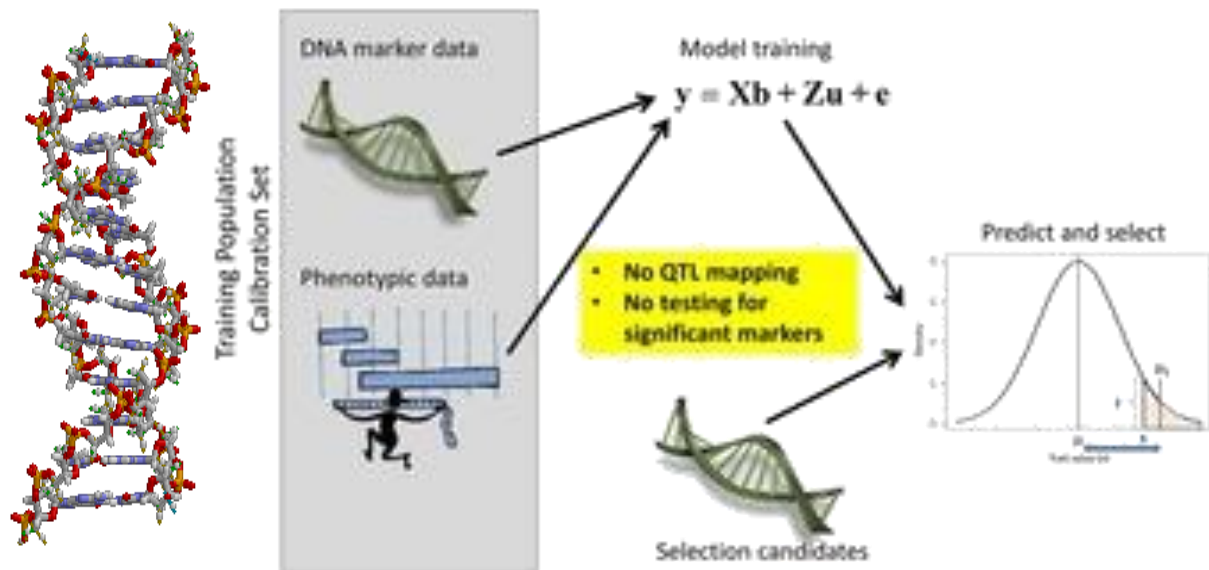


Accelerating genetic gains in potatoes through genomics-led breeding



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The Potato

Originated in Andean region

Domesticated ~ 8,000 years ago

Third most important food crop

Petota section has >100 tuber bearing species

Important cultivated species

S. tuberosum Chilotanum Group (long day adapted)

S. tuberosum Andigenum Group (short day adapted)

Complex Genetics

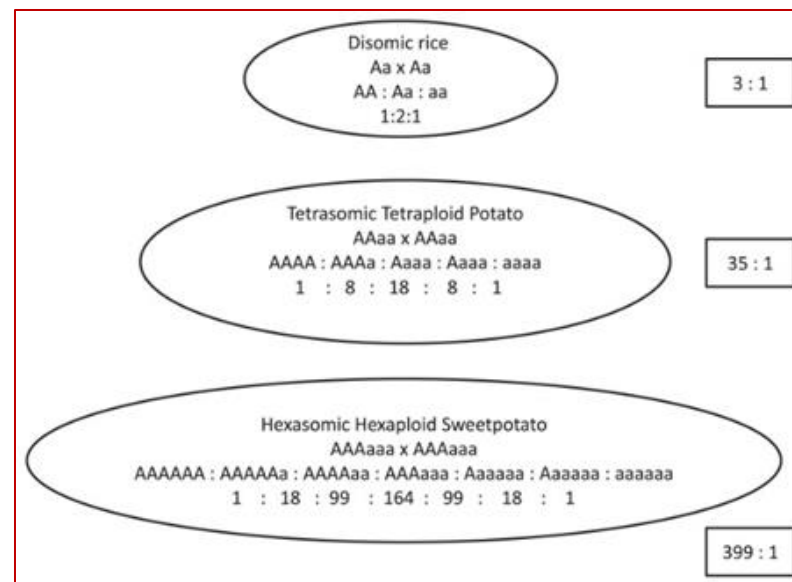
***Solanum tuberosum* ($2n=4x=48$)**

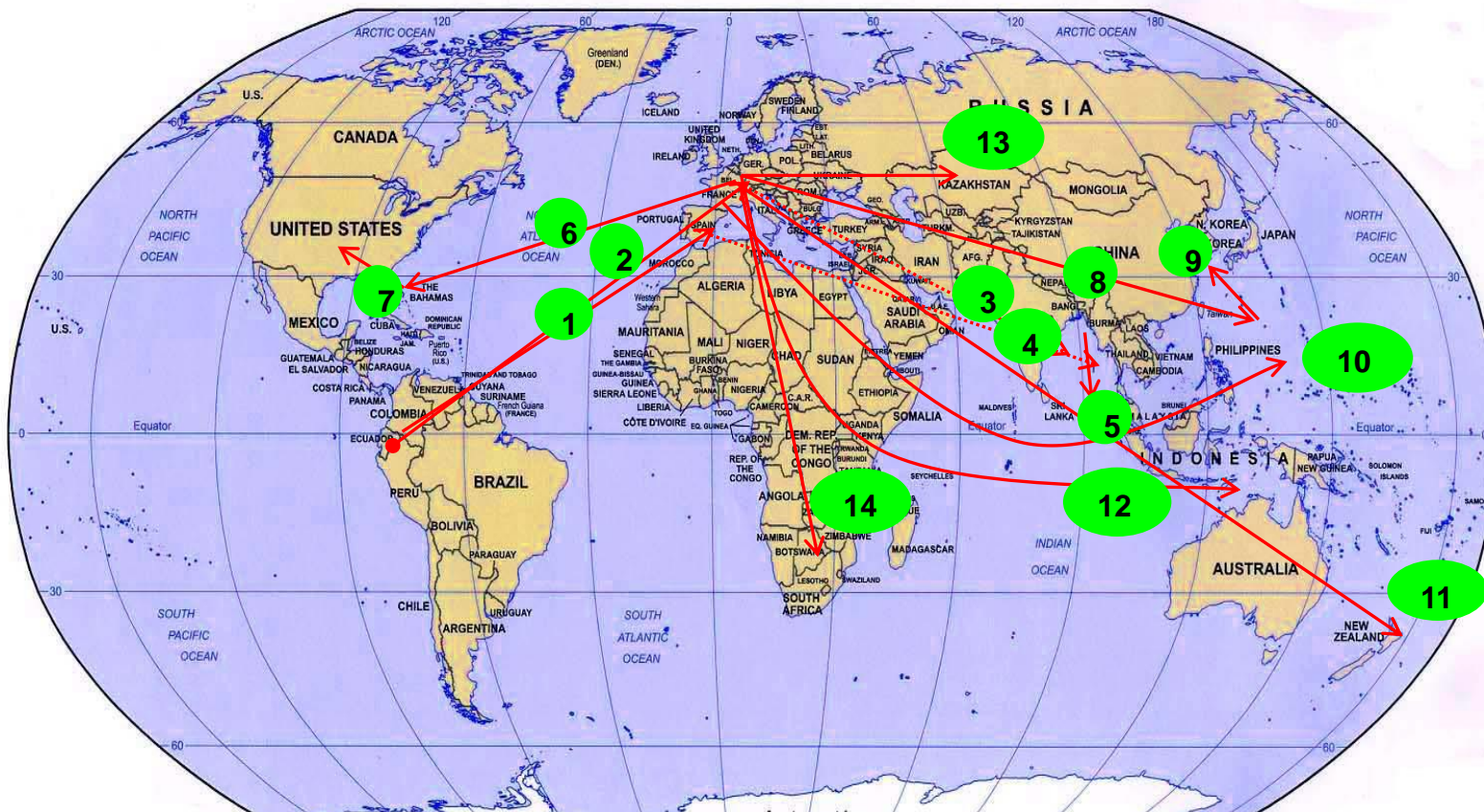
Genome size= ~850Mb

Autotetraploid

Vegetatively propagated

Heterozygosity





Potato's journey from centre of its origin

- South America (Centre of origin)
- 1. South America → Spain 1570
- 2. South America → UK 1590
- 3. UK → India <1610
- 4. Portugal → India <1610
- 5. India → Sri Lanka <1610
- 6. UK → Bermuda 1613
- 7. Bermuda → Virginia, USA 1621
- 8. Holland → Taiwan <1650
- 9. Taiwan → China <1650
- 10. Spain → Philippines <1700
- 11. UK → New Zealand 1773
- 12. Holland → Java 1794
- 13. Holland → Russia <1800
- 14. UK → South African continent 1830

Production

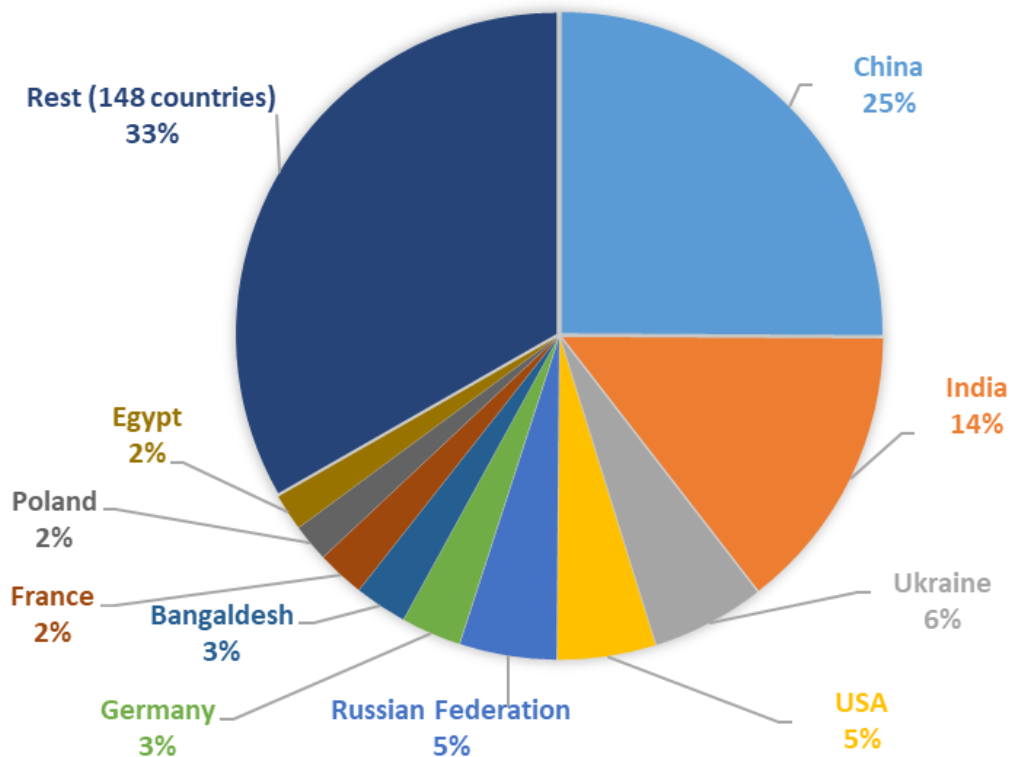
World: 376 million tonne

Asia + Europe: ~ 80%

India

53.03 million tonnes

25 t/ha



~50% consumed as fresh food

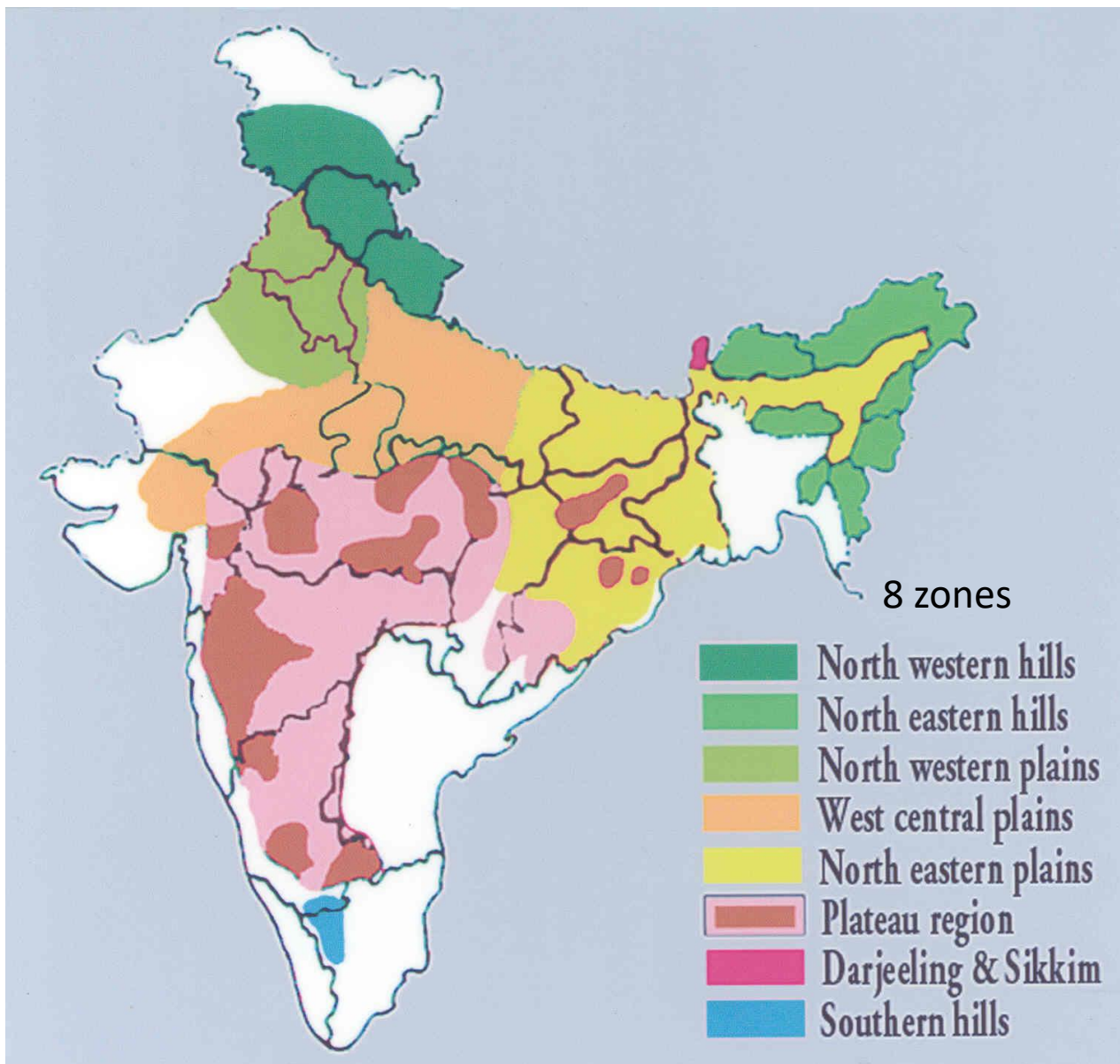


- **Sub-tropical crop**
- **Predominant vegetable**
- **Fresh consumption**
- **Growing processing sector**
- **Inadequate storage capacity**

Indian Scenario

- India is producing **53.0m** tons from 2.2 m ha at an average productivity of **25t/ha**
- **4.5m tons (8.5%) of the produce is used as seed.**
- **5.3m tons (~10%) of the produce is processed.**
- **0.5m tons exported (in 2022)**
- **Post-harvest losses are nearly 20% of the total produce**

Agro-ecological zones of the country



- Organized research started in 1935
- ICAR-CPRI established in 1949
- Headquarter shifted to Shimla in 1956
- First indigenous variety released in 1958
- Seed Plot Technique in 1960s
- Nucleus Seed Production at Kufri (Fagu) in 1963
- Seed Production Stations: Jalandhar 1969, Daurala (Meerut) 1971, Kodiakanal 1975, Gwalior 1979



Central Potato Research Institute, Shimla (CPRI)

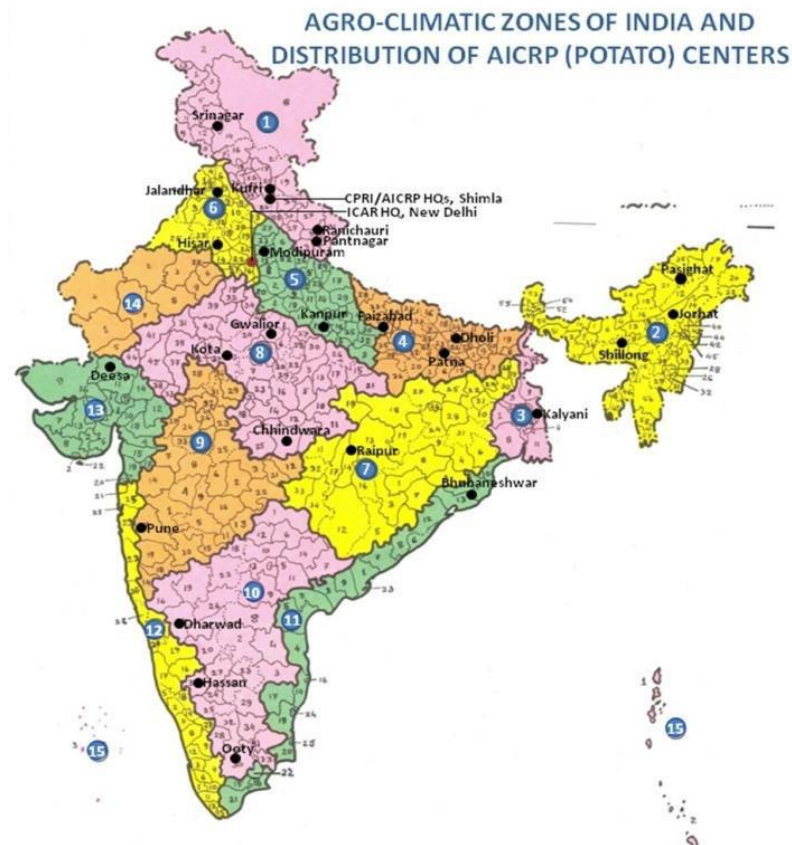
6 research centres

- CPRIC, Modipuram, Meerut (UP)
- CPRS, Jalandhar (Punjab)
- CPRS, Gwalior (MP)
- CPRS, Patna (Bihar)
- **CPRS, Kufri-Fagu, Shimla (HP)**
- CPRS, Ooty (Tamilnadu)
- CPRS, Shillong (Meghlaya)

All India Coordinated Research Project Potato (AICRP), 1970

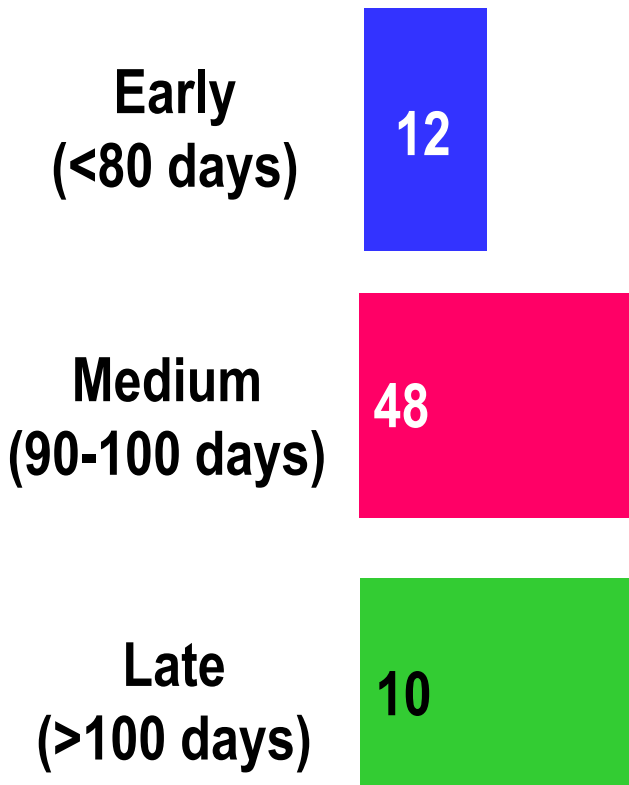
has headquarter at CPRI, Shimla has a nationwide network of **25**

centers (7 CPRI based centers, 17 SAU based centers and 1 Voluntary center)

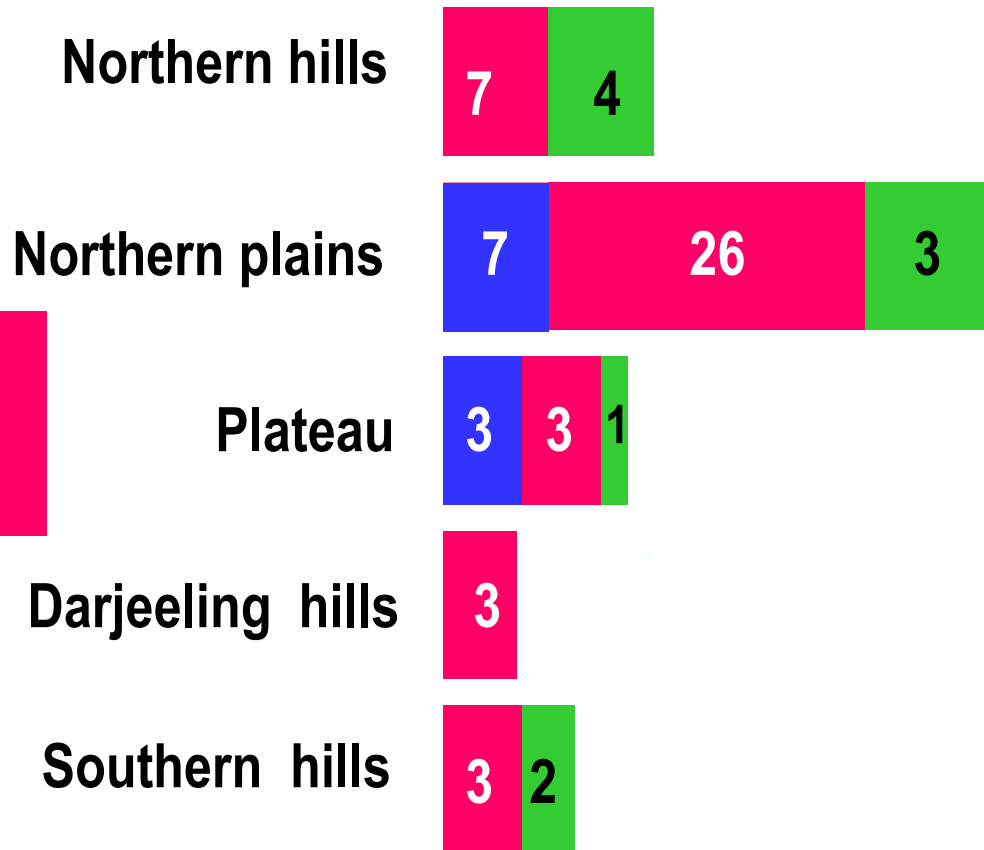


Varieties Developed: 70

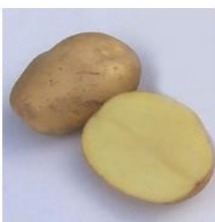
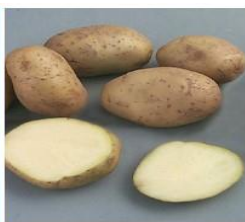
Varieties as per duration



Varieties as per adaptability



Varieties with special attributes: Processing-7; Heat tolerance-3



Work done with EiB

- **Genetic gain - potato breeding in India**
- **Low-density genotyping for forward breeding**
- **Mid-density genotyping for genomic selection**

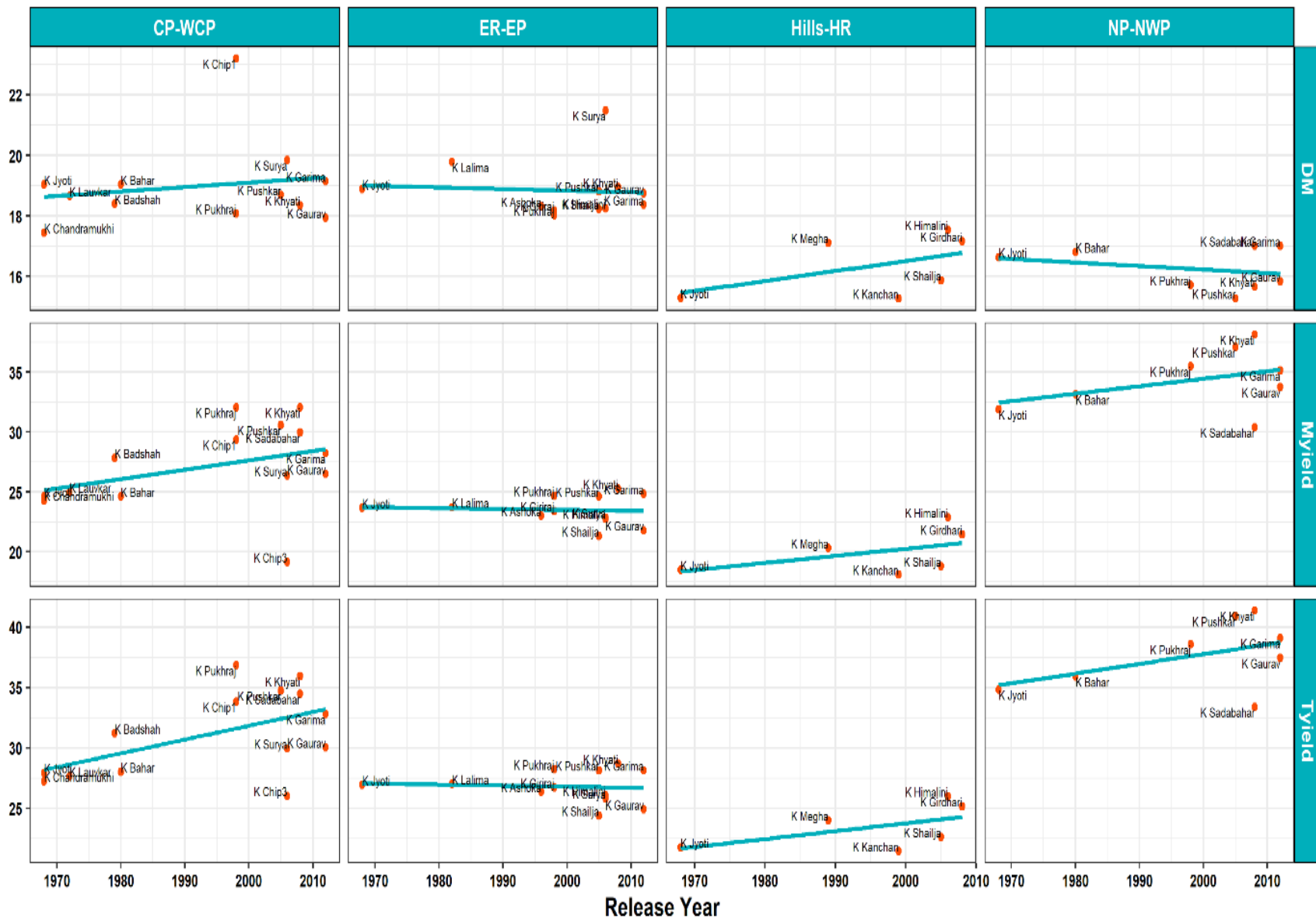
Realized Genetic gains in ERA Trials

- Twenty-two potato varieties released in different decades from 1968-2012
- Evaluated for three consecutive years (2014-15 to 2016-17) in four potato-growing zones of the country

Zone	Varieties	Locations	Trait	Base Predicted Mean	Relative Genetic Gain (%)
NWP	8	4	Total tuber yield	35.11	0.230
			Marketable tuber yield	32.52	0.192
			Dry matter	16.69	-0.070
WCP	13	6	Total tuber yield	28.26	0.404
			Marketable tuber yield	25.23	0.308
			Dry matter	18.68	0.079
EP	12	7	Total tuber yield	27.05	-0.031
			Marketable tuber yield	23.66	-0.032
			Dry matter	19.09	-0.028
HR	6	2	Total tuber yield	21.67	0.302
			Marketable tuber yield	18.46	0.320
			Dry matter	15.42	0.214

NWP-North-Western Plains; WCP-West Central Plains; EP-Eastern Plains; HR-Hills Region

Realized Genetic gains in ERA Trials



DM

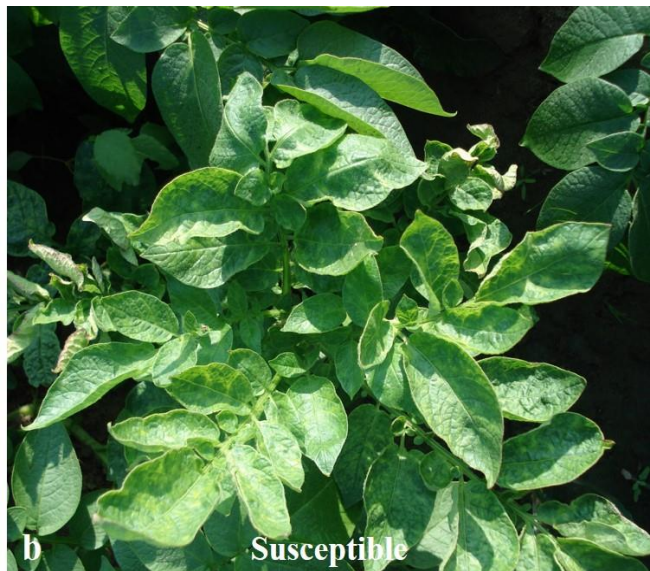
Myield

Tyield

Release Year

Several biotic stresses hamper quantity and quality of tuber production

- Late blight
- Viruses – PVY
- PCN

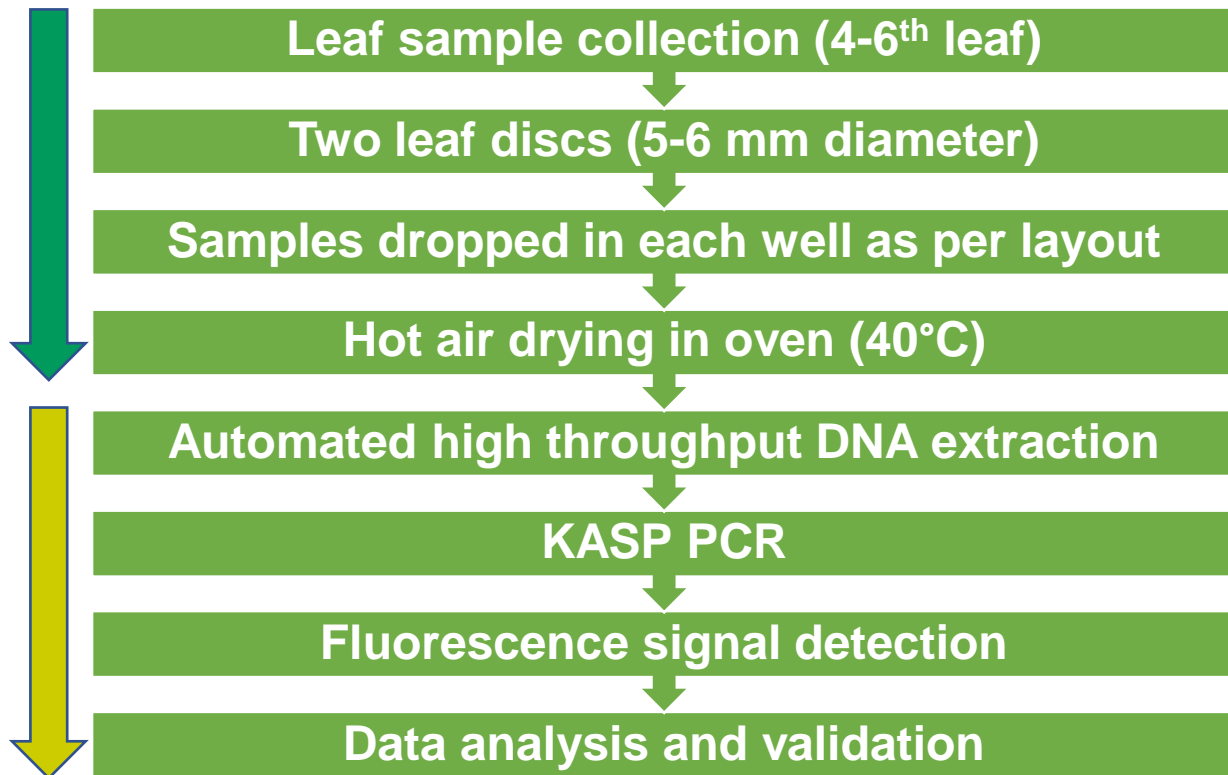


Low density genotyping –KASP markers

- ✓ SNP KASP markers for late blight, PVY, PCN and common scab resistant genes were designed and used
- ✓ A set of 1447 potato accessions were used for screening
- ✓ Phenotypic data on late blight, PVY and PCN recorded earlier at Shimla, Kufri, Shillong and Ooty over the years was used for validation

Trait	Gene	Number
Late blight	R2, R8-QTL, unknown genes	17
PVY	Ryadg, Rysto, Ny(o,n)sto	5
Potato Cyst Nematode	H1, H2, H3, H6, Pa2/3	20
Plant Maturity & MCR	-	17
Chip colour	-	1
Common Scab	-	10

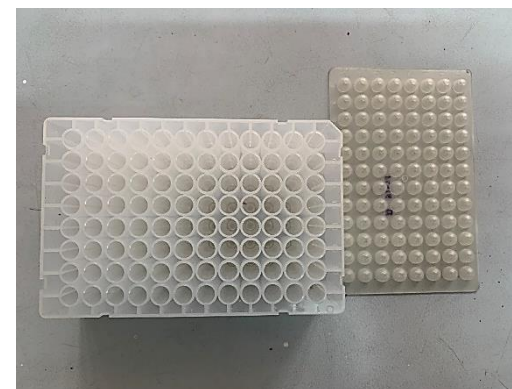
Flow chart of KASP analysis



Puncher



Deep well plates



Markers Validation

SNP ID	Marker	Trait	Resistant Allele	Susceptible allele	Gene associated
snpST00020	S9_61261167	Late blight	C	A	R8-QTL
snpST00023	solcap_snp_c2_56418	Late blight	G	T	R8-QTL
snpST00052	M6F1R4_711	PVY, Ryadg	A	G	Ryadg
snpST00073	M6F1R4_817	PVY, Ryadg	G	A	Ryadg
snpST00082	YES3_a	PVY, Rysto	T	G	Rysto
snpST00083	YES3_b	PVY, Rysto	DEL	INS	Rysto
snpST00094	CPRISNP01	PCN	A	G	H2 (Pa1)
snpST00106	CPRISNP13	Late blight	CGAAA	TGATT	R2
snpST00107	CPRISNP14	PVY, Rysto	CAATTCC	TAATTCT	Ny(o,n)sto

Allele calls of KASP assays for late blight, PVY and PCN

Trait & Gene/QTL	SNP ID	Allele/call	Count	Freq (%)
Late blight R2	snpST00106	CGAAA:CGAAA	10	0.7
		CGAAA:TGATT	165	11.2
		TGATT:TGATT	1301	88.1
Late blight R8-QTL	snpST00023	G:G	13	0.9
		G:T	579	39
		T:T	892	60.1
PVY Ny(o,n)sto	snpST00107	CAATTCC:CAATTCC	35	2.4
		CAATTCC:TAATTCT	128	8.7
		TAATTCT:TAATTCT	1301	88.9
PVY Ryadg	snpST00052	A:A	1	0.1
		G:A	159	10.8
		G:G	1308	89.1
PVY Rysto	snpST00082	T:T	27	1.8
		G:T	1	0.1
		G:G	1459	98.1
PCN H2	snpST00094	A:A	2	0.1
		A:G	208	14
		G:G	1271	85.8

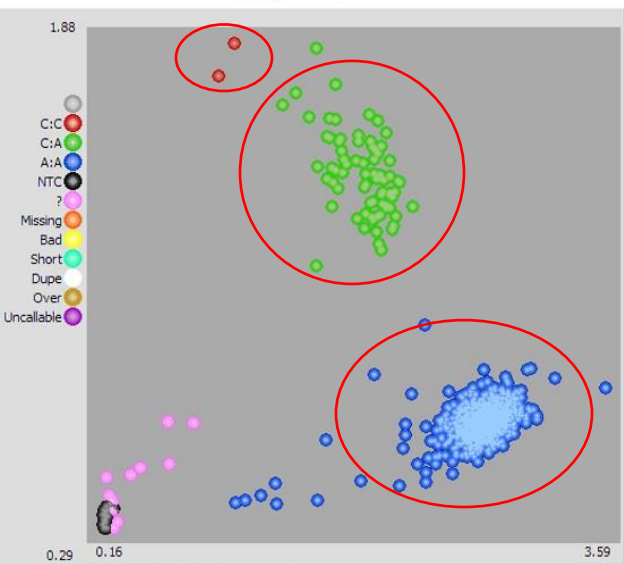
Validation of KASP markers with phenotype

Gene/QTL	Marker	Genotype (type of allele)	No. of accessions		
			R	MR	S
Late blight					
R2	snpST00106	Favourable (CGAAA:CGAAA)	3 (0.32)	4 (0.43)	0 (0)
		Heterozygous (CGAAA:TGATT)	31 (3.35)	24 (2.59)	47 (5.08)
		Unfavourable (TGATT:TGATT)	117 (12.63)	146 (15.77)	554 (59.83)
R8-QTL	snpST00020	Favourable (C:C)	0 (0)	2 (0.22)	0 (0)
		Heterozygous (C:A)	14 (1.51)	10 (1.08)	17 (1.84)
		Unfavourable (A:A)	135 (14.59)	162 (17.51)	585 (63.24)
R8-QTL	snpST00023	Favourable (G:G)	2 (0.22)	4 (0.43)	1 (0.11)
		Heterozygous (G:T)	62 (6.68)	59 (6.36)	247 (26.62)
		Unfavourable (T:T)	88 (9.48)	112 (12.07)	353 (38.04)

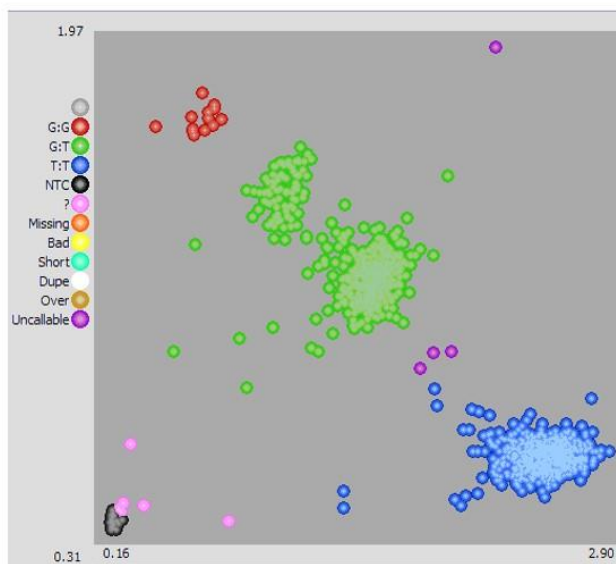
- Rapid, high throughput diagnostic markers for MAS
- KASP assays for late blight and PVY demonstrated a good diagnostic potential
- Effective for screening large potato germplasm collection

Late Blight KASP assay

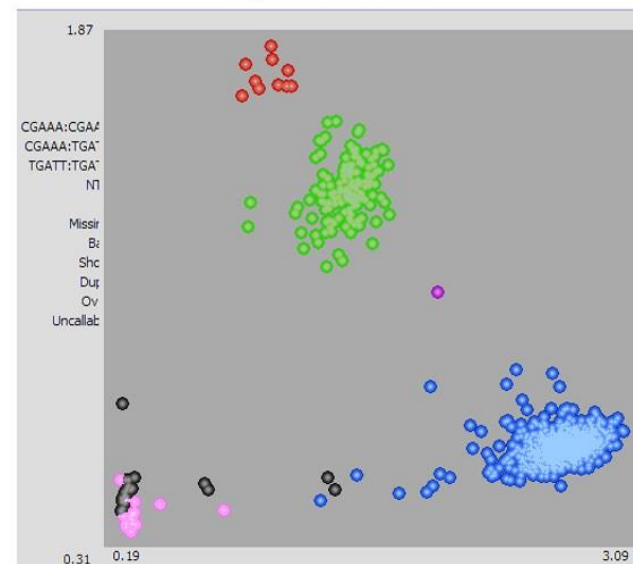
Snp ST00020



Snp ST00023



Snp ST00106



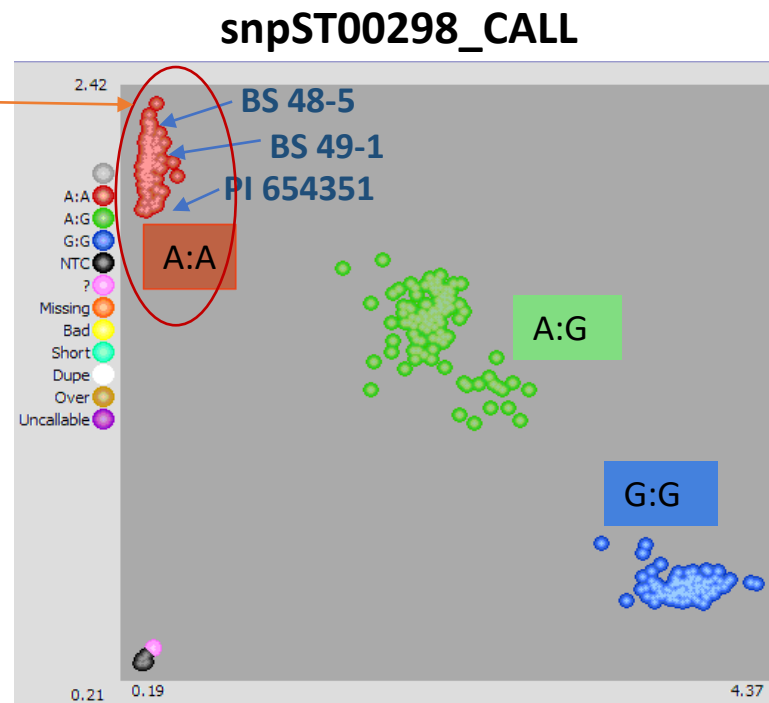
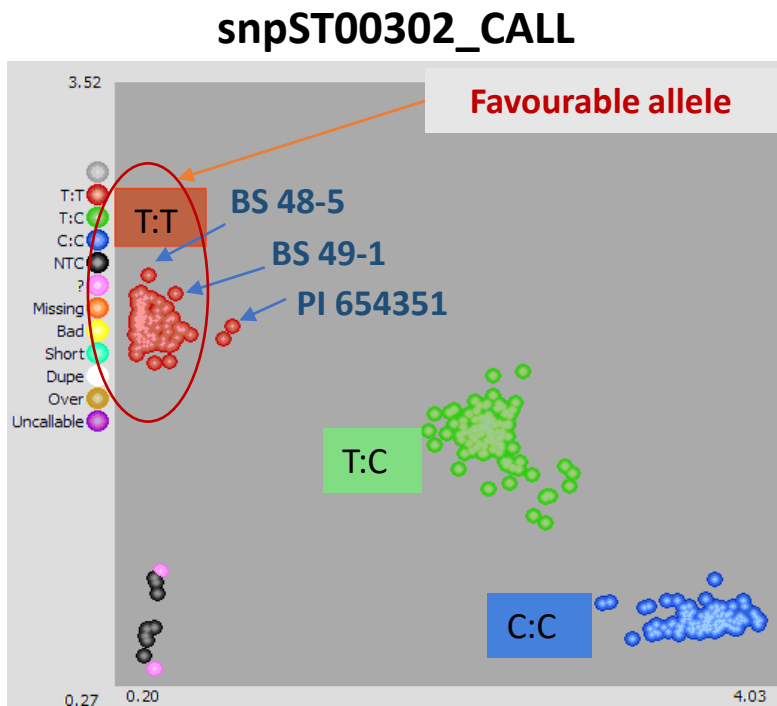
KASP assay for self-compatibility

Marker ID	SNP_ID	Chr	Position	Favourable allele	Unfavorable allele	SNP
snpST00297	ST4_03ch12_58961580	12	58961580	A	G	A/G
snpST00298	ST4_03ch12_58962561	12	58962561	A	G	A/G
snpST00299	ST4_03ch12_58974932	12	58974932	A	T	A/T
snpST00300	ST4_03ch12_59002442	12	59002442	T	C	T/C
snpST00301	ST4_03ch12_59019319	12	59019319	A	T	A/T
snpST00302	ST4_03ch12_59023684	12	59023684	T	C	T/C
snpST00303	ST4_03ch12_59155291	12	59155291	C	A	C/A
snpST00304	ST4_03ch12_59184424	12	59184424	C	T	C/T
snpST00305	ST4_03ch12_59211572	12	59211572	A	G	A/G
snpST00306	ST4_03ch12_59271443	12	59271443	T	C	T/C

Clot et al. (2020)

KASP assay for self-compatibility

➤ Validated 10 SNP markers to screen self-compatible diploid clones



Association of KASP marker genotypes with self-compatible phenotype through Chi-squared likelihood ratio test

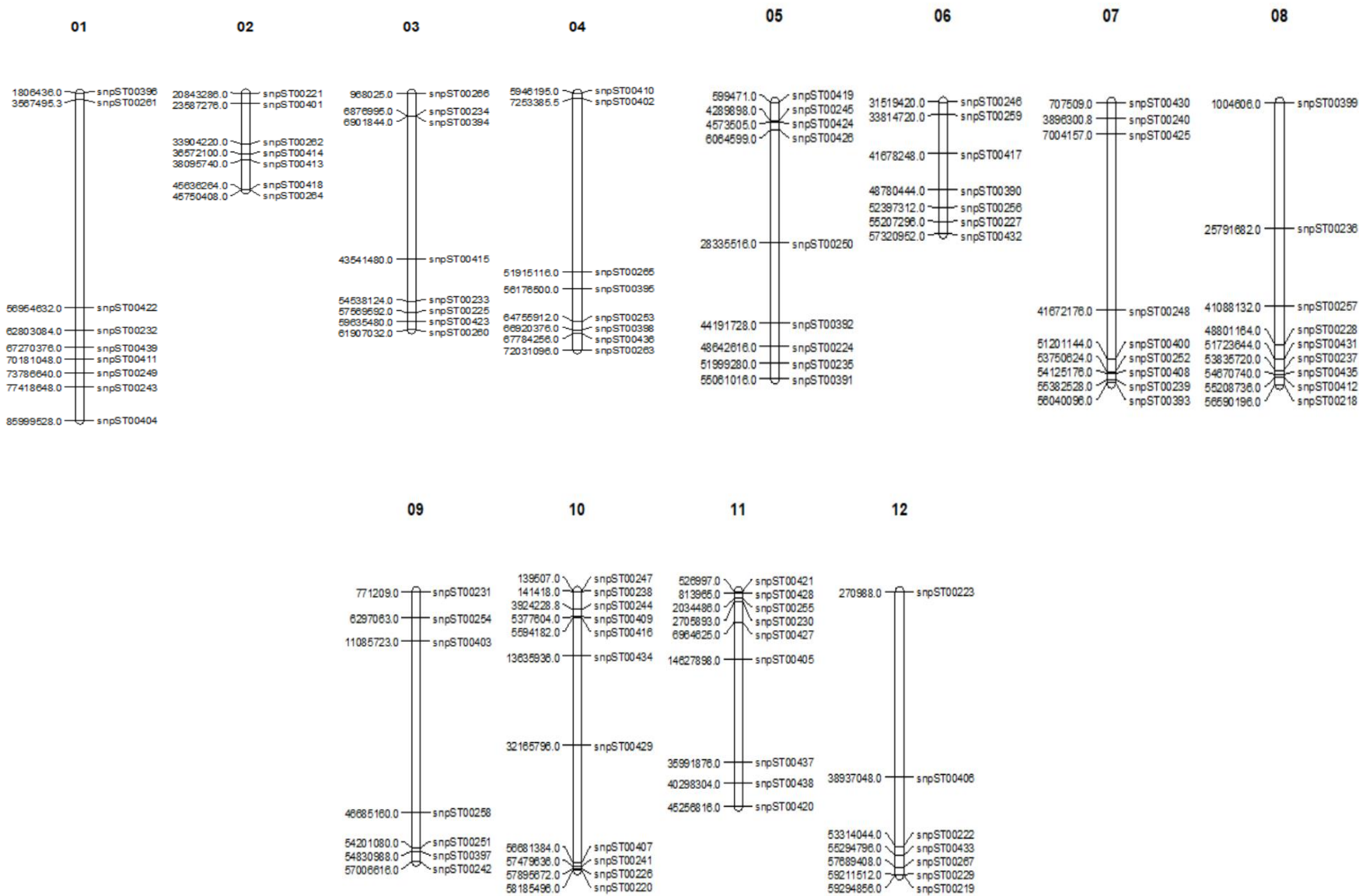
Marker ID	Chi-square	P value	Critical value at p =0.05
snpST00297	5.18	0.02*	3.84
snpST00298	2.05	0.15	
snpST00299	2.26	0.13	
snpST00300	1.94	0.16	
snpST00301	2.61	0.11	
snpST00302	2.18	0.14	
snpST00303	0.18	0.67	
snpST00304	0.07	0.79	
snpST00305	0.07	0.79	
snpST00306	0.05	0.83	

*Significant at $P \leq 0.05$; means observed genotype through marker alleles differ significantly from expected phenotype; non-significant differences suggest that observed marker genotypes agree with the SC phenotype

SNP for Homozygosity

- 100 SNPs distributed across the potato genome were used for homozygosity analysis
- ~10 SNPs per chromosome were selected, SNPs were evenly distributed across the genome, including the most distal telomeric and centromeric markers
- The SNP sequences were taken from potSNP information generated in earlier studies (AnithaKumari et al., 2010)

100 SNPs distributed across the 12 potato chromosomes

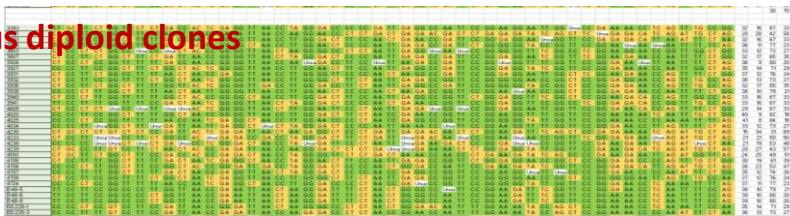


Homozygosity percentage in different diploid potato generations assessed through 100 KASP assay

Inbreeding Generation	N	Homozygosity (%)		
		Min	Max	Average
Founder diploid clones	132	20.1	78.3	56.7
<i>Sli</i> introgressed lines	18	45.6	80.9	68.2
First generation selfing	62	51.2	82.8	65.8
Second generation selfing	95	59.5	85.4	76.6
Third generation selfing	50	69.3	87.6	80.7

Homozygosity in inbreeding generations

Heterozygous diploid clones



➤ Average homozygosity in founder diploid clones was 57%.

Diploid clones-One generation of selfing



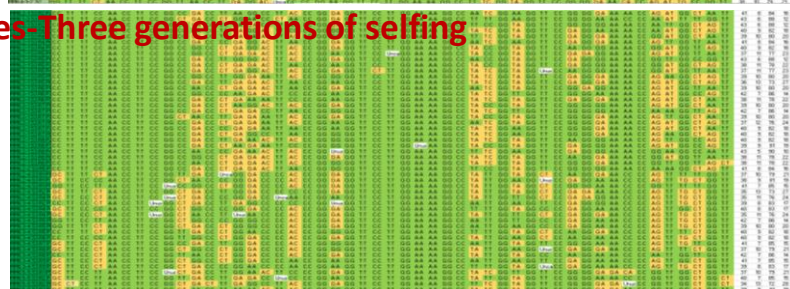
➤ Homozygosity

- S_0 : 20-78%
- S_1 : 45-80%
- S_2 : 51-82%
- S_3 : 60-85%
- S_4 : 69-88%

Diploid clones-Two generations of selfing



Diploid clones-Three generations of selfing



Homo

Hetero

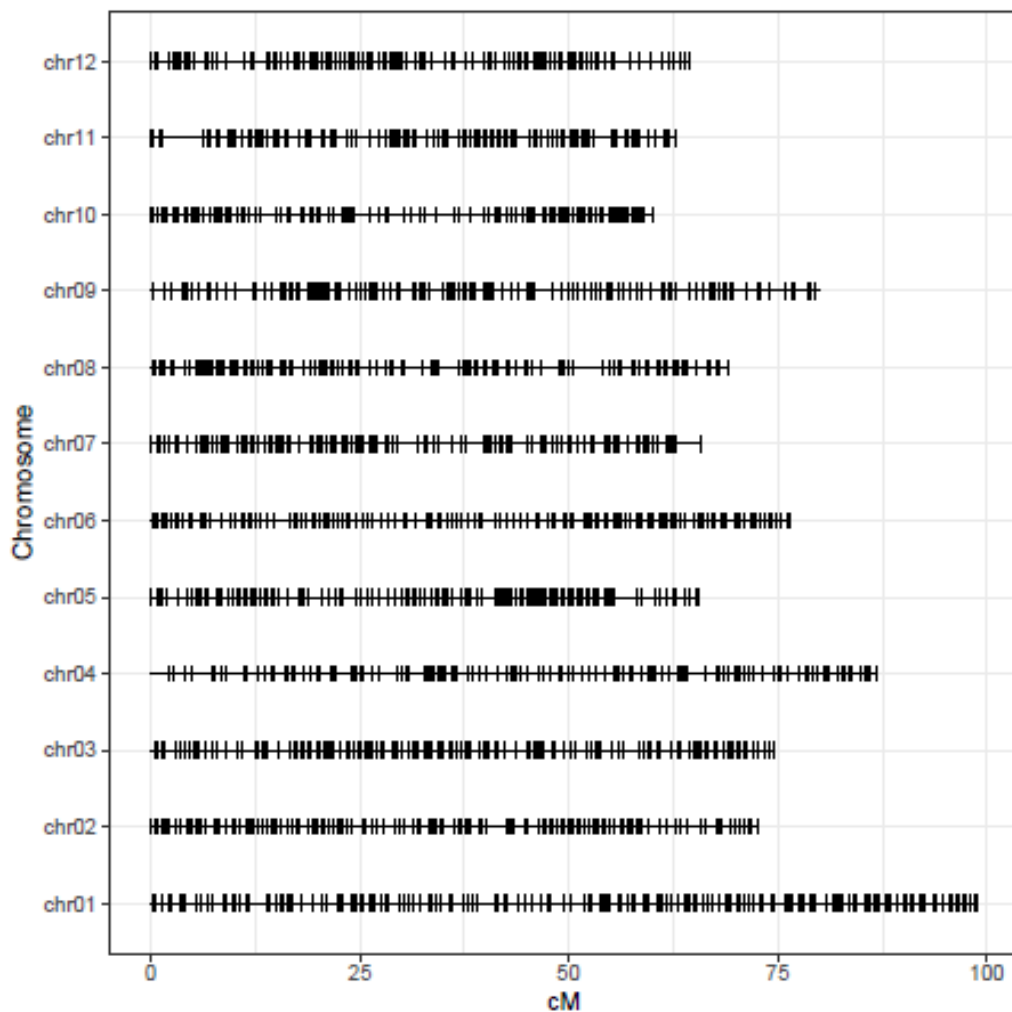
Genomic Selection

- Mid-density genotyping data generated on potato clones using 2502 SNP loci using DArTag platform
- Allele read depth varied from 1-13299, ref allele: 1-934; alternate allele: 1-13125
- 60 Loci having read depth of less than 10 were removed
- Phenotype data generated in two locations on qualitative and quantitative traits
- GS models were tested with available phenotype data

Chromosome	No of SNP loci
Chr 1	272
Chr 2	242
Chr 3	221
Chr 4	220
Chr 5	199
Chr 6	211
Chr 7	198
Chr 8	193
Chr 9	201
Chr 10	178
Chr 11	190
Chr 12	177
Total	2502

10	PotVar0120130	chr01	602954	104.7109	27.46048	4	1	3	3	1	4	3	4	4	4	4	4	4	4
11	solcap_snp_c2_36639	chr01	717629	70.74783	63.76173	3	3	2	4	0	4	1	2	1	1	3	4	2	2
12	solcap_snp_c1_10926	chr01	828025	25.88184	9.109635	3	1	3	2	0	4	1	3	2	3	3	3	3	3
13	solcap_snp_c1_2426	chr01	1177430	164.4073	105.1107	3	3	3	4	0	3	1	2	1	2	3	4	2	2
14	PotVar0071738	chr01	1254782	127.8283	95.15942	1	1	2	1	4	1	3	2	3	2	2	1	2	2
15	PotVar0071966	chr01	1259087	30.38056	2.375	4	4	4	4	4	4	4	4	4	4	4	4	4	4
16	PotVar0072076	chr01	1692167	68.62953	9.053061	3	3	4	4	1	3	1	3	1	2	3	4	2	2
17	solcap_snp_c1_2417	chr01	1916269	175.0251	87.97727	3	3	3	4	2	2	1	3	1	2	3	4	2	2
18	PotVar0044821	chr01	2537458	120.0567	25.18006	2	1	2	4	4	1	0	3	1	2	3	2	1	1
19	solcap_snp_c2_21098	chr01	2617236	250.6017	184.7109	3	1	4	2	3	4	4	2	4	3	1	3	4	4
20	solcap_snp_c2_21122	chr01	2690797	240.2636	223.6147	0	3	1	0	3	2	3	2	3	1	2	2	2	2
21	solcap_snp_c2_21178	chr01	2829162	38.05476	15.03762	2	3	3	2	2	2	1	2	3	2	2	3	3	3
22	PotVar0044963	chr01	2868145	16.4184	15.32722	4	1	1	4	2	3	2	3	1	2	2	2	3	3
23	PotVar0044998	chr01	2868837	94.42137	36.93598	2	1	0	4	3	4	2	3	1	1	3	2	2	2
24	solcap_snp_c2_19358	chr01	3730701	113.4556	86.21605	3	1	2	2	4	2	1	3	0	3	2	1	0	0
25	solcap_snp_c2_19353	chr01	3744040	274.9912	230.4783	2	2	2	0	3	1	1	2	0	3	2	2	0	0
26	PotVar0045428	chr01	4013228	22.14887	23.25387	1	3	3	3	1	2	3	0	4	2	2	2	4	4
27	solcap_snp_c2_51811	chr01	4592988	38.53448	42.34043	4	3	3	4	3	4	4	3	4	3	4	1	4	4
28	solcap_snp_c2_51791	chr01	4643672	586.3536	140.4933	3	3	3	2	4	4	3	4	2	4	4	3	1	1
29	solcap_snp_c2_49936	chr01	4996079	443.0829	152.623	2	3	3	3	2	0	3	2	4	2	2	4	4	4
30	solcap_snp_c2_48051	chr01	5729429	388.9503	68.86855	4	3	4	4	4	4	3	4	3	3	2	4	4	4
31	solcap_snp_c2_56125	chr01	6012003	152.055	347.7452	1	1	1	0	3	2	2	1	2	2	1	1	2	2
32	solcap_snp_c1_13307	chr01	6097814	272.058	126.1647	2	3	3	3	3	3	2	4	2	2	2	3	3	3
33	solcap_snp_c1_13312	chr01	6105530	318.0499	151.8607	3	2	4	3	3	2	3	3	3	3	2	3	4	4
34	solcap_snp_c1_13290	chr01	6218999	164.1262	258.2712	2	1	1	0	3	0	2	1	2	2	1	2	2	2
35	solcap_snp_c1_13297	chr01	6242823	92.49425	1.886905	4	4	4	3	4	4	4	4	4	4	4	4	4	4
36	solcap_snp_c2_27882	chr01	6953278	231.9917	134.214	4	2	1	2	4	4	4	2	4	3	4	3	3	3
37	solcap_snp_c1_8608	chr01	7025123	428.8421	175.3097	4	3	2	2	4	4	4	2	4	4	4	3	3	3
38	solcap_snp_c2_27900	chr01	7184764	54.43491	59.63127	1	2	2	2	1	2	1	2	1	1	2	4	1	1
39	solcap_snp_c2_53842	chr01	7501568	110.1381	41.5678	3	3	4	2	4	4	2	3	1	4	4	3	1	1
40	solcap_snp_c2_38350	chr01	8378536	358.9006	232.4578	3	3	4	4	2	3	3	3	2	4	2	2	2	2
41	solcap_snp_c1_11430	chr01	8604059	62.94286	25.87981	4	3	1	4	4	4	4	3	4	3	4	4	3	3
42	solcap_snp_c1_14511	chr01	10925976	475.6657	169.2897	4	3	2	4	4	3	4	3	4	4	4	4	3	3
43	solcap_snp_c1_14731	chr01	11138798	258.6359	116.4575	4	3	2	4	4	3	4	3	4	4	4	4	3	3
44	solcap_snp_c2_50030	chr01	11139408	148.5069	51.45763	4	3	4	4	4	3	4	4	4	4	4	4	4	3
45	solcap_snp_c2_55008	chr01	11987796	452.6898	99.37676	3	2	2	2	4	4	3	2	1	2	4	3	4	4
46	solcap_snp_c2_43970	chr01	12917838	130.0778	158.9302	1	0	1	1	3	2	2	1	0	1	1	2	1	1
47	solcap_snp_c1_8906	chr01	13027433	125.2833	84.11741	4	3	2	4	3	3	4	4	4	4	4	4	3	4

Potato mid density genotyping panel



- 2-3 SNP per cM
- Low genotyping cost
- Possible inclusion of any mapped marker
- US \$12 per sample

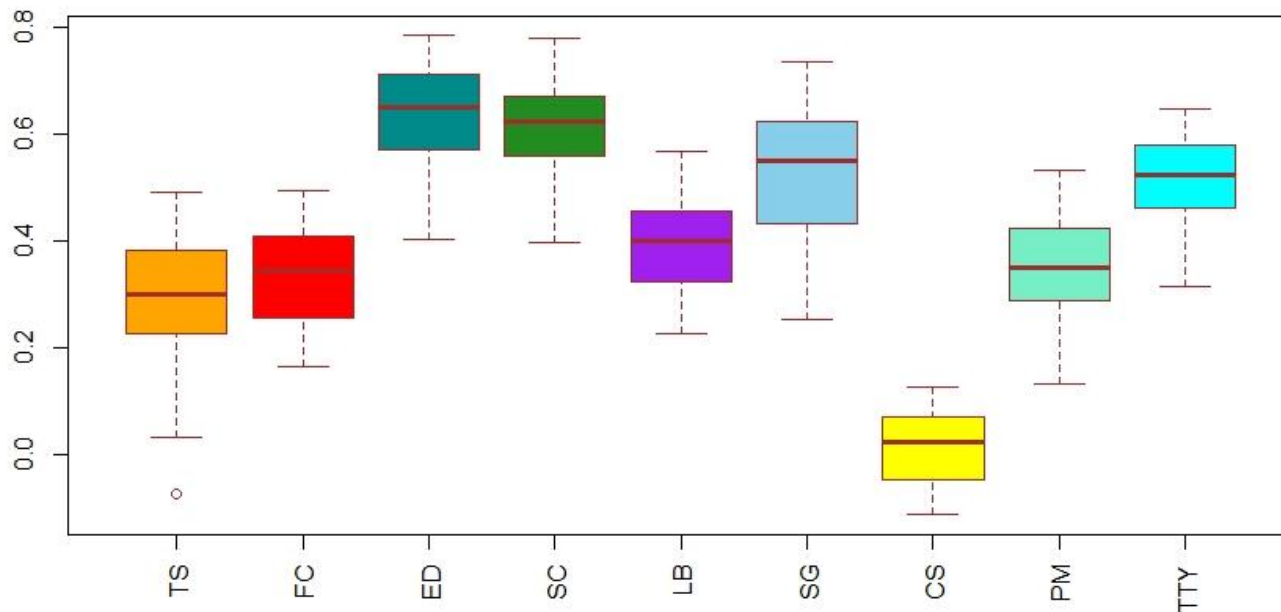
Genomic prediction accuracy (GBLUP)

Trait	TP	h ² (ns)	Prediction accuracy	
			Range	Average±S.E.
Tuber Shape	171	0.21	-0.10-0.45	0.17±0.021
Flesh Colour	171	0.34	0.11-0.49	0.28±0.010
Eye depth	143	0.53	0.40-0.78	0.64±0.014
Skin colour	143	0.41	0.40-0.78	0.62±0.012
GR resistance	97	0.21	0.00-0.38	0.19±0.016
GP resistance	97	0.30	-0.23-0.21	0.06±0.013
Late blight resistance	191	0.56	0.18-0.67	0.42±0.016
Specific Gravity	171	0.74	0.25-0.74	0.52±0.017
Chip score	183	0.16	-0.11-0.13	0.02±0.009
Plant Maturity	171	0.24	0.13-0.53	0.35±0.013
Total tuber yield	171	0.50	0.32-0.65	0.52±0.011

Test population size -50 for all the traits; Results are means ± s.e. across 50 replicates

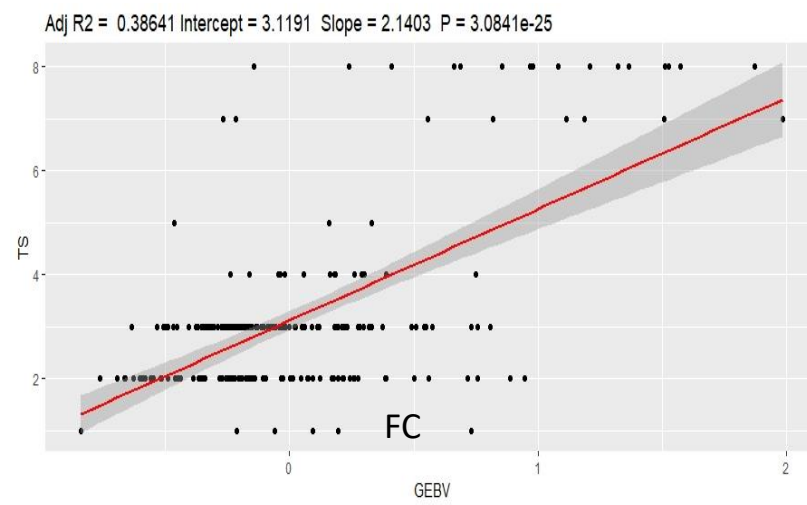
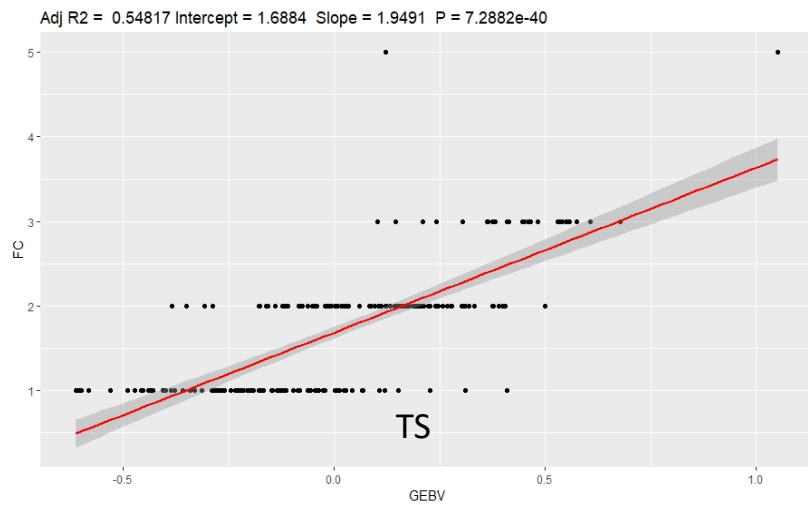
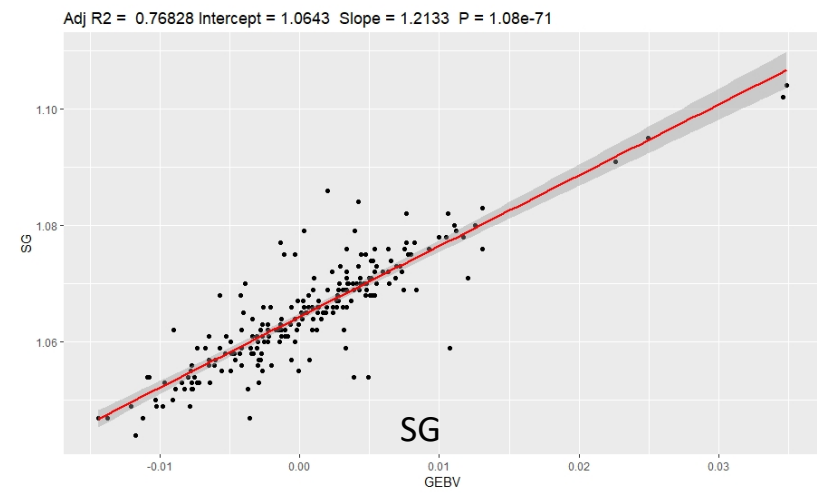
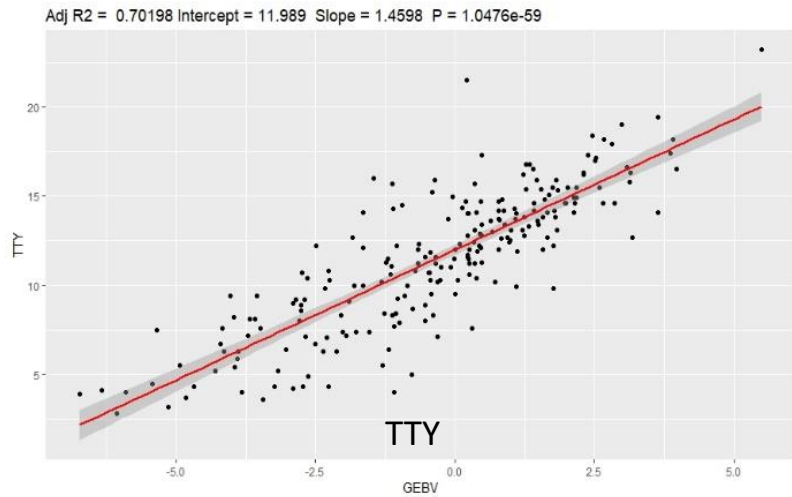
GS Prediction Accuracy

GBLUP - Genomic prediction accuracy range of different traits

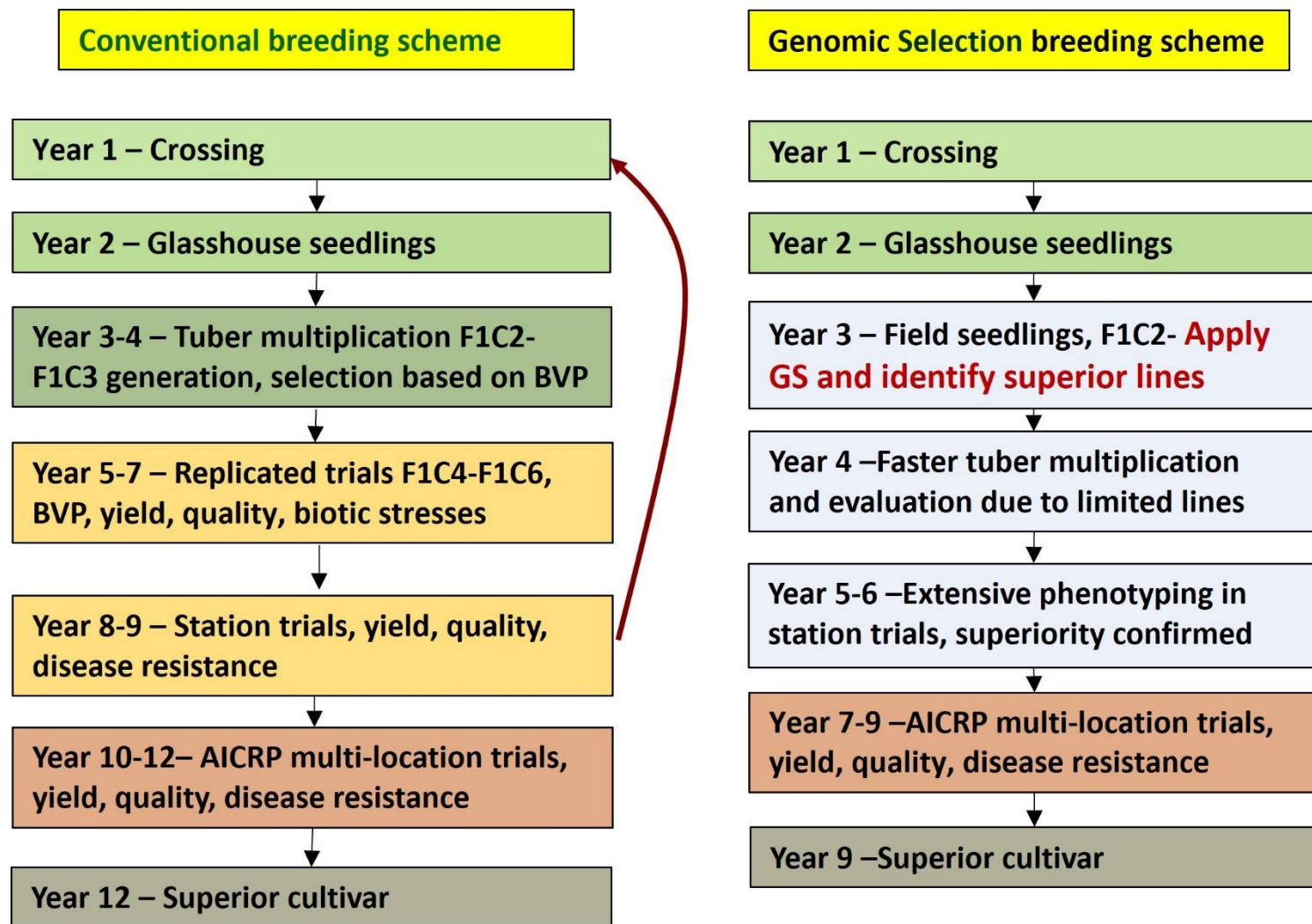


TS- Tuber shape; FC-Flesh colour; ED- Eye depth; SC- Skin colour; LB- Late blight resistance; SG- Specific gravity; CS- Crisp score; PM- Plant maturity; TTY-Total tuber yield
Results are means \pm s.e. across 50 replicates

Genomic prediction bias



Proposed GS Breeding Pipeline



Summary

- ✓ Genetic gain is low in potato breeding
- ✓ KASP assays demonstrate the usefulness in high throughput cost effective MAS for important biotic stress traits
- ✓ Genomic prediction accuracy is moderate to high for most of the traits
- ✓ Robust and accurate data could further improve the prediction accuracy
- ✓ Genomic selection shows promise for enhanced genetic gain in potato breeding



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Genetic progress in 50 years of potato breeding in India: Where do we stand?

Salej Sood ^a, Vinay Bhardwaj ^a, Vinod Kumar ^a, Roma Das ^b, VK Gupta ^c, Vikas Mangal ^a, SK Luthra ^c, Raj Kumar ^d, Shambhu Kumar ^e, RK Singh ^a, Manoj Kumar ^{a,c}, Abhishek Rathore ^b, NK Pandey ^a, AK Singh ^f

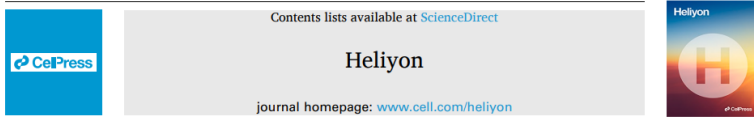
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Review article

Digitalization of potato breeding program: Improving data collection and management

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ARTICLE INFO

Keywords:
Breeding data management
Data digitalization
Phenotyping
Precision breeding

ABSTRACT

A plant breeding program involves hundreds of experiments, each having number of entries, genealogy information, linked experimental design, lists of treatments, observed traits, and data analysis. The traditional method of arranging breeding program information and data recording and maintenance is not centralized and is always scattered in different file systems which is inconvenient for retrieving breeding information resulting in poor data management and the loss of crucial data. Data administration requires a significant amount of manpower and resources to maintain nurseries, trials, germplasm lines, and pedigree records. Further, data transcription in scattered spreadsheets and files leads to nomenclature and typing mistakes which affects data

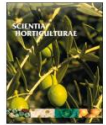
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KASP markers validation for late blight, PCN and PVY resistance in a large germplasm collection of tetraploid potato (*Solanum tuberosum* L.)

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ARTICLE INFO

Keywords:
Biotic stress resistance
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ABSTRACT

Molecular markers are important and valuable tools in crop breeding programmes to help in the discovery and manipulation of important genes governing resistance reaction. In potato, several biotic stresses hamper quantity and quality of tuber production. Availability of molecular markers and high throughput screening method

P-105



Genome-wide association and genomic prediction for late blight and PCN resistance in potato

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Overview

Potato is the most important tuber crop and is a staple food for ~1.3 billion people worldwide. Late blight and PCN are two important biotic stresses which hamper the quantity and quality of tuber production. Although the potato genome was deciphered in the year 2011, various genetic complexities like autotetraploid inheritance, heterozygosity, etc. constrained the identification of genomic loci's governing these traits in comparison to major crops. The genomic-assisted

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Bohar



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