



AfricaYam: A project to strengthen yam breeding in West Africa

Primary Outcome 2: IITA progress report Year

AfricaYam
Annual Planning Meeting
September 15-17, Abuja,
Nigeria

Paterne Agre, Asrat Amele,
Patrick Adebola et al.,



Key Achievements (June 2021 – 2022)

- 50 QC/QA markers developed and validated
- Additional QTLs linked with key agronomic and tuber quality developed
- QTL markers related to 7 traits developed and validated
- YamBase fully operational and used in the breeding program with additional functionalities

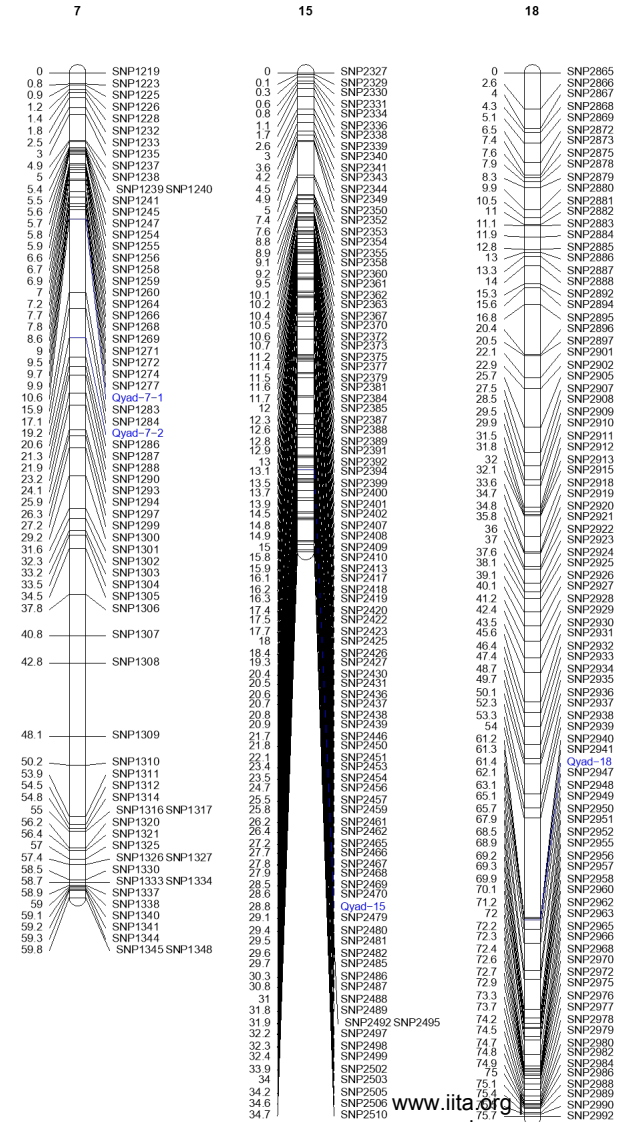
Different genotyping platforms used

- **DArT**
 - 506 *D. rotundata* == GWAS and for pop validation, forward marker development
 - 100 *D. alata* GWAS for key agronomic, tuber quality traits and textural traits
 - 86 *D. rotundata* farmer varieties (trait profiling)
 - 2903 *D. rotundata* for parental selection and breeding advancement using GPCP
 - 940 *D. rotundata* (SCG Abuja)
 - 1624 *D. rotundata* (Seedling nursery Ibadan)
- **Intertek**
 - 374 multiple yam species (QC/QA markers development/validation)
 - 940 *D. rotundata* for markers validation targeting 7 traits
 - 374 *D. rotundata* used for varietal tracking and verification

Linkage analysis for QTL detection for anthracnose resistance in *D. alata*

Summary of significant QTLs detected for yam anthracnose disease tolerance in water yam

Markers	Chr	Pos (cM)	LOD	R ² (%)	Gene function
Qyad-7-1	7	10.60	4.51	33.7	DRNTG_08663.1
QTL-7-2	7	19.21	5.28	29.54	DRNTG_08664.1, DRNTG_23336.1
Qyad-15	15	28.80	4.43	30.90	DRNTG_14305.1
Qyad-18	18	61.4	4.65	39.40	DRNTG_18245.1, DRNTG_29617.1



> [Genes \(Basel\). 2022 Feb 14;13\(2\):347. doi: 10.3390/genes13020347.](#)

Identification of QTLs Controlling Resistance to Anthracnose Disease in Water Yam (*Dioscorea alata*)

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Affiliations + expand

PMID: 35205389 PMCID: [PMC8872494](#) DOI: [10.3390/genes13020347](#)



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D. rotundata

Set of materials used:

- Diversity panel
 - 332 yam genotype sequenced using WGRS
- Breeding panel
 - 406 genotypes sequenced using DArT
 - 206 genotypes using GBS (historical data)

Traits

- YMV, tuber appearance, tuber yield per plant, plant sex, flowering intensity, cross-compatibility related traits such as average crossability rate (ACR), and percentage of high crossability (PHC)

Analysis

- Phenotypic value as BLUE estimated for respective traits of the study populations
- GWAS analysis using mixed linear model implemented in mrMLM, CMPLOT and GAPIT R package
- Gene annotation conducted for gene prediction
 - Promising SNP markers identified and converted into Kasp-PCR with INTERTEK

D. alata

Set of materials used:

- Diversity panel
 - 100 yam genotype sequenced using DArT
- Historical trials
 - 72 genotypes (historical data)

Traits

- YAD, tuber yield, plant sex, flowering intensity, average crossability rate (ACR), percentage of high crossability (PHC), tuber shape, tuber browning index/oxidation, dry matter content

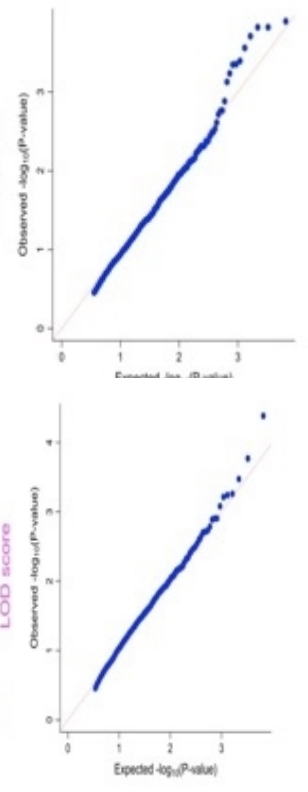
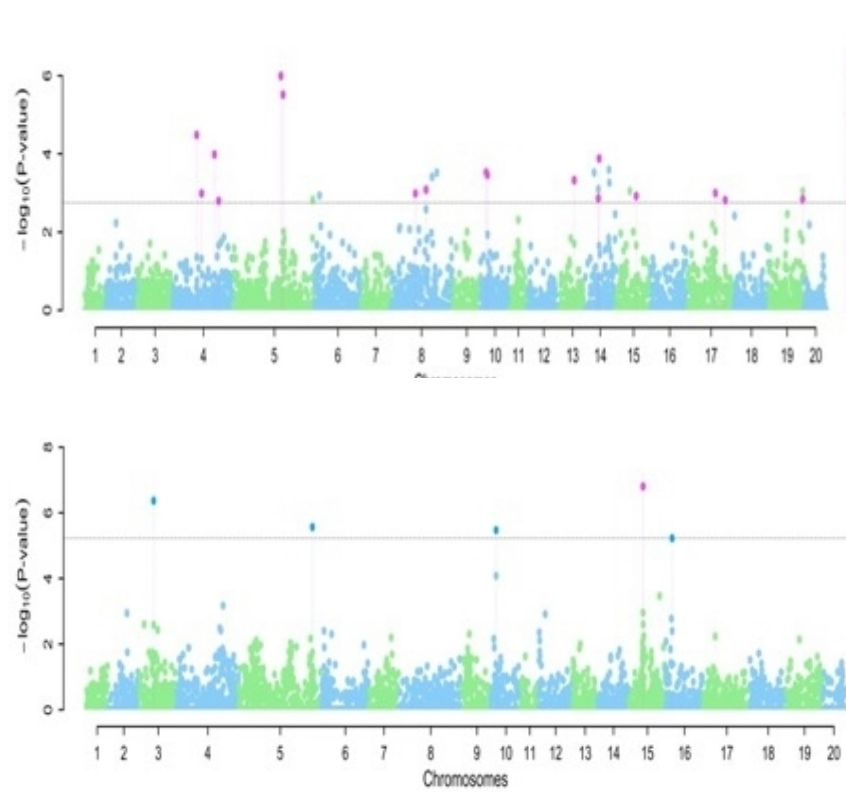
Analysis

- Phenotypic value as BLUE estimated for respective traits of the study populations
- GWAS analysis using mixed linear model implemented in GWASPOLY using K+Q model
- Gene annotation conducted for gene

prediction

Primary Outcome 2: Methods and Tools

Association mapping in *D.rotundata* breeding panel



Multiples SNPs marker located on chromosome 6, 8, 14, 15 and 19 were identified to be associated with the TTY/Plant

Multiples SNPs marker located on chromosome 3, 4, 10 and 16 were identified for YMV

Trait	SNP	Chro	R ²	effect	LOD	Putative genes identified
Yield	chr14_14300070	14	62.74	-0.08	4.71	Zinc finger, CCHC-type
	chr14_11128124	14	62.74	0.05	4.70	Mlo-related protein
	chr14_14292173	14	62.62	-0.07	4.44	Transcription factor TFIIIB
	chr14_15507116	14	62.53	0.05	4.24	UDP-glucuronosyl/UDP-glucosyltransferase
	chr15_4138634	15	62.36	-0.03	4.00	Survival protein SurE-like phosphatase/nucleotidase
	chr08_21789522	8	62.19	0.05	4.35	Protein with unknown function
	chr06_965642	6	62.13	-0.02	4.12	DNA polymerase alpha/epsilon, subunit B
	chr14_8143018	14	62.13	0.03	4.06	Unknown
	chr08_13478676	8	62.08	0.04	3.95	ATPase, F1/V1/A1 complex, alpha/beta subunit, nucleotide-binding domain
	chr19_9446619	19	62.03	0.03	4.00	Translation protein SH3-like domain superfamily
YMV	chr16_1325272	16	13.52	295.41	4.12	ABC-2 type transporter, and
	chr04_23336802	4	12.95	-225.25	4.10	SNF2-related domain; Geminivirus AL3 coat protein ; SANT/Myb domain ; Geminivirus AL1 replication-associated protein .
	chr10_1116193	10	12.85	-240.87	4.00	
	chr03_6338751	3	12.42	169.09	4.28	AP2/ERF domain; Gdt1 family ; NB-ARC; Probable transposase, Pita/Eni/Spm; plant
	chr10_613339	10	12.38	138.99	4.36	Geminivirus AL1 replication-associated protein catalytic domain ; Kinesin-like protein and Geminivirus Rep catalytic domain .
						www.ncbi.nlm.nih.gov/
						www.katoh.org/
						www.uniprot.org/
						www.ebi.ac.uk/EMBL/BLAST/
						www.ncbi.nlm.nih.gov/blast/

BMC Plant Biology

Research | Open Access | Published: 22 November 2021

Identification of quantitative trait nucleotides and candidate genes for tuber yield and mosaic virus tolerance in an elite population of white guinea yam (*Dioscorea rotundata*) using genome-wide association scan

Patrice A. Agre | Prince E. Norman, Robert Asiedu & Asrat Asfaw

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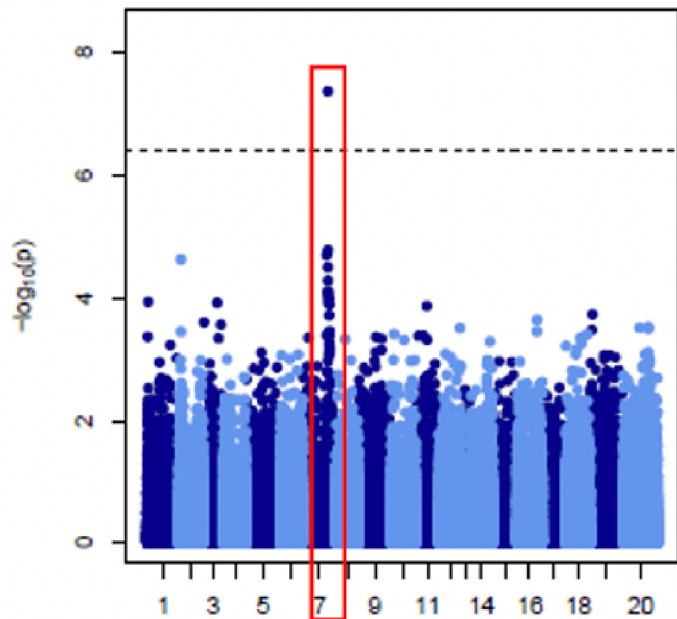
Sections: Abstract, Background, Material and methods, Results, Discussion, Conclusion

IITA is a member of the CGIAR System Organization.

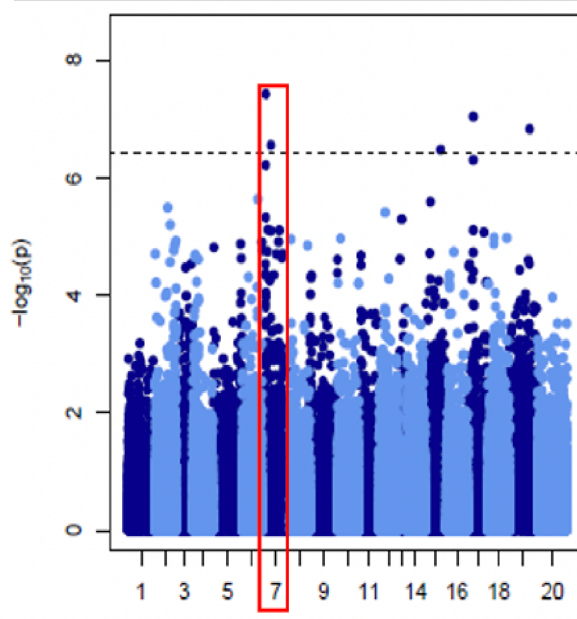
Primary Outcome 2: Methods and Tools

Association mapping in *D.rotundata* diversity panel

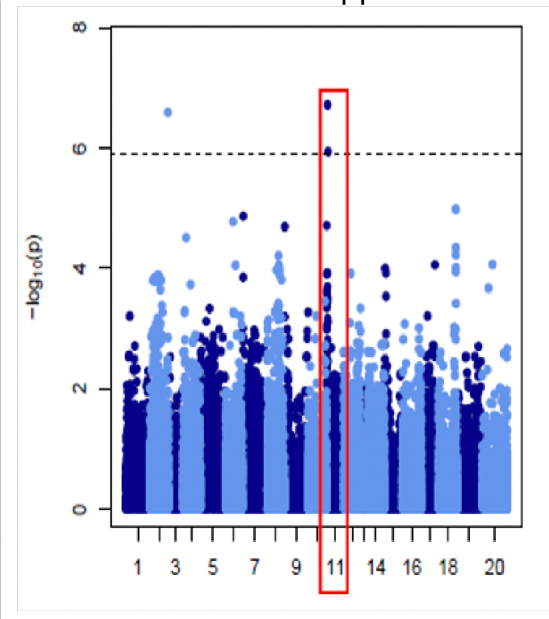
Tuber yield per plant



YMV



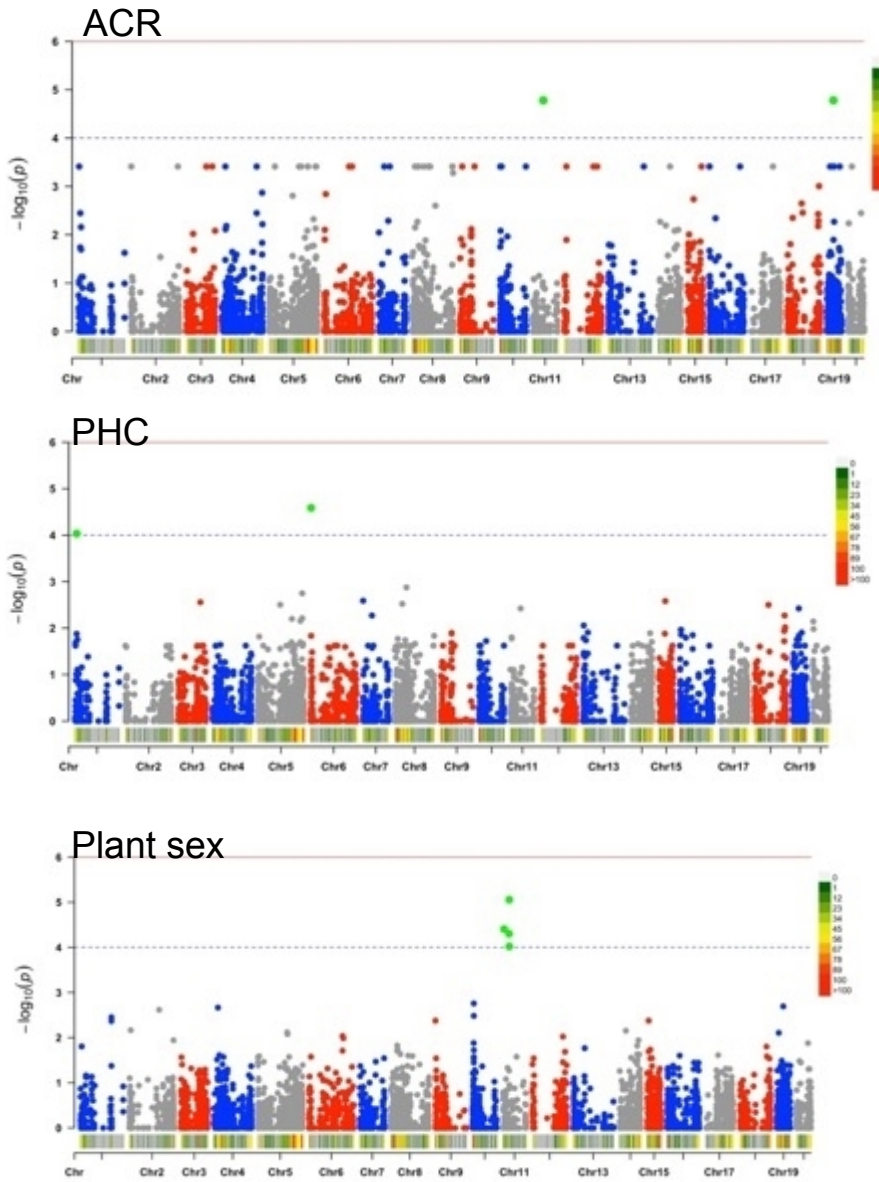
Tuber Appearance



Trait	Chr.	Position	Candidate genes	Description
Plant vigour	3	880906	DRNTG_27903.4	MSF1-like family protein
			DRNTG_27904.1	Sm-like protein LSM5
			DRNTG_27907.1	Zinc finger protein WIP2
Plant Sex	11	1819621	DRNTG_10433.1	Transposase-associated domain
	1	7175652	DRNTG_18989.1	Zinc finger, CCHC-type
			DRNTG_18987.3	Plant transposase (PttA/En/Spm family)
Flowering intensity	11	93339	DRNTG_18807.1	BAG family molecular chaperone regulator 1
		222725	DRNTG_22443.1	Vacuolar-sorting-associated 13 protein C-terminal
		260263	DRNTG_22446.1	60s Acidic ribosomal protein
		278178	DRNTG_22448.1	Polyadenylate-binding protein-interacting
		353466	DRNTG_13800.1	No apical meristem (NAM) domain-containing protein 43
		553347	DRNTG_25602.3	Cyclophilin type peptidyl-prolyl cis-trans isomerase
		1450774	DRNTG_18497.2	Cyclophilin type peptidyl-prolyl cis-trans isomerase

Primary Outcome 2: Methods and Tools

Association mapping in *D. rotundata* based historical information



Trait	SNP	Chr	PVE (%)	Orthologs	Putative function
ACR	chr11_7229882	11	5.67	PPM-type_phosphatase_dom	Abscisic acid signal transduction
	chr11_7229910	11	3.65		
	chr11_7229912	11	6.78		
	chr11_7229926	11	4.18		
	chr19_4269172	19	3.78	Cyt_P450	Biosynthesis of hormones
PHC	chr19_4269173	19	2.12		
	chr06_463969	6	4.70	Pectinesterase_cat	Important role in fruit ripening
Sex	chr01_1068963	1	8.90	BLH1	Cell-fate switch of synergid to egg cell
				LEA_2	Active during seed formation
Sex	chr11_867049	11	10.34	LIM-bd/SEUSS	Regulates flower development
				AP2/ERF_dom	Regulates meristem identity, floral organ specification, and seed coat development.
				TraB/PrgY/GumN_fam	Acts as a protease to inactivate the mating pheromone
	chr11_4499228	11	11.23	WD40_repeat	Key regulator of plant-specific developmental events
				Gprotein_alpha_su	Cell growth and hormonal regulation
	chr11_4664050	11	9.76	NmrA	Involved in asexual and sexual development
	chr11_4664100	11	12.45	Haem_peroxidase	Ethylene biosynthesis

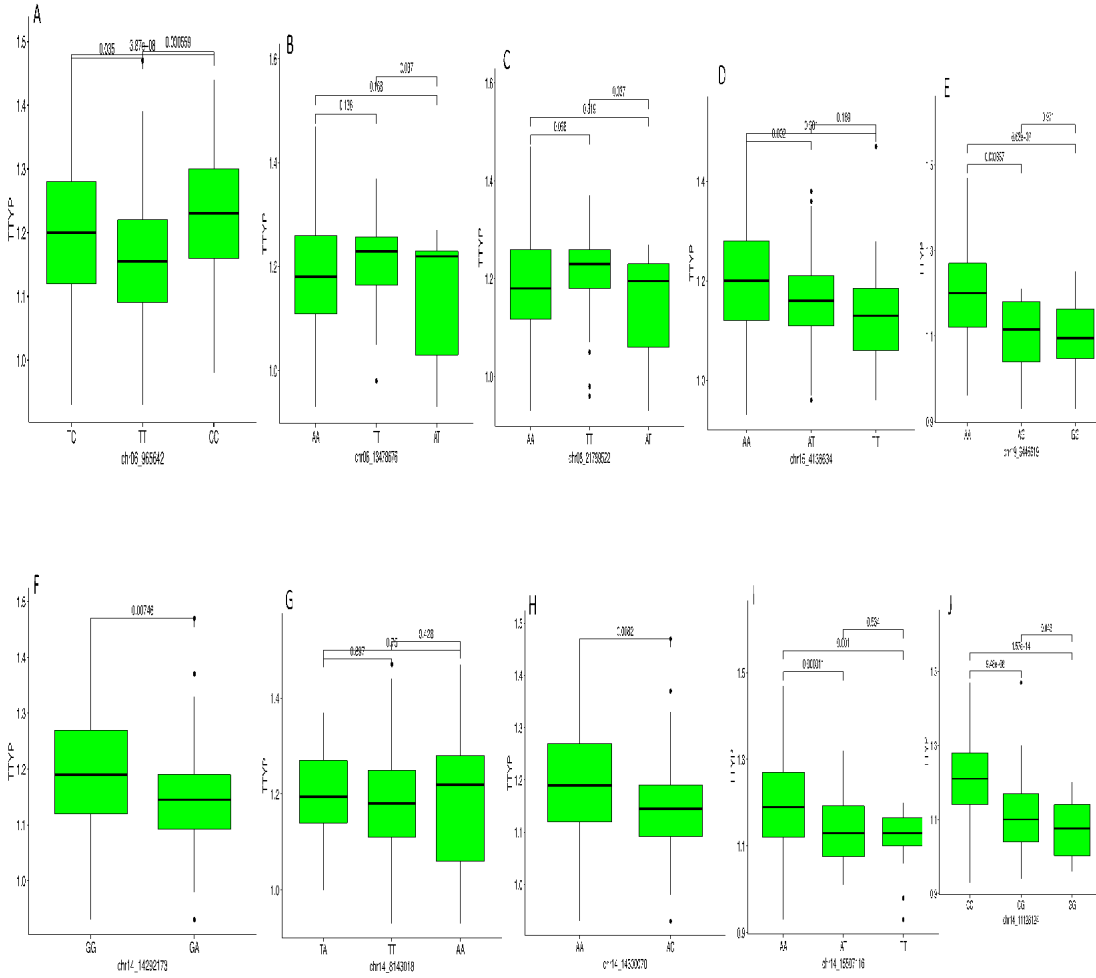
Markers development for forward breeding

SNP markers already identified to be associated with different traits using different breeding population and technics

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	-	

GWAS result in *D. rotundata* breeding panel

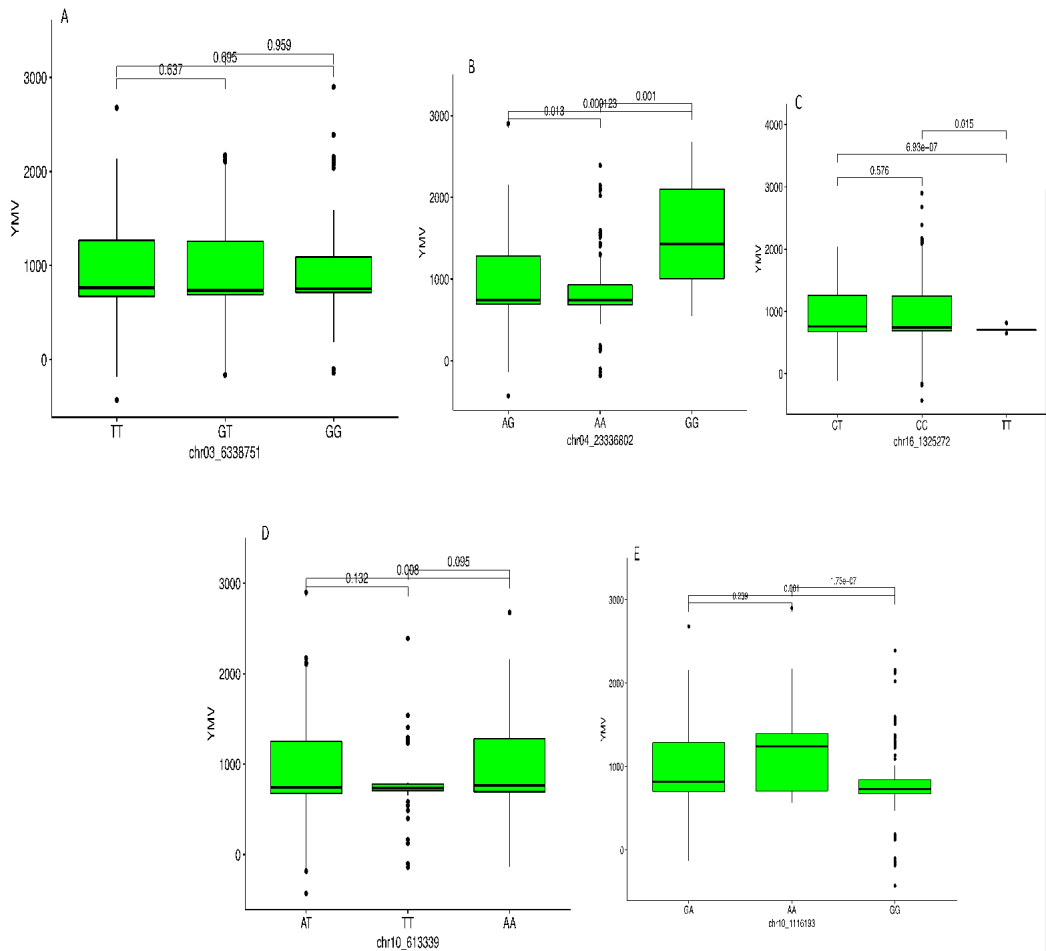
Haplotypes associated TTY: Frequency and markers prediction effect



Traits	Markers	Hap	Seq	Freq	Adjusted probability	Prob. significance
Yield	chr04_6236404	Hap1	CCCT	0.475	3.74 e ⁻⁰⁵	****
		Hap2	CCTT	0.296	7.11 e ⁻⁰⁷	****
		Hap3	CTTT	0.228	0.001	***
	chr04_8196378	Hap1	CCCT	0.481	0.218	ns
		Hap2	CCTT	0.364	0.041	*
		Hap3	CTTT	0.154	0.218	ns
	chr04_18269860	Hap1	AAAC	0.328	0.399	ns
		Hap2	AACC	0.359	0.814	ns
		Hap3	ACCC	0.312	0.814	ns
	chr04_23401186	Hap1	AAAG	0.274	0.029	*
Hap2		AAGG	0.396	0.001	***	
Hap3		AGGG	0.330	0.619	ns	
chr05_24237388	Hap1	CCCT	0.367	0.020	*	
	Hap2	CCTT	0.316	3.57 e ⁻¹¹	****	
	Hap3	CTTT	0.317	1.02 e ⁻⁰⁵	****	
chr05_24682916	Hap1	AAAC	0.295	0.921	ns	
	Hap2	AACC	0.305	0.044	*	
	Hap3	ACCC	0.400	0.043	*	
chr08_7046574	Hap1	AAAC	0.142	0.294	ns	
	Hap2	AACC	0.423	1.25 e ⁻¹¹	****	
	Hap3	ACCC	0.435	2.16 e ⁻⁰⁸	****	
chr08_10135940	Hap1	CCCG	0.217	0.363	ns	
	Hap2	CCGG	0.326	0.522	ns	
	Hap3	CGGG	0.457	0.522	ns	
chr10_1317508	Hap1	CCCT	0.363	0.079	ns	
	Hap2	CCTT	0.359	0.713	ns	
	Hap3	CTTT	0.278	0.246	ns	
chr10_1571815	Hap1	CCCT	0.144	0.873	ns	
	Hap2	CCTT	0.362	0.873	ns	
	Hap3	CTTT	0.494	0.978	ns	
chr13_13467988	Hap1	CCCT	0.364	0.912	ns	
	Hap2	CCTT	0.365	6.12 e ⁻⁰⁴	***	
	Hap3	CTTT	0.270	0.001	***	
chr14_11301309	Hap1	AAAG	0.110	0.705	ns	
	Hap2	AAGG	0.393	0.386	ns	
	Hap3	AGGG	0.498	1.01 e ⁻²⁰	****	
chr14_11128124	Hap1	CCGG	0.414	6.59 e ⁻¹⁸	****	
	Hap2	CCTT	0.192	0.242	ns	
chr15_5858214	Hap1	CCCT	0.394	0.003	**	
	Hap2	CCTT	0.315	0.057	ns	
chr17_15363223	Hap1	AAAT	0.539	1.20 e ⁻¹³	****	

GWAS result in *D. rotundata* breeding panel

Haplotypes associated YMV: frequency and markers prediction effect



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

Traits	SNP ID	Chr	Pos	Flanking sequence	GC %	FA	UA
SpTu	snpDR00165	4	2381068	GGAATTCTTGACTCCAGAAATCCCTGATGATGAGATATA TTAGCTAGTG [Y]TGCTTTGTTTTGTAATACYATGGACATATGCTGCTTGT TTTTTTCTTT	0.35	C	T
	snpDR00166	17	5305858	TTAACCTTGAGTGACCCCACTGCTAGGTCACCTCAACGG GCACACCAGAC[Y] GGTTTCATGCATCAATGGACTTTTAAATTTGAACCAGGGA AGTACTCATT	0.46	C	T
App	snpDR00167	2	23410203	AACACAGCTCCCCAGCTGCATGGGAGTTGGTYAGGTAT GGTGTGTTTGG[R] TGTATTCTTTAAAGAAKTCAGTTGCATTCCATTTAGGCC TCTCTTTCAC	0.46	Bad	Bad
	snpDR00168	11	2022871	GCCTCTTGCTTTTGCCTTCATTGATGGTATTCTTGATTT ACTTTTCTA[W] TACTAGTTAAGTAGAAAACCTTCTATTTAAGAGTTAGGTTA GAAAGTAGGC	0.31	T	A
Flower Inten	snpDR00154	11	203612	AGAAGCATGTAGCTTGCTGAAGGCTATTAATTTGTCAGTT ATCCTCTGTC[R] CCAGTTTCCATGGTCTCCTATTATTTTTGTTACTACGATT ACAACCTTAT	0.35		
	snpDR00155	11	353466	TCATATAGGGTGAGATAATACAGGTGTTTTACGGTAATAA TTCATTGGTG[S] CTTGTCATTATTTGGCAACAAAAAATAATAATATTTTT TTTTACTTA	0.34		
	snpDR00156	11	508869	CACGTGCYCTCTTAAATGACGTGCATATCTGTGATGCA AATGGAGGGG[Y] GAGCTGGTGTAAAGTGGCAACTATGGYATCAAATTCTC TCCAGGATCCT	0.46		
	snpDR00159	11	1758116	AGATGACTATCATCCAAGCATTGAAACGGTYGACCATCK TTYCCTTAACT[R] TTMTTTCACTAGGCGGATCTGGGATTACTTTATTCATCTG TTCCGCCTC	0.40		
Plant sex	snpDR00152	11	1819621	ATCAACGCATATGCCTTTTGATCCTTTTCAATTTTTTGAA AAATTTTT[Y] TTTTCTGTTTTTCTCTTTTGATGTTAATGCTTTATACTAT GGTGTATT	0.24	NA	NA
	snpDR00153	11	1892426	GAAACCCCAACAGTCAAAAAAAGGCGCCAAATTA GACTCCACCA[Y] ATATGAAAACAGAAAATCAGCAAATAAAACAAAATCACCA GCGCCTTGCT	0.34	NA	NA
Plant vigor	snpDR00151	3	880906	GCGCTGTTCTGCAAGAACCCTCTCAGCGCACCGTTGCTCM ACCTTCTCAGC[R] ATAGACGCCAAGCGGACAAGGGCTTGCATCGGATCCT CGTCTCTTGCCG	0.59	G	A
Yield	snpDR00163	7	24207228	TKATTGTTTCTCTTTGTTTRATTKAGTGTATGCCMCC GAAGGGTAAA[K] CACCAAGATTGGTAGAAGATGAGAATWGTGCAGAAAGA GTRATTAGAACC	0.39	T	G
	snpDR00164	7	24200191	TTGGTGGAAAAGCGGGTGGGAAGGTGGAGGCATGGTGA AAGAAAAGAACA[K] CTTATTATTTGTAAGACGYTTTGACTWGGTAAAACGTTG AAGTATCCCTC	0.42	T	G
YMV	snpDR00160	7	10278867	TATTATACCCTTGGAAATAACCAATATTTTGGAGAGCAAA GTGATAGATT[K] ATATTTTGCATKTATATCATTCTTTCMATTCTTGCTTGT GCTAAATAG	0.29	G	T
	snpDR00161	7	10332993	AAAAGTGGSTAAGTGTCCACAYGCCCTTGTAGCAATTC CACACAGGCAT[K] TGGATGCGCACAGCGTACTCACAGGGTACTCACACG SCCCTGTGTCTT	0.53	Bad	Bad
	snpDR00162	7	10293618	GCCATCAGTRATATTTGAATTTAAAATTAGCAGCCTCC CGTTTGCCTA[W] WAAGAGTTCTCATTGCTCCCAAGAGGATTCCAGTAAGC CACTTAAGCA	0.39	A	T

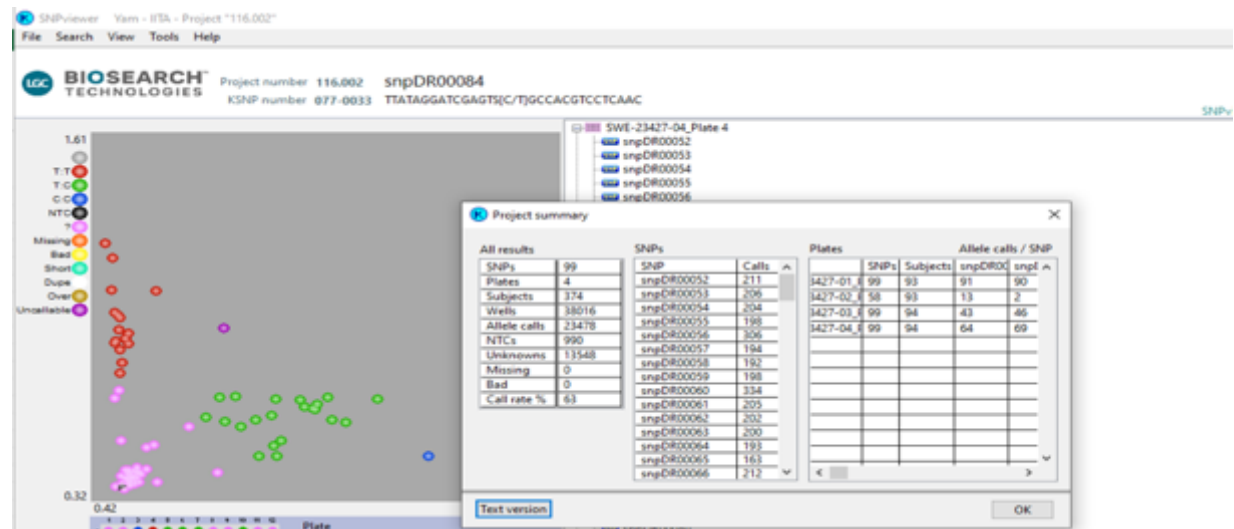
Markers validation and deployment

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

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

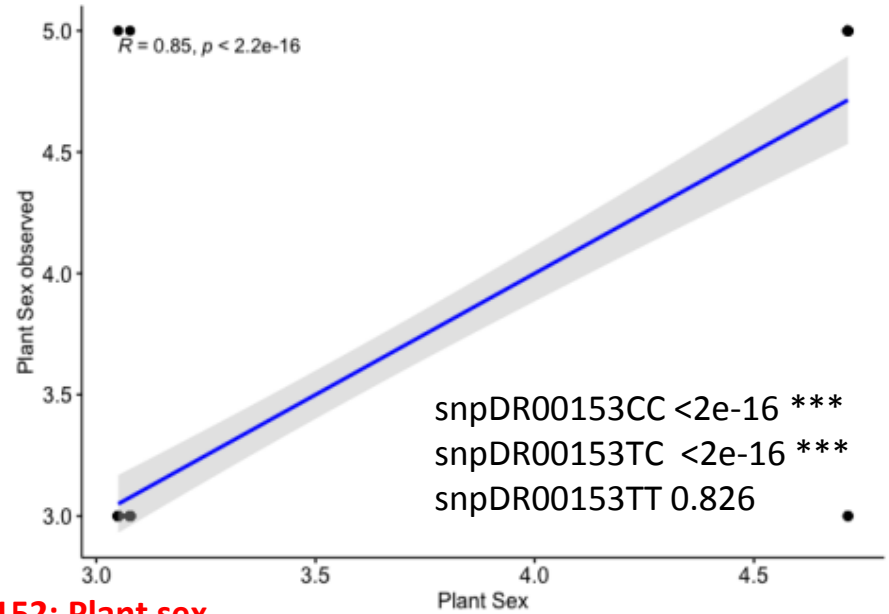
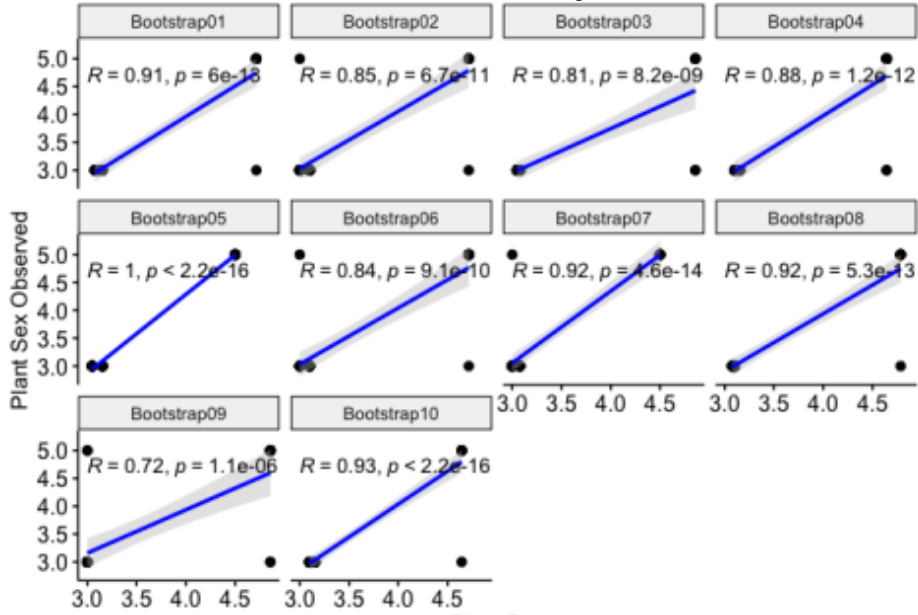
Flanking sequencing around the target region associated with each trait was developed and sent to INTERTEK for conversation into KASP-PCR

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

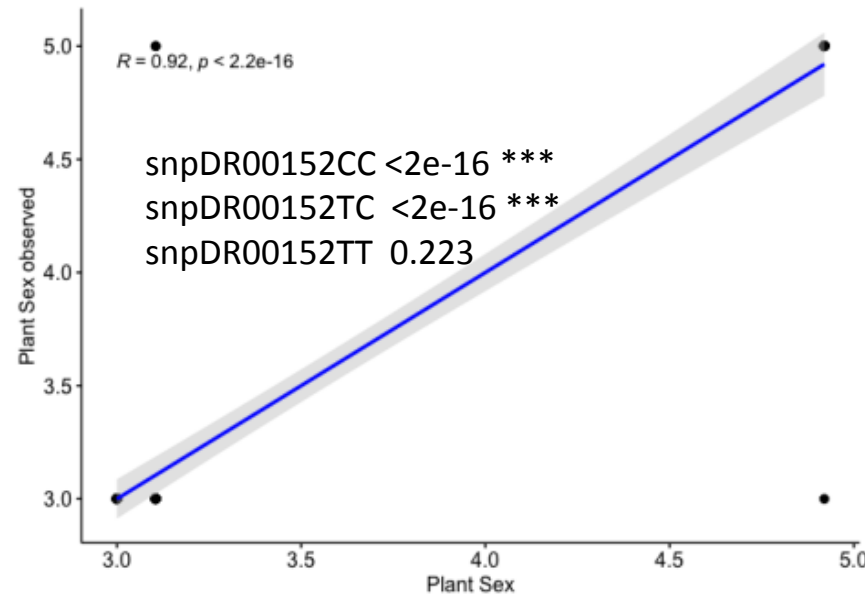
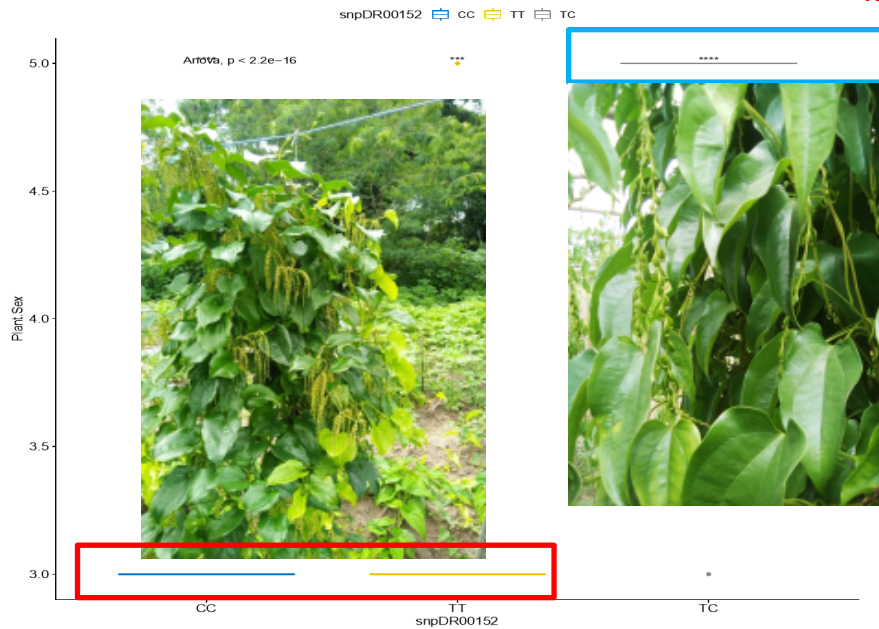


Primary Outcome 2: Methods and Tools

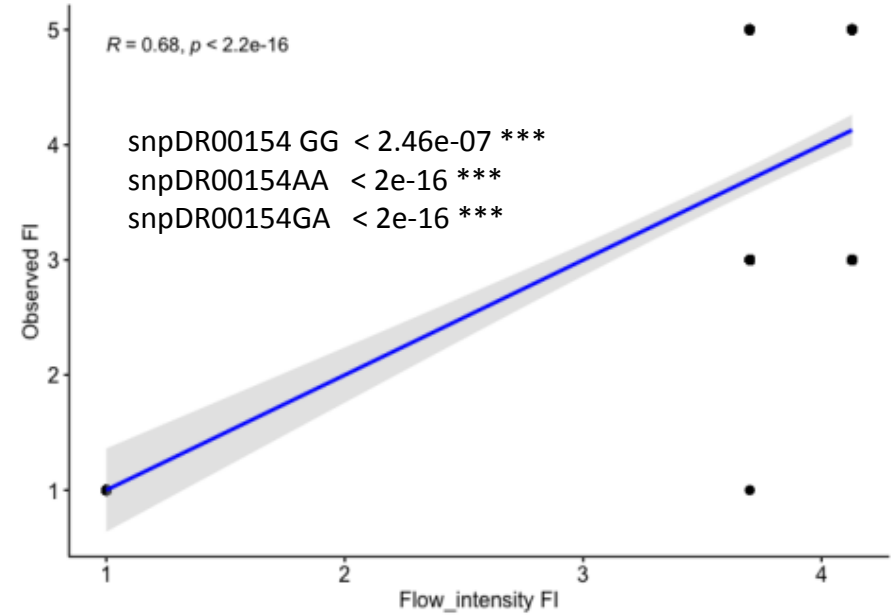
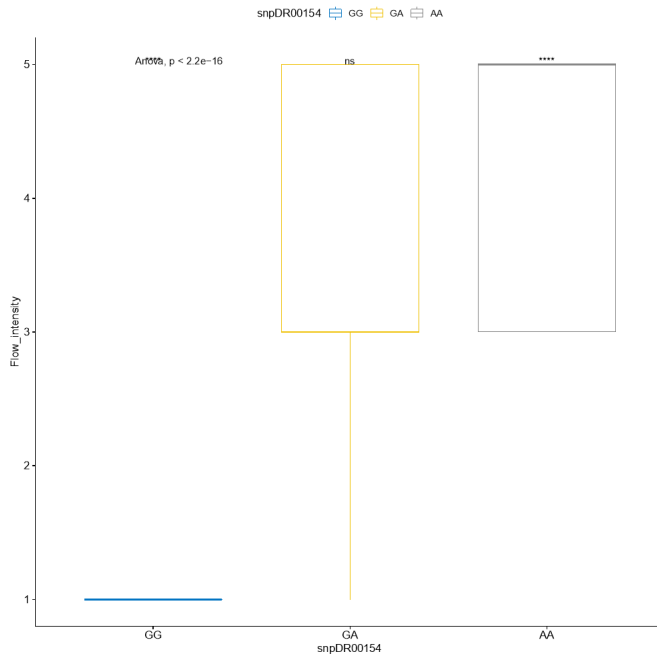
snpDR00153: Plant sex



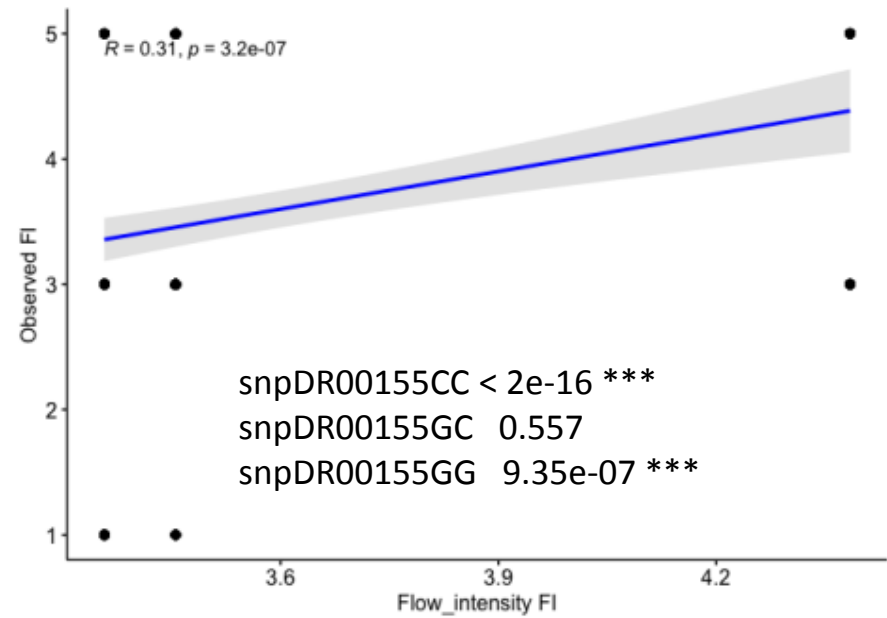
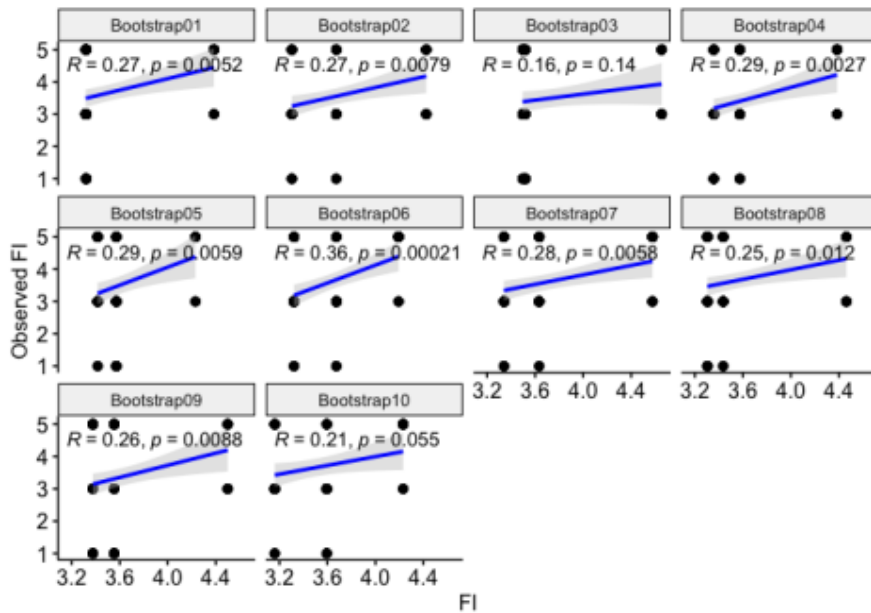
snpDR00152: Plant sex



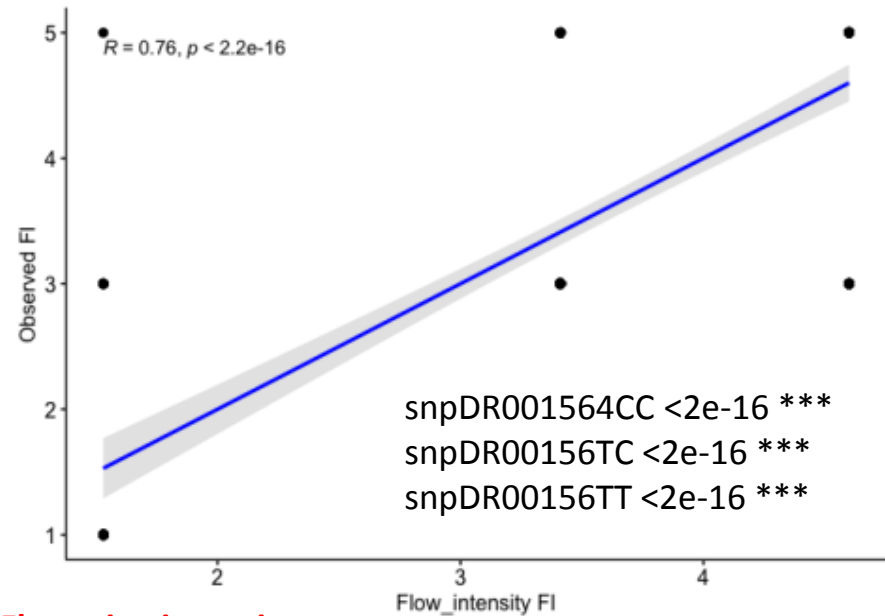
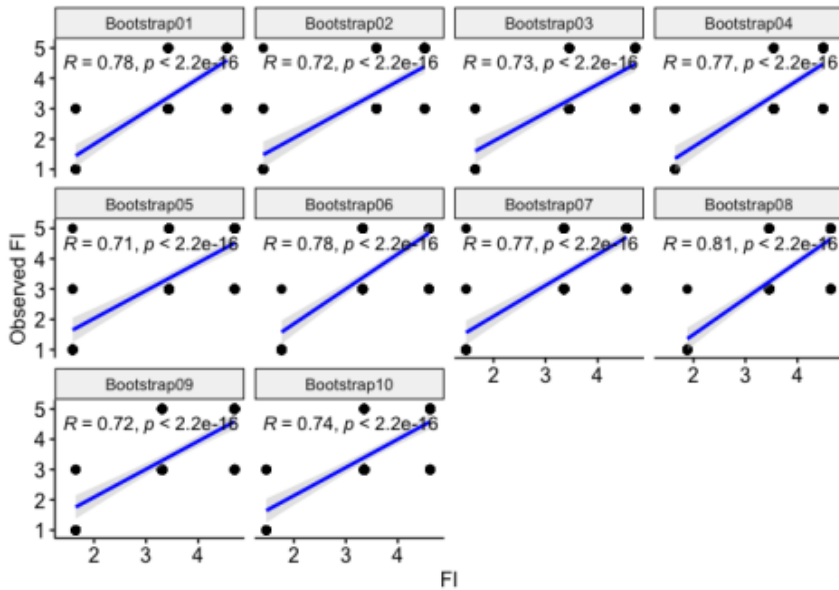
snpDR00154: Flowering intensity



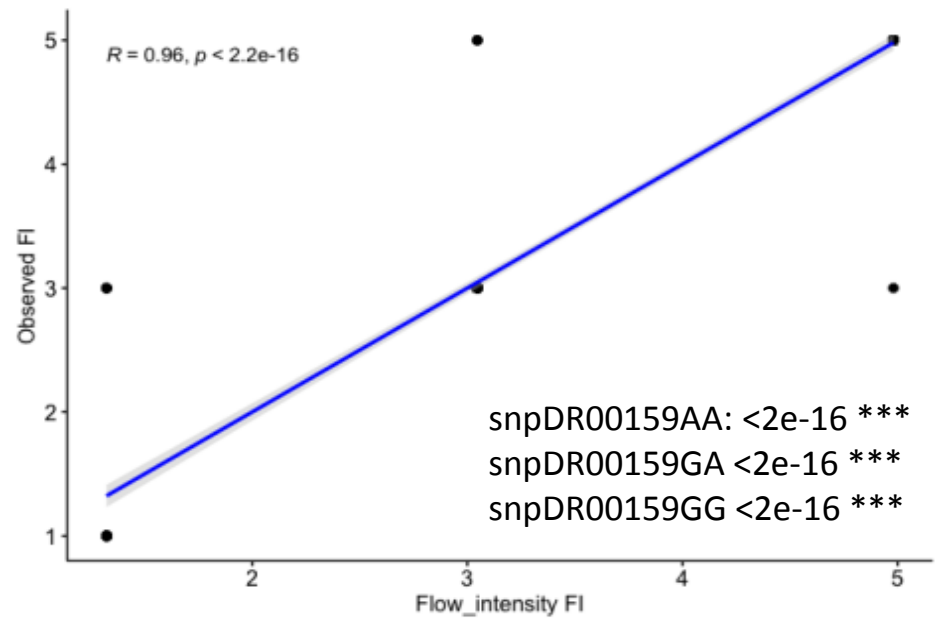
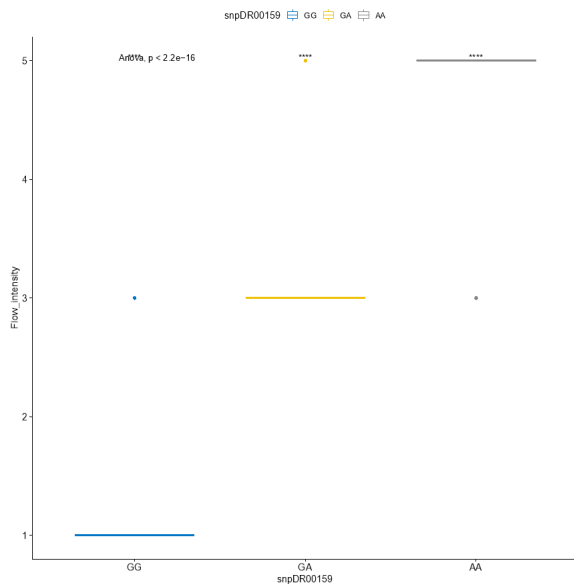
snpDR00155: Flowering intensity



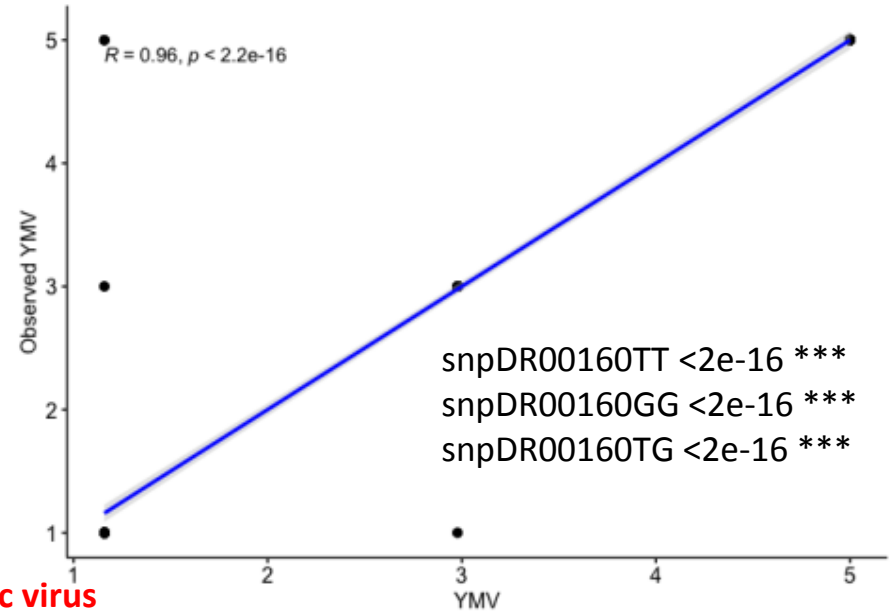
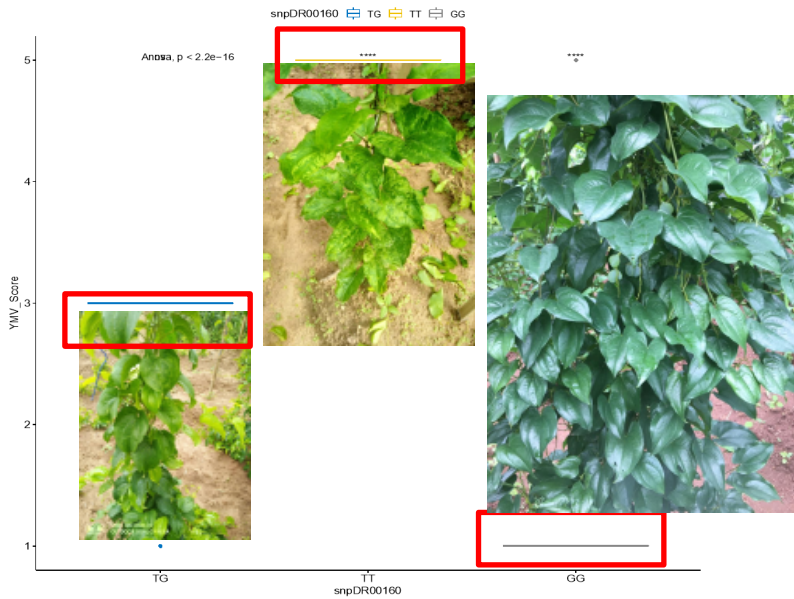
snpDR00156: Flowering intensity



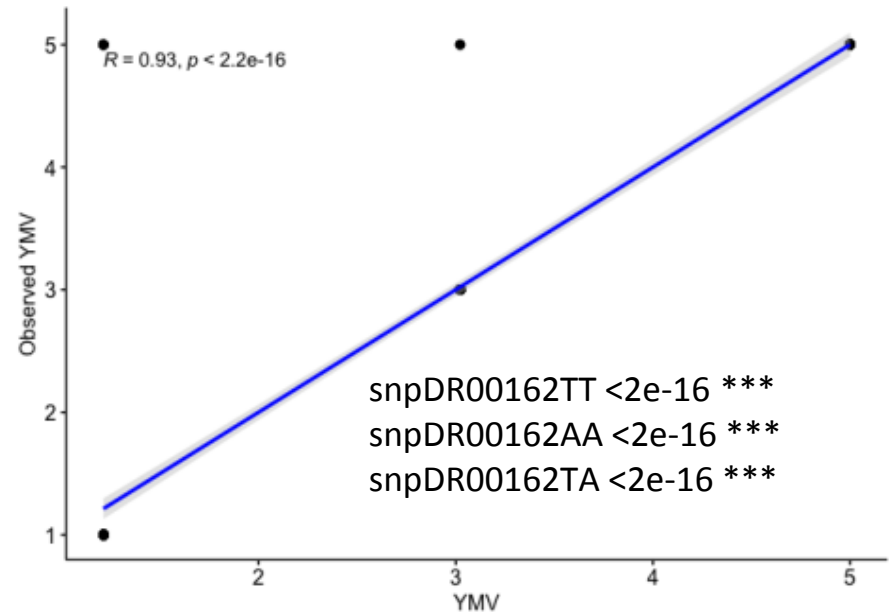
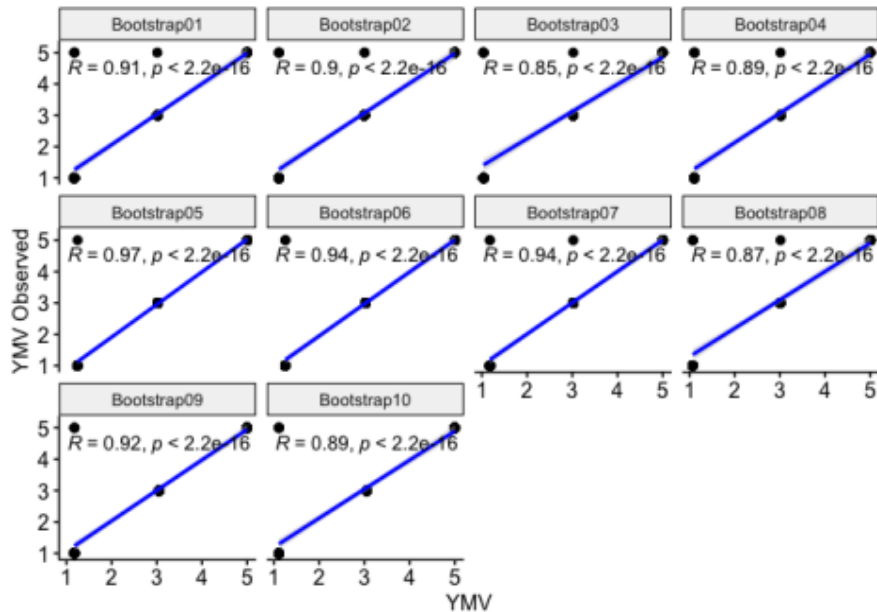
snpDR00159: Flowering intensity

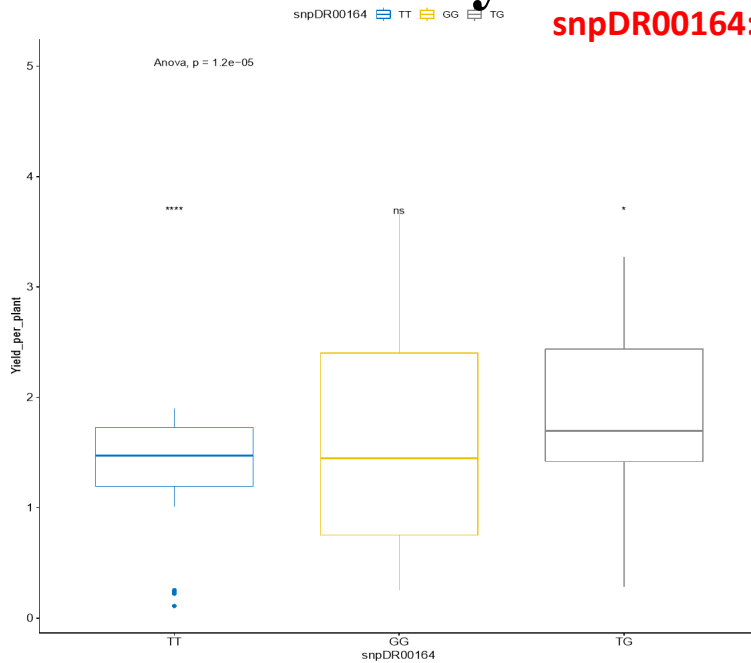


snpDR00160: Yam mosaic virus

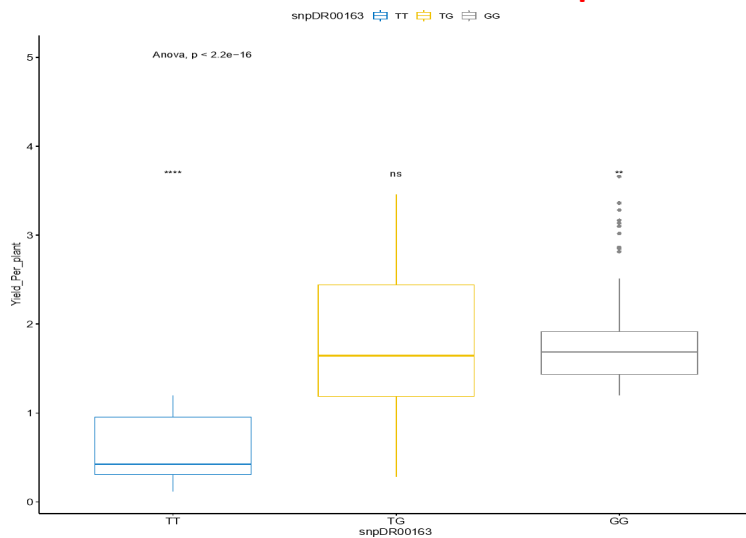
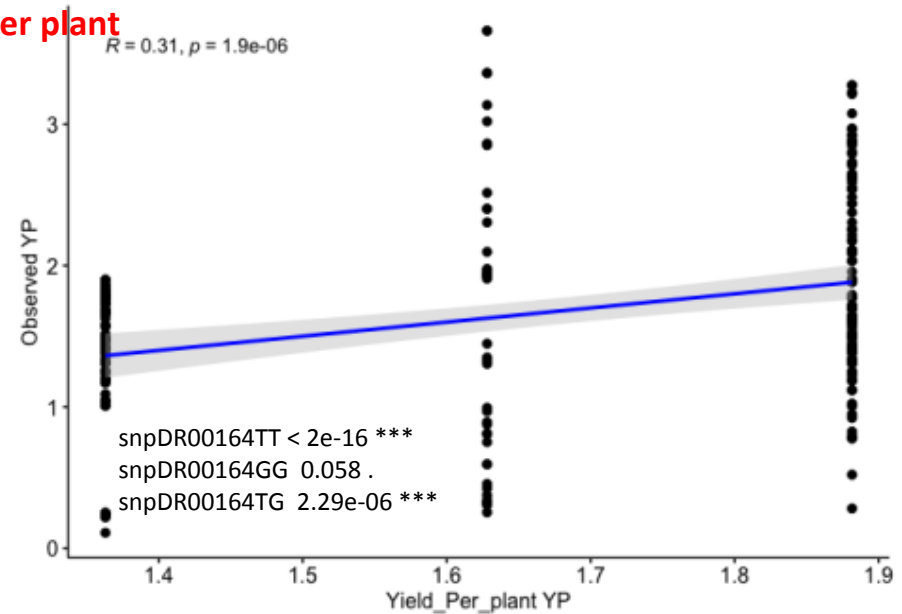


snpDR00162: Yam mosaic virus

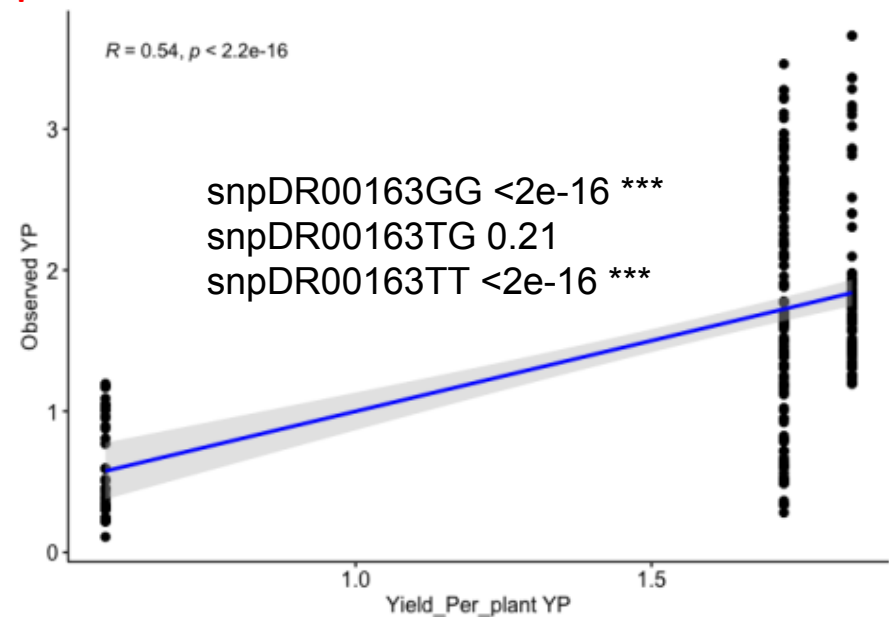




snpDR00164: Yield per plant



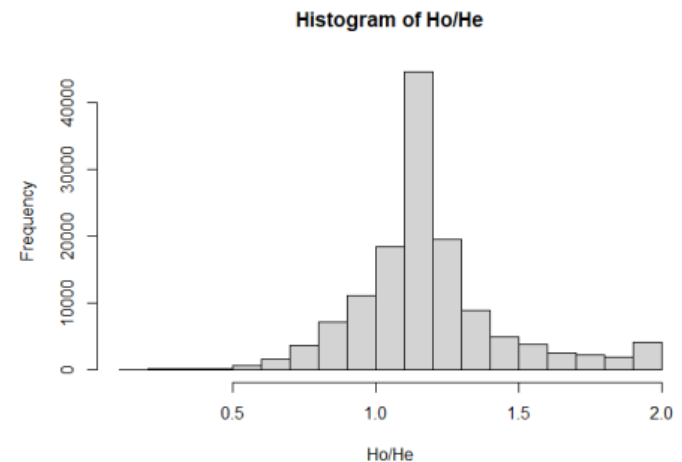
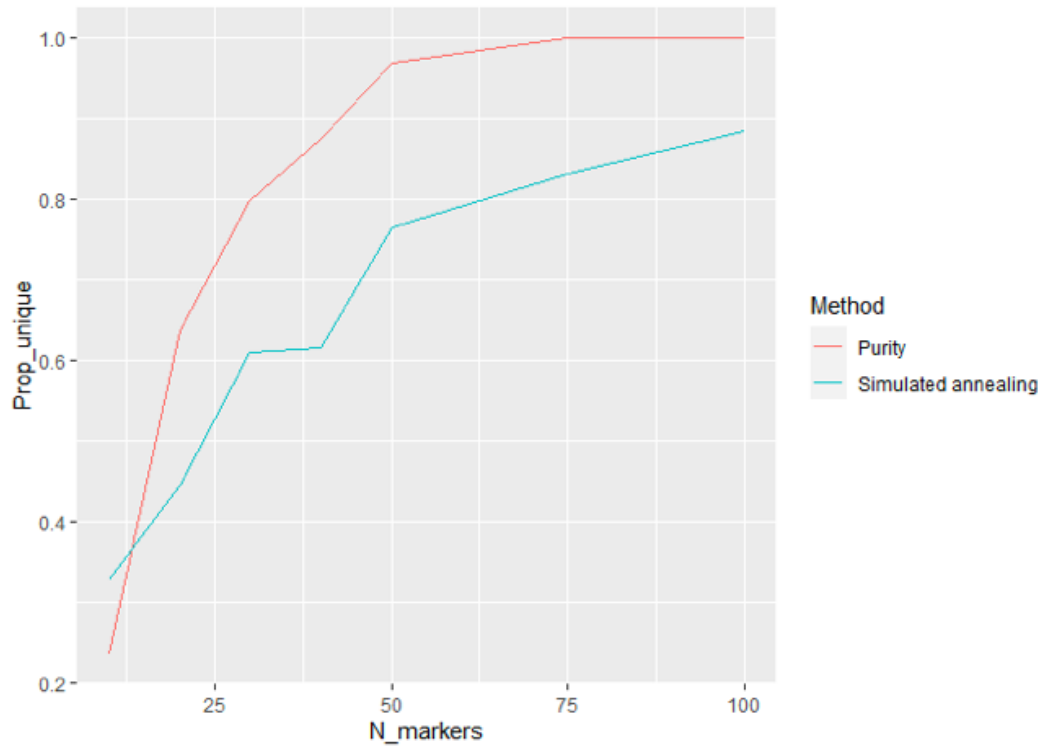
snpDR00163: Yield per plant



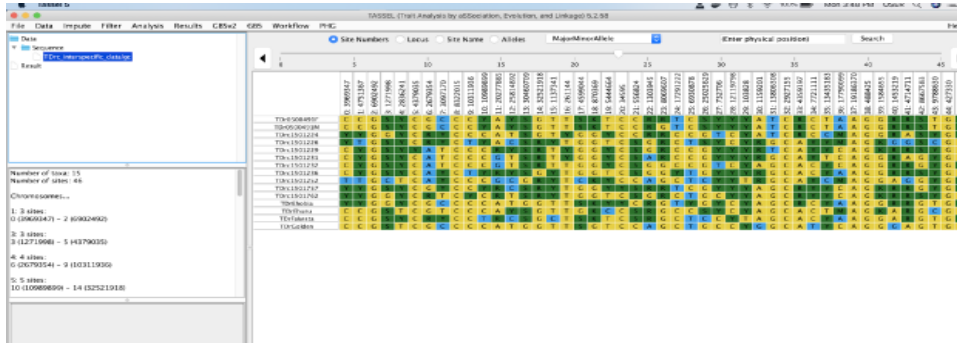
2.1.3. Molecular tool-kits available for routine use (quality control and assurance) in yam breeding

Milestone: Ultra low SNP markers (at least 50) for QA/QC selected from the previous data IITA

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

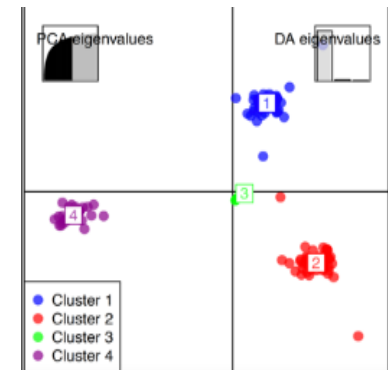
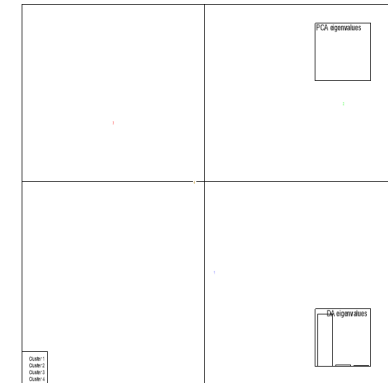
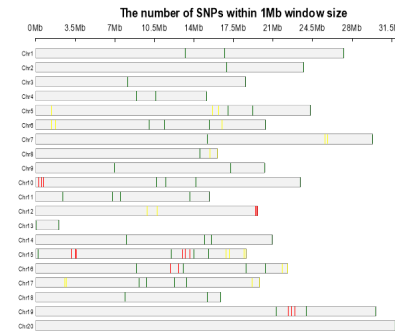
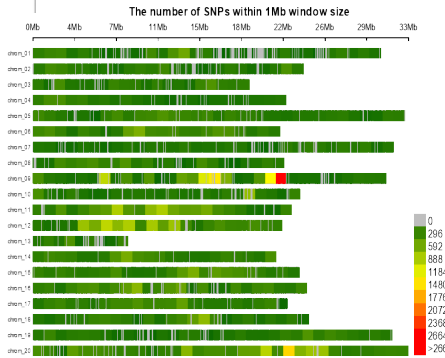


QC Marker selection procedure



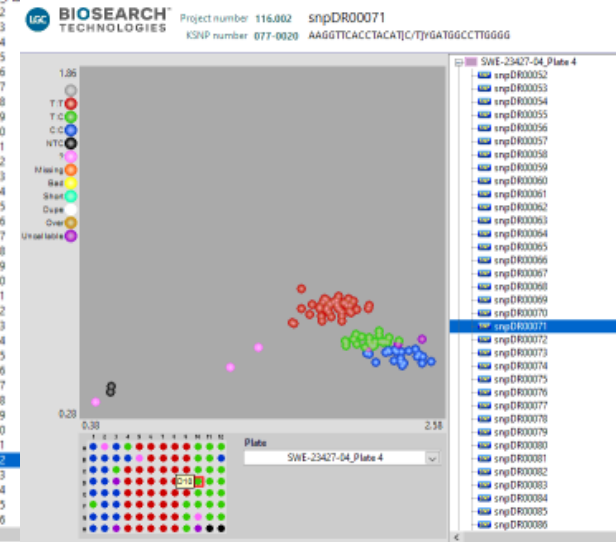
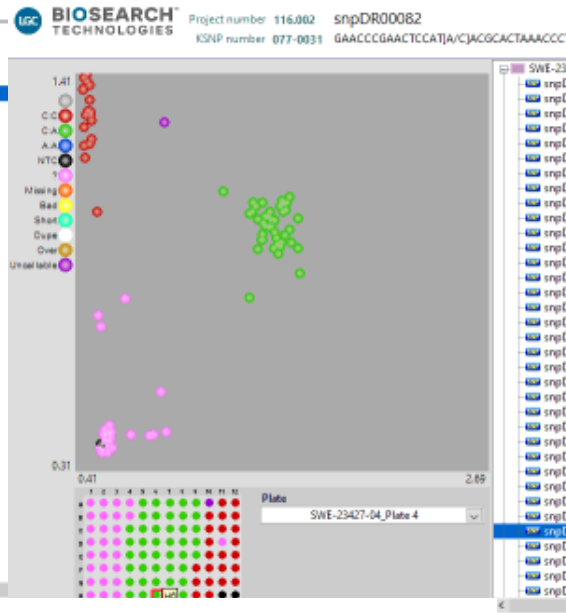
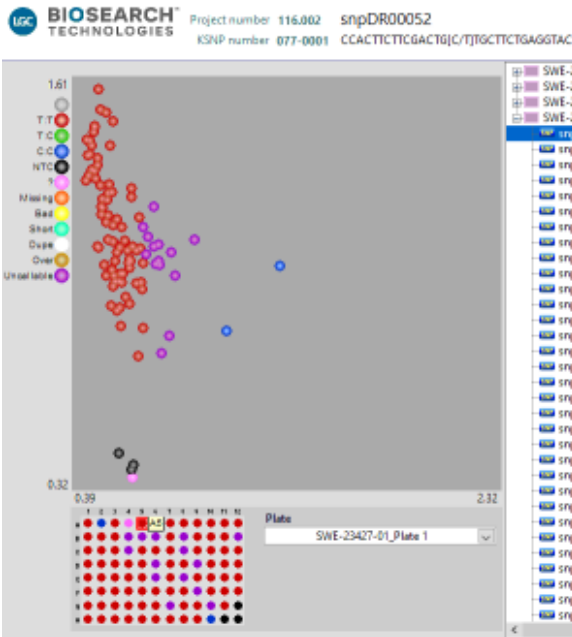
99 SNP markers well distributed across the genome have been selected and successfully converted to KASP markers and are yet to be validated in a diversity panel for QC/QA usage

- 374 divers clones representing *D. alata*, *D. rotundata*, *D. prehensilis*, *D. esculenta* *D. cayennensis* sent to INTERTEK for validation



Primary Outcome 2: Methods and Tools

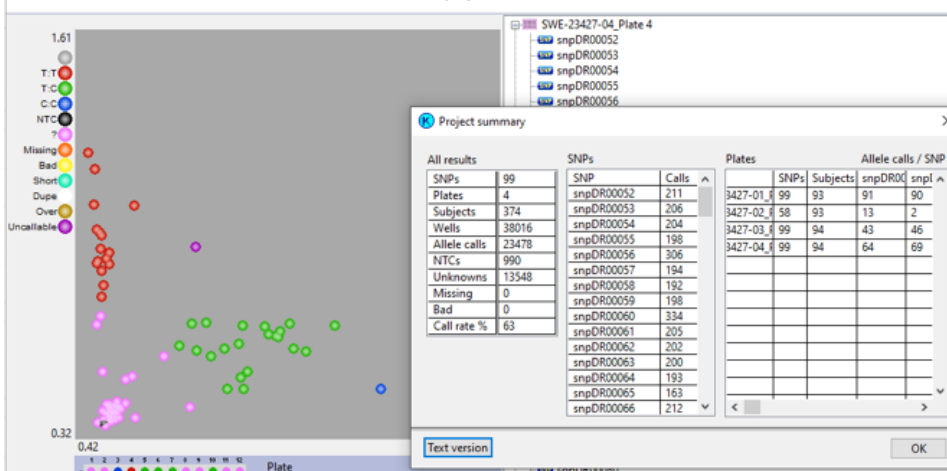
SNP markers quality view



SNP-viewer Yam - IITA - Project "116.002"

File Search View Tools Help

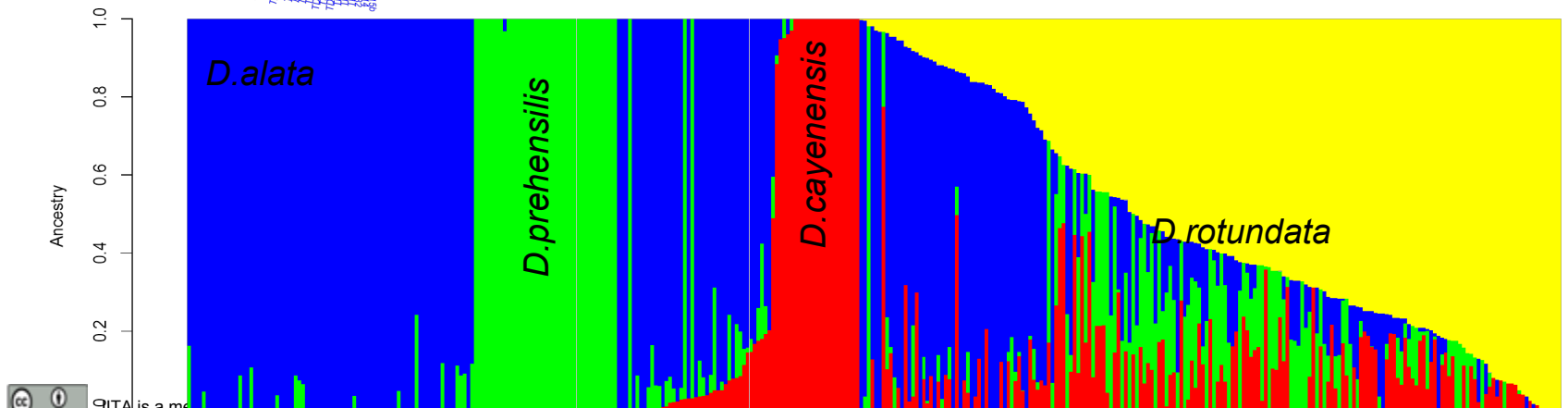
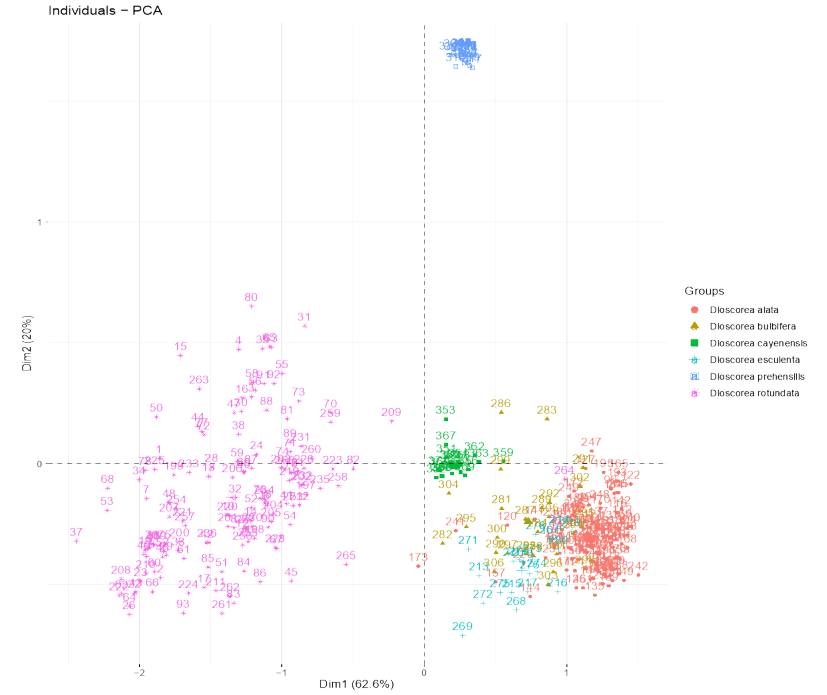
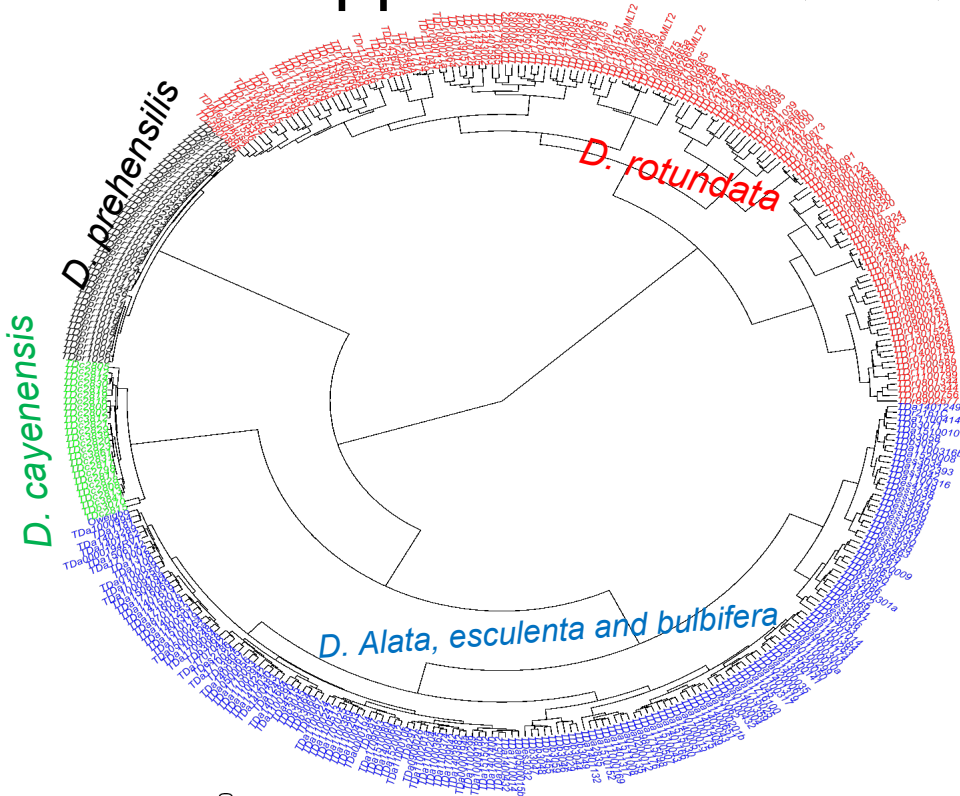
BIOSEARCH TECHNOLOGIES Project number 116.002 snpDR00084
KSNP number 077-0033 TTATAGGATCGAGT[C/T]GCCAGCTCTCAAC



In general, high-quality data was obtained

Primary Outcome 2: Methods and Tools

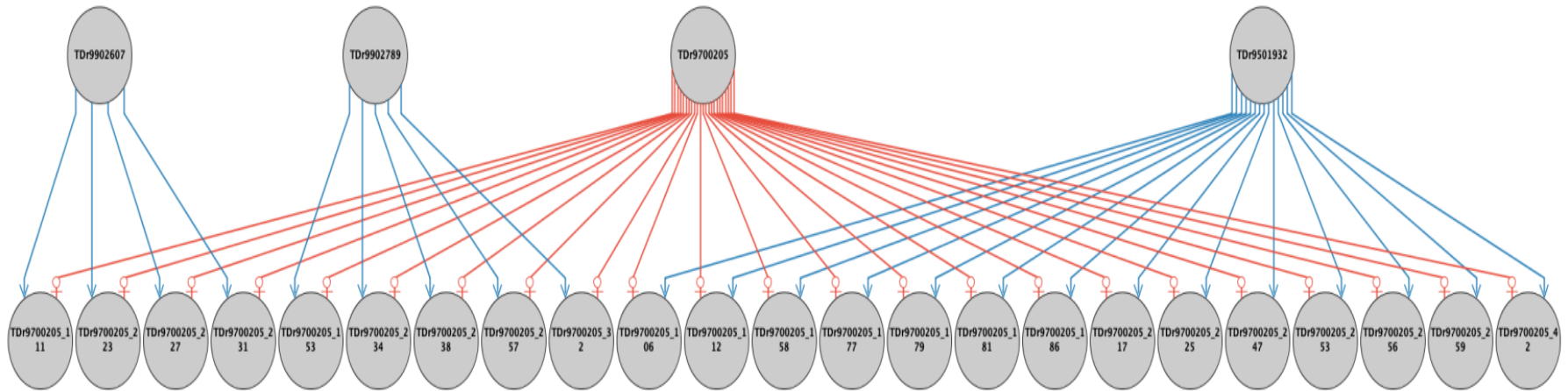
Application of QC/QA marker in yam breeding



Primary Outcome 2: Methods and Tools

Application of QC/QA marker in yam breeding

- Pedigree verification and reconstruction



Application of QC/QA marker in yam breeding

- Fourteen SNP selected for varietal tracking, verification
- Selected of advanced trials (APT, NPT, RVT, VVT)
- Six plants selected per plot and rep across various locations'
- Disc leave sent to INTERTEK

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
2022VVT_IWO_104	TDr8902665	TC	TT	GC	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
2022VVT_EDE_4	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrNPT2_2022Ubiaja_6	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrNPT2_2022Ubiaja_28	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	GA	TC	TC	TC
TDrRVT2022Ubiaja_116	TDr8902665	TC	TT	GG	TC	GA	TC	GG	TC	TT	AA	TC	CC	CC

Yam Breeding Unit
Bioscience IITA Ibadan
Polyploidy group
Excellence in Breeding
INTERTEK
University of Illinois
AfricaYam Partners'

BILL &
MELINDA
GATES
foundation



Thank you

