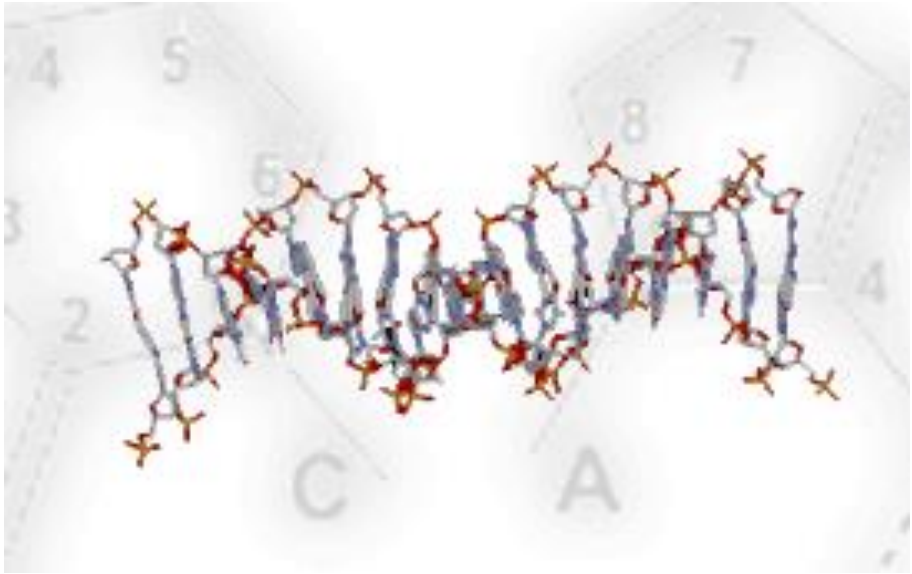
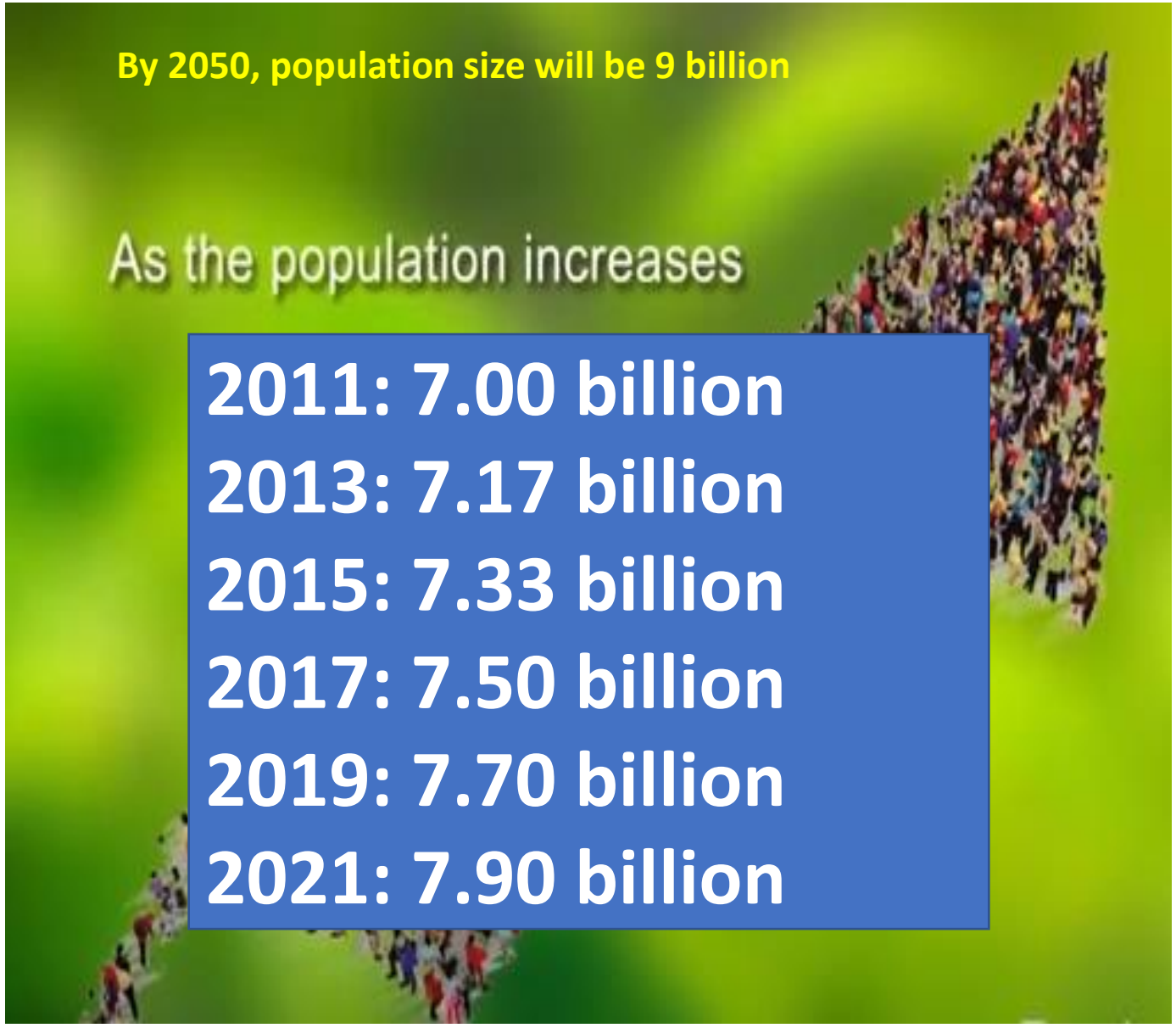
CIMMYT Headquarters, Mexico

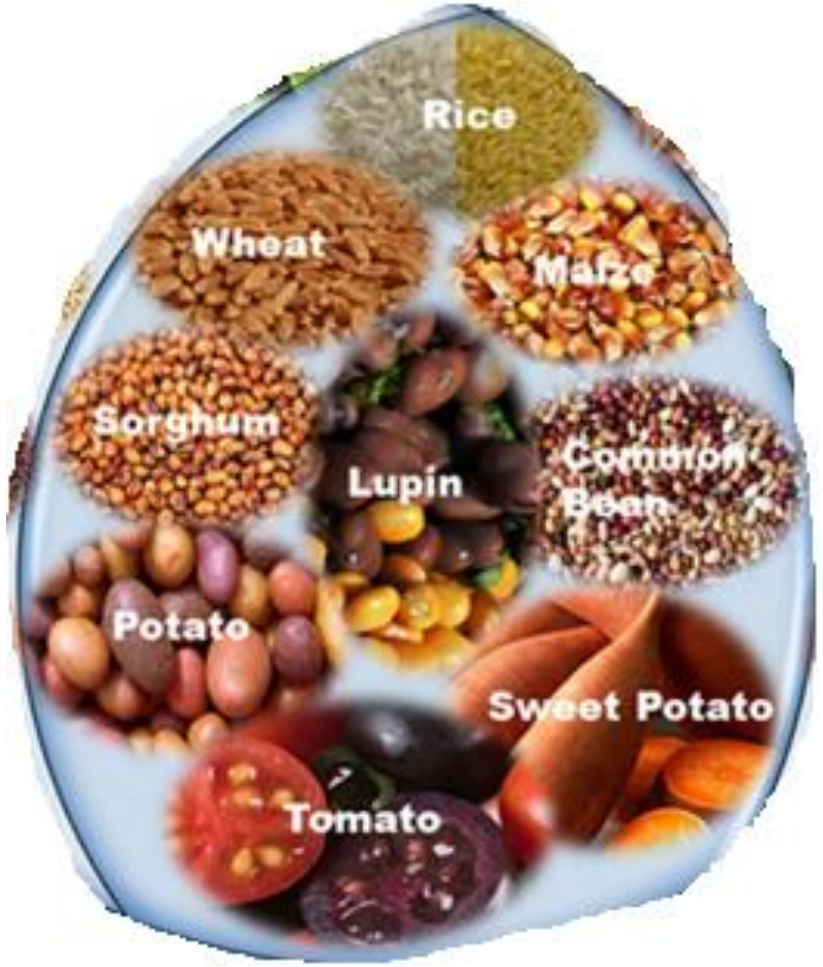
Genome-wide association study: a powerful approach to discover novel alleles from germplasm collections

Deepmala Sehgal
Wheat Geneticist
Global Wheat Program
CIMMYT MR
International Maize and Wheat Improvement Center

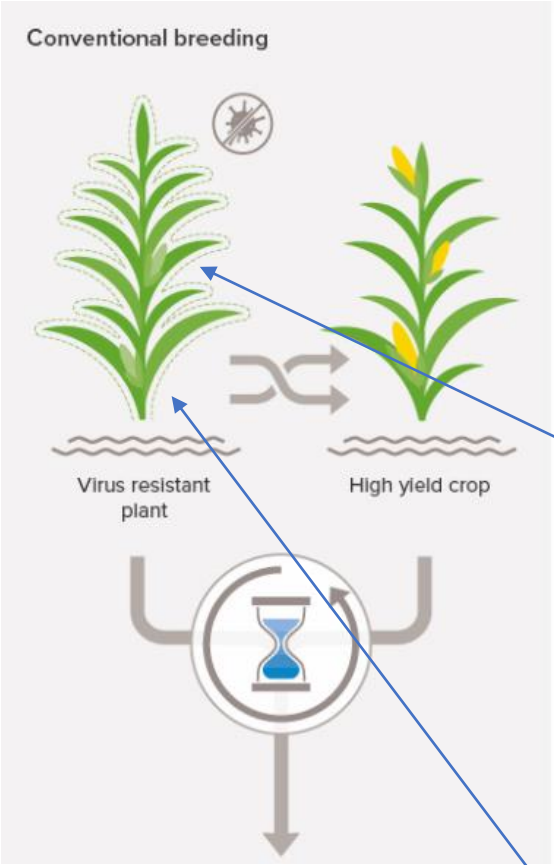


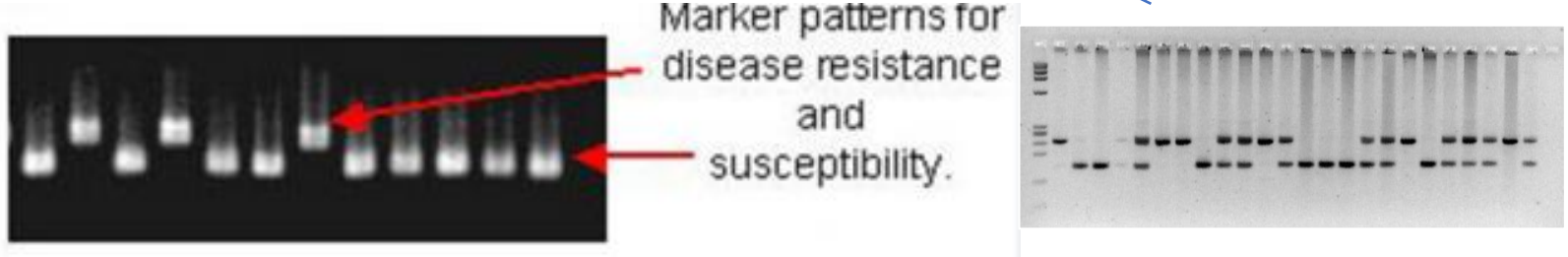
“Food is the moral right of all who are born into this world”
Nobel prize winner in 1970, Norman Borlaug, known as <u>Father of the Green Revolution</u>





Integration of molecular genetics can help to accelerate the development of varieties that are desired





By using molecular genetics approaches

- Understand the genetic architecture of trait(s)
- Identify trait-linked markers
- Increase the selection intensity
- Decrease the cycle time
- Accelerate genetic gain

Approaches to identify trait-linked markers

- **Traditional QTL mapping**

- **Genome wide association study; a new genetics approach for crop improvement**

What is a QTL?

Grain weight

Quality

The ge
gene
‘
multiple
called a
TL)

Plant height

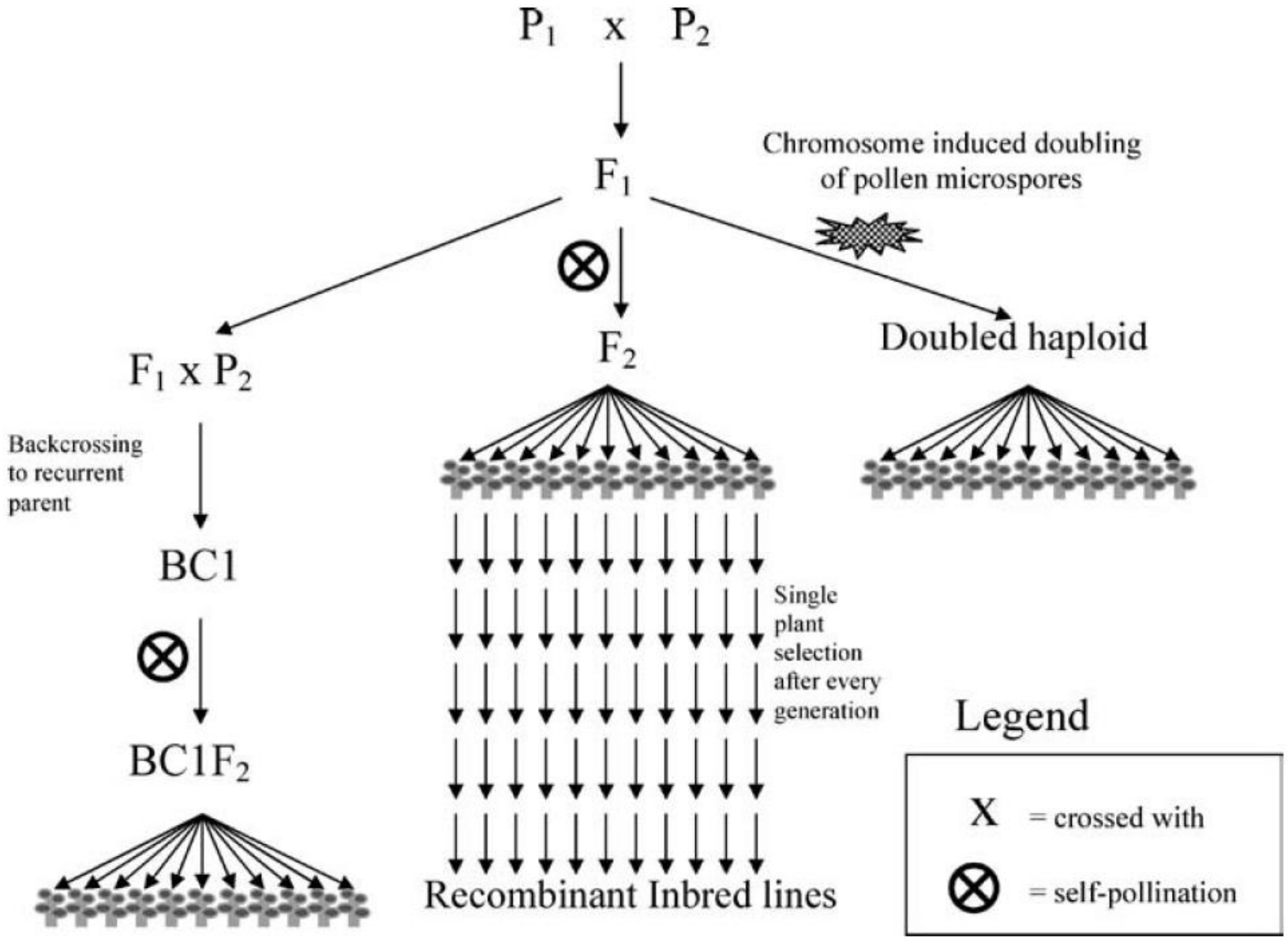
Pea trait	Dominant trait		Recessive trait	
Seeds				
Seed shape	Round		Wrinkled	
Seed colour	Yellow		Green	
Whole plants				
Flower colour	Purple		White	
Flower position	Axial		Terminal	
Plant height	Tall		Short	
Pod shape	Inflated		Constricted	
Pod colour	Green		Yellow	

Approaches to identify trait-linked markers

- **Traditional QTL mapping**

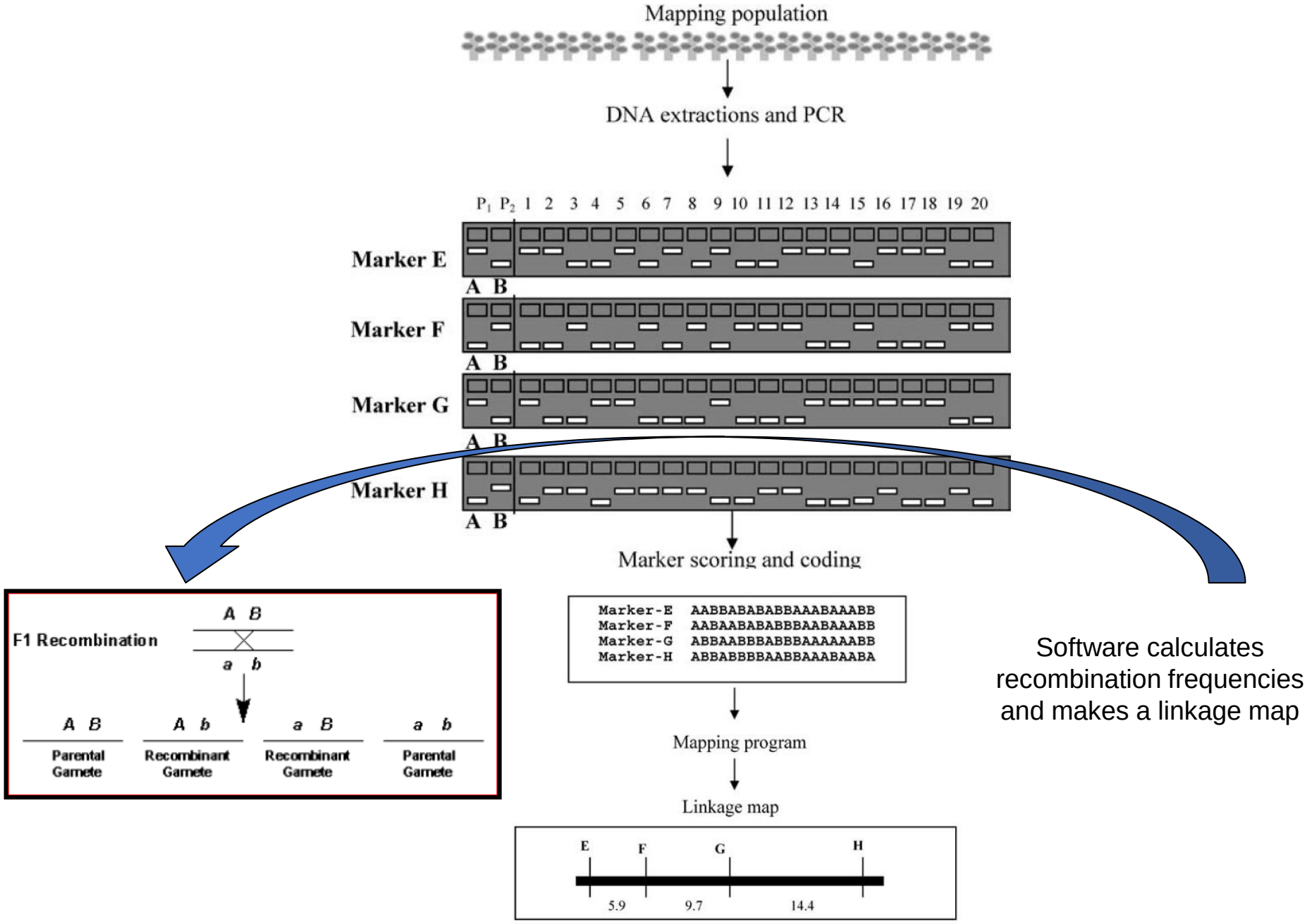
- **Genome wide association study; a new genetics approach for crop improvement**

Step1: Develop Mapping populations

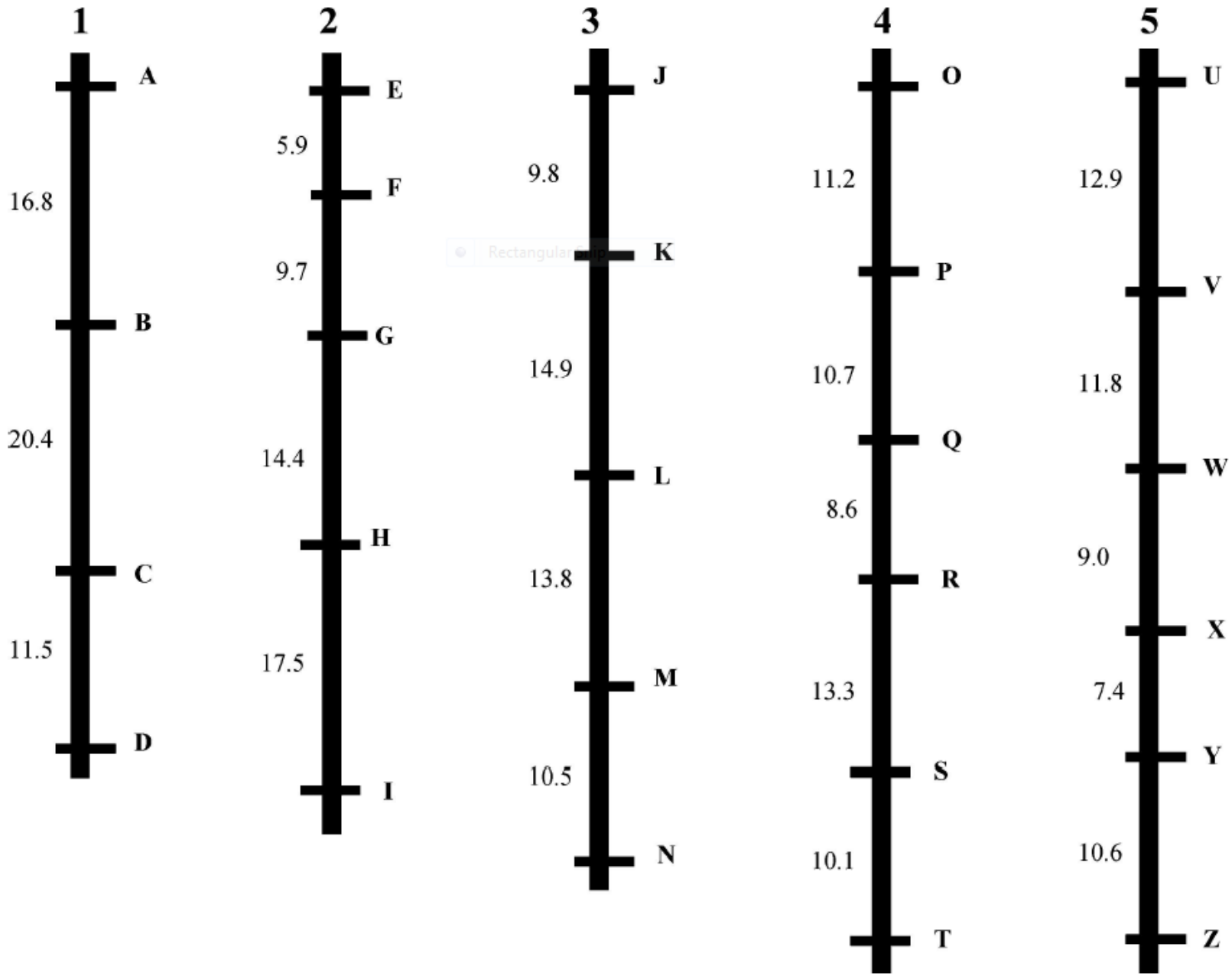


RIL

Step 2: Construct a linkage map



Software calculates recombination frequencies and makes a linkage map

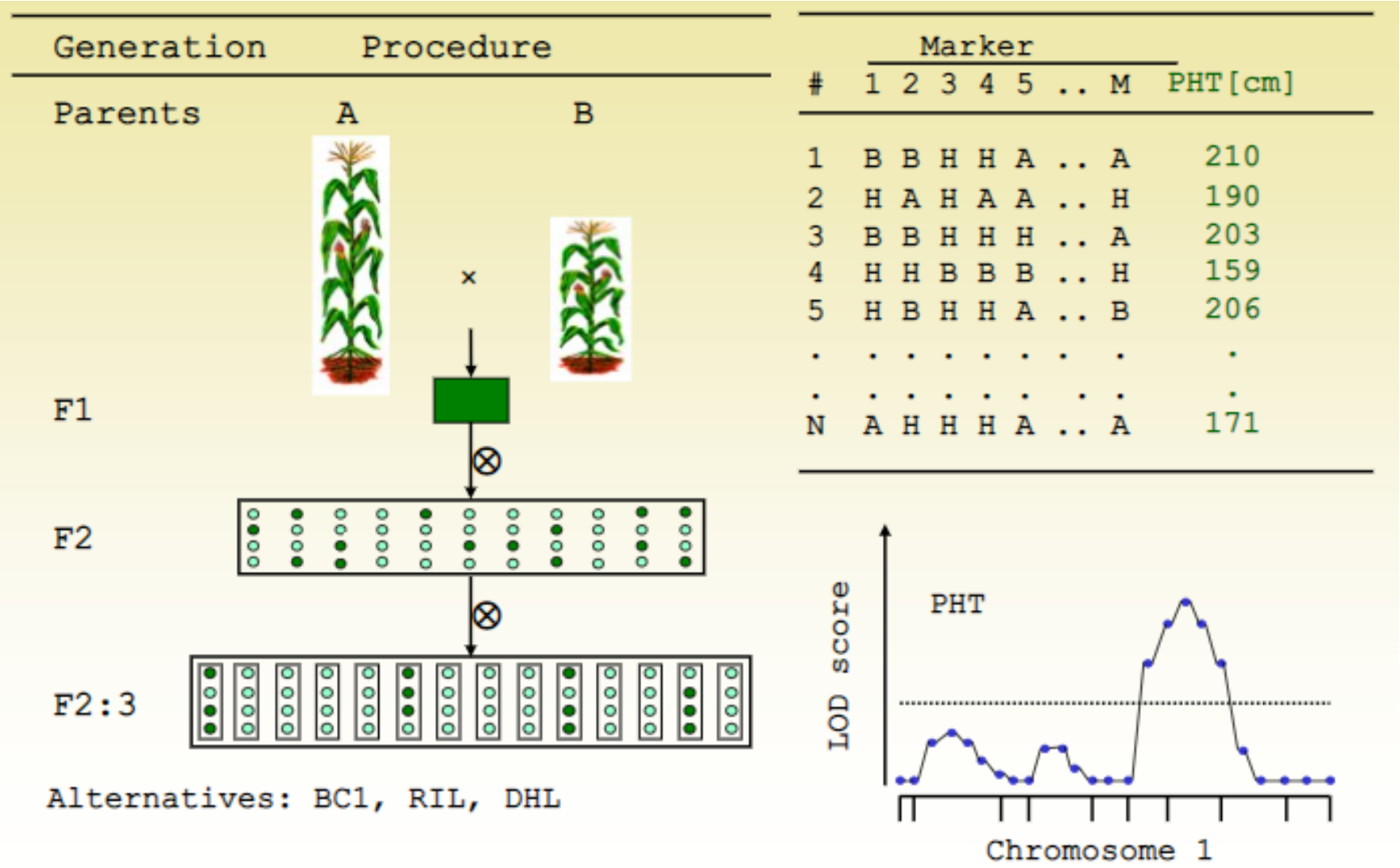

1
A
16.8
B
20.4
C
11.5
D
2
E
5.9
F
9.7
G
14.4
H
17.5
I
3
J
9.8
K
14.9
L
13.8
M
10.5
N
4
O
11.2
P
10.7
Q
8.6
R
13.3
S
10.1
T
5
U
12.9
V
11.8
W
9.0
X
7.4
Y
10.6
Z

Step 3: Generate phenotypic data

Events
plant-phenotyping.org

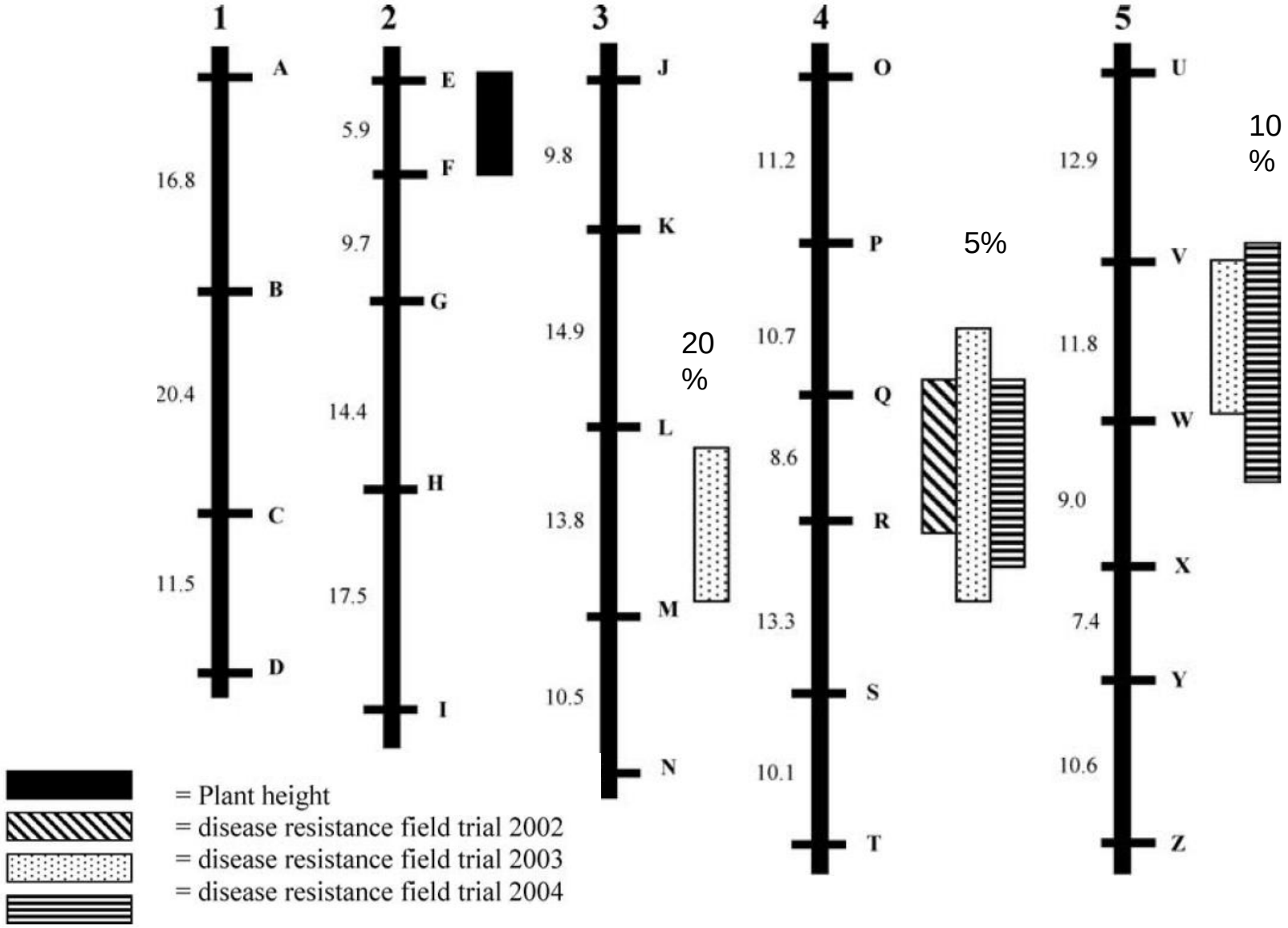
Trevor Garnett (@TrevorGarnett) | Twitter
twitter.com

QTL mapping



	Marker							
#	1	2	3	4	5	..	M	PHT[cm]
1	B	B	H	H	A	..	A	210
2	H	A	H	A	A	..	H	190
3	B	B	H	H	H	..	A	203
4	H	H	B	B	B	..	H	159
5	H	B	H	H	A	..	B	206
.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.
N	A	H	H	H	A	..	A	171

QTLs on a genetic linkage map



Current status of molecular breeding

- A literature review indicates thousands of QTL mapping studies but not many *actual* reports of the application of MAS in breeding

- *Why is this the case?*

Reliability of QTL mapping is critical to the success of MAS

- Reliable phenotypic data critical!
  - Multiple replications and environments
- Confirmation of QTL results in independent populations
- "Marker validation" must be performed
  - Testing reliability for markers to predict phenotype
  - Testing level of polymorphism of markers
- Effects of genetic background need to be determined

Recommended references:

Young (1999). A cautiously optimistic vision for marker-assisted breeding. Mol Breeding 5: 505-510.

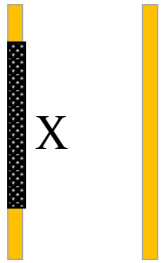
**Holland, J. B. 2004 Implementation of molecular markers for quantitative traits in breeding programs - challenges and opportunities. Proceedings of the 4th International *Crop Sci.* Congress., Brisbane, Australia.

Case of drought tolerance QTLs in wheat

Reports	Traits	QTLs	Interval
Kirigwi et al. 2007	Grain yield and yield components	4AL	10.7 cM
Maccaferri et al. 2008	Grain yield, heading date, plant height	2BL, 3B	19 cM

Generation of fine-mapping population

(Near isogenic line introgressed with drought tolerance QTL background of susceptible parent



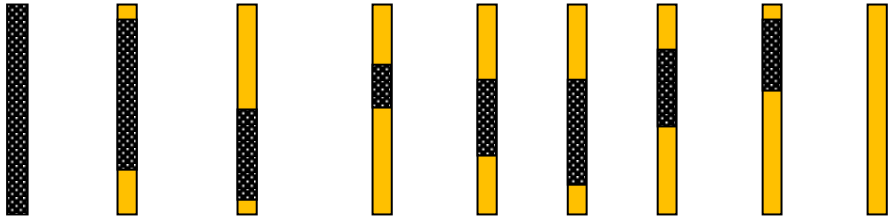
X

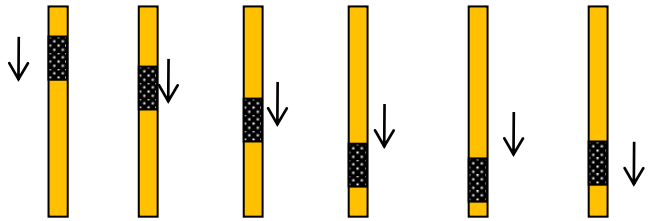
(Elite)

BC5F1

Self (Fine mapping population)

Recombinants (BC5F2s)



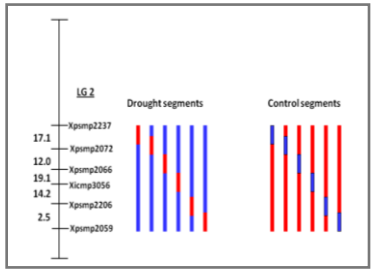


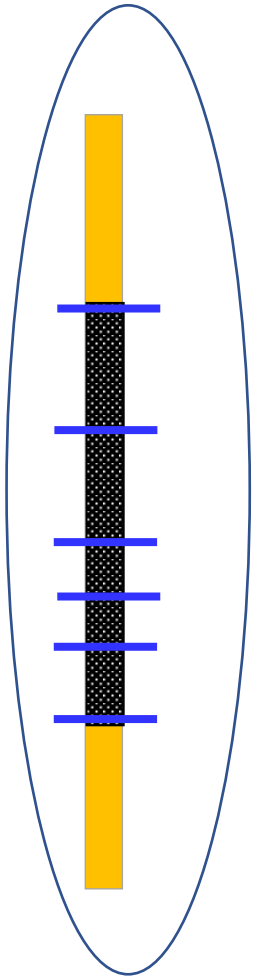
Selection of stepped recombinants covering ~ 10cM

2,500 individuals in fine mapping population

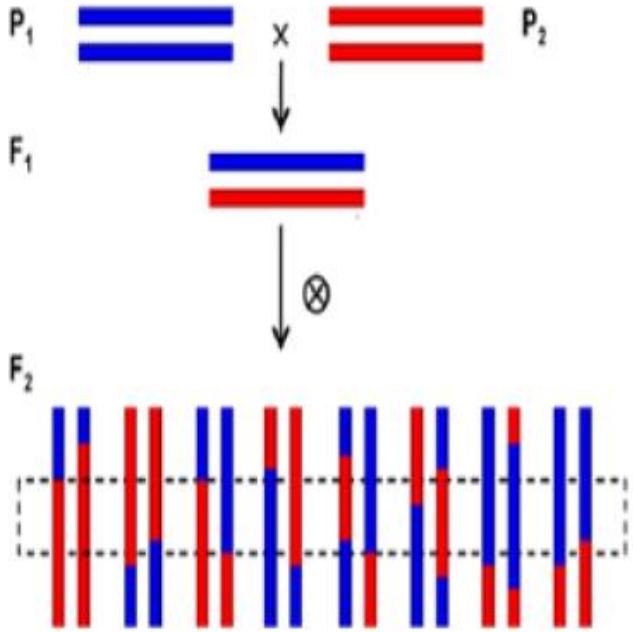
Expected recombinants

ABBBBB	BAAAAA
AABBBB	BBAAAA
AAABBB	BBBAAA
AAAABB	BBBBAA
AAAAAB	BBBBBA
AAAAAA	BBBBBB

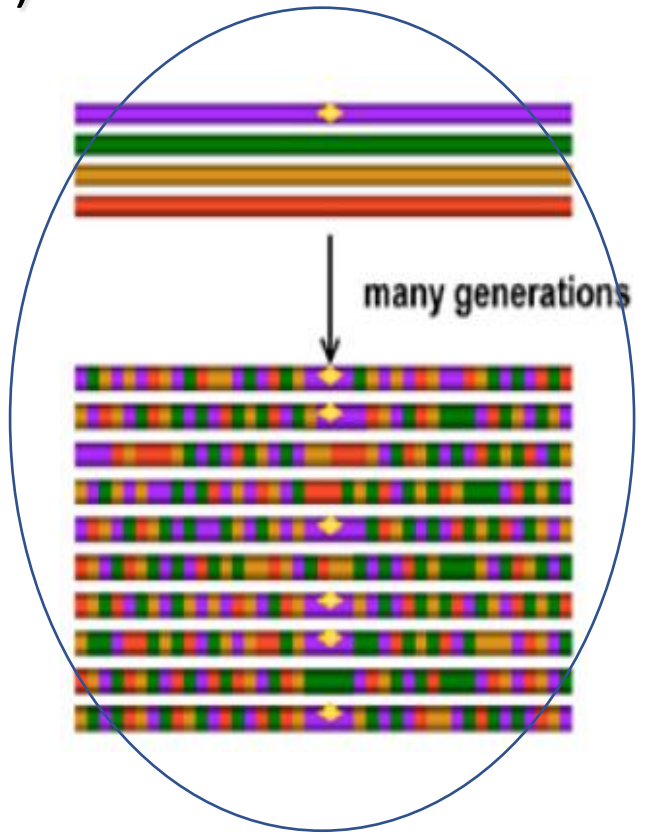




Linkage Analysis *vs* Association Mapping (mapping population *vs* diverse collections)



A Biparental population: QTL Mapping



B Diverse germplasm population: Association Mapping

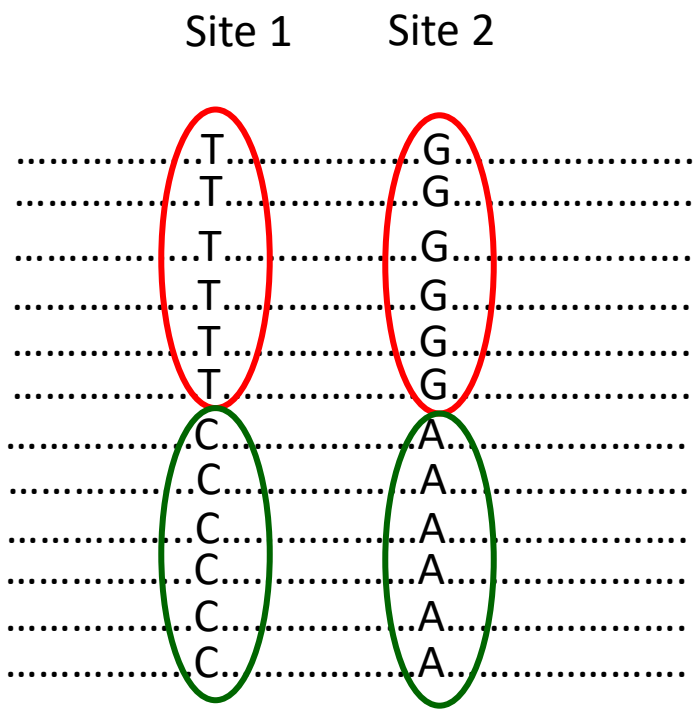
Association Mapping
A New Paradigm for Dissection of Complex Traits in Crops

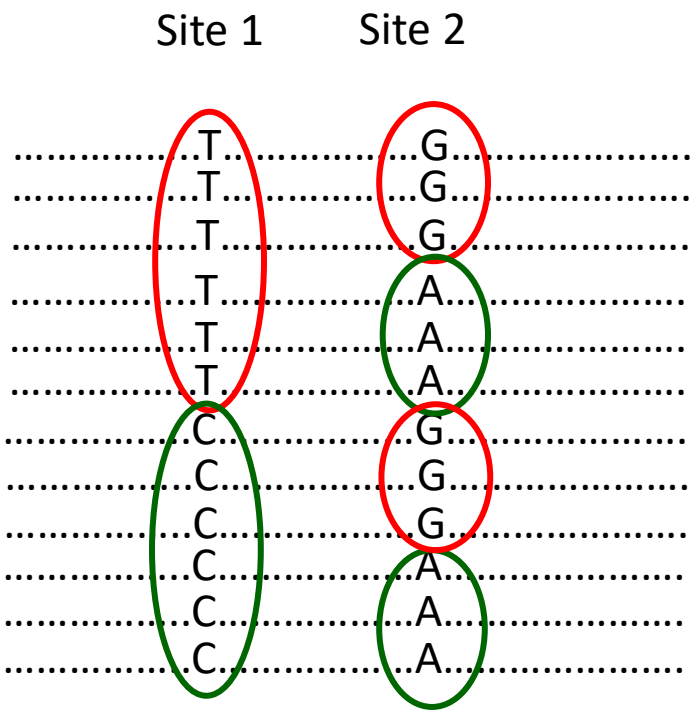
“Association mapping, also known as Linkage Disequilibrium mapping, is a germplasm-based survey to identify trait-marker relationships based on linkage disequilibrium”

What is Linkage Disequilibrium?

Linkage disequilibrium is the non-random association of alleles at different loci in a given population

What is Linkage Disequilibrium?





Site 1 \ Site 2	A	G
C	6	0
T	0	6

Complete LD (D' = 1)

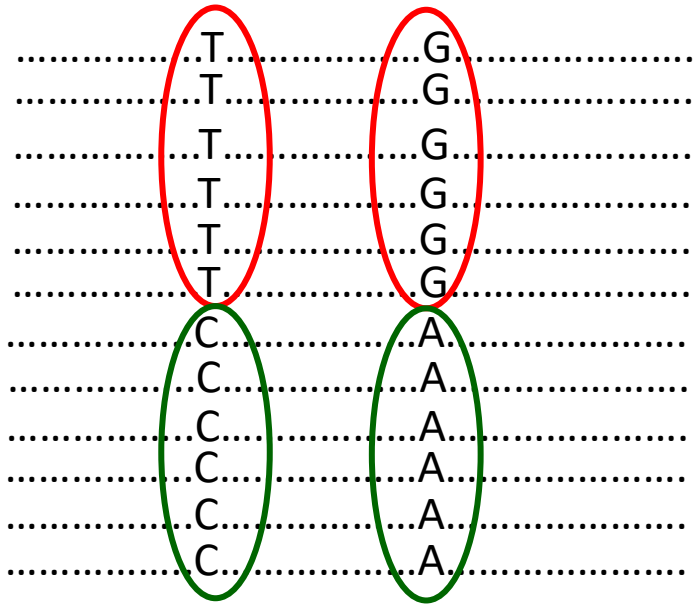
Fisher's Exact Test P = 0.002

Site 1 \ Site 2	A	G
C	3	3
T	3	3

No LD (D' = 0)

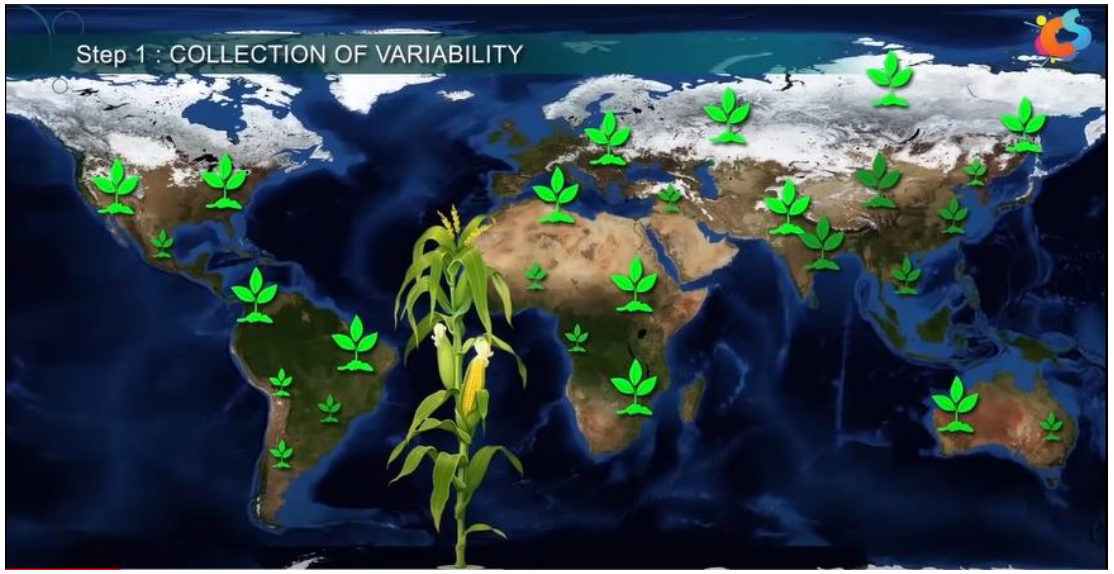
Fisher's Exact Test P = 1.00

Linkage Disequilibrium can also be due to selection practiced by breeders

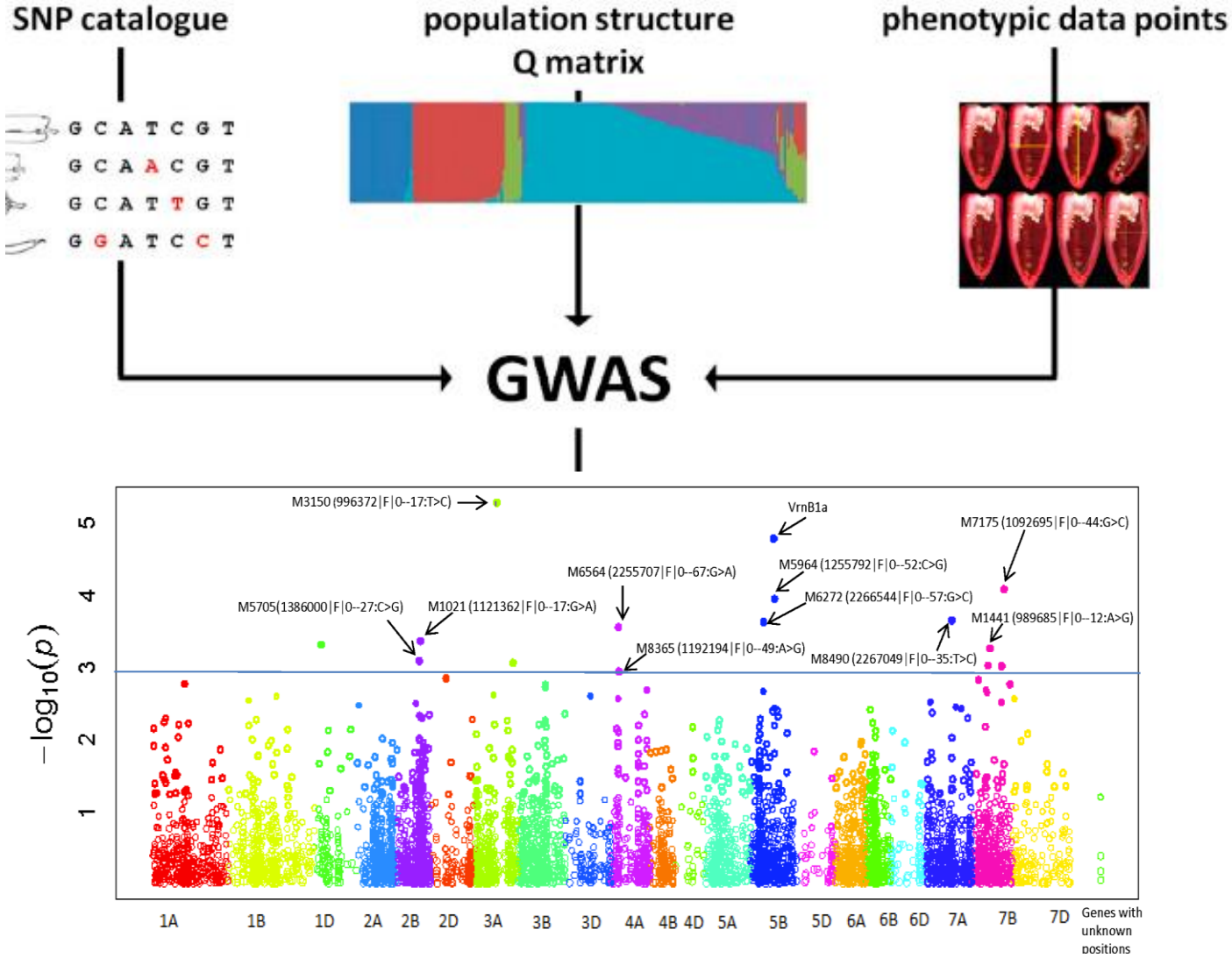


Steps in Association mapping

- **No need of population development-saves 2 years**

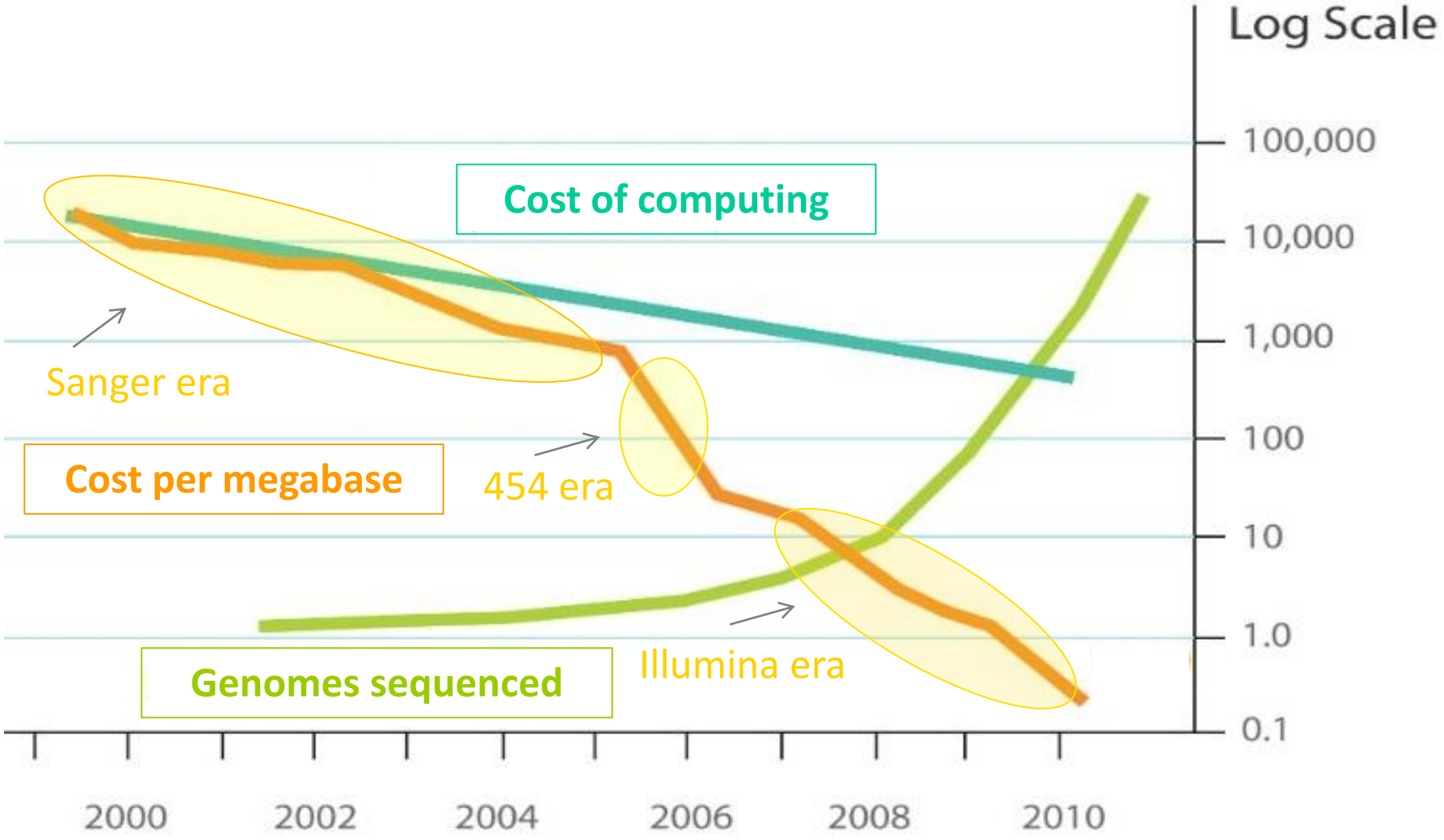


Genbank accessions
Or
Breeder's germplasm



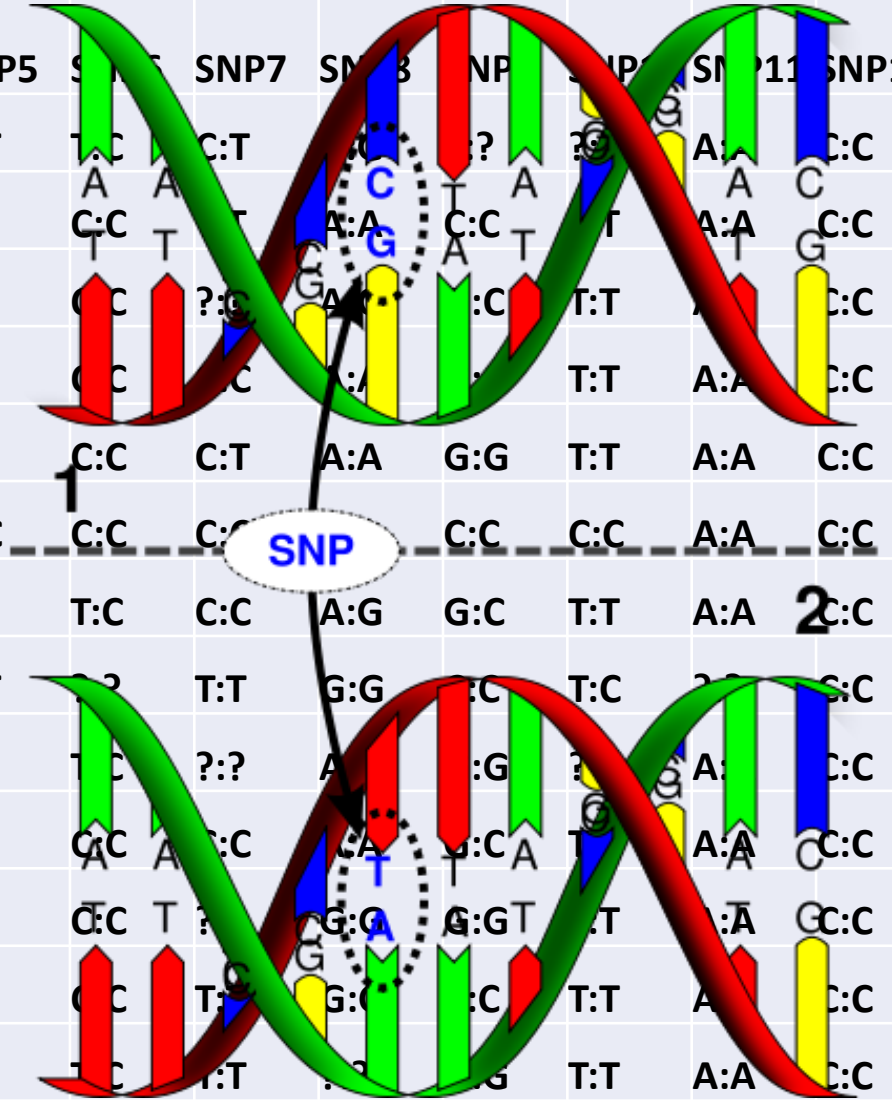
Why Association Mapping has become more relevant now than before?

The sequencing explosion……



Why Association Mapping has become more relevant now than before?

SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SNP10	SNP11	SNP12	SNP13	SNP14	SNP15	SNP16
G:T	?:?	C:C	G:G	C:T	T:C	C:T	C:C	?:?	?:?	A:A	C:C	C:C	?:?	?:?	C:C
?:?	C:C	C:C	?:?	T:T	C:C	T:T	A:A	C:C	T:T	A:A	C:C	?:?	G:G	A:A	C:C
G:T	?:?	C:C	G:G	T:T	C:C	?:G	A:A	C:C	T:T	A:A	C:C	?:?	G:G	A:A	C:C
G:G	T:T	C:C	G:G	T:T	C:C	C:C	A:A	C:C	T:T	A:A	C:C	C:C	G:G	A:A	?:?
?:?	C:C	C:C	G:G	T:T	C:C	C:T	A:A	G:G	T:T	A:A	C:C	C:C	G:G	A:A	C:C
?:?	T:T	C:C	G:G	C:C	C:C	C:C	A:A	C:C	C:C	A:A	C:C	C:C	A:A	C:C	C:C
G:T	T:C	C:C	G:G	T:T	T:C	C:C	A:G	G:C	T:T	A:A	C:C	C:C	G:G	A:A	C:C
?:?	T:T	C:C	G:G	C:T	C:C	T:T	G:G	C:C	T:C	A:A	C:C	C:C	?:?	A:A	T:C
G:T	T:T	C:C	G:G	?:?	T:C	?:?	A:A	C:G	?:?	A:A	C:C	C:C	G:G	A:A	C:C
T:T	T:T	C:C	G:G	T:T	C:C	C:C	C:A	C:C	T:T	A:A	C:C	C:C	?:?	C:C	C:C
T:T	C:C	C:C	G:G	?:?	C:C	T:?	G:G	G:G	T:T	A:A	C:C	C:C	G:G	A:A	C:C
?:?	C:C	?:?	?:?	T:T	C:C	T:T	G:G	C:C	T:T	A:A	C:C	C:C	G:G	A:A	C:C
T:T	?:?	C:C	G:G	T:T	T:C	T:T	A:G	G:G	T:T	A:A	C:C	C:A	G:G	?:?	C:C



SNP Explosion in the Genomics Era

3K RGP *GigaScience* 2014, **3**:7
http://www.gigasciencejournal.com/content/3/1/7

Rice

DATA NOTE

The 3,000 rice genomes project

The 3,000 rice genomes project[1,2,3*†]

- ✓ Approximately 18.9 million single nucleotide polymorphisms (SNI discovered when aligned to the reference genome of the temper Nipponbare.
- ✓ Phylogenetic analyses based on SNP data confirmed differentiation of the O. sativa gene pool into 5 varietal groups – indica, aus/boro, basmati/sadri, tropical japonica and temperate japonica.

Plant Biotechnology Journal

Plant Biotechnology Journal (2020) **18**, pp. 1354–1360 doi: 10.1111/pbi.13361

Wheat

Review

The Wheat 660K SNP array demonstrates great potential for marker-assisted selection in polyploid wheat

Congwei Sun, Zhongdong Dong, Lei Zhao, Yan Ren, Ning Zhang and Feng Chen

National Key Laboratory of Wheat and Maize Crop Science/Agronomy College, Henan Agricultural University, Zhengzhou, China

Mol Breeding (2017) 37: 20
DOI 10.1007/s11032-017-0622-z

CrossMark

Maize

Development of a maize 55 K SNP array with improved genome coverage for molecular breeding

Cheng Xu · Yonghong Ren · Yinqiao Jian · Zifeng Guo · Yan Zhang · Chuanxiao Xie · Junjie Fu · Hongwu Wang · Guoying Wang · Yunbi Xu · Ping Li · Cheng Zou

Search

- Search & Browse GrainGenes
- Genetic Maps at GrainGenes

Submit Your Data to GrainGenes

- Submit Your Data to GrainGenes
- GrainGenes Data Formats

Community Services

- Calendar
- Current Hot Topics
- Data Download
- Database Information
- GrainGenes Mailing List
- Job Listings
- Oatmail Mailing List
- Tutorials

Species Portals on GrainGenes

- Annual Wheat Newsletter
- Barley Boulevard
- Barley Genetics Newsletter
- Oat Newsletter
- Wheat Gene Catalogue

The GrainGenes Genome Browsers

Share this on: SHARE

Popular Browsers

- Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)
- Barley Morex, MorexV2 assembled by TRITEX (2019)
- PepsiCo OT3098 Hexaploid Oat (2020)

Wheat

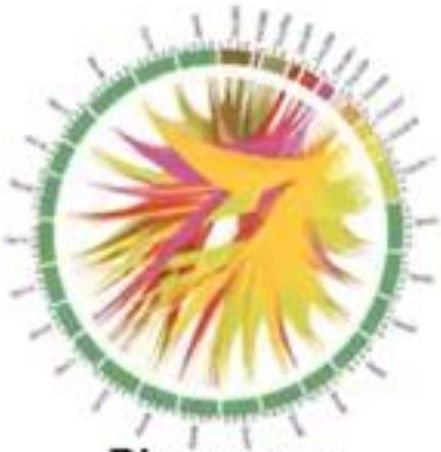
- 10+ Wheat Genome Project
- Triticum turgidum Durum Wheat Svevo (RefSeq Rel. 1.0) (2019)
- Wild Emmer Wheat Zavitan WEWSeq v2.0 genome assembly (2019)
- Wheat Chinese Spring IWGSC RefSeq v1.0 genome assembly (2018)
- Aegilops tauschii Aet v4.0 genome assembly (2017)
- Wild Emmer Wheat Zavitan WEWSeq v1.0 genome assembly (2017)
- Hexaploid Wheat Pangenome, Montenegro et al., 2017
- Wheat Physical EST Maps (2004)
- D Genome Physical Map

Barley

- Barley Morex V3 (2021)
- Barley Pangenome Project - 2020
- Barley Morex, MorexV2 assembled by TRITEX (2019)
- Barley Morex IBSC genome assembly (2017)
- Barley (2016) (Ensembl Release 31)
- Barley Bin Maps

Oat

- PepsiCo OT3098 Hexaploid Oat (2020)
- Avena atlantica Diploid Oat (2019)
- Avena eriantha Diploid Oat (2019)
- Hexaploid Oat (2013)

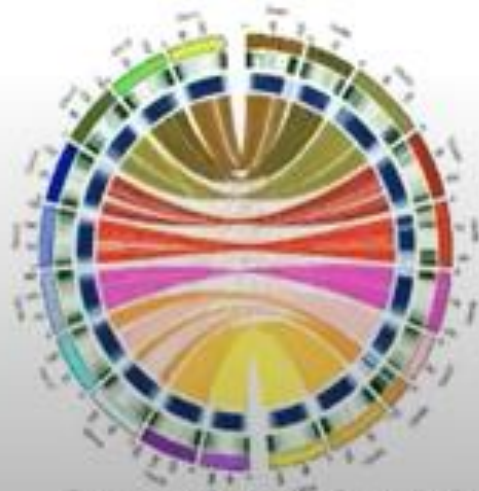


Pigeonpea
(*Nature Biotechnology 2012*)

Chickpea
(*Nature Biotechnology 2013*)

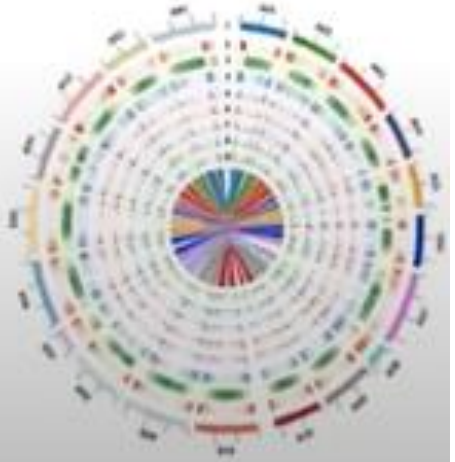
Pearl millet- 2017
(*Nature Biotechnology 2017*)

Wild ancestors of groundnut



Subspecies *fastigiata*

Cultivated tetraploid groundnut



Subspecies *hypogaea*

Molecular marker availability

Number of molecular markers is not an unlimited factor in wheat

SNP markers/chips

1534 Illumina Golden Gate (2010)

5000 KASP markers (2011)

9000 Illumina Golden Gate (2011)

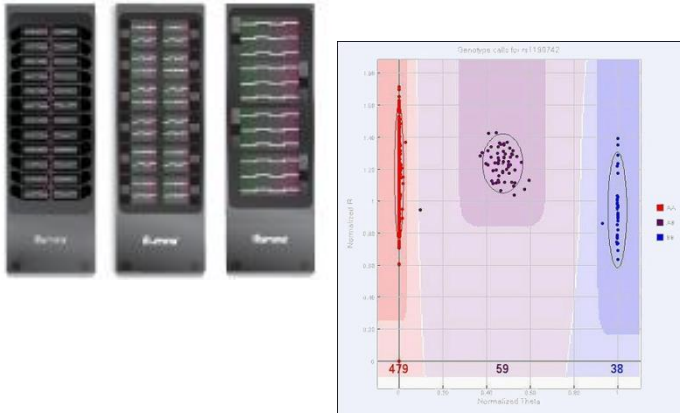
90000 Illumina infinitum (2012)

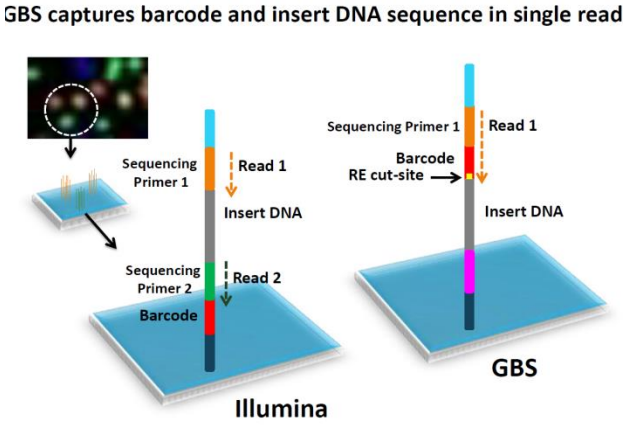
Genotyping by Sequencing (GBS)

20-40000 markers (2012)

384000 SNPs Affimetrix Axiom (2013)

660000 SNP Array (2020)





SNP marker availability in crops

Crop	Size	Technology	Information/resource	Reference
Apple	20K	Illumina Infinium BeadChip		Bianco et al. (2014)
Apple	480K	Affymetrix Axiom	Axiom Apple480K	Bianco et al. (2016)
Apple	8K	Illumina Infinium BeadChip		Chagné et al. (2012)
Barley	9K	Illumina Infinium BeadChip		Comadran et al. (2012)
Brassica	60K	Illumina Infinium BeadChip	International Brassica SNP Consortium	Clarke et al. (2016)
Brassica	15K	Illumina Infinium BeadChip	TraitGenetics	Unpublished
Cherry	6K	Illumina Infinium BeadChip	RosBREED 6K SNP	Peace et al. (2012)
Chickpea	50K	Affymetrix Axiom	Axiom *CicerSNP* Array	
Cotton	63K	Illumina Infinium BeadChip	In development	Hulse-Kemp et al. (2015)
Cotton	35K	Affymetrix Axiom	Axiom cotton Genotyping array	
Cowpea	60K	Illumina Infinium BeadChip		Close et al. (2015)
Grape	18K	Illumina Infinium BeadChip	GrapeReSeq 18K Vitis	Le Paslier et al. (2013)
Grape	9K	Illumina Infinium BeadChip	Vitis9KSNP	Myles et al. (2010)
Lettuce	35K	Affymetrix GeneChip		Stoffel et al. (2012)
Maize	50K	Illumina Infinium BeadChip	MaizeSNP50 BeadChip	Ganal et al. (2011)
Maize	3K	Illumina Infinium BeadChip	Subset of MaizeSNP50	Rousselle et al. (2015)
Maize	600K	Affymetrix Axiom	Axiom 600K	Unterseer et al. (2014)
Maize	50K	Affymetrix Axiom	Maize 55K Axiom	Xu et al. (2017a)
Oat	6K	Illumina Infinium BeadChip	Infinium 6K Oat array	Tinker et al. (2014)
Peach	9K	Illumina Infinium BeadChip		Verde et al. (2012)
Pear	1K (9K)	Illumina Infinium BeadChip	8K apple chip + 1K Pear	Montanari et al. (2013)
Peanut	58K	Affymetrix Axiom	Axiom_Arachis array	Pandey et al. (2017)
Pepper	16K	Illumina Infinium BeadChip		Ashrafi et al. (2012)
Pepper	640K	Affymetrix GeneChip	https://pepchip.genomecenter.ucdavis.edu	In progress
Poplar	12K	Illumina Infinium BeadChip		Faivre-Rampant et al. (2016)
Potato	20K	Affymetrix Axiom	SolSTW array	Vos et al. (2015)
Potato	8K	Illumina Infinium BeadChip		Hamilton et al. (2011)
Rice	1M	Affymetrix		McCouch et al. (2010)
Rice	50K	Illumina Infinium BeadChip	RiceSNP50	Chen et al. (2014)
Rice	6K	Illumina Infinium BeadChip	RICE6K	Yu et al. (2014)
Rice	50K	Affymetrix Axiom	OsSNPnks	Singh et al. (2015)
Rice	44K	Affymetrix GeneChip		Tung et al. (2010)

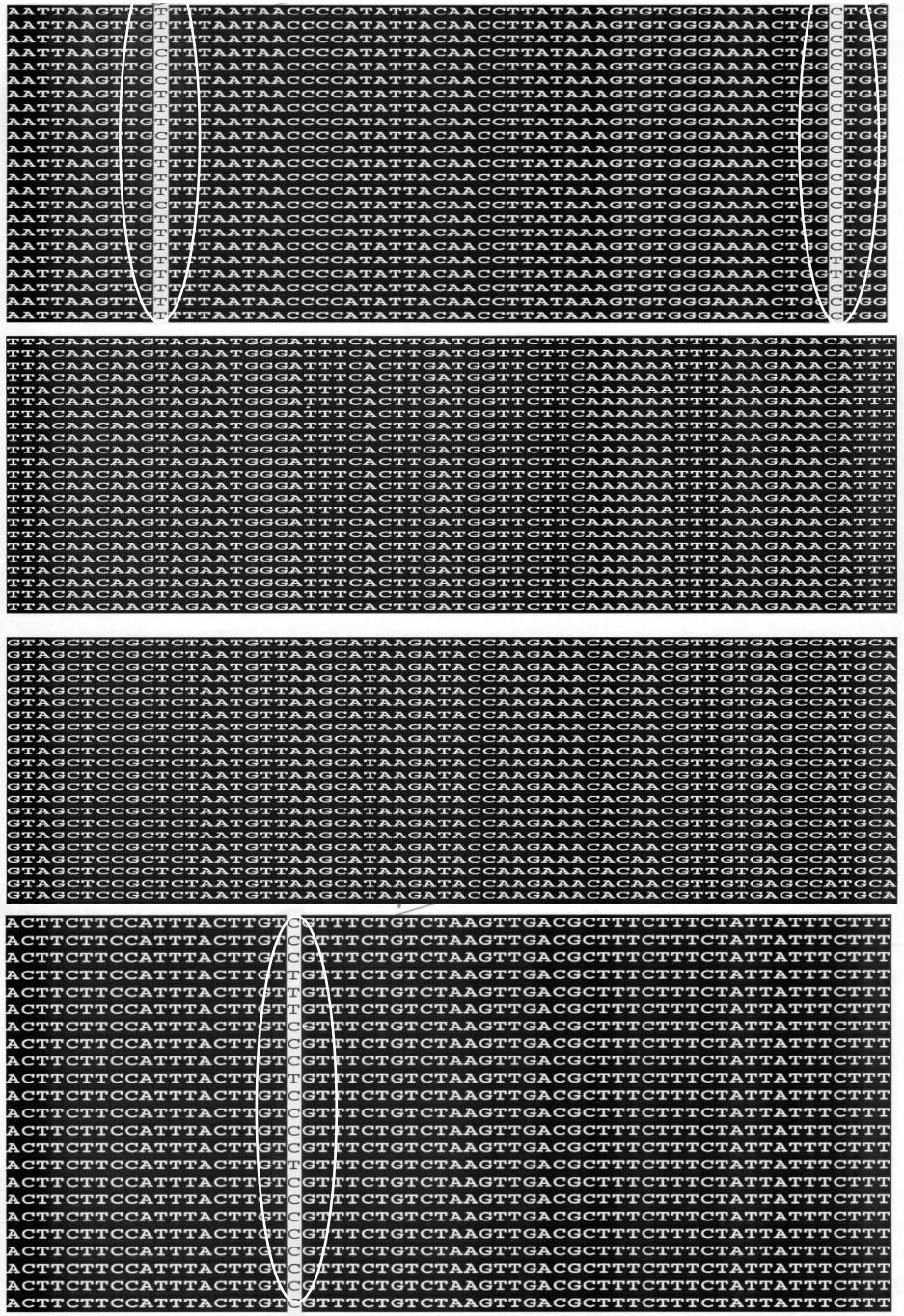
SNP marker availability in crops

Crop	Size	Technology	Information/resource	Reference
Rose	68K	Affymetrix Axiom	WagRhSNP68K	Koning-Boucoiran et al. (2015)
Rye	600K	Affymetrix Axiom	Rye600K	Bauer et al. (2017)
Ryegrass	9K	Illumina Infinium BeadChip		Blackmore et al. (2015)
Soybean	50K	Illumina Infinium BeadChip	SoySNP50K	Song et al. (2013)
Soybean	180K	Affymetrix Axiom	SoyaSNP180K Axiom	Lee et al. (2015)
Strawberry	90K	Affymetrix Axiom	IStraw90	Bassil et al. (2015)
Sunflower	25K	Illumina Infinium BeadChip		Livaja et al. (2016)
Sunflower	10K	Illumina Infinium BeadChip		Bachlava et al. (2012)
Tomato	10K	Illumina Infinium BeadChip		Sim et al. (2012)
Wheat	9K	Illumina Infinium BeadChip	Wheat 9K iSelect	Cavanagh et al. (2013)
Wheat	90K	Illumina Infinium BeadChip	Wheat 90K iSelect	Wang et al. (2014)
Wheat	660K	Affymetrix Axiom	Wheat 660K Axiom	Jia Jizeng (personal communication)
Wheat	820K	Affymetrix Axiom	Wheat HD genotyping array	Winfield et al. (2016)
Wheat	35K	Affymetrix Axiom	Wheat Breeder's genotyping array	Allen et al. (2017)
Crop specific	Scalable	Exome capture	Exome sequencing	Allen et al. (2013); Henry et al. (2014)
De novo (applicable to multiple crops)	50–300K	GBS	Genotype-by-sequencing	Elshire et al. (2011)
	~50K	DArT-seq	DArT sequencing	http://www.diversityarrays.com
	1-2K	rAmpSeq	Repeat amplification sequencing	Buckler et al. (2017)
	Depend on genome size, sequencing depth and technology	SLAF-seq	Specific length amplified sequencing	Sun et al. (2013)
		RAD-seq	Restriction site-associated DNA sequencing	Baird et al. (2008)
		Two-enzyme GBS		Poland et al. (2012)
		ddRAD	Double digest RAD	Peterson et al. (2012)
		SBG	Sequencing-based genotyping	Truong et al. (2012)
		REST-seq	Restriction fragment sequencing	Stolle and Moritz (2013)
		RAD capture	Rapture	Ali et al. (2016)
		MSG	Multiplexed shotgun genotyping	Andolfatto et al. (2011)
		ezRAD		Toonen et al. (2013)

Types of Association mapping

- Whole-genome association studies; also called Genome wide association mapping
- Candidate genes-based (direct approach); candidate genes known through synteny, biochemical pathways, functions of genes known in model crops etc.

Candidate genes-based association mapping



Sequencing of candidate genes in the germplasm collection

Association Mapping as a Plant Breeding Strategy

AM versus QTL Mapping

- **Association Mapping can be conducted directly on the breeding material, therefore:**
  - **Direct inference from research to breeding is possible**
  - **Phenotypic variation is observed for most traits of interest**
  - **Marker polymorphism is higher than in biparental populations**
  - **Routine evaluations provide phenotypic data**

EXAMPLES OF NOVEL GENE/ALLELE DISCOVERY USING GWAS APPROACH

With collaborators from Kazakhstan-under IWWIP (International Winter Wheat Improvement Programme)

Kazakhstan is one of the great wheat producers in Central Asia; among the 10 largest wheat producers

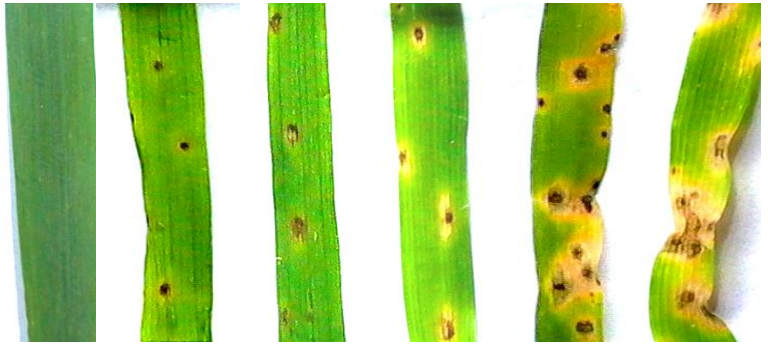
Wheat production in Kazakhstan is important for food security

Tan spot, caused by *Pyrenophora tritici-repentis*

- Tan spot, caused by *Pyrenophora tritici-repentis*, is a serious foliar disease of wheat, especially in Kazakhstan and Russia. Under conditions favorable for disease development, yield losses can rise beyond 50%. This disease is favoured by reduced tillage systems and monoculture of wheat.

- Many races of *P. tritici-repentis* have been identified in Kazakhstan, including races 1, 2, 3, 5, 7 and 8.

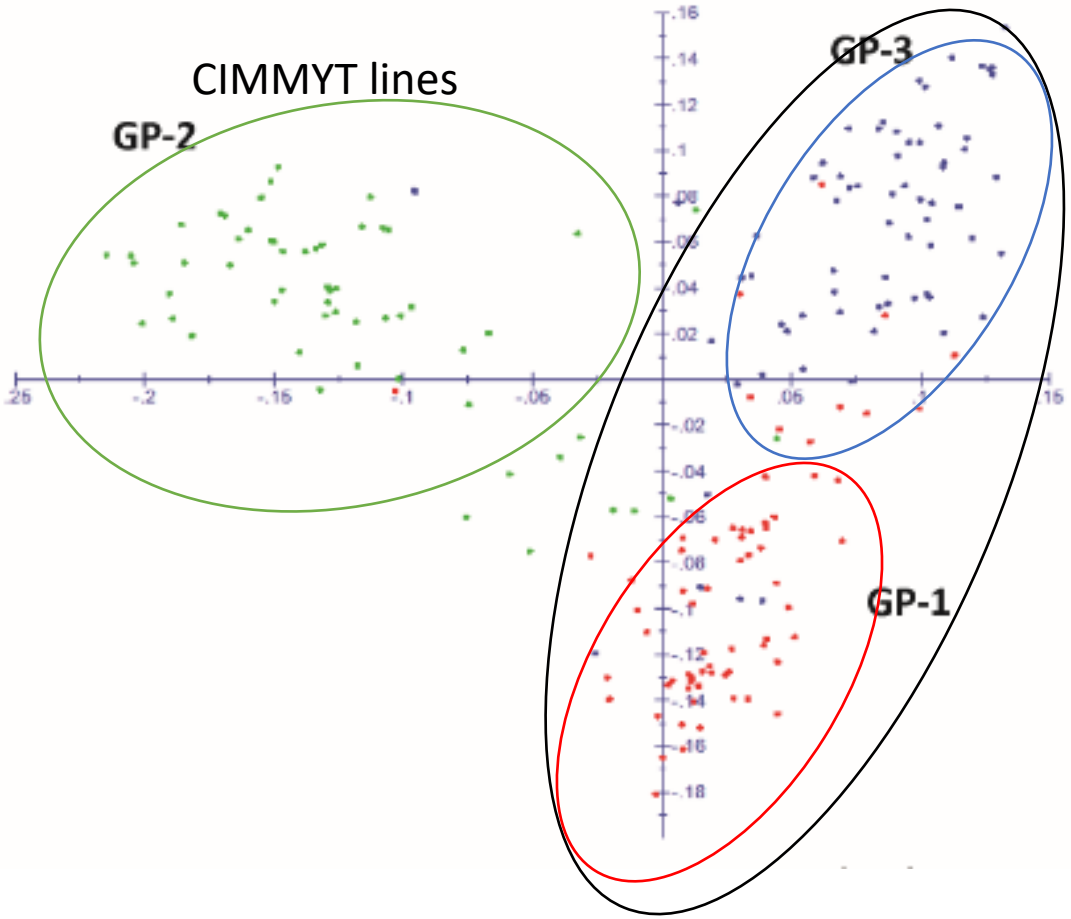
- In spite of the economic importance of disease, wheat germplasm from Kazakhstan and Russia have not been evaluated for genetic resistance to tan spot.



Phenotyping for tan spot resistance in Kazakhstan

A panel of 191 spring and winter wheat lines from Kazakhstan and CIMMYT spring wheat lines

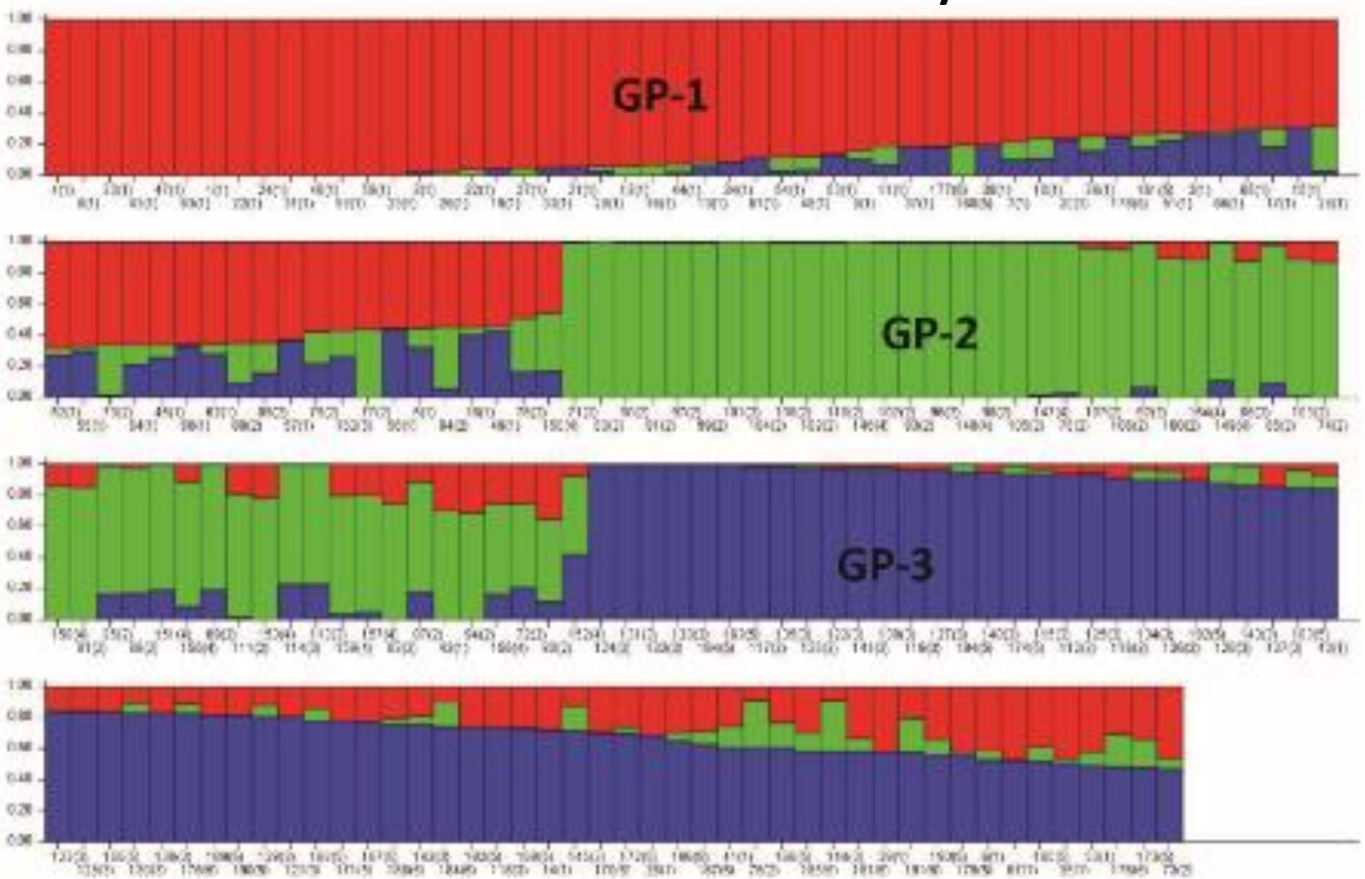
Genotyped by a NGS approach Genotyping-by-Sequencing (GBS)



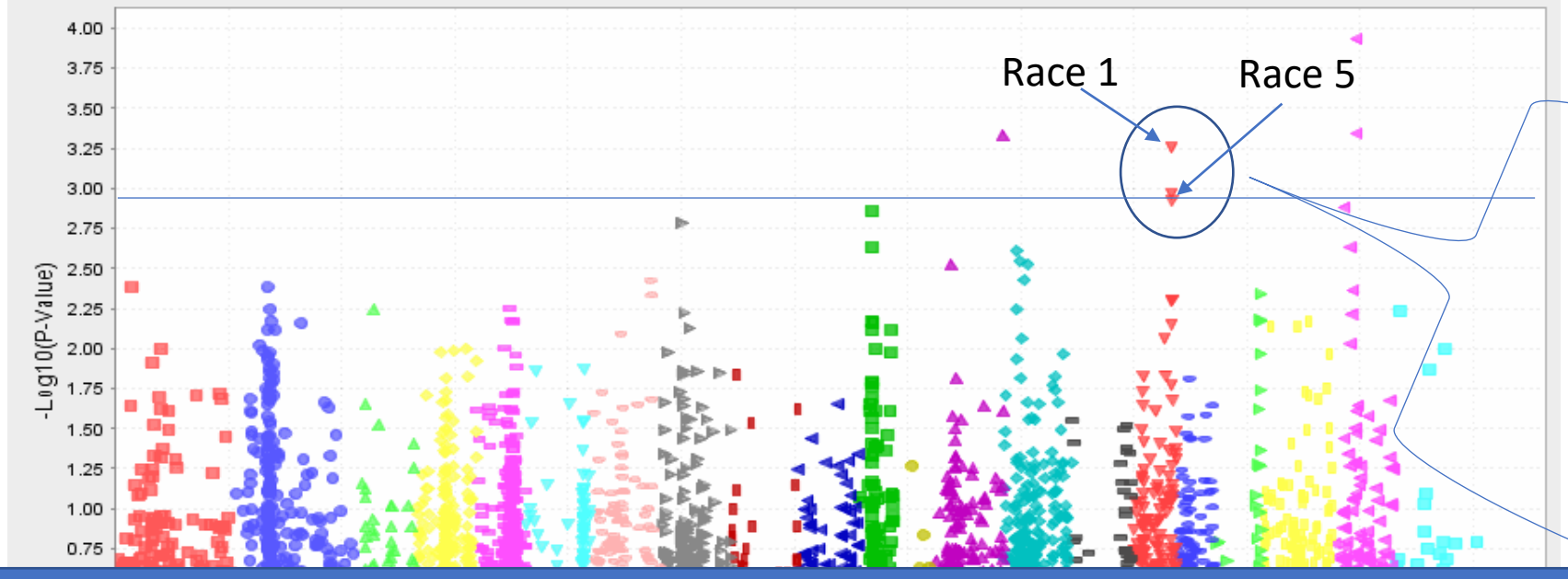
2D Principal component analysis

Kazakhstan lines

Admixture analysis



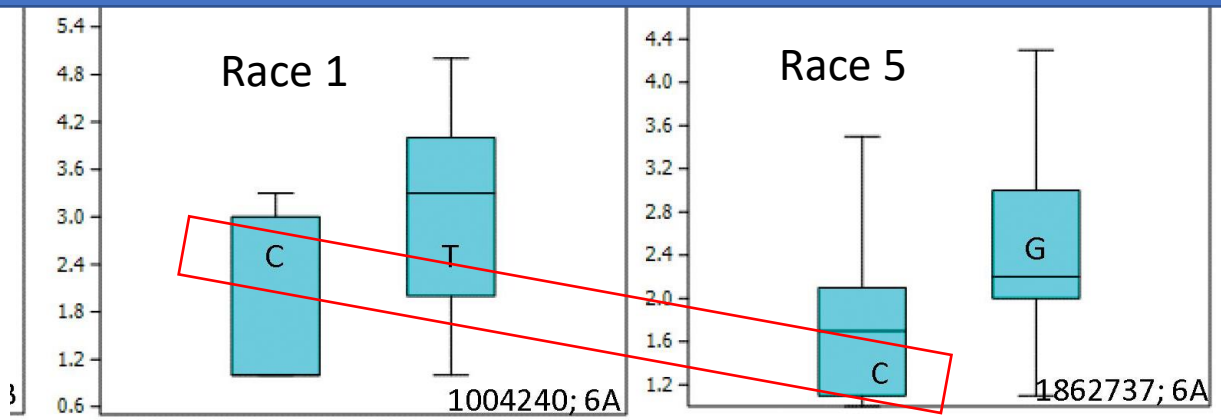
Structure of Kazakhstan wheat panel



TraesCS6A02G384600

7880

Both candidate genes code for proteins having oxidoreductase activity. Oxidoreductase family of proteins are known as important components of pathogen-associated molecular pattern-triggered immunity *via* production of reactive oxygen species in response to pathogen attack (Heiser and Elstner, 2002).



"CC" combination

Implications of these results for Breeding

Novel

Novel

ID	Name	Origin	Growth habit	Race 1 1B_ 140 6319	3B_ 114 7153	4B_ 395 8510	5A_ 113 4493	5B_ 394 6488	6A_ 1004 240	7B_ 302 1234	7B_ 108 1730	Race 1_ average	Race 5 5A_10 08802	5D_10 93048	6A_18 62737	Race 5_ average
				T>C	G>C	C>T	T>C	C>T	T>C	T>C	G>A		G>C	T>G	C>G	
908618316005_D_1	Alikhan	KZ	Winter	C	C	T	C	C	T	C	A	1	G	T	C	2
908618316005_E_2	Derbes	KZ	Winter	C	C	T	C	C	T	T	G	1,3	S	T	C	1
908618316005_A_3	Konditerskaya	KZ	Winter	N	C	T	C	C	T	T	G	1	G	T	C	2
908618316005_D_3	Kokbiday	KZ	Winter	T	C	C	C	C	T	C	A	1,3	N	T	C	1
908618316005_G_3	Manshyk	KZ	Winter	C	C	N	T	C	T	T	G	2	G	T	C	2
908618316005_F_5	Tyngysh	KZ	Winter	T	C	Y	C	C	T	C	A	1	N	G	C	1
908618316005_A_6	Ybileinaya 60	KZ	Winter	C	G	T	T	C	T	T	G	1	C	G	C	1
908618316005_D_7	Naz/GF55-5	KZ	Winter	C	C	T	T	C	C	C	A	1	N	T	C	1
908618316005_F_7	428g/MK-122A-1	KZ	Winter	C	C	T	C	C	T	C	A	1	N	T	C	1
908618316005_D_9	Astana	KZ	Spring	N	N	T	C	C	T	T	G	2	G	G	C	1
908618316005_E_9	Aktubinka	KZ	Spring	C	C	T	C	C	T	T	G	1,3	G	T	C	1
908618316005_G_9	Karabalykskaya 92	KZ	Spring	C	C	T	C	C	T	T	G	1	G	T	C	1
908618316005_H_9	Kazakhstan-skaya 25	KZ	Spring	C	C	T	C	C	T	T	G	1,7	G	T	C	1
908618316005_B_10	Kazakhtanskaya rannespelaya	KZ	Spring	N	C	T	C	C	T	T	G	1,7	G	T	C	2

Footnote: Green highlighted cells represent favorable allele of each associated SNP

Lines showing resistances to Race 1 and Race 5 with best allele combinations

PLOS ONE

OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

Exploring Potential of Pearl Millet Germplasm Association Panel for Association Mapping of Drought Tolerance Traits

Deepmala Sehgal, Leif Skot, Richa Singh, Rakesh Kumar Srivastava, Sankar Prasad Das, Jyoti Taunk, Parbodh C. Sharma, Ram Pal, Bhasker Raj, Charles T. Hash, Rattan S. Yadav

Published: May 13, 2015 • https://doi.org/10.1371/journal.pone.0122165

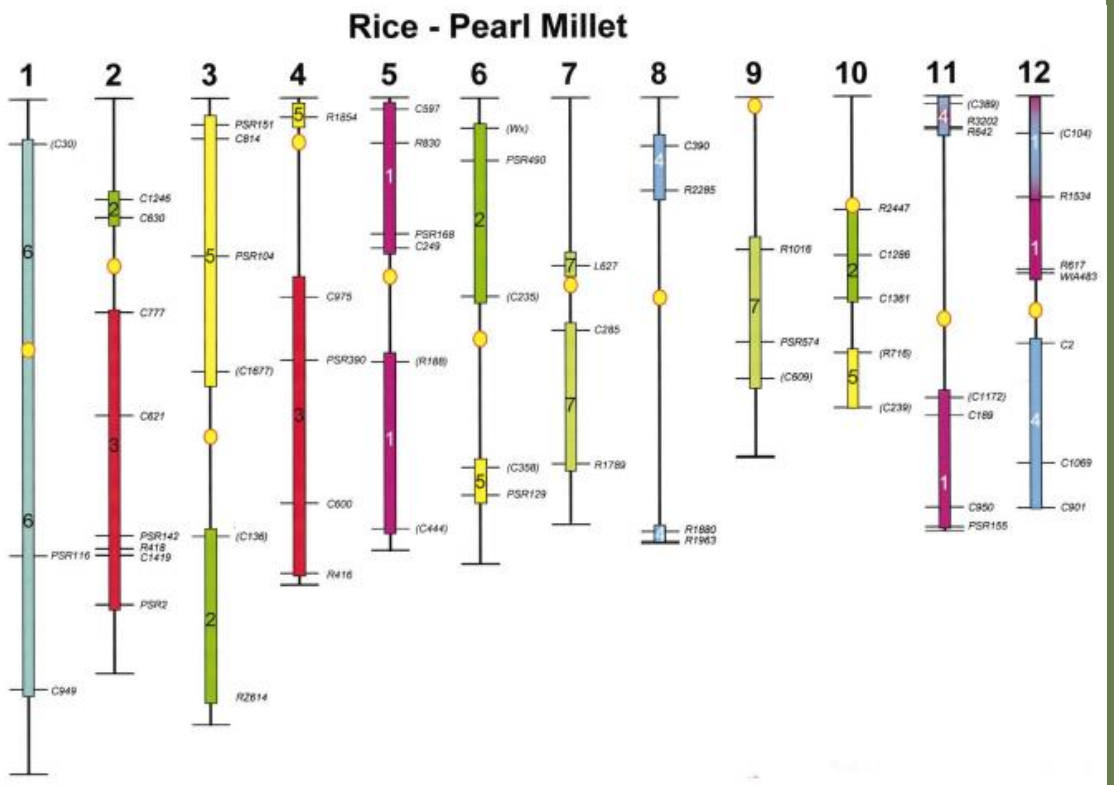
Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is the sixth most important global cereal crop which is grown by subsistence farmers in the semi-arid regions of sub-Saharan Africa and the Indian subcontinent

It can be grown in a vast range of harsh environmental conditions where other major crops such as wheat rice and maize fail to grow; environments with high mean temperatures and frequent droughts and/or with poor soil fertility

A Pearl Millet Germplasm Association Panel (PMiGAP) comprising 250 inbred lines has been assembled by ICRISAT from a large set of 1000 diverse breeding lines and accessions of landraces and elite cultivars for association mapping of complex traits

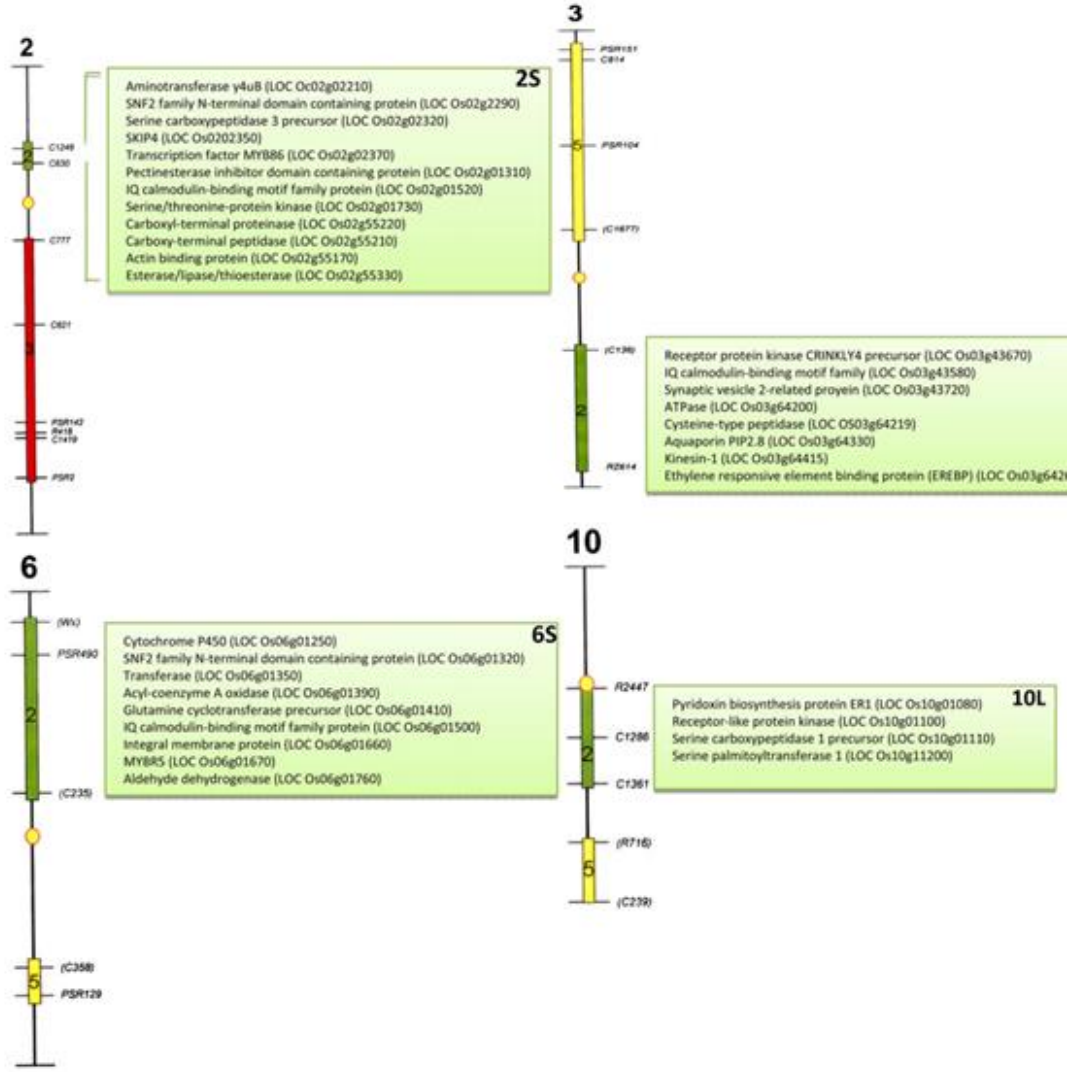
Candidate gene-based association mapping in PMiGAP

Synteny

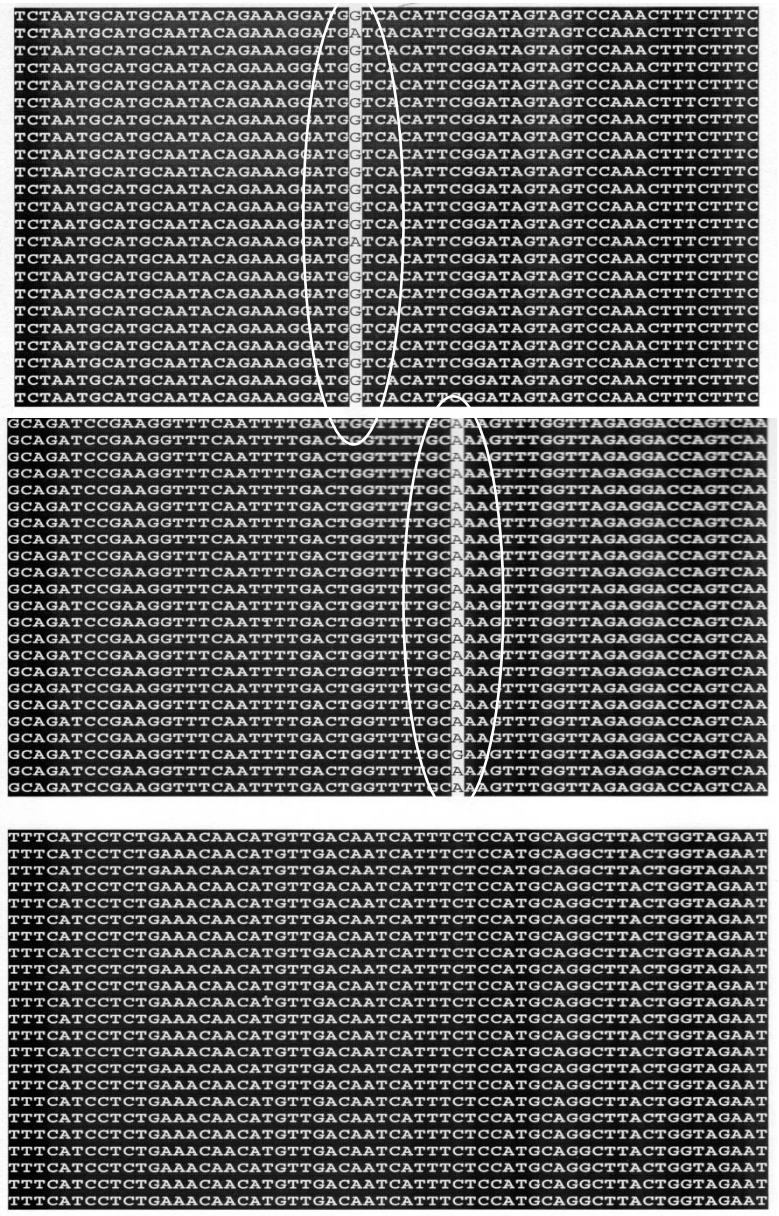


Source: Devos et al. 2000

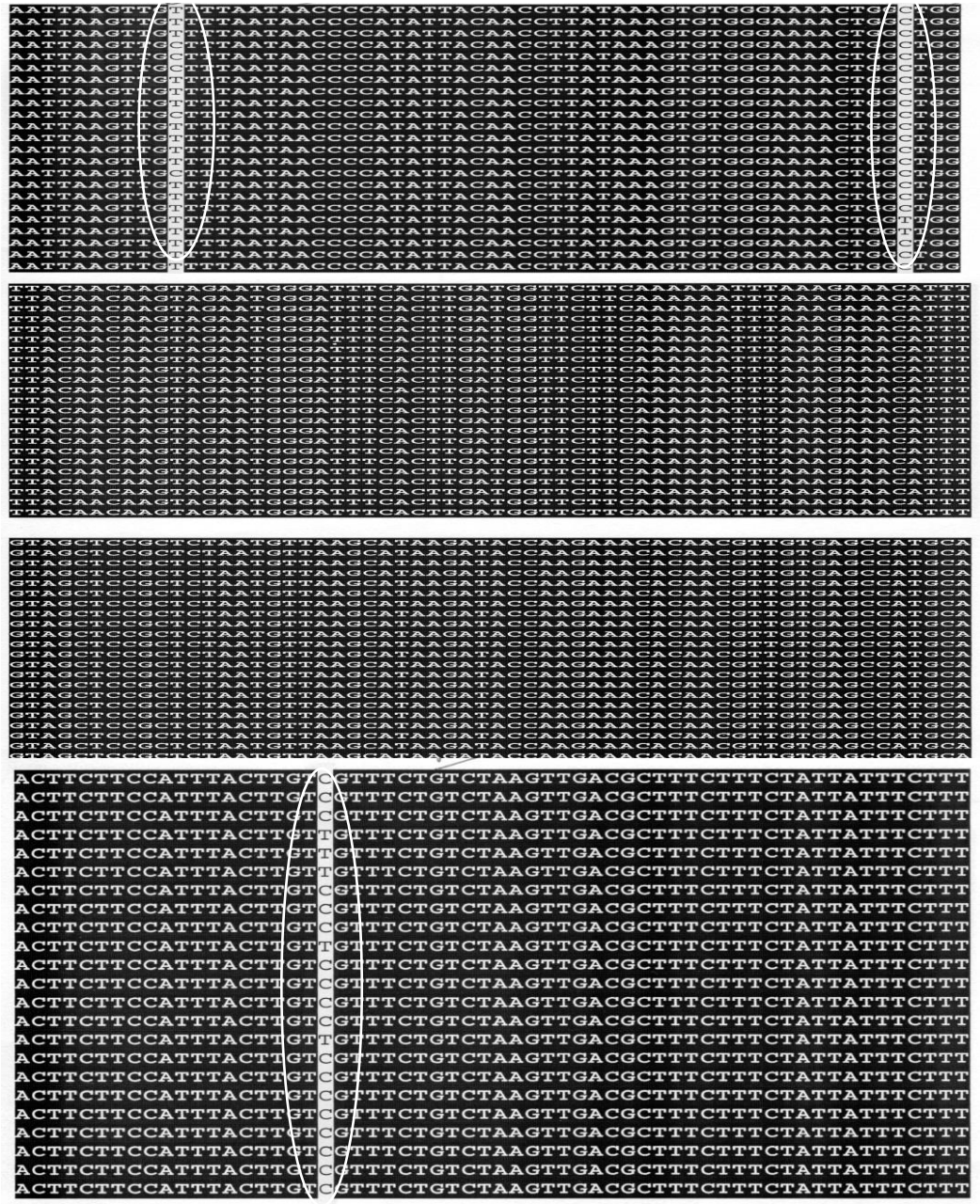
Rice chromosomes syntenic to pearl millet LG2



Sequencing of candidate genes in PMiGAP

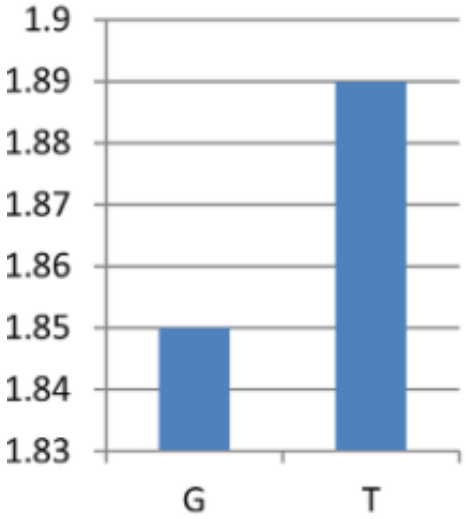


Sequencing of Zn finger CCCH type transcription factor gene

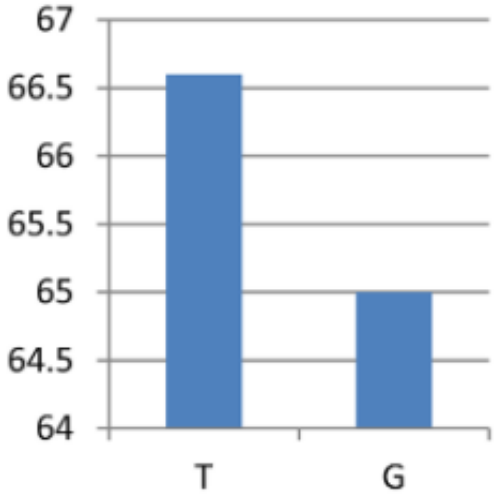


Sequencing of Serine/threonine protein kinase gene

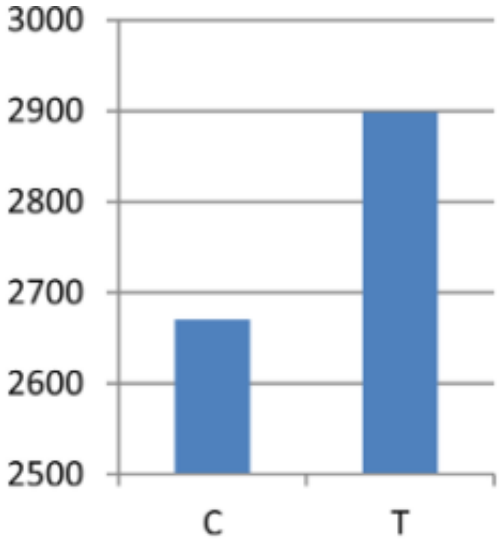
Allelic effects of genes on agronomic traits of pearl millet under drought stress



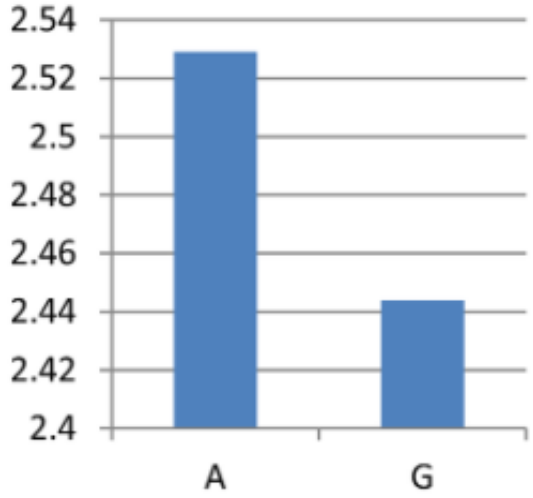
Uridylate kinase gene
Tiller per plant



Serine/threonine protein kinase gene
Panicle harvest index



Acetyl CoA carboxylase gene
Grain yield

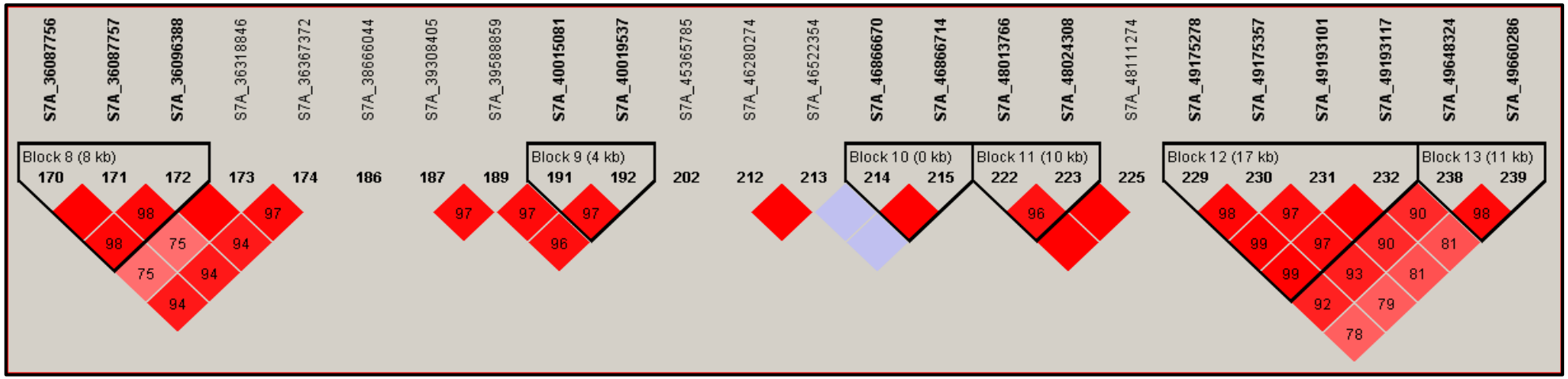


Zn finger CCCH type transcription factor
Panicle diameter

Haplotypes-based GWAS-A paradigm shift in GWAS analysis

What are haplotype blocks?

A haplotype block (haploblock) defines a region of the genome that comprises a set of neighboring genetic markers (i.e. SNPs), whereby their phased alleles are likely inherited together



Haplotypes are multiallelic

Biallelic SNPs

Two alleles A or G

Two alleles C or T

S1B_121281093	S1B_121290405
A/G	C/T
1B	1B
6.1cM	7.2cM
A	C
G	T
A	C
G	T
A	C
G	T
A	C
G	T
A	C
G	T
A	C
A	C
A	C
A	C
A	T
A	C
A	C
A	C
G	C
G	C
G	C
G	C

Haplotypes

S1B_121281093S1B_121290405
A/GC/T
1B1B
6.1cM7.2cM
AC
GT
AC
GT
AC
GT
AC
GT
AC
AC
AC
AC
AT
AC
AC
AC
GC
GC
GC
GC

Four alleles

AC

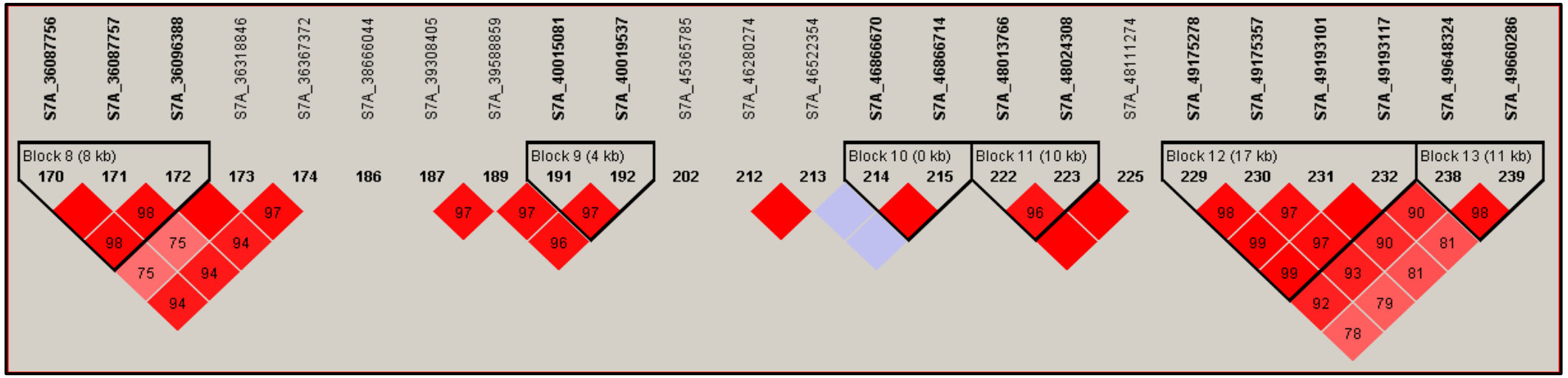
GT

AT

GC

Advantages of Haplotypes for GWAS?

- Being multiallelic, haplotypes are more informative than single SNPs
- Use of haplotypes instead of single SNPs maximizes linkage disequilibrium between markers and QTLs
- Use of multi-allelic haplotypes has significantly improved the power and robustness of GWAS in animals.
- Haplotype blocks exploit local epistasis among markers and improve prediction accuracies



Haplotypes-based GWAS identified exotic introgressions in elite lines of wheat and exotic-specific associations with grain yield under abiotic stress environments

SCIENTIFIC REPORTS

OPEN

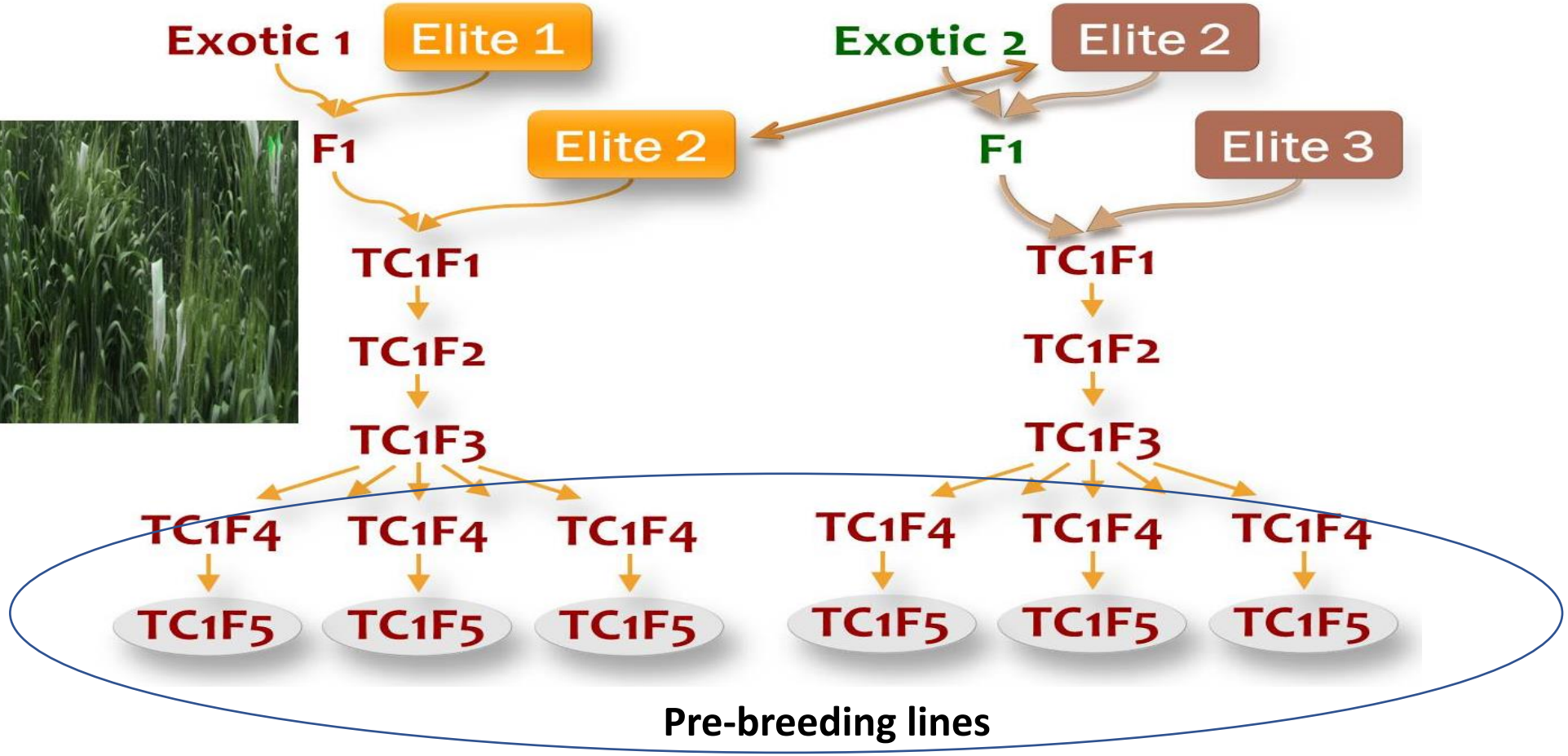
Harnessing genetic potential of wheat germplasm banks through impact-oriented-prebreeding for future food and nutritional security

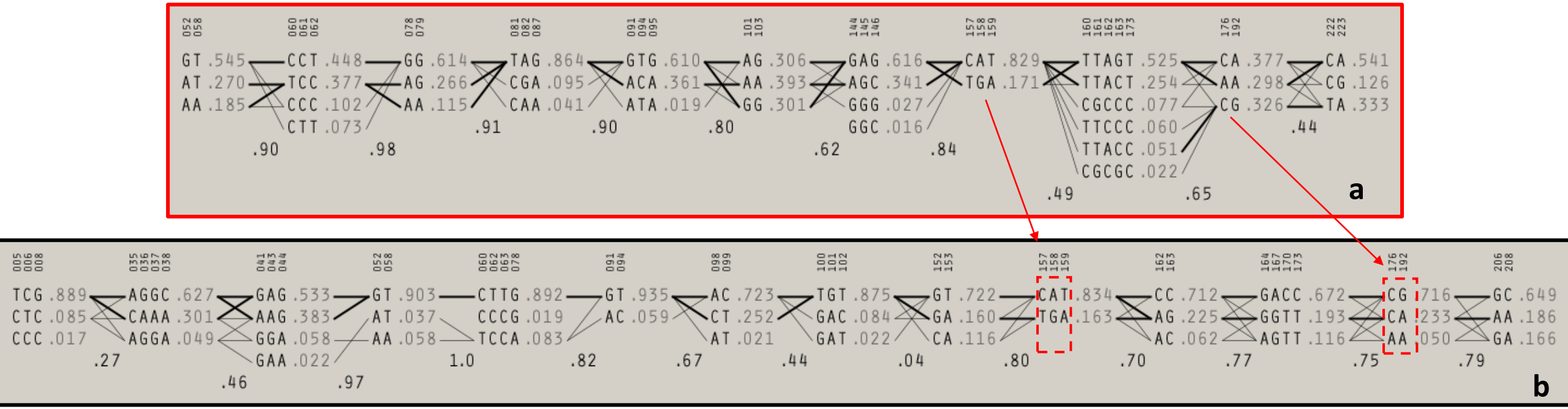
Received: 27 April 2018
Accepted: 2 August 2018
Published online: 21 August 2018

Sukhwinder Singh[1], Prashant Vikram[1], Deepmala Sehgal[1], Juan Burgueño[1], Achla Sharma[2], Sanjay K. Singh[3], Carolina P. Sansaloni[1], Ryan Joynson[4], Thomas Brabbs[4], Cynthia Ortiz[1], Ernesto Solis-Moya[5], Velu Govindan[1], Naveen Gupta[6], Harminder S. Sidhu[6], Ashwani K. Basandrai[7], Daisy Basandrai[7], Lourdes Ledesma-Ramires[5], Maria P. Suaste-Franco[5], Guillermo Fuentes-Dávila[8], Javier I. Moreno[9], Kai Sonder[1], Vaibhav K. Singh[10], Sanjay Singh[11], Sajid Shokat[12,13], Mian A. R. Arif[12], Khalil A. Laghari[14], Puja Srivastava[2], Sridhar Bhavani[15], Satish Kumar[3], Dharam Pal[16], Jai P. Jaiswal[17], Uttam Kumar[6], Harinder K. Chaudhary[7], Jose Crossa[1], Thomas S. Payne[1], Muhammad Imtiaz[18], Virinder S. Sohu[2], Gyanendra P. Singh[3], Navtej S. Bains[2], Anthony Hall[4,19] & Kevin V. Pixley[1]

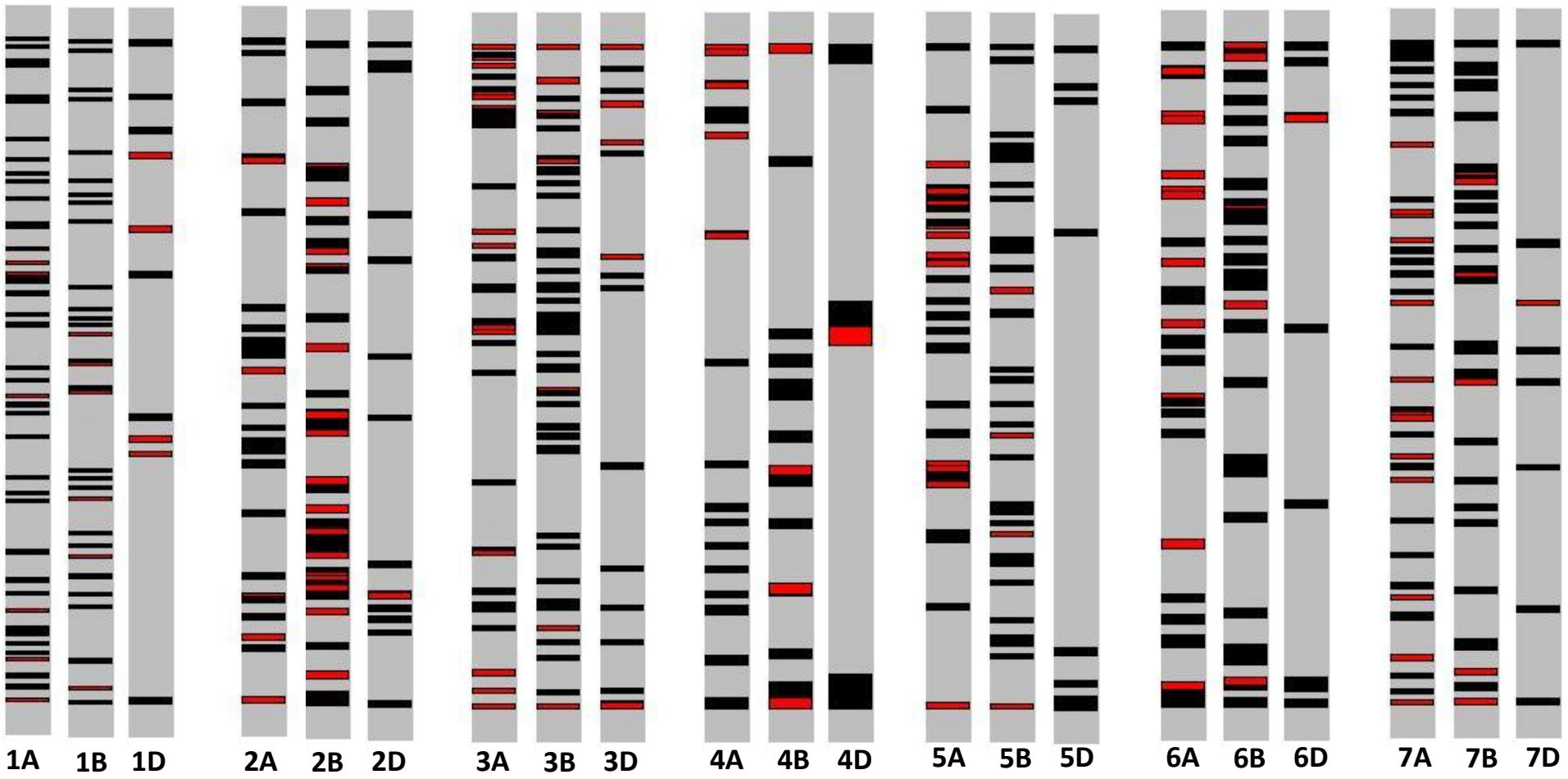
SEED of Discovery Project

Pre-breeding Strategy

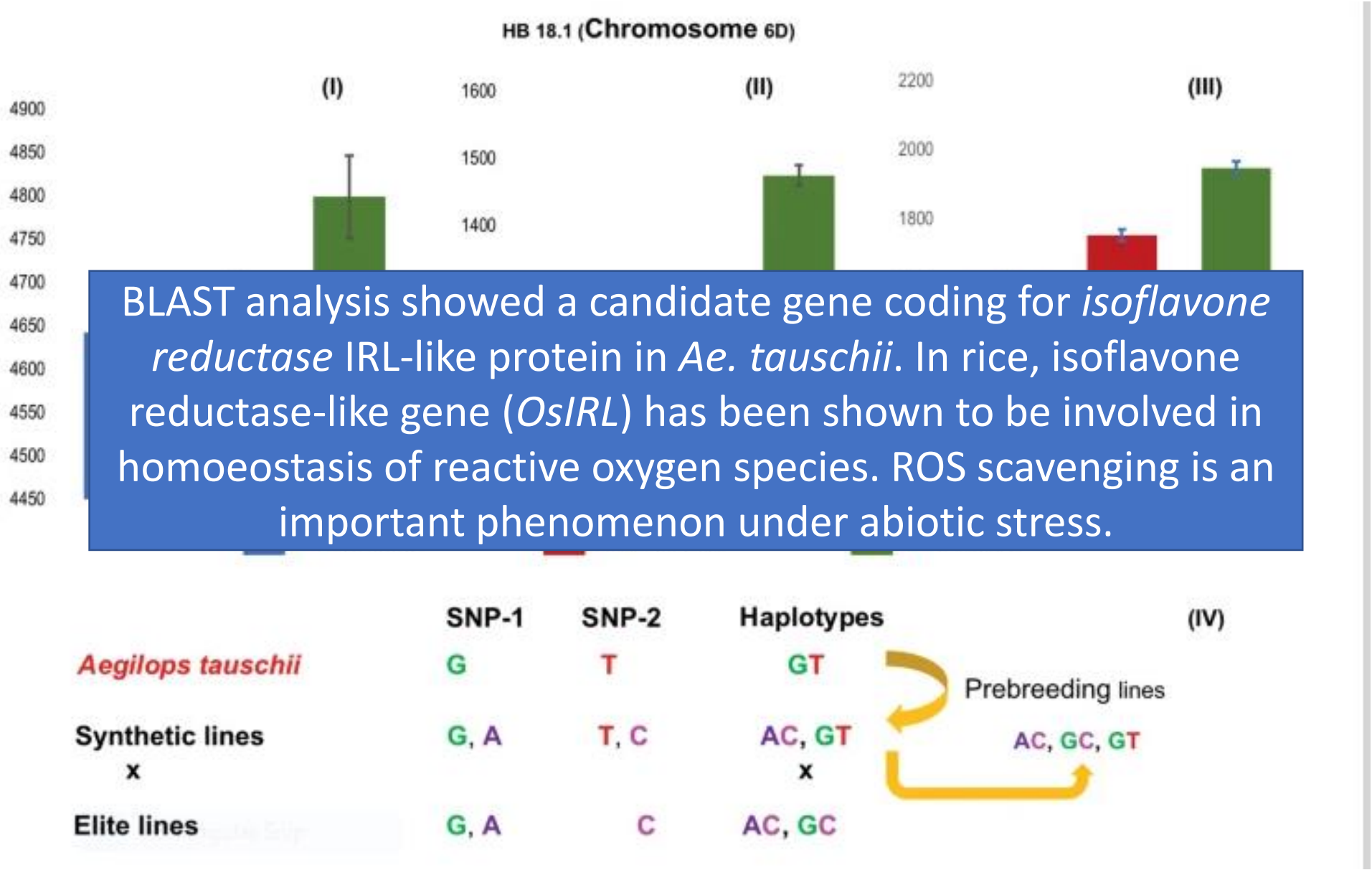




Comparison of Haplotype maps between Exotics and Elites



Haplotype maps of pre-breeding lines showing introgressed genomic regions from exotics as red bars


HB 18.1 (Chromosome 6D)
(I)
(II)
(III)
4900
4850
4800
4750
4700
4650
4600
4550
4500
4450
1600
1500
1400
2200
2000
1800
BLAST analysis showed a candidate gene coding for *isoflavone reductase* IRL-like protein in *Ae. tauschii*. In rice, isoflavone reductase-like gene (*OsIRL*) has been shown to be involved in homoeostasis of reactive oxygen species. ROS scavenging is an important phenomenon under abiotic stress.
SNP-1
SNP-2
Haplotypes
(IV)
Aegilops tauschii
G
T
GT
Synthetic lines
x
G, A
T, C
AC, GT
x
Elite lines
G, A
C
AC, GC
Prebreeding lines
AC, GC, GT

Thank you for your interest!