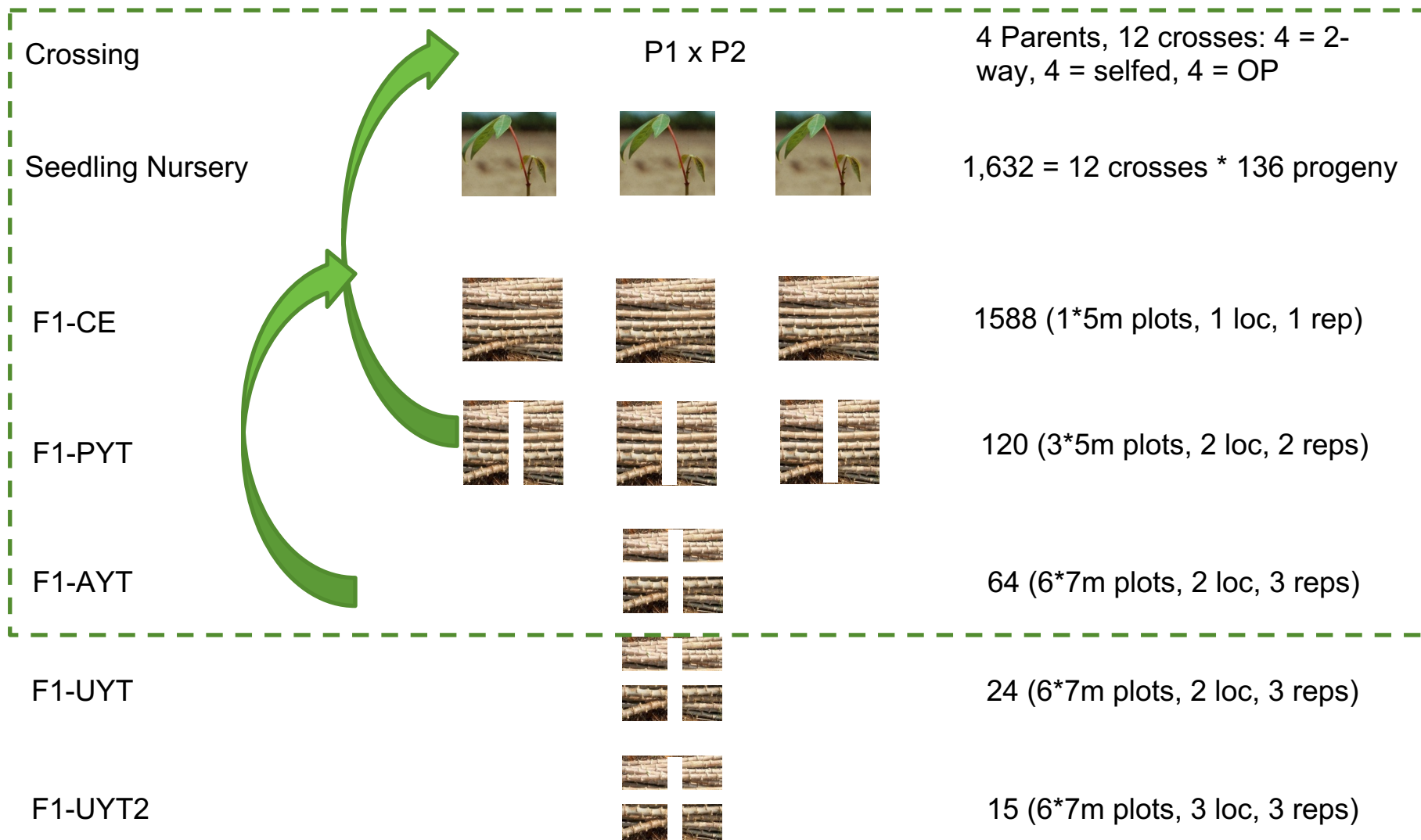


Report(IP1): Finding Optimal Number of Parents, Crosses

EIB-Roslin Collaboration
June 2nd 2020

Baseline



1. Introduction to the problem

Crop by Region

IITA-EACassava

Problem Specification

Currently, only four parents are used. Too few parents may make it difficult to maintain adequate diversity required to increase genetic gain over time

Breeding strategy component tackled

Crossing / Evaluation / Selection

Breeders' equation terms tackled

σ_a, i, L

Hypothesis

Increasing the number of parents in the program will lead to increased genetic gains over time



Excellence in
Breeding
Platform

2. Materials and Methods

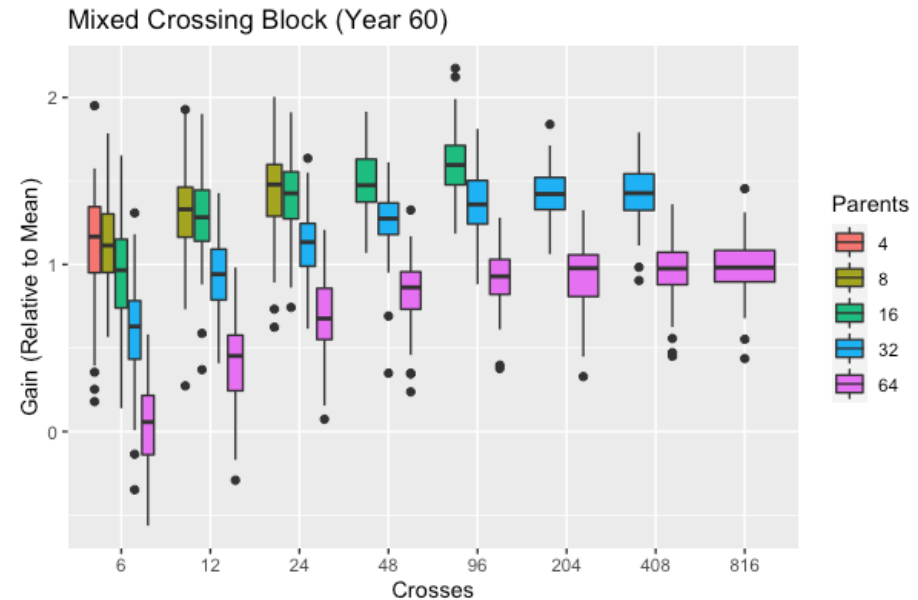
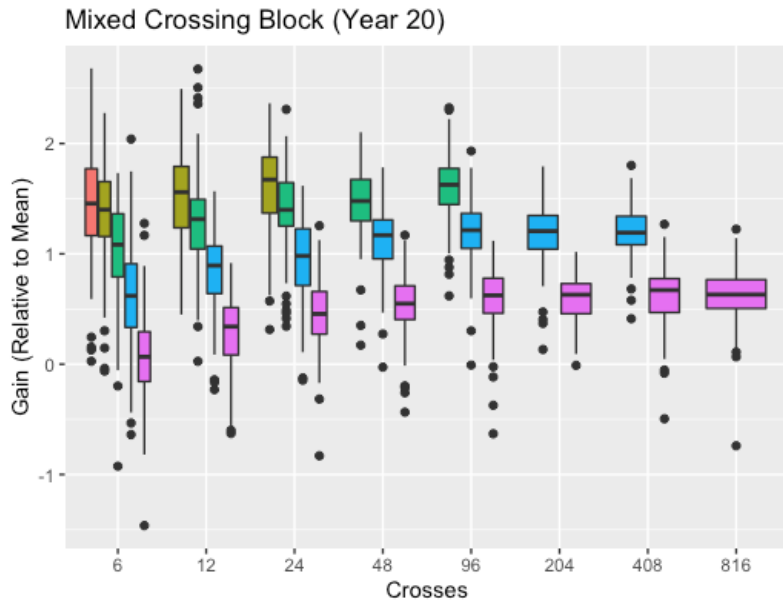
Treat	Description
T1 (Baseline)	Use of current #parents, #crosses, #progeny (4 parents, 12 crosses, 136 progeny). Parents recycled from PYT and AYT (mixed crossing block)
T2 (Grid)	A grid of different combinations of nParents(4-64), nCrosses(6-816, $[n(n-1)/2]$), nProgeny determined by restricting genotypes to 1632. Parents recycled from PYT and AYT (mixed crossing block)
T3 (PYT/AYT)	nParents (4-64), largest nCrosses/nParents and nProgeny determined by restricting genotypes to 1632. Recycling new parents at PYT, AYT and PYT+AYT were compared.

- Simulation: 20-year burnin based on the current scheme (Baseline), and followed by 20-year and 60-year period of breeding for each treatment
- varGxY assumed = varG
- Plant $H^2 = 0.01$, row $H^2 = 0.2$ and plot $H^2 = 0.5$
- Genetic gain and relative variance tracked at F1



3. Results

Genetic gain at F1: T1&T2(Grid: $[n(n-1)]/2$: #F1 = 1632)



- There is a plateau to the number of crossCombs: $<nParents$ do not allow reaching this plateau
- With a longer breeding period, the comparative advantage of $<nParents$ diminishes
- There is a sweetspot for $nParents$
- No need to do all possible crosses, just sampling % of crosses is adequate

3. Results

Genetic gain at F1: T1&T2(Grid: $[n(n-1)]/2$: #F1 = 1632)

Table: Summary of nParents, nCrosses and nProgeny combinations from the results from the previous slide. Number of genotypes (nIndTotal) remains constant based on the program size. The blue color indicates where the plateau of the scenarios lies

nParents	4	8	8	8	16	16	16	16	16	32	32	32	32	32	32	32	64	64	64	64	64	64	64	64
nCrosses	6	6	12	24	6	12	24	48	96	6	12	24	48	96	204	408	6	12	24	48	96	204	408	816
nProgeny	272	272	136	68	272	136	68	34	17	272	136	68	34	17	8	4	272	136	68	34	17	8	4	2
nIndTotal	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632	1632

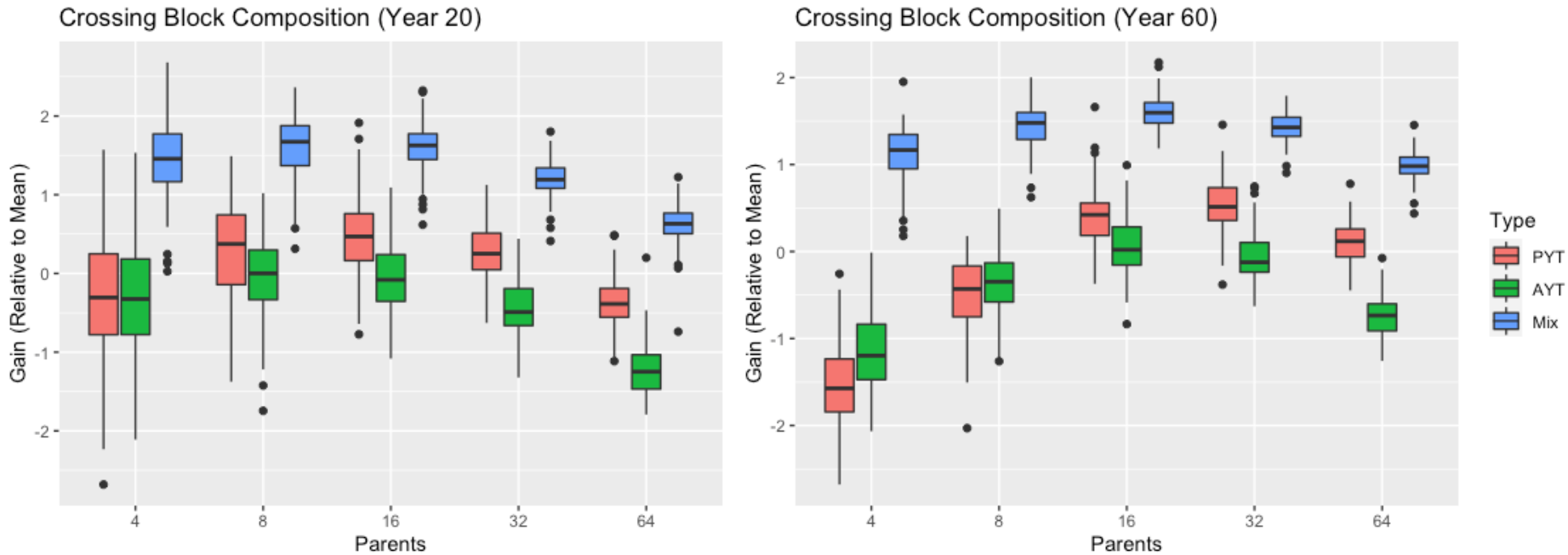
Based on the results presented on the previous slide,

- Optimal nParents ranges from 16-32
- Optimal nCrosses ranging from 96 – 204 depending on nParents
- Optimal nProgeny per cross ranging from 8-17 depending on nCrosses



3. Results

Genetic gain at F1: T3(Largest nCrosses/nParent: #F1 = 1632)



- Given the current evaluation strategy, it is better to select new parents from both PYT and AYT.

4. Conclusion

1. Even though $nParents$ appears to sustain genetic gains, for medium to long term objectives, it is advisable to find a sweetspot for parents that allows sustained genetic gains and enough diversity to adapt to changing situations.
2. The data suggests this sweetspot to be between 16-32 $nParents$ for this program and the $nCrosses$ between 96-204. However, $nCrosses/nProgeny$ Combs should be managed such as to allow optimal sampling of the diversity ($nCrosses$) and the value of each cross($nProgeny$)
3. Given the current evaluation strategy and accuracy, recycling parents from both PYT and AYT is optimal. After deciding on $nParents$, a follow up IP may be to examine recycling at PYT and AYT using a different evaluation strategy.





**Thank you for
your interest!**

