

WHAT THE WORLD EATS: WHEAT



Genetic strategies and challenges to mitigate rust pathogens in wheat

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CIMMYT

20/8/2019 ASPEN GLOBAL

Importance of wheat

- Globally the most important food crop
- Food for 2.5 billion poor (< US\$2) in 89 countries
- 20% of daily calories both developed and developing countries
- Most important protein source (20%) in less developed countries


2.5 billion people
in **89** countries


GROWN ON
 **215mm** 
HECTARES

 **\$50 billion**
IN TRADE EACH YEAR



WHEAT IS THE LARGEST
PRIMARY COMMODITY

GLOBAL PRODUCTION IS OVER
700 million tons



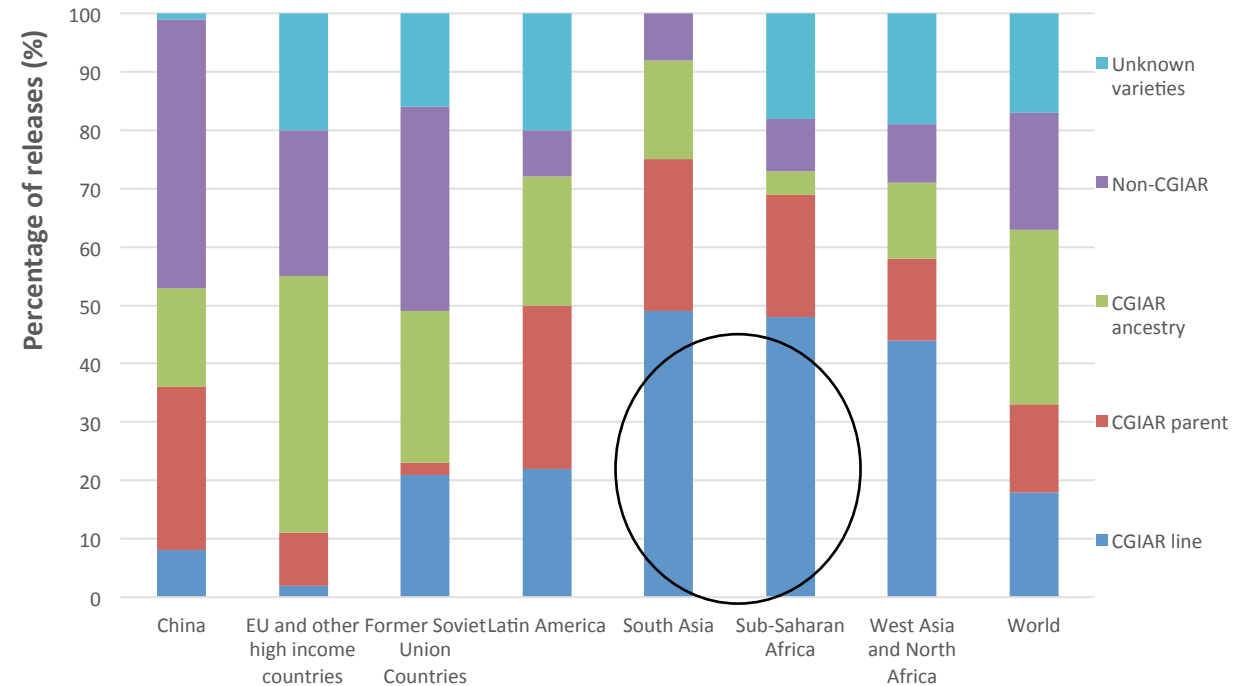
WHEAT PROVIDES **19%** OF OUR
TOTAL AVAILABLE CALORIES

CIMMYT Wheat Improvement Program in Mexico-

Targeted area: 60 million hectares (150 million acre)

- Irrigated (Mega-environment 1):
30 million hectares
- High rainfall (Mega-environment 2):
5 million hectares
- Semiarid (Mega-environment 4):
15 million hectares
- Irrigated-Warmer (Mega-environment 5):
10 million hectares

Wheat varieties releases by region and origin 1994-2014
(Source: Lantican et al. 2016)



About 50% of the varieties released in South Asia, Sub-Saharan Africa and West Asia & North Africa are direct CGIAR derived; and >30% have at least one parent.

Priority diseases for CIMMYT wheat breeding

Core traits

All mega-environments

Rust diseases

- Stripe rust
- Stem rust (including Ug99)
- Leaf rust



Key traits for specific mega-environments

- Septoria leaf blight (ME2) **high rainfall**
- Spot Blotch (ME5)
- Tan Spot (ME4)
- Fusarium – head scab and myco-toxins (ME2/4/5) **high rainfall**
- Karnal bunt (ME1)
- Root rots and nematodes (ME4)
- Aphids- (ME5)-**warm and irrigated**
- Wheat blast (ME5)-**warm and humid**

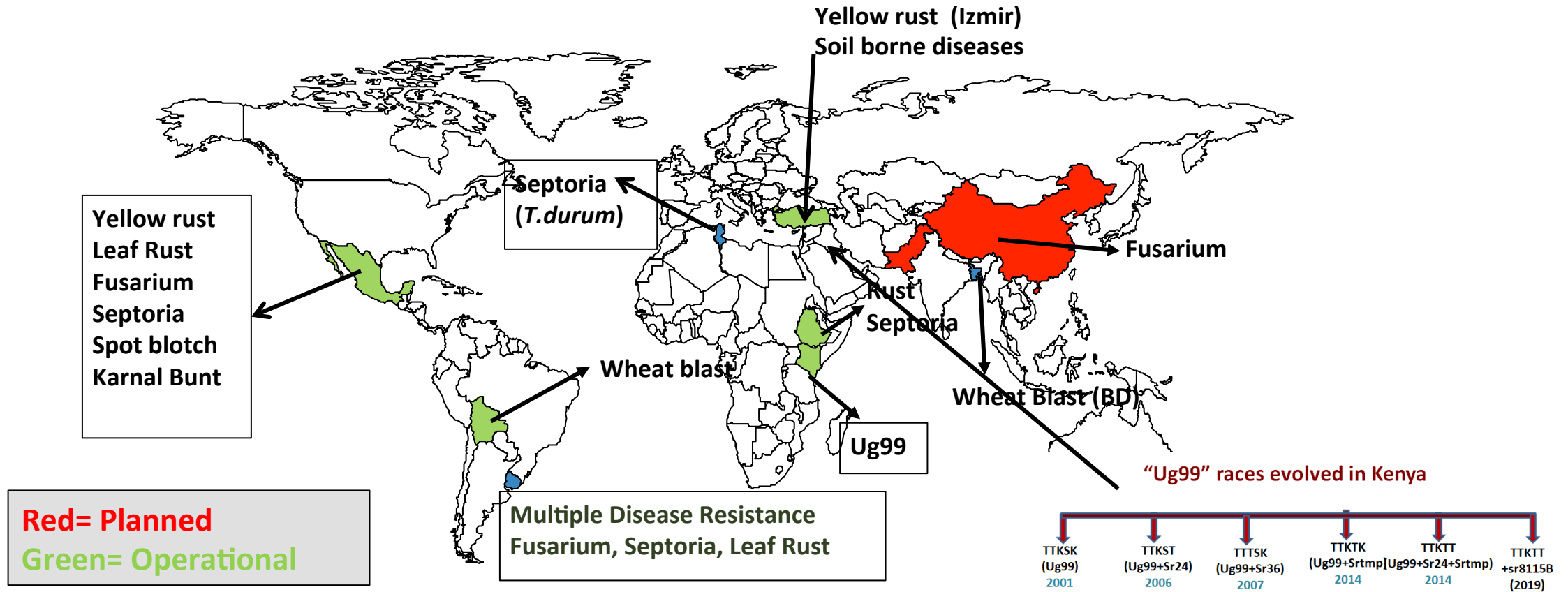


Annual losses due to rust diseases alone 4.5-5 billion USD

Main objective is to achieve resistance durability, averting major epidemics, and minimizing chemical control



A global disease phenotyping network for wheat improvement



Phenotyping Platforms

- Hubs for generating high quality phenotypic data, under defined good practices, and promoting training and sharing of the generated knowledge.
- Sites represent hotspots for specific diseases for evaluation and selection

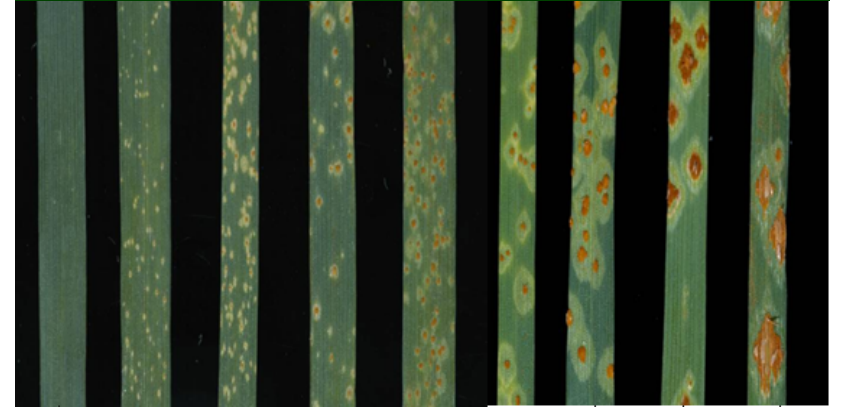
Race Specific resistance

often called major or seedling genes

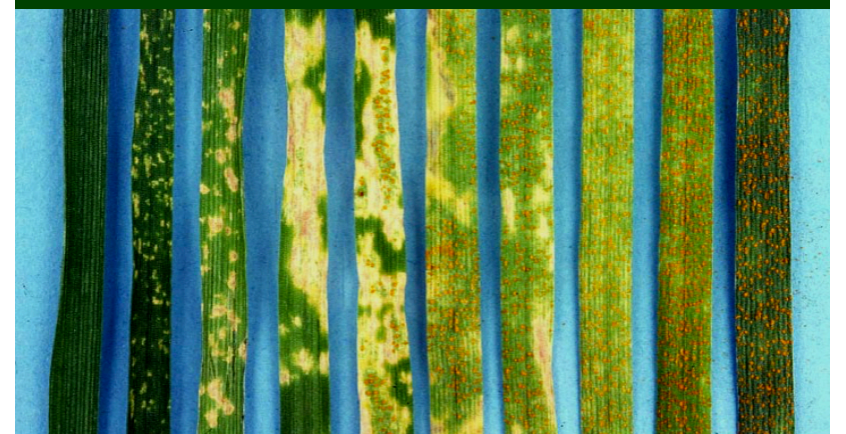
Widely used strategy in many breeding programs

- Have large to small effects
 - Effective in seeding and/or adult plants
 - hypersensitive host reactions
 - Rapid breakdown if deployed singly
 - (Boom & Bust) eg: *Yr27*, *Sr31*, *Srtmp*
 - Cloned genes have NBS-LRR structure
-
- Leaf rust (*Lr1*, *Lr21*, and *Lr10*)
 - Stem rust (*Sr13*, *Sr22*, *Sr33*, *Sr35*, *Sr45*, and *Sr50*)
 - Stripe or yellow (*Yr5*, *Yr7*, *YrSp*, *Yr10*)
 - Gene cassettes: 2 blades –Transgenic solution

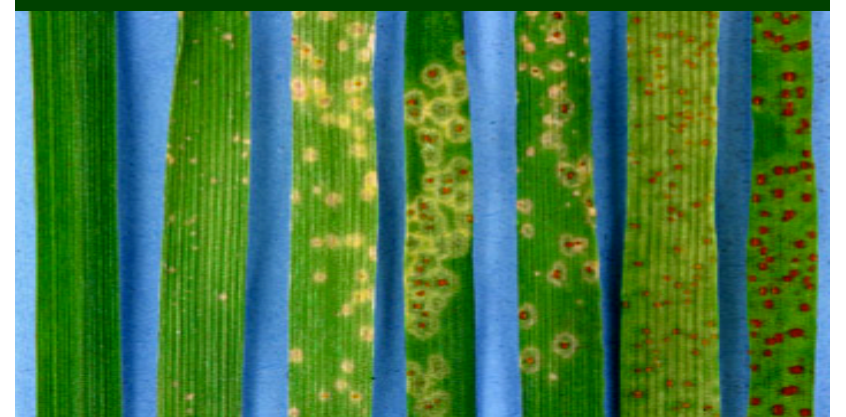
Seedling reactions- stem rust



Seedling reactions- yellow rust



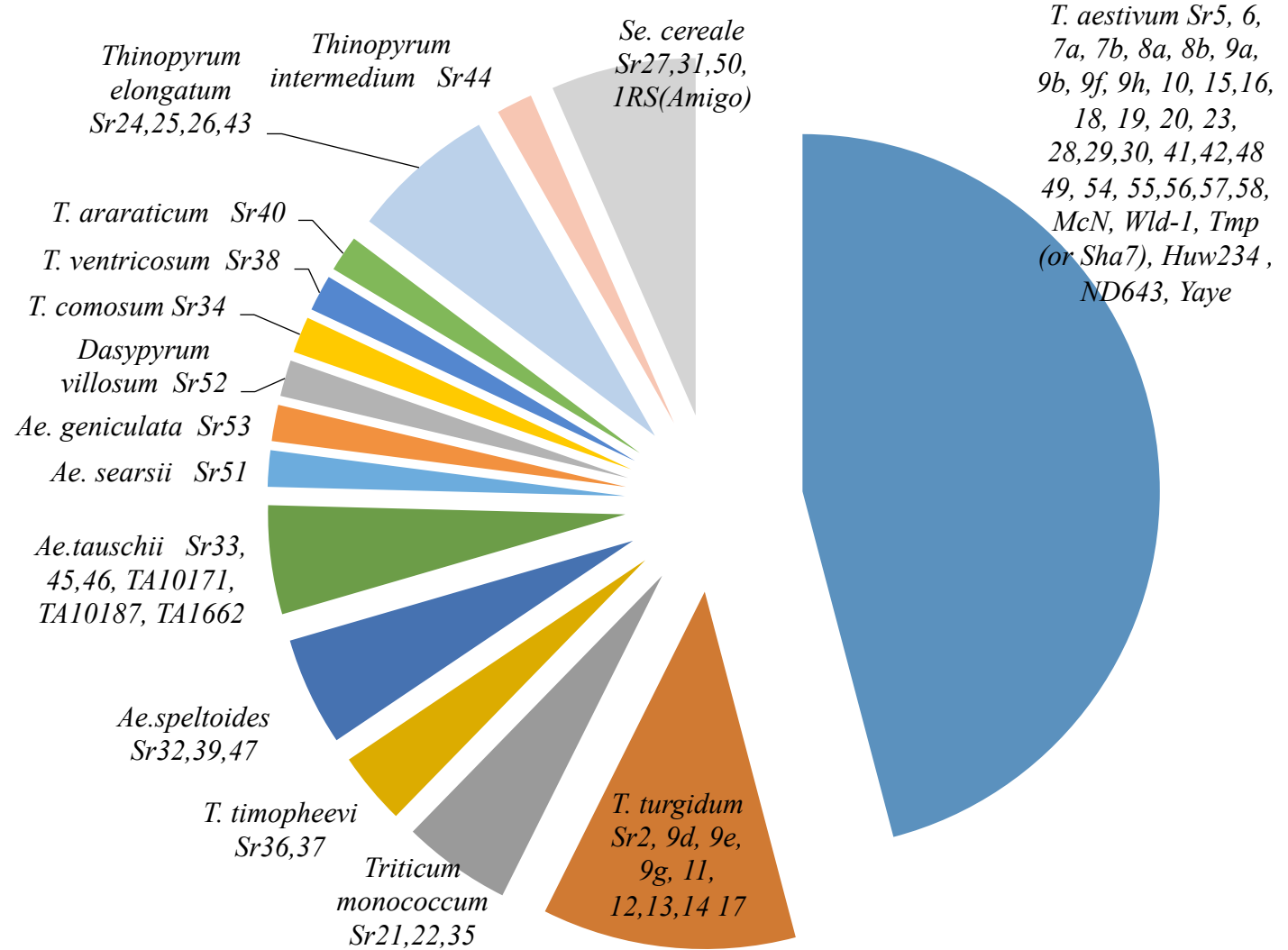
Seedling reactions- leaf rust



Stem (black) rust- known resistance genes



- 35 genes from *Triticum aestivum*
- 38 genes from 14 different species and genera
- Majority race-specific
- Some alien genes successfully used



APR: Sr2, Sr55, Sr56, Sr57 and Sr58

Adult plant resistance-CIMMYT breeding strategy



IT-4



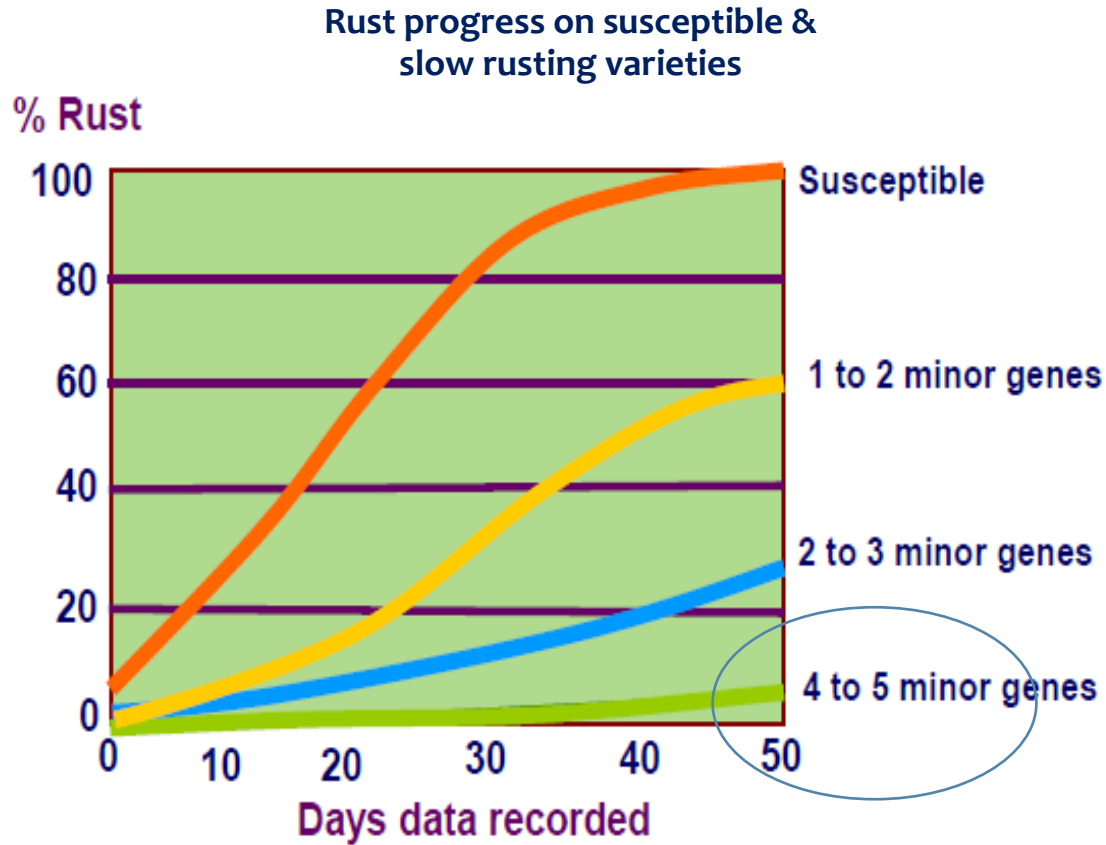
MS-S

- Minor genes with small to intermediate effects/slow rusting/partial resistance
- Gene effects are additive
- Race- non specific
- Compatible host interactions at seedling stage (SR and LR), Effective in post seedling growth stages
- Associated with slower disease progress due to increased latency period, lower infection frequency, pustule size and spore production
- Quantitative trait variation, Complex inheritance
- Significant Interactions with environment
- Often associated with resistance durability- Sr2 (1920), Lr34 (1940), Lr67 (1976), Lr68 (1981)
- Cloned APR genes ABC- Transporter -Lr34, Hexose transporter –Lr67

Krattinger et al. Science (2009) 323:1360-1363 Collaboration with CSIRO

Moore et al. 2015. Nature Genetics 47:1494-1498 Collaboration with CSIRO

Pleiotropic multi-pathogen & other slow rusting genes for achieving resistance durability in CIMMT germplasm

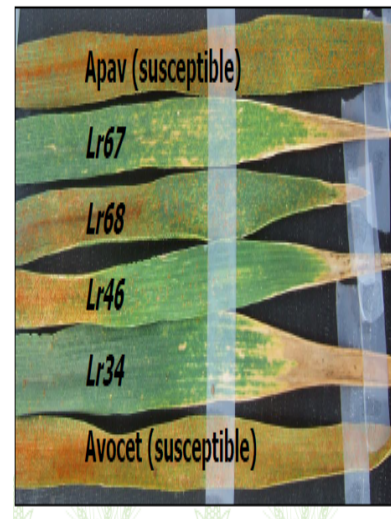


Near-immunity (trace to 5% severity) achieved by combining 4-5 genes

(similar approach for other leaf spotting diseases, fusarium head blight and wheat blast)

- *Lr34* [Syn. = *Yr18*=*Sr57*=*Pm38*=*Sb1*=*Bdv1*=*Fhb?*=*Ltn1*] **chromosome 7DS**
(leaf rust, yellow rust, stem rust, powdery mildew, spot blotch, barley yellow dwarf virus, fusarium head blight, leaf tip necrosis)
- *Lr46* [Syn.=*Yr29*=*Sr58*=*Pm39*=*Ts?*=*Ltn2*] **chromosome 1BL**
- *Lr67* [Syn.= *Yr46*=*Sr55*=*Pm46*=*Ltn3*] **chromosome 4DL**
- *Sr2/Yr30/Lr* **chromosome 3BS**
- *Lr68* **chromosome 7BL**

Lr67/Yr46/Sr55/Pm46 (present in C306, Sujata and some other old tall varieties) mediated resistance in resistant (R) and susceptible (S) mutant sibs



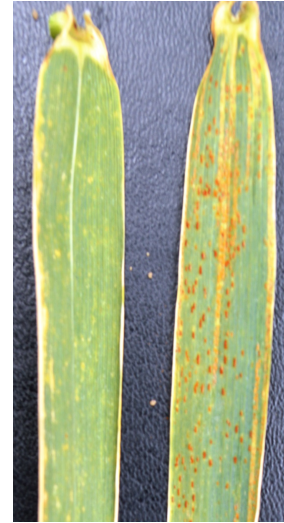
LTN



R S
Stem rust
(Obregon, Mexico)



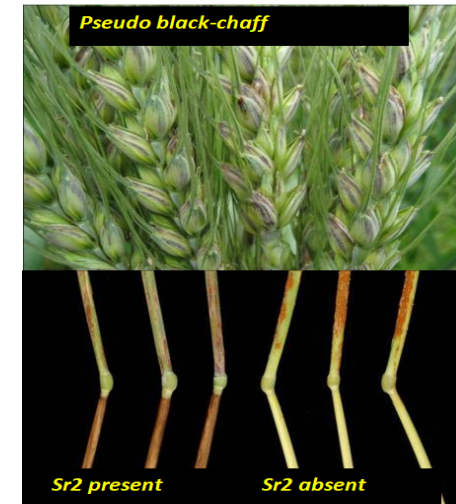
R S
Leaf rust



R S
Leaf & Yellow rusts
(Cobbitty, Australia)



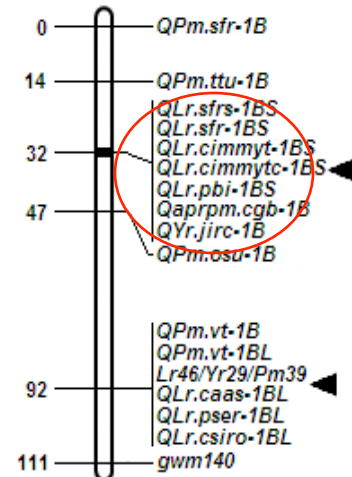
R S
powdery mildew
(Vollebekk, Norway)



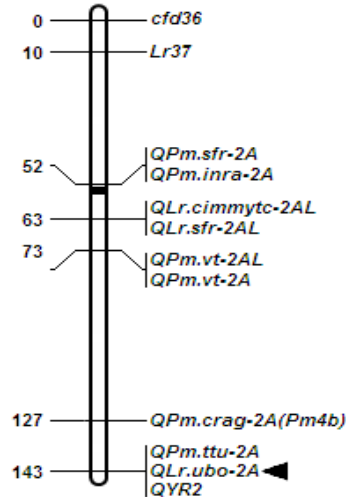
S Sr2-pbc

- Lr67 encodes a hexose transporter- a novel resistance mechanism
- Gene sequence based molecular markers available for MAS

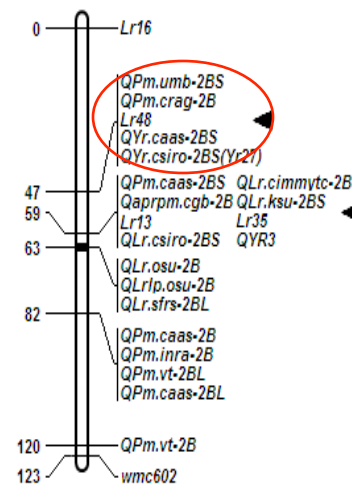
Potential PAPR -QTLs for leaf rust, stripe rust and powdery mildew



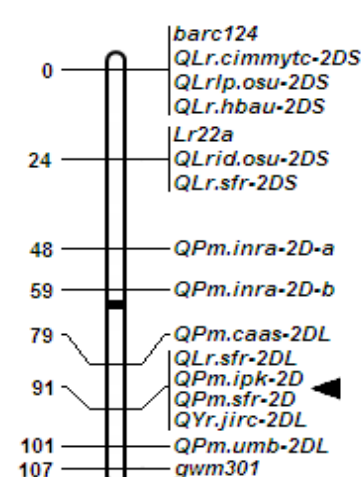
Chromosome 1B



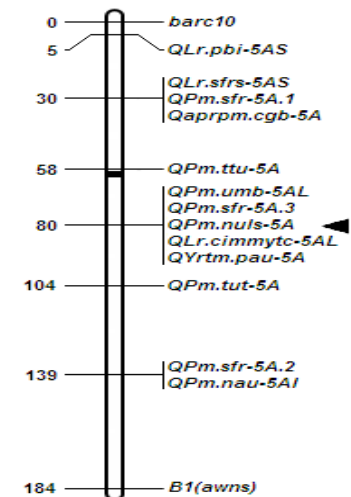
Chromosome 2A



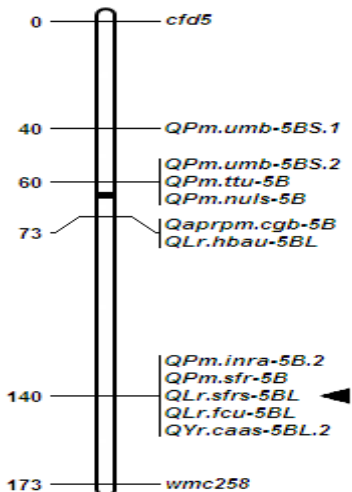
Chromosome 2B



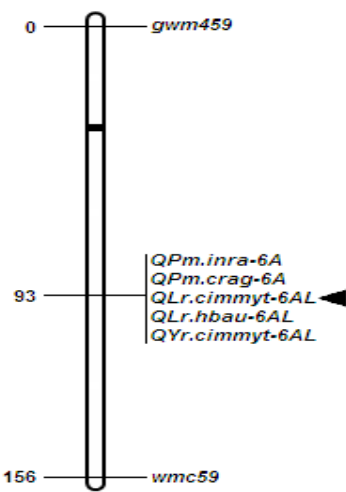
Chromosome 2D



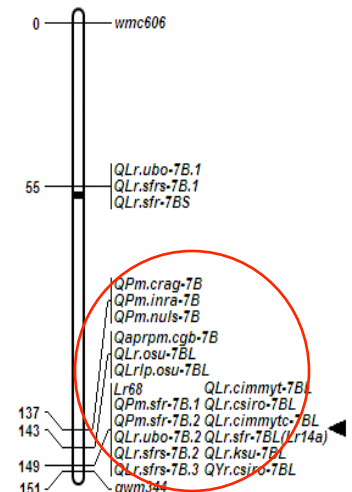
Chromosome 5A



Chromosome 5B



Chromosome 6A



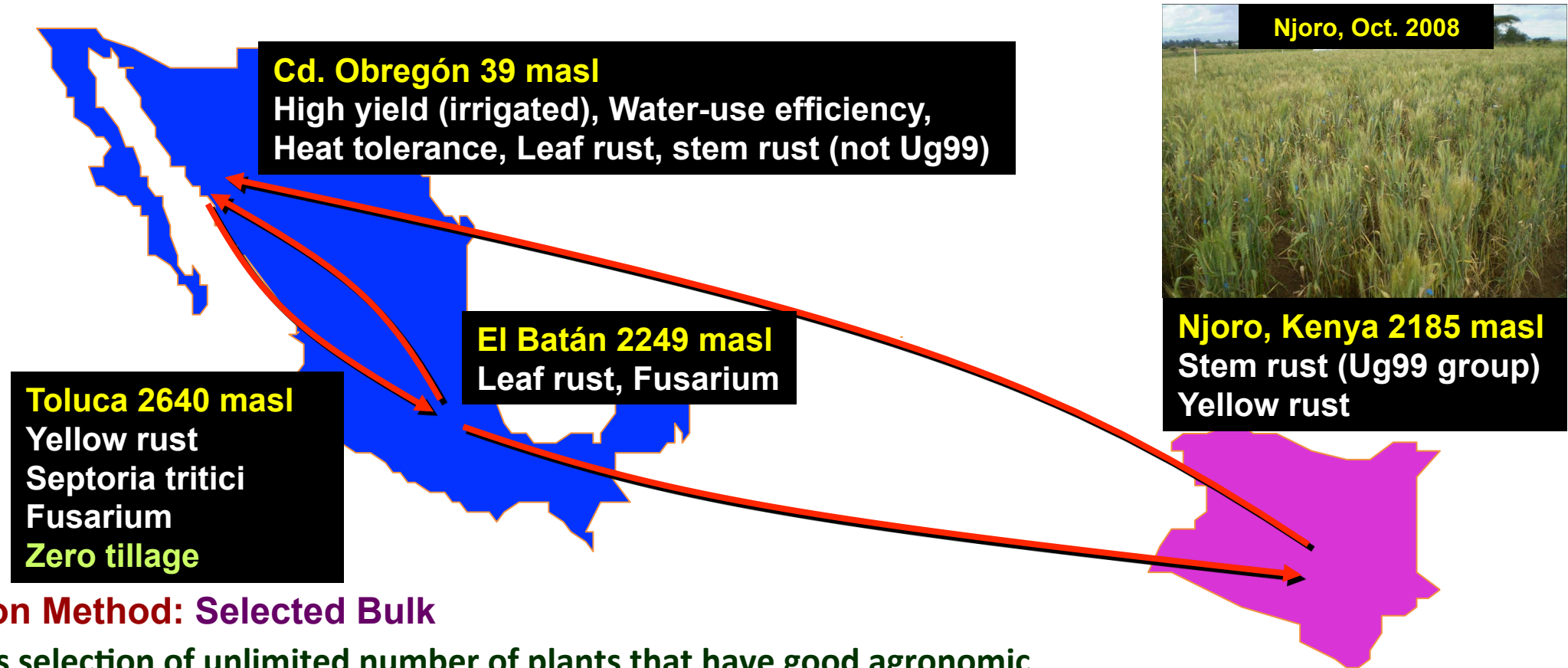
Chromosome 7B

1BS, 2AL, 2BS, 2DL, 5AL, 5BL, 6AL and 7BL and many unknown genes from other sources

Rapid cycling of breeding materials

Mexico (Cd. Obregon-Toluca/El Batán)- Kenya International Shuttle Breeding

A five-year recurrent breeding cycle

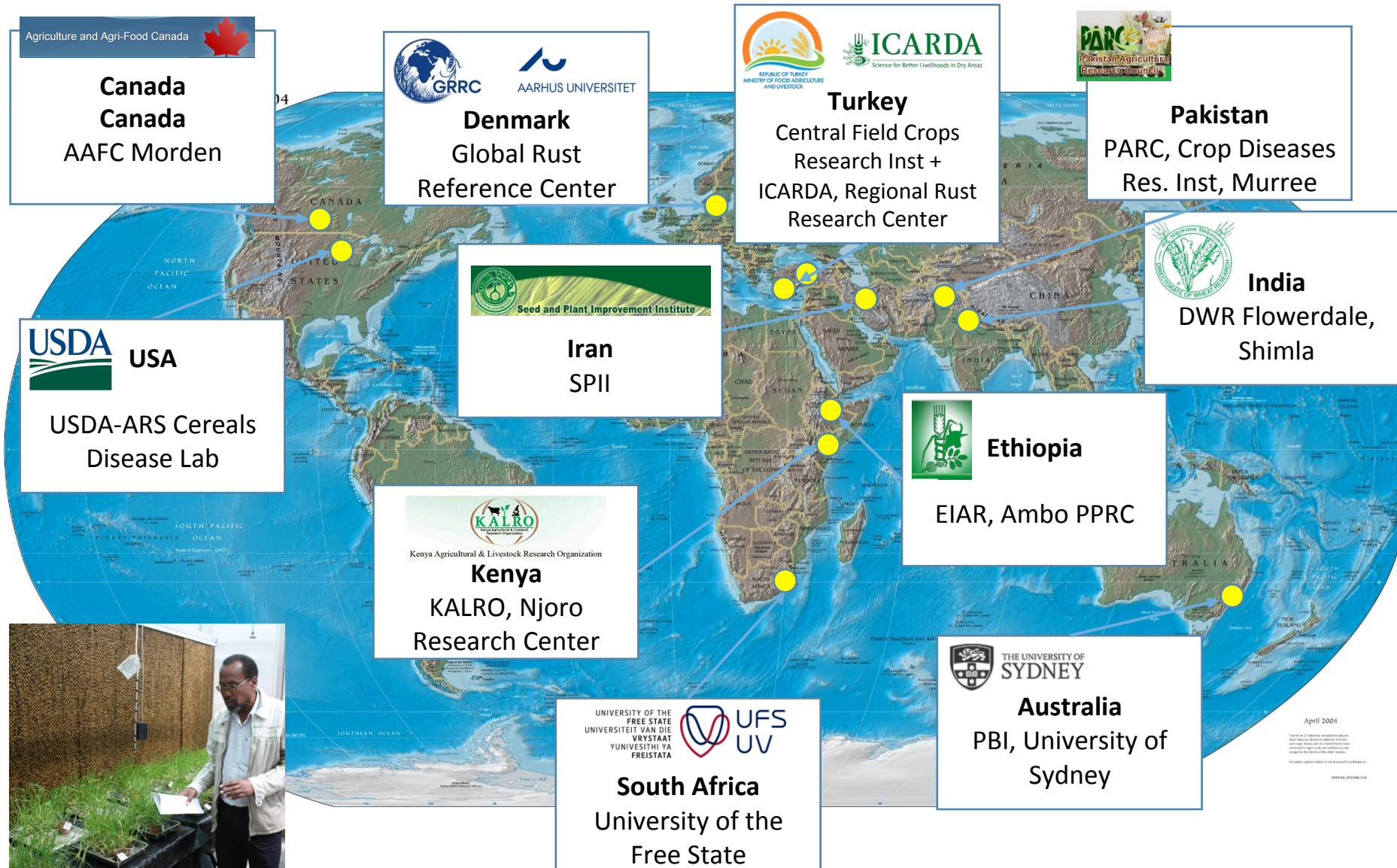


Selection Method: Selected Bulk

- ❖ Permits selection of unlimited number of plants that have good agronomic features and desired level of resistance to diseases
- ❖ Increases possibility to identify transgressive segregants due to larger population sizes (1200-1500)
- ❖ Field operation is easy, fast and economic

- 1st group of populations planted in Kenya in 2008
- 2000 F3/F4 populations undergo Mexico-Kenya shuttle

Rust Pathotyping Lab Network-Survey and surveillance information integrated in to breeding



Progress in breeding Ug99 stem rust resistance in CIMMYT wheats: resistance in current international trials and nurseries

- 10-15% lines with high levels of adult plant resistance
- 40-50% lines with adequate adult plant resistance
- 20-30% lines with race-specific resistance genes
- 20-30% lines with inadequate resistance

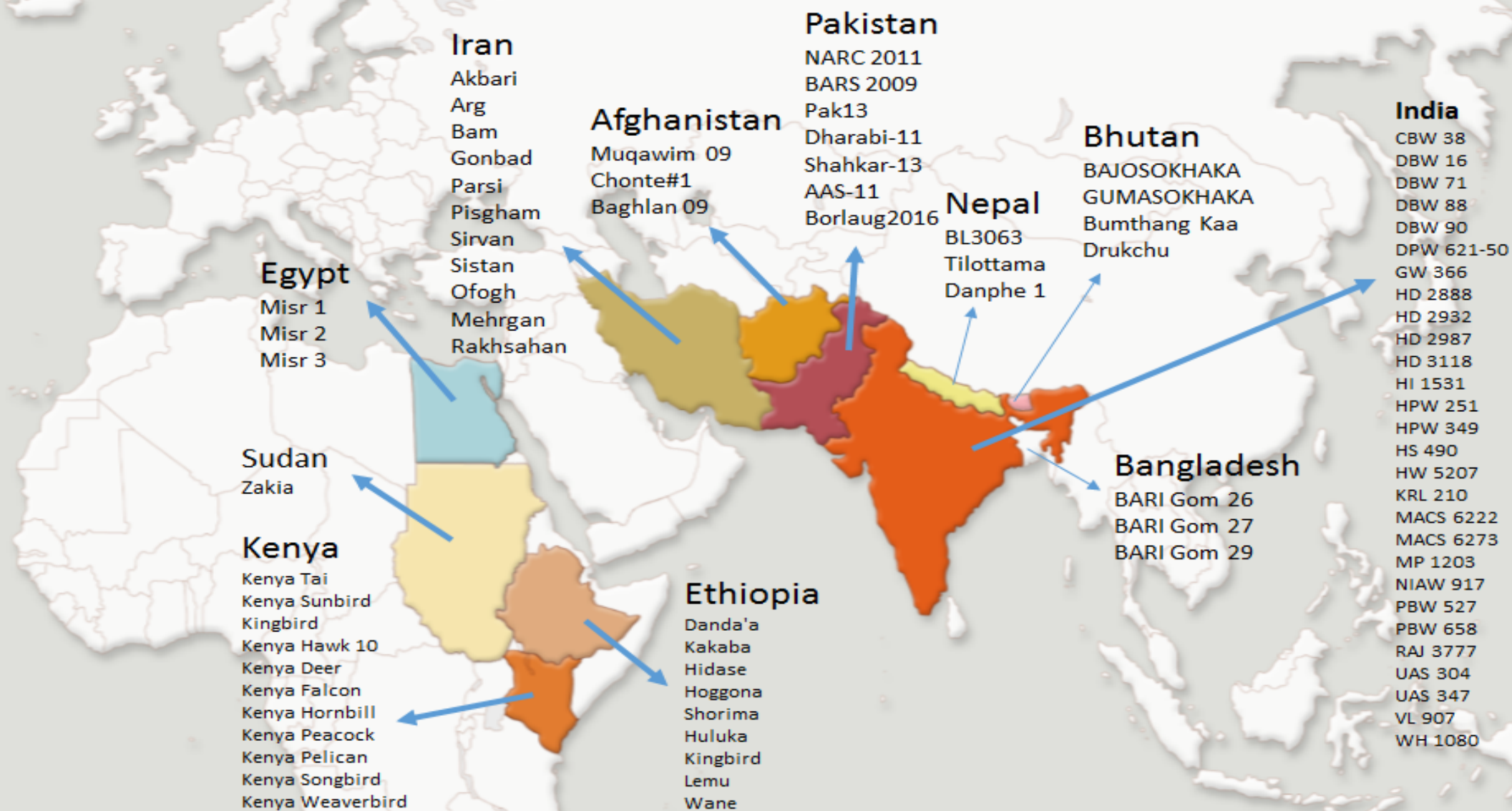


New lines with high yields and high levels of complex adult-plant resistance to stem rust (Njoro, Kenya 2018)



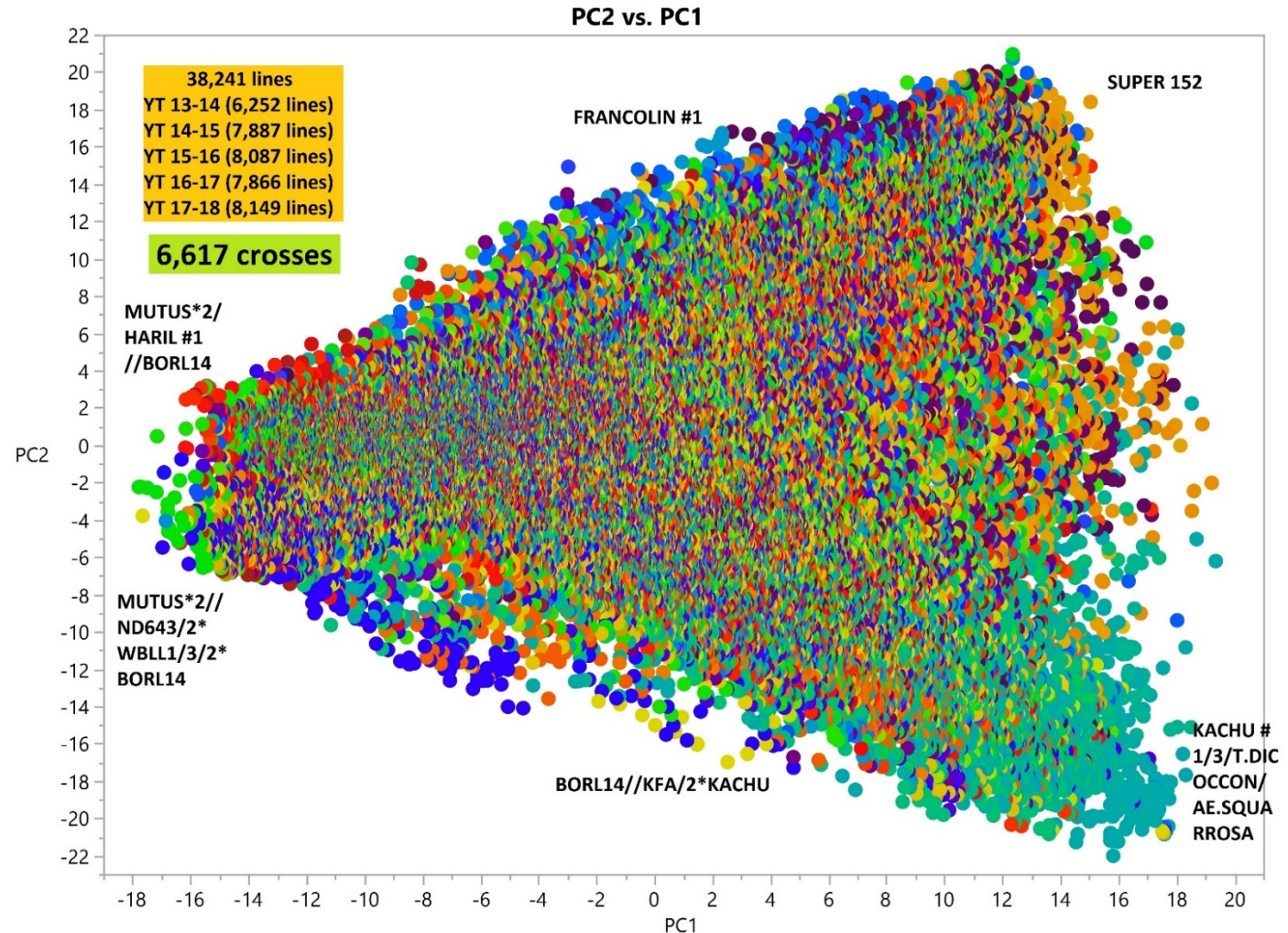
King bird – APR variety

Wheat varieties released during 2005-2016 showing high to adequate resistance to Ug99 race group



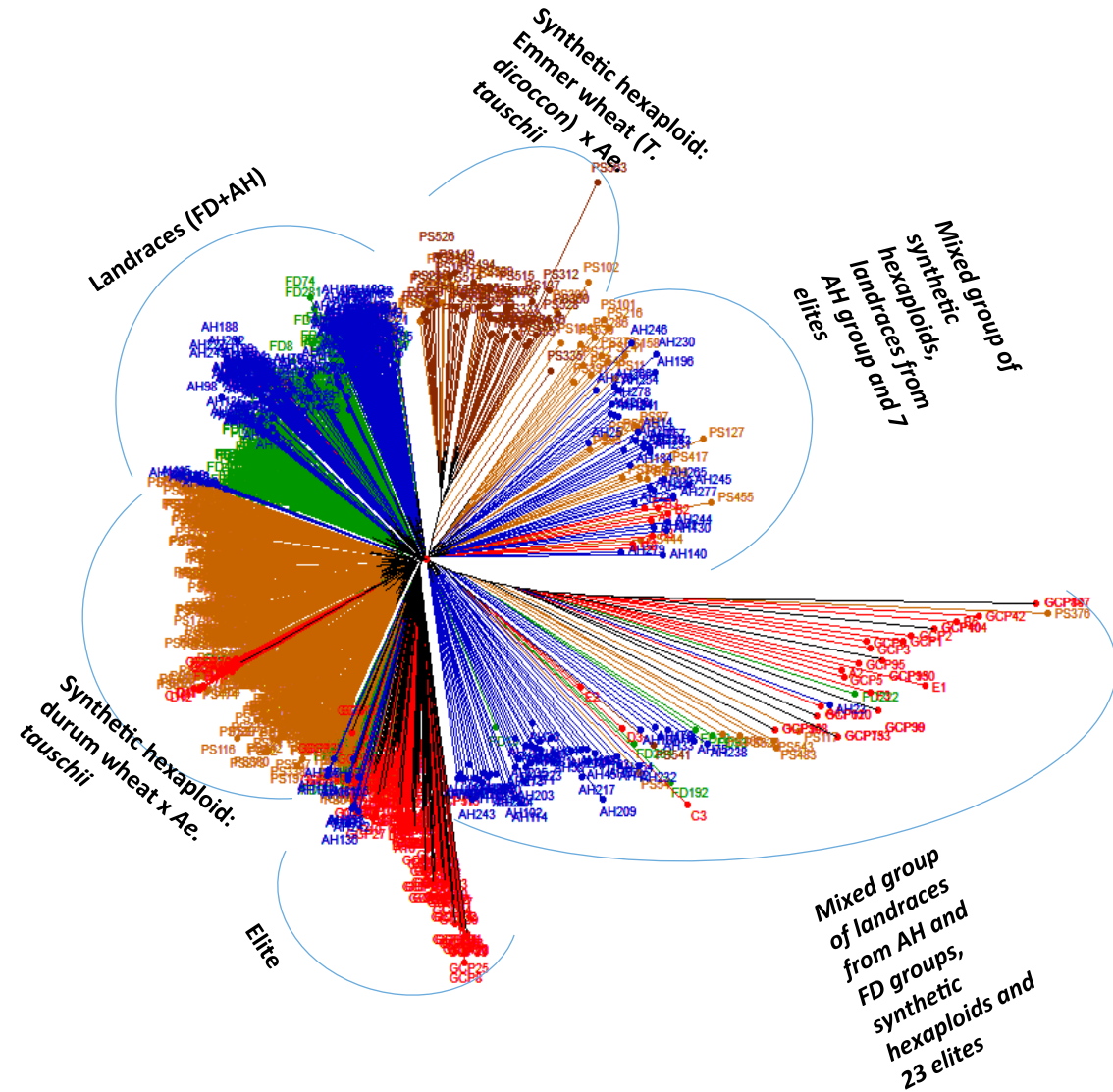
Genetic diversity in CIMMYT's first year yield trials

- The genetic diversity of 5 yield trial panels (38,241 lines) visualized by plotting the principal components 1 vs 2 derived from 9,832 GBS markers.
- The color of the points represent the 6,617 crosses
- Some cross annotations show big families at the end of the clusters, however there are many other
- Some families very different from the rest of the germplasm in the central & other clusters

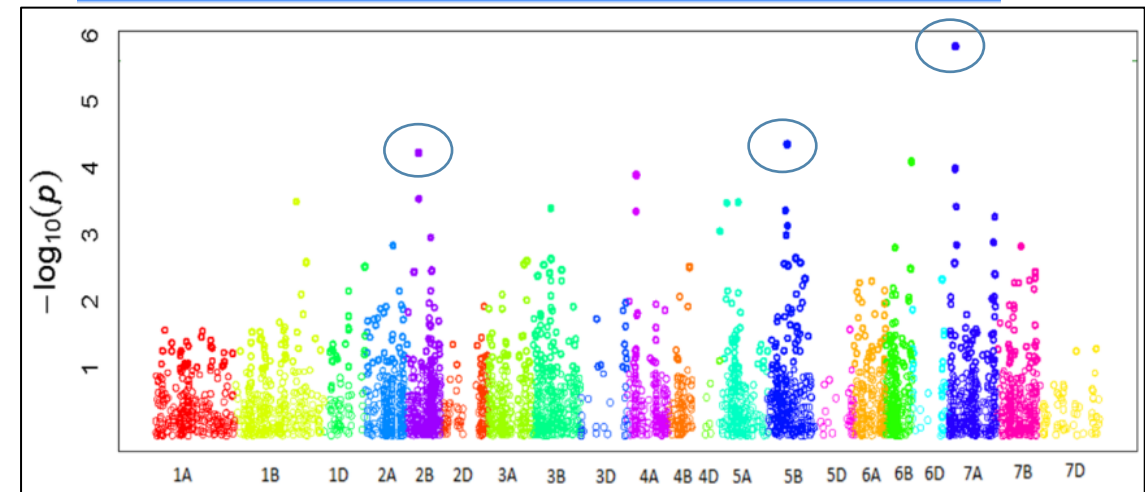
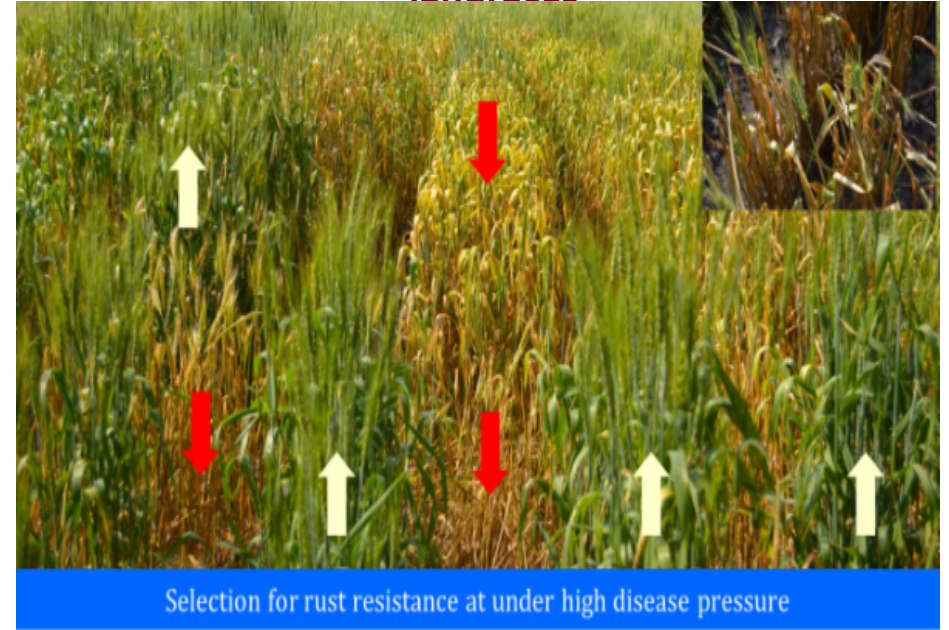


Source: P. Juliana et al., Unpublished

Unlocking the diversity in gene bank (150,000 accessions -Core Sets)

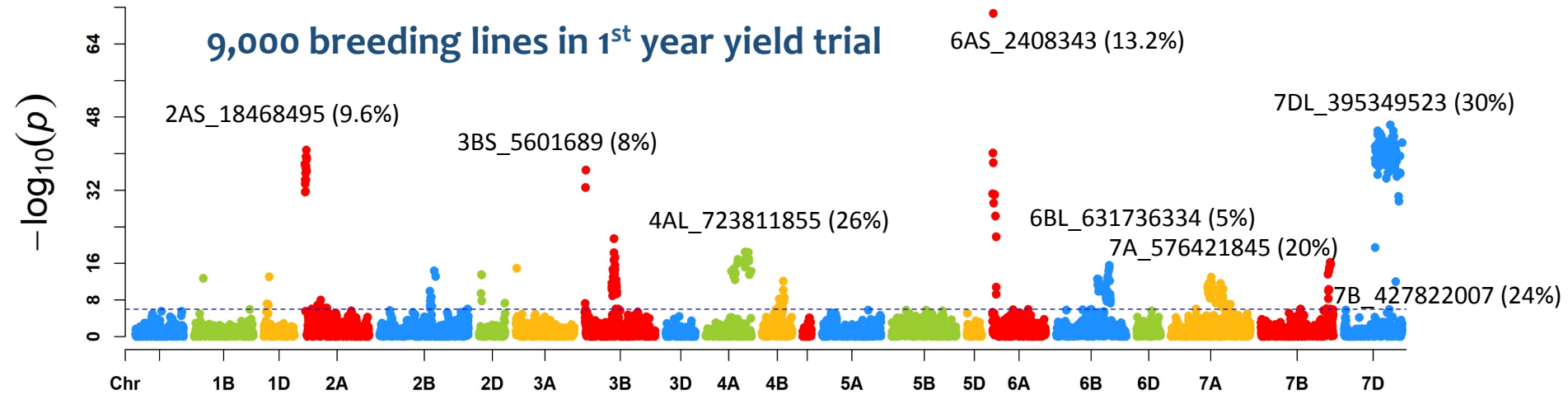


Yellow rust resistant wheat
landraces

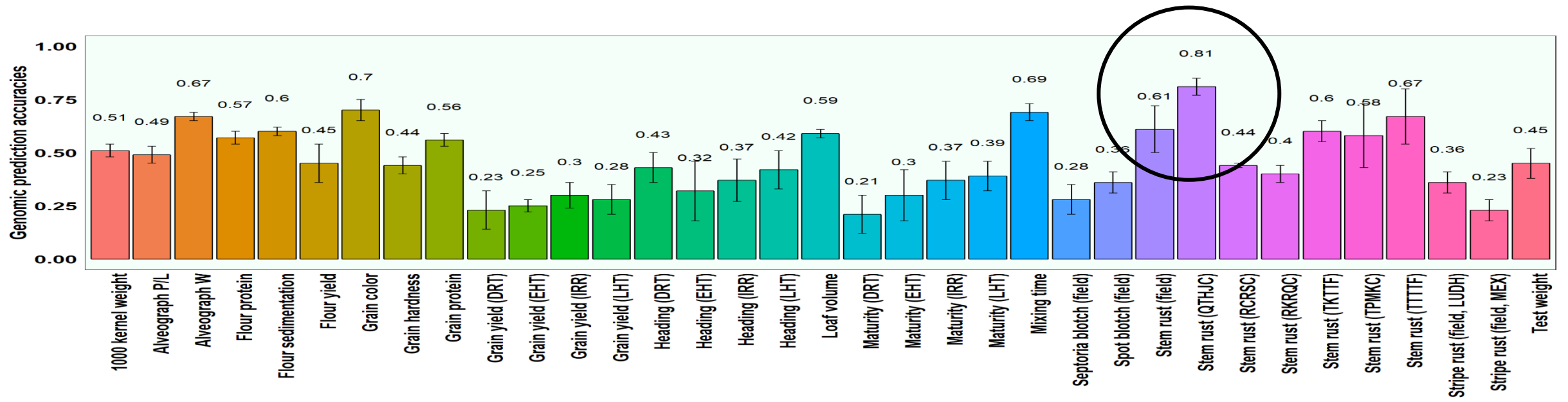


Association mapping for Yellow rust in wheat landraces

Meta-GWAS for stem rust



Genomic predictabilities of traits across environments in the elite yield trials (using historic training sets)



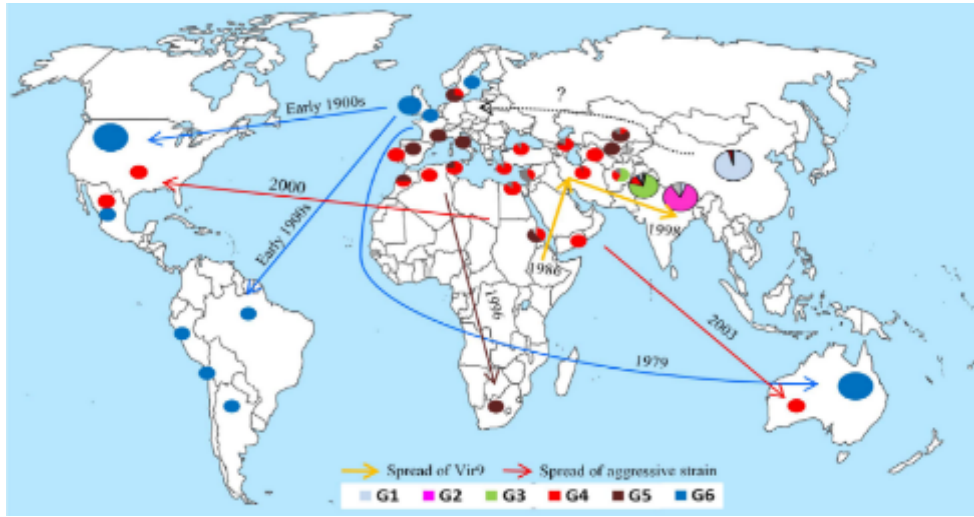
Enhancing the current genetic diversity in breeding materials: Incorporation of 23 new genes through 'Marker Assisted Backcrossing'

Source	Gene	
RL6077/AOC-YR	Lr67/Yr46/Sr55/Pm46	Pleiotropic APR
SUJATA	Lr67/Yr46/Sr55/Pm46 +YrSuj-7BL	
H-S A/2*MUNAL #1	Sr2 + Fhb1	Stem rust resistance genes
SWSR22T.B.	Sr22	
KACHU/3/WHEAR//2*PRL/2*PASTOR	Sr25	
SHORT SR26 TRANS./4/3*CHIBIA//...	Sr26	
SR32	Sr32	
W3763-SR35	Sr35	
SR47	Sr47	
SR50	Sr50	
ALPOWA	Yr39	Stripe rust resistance genes
CHUAN NONG 19	Yr41	
BLANCA GRANDE 515	Yr5 + Yr15	
SUMMIT 515	Yr5 + Yr15	
YR51#5515-1	Yr51	
KOELZ W 11192:AE	Yr52	
YR57#5474-6	Yr57	
IRAGI	Yr59	
LALBMONO1*4/PVN	Yr60	Aluminum tolerance, Aphid resistance, Grain Zinc Hessian fly
CZHO	ALMT1	
SERI//T.DIC. PI94623/AE.SQ. (1027)	Gba + QRp.slu-5AL + QRp.slu-5BL + QZn.Across_4BS	
PI592729	H25	
PI572542	H26	

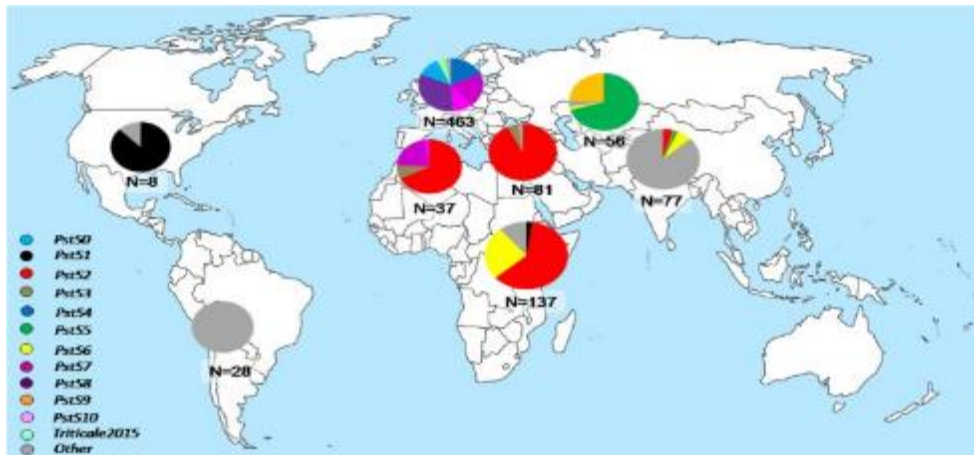
Conclusions

- High genetic diversity is present in wheat germplasm to diseases and pests
- New races of rust fungi, especially yellow rust and stem rust, continue to evolve, mutate and migrate
- Pyramiding 4-5 genes, that individually have small to intermediate effect genes, leads to near-immune, durable resistance to rusts and other fungi
- Breeding should emphasize development of more productive varieties that carry resistance to all important diseases to protect crop without a cost to farmer

Continuing challenge: Spread of aggressive *Puccinia striiformis* (yellow rust) races (e.g. PstS1/PstS2, Warrior & other) adapted to warmer temperatures



Countries with red dots with confirmed presence of PstS1/PstS2 race group Source: Ali et al. (2014) PLoS



Different colors show different lineages identified from global samples during 2009-2015 at GRRRC, Denmark Source: Ali et al. (2017) Front Plant Sci 8: 1057.

- Early infection
- Faster disease build up
- Disease progression under warmer temp.
- New areas of adaptation
- Faster evolution of new virulences
- Reduced effectiveness of resistance

- Pst11 from Afghanistan (2012) to Ethiopia in 2016, by 2018 most prevalent in East Africa
- Pst13 From Europe to South America in 2017

- Breeding programs challenged with diverse, evolving & migrating *Pst* population
- In Mexico virulence evolved for: Yr1, Yr3, Yr10, Yr24(=Yr26), Yr17, Yr27 & Yr31 in *Pst1* lineage in 12 years
(a new virulence every alternate year)

Combating wheat blast disease in Bangladesh

- Since 2010 pre-emptive screening for wheat blast in Bolivia
- **Blast** migrated to Bangladesh from South America (1st detected in 2016)
- Bangladesh scientists observed a resistant CIMMYT breeding line in 'National Variety Registration Trial'
- Resistant variety 'BARI Gom 33' released in 2017: *>5% higher yield than the best check & biofortified*
- Resistance confirmed in USDA-ARS biosafety greenhouse and in field in Bolivia
- 2NS translocation (*Ae. ventricosa*) Lr37/Yr17/Sr38



Bengal farmers burn crops as devastating fungi threaten wheat

WHEAT BLAST Disease damaged 20K hectare crops in B'desh in 2016



• Standing wheat crop set ablaze in Sonpukur village in Nadia district of West Bengal on Saturday.

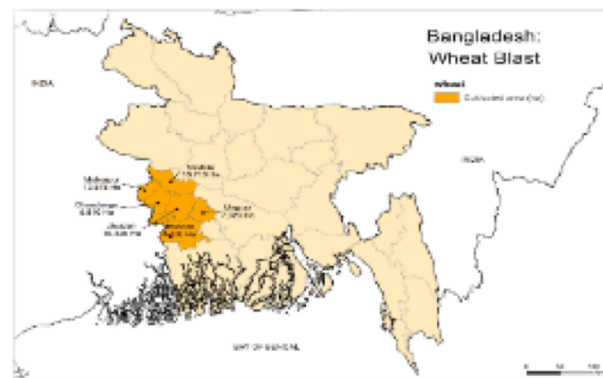
HT SPECIAL

Ravik Bhattacharya & Halim Maital
• info@thehindu.co.in

CHAPRA WEST BENGAL: Sixty-year-old Dulal Shukla of Sonpukur village in Nadia district in West Ben

OFFICIALS ARE IN A RACE TO CLEAR FIELDS TO ENSURE THE FUNGAL SPORES DON'T TRAVEL FROM BENGAL TO THE HINDI HEARTLAND

Bangladesh, where crops of over 20,000 hectares had to be burnt. Both Nadia and Murshidabad border Bangladesh, alarming the government in West Bengal. The anti-fungal drive is said to be for protecting wheat crops. But Dulal Shukla is desolate watching his crops go up in flames. "I had



Projected losses:
1.32 billion USD in epidemic years



Photo source: BARI

BARI Gom 33: Blast resistant & biofortified

Supported by ACIAR

The big impact



**Annual benefits of
\$3.5-4 billion.**



**50% of maize and wheat
in the developing world
are based on CIMMYT
varieties.**



**Trained over 10,000
agricultural experts and
scientists.**

Acknowledgements

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