Genomic Selection in Wheat Breeding

A Program Establishment and Prospective

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Wheat is the most important worldwide cultivated staple crops and currently provides 20 percent of the overall daily protein and calories consumed throughout the world.

THE WHEAT SITUATION IN CHINA

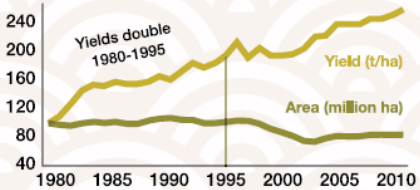
#1 WORLD'S WHEAT PRODUCER

120 MILLION TONS of wheat grain harvested annually

17% OF WORLD WHEAT PRODUCTION

Wheat comprises **40%** of China's grain consumption

Wheat yield and area growth



24 million hectares of wheat area

CIMMYT 2014

Next generation breeding

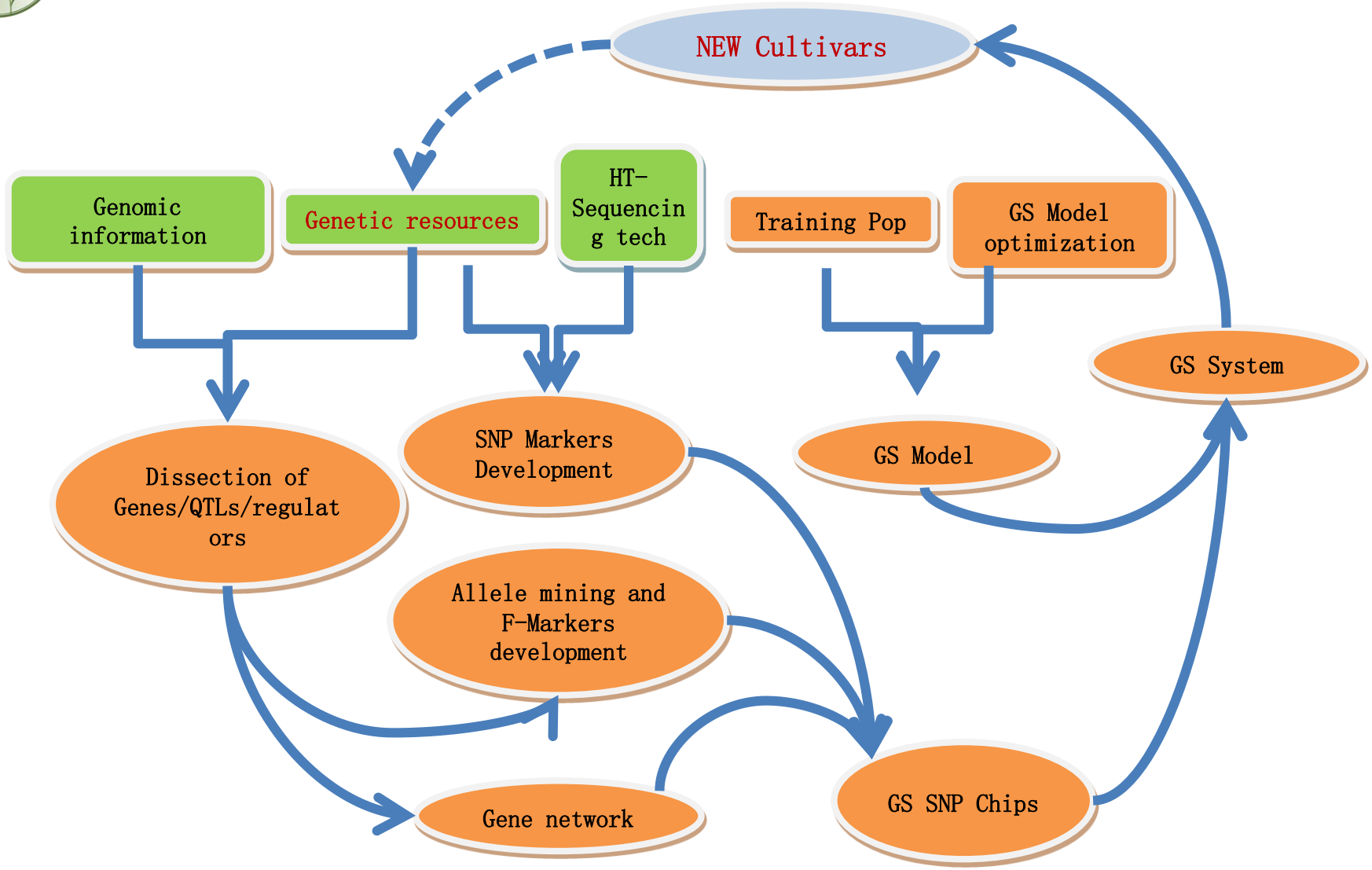
- Genome sequencing and sequence-based markers
- Mining plant diversity: from genotype to phenotype
- Collecting genetic information through meta-analysis
- Marker-trait association in large germplasm collections
- **Genome-wide prediction of breeding value and genomic selection**
- Plant improvement through genome-editing
- The control of genetic recombination

Barabaschi 2016

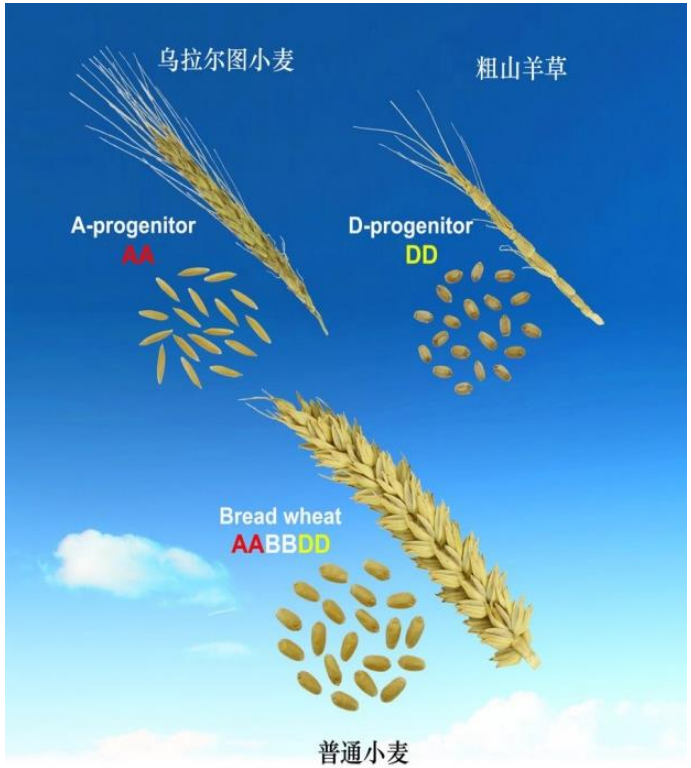
Goal of the Project

- Genetic dissection of complex traits of yield and quality in wheat
- Development optimized genomic selection models for wheat and application in wheat genetic improvement

Working Plan of the Project



Wheat Genome Sequencing



LETTER

OPEN
doi:10.1038/nature11997

Draft genome of the wheat A-genome progenitor *Triticum urartu*

Hong-Qing Ling[1]*, Shancen Zhao[2,3]*, Dongcheng Liu[1]*, Junyi Wang[1,2]*, Hua Sun[1]*, Chi Zhang[2]*, Huajie Fan[1], Dong Li[2], Lingli Dong[1], Yong Tao[2], Chuan Gao[2], Huilan Wu[1], Yiwen Li[1], Yan Cui[1], Xiaosen Guo[2], Shusong Zheng[1], Biao Wang[1], Kang Yu[1], Qinsi Liang[2], Wenlong Yang[1], Xueyuan Lou[1], Jie Chen[2], Mingji Feng[2], Jianbo Jian[2], Xiaofei Zhang[1], Guangbin Luo[1], Ying Jiang[2], Junjie Liu[2], Zhaobao Wang[2], Yuhui Sha[2], Bairu Zhang[1], Huajun Wu[4], Dingzhong Tang[1], Qianhua Shen[1], Pengya Xue[1], Shenhao Zou[1], Xiujie Wang[4], Xin Liu[1], Famin Wang[1], Yanping Yang[1], Xueli An[1], Zhenying Dong[1], Kunpu Zhang[1], Xiangqi Zhang[1], Ming-Cheng Luo[5], Jan Dvorak[5], Yiping Tong[1], Jian Wang[2], Huanming Yang[2], Zhensheng Li[1], Daowen Wang[1], Aimin Zhang[1] & Jun Wang[2,6,7]

LETTER

OPEN
doi:10.1038/nature12028

Aegilops tauschii draft genome sequence reveals a gene repertoire for wheat adaptation

Jizeng Jia[1]*, Shancen Zhao[2,3]*, Xiuying Kong[1]*, Yingrui Li[2]*, Guangyao Zhao[1]*, Weiming He[2]*, Rudi Appels[4]*, Matthias Pfeifer[5], Yong Tao[2], Xueyong Zhang[1], Ruilian Jing[1], Chi Zhang[2], Youzhi Ma[1], Lifeng Gao[1], Chuan Gao[2], Manuel Spannagl[5], Klaus F. X. Mayer[5], Dong Li[2], Shengkai Pan[2], Fengya Zheng[2,3], Qun Hu[6], Xianchun Xia[1], Jianwen Li[2], Qinsi Liang[2], Jie Chen[2], Thomas Wicker[7], Caiyun Gou[2], Hanhui Kuang[6], Genyun He[2], Yadan Luo[2], Beat Keller[7], Qiuju Xia[2], Peng Lu[2], Junyi Wang[2], Hongfeng Zou[2], Rongzhi Zhang[1], Junyang Xu[2], Jinlong Gao[2], Christopher Middleton[7], Zhiwu Quan[2], Guangming Liu[8], Jian Wang[2], International Wheat Genome Sequencing Consortium†, Huanming Yang[2], Xu Liu[1], Zhonghu He[1,9], Long Mao[1] & Jun Wang[2,10,11]

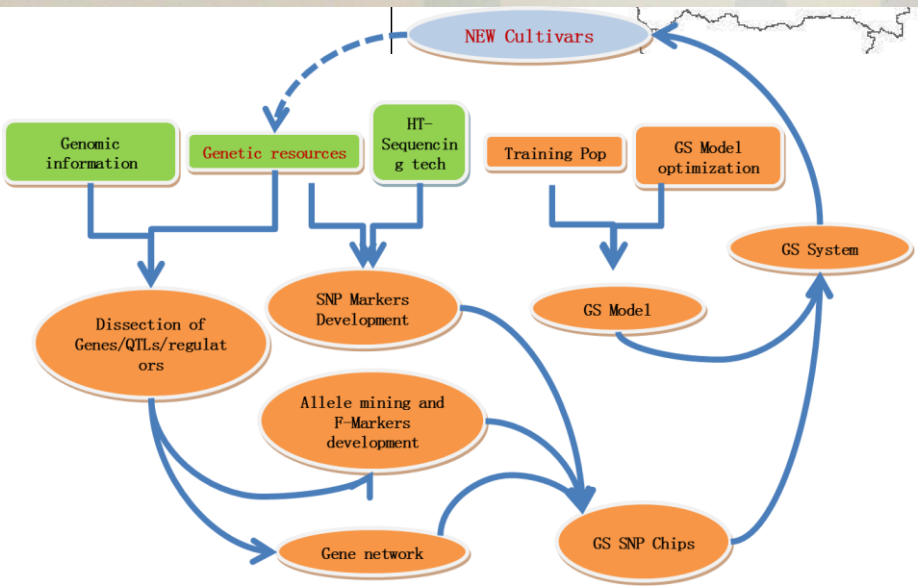
WHEAT GENOME

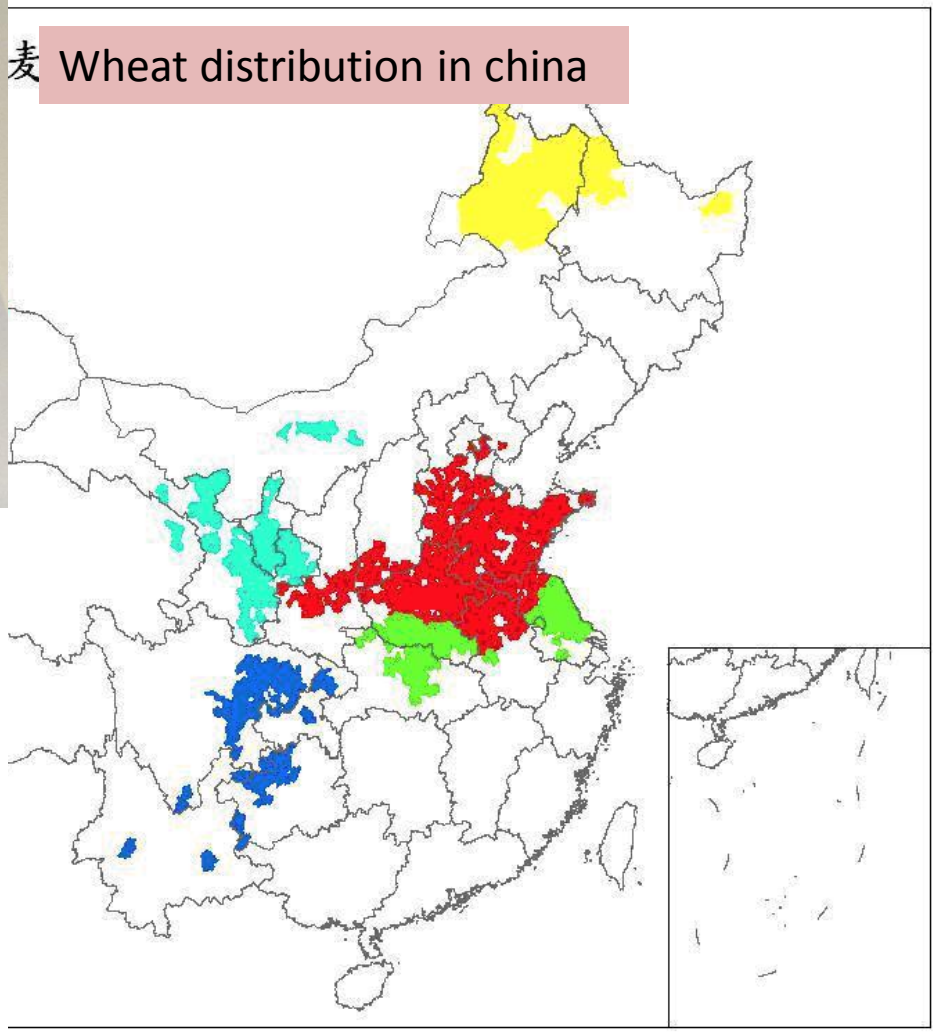
A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome

The International Wheat Genome Sequencing Consortium (IWGSC)*†

An ordered draft sequence of the 17-gigabase hexaploid bread wheat (*Triticum aestivum*) genome has been produced by sequencing isolated chromosome arms. We have annotated

Three Training Population





Three Training Population

NORTH of HHR TP

- ◆166 cultivars including new advanced breeding lines
- ◆Phenotyped in 2 years in 2 locations
- ◆Quality parameters including protein quality and starch quality
- ◆Genotyped by 90K and wheat660

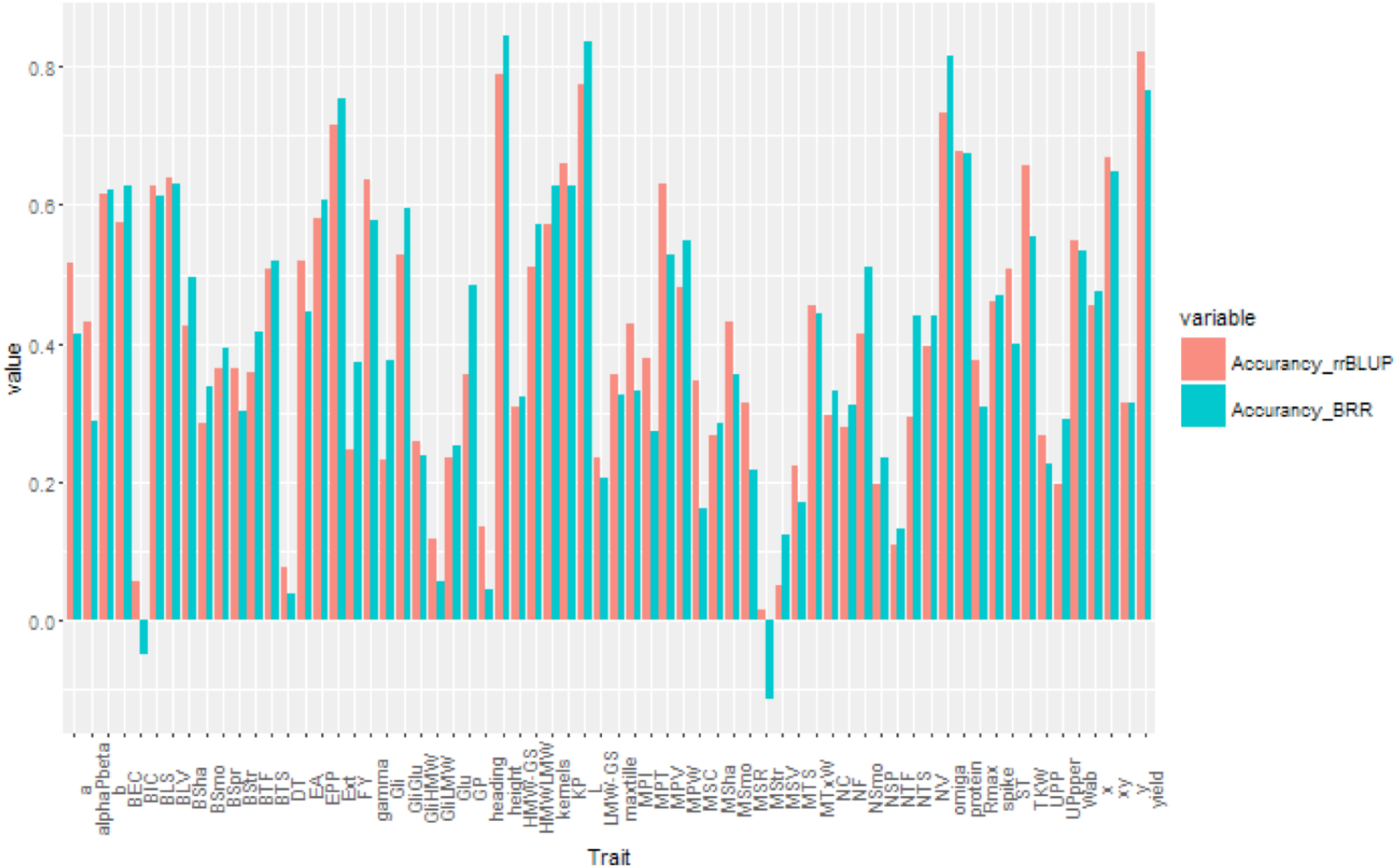
Traits	Average	Scope	SE	Genotype
HD	185	170-202	7.1	7111***
PH	81	54-150	13.4	154520***
SL	8.9	5.7-12.8	1.0	786***
SN	29.4	22.5-60.2	6.9	24604***
KN	39.2	20.7-72.8	7.3	39634***
TKW	45.5	22.3-64	7.0	26834***
KL	14.2	11.1-17.1	1.0	470***
KW	7.0	4.9-8.3	0.5	110***
YIELD	506	209-816	111.7	29396***

Traits	Average	Scope	SE
Protein content	13.0	10.2-15.7	1.4
Kernel Hardness	50.3	8.1-89.5	19.1
Peak viscosity	3294	2608-4211	294
Developing time	3.4	1.3-7.5	1.4
Water absorption	61.3	52.6-70.0	3.2
Stability time	7.5	1.0-12.6	3.1
Mixsolab C1	1.12	1.03-1.19	0.03
Mixsolab C2	0.45	0.20-0.67	0.09

GSBP（Genomic Selection Breeding Platform）

Three prediction methods： Stepwise Regression, Ridge Regression and Generalized Inverse Regression

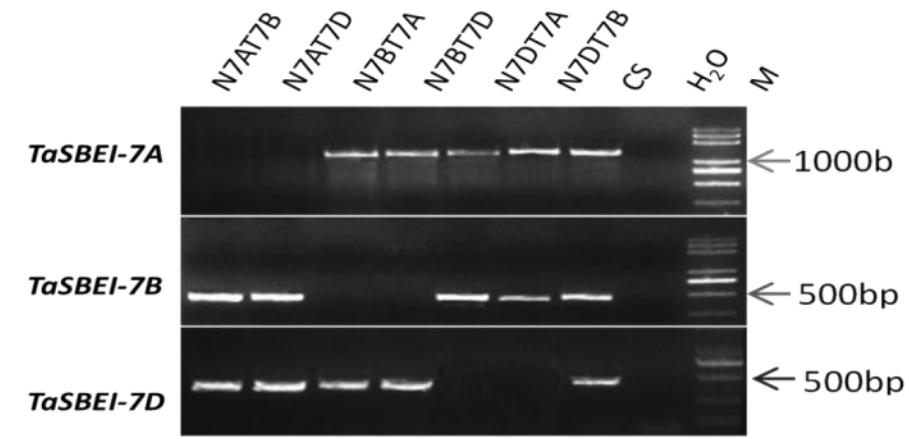
Accuracy of two prediction methods

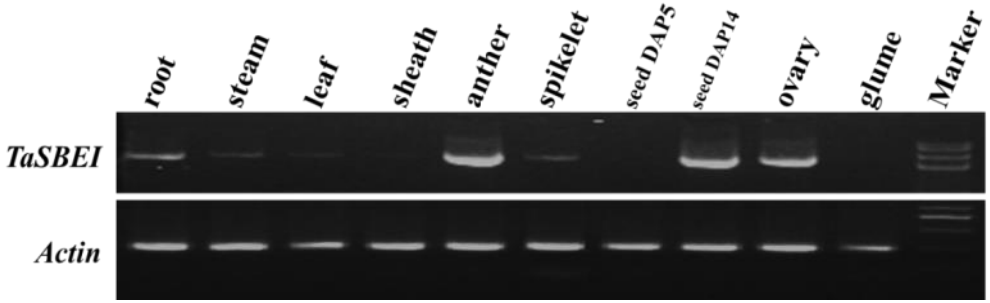


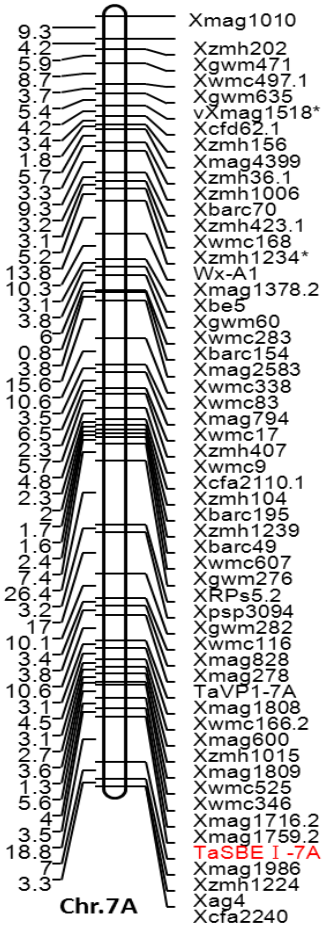
57 genotypes, 64 traits, 90K

Problems and Challenges

Limited genes/loci



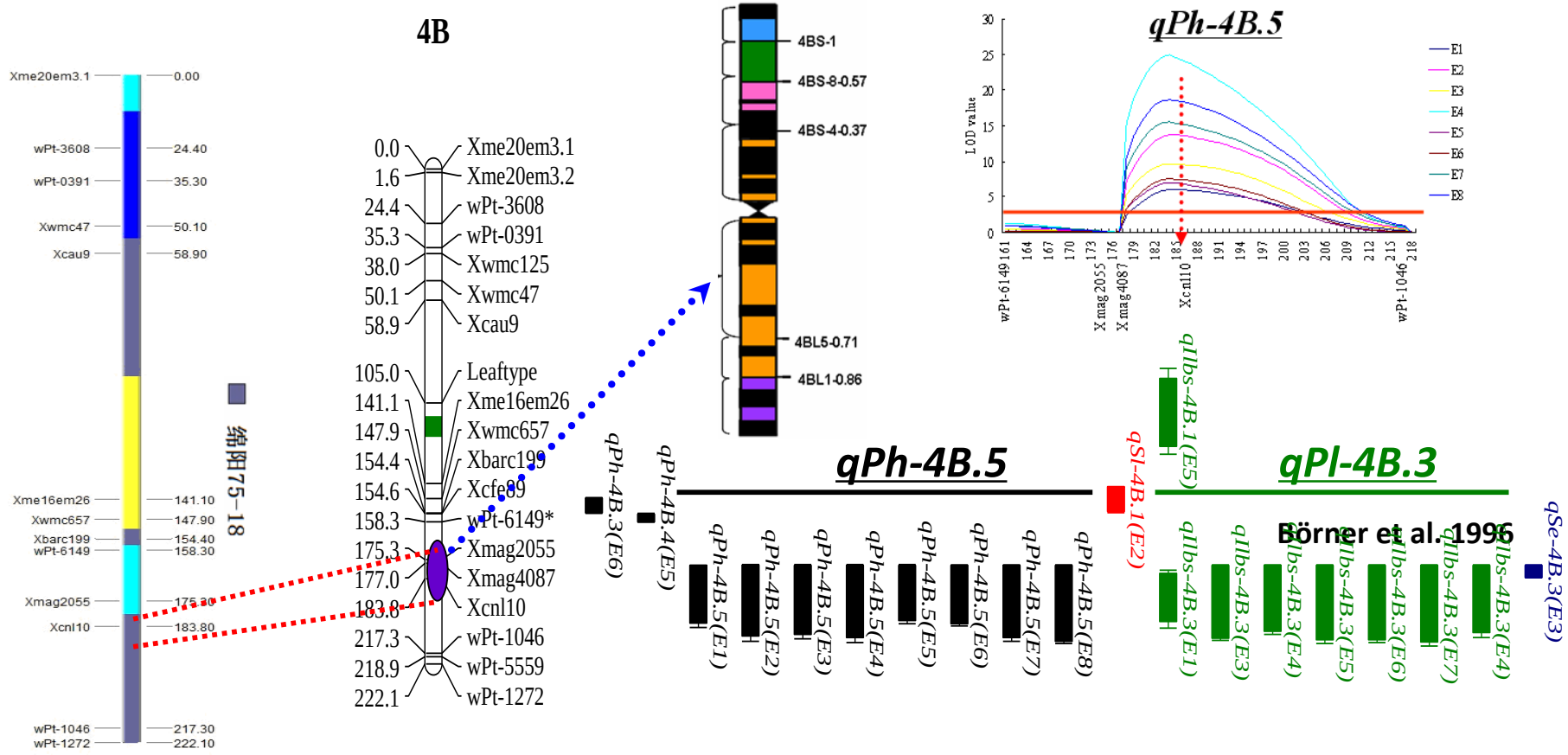




***Starch branching enzyme I* for quality and kernel number per spike**

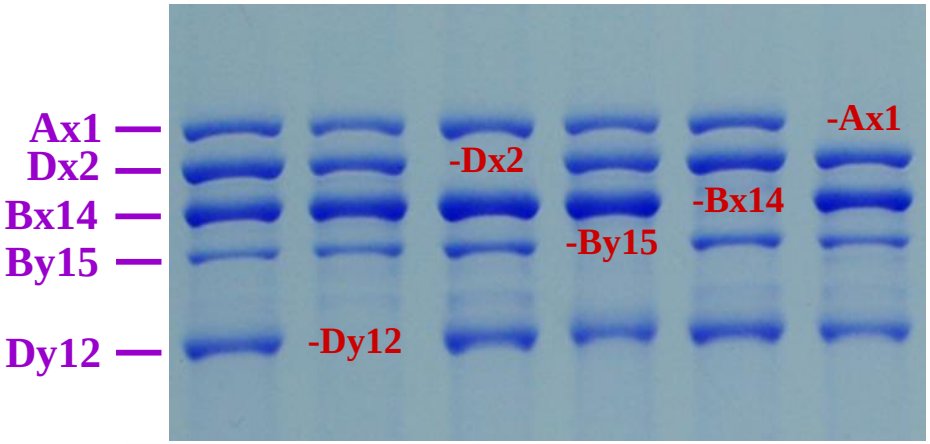
Problems and Challenges

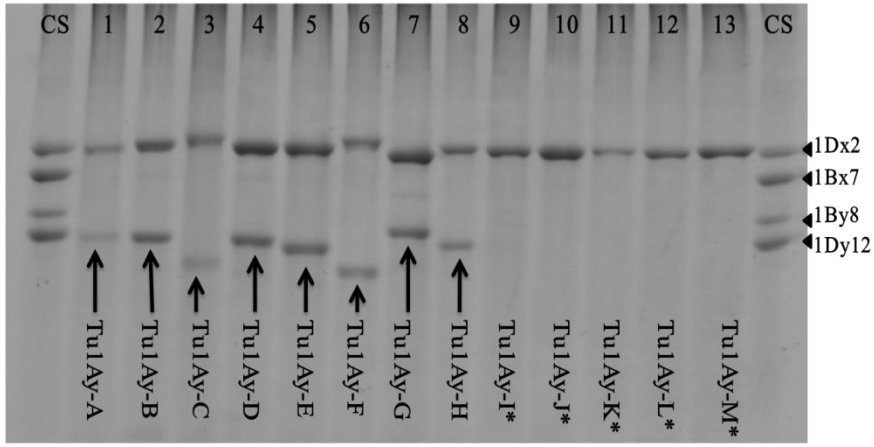
Limited genes/loci

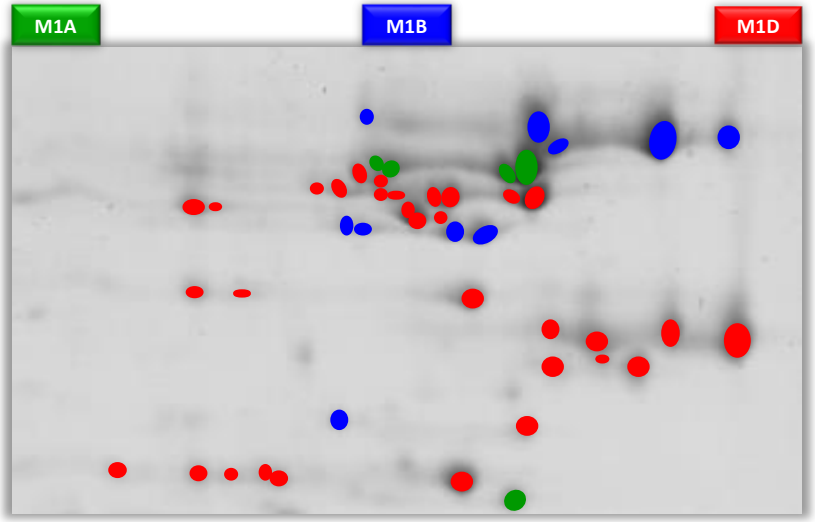


Problems and Challenges

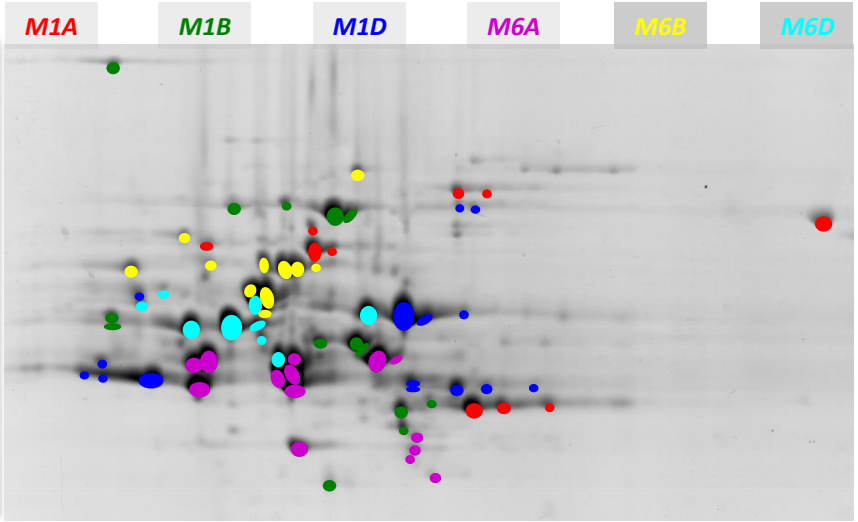
Limited germplasm







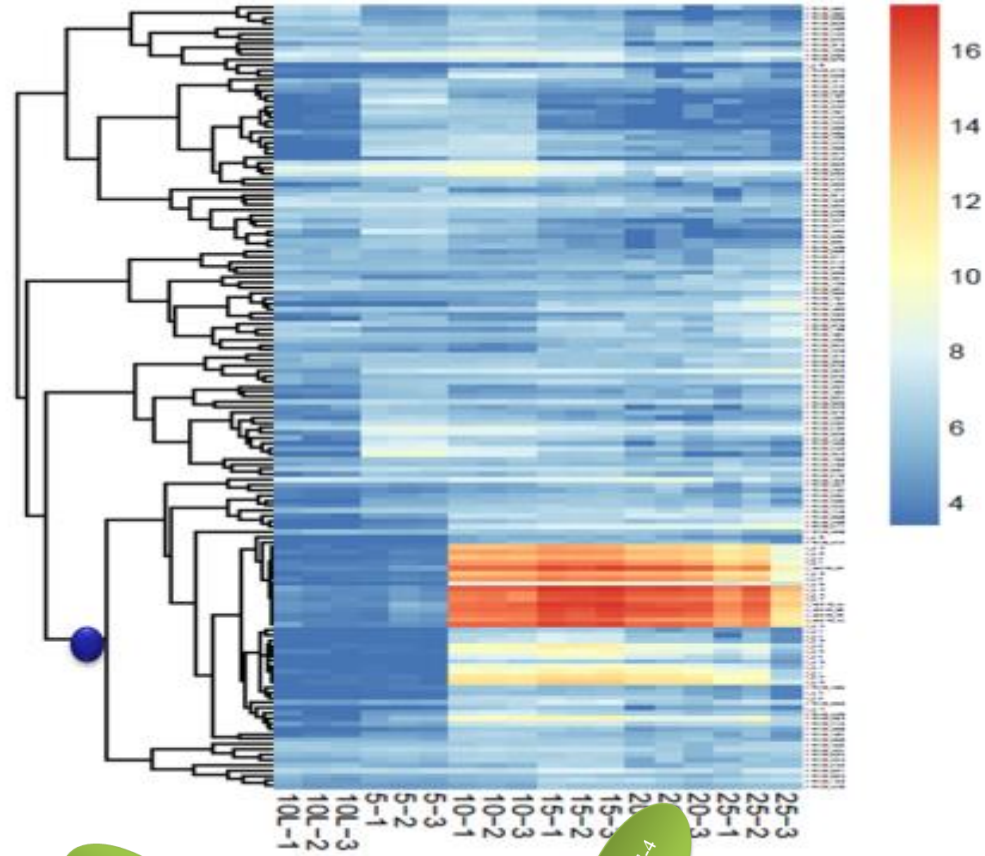
LMW-GS mutant

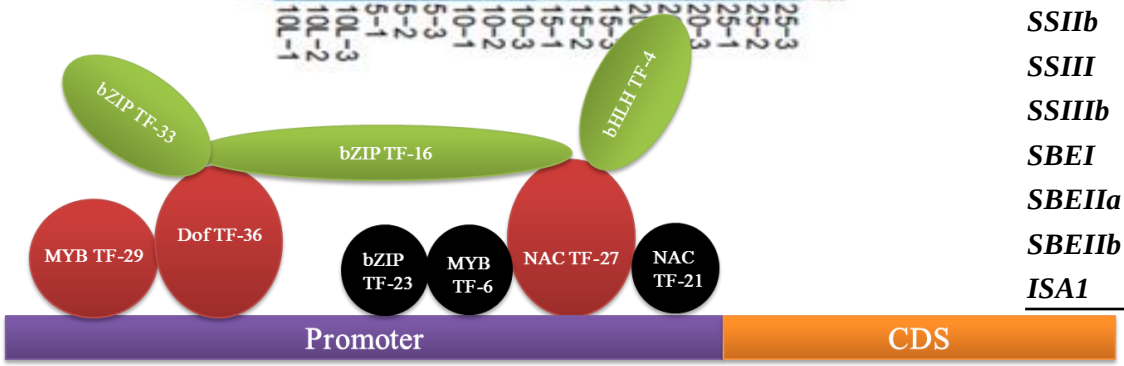


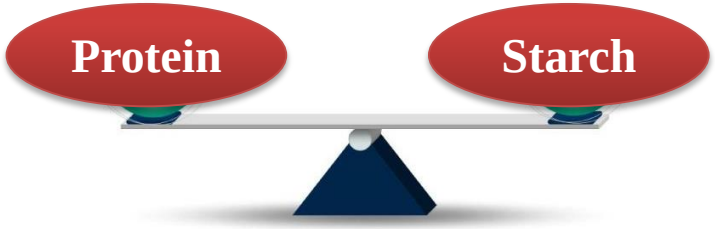
Gliadin mutant

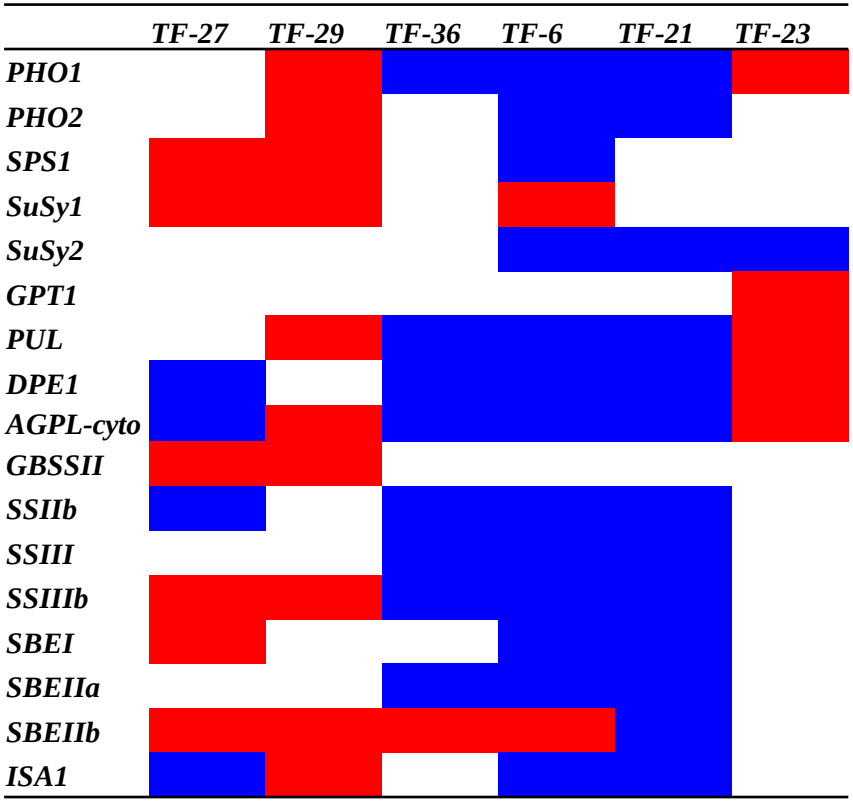
Problems and Challenges

Trait development poorly understood









Prospectives

- ◆Exchange knowledge, germplasm and genes, especially lines with elite dough quality
- ◆Collaborate to dissect the genetic components of yield potential and dough quality
- ◆Collaborate to develop molecular markers, breeding methodology, etc. for molecular breeding.

Acknowledgement

国家重点基础研究发展计划

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ICS,CAAS BIC,CAS

SDAU HNAU

Thanks for your attention !