, institutional, environmental, technological or of other types¹, sphere of interest; see annex 4, and phase of scaling in annex 5.
- **Impact assessment:** In CGIAR, this term is generally used for an ex-post study which uses specialized methods to estimate the changes in selected development parameters and the extent to which these are attributable to defined research activities or programs of the CGIAR¹. However, in phase II and under the new strategy and results framework 2017-2030, the CGIAR Research Programs are taking on a wider definition of the term, recognizing that there are different forms of impact assessment built into the programs of work, e.g. Theories of Change as one ex-ante impact assessment.
- **Indicator:** A quantitative or qualitative variable that represents an approximation of the characteristic, phenomenon or change of interest (for instance, efficiency, quality or outcome). Indicators can be used to monitor research or to help assess for instance organizational or research performance¹.
- **Inputs:** the financial, human, and material resources used in research.¹
- **Output:** the products, new knowledge and services which result from research, capacity building and other activities related to research for development¹, sphere of control, see annex 4. Outputs are resulting of discovery and proof of concept phases; see annex 5.
- **Outcome:** the intended or unintended short-term and medium-term effects resulting from an intervention's outputs¹, change in knowledge, attitudes and skills, manifest as change in discourse, institutions, policy and practice that result in part of in while from the CRP's research and associated activities, sphere of control and influence, see annex 4. Research outcomes are resulting of pilot phase and development outcomes from scaling up phase; see annex 5.
- **Milestone:** is a progress marker towards our Flagship 2022 outcomes and into which they are divided for monitoring intermediate performance along a timeline. Milestones are measurable and observable. Annual milestones are defined to reflect some reasonable achievement for the specified time period (challenging but achievable). Milestones could be outputs or outcomes as appropriate to the scale and maturity.
- **Performance management:** the continuous process of setting goals, measuring progress, giving feedback, coaching for improved performance, and rewarding achievement.¹
- **Target:** an amount of change that is to be achieved over a specific time frame in an indicator.²
- **Theory of Change (ToC):** includes the impact pathways and the assumptions along the way. Presents a hypothetical identification of the ways by which change is expected to occur from output to outcome and impact along an impact pathway. The ToC questions the assumptions about causality underlying the relationships between outputs, outcomes and impact. In ToC the assumptions present the mechanisms of change.¹

¹ From "CGIAR standards for independent external evaluation", IEA, Dec 2015

² L.G. Morra Imas and R.C. Rist, Road to Results, World Bank, 2009

Annex 2: Excellence in Breeding Theory of Change



Annex 3: Guidance on Tables

To make this process of planning more efficient in the future we are working towards an ICT supported performance management on the program and system level for the planning of work and budget.

While table 1 is the overarching presentation of the Platform budget broken down by modules and management & support costs by W1/W2 and W3/bilateral, table 2-3 are giving more detailed information on the work for each module.

Table 2 3 shows the module 2022 outcomes with annual progress markers (milestones). Table 3 gives an overview of key outputs expected to be delivered related to module outcomes 2022 and their associated contribution to the cross-cutting topic (gender, youth, capacity development).

Additional specific notes

For table 2:

- Any number of between 1 – max. of 3 milestones per year for one module outcome.
- To make the term milestone corresponding with results-based-management concept laid out in the CGIAR Strategy and Results Framework 2017-2030, they are progress markers towards the module Outcome 2022, see annex 1 glossary.
- Note that budget amounts are only mapped to outcomes from costing outputs and activities that are required to enable changes that we expect to happen. It is important to acknowledge that the budget amounts are most likely directly correlated to the work proposed in this year, but building on investment and outputs from the past.

For table 3:

We are testing the usage of Organisation for Economic Co-operation and Development (OECD) scheme for tracking some of our cross-cutting topics from the CGIAR Strategy and Results Framework 2017-2030 at outputs level. The OECD Development Assistance Committee (DAC) gender equality policy marker are a qualitative statistical tool to record aid activities that target gender equality as a policy objective. The gender equality policy marker is based on a three-point scoring system. For more information, <http://www.oecd.org/dac/gender-development/dac-gender-equality-marker.htm>

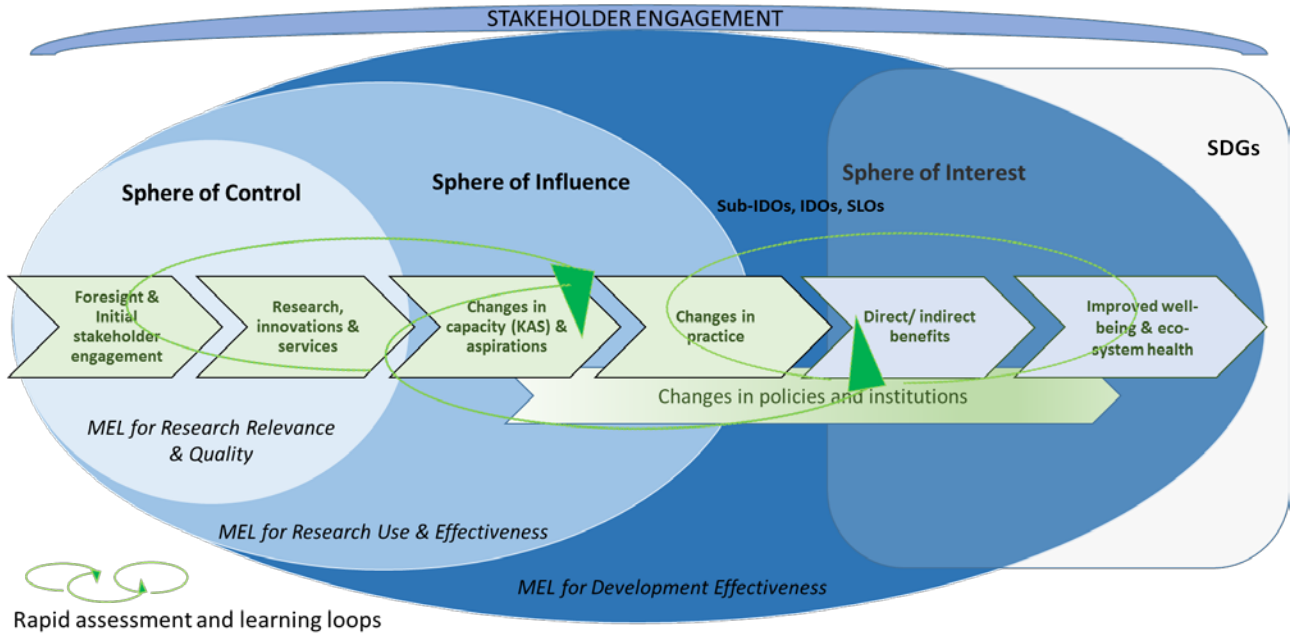
For the CGIAR we are suggesting the scoring system adjusted to gender, youth and capacity development:

2 = Principal means that gender, youth and capacity development is the main objective and is fundamental in its design and expected results. The output would not have been undertaken without this objective.

1 = Significant means that gender, youth and capacity development is an important and deliberate objective, but not the principal reason for the output.

0 = Not targeted means that the output has been screened against gender, youth and capacity development marker but has not been found to target it.

Annex 4: Draft Integrated Framework for a Performance Management System for CGIAR Research



Annex 5: Different phases in flagship projects

