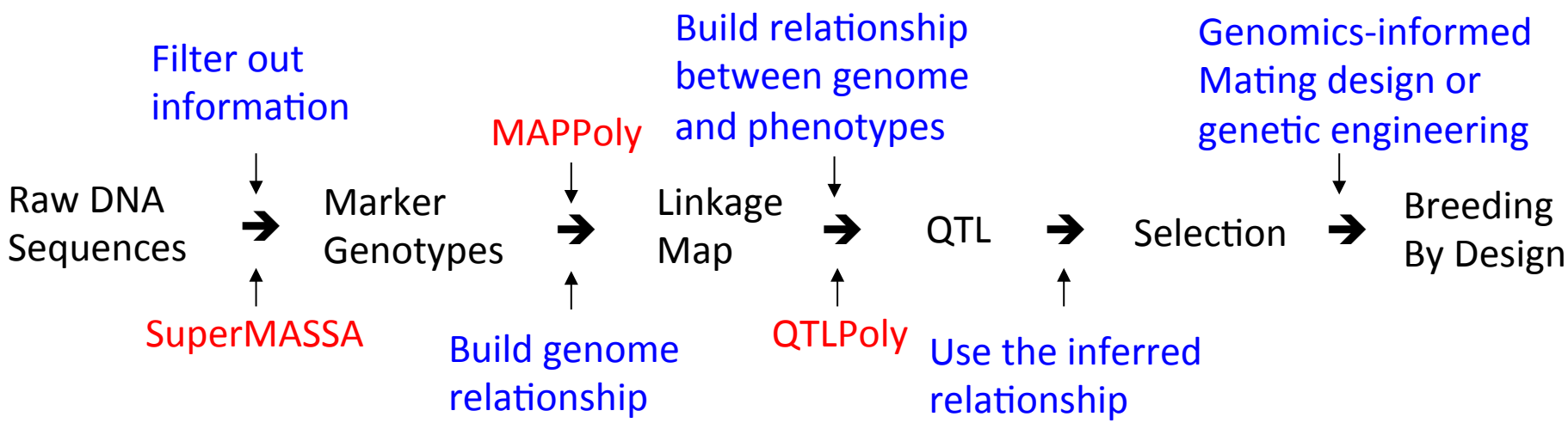
GT4SP (Genomic Tools for Sweetpotato Improvement)

https://sweetpotatogenomics.cals.ncsu.edu/

BILL & MELINDA GATES foundation

Zhao-Bang Zeng

- Develop computational tools for the whole pipeline data analysis.

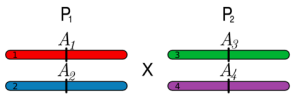


- Sweetpotato is one of the most complex genetic systems for breeding due to (auto)hexaploid (6x).
- If we can solve the whole analytical problems for this system, we can use it or adapt it for almost any system.

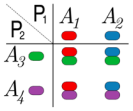
Autohexaploid complexity

Diploid

Multiallelic



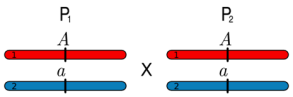
Gametes



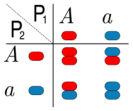
4 possible genotypes

1:1:1:1

Biallelic



Gametes

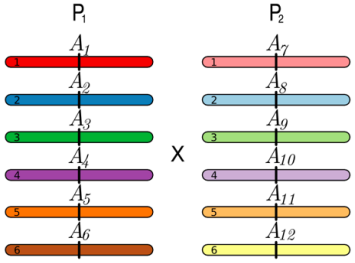


3 possible genotypes

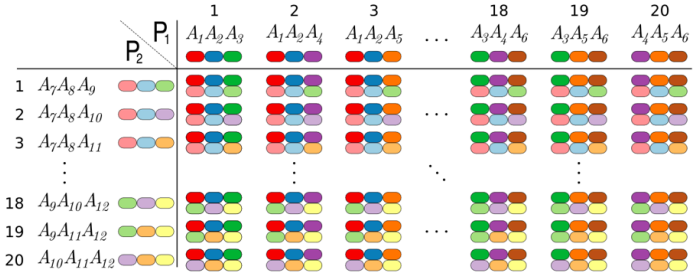
1:2:1

Hexaploid

Multiallelic



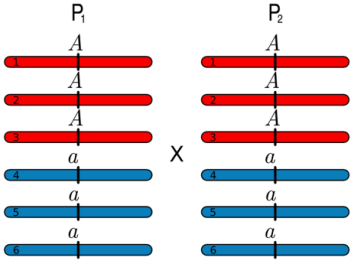
Gametes



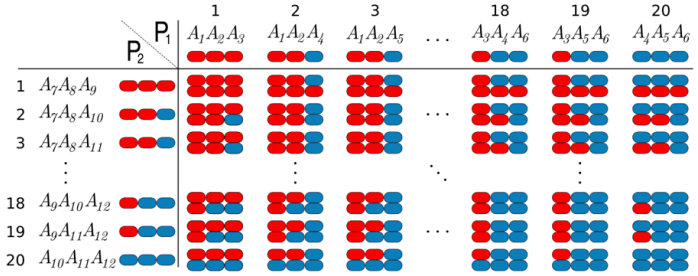
400 possible genotypes

1 : 1 : … : 1 : 1

Biallelic



Gametes



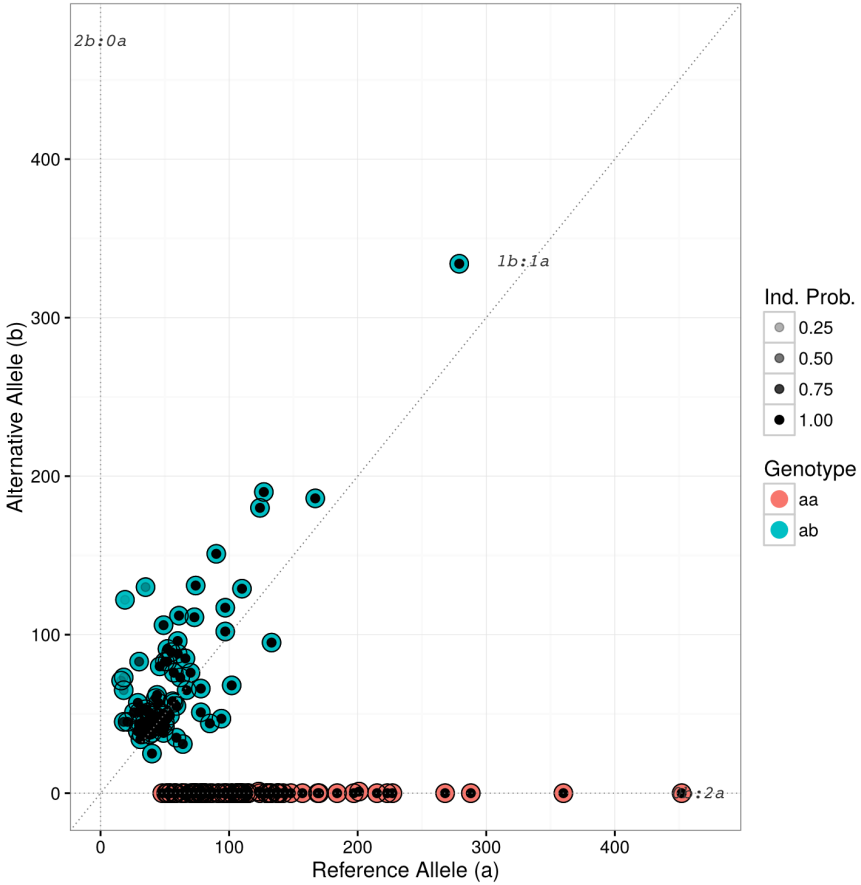
7 possible genotypes

1 : 18 : 99 : 164 : 99 : 18 : 1

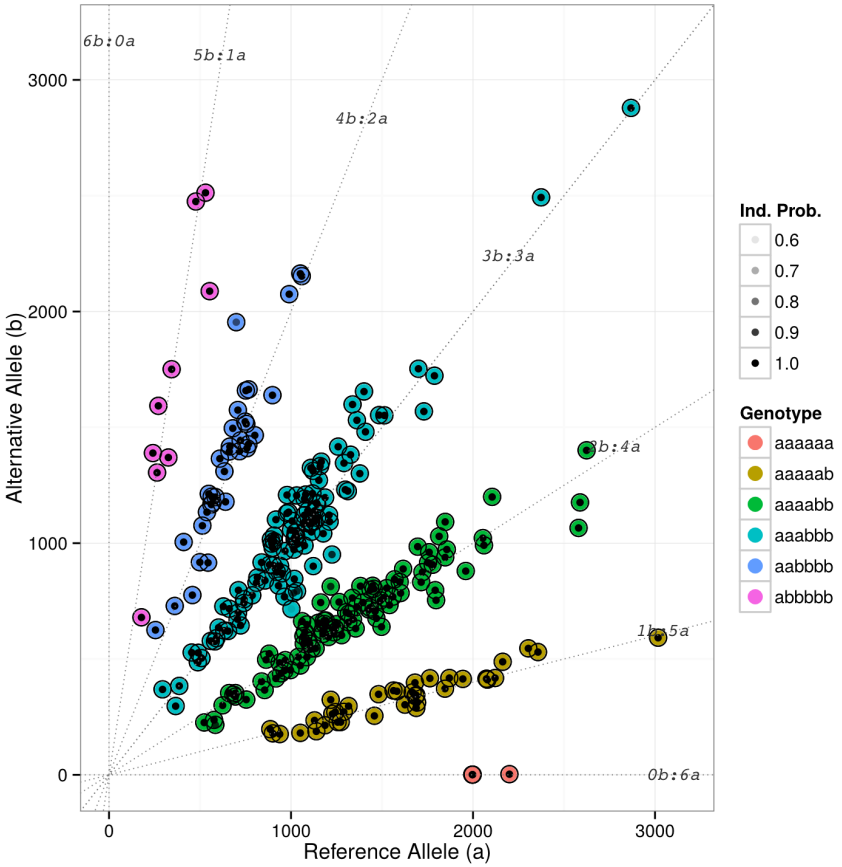
Genotype calling

SuperMASSA

Diploid



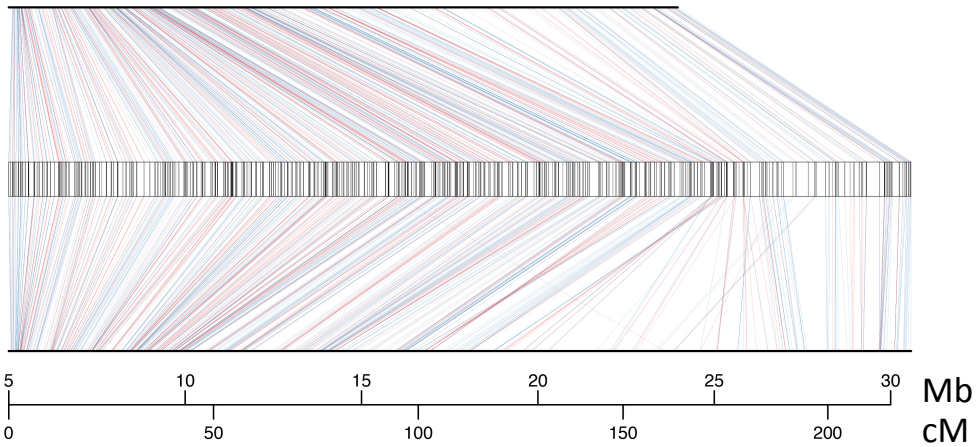
Hexaploid

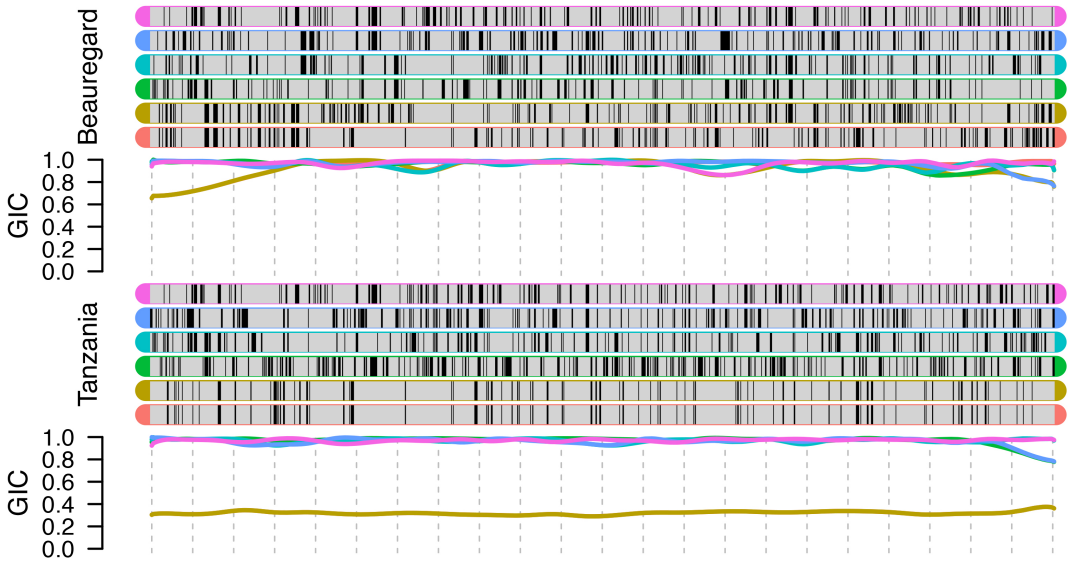


Sweetpotato map - 22,793 SNPs

MAPPoly

Tf and Tl (private)
Tf_Tl (shared)

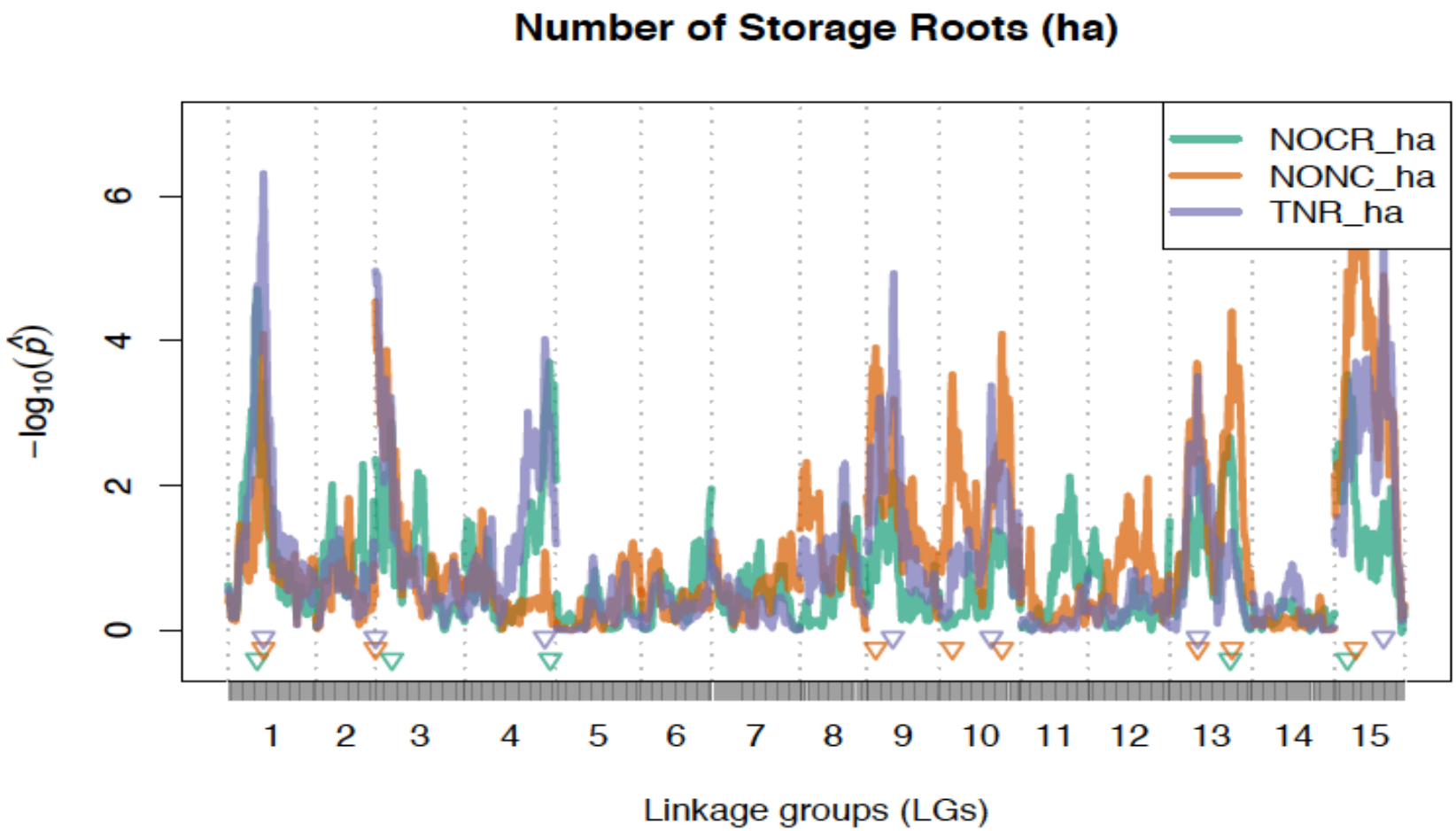




QTL mapping

QTLPoly

Number of roots



QTL Characterization: NOCR (ha)

QTLPoly

QTL	LG	Pos	Score	$\hat{p}$-value	μ	$\hat{\sigma}_q^2$	$\hat{\sigma}_e^2$	H_q^2
1	1	32.01	210.64	1.46e-5		25338117		0.1076
2	3	18.07	141.39	7.72e-4		27415108		0.1164
3	4	95.03	180.69	1.20e-4		20758803		0.0881
4	13	67.05	124.77	1.18e-3		14748822		0.0626
5	15	14.03	172.15	2.07e-4		25071513		0.1064
					64699		122165237	0.4812