



Harnessing the potential of highly informative KASP and middle density SNP markers panel for yam breeding
Crops to End Hunger webinar
August, 2023



Introduction

Low density SNP markers

- QC/QA marker development, validation and application
- Trait marker validation

Middle density SNP markers

- Panel SNP markers: Middle density of 3092 SNP for GS/GPCP

Development of reference genome

Ongoing molecular activities

Take home message



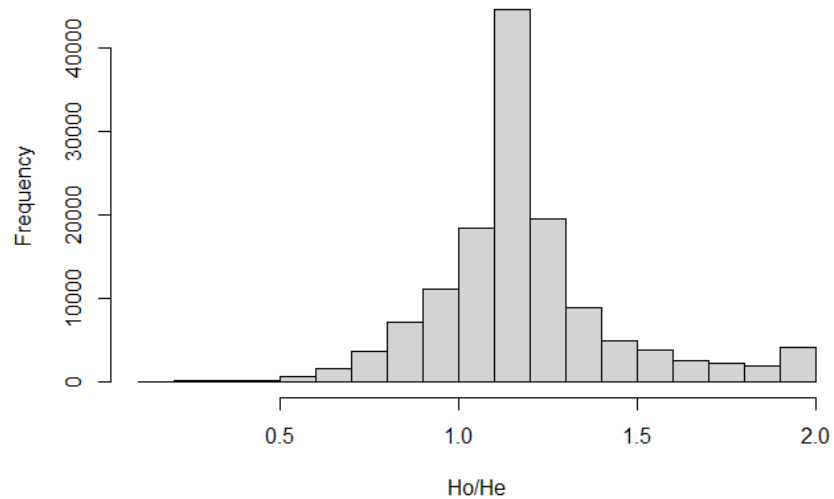
- Mis-labelling error frequently occurred in germplasm management
- Genetic purity and variety tracking
- Pedigree verification (intra and inter specific)
- Trait performance prediction at early generation through MAS
- Optimizing the breeding program
- Parental selection & heterotic group
- Implementation of genomic prediction and cross performance



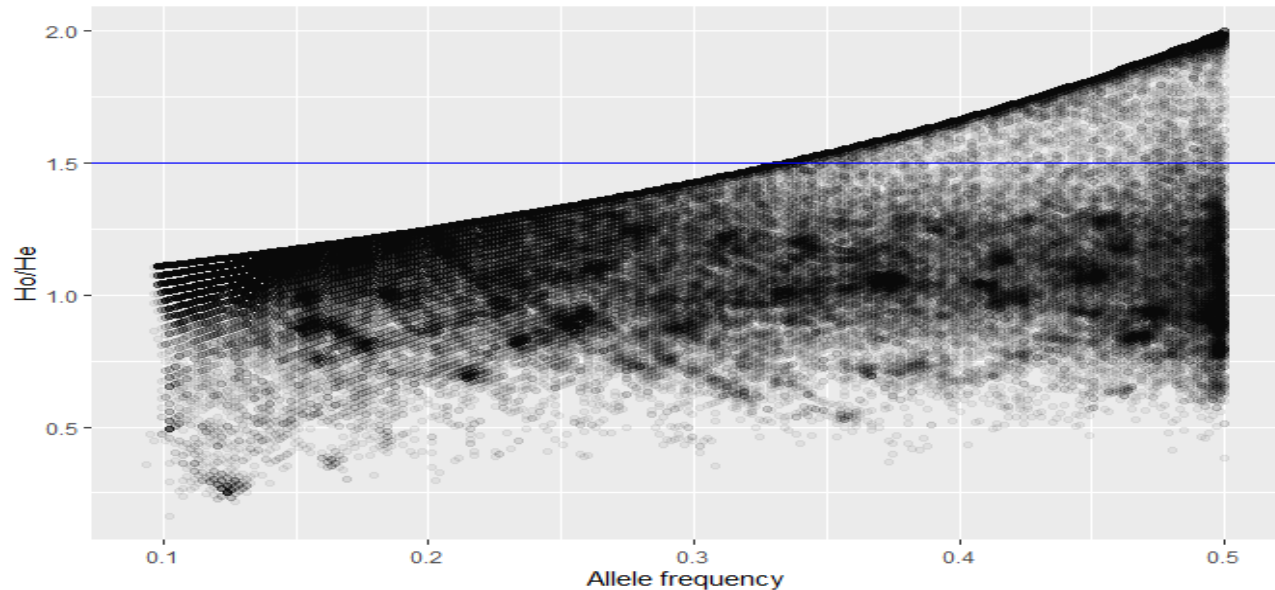
QC/QA Marker: Selection procedure

- PIC
- Ho/He
- MAF
- Putative Paralogs
- GC content
- Duplicate
- Missing %
- INDELS

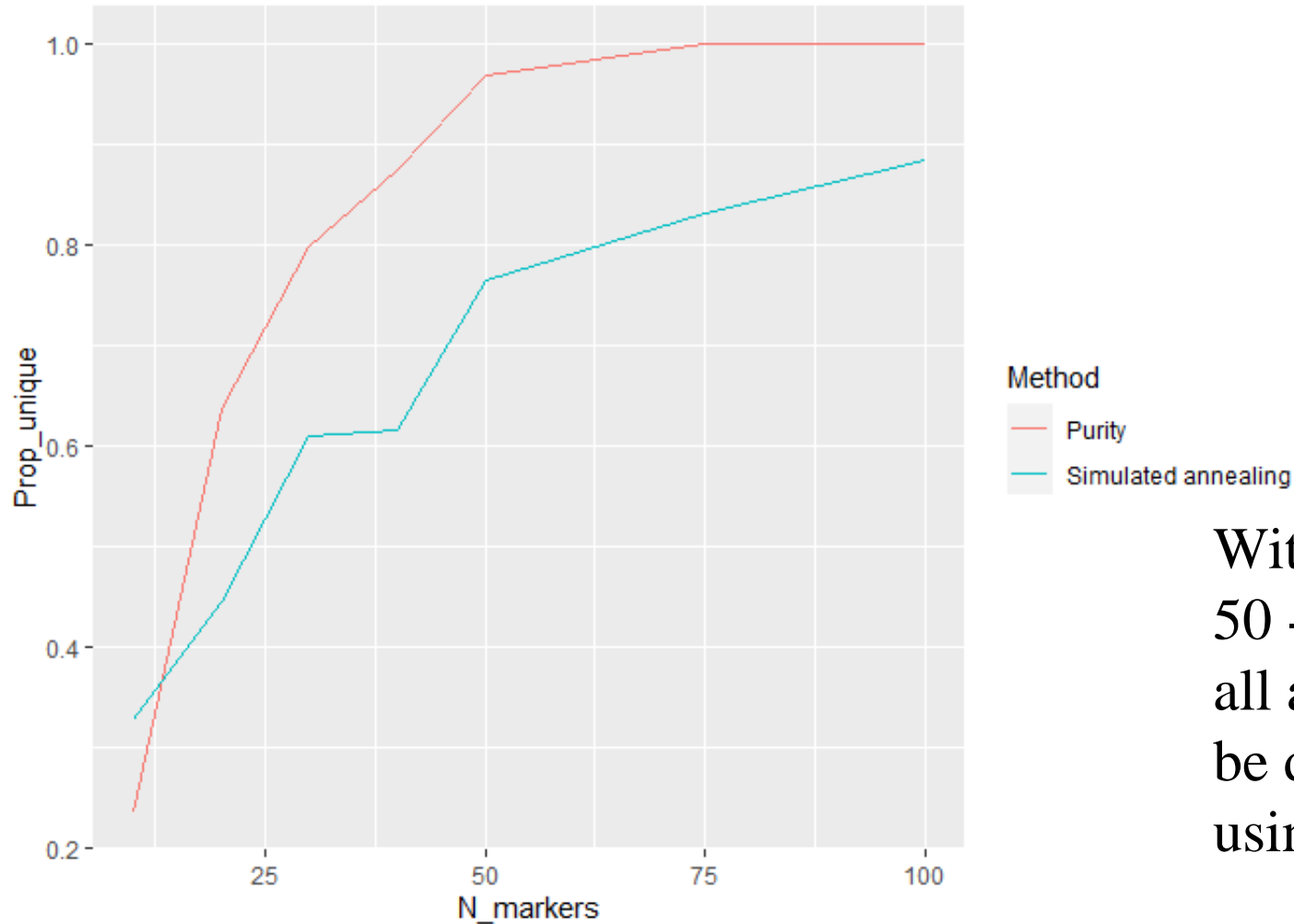
Histogram of Ho/He



Filtering for putative paralogs



QC/QA Marker: Selection procedure



With a range from 50 - 100 markers, all accessions could be distinguished using Purity method

https://github.com/HPCBio/eib-marker-design/blob/main/Pedigree_verification.md

QC/QA Marker: selection procedure

TASSEL (Trait Analysis by aSSociation, Evolution, and Linkage) 5.2.58

PHC Help

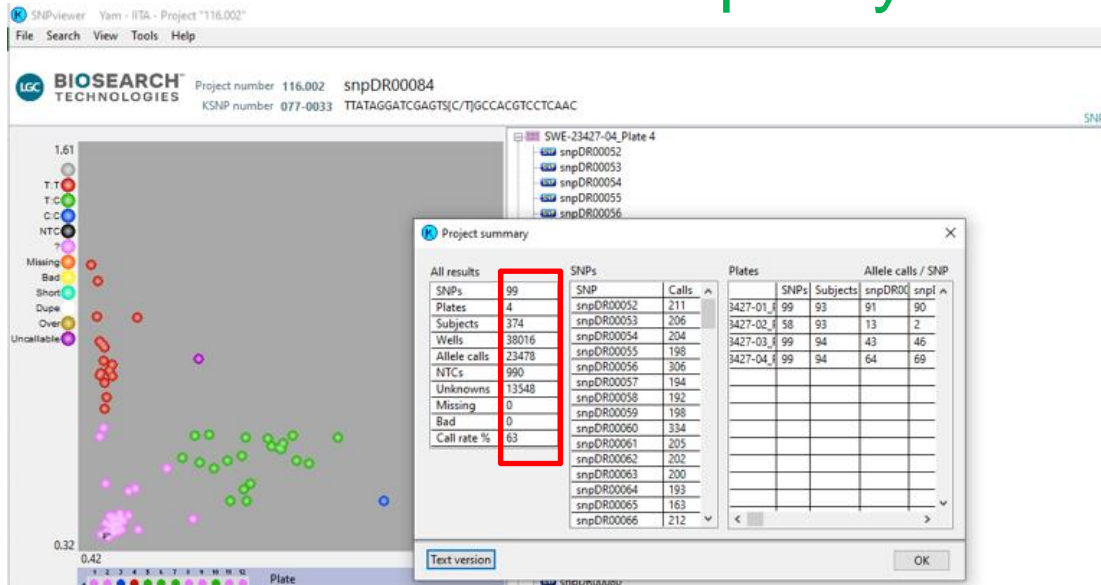
Site Numbers
 Locus
 Site Name
 Alleles
 MajorMinorAllele (Enter physical position) Search

67	134	201	268	335	402	469	536	603
273: 530262								
274: 571765								
275: 657724								
276: 1127230								
277: 1484891								
278: 1967677								
279: 1967684								
280: 2032338								
281: 2058730								
282: 2384490								
283: 2888289								
284: 3111534								
285: 3111580								
286: 3498764								
287: 3498790								
288: 4119373								
289: 4119381								
290: 4345538								
291: 4849054								
292: 5132309								
293: 5952249								
294: 6366323								
295: 6683221								
296: 7102052								
297: 14238010								
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299: 15703503								
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301: 16529478								
302: 17630762								
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305: 19144152								
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307: 20153048								
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319: 25559854								
320: 24985								
321: 25833								
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325: 4665817								
326: 5269889								
327: 12300807								
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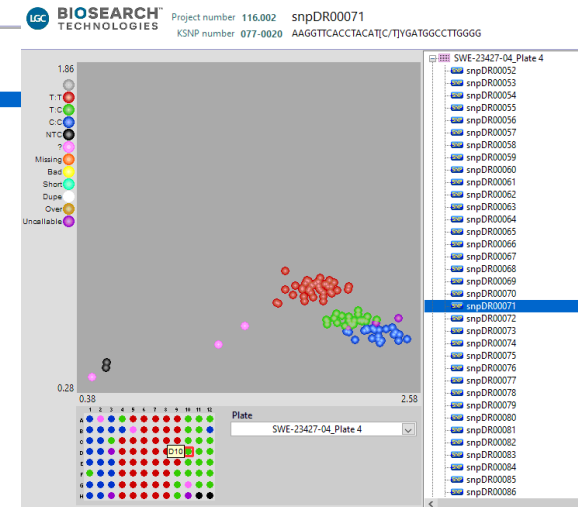
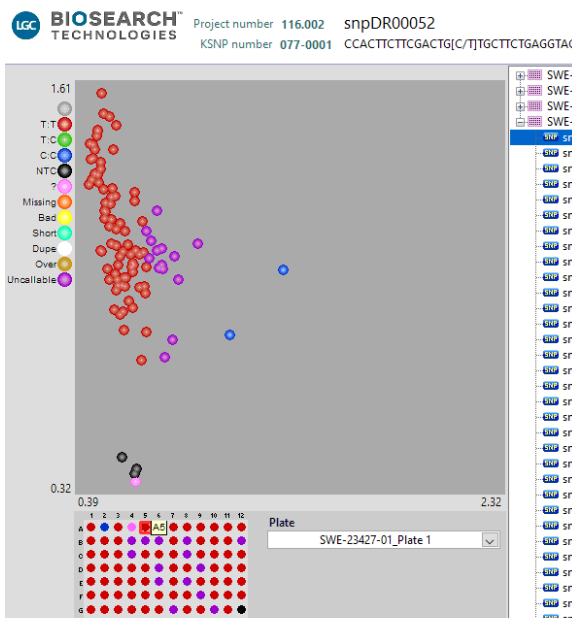
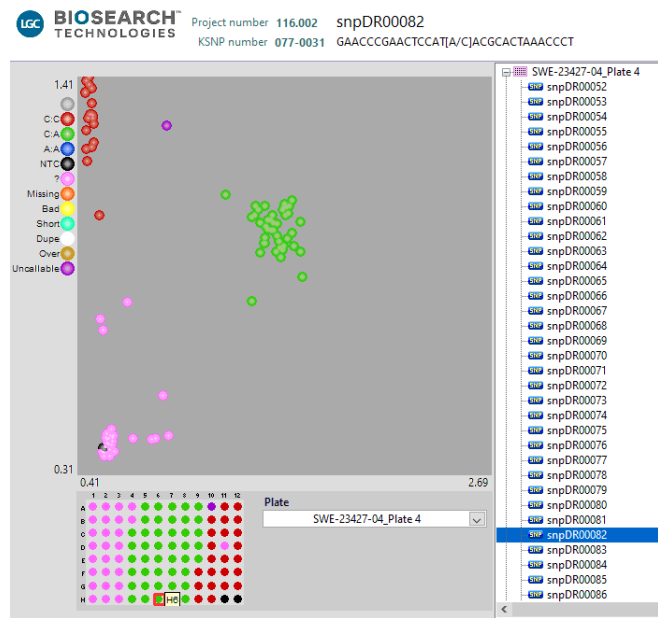


- 99 SNP markers well distributed across the genome were selected and successfully converted to KASP
- 374 diverse clones representing *D. alata*, *D. rotundata*, *D. praeensis*, *D. esculenta* *D. cayenensis* sent to INTERTEK for validation

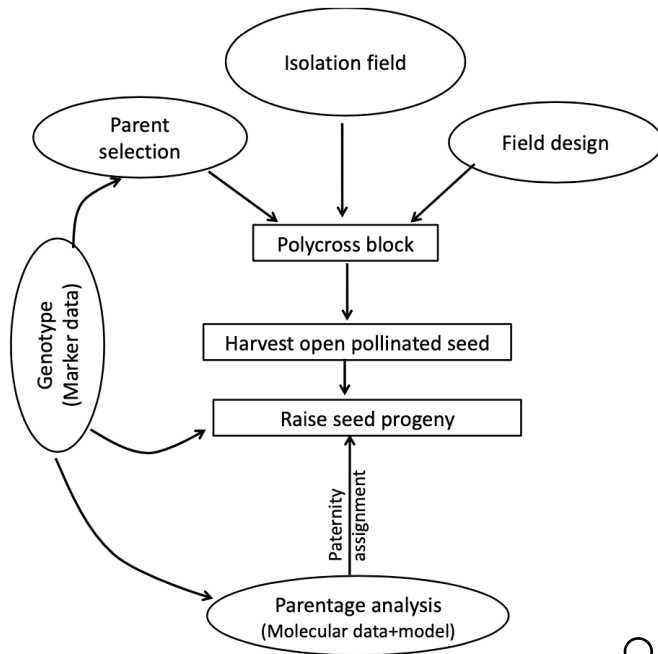
SNP markers quality view



In general, high-quality data were obtained



Application of QC/QA markers: Pedigree reconstruction



Plants (Basel), 2020 Apr; 9(4): 527.
 Published online 2020 Apr 19. doi: [10.3390/plants9040527](https://doi.org/10.3390/plants9040527)

PMCID: PMC7238154
 PMID: 32325826

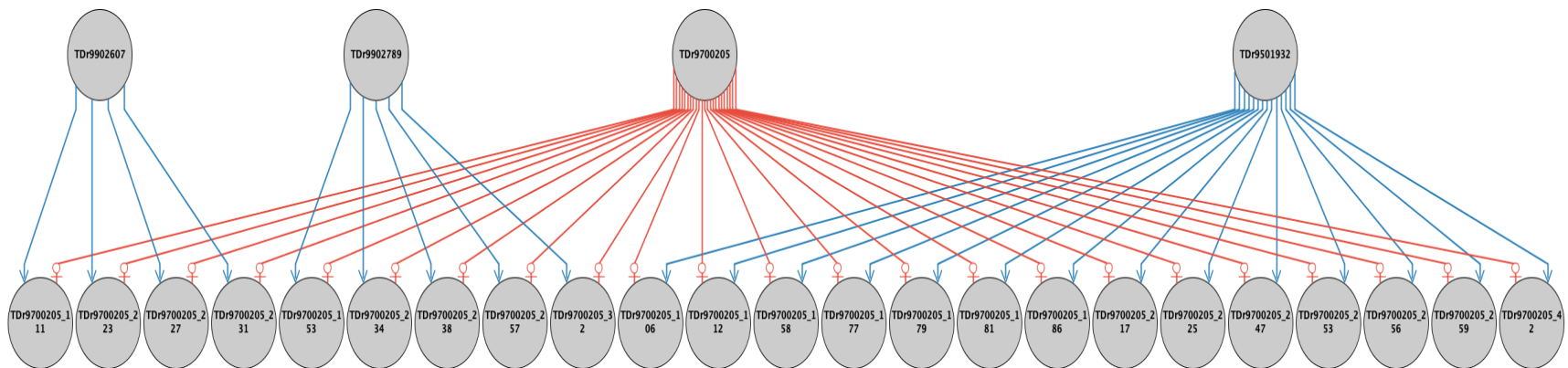
Paternity Assignment in White Guinea Yam (*Dioscorea Rotundata*) Half-Sib Progenies from Polycross Mating Design Using SNP Markers

Prince E. Norman,^{1,2,3,*} Agre A. Paterne,² Agyemang Danquah,³ Pangirayi B. Tongoona,³ Eric Y. Danquah,³ David De Koeber,⁴ Ugochukwu N. Ikeogu,⁵ Robert Asiedu,² and Asrat Asfaw²

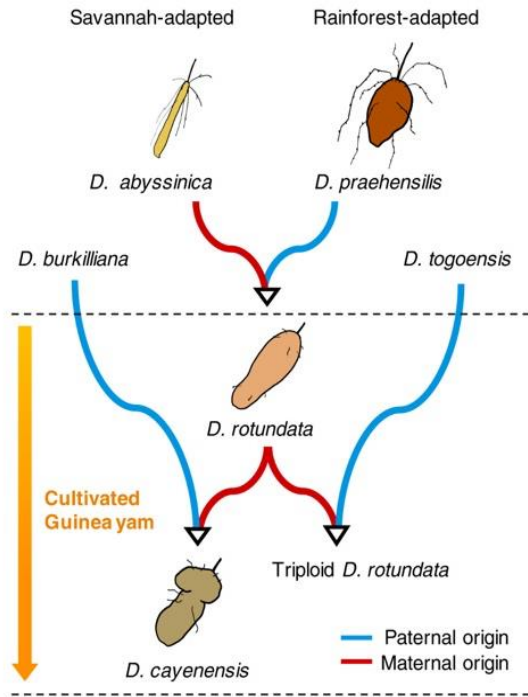
▶ Author information ▶ Article notes ▶ Copyright and License information ▶ PMC Disclaimer

- First approach analysis conducted using 6K SNP markers from DArT

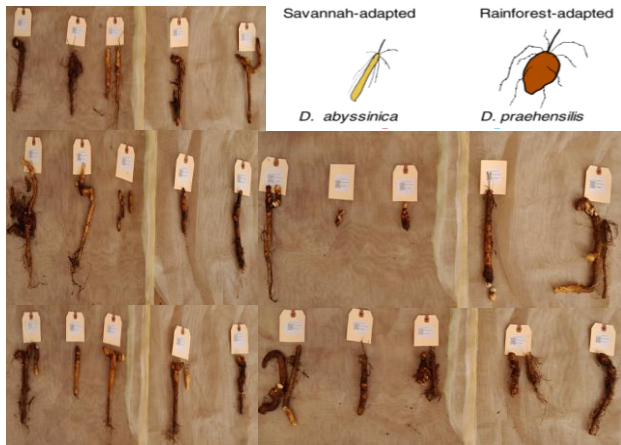
- Replicated work using only 50 QC markers



Application of QC/QA markers: Fidelity of crosses/hybridity test



Sugihara et al. 2020



SUBJECT_ID	homozygote markers												heterozygosity markers				
	snpDR00071	snpDR00074	snpDR00091	snpDR00103	snpDR00104	snpDR00109	snpDR00113	snpDR00123	snpDR00126	Comment	snpDR00134	snpDR00140	snpDR00143	snpDR00148	snpDR00108		
TDf	CC	AA	CC	TT	AA	TT	CC	TT	CC	Pfemale	GG (100%G)	TT (100%T)	TT (100%T)	TT (100%T)	TT (100%T)		
INTERSPEC-008	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA (50%G&50%A)	TC (50%T & 50%G)	TC (50%T & 50%G)	TC (50%T & 50%G)	TC (50%T & 50%G)		
INTERSPEC-008	TC	AA	CC	TT	AA	CC	CC	TT	CC	Non-hybrid	GG	TT	TT	TT	TT		
INTERSPEC-008	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GG	TC	TC	TC	CC		
INTERSPEC-E08	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GG	TC	TC	TC	CC		
INTERSPEC-F08	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GG	TT	TC	TC	TC		
INTERSPEC-G08	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-H08	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-A09	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-B09	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-C09	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-D09	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-E09	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-F09	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GG	TC	TC	TC	CC		
INTERSPEC-G09	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GG	TC	TC	TC	CC		
INTERSPEC-H09	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GG	TC	TC	TC	TC		
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INTERSPEC-B10	TC	AA	CC	TT	AA	CC	CC	TT	CC	Non-hybrid	GG	TC	TC	TC	CC		
INTERSPEC-C10	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GG	TC	TC	TC	CC		
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INTERSPEC-E10	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-F10	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-G10	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
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INTERSPEC-F03	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
INTERSPEC-G03	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
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INTERSPEC-F04	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	CC		
INTERSPEC-G04	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		
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INTERSPEC-A05	TC	TA	GC	TC	GA	TC	GC	TC	TC	Hybrid	GA	TC	TC	TC	TC		

Marker segregation among the inter-specific progenies

Genetic purity

- Fourteen SNP selected for varietal tracking, verification
- Genotypes were selected from trials: APT, NPT, RVT & VVT
- Six plants selected per plot and rep across various locations

TDrRVT2022IBN_106	Oju-iyawo	TC	TA	GG	TC	GA	TC	GC	TC	TC	GA	TC	TC	TC
TDrRVT2022IBN_127	Oju-iyawo	TC	TA	GG	TC	GA	TC	GC	TC	TC	GA	TC	TC	TC
TDrNPT1_2022IBN_11	Ojuiyawo	TC	TT	GG	TC	GA	TC	GG	TC	TC	GA	TC	TC	TC
TDrNPT1_2022IBN_21	Ojuiyawo	TC	TT	GG	TC	GA	TC	GG	TC	TC	GA	TC	TC	TC
TDrNPT1_2022IGO_11	Ojuiyawo	TC	TT	GG	TC	GA	TC	GG	TC	TC	GA	TC	TC	TC
TDrNPT1_2022IGO_21	Ojuiyawo	TC	TT	GG	TC	GA	TC	NN	TC	NN	GA	TC	TC	TC
TDrNPT1_UB111	Ojuiyawo	CC	NN	NN	CC	NN	NN	NN	CC	TT	NN	NN	NN	CC
TDrNPT1_UB121	Ojuiyawo	CC	NN	GG	NN	NN	NN	GG	TC	NN	NN	CC	CC	CC
TDrRVT2022Ubiaja_103	Ojuiyawo	TC	TT	GG	TC	GA	TC	GG	TC	TC	GA	TC	TC	TC
TDrAPT_2022IBN__3	TDr1000048	TC	TT	GG	TC	GA	TC	GC	TC	TT	GA	TC	TC	TC
TDrAPT_2022IBN__12	TDr1000048	TC	TT	GG	TC	GA	TC	GC	TC	TT	GA	TC	TC	TC
TDrAPT_2022IBN__23	TDr1000048	TC	TT	GG	TC	GA	CC	GC	TC	TT	GA	TC	TC	TC
TDrAPT_2022IBN__25	TDr1000048	TC	TT	GG	TC	GA	CC	GC	TC	TT	GA	TC	TC	TC
TDrAPT_2022IBN__37	TDr1000048	TC	TT	GG	TC	GA	TC	GC	TC	TT	GA	TC	TC	TC
TDrNPT2_2022IBN_2	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrNPT2_2022IBN_27	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrNPT2_2022_IGO_6	TDr8902665	TC	TT	GC	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrNPT2_2022_IGO_28	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrRVT2022IBN_112	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrRVT2022IBN_132	TDr8902665	TC	TA	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrAPT_2022IBN__6	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrAPT_2022IBN__13	TDr8902665	TC	TT	GG	TC	GA	TC	GC	TC	TT	GA	TC	TC	TC
TDrAPT_2022IBN__24	TDr8902665	TC	TT	GG	TC	GA	TC	GC	TC	TT	AA	TC	TC	TC
TDrAPT_2022IBN__26	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrAPT_2022IBN__38	TDr8902665	TC	TT	GG	TC	GA	TC	GC	TC	TT	GA	TC	TC	TC
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2022VVT_EDE_4	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
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TDrNPT2_2022Ubiaja_28	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
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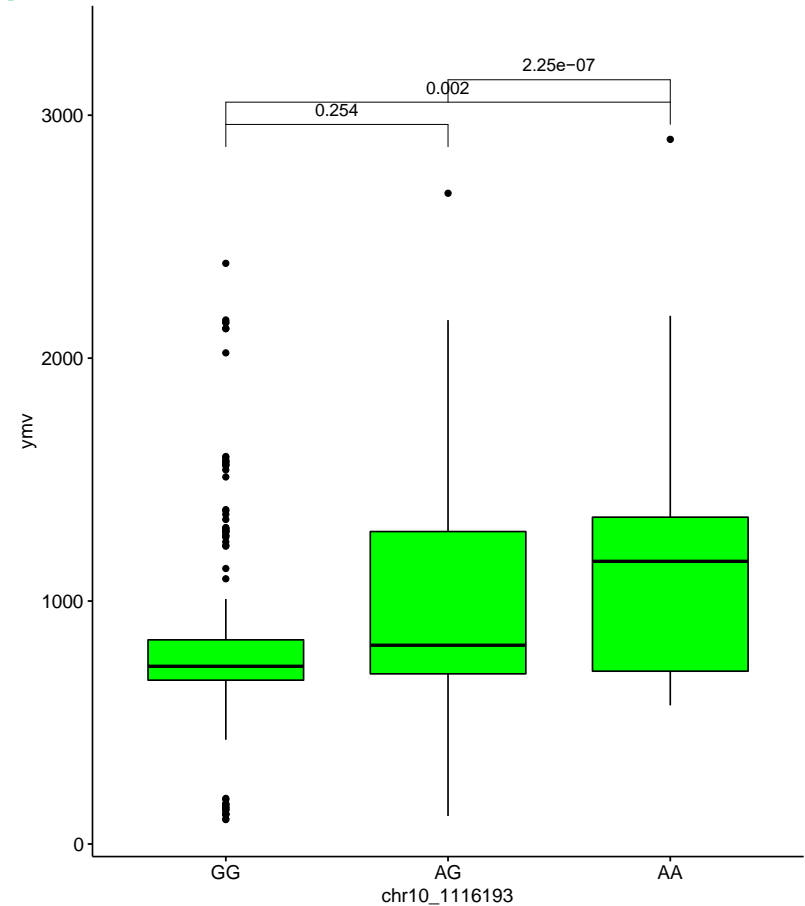
Selection of promising markers

SNP markers already identified using GWAS and QTL mapping

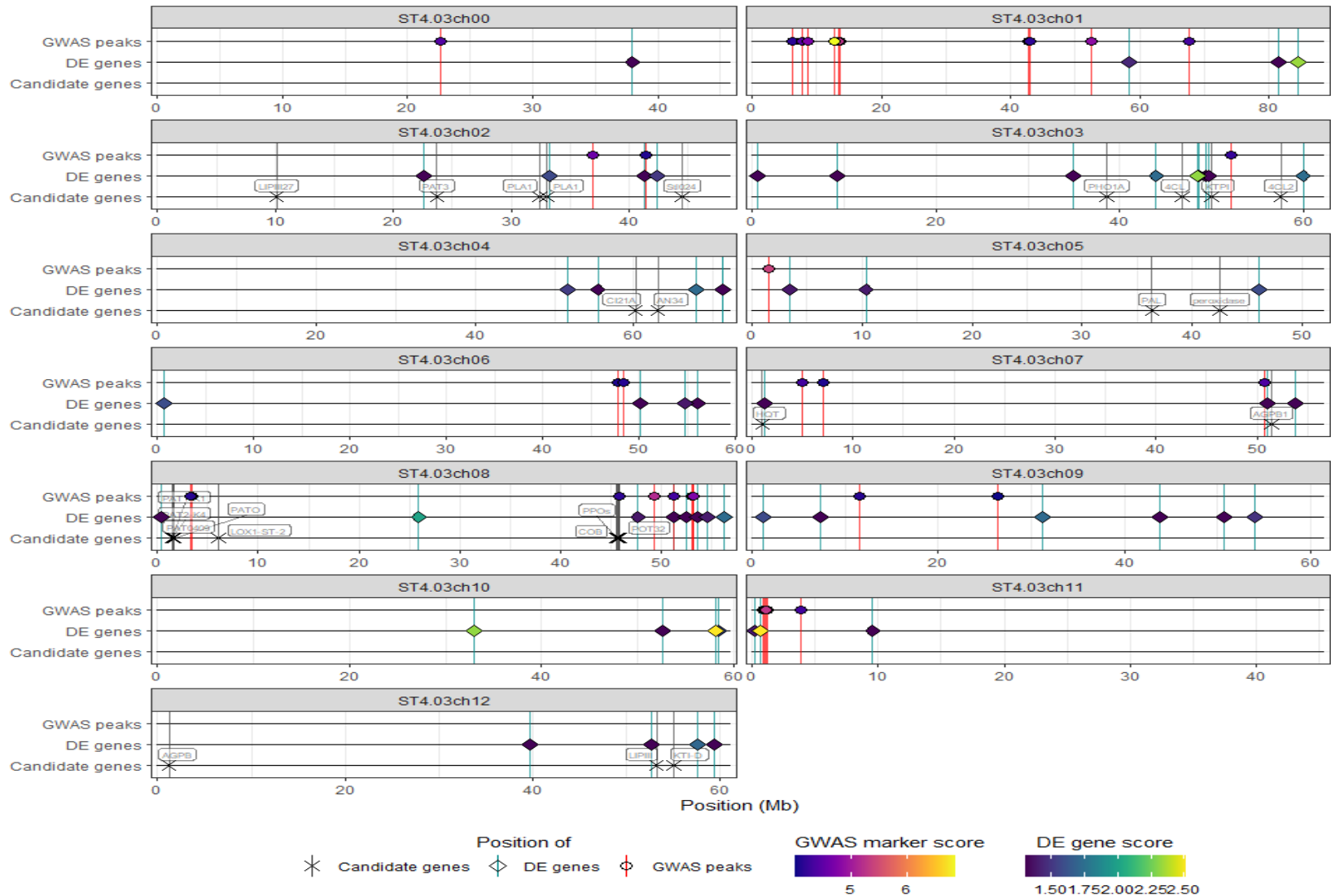
Traits	Species	Sources	Number of QTL	Promising QTL	Validated QTL
YMV	<i>D.rotundata</i>	Association mapping	15	4	2
Yield per plant	<i>D.rotundata</i>	Association mapping	18	3	2
Plant sex	<i>D.rotundata</i>	Association mapping	14	2	2
Flowering Intensity	<i>D.rotundata</i>	Association mapping	7	4	2
Plant vigor	<i>D.rotundata</i>	Association mapping	3	1	1
Tuber appearance	<i>D.rotundata</i>	Association mapping	4	2	1
YAD	<i>D.alata</i>	Linkage mapping	5	2	NA
Dry matter	<i>D.alata</i>	Association mapping	2	2	NA
Oxidation	<i>D.alata</i>	Association mapping	4	2	NA
Plant sex	<i>D.alata</i>	Association mapping	57	-	-
ACR	<i>D.alata</i>	Association mapping	12	-	-
PHC	<i>D.alata</i>	Association mapping	6	-	-
PHC	<i>D.rotundata</i>	Association mapping	2	-	
ACR	<i>D.rotundata</i>	Association mapping	2	-	

Selection of promising markers

YMV	Marker	Haplotype	Frequency	Linkage Disequilibrium (r ²)	P-value	Significance
YMV	chr03_6338751	Hap1	GGGT	0.427	1.000	ns
		Hap2	GGTT	0.320	1.000	ns
		Hap3	GTTT	0.466	1.000	ns
	chr10_1116193	Hap1	AAAG	0.226	0.254	ns
		Hap2	AAGG	0.309	0.003	**
		Hap3	AGGG	0.465	6.75 e ⁻⁰⁷	****
	chr15_3906069	Hap1	AAAC	0.214	0.882	ns
		Hap2	AACC	0.281	0.882	ns
		Hap3	ACCC	0.412	0.882	ns
	chr16_1482029	Hap1	AAAT	0.307	0.096	ns
		Hap2	AATT	0.424	2.01 e ⁻⁰⁴	***
		Hap3	ATTT	0.576	0.006	**
	chr05_30671001	Hap1	AAAG	0.365	1.000	ns
		Hap2	AAGG	0.265	1.000	ns
		Hap3	AGGG	0.369	1.000	ns



Selection of promising markers

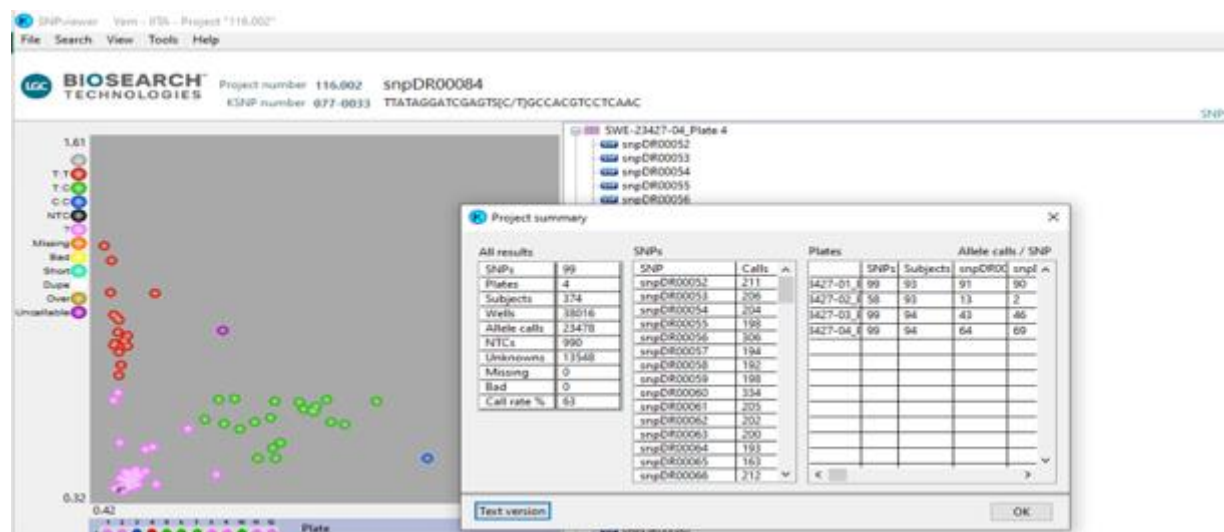


Seven traits were considered for the marker validation in *D. rotundata*

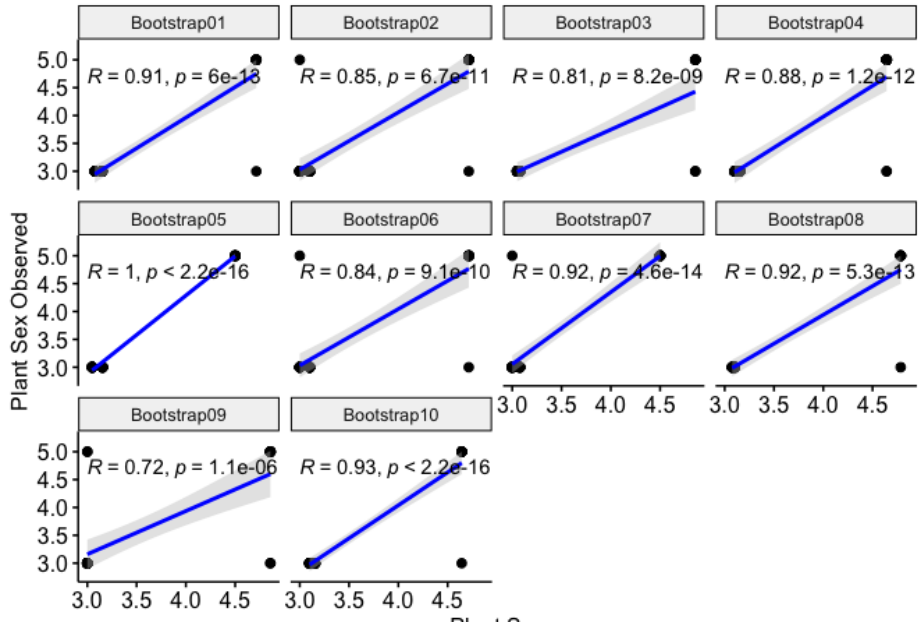
- Tuber yield per plant
- Yam mosaic virus
- Plant sex,
- Flowering intensity
- Plant vigor
- Tuber appearance
- Tuber shape

Flanking sequencing around the target region associated with each trait was developed and sent to INTERTEK for conversion into KASP-PCR

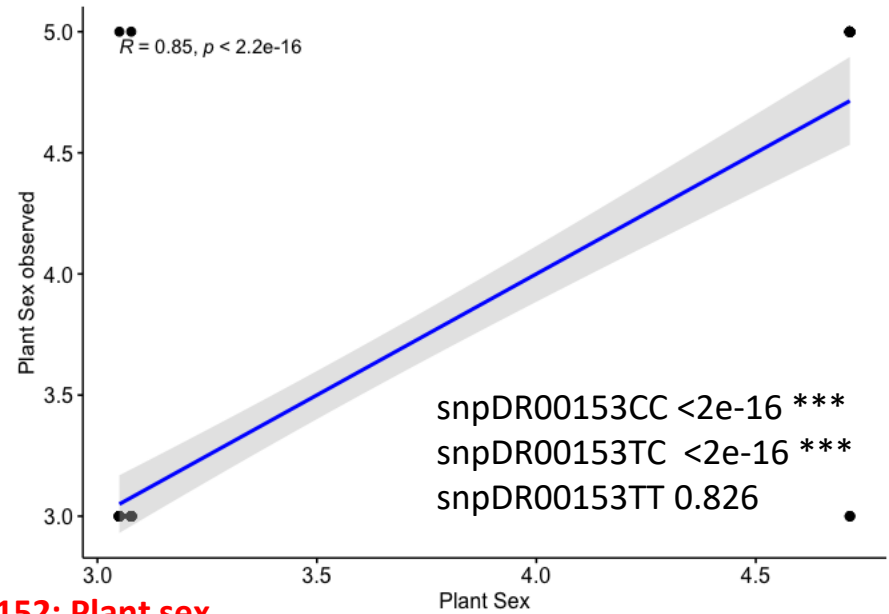
- For traits like sex, clones with well known sex information and those with unknown sex status were selected for the validation
- For disease, clones susceptible or tolerant to disease were used for the validation
- We then developed haplotype variant to estimate the marker prediction accuracy of each marker and for each trait



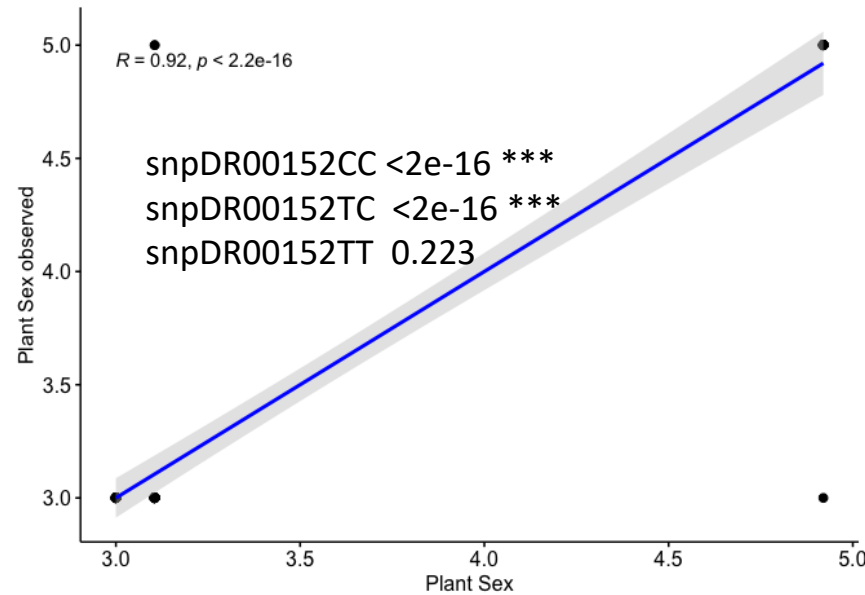
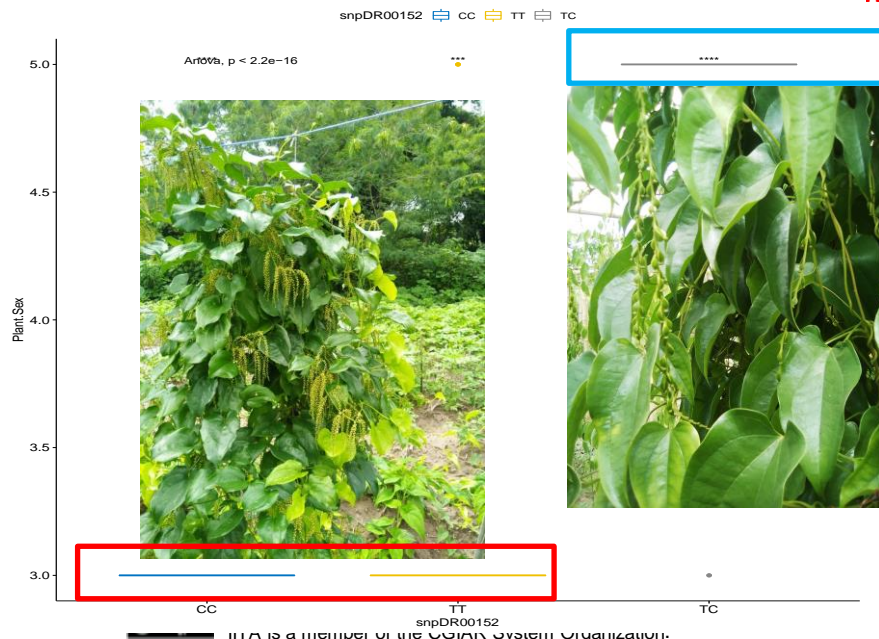
Low density SNP markers: Trait markers

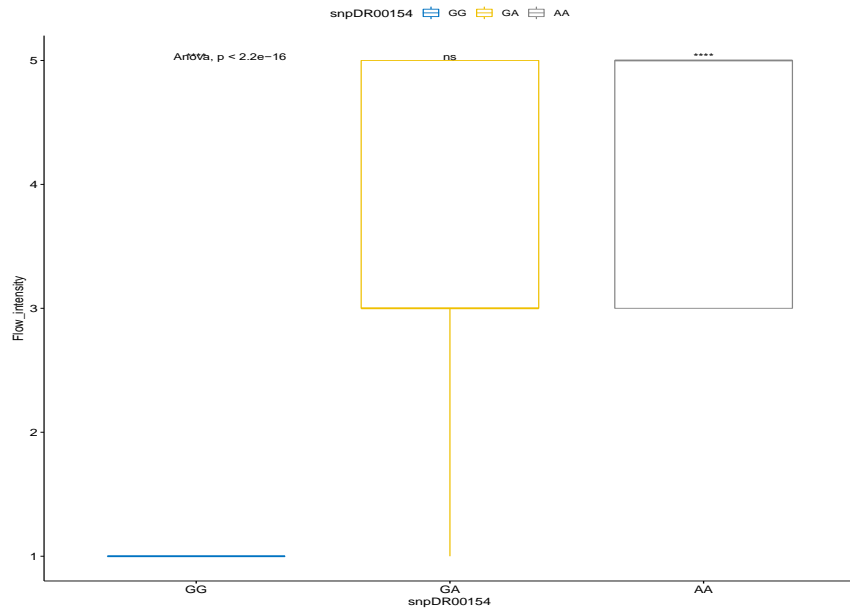


snpDR00153: Plant sex

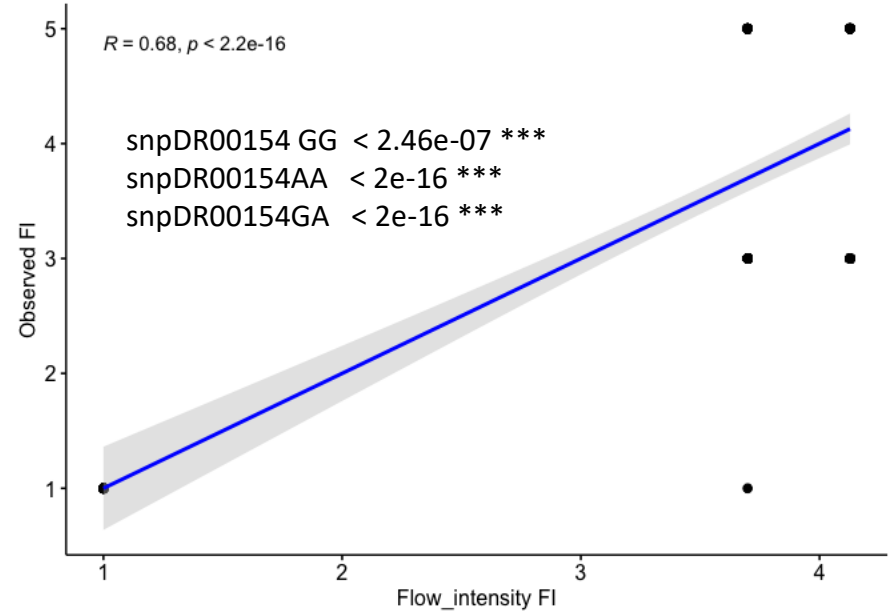


snpDR00152: Plant sex

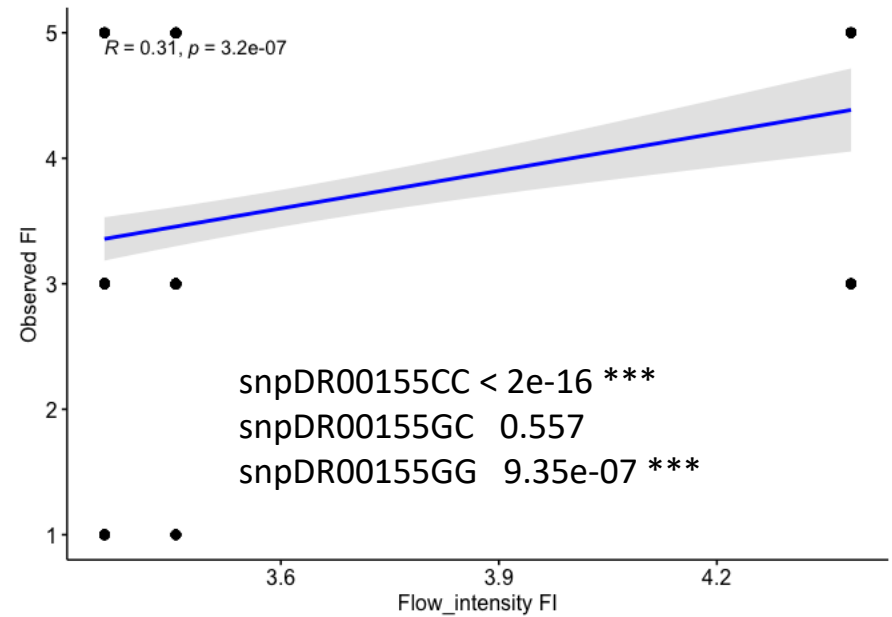
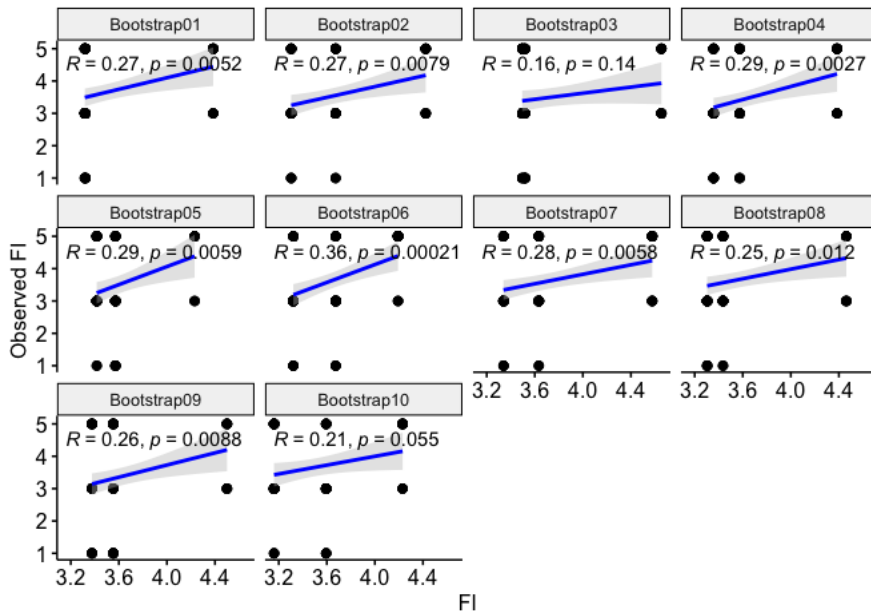




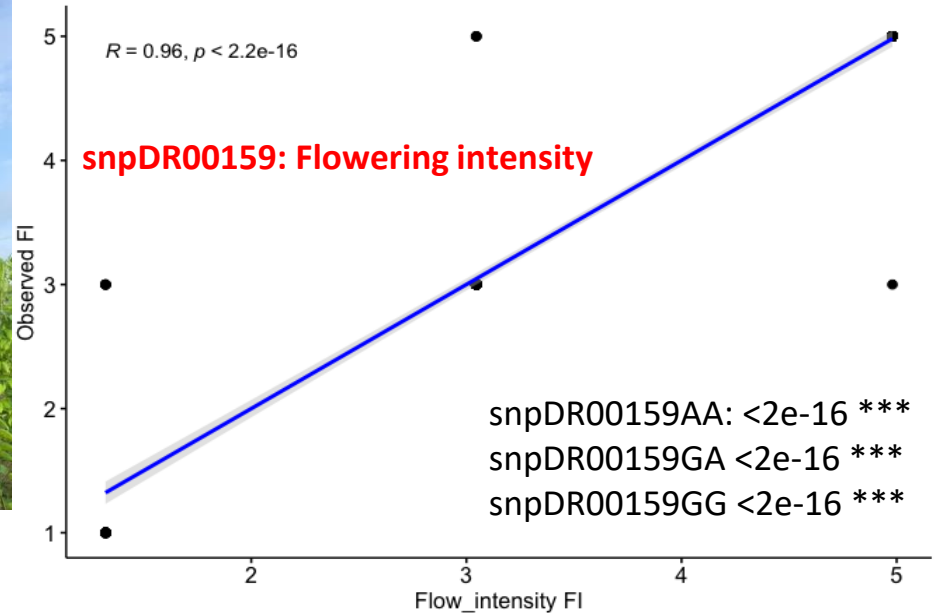
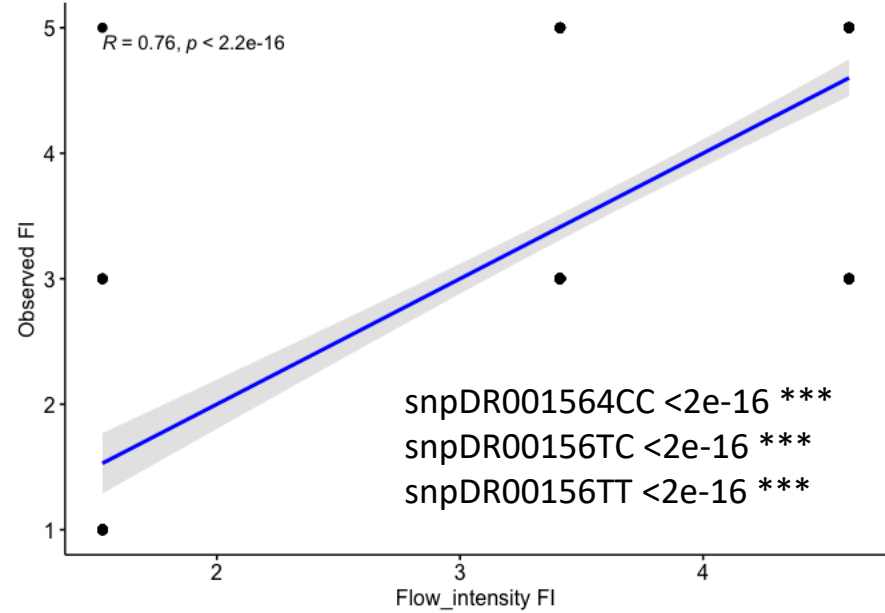
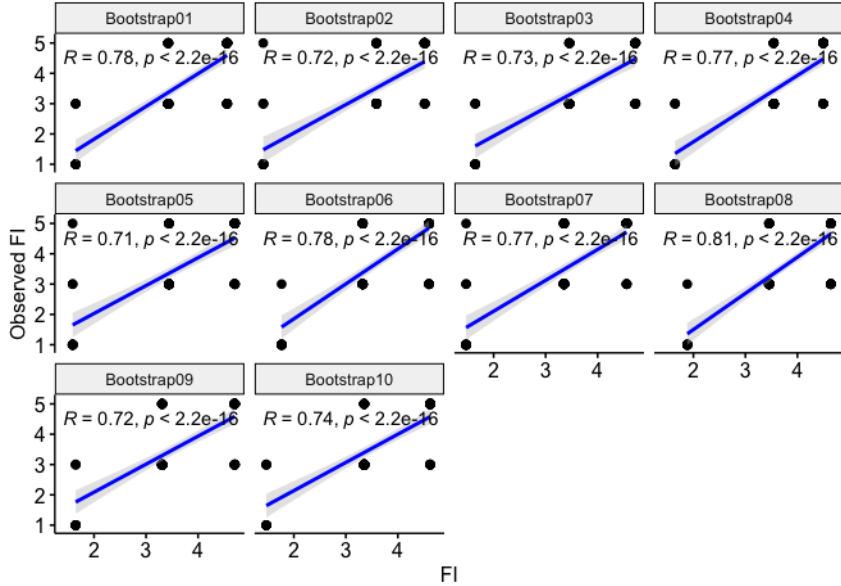
snpDR00154: Flowering intensity



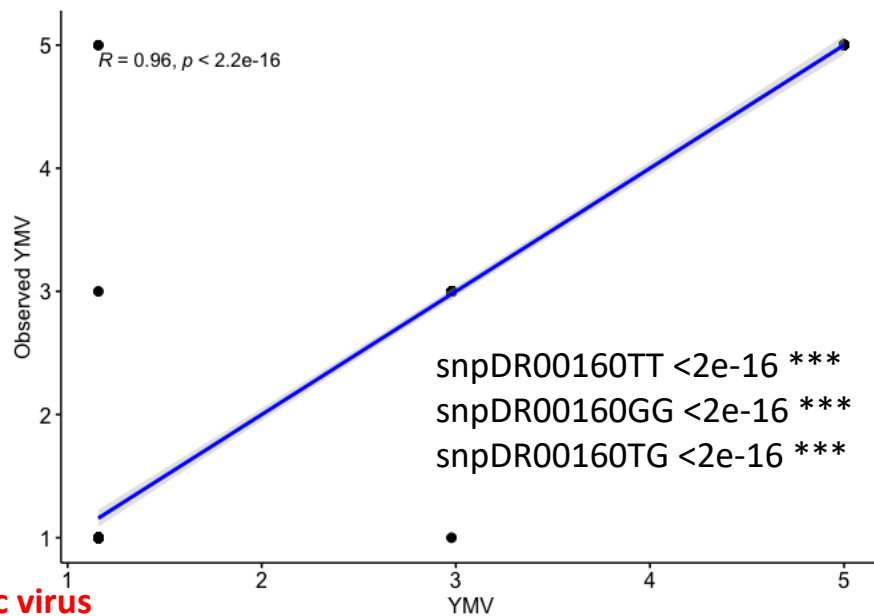
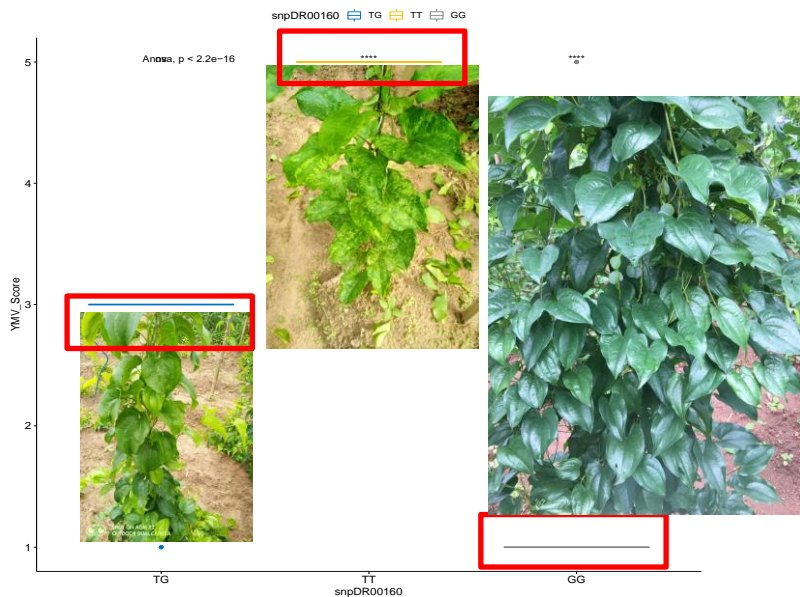
snpDR00155: Flowering intensity



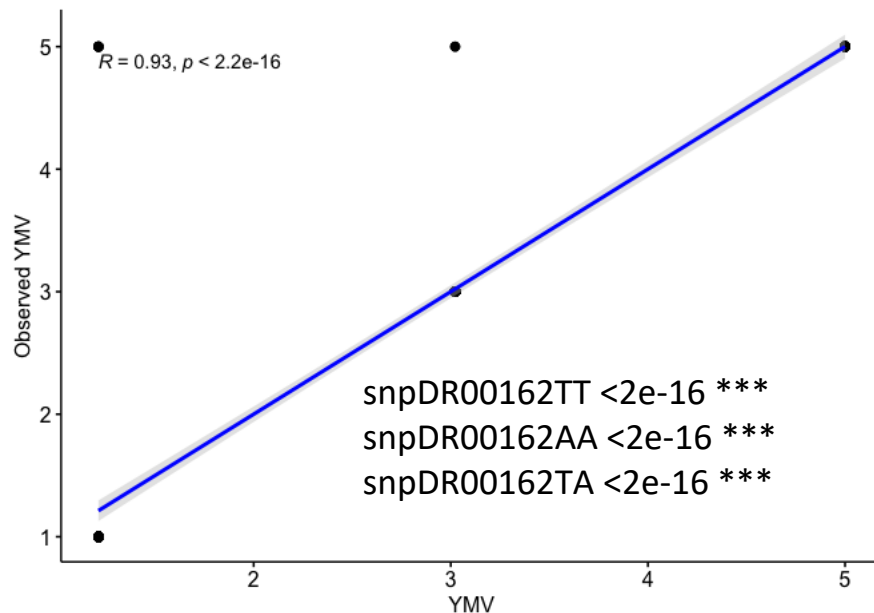
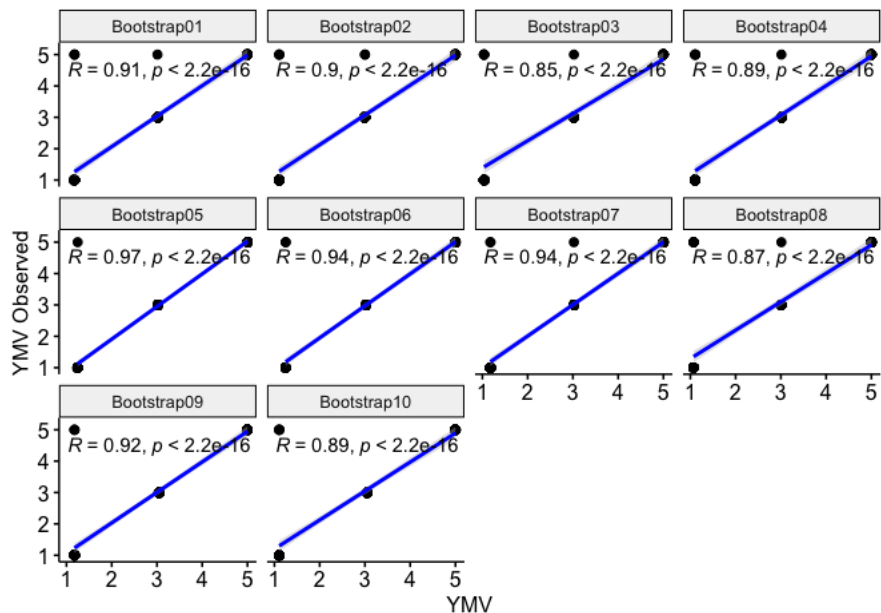
snpDR00156: Flowering intensity

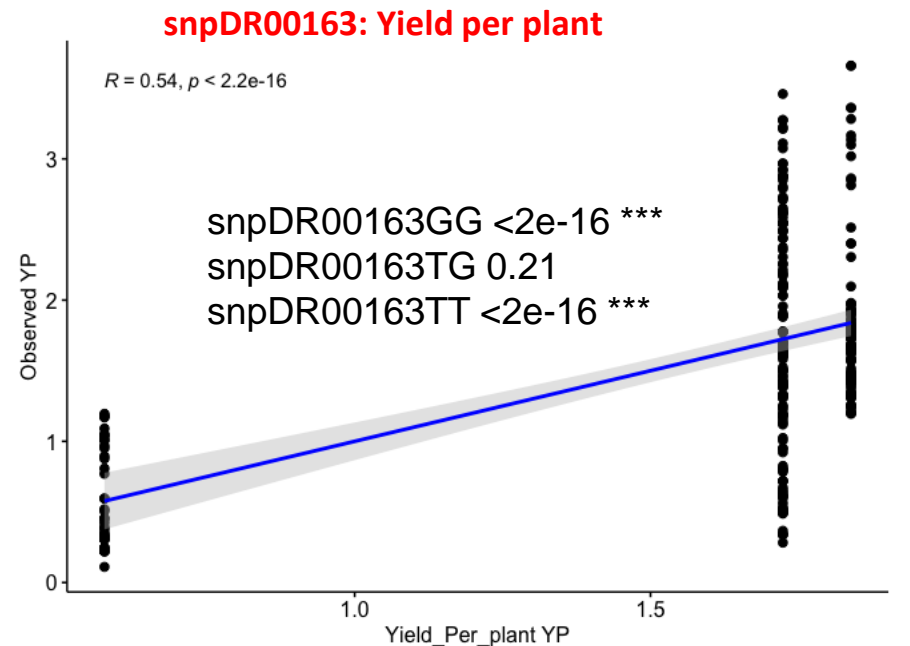
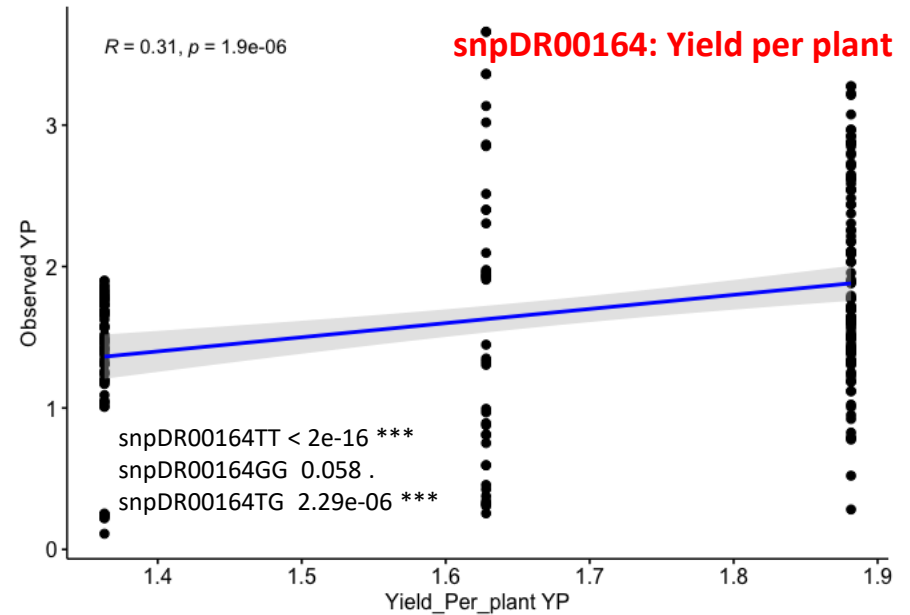
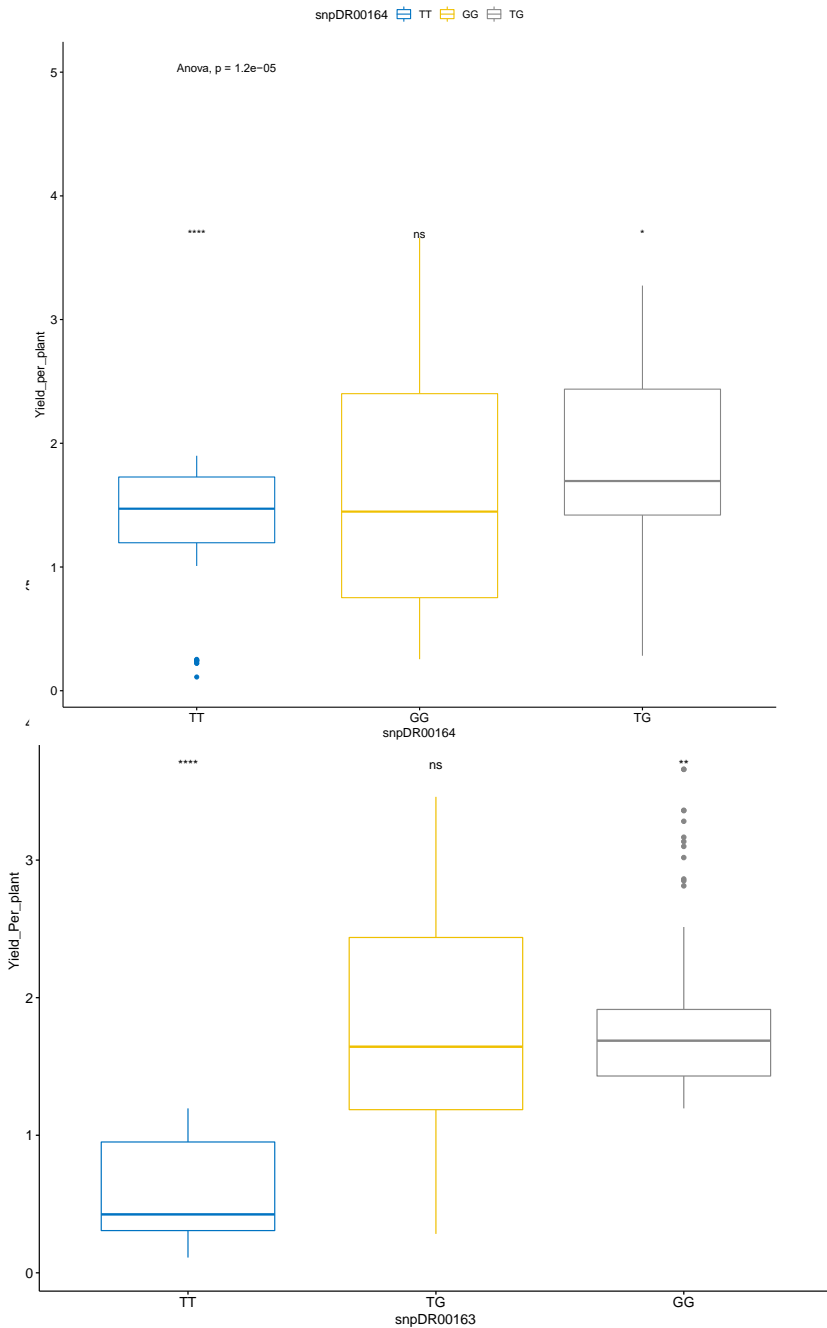


snpDR00160: Yam mosaic virus

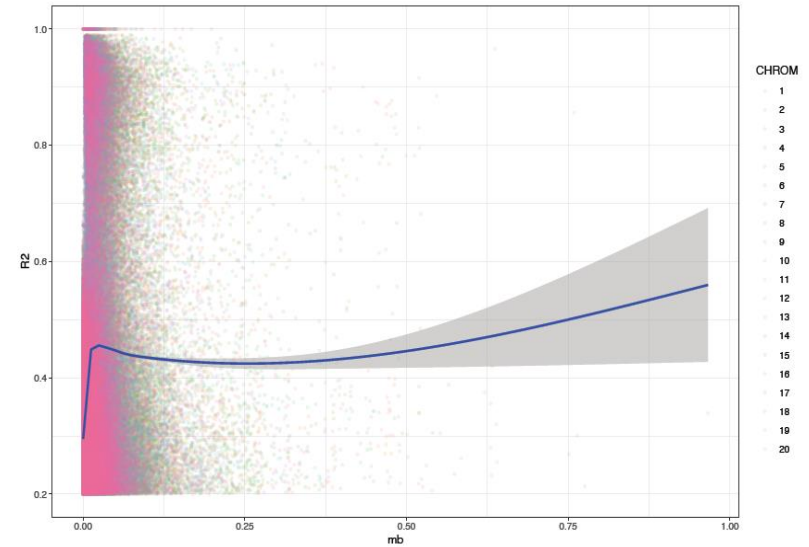
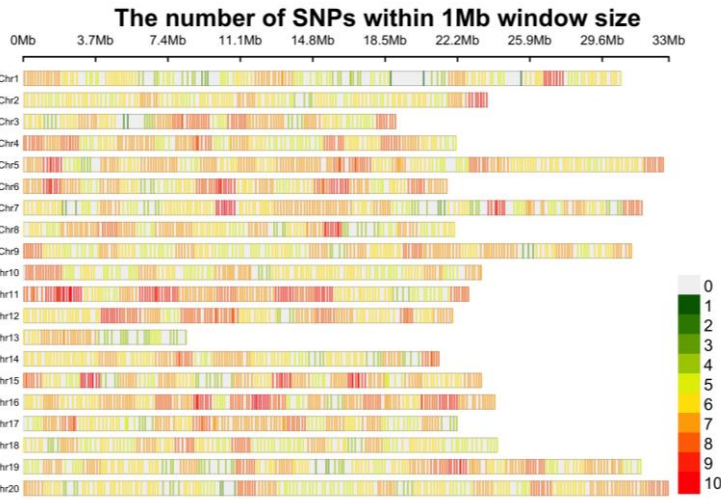
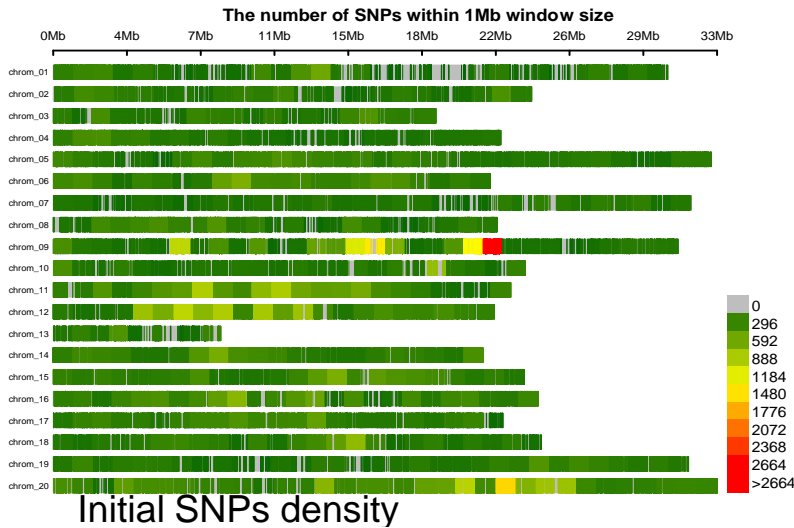


snpDR00162: Yam mosaic virus





Highly Informative SNP Marker Panels in Yam



SNP_ID	Chrom	Posi	Sequence
chrom_01_1010395	1	1E+07	YTTGGGAAATTAATGCATGTGTGTGGAAATTCACACGCCGTGTGGCT(M)CTCTATTGTTTCTTCTCCGGCCGTGTGAACAGTACCTGCTACTGTG
chrom_01_10210644	1	1E+07	GTGGCGAAGCACCTTCAAGGGGAAGAAACCCCAATAGTGTGCTGTTTTCACGGCGAGGCACATGTTCTGTGATGGGTATGTAGTGCACAAAT
chrom_01_10319388	1	1E+07	AGTCCCTTTGGCATGAATCATAGACAAGTAGGAGTCTTTTCTCC(R)ACAACTTCCAAGAGCTGCAAGGTCGGATGAGGAGACCTTCCAAAT
chrom_01_1045661C	1	1E+07	CTTCCAAAGACGGTGTGTTGGCTGGAAATTAAGATGAAGTGGCCG(R)TGTGAAATGTGTGGCATTTTAGATGGCATAATGTCATATACATGT
chrom_01_1054556	1	1054556	ATATTTCATAGGGTTTCGGTTCGGCACTTACCATCAATCCACACAG(M)ACCACCAATCGCGACATCCCGGGCCCGGACGTGATTCACAACTCCCC
chrom_01_10743101	1	1.1E+07	ATATTAGTGTGGAGGGATAGTGTCTCCACGGCTCGAAGGACTCGATGCTCGTGGAATCTGAGTGTGCACTGAGAGCTGTGTCACACAGACAGCCCTT
chrom_01_1088673C	1	1.1E+07	GGAGCTACTGTACTTACTCTGACGTAGCAGGTGTACCGATCTCACTA(R)GCGACACTTCGACAGTACTCAGACACGGGCACTATGTAGACTGG
chrom_01_11001424	1	1.1E+07	GATCGTACAATCCGAGATACATCAAGAATGGGTCAAGACATCCCATC(R)GCGCCGAAGGCTCAGAAATGAGTGTATCTCTGTCCAAAGTATAGT
chrom_01_11133068	1	1.1E+07	AGTCAACATGATCAGGACGTGTGTGTGGTATAGCAAGCTCCCA(N)AATCGTTCGATATCTTTTCATGCACTCTCCAGACTTCTCCCACTG
chrom_01_11275766	1	1.1E+07	GTTATAGACTTAACTTGGTCAAGGTGAAGATGGCTAGCACAAAT(S)CCCTAGATGCTTAAATGCTCAATGCTTCTACTGCTGGACTGGAGT
chrom_01_11445944	1	1.1E+07	AAGAGGGATTACCTAGCATCAAGAGGATTGAAGTTATAGTCATC(G)A(K)CTCAACTGAGGGCTGTGGGAAAGCTCCGGTCACTCCATCATG
chrom_01_11663472	1	1.2E+07	TTATGCTAGTCCCTCAGTTTGGGCAAAAATCGAGTATGTGCGATCC(C)Y(G)ATTACAGCTT(G)AATCTGAGCTAAAGTTCGCAATCATCAACGATTC
chrom_01_11865975	1	1.2E+07	GTGTCTTCCACAGCTCCACTCTTCCACACACTCACTTACAC(R)SCTCTCACTCACTACTCTTCAAGTCTCTTCAAGCAAGTITTAGSCATGTT
chrom_01_1197688	1	1197688	AAAGCTGGCTCTYTGAACTTCTTACTACCACTACCAACTAGT(Y)AGTGTATTTACCAAAGCCCTGGCAAGACTCGCTTTTTGTTTACTGG
chrom_01_1203053C	1	1.2E+07	TTTGTGATGATGCTTGTAGCTTCTCACTCCCACTCTCTCTCTTCC(W)CTCCCTCTGGTGTATGTGTCTCAITTCACAAAGATCACTCGCCGG
chrom_01_12191041	1	1.2E+07	TACGGTGTGCTCAATGAAAGAAATAGTGTGCCCACTAGAAATGTC(N)AAGAGGTGGGGGTGTGCATAGACTATATAAACATCAAGCTCTACTAGAA
chrom_01_12211182	1	1.2E+07	CAGGTATCCATATAGCACACTCACTACGGTGGAGAGACTC(Y)M(A)CTTTCTGTGGACACACGGATACCCAAAGGCCATGGCCACCAAG
chrom_01_1246508E	1	1.2E+07	AATGAAAGATGATGATGCTGGTCTGACTGAAAGAACTACATCC(C)R(J)AGGATATGAGCAGGCTGTCCGGAAATGAAAGGCTAGAAAGCACCA
chrom_01_1257280E	1	1.3E+07	GAAAGTGGCCGGCTCATGAATAGATGCACTCACTTTTGGCAACC(W)AATGAATCAATGTAAGAAGTATAGACCTTCAACTTGAATAGAGTGG
chrom_01_1278963C	1	1.3E+07	GAGTGCATGGCAAGTCAACATGCTGGCATCACCCTGGCTAGGTT(Y)GATTCGAAATTTCCCGAACAAGACATCTCCGAAGGACCTCCGGTACCA
chrom_01_12892824	1	1.3E+07	CTCACAGGCTACTATATACTTGTGGCCCTACTTCTGGAG(M)CACAGCTCAAGTITGGCGCACTGTGAGGATAGCACAGATTAAFAA
chrom_01_1300093	1	1300093	GAACTTATCTGGCCGTGACTCTCTAGTTTGTCAACTTGGAG(M)CACAGCTCAAGTITGGCGCACTGTGAGGATAGCACAGATTAAFAA
chrom_01_1306559E	1	1.3E+07	TCAGAGTTGGCTTCCAACTCACGGAAACAGAGATACAACTGGAT(Y)CATCCAGCAAGTGTGAATGATTTTCAACAATCAGGGACACAAGATC
chrom_01_13215574	1	1.3E+07	CAGCGTGGAGGATGATATAGATGATGAGCTCCAGCTCTCTGGACTG(R)TCTTGGATGATCCMSGTAGSTAGAGATACCCCTTCCACACATGA
chrom_01_13265621	1	1.3E+07	GATCGTAACTGACAAATGGAGAAATCTGAAAGGATCAAAACCGT(C)A(J)ACTGGTTCGAAAGATGCAAGATGCTTCAACCTCCCGCTATT
chrom_01_1339547E	1	1.3E+07	CTGTAGATCGCTGCTTCTCAATAAGGGATGACATTGACAAAAT(T)S(J)CTACTGTCCAAAGTGGAAACAAATGAGTGTACTTGTAGCTCT
chrom_01_13588151	1	1.4E+07	ATTAATTTATAAGAAACGGAGCTTTAAGTCTGTACATCCAC(N)GGGGCTGTGGATACCCAGTCCGATGACTCACAGGAAGACACT
chrom_01_13748093	1	1.4E+07	CTTACCCTGATGAATATAGTAAGGAACTTACAGTGG(G)A(G)A(C)TBTATAGCAAC(T)TATAGCAACATATAGCACATCTTCTTCTTCTTCTT
chrom_01_1386017E	1	1.4E+07	AGTGTGGTGGCAGCCAAAACGGCCAAAGAAATCTCCATCAAT(Y)G(C)TCAACATCTGATTTATACATCAAGAACATCGGGCCATATGGGAC
chrom_01_1398580E	1	1.4E+07	GGCTCTCTGTCCAAAGAACTCGTCAATGGTGGGCTGCTATTAGGC(R)AAGCGGCGCTGAAAGAGTCAATCTTCTTCTTCTTCTTCTT
chrom_01_1414446E	1	1.4E+07	GATGACACTTCTGATATGCTAGACCTTAGTTTGGCACAACTG(A)K(C)ATTATCCCAATAGCTCCCAATTTGAGCTGAACCTGGCATCTC
chrom_01_1424388E	1	1.4E+07	GTGATAGCTCTCAGAGAGCTTGTCACTTAAATATATGGAACT(M)ACATCTGTGCAAGACT(C)TGTGCGCATATGAGGCTCTCTTCTTCTTCTT
chrom_01_1438085	1	1438085	CTCGATTTATGATCAAAATCTCAGCAACTCCCTCTGTGCAAACT(M)ACATCTGTGCAAGACT(C)TGTGCGCATATGAGGCTCTCTTCTTCTTCTT
chrom_01_1468293E	1	1.5E+07	CAGTTCATCACTTCTCTAGTAAGATAGTCCCTATCTGCTT(C)R(C)CATGCTCCACCTCTTTTCCAAACCTGGCTTTGATACAGTGTGG
chrom_01_1489212E	1	1.5E+07	GTATTGCTGGGATCCAGCCGTAAGAATTTGATGACTATAGG(M)M(C)AAGCACATCCCGAGGCTTACTGCTAGTCTTCAATAGATG
chrom_01_1509414E	1	1.5E+07	AACATCAACAAAGCCGCAAGACTGAAATCGATTTCAGGCTTGAAG(R)AATGATGATGCAAGACTGAGAAAGACTCAACTGATCTCAATATG
chrom_01_15240184	1	1.5E+07	ACGTAGCTCCCCCGCTGCTCTCTTCCAGCCGGCGATCTTTT(K)AATGTTGGATGTGTTACTCGATATCTTATCGCTTTTTGGGGATC

A total of 3092 SNP markers selected across the yam genome including the QC/QA the traits associated markers

TO END HUNGER (CtEH)

Crops to End Hunger (CtEH) Data (CIMMYT)

CIMMYT Research Data & Software Repository Network > Crops to End Hunger (CtEH) Data >

The reference genomes of four yam (*Dioscorea* spp.) clones.

Version 1.1



Agre, Paterne; Asfaw, Asrat, 2023. "The reference genomes of four yam (*Dioscorea* spp.) clones.", <https://hdl.handle.net/11529/10548882>, CIMMYT Research Data & Software Repository Network, V1

Cite Dataset

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Link Dataset	
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Description

1. TDa0000194 is a female flowering and white tuber fleshed water yam clone (*Dioscorea alata*) with less tendency to oxidize often used as trait progenitor in IITA breeding program. It is a released variety in Nigeria.
2. TDa0200012 is a male flowering and anthracnose tolerant water yam (*Dioscorea alata*) parental clone.
3. TDr9902789 is male flowering white Guinea yam (*Dioscorea rotundata*) breeding line tolerant to yam mosaic virus often used as a trait progenitor in IITA white Guinea yam breeding program.
4. Gwagwa is a female flowering white Guinea yam (*Dioscorea rotundata*) landrace variety in Nigeria. It is a short vine length and less tendency to climb landrace clone producing multiple shoots and tubers.

Subject

Agricultural Sciences

Keyword

genomes, genome, reference_genome

Notes

For the description of each file, please see: Yam_v.01.xlsx, included in this dataset.

License/Data Use Agreement

Custom Dataset Terms

- Files
- Metadata
- Terms
- Versions

<https://data.cimmyt.org/dataset.xhtml?persistentId=hdl%3A11529%2F10548882>



- Deployment of MAS in the breeding program
- Annotation and gene model prediction
- Gene expression analysis for semi-dwarf genotypes
- Validation of middle density SNP markers and deployment for product advancement and for GPCP
- Identification of tolerant/resistant inter-specific genotype-based marker coupled with quantitative method
- Variety tracking and monitoring adoption of improved yam varieties
- Implementation of GS and prediction
- Effect of heterozygosity level on trait association

Take home message



QC/QA markers were successfully developed and deployed in yam breeding for routine activities



Trait linked markers developed and deployed for MAS for key traits; ongoing work on validating additional markers



Middle density SNP markers developed and in the process of validation for GS as well as for GPCP



Additional reference genome developed to accelerate discovery in yam with the support of EiB/CtEH



Continuing application of low, middle and high-density SNP markers in the breeding program for breeding optimization.



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in Breeding**
PLATFORM



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GATES**
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