Development of high-density gene chip and identification of soil-borne disease regulatory genes in wheat

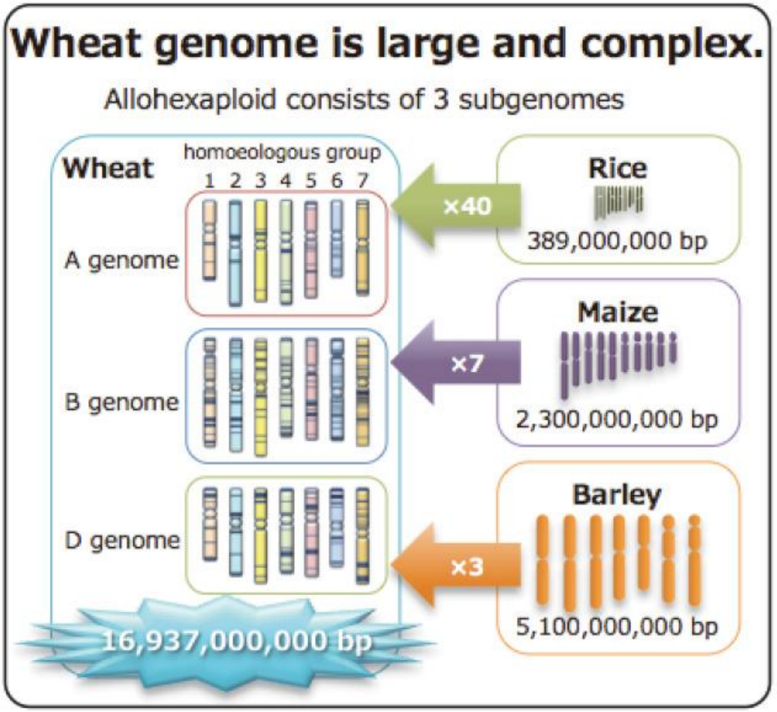
Feng Chen

Henan Agricultural University

March, 2026

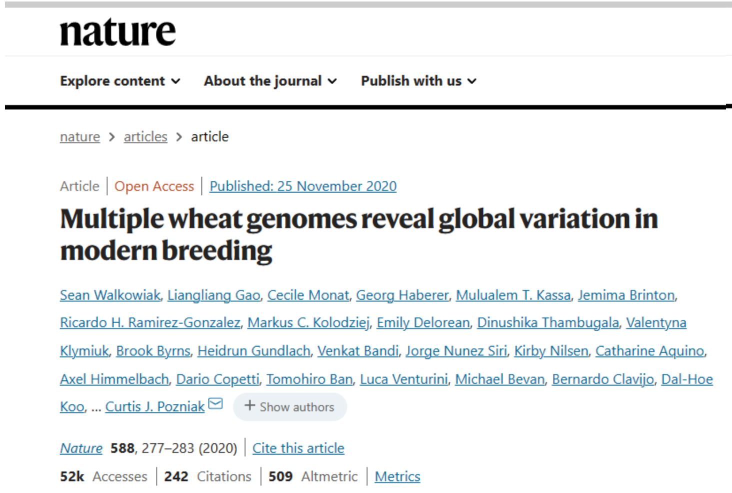
1. Challenge of cloning wheat genes

- ➢Wheat is one of the most important food crops
- ➢Large genome size and high duplication
- ➢Allohexaploid (AABBDD)



2014

2018



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Multiple wheat genomes reveal global variation in modern breeding

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Nature **588**, 277–283 (2020) | Cite this article

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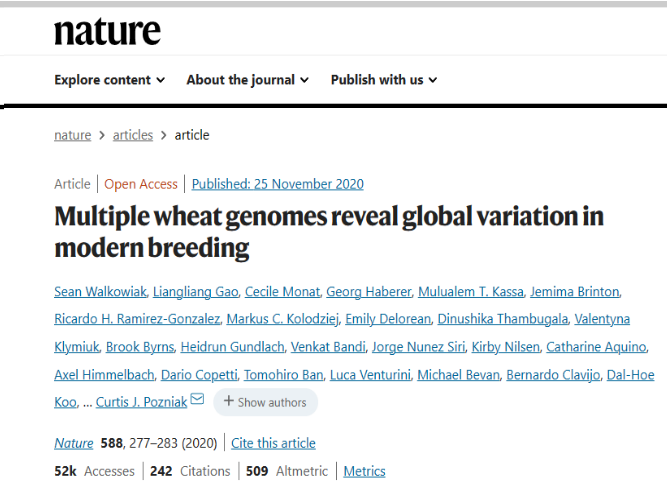
2020



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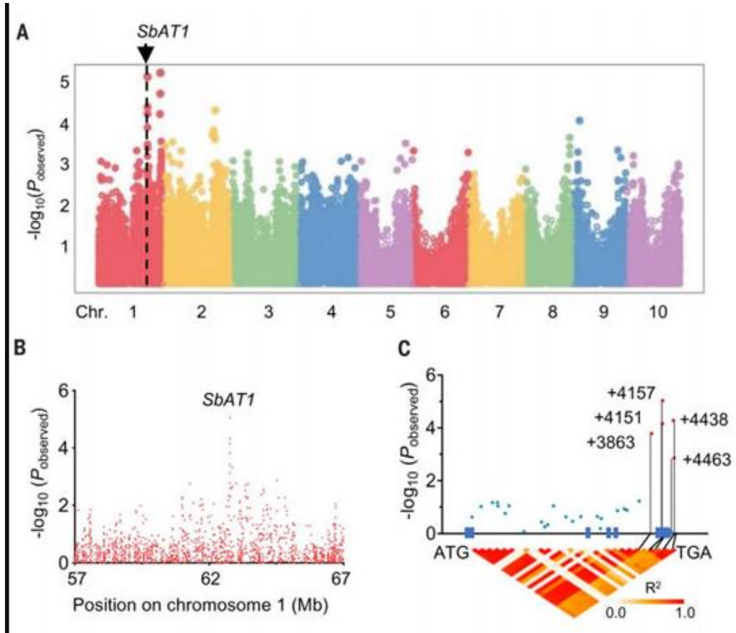
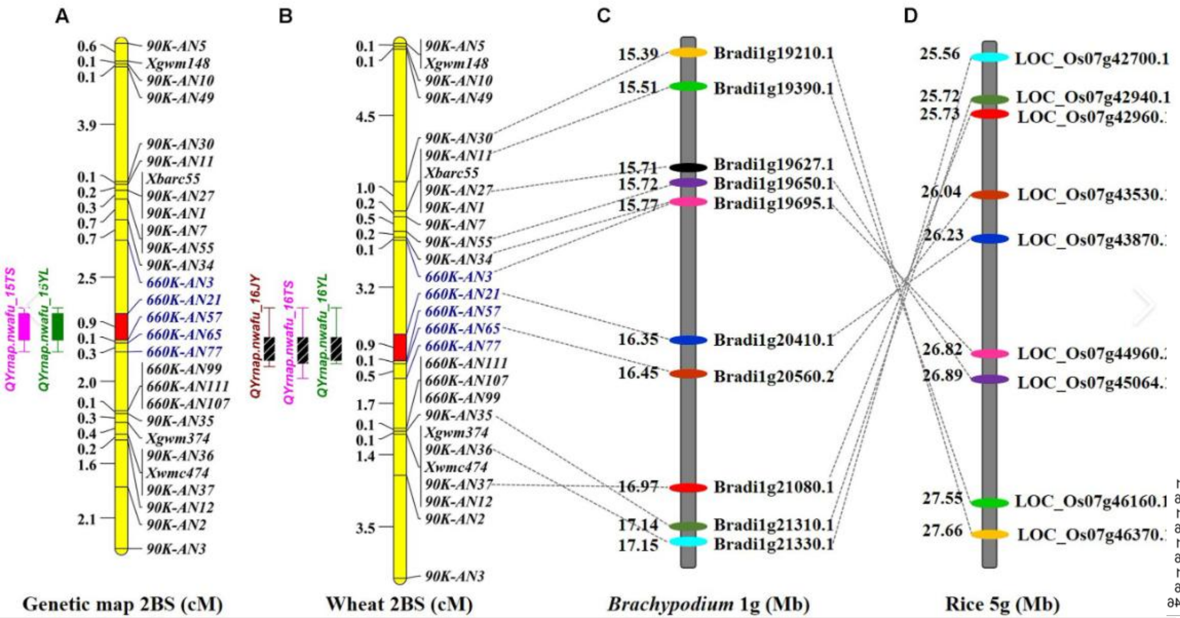
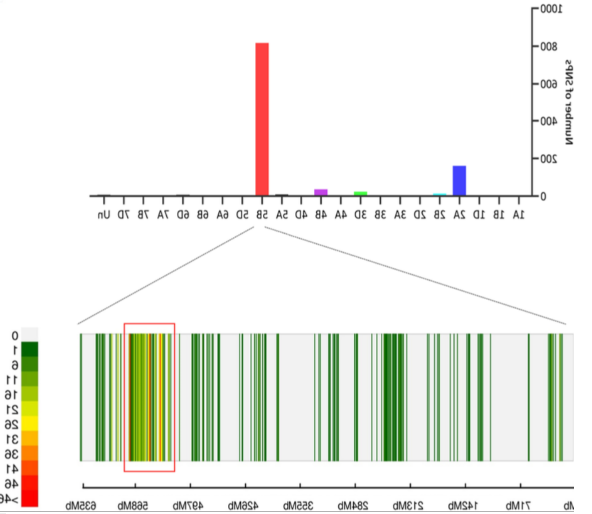
2024

Forward genetic strategy is a key to uncover wheat important genes

- GWAS (Genome-wide association study)
- Linkage/QTL mapping
- BSA (Bulk segregation analysis)
- ……







Markers selection for physical mapping

PCR-Based marker

- RPAD
- RFLP
- AFLP
- SSR
- DArT
- EST
- …

Time-consuming
Less density

Sequencing marker

- GBS
- SLAF
- Exome capture
- Genome resequencing

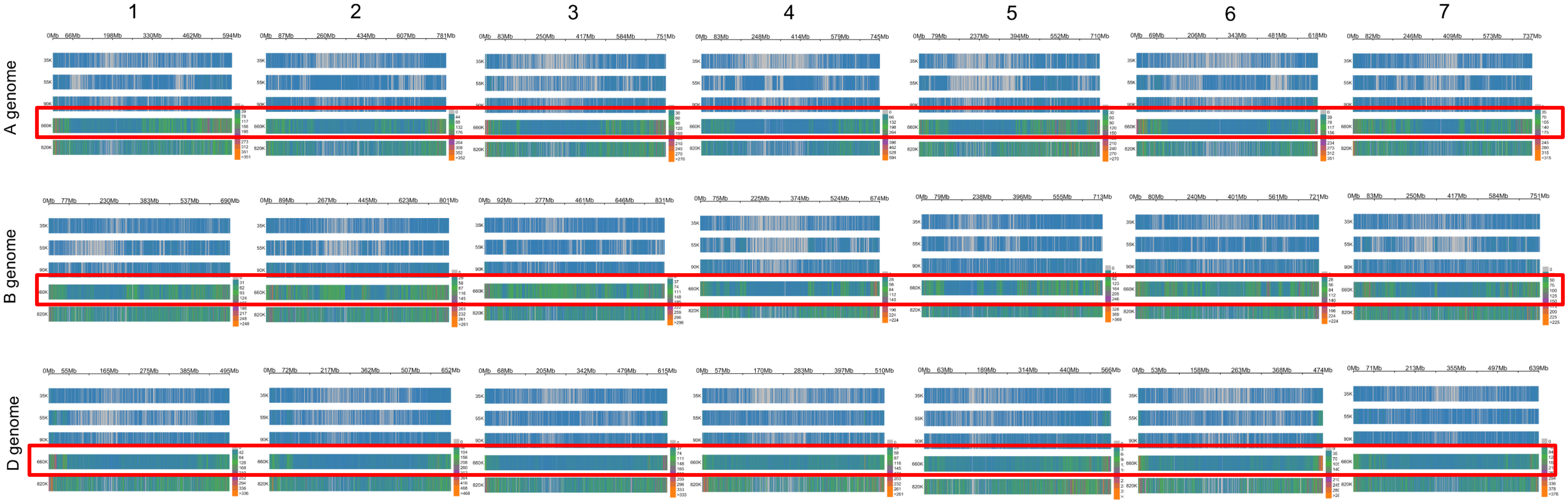
High cost
Professional

Chip marker

- 9K SNP Array
- 10K SNP Array
- 15K SNP Array
- 35K SNP Array
- 50K SNP Array
- 55K SNP Array
- 90K SNP Array
- 660K SNP Array
- 820K SNP Array

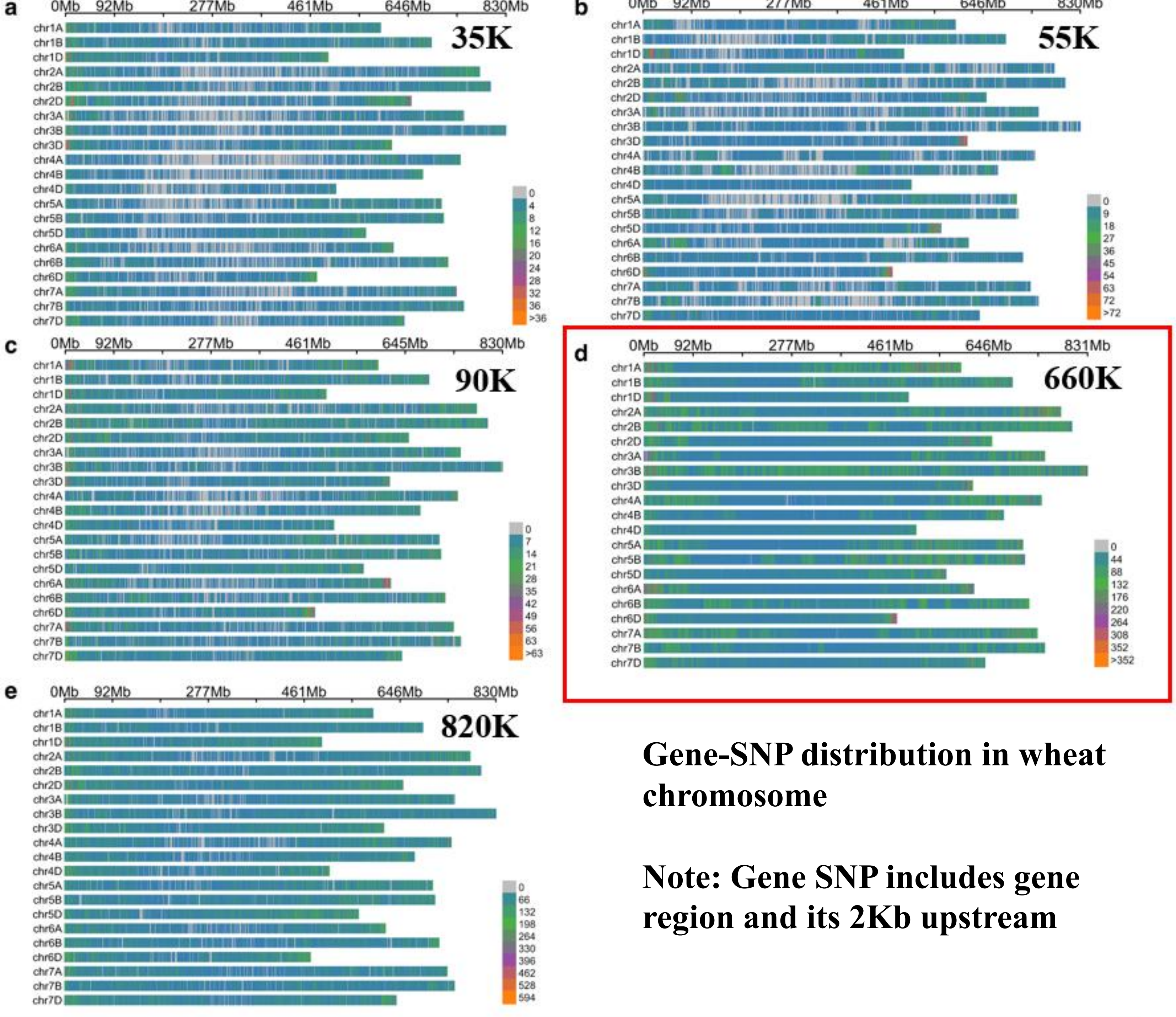
Low cost
Non-professional

SNP distribution revealed the highest density of 660K in wheat chromosome



Chromosomal distribution of SNP density for five Chips

Up to down: 35K, 55K, 90K, 660K and 820K



Gene-SNP distribution in wheat chromosome

Note: Gene SNP includes gene region and its 2Kb upstream

Gene-SNP distribution revealed the highest density of 660K Chip among five common chips

Plant Biotechnology Journal

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

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

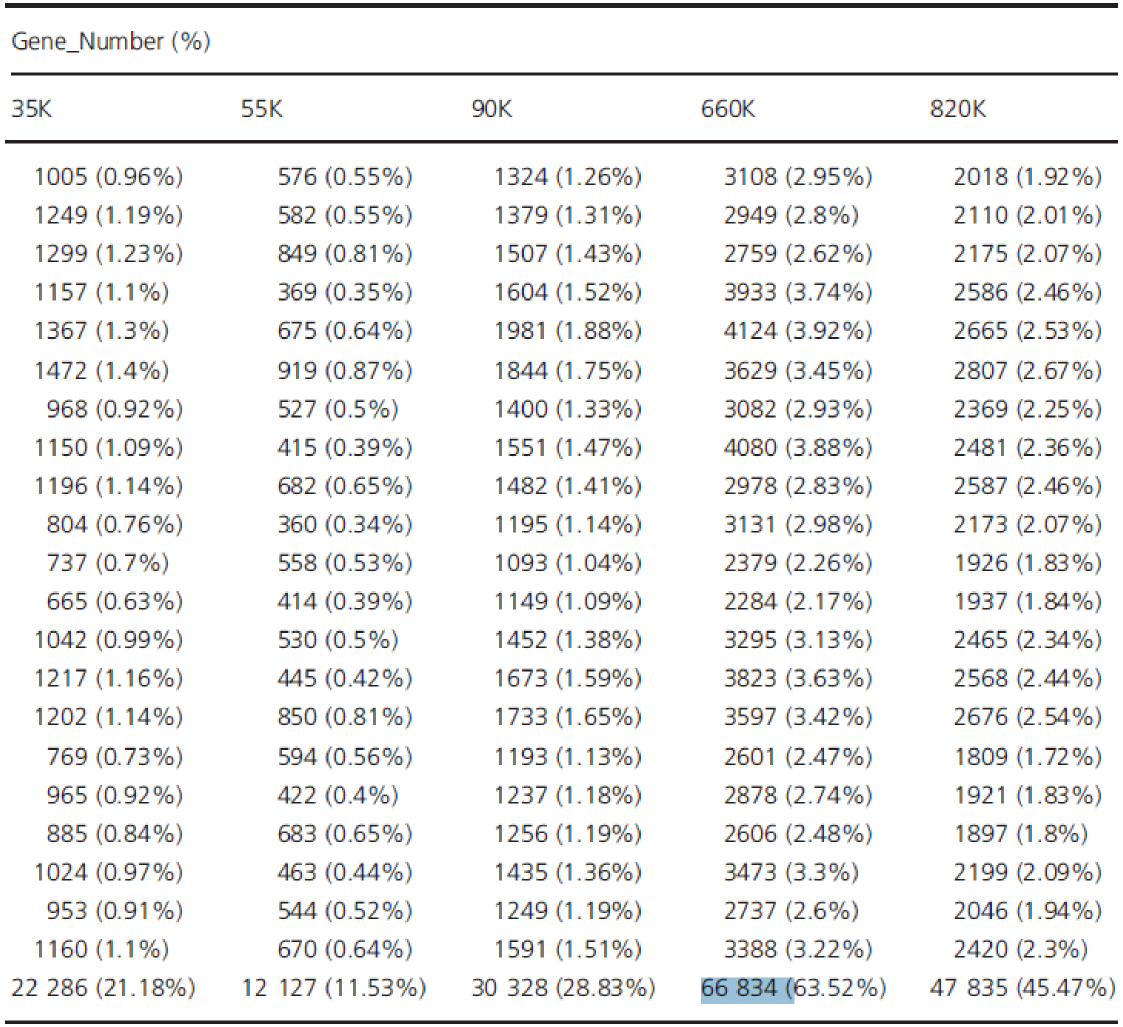
Received 21 October 2019;
revised 22 January 2020;
accepted 1 February 2020.
*Correspondence (Tel +86 37156990337;

Abstract

The rapid development and application of molecular marker assays have facilitated genomic selection and genome-wide linkage and association studies in wheat breeding. Although PCR-based markers (e.g. simple sequence repeats and functional markers) and genotyping by

Based on current wheat genome database, it’s feasible to explore more high-throughput wheat chips

- ◆ **More than 200K genes in wheat pan-genome**
- ◆ **More than 160K genes in single variety (e.g. Chinese Spring)**
- ◆ **The 660K Chip only covers 67K genes (including ±2K downstream/upstream)**
- ◆ **More high-throughput wheat chips?**

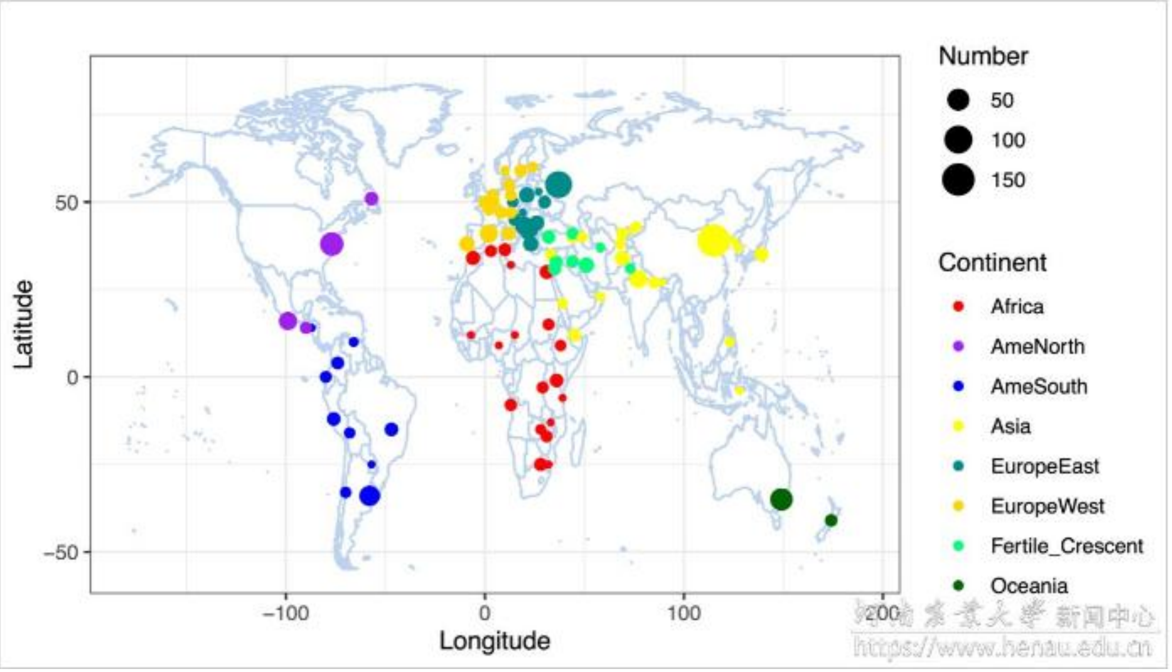


Gene_Number (%)				
35K	55K	90K	660K	820K
1005 (0.96%)	576 (0.55%)	1324 (1.26%)	3108 (2.95%)	2018 (1.92%)
1249 (1.19%)	582 (0.55%)	1379 (1.31%)	2949 (2.8%)	2110 (2.01%)
1299 (1.23%)	849 (0.81%)	1507 (1.43%)	2759 (2.62%)	2175 (2.07%)
1157 (1.1%)	369 (0.35%)	1604 (1.52%)	3933 (3.74%)	2586 (2.46%)
1367 (1.3%)	675 (0.64%)	1981 (1.88%)	4124 (3.92%)	2665 (2.53%)
1472 (1.4%)	919 (0.87%)	1844 (1.75%)	3629 (3.45%)	2807 (2.67%)
968 (0.92%)	527 (0.5%)	1400 (1.33%)	3082 (2.93%)	2369 (2.25%)
1150 (1.09%)	415 (0.39%)	1551 (1.47%)	4080 (3.88%)	2481 (2.36%)
1196 (1.14%)	682 (0.65%)	1482 (1.41%)	2978 (2.83%)	2587 (2.46%)
804 (0.76%)	360 (0.34%)	1195 (1.14%)	3131 (2.98%)	2173 (2.07%)
737 (0.7%)	558 (0.53%)	1093 (1.04%)	2379 (2.26%)	1926 (1.83%)
665 (0.63%)	414 (0.39%)	1149 (1.09%)	2284 (2.17%)	1937 (1.84%)
1042 (0.99%)	530 (0.5%)	1452 (1.38%)	3295 (3.13%)	2465 (2.34%)
1217 (1.16%)	445 (0.42%)	1673 (1.59%)	3823 (3.63%)	2568 (2.44%)
1202 (1.14%)	850 (0.81%)	1733 (1.65%)	3597 (3.42%)	2676 (2.54%)
769 (0.73%)	594 (0.56%)	1193 (1.13%)	2601 (2.47%)	1809 (1.72%)
965 (0.92%)	422 (0.4%)	1237 (1.18%)	2878 (2.74%)	1921 (1.83%)
885 (0.84%)	683 (0.65%)	1256 (1.19%)	2606 (2.48%)	1897 (1.8%)
1024 (0.97%)	463 (0.44%)	1435 (1.36%)	3473 (3.3%)	2199 (2.09%)
953 (0.91%)	544 (0.52%)	1249 (1.19%)	2737 (2.6%)	2046 (1.94%)
1160 (1.1%)	670 (0.64%)	1591 (1.51%)	3388 (3.22%)	2420 (2.3%)
22 286 (21.18%)	12 127 (11.53%)	30 328 (28.83%)	66 834 (63.52%)	47 835 (45.47%)

Sun et al. PBJ, 2020,18:1354-1360

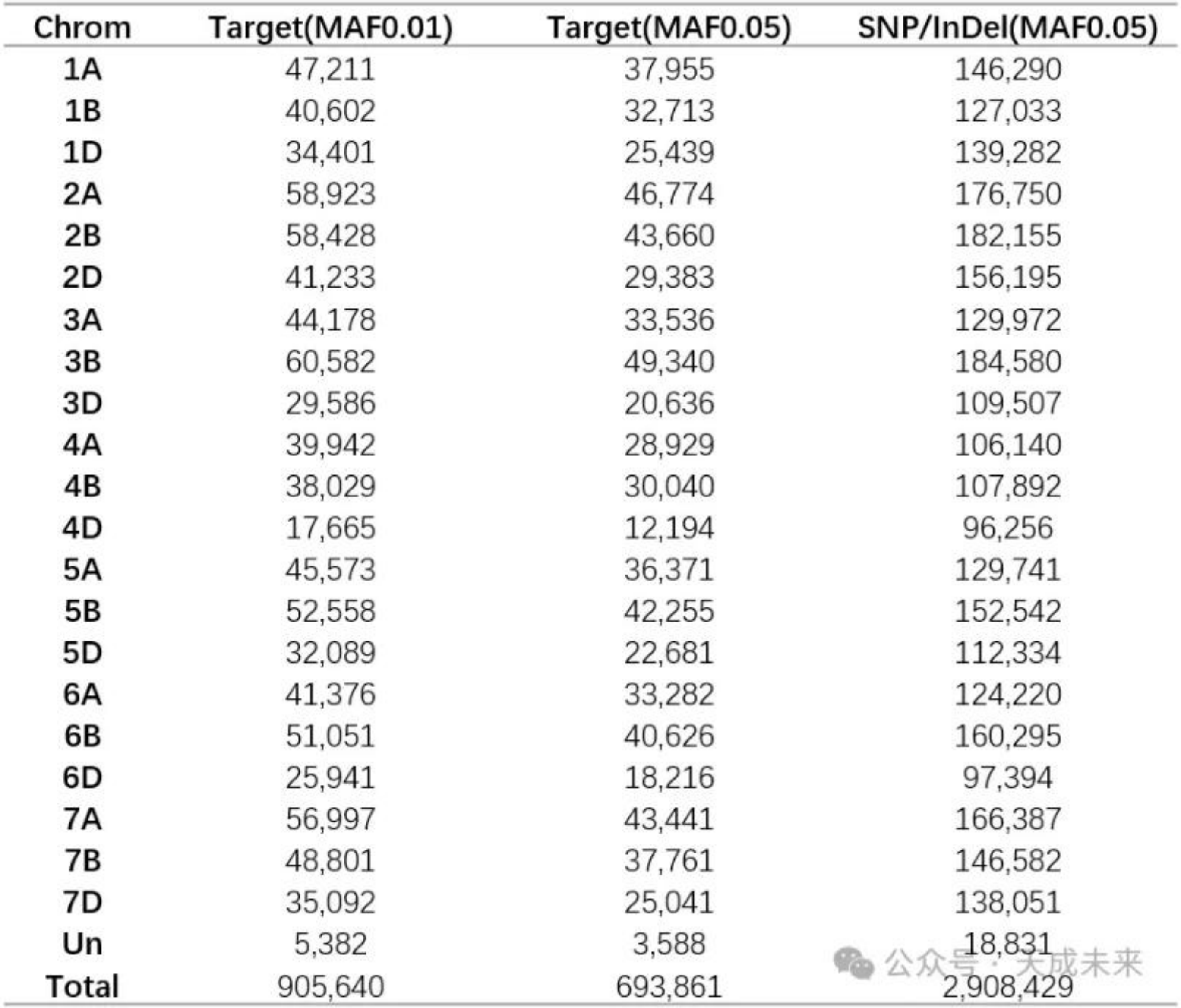
Explore wheat Pan800K gene chip

- ➢ Construct a pan-genome variant atlas based on *de novo* seq/re-seq/ exome seq of 3000 global wheat
- ➢ Select 800K variants as probes in gene regions (±5K)
- ➢ Balanced variants： 50K SNPs as probes was added in Chip
- ➢ Method: Next-generation sequencing (capture 200-300 bp variants around site)
- ➢ Finally obtain more variants than designed probe



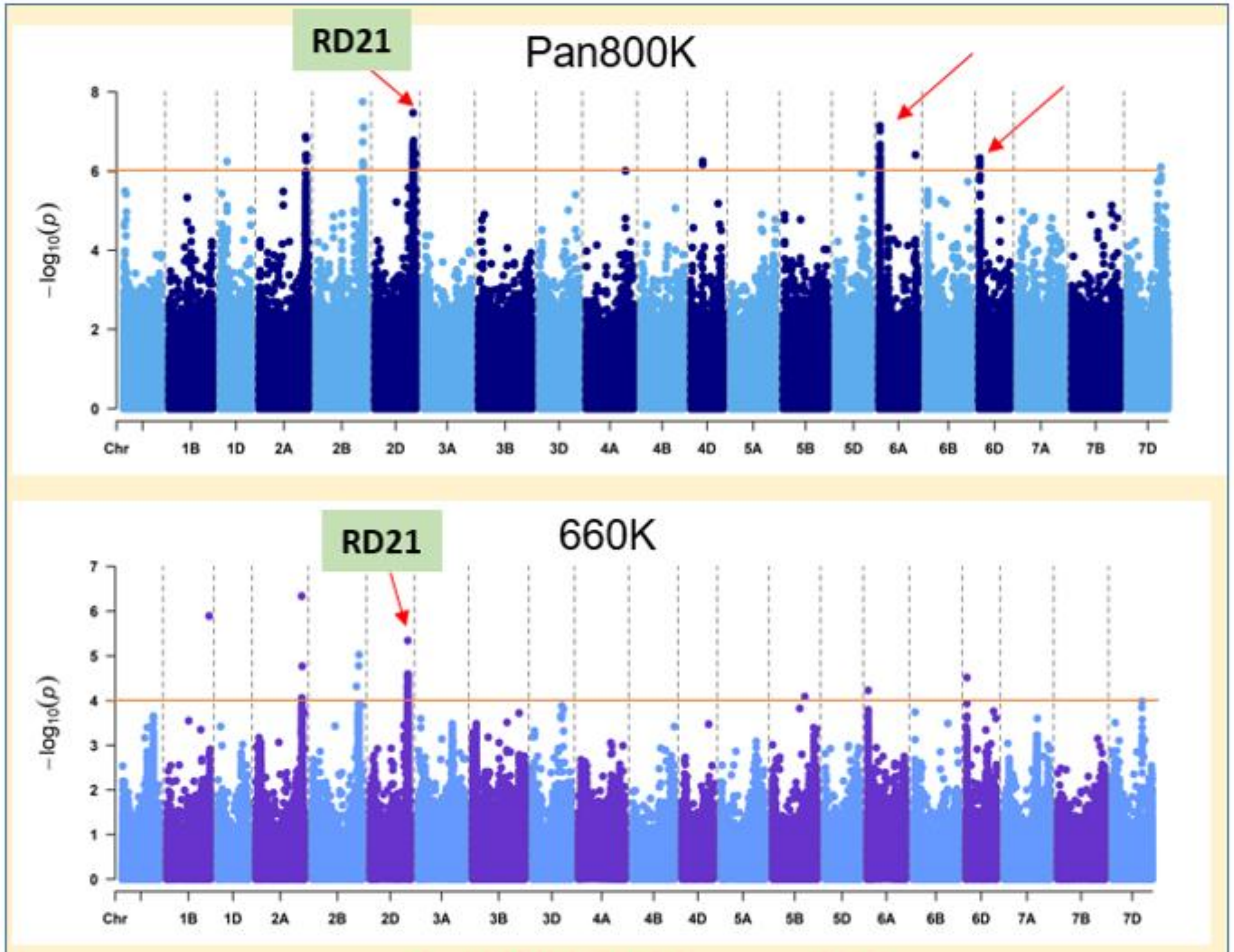
Sequencing results by Pan800K gene Chip

- Sequence 480 Chinese wheat varieties
- Obtain 693K high-quality variant fragments (MAF≥0.05), containing 2.9M SNP/InDel（see Table）
- Cover ~180K genes (±5K)
- More than 50% variants were in HC genes (±5K)

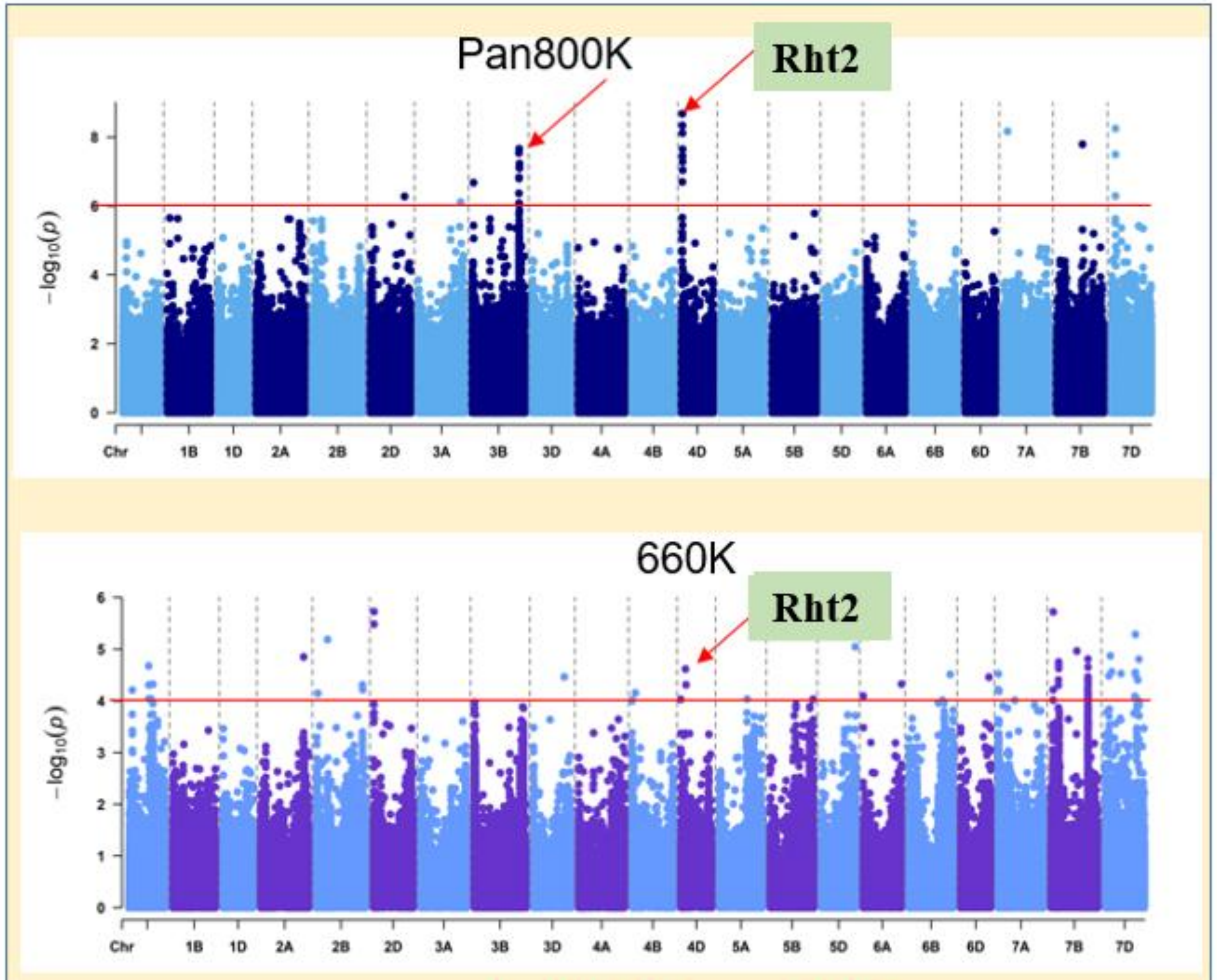


Chrom	Target(MAF0.01)	Target(MAF0.05)	SNP/InDel(MAF0.05)
1A	47,211	37,955	146,290
1B	40,602	32,713	127,033
1D	34,401	25,439	139,282
2A	58,923	46,774	176,750
2B	58,428	43,660	182,155
2D	41,233	29,383	156,195
3A	44,178	33,536	129,972
3B	60,582	49,340	184,580
3D	29,586	20,636	109,507
4A	39,942	28,929	106,140
4B	38,029	30,040	107,892
4D	17,665	12,194	96,256
5A	45,573	36,371	129,741
5B	52,558	42,255	152,542
5D	32,089	22,681	112,334
6A	41,376	33,282	124,220
6B	51,051	40,626	160,295
6D	25,941	18,216	97,394
7A	56,997	43,441	166,387
7B	48,801	37,761	146,582
7D	35,092	25,041	138,051
Un	5,382	3,588	18,831
Total	905,640	693,861	2,908,429

Comparison of Pan800K and 660K Chips by GWAS

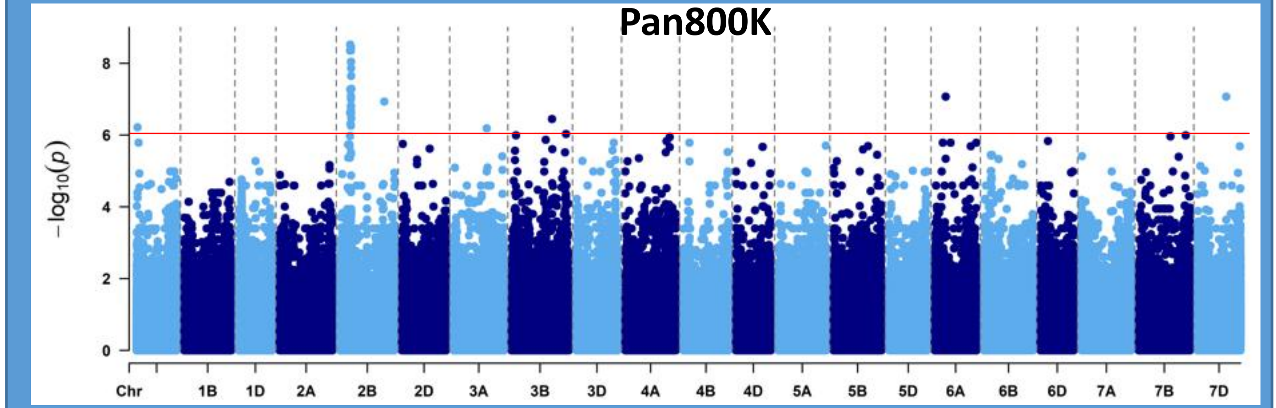


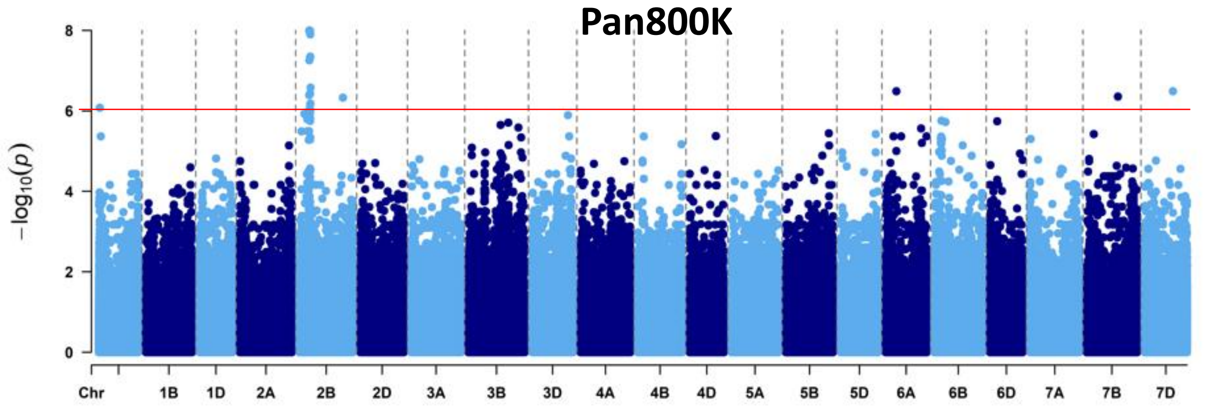
小麦黄花叶病GWAS分析

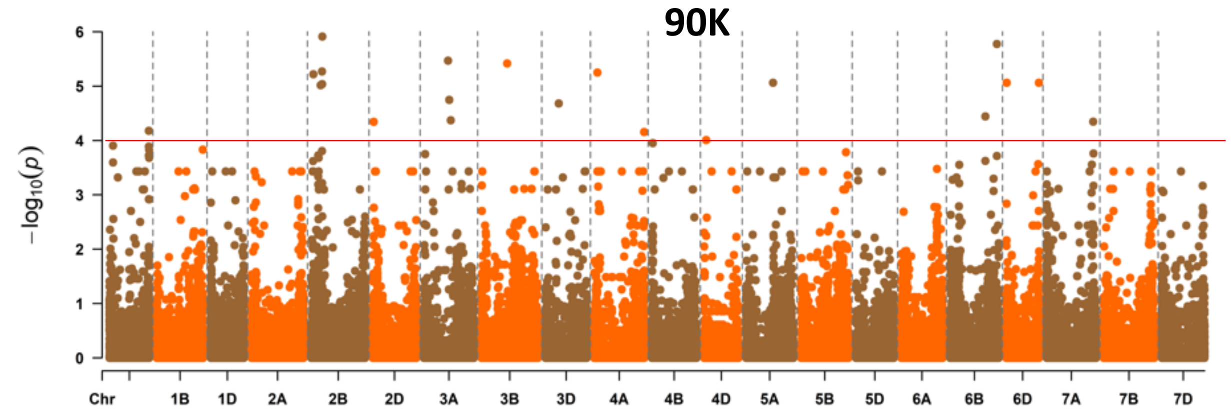


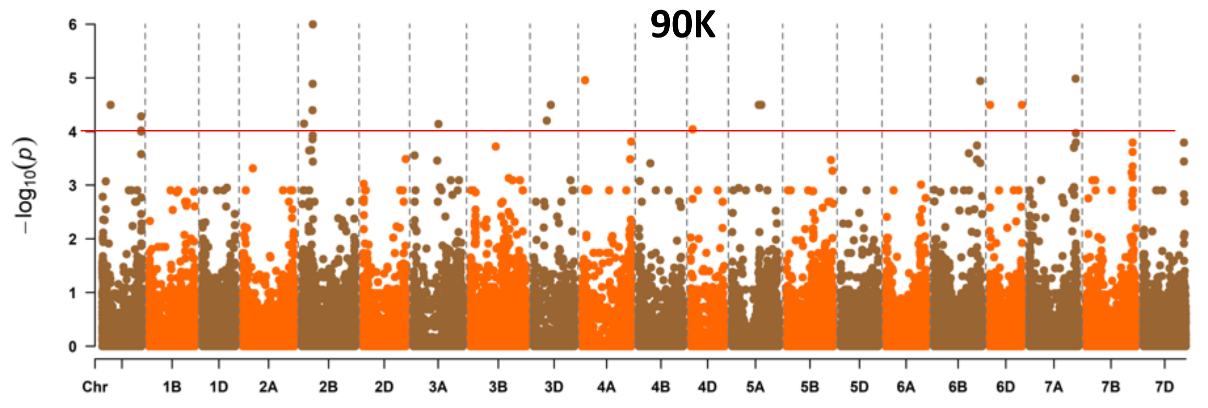
小麦株高GWAS分析

Comparison of GWAS results between Pan800K and 90K

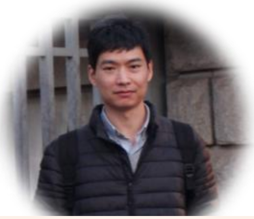

Pan800K


Pan800K


90K


90K

Transfer the right of Pan800K gene Chip to Chengdu Tiancheng Future Sci&Tech Co., Ltd. for a price of 15 million Yuan



Congwei Sun

我院陈锋教授团队研发小麦超高密度芯片的智慧基因挖掘和育种选择系统成功转让

发布时间： 2024-11-09 22:12　点击数:188

本网讯11 月 9 日上午，我院陈锋教授团队与成都天成未来科技有限公司总经理陈中旭在校图书馆举办的“2024第八届作物学黄河国际论坛”上签署了基于小麦超高密度基因芯片WheatPan800K的智慧基因挖掘和育种选择系统转化协议，转让金额1500万元。

高端人才引领 守护沃土粮仓

——河南农业大学作物学科成果频出的秘诀

2024年11月22日08：45 | 来源：光明日报

原标题：高端人才引领 守护沃土粮仓

“小麦Pan800K基因芯片转让费1500万元！” “豫农905、907、912、931品种经营权买断费1040万元！” 日前，在第八届作物学黄河国际论坛上，河南农业大学作物学科最新成果成为全场焦点。

2. Identification of fusarium crown rot resistance gene in wheat

- Fusarium crown rot (FCR), mainly caused by *F. pyseudgraminearum*, is one of the most serious wheat soil-born diseases.
- FCR could cause yield reduction by 10～30%, even by more than 70% in some serious region.
- FCR frequently occurs in all of the world, e.g. Australia, North America and South Asia
- Necrotrophic or hemi-biotrophic disease?

Occurrence of FCR in China

- In China, FCR was reported in 1990s and is becoming an important wheat diseases.
- More than 6M-hectare wheat is suffering from FCR annually in China.
- Most popular wheat varieties are susceptible or highly-susceptible to FCR.
- No FCR high-resistance or immunity wheat germplasm was publicly reported so far.

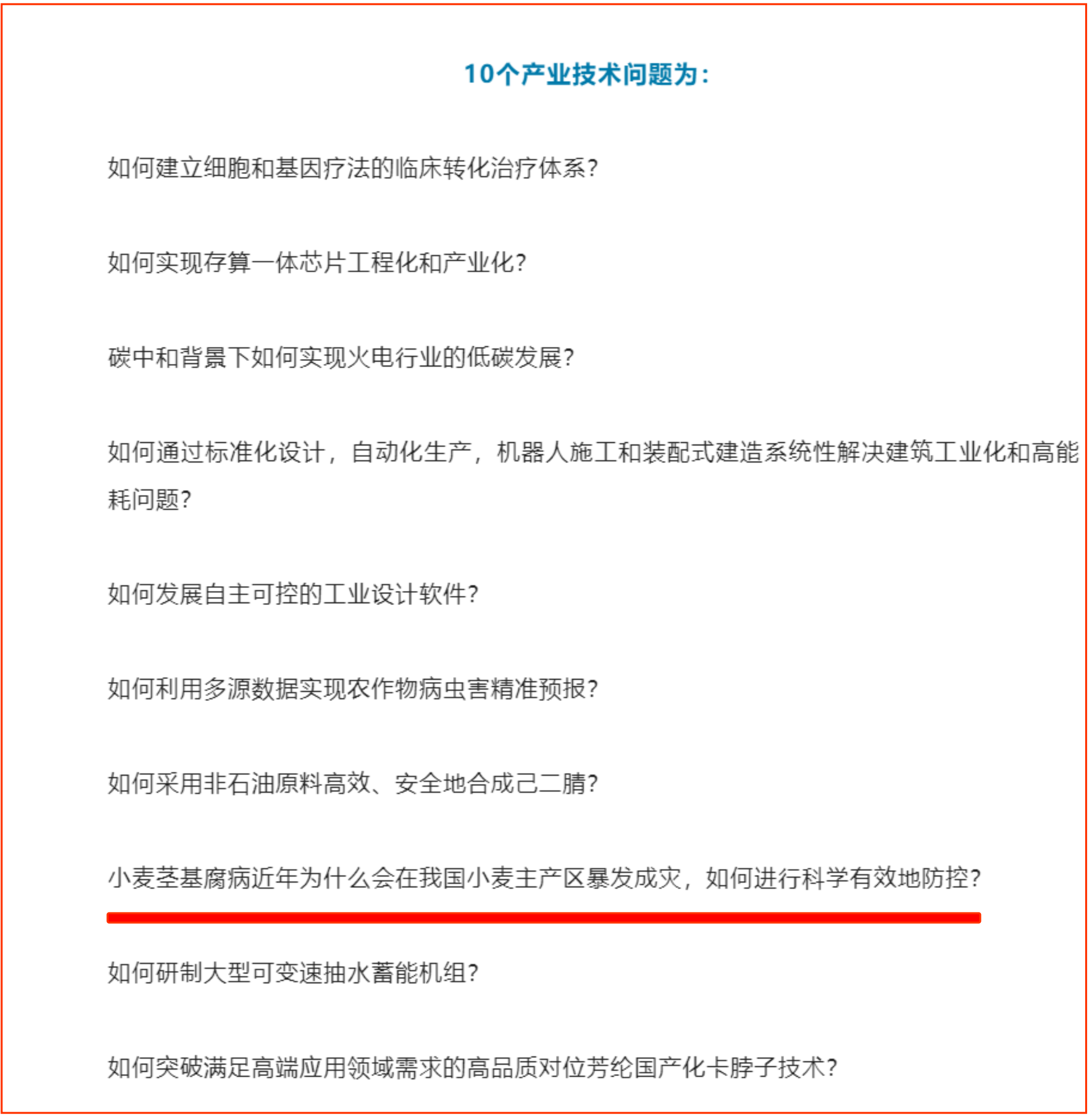
FCR was listed as one of the top ten in industrial technical issues by the China Association for Sci & Tech

30个！中国科协发布2022重大科学问题、工程技术难题和产业技术问题

锐动源 2022-06-27 16:50 发表于北京

6月27日，在第二十四届中国科协年会闭幕式上，中国科协隆重发布**10个对科学发展具有导向作用的前沿科学问题、10个对工程技术创新具有关键作用的工程技术难题**和**10个对产业发展具有引领作用的产业技术问题**，由中国科协副主席、中国工程院院士尤政发布。发布活动中还向推荐入选问题难题的中国化学会、中国环境科学学会等28个学会颁发"优秀推荐单位"牌匾。

2022重大科学问题、工程技术难题和产业技术问题征集发布活动，重点围绕数理化基础科



10个产业技术问题为：

如何建立细胞和基因疗法的临床转化治疗体系？

如何实现存算一体芯片工程化和产业化？

碳中和背景下如何实现火电行业的低碳发展？

如何通过标准化设计，自动化生产，机器人施工和装配式建造系统性解决建筑工业化和高能耗问题？

如何发展自主可控的工业设计软件？

如何利用多源数据实现农作物病虫害精准预报？

如何采用非石油原料高效、安全地合成己二腈？

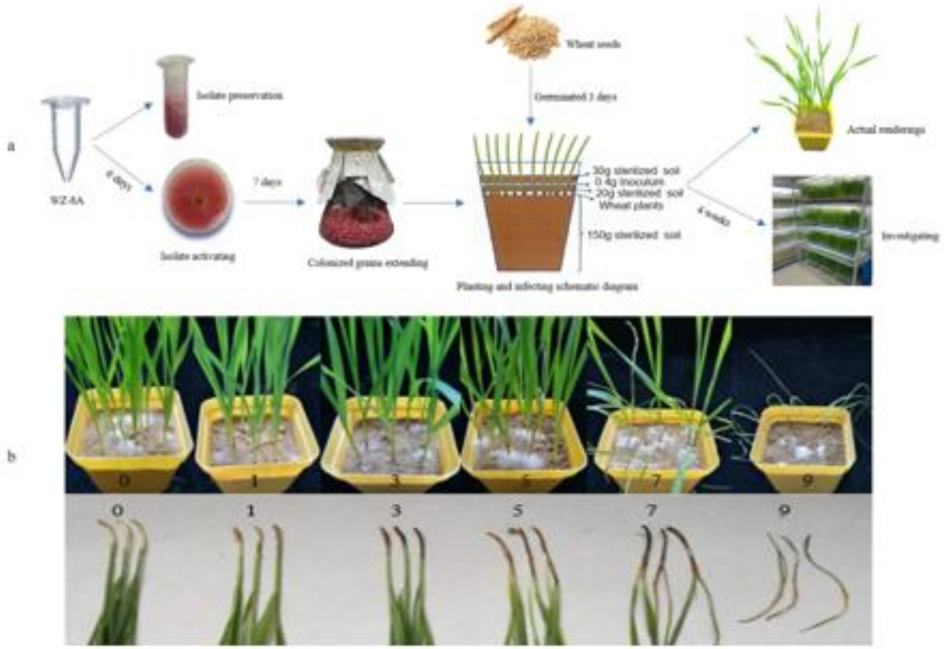
小麦茎基腐病近年为什么会在我国小麦主产区暴发成灾，如何进行科学有效地防控？

如何研制大型可变速抽水蓄能机组？

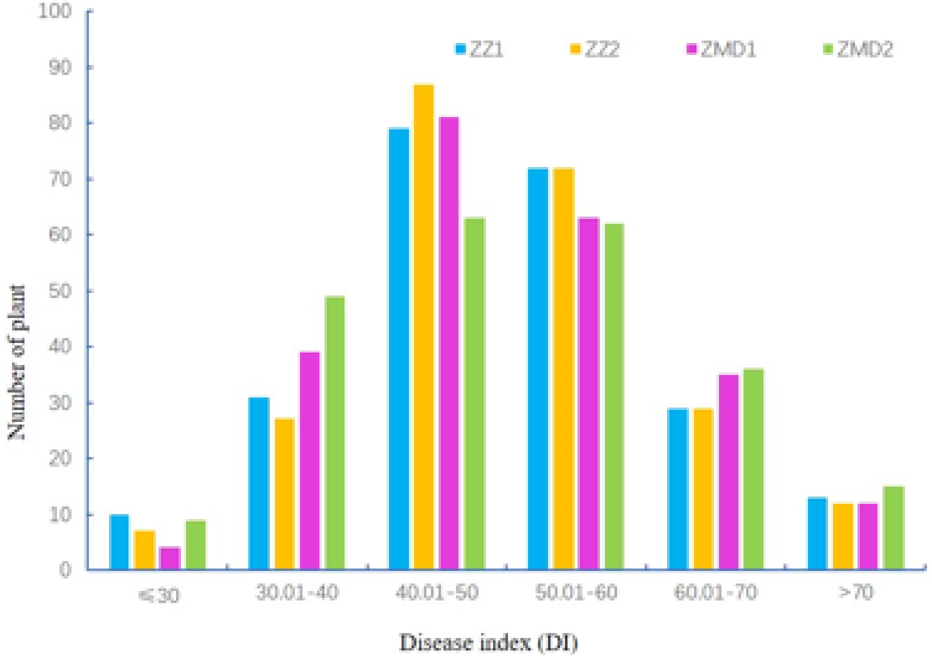
如何突破满足高端应用领域需求的高品质对位芳纶国产化卡脖子技术？

3. Physical mapping and identification of FCR genes

- Develop a rapid approach for scoring wheat FCR in greenhouse
- Score FCR resistance in >1000 wheat accessions
- Most of them are susceptible or highly-susceptible to FCR
- It’s urgent to improve FCR resistance in China



Yang et al. 2019, BMC Plant Biology

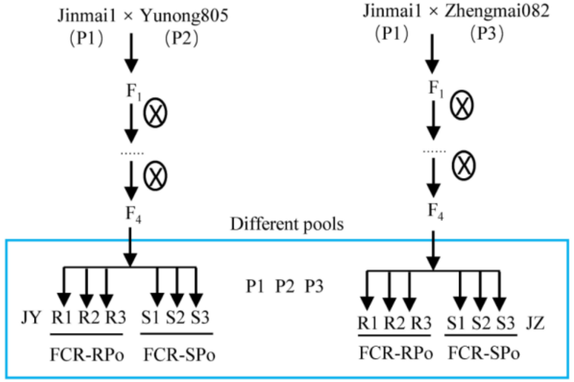


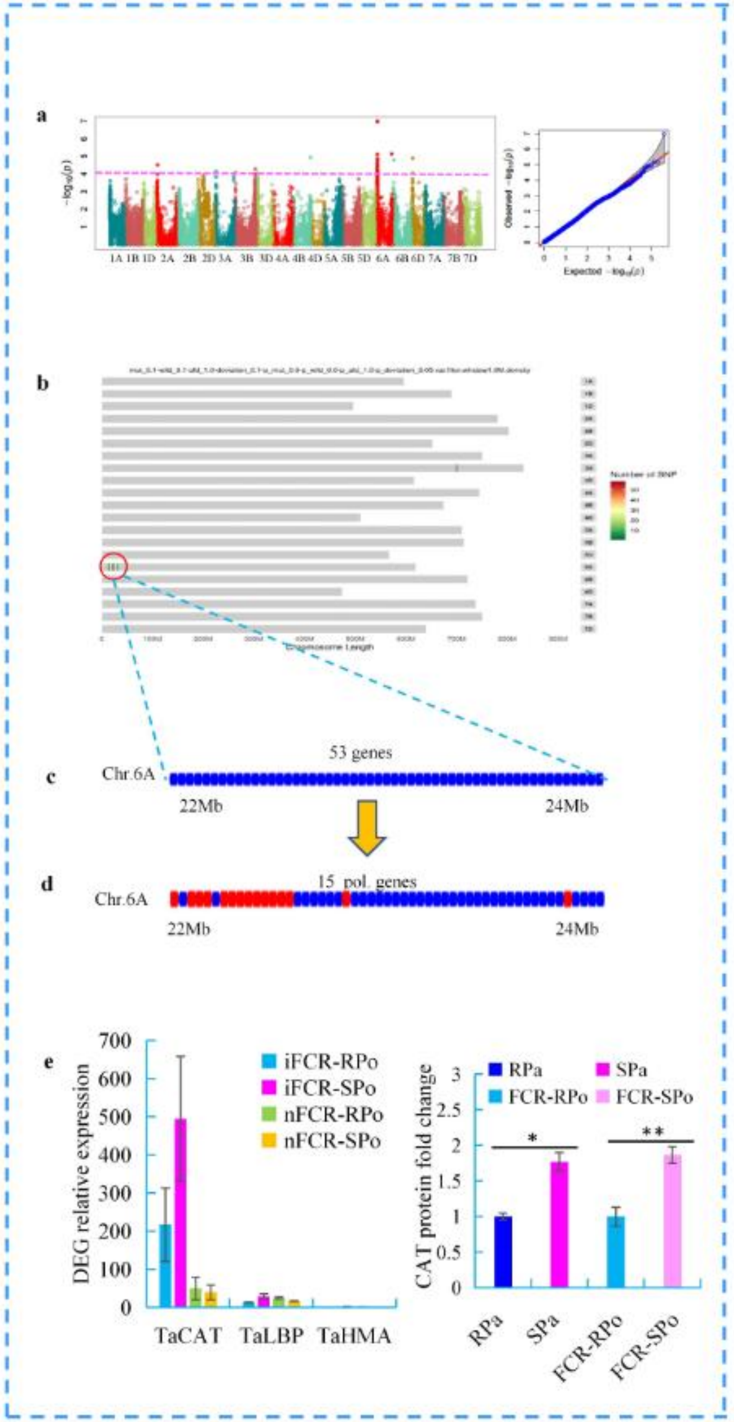
Genotyping for GWAS on FCR

- Genotyped by 660K or 90K SNP chips
- 480 accessions genotyped by Pan800K gene chip
- GWAS results showed almost all chrom. have FCR regulatory loci in wheat
  - Chrom. 4B, 6A, 2A, 3B etc.
  - Showed big difference of significant SNP in different populations
- Multi-omics were used to clone different loci

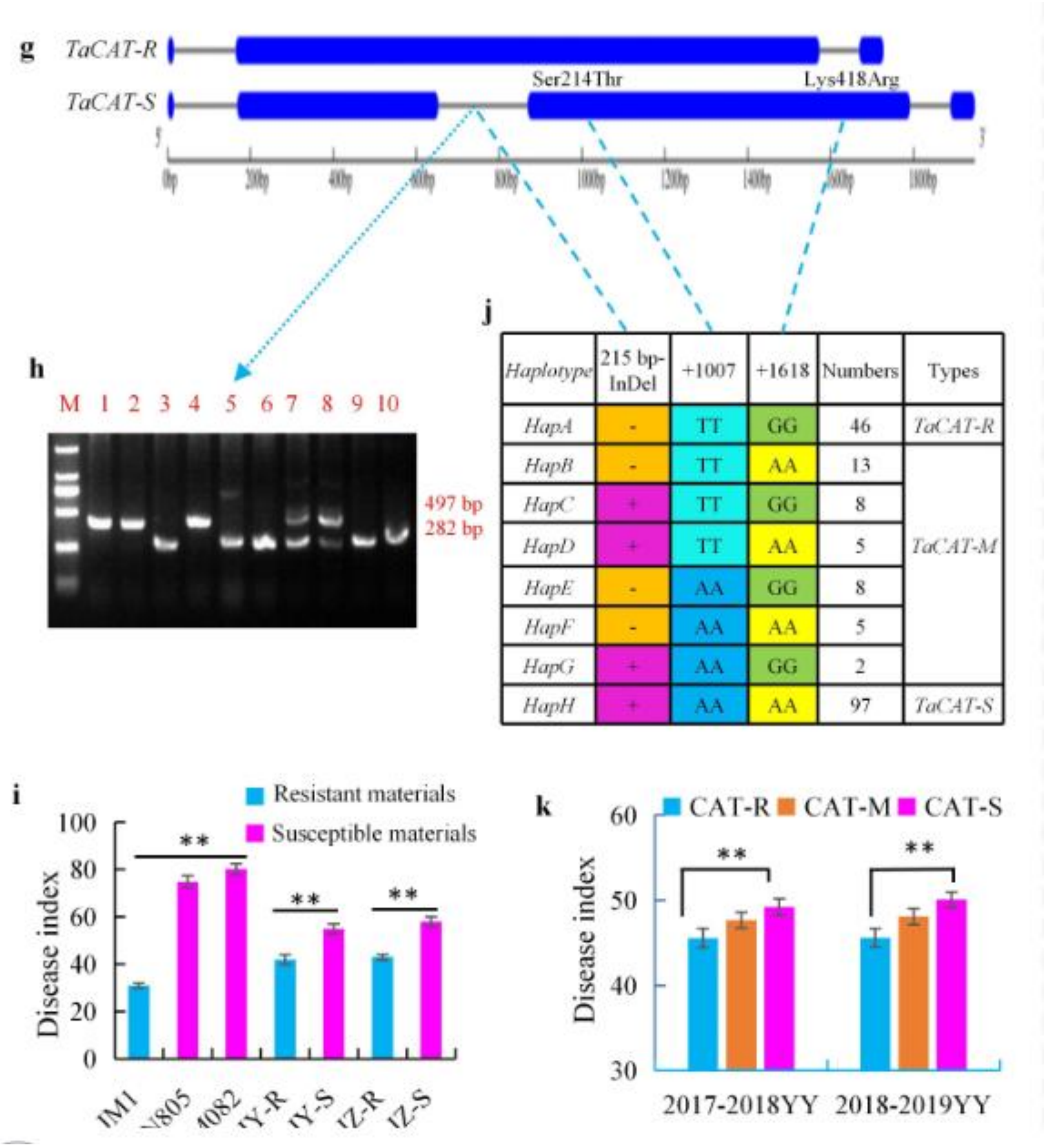
1) Cloning of TaCAT2 positively regulating FCR

- **Identify a key locus in the 14-Mb interval of 6A by GWAS**
- **Build two nested RIL populations:**
  - Jinmai1/Yunong805, Jinmai1/Zhengmai802
- **Narrow into 2-Mb interval by whole exome sequencing**
- BSR-Seq, BS-iTRAQ
- **TaCAT2（Catalase）as candidate**

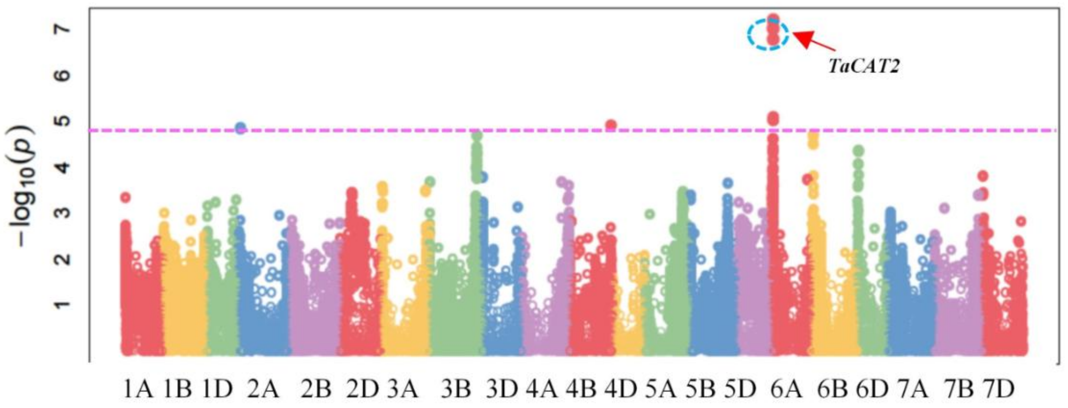




- **TaCAT2 shows 8 haplotypes in Chinese wheat**
- **Divide into R, mid-S and S types**
- **Hapl-A as R-type shows variants of Ser214Thr, Lys418Arg and 215bp InDel (intron)**
- **Develop a marker for TaCAT2 and re-run GWAS revealed *TaCAT2* as a lead SNP**

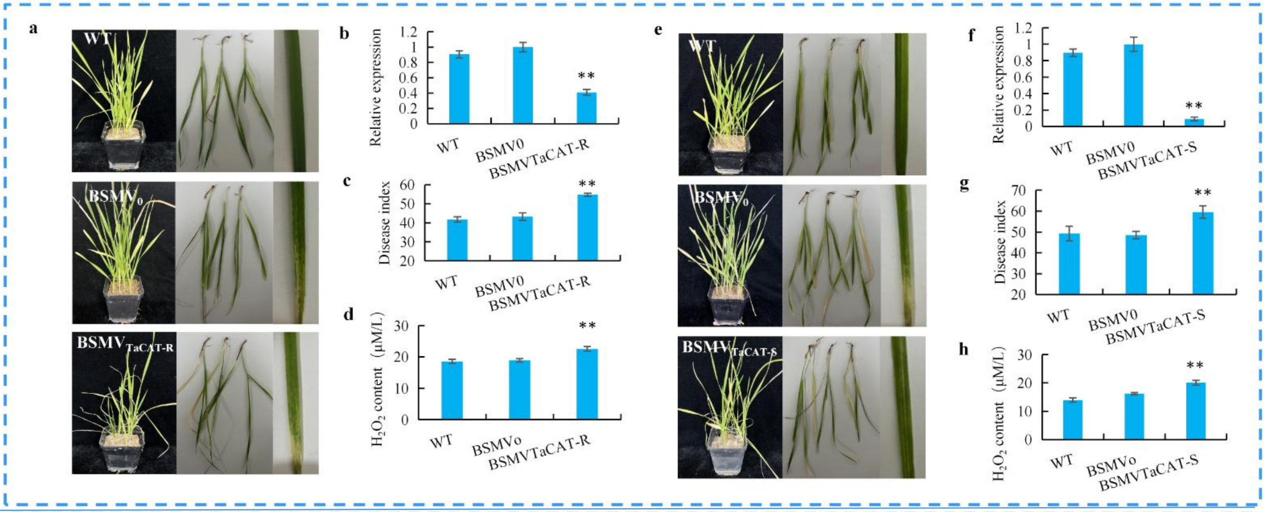


Haplotype	215 bp-InDel	+1007	+1618	Numbers	Types
HapA	-	TT	GG	46	*TaCAT-R*
HapB	-	TT	AA	13	*TaCAT-M*
HapC	+	TT	GG	8	
HapD	+	TT	AA	5	
HapE	-	AA	GG	8	
HapF	-	AA	AA	5	
HapG	+	AA	GG	2	
HapH	+	AA	AA	97	*TaCAT-S*

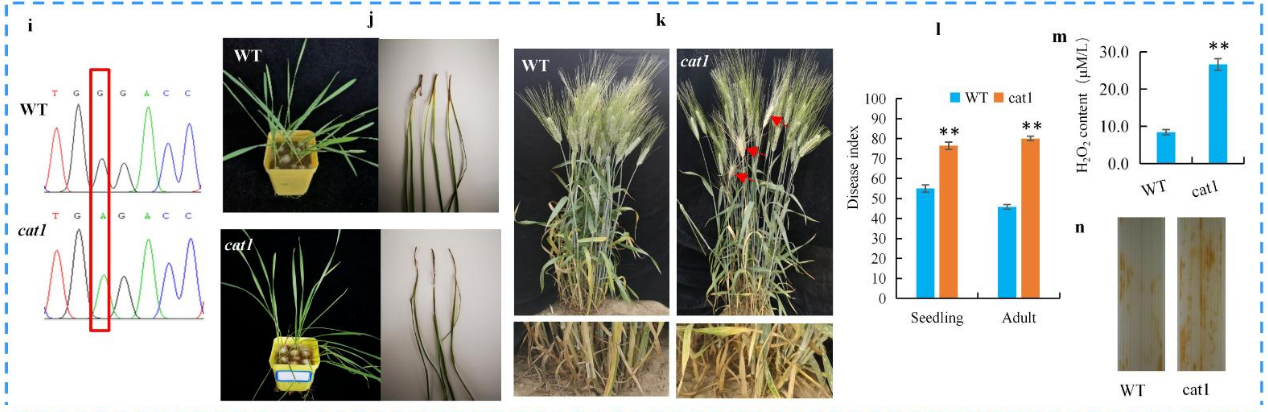


Functional verification of TaCAT2

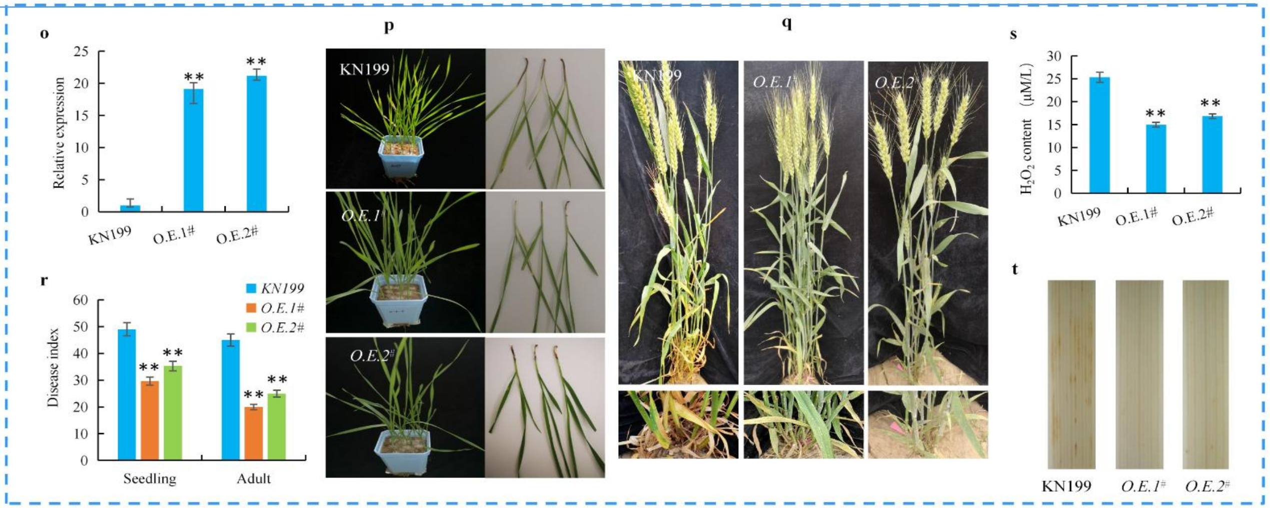
Silencing TaCAT2 by VIGS sharply increased FCR disease index (DI) as well as ROS (Reactive oxygen species) content



EMS mutants showed increased FCR DI as well as ROS content

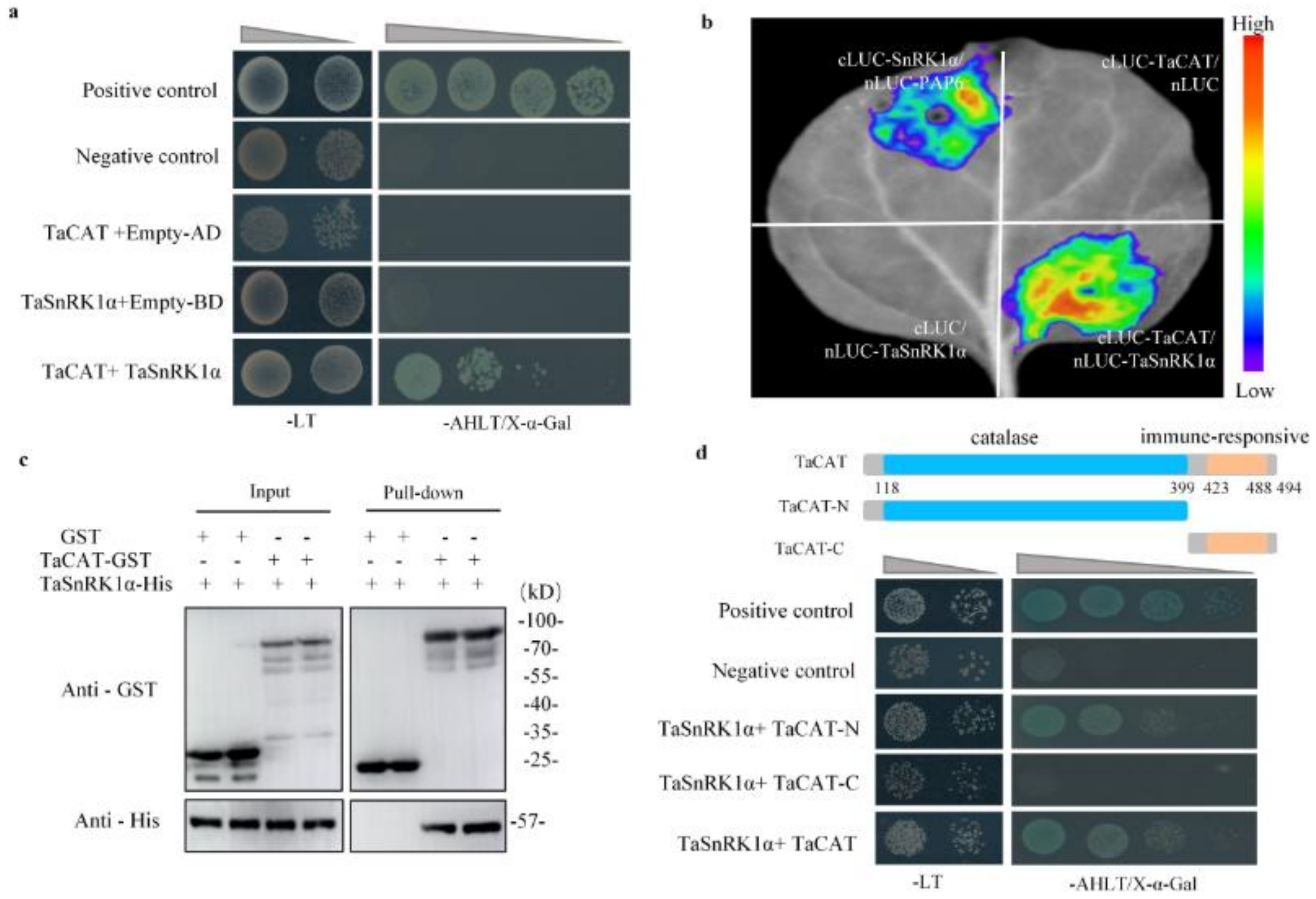


Overexpression of TaCAT2 showed decreased FCR DI as well as ROS content

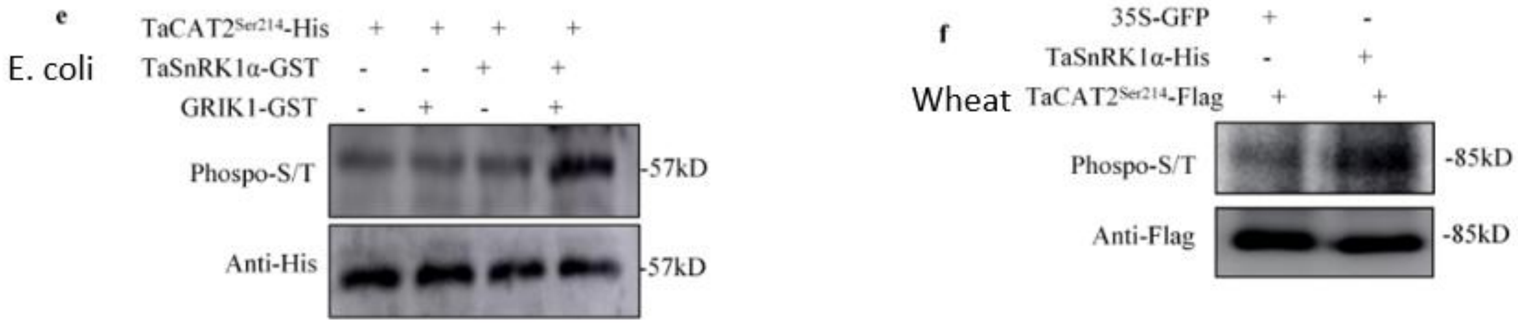


Dissection of molecular mechanism of TaCAT2 mediating FCR

- ➢TaSnRK1a interacted with TaCAT2 by Y-2H
- ➢The interaction was confirmed by Y-2H, Luciferase, Pull-down
- ➢TaSnRK1a interact with the N terminal of TaCAT2

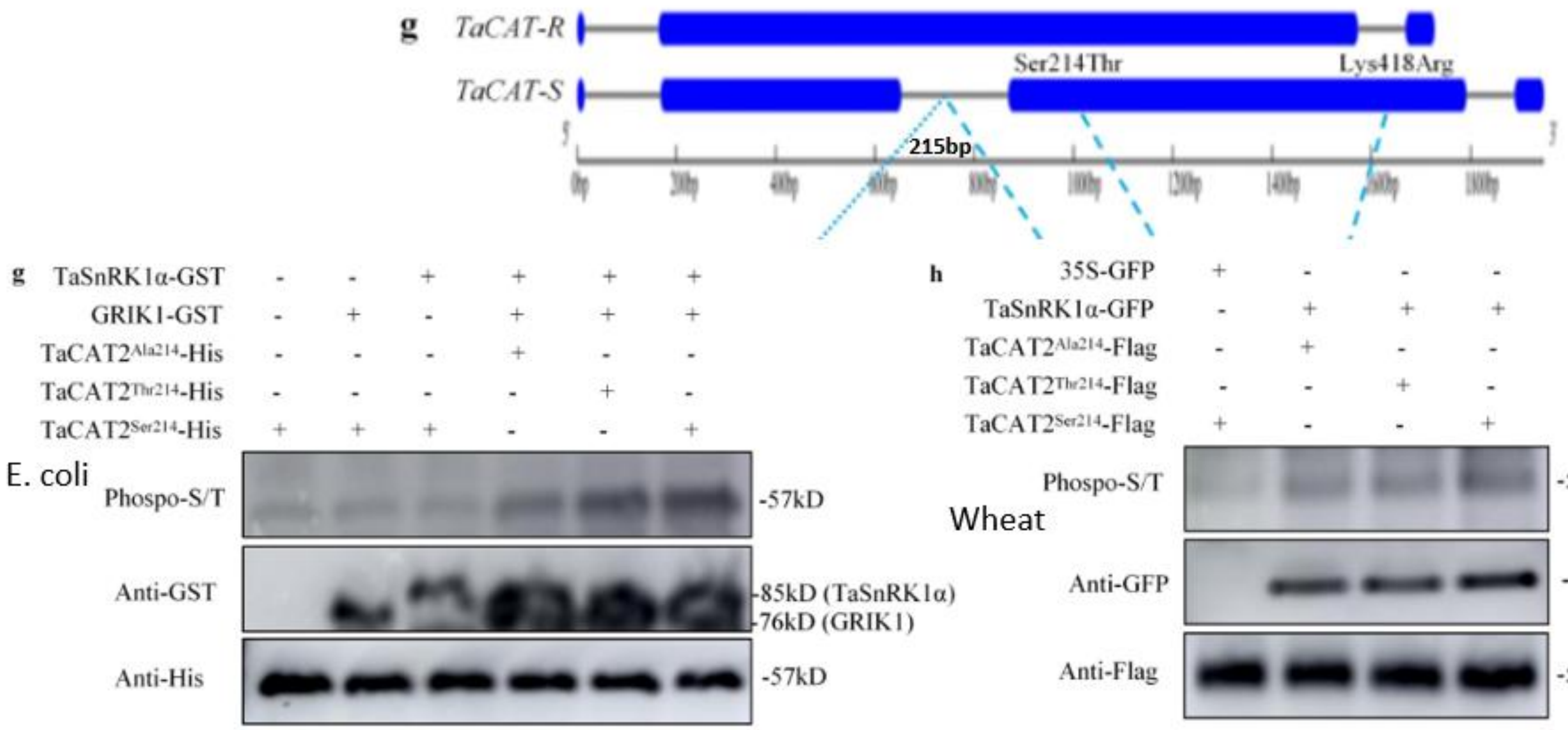


◆ **TaSnRK1a as a kinase phosphorylate TaCAT2 *in vivo* and *in vitro***



◆ **214aa is a key site of TaSnRK1a phosphorylating TaCAT2**

◆ **TaSnRK1a more strongly phosphorylates TaCAT2-R than TaCAT2-S**

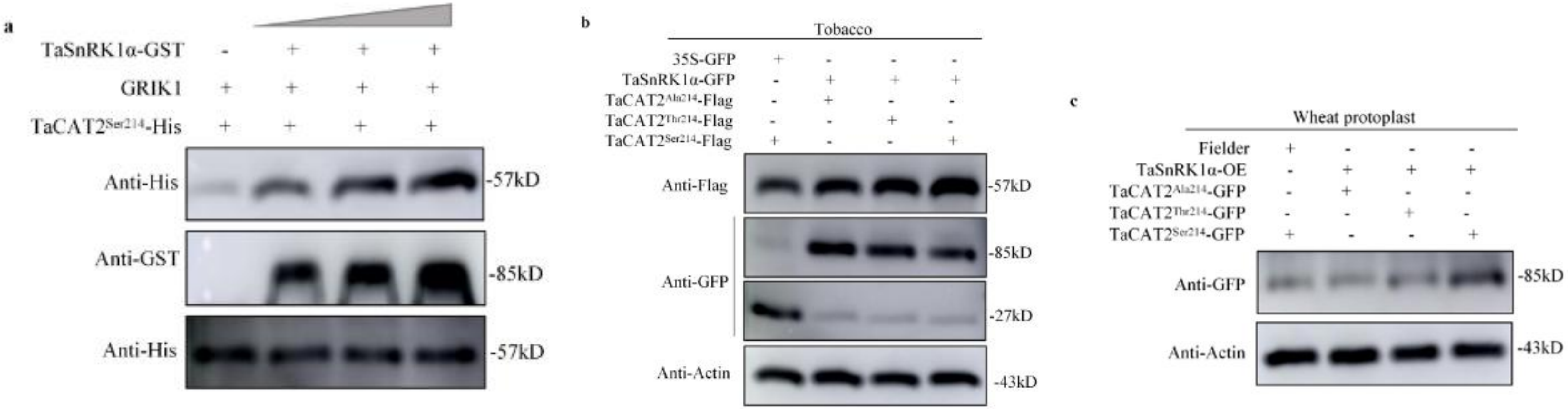


TaCAT2-R：Serine214
TaCAT2-S：Threonine214

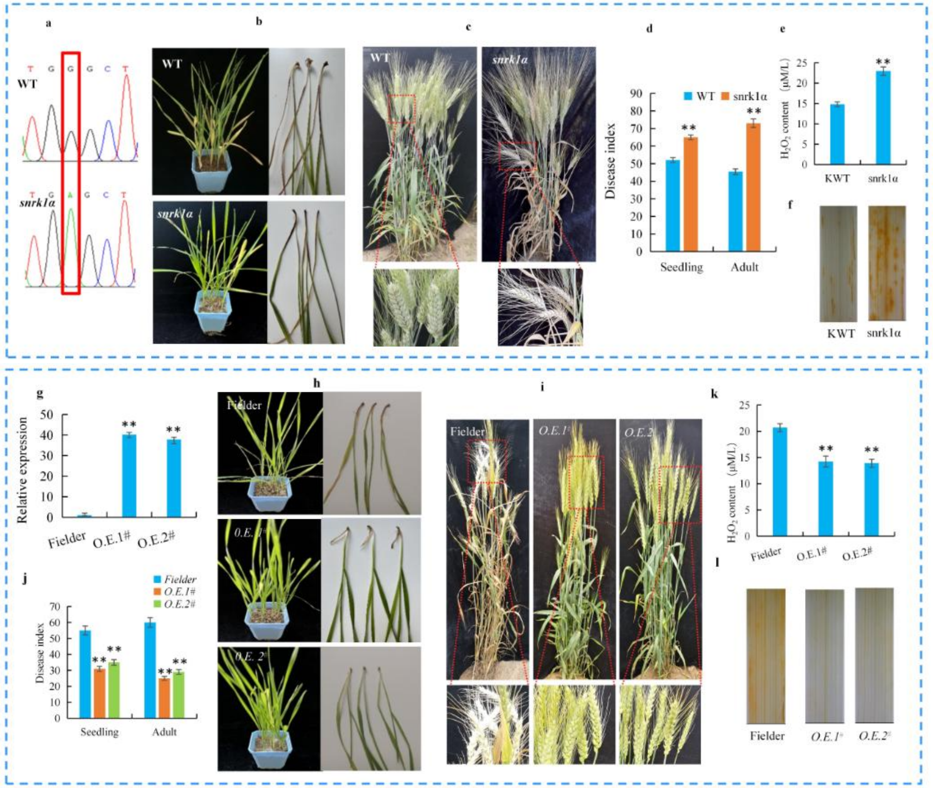
Note: Alanine (Ala) is non-phosphor AA.

Affect protein stability of TaCAT2 by phosphorylation of TaSnRK1a?

- **TaSnRK1a improves the abundance of TaCAT2 in**
  - E.coli
  - Tobacco
  - TaSnRK1a-OE

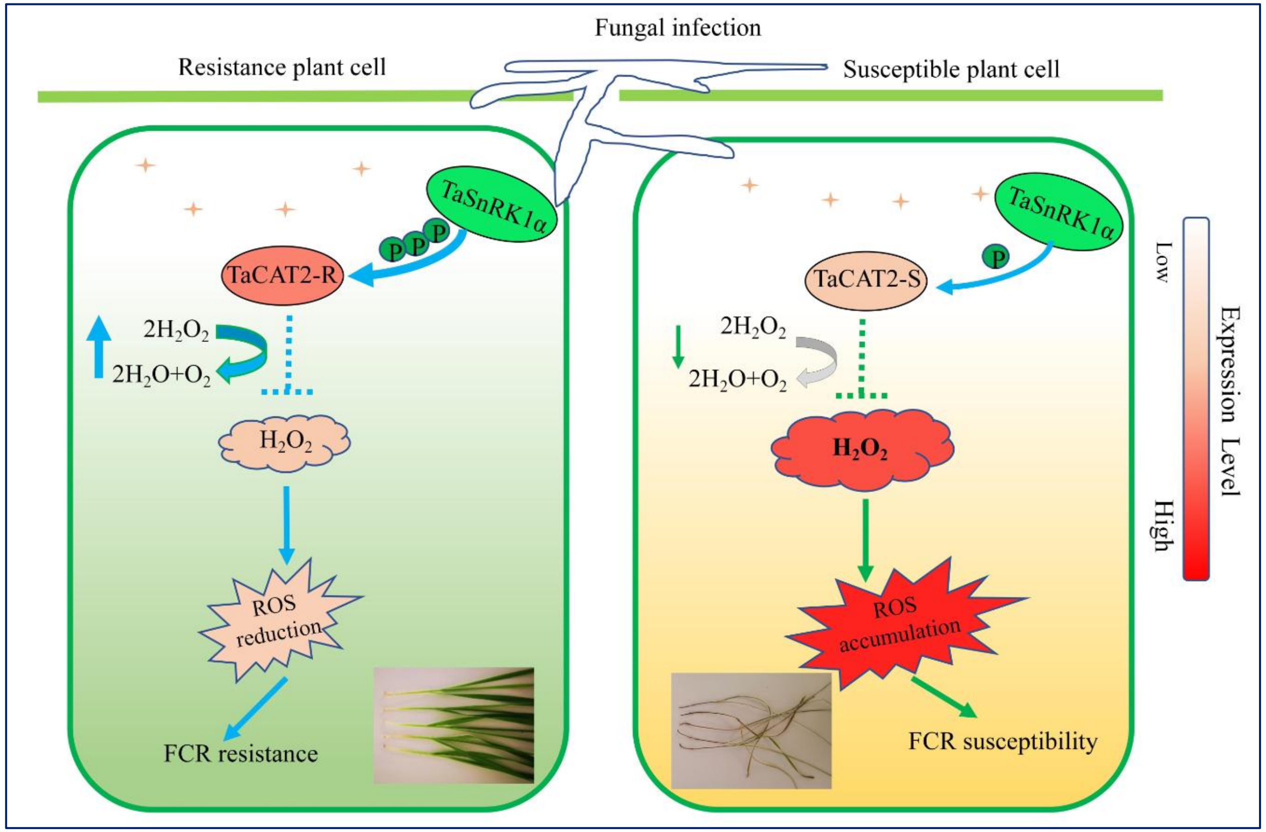


- **TaSnRK1a EMS mutants decreased FCR resistance and ROS content**
- **TaSnRK1a-OE plants exhibit increased FCR resistance and ROS**



Conclusion:

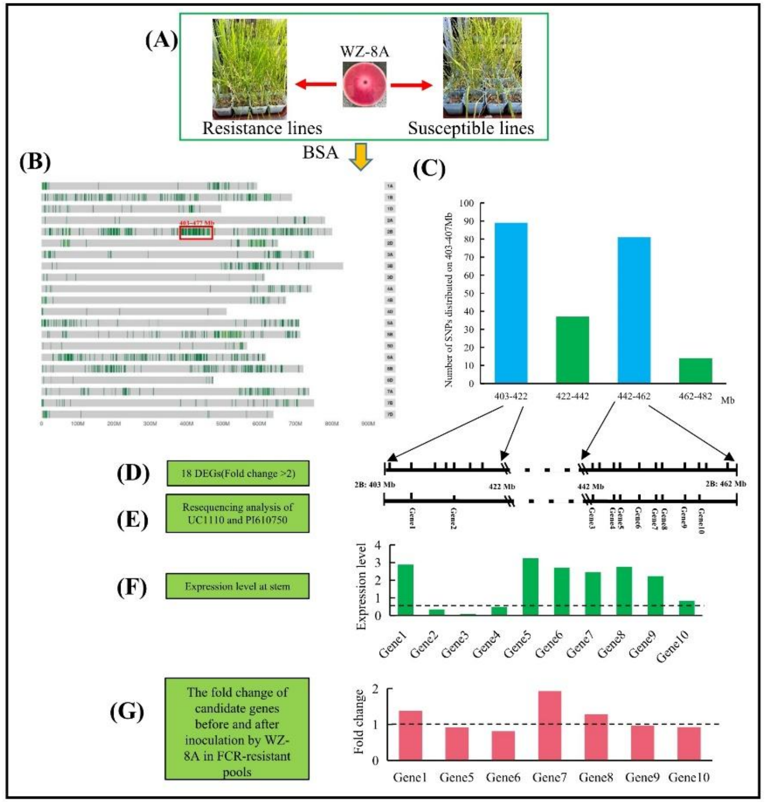
Differential phosphor of TaCAT2 by TaSnRK1a altered wheat FCR resistance

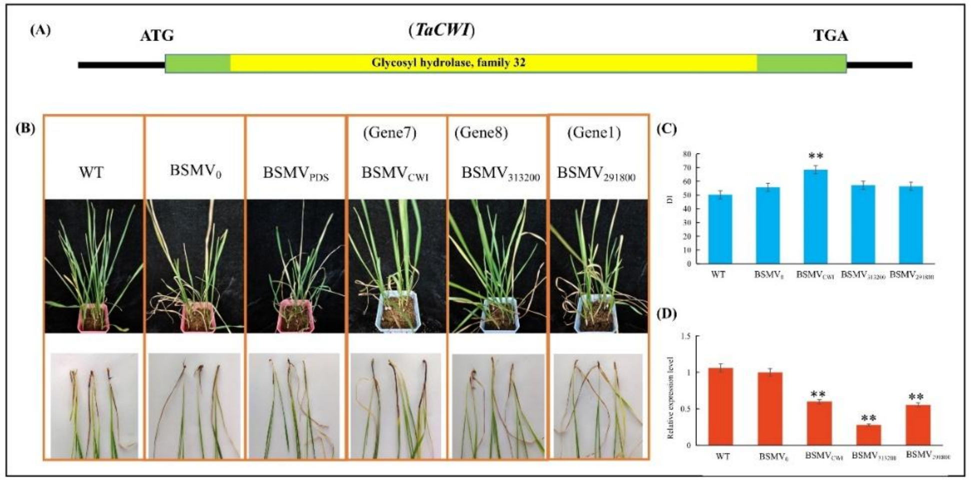


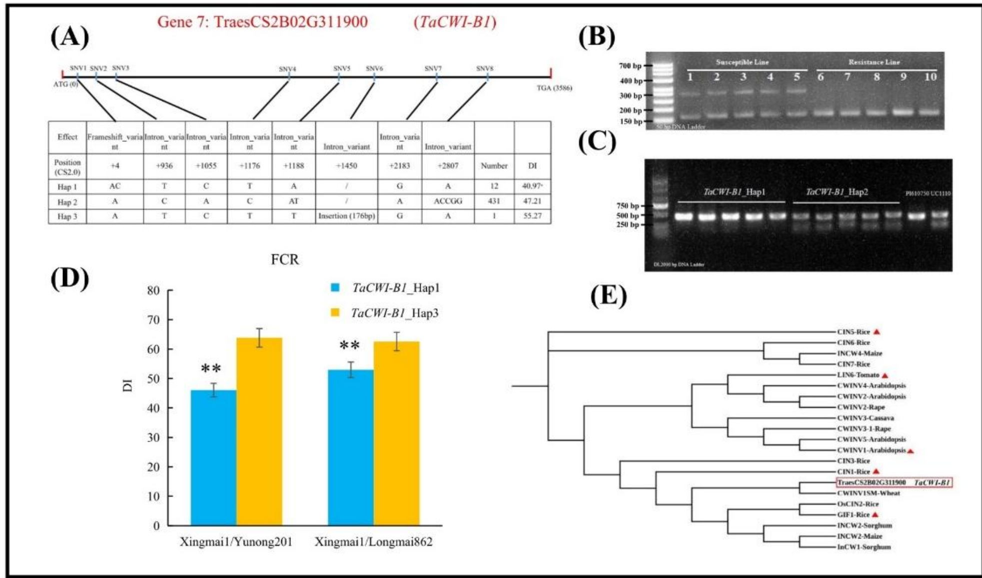
Nature Communications, 2025, 16(1):2549

2) Cloning of TaCWI regulating FCR

- In RIL (UC1110/PI610750), we identified 7 candidates by integration of BSA, BSR-seq and re-sequencing
- Silence 3 highly expressed genes in root by VIGS
- *TaCWI* (cell wall invertase) was induced by *F. pg*
- Three haplotypes in Chinese wheat
- Create 2 RILs based on Hapl:
  - Xingmai1/Yunong201, Xingmai1/Longmai862

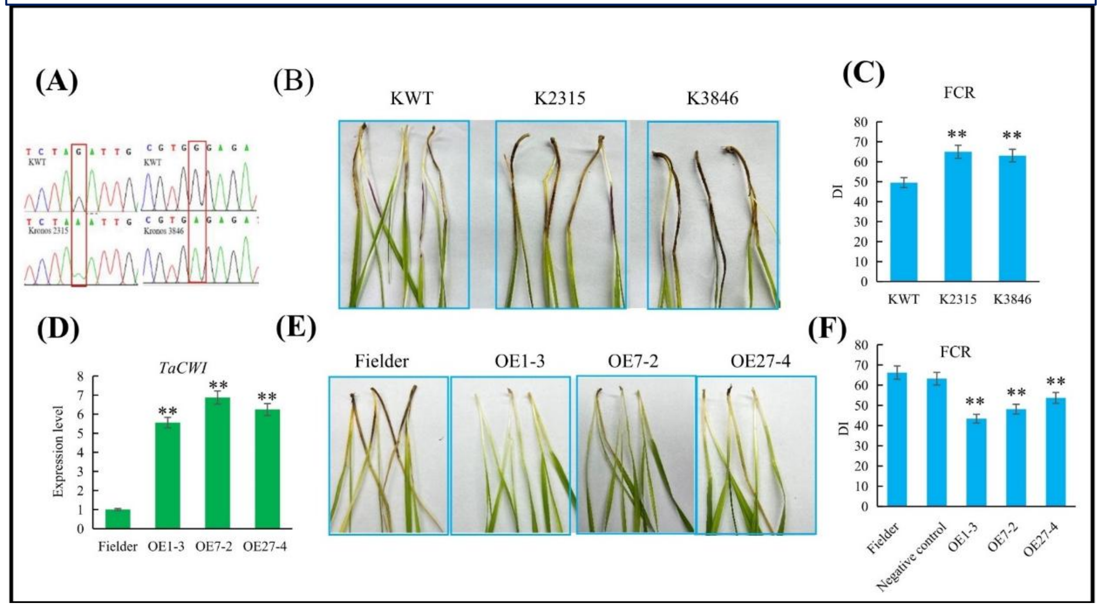






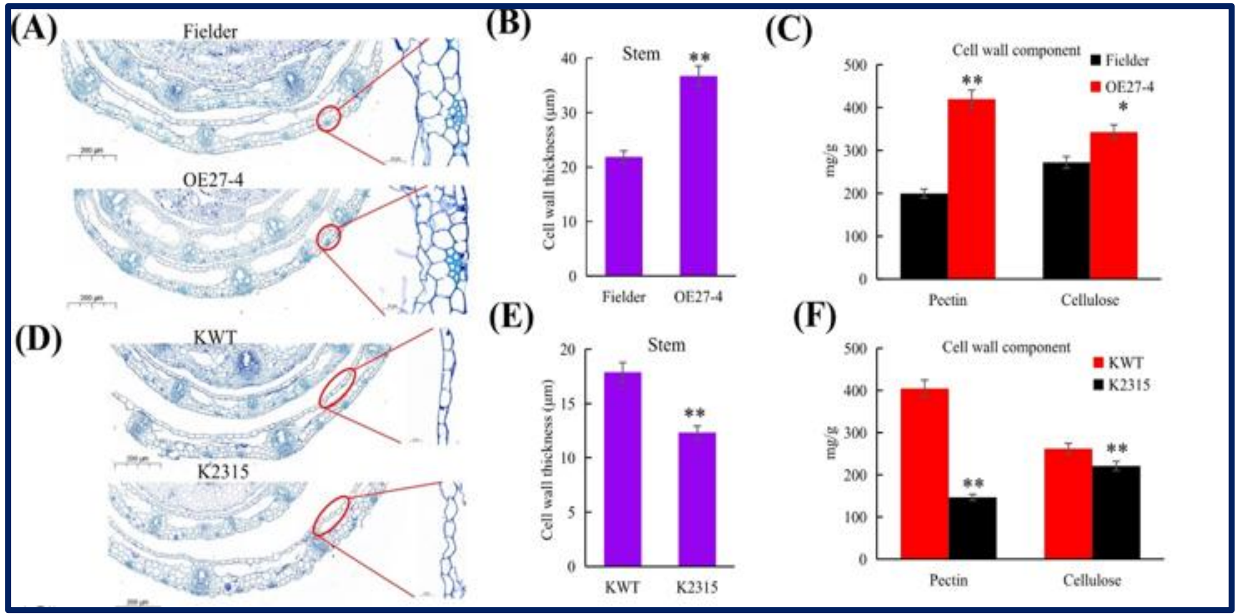
Effect	Frameshift_variant	Intron_variant	Intron_variant	Intron_variant	Intron_variant	Intron_variant	Intron_variant	Intron_variant		
Position (CS2.0)	+4	+936	+1055	+1176	+1188	+1450	+2183	+2807	Number	DI
Hap 1	AC	T	C	T	A	/	G	A	12	40.97*
Hap 2	A	C	A	C	AT	/	A	ACCGG	431	47.21
Hap 3	A	T	C	T	T	Insertion (176bp)	G	A	1	55.27

- *TaCWI*-EMS decreased FCR resistance
- *TaCWI*-OE plants increased FCR resistance



Why is *TaCWI* resistant to FCR

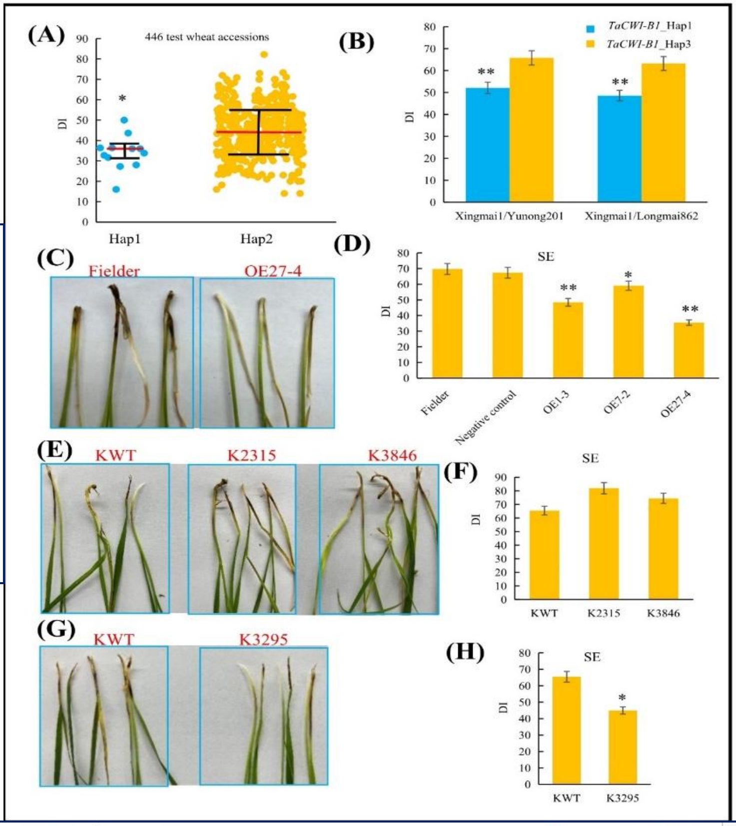
- *TaCWI*-OE increased cell wall thickness
- *TaCWI* EMS mutants decreased cell wall thickness

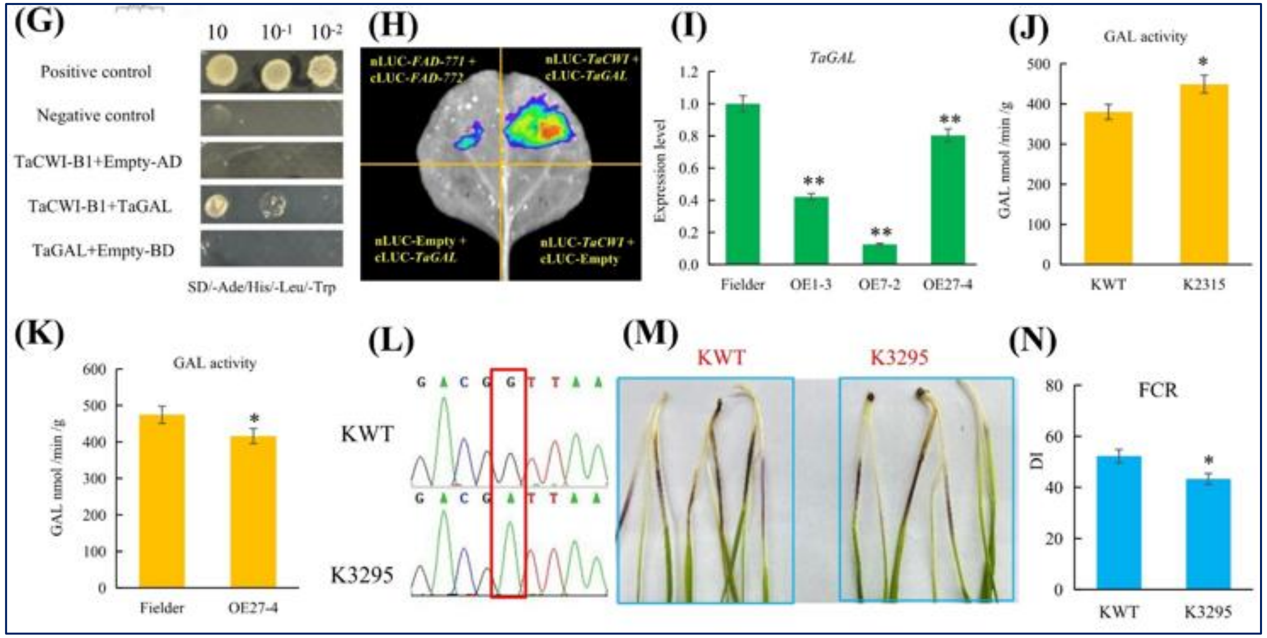


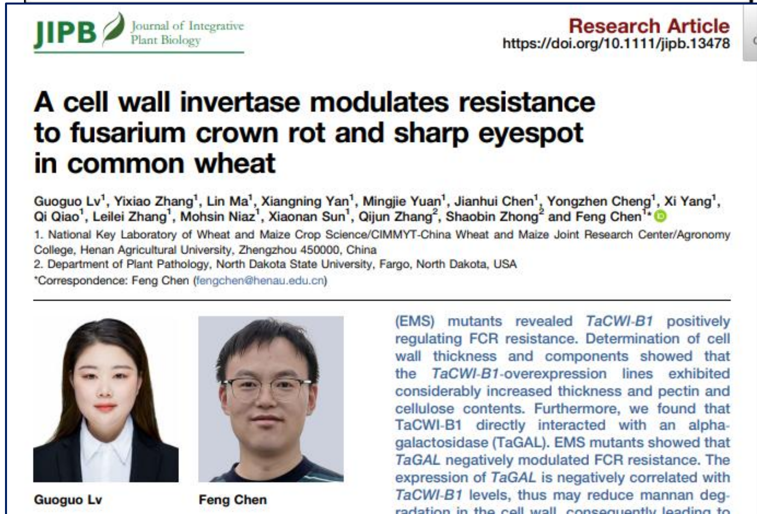
TaCWI mediating cell wall thickness showed broad-spectrum resistance to FCR and SE (sharp eyespot)

- TaCWI interacts with TaGAL (alpha-galactosidase) that is a cell well lytic enzyme
- TaGAL EMS mutants improved FCR resistance
- Conclusion: TaCWI regulates FCR resistance by mediating TaGAL to affect cell wall thickness

TaCWI shows broad-spectrum resistance to FCR and SE






JIPB Journal of Integrative Plant Biology
Research Article
https://doi.org/10.1111/jipb.13478

A cell wall invertase modulates resistance to fusarium crown rot and sharp eyespot in common wheat

Guoguo Lv[1], Yixiao Zhang[1], Lin Ma[1], Xiangning Yan[1], Mingjie Yuan[1], Jianhui Chen[1], Yongzhen Cheng[1], Xi Yang[1], Qi Qiao[1], Leilei Zhang[1], Mohsin Niaz[1], Xiaonan Sun[1], Qijun Zhang[2], Shaobin Zhong[2] and Feng Chen[1*]
1. National Key Laboratory of Wheat and Maize Crop Science/CIMMYT-China Wheat and Maize Joint Research Center/Agronomy College, Henan Agricultural University, Zhengzhou 450000, China
2. Department of Plant Pathology, North Dakota State University, Fargo, North Dakota, USA
*Correspondence: Feng Chen (fengchen@henau.edu.cn)

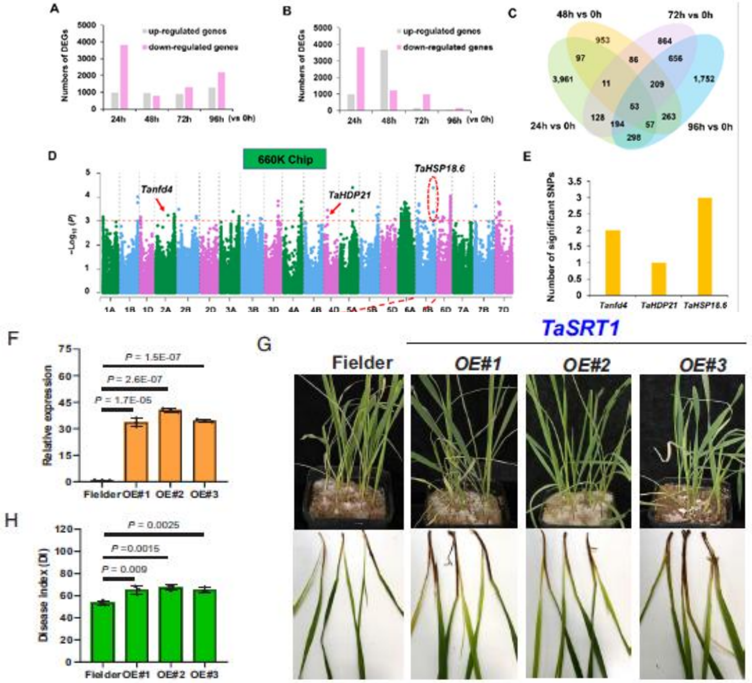
Guoguo Lv

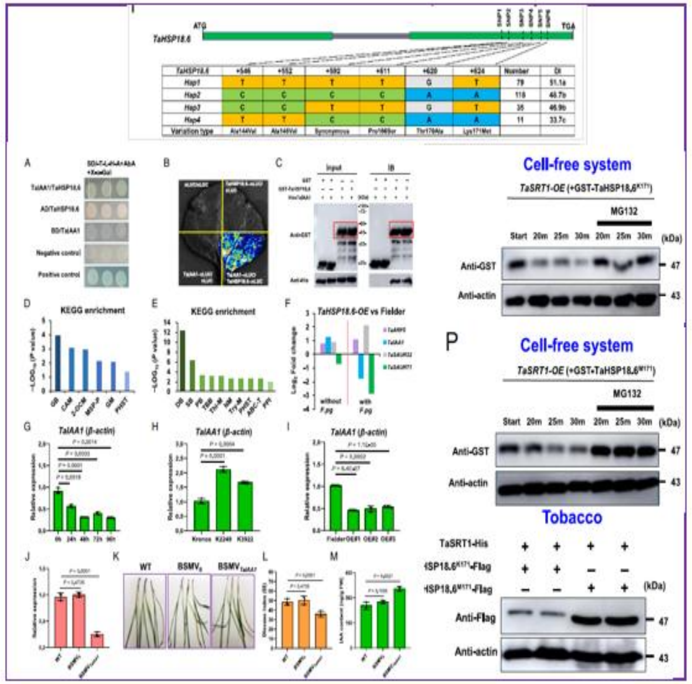
Feng Chen

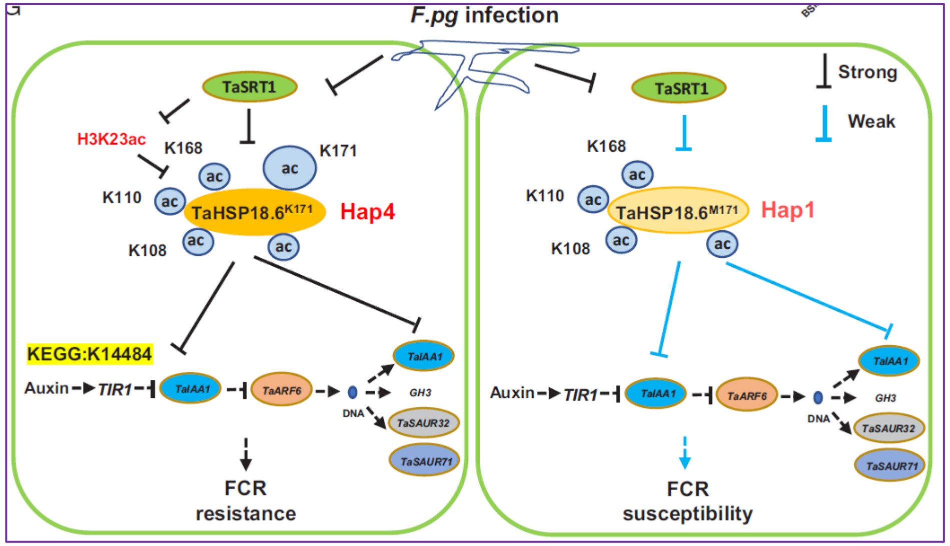
(EMS) mutants revealed *TaCWI-B1* positively regulating FCR resistance. Determination of cell wall thickness and components showed that the *TaCWI-B1*-overexpression lines exhibited considerably increased thickness and pectin and cellulose contents. Furthermore, we found that TaCWI-B1 directly interacted with an alpha-galactosidase (TaGAL). EMS mutants showed that *TaGAL* negatively modulated FCR resistance. The expression of *TaGAL* is negatively correlated with *TaCWI-B1* levels, thus may reduce mannan degradation in the cell wall, consequently leading to

3) Cloning of TaHSP18.6 regulating FCR resistance

- ➢ RNA-seq+GWAS: TaHSP18.6
- ➢ Four haplotypes: TaHSP18.6^{Hap4} is resistance
- ➢ TaSRT1 dual-inhibited TaHSP18.6 through de-acetylation of non-histone and histone
- ➢ TaSRT1-TaHSP18.6 model regulate wheat FCR resistance by mediating auxin content



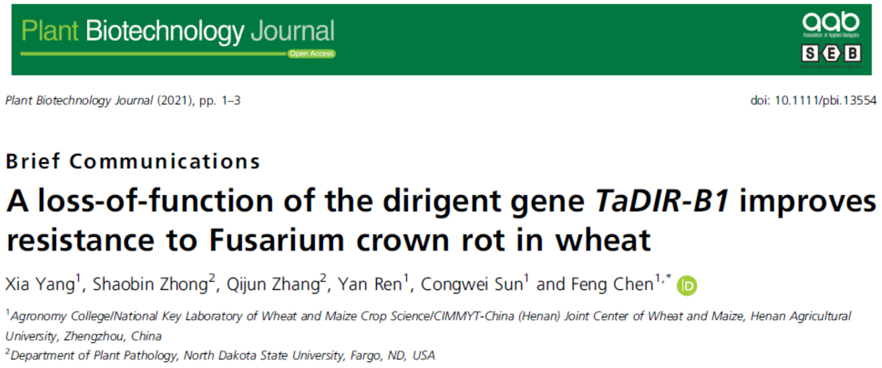




PNAS, 2025, 122(28):e2500029122

4) Cloning of *TaDIR* (dirigent)

- **Clone TaDIR by combination of GWAS, QTL, BSA, BSR-Seq**
- ***TaDIR* shows premature stop codon in R-parent Bainong 64**
- ***TaDIR*-silenced plants exhibited increased FCR resistance by VIGS**
- ***TaDIR*-EMS mutants exhibited increased FCR resistance and lignin content in tetraploid and hexaplod wheat**
- **Conclusion: TaDIR regulates FCR resistance through mediating lignin content**



Plant Biotechnology Journal

Plant Biotechnology Journal (2021), pp. 1–3

doi: 10.1111/pbi.13554

Brief Communications

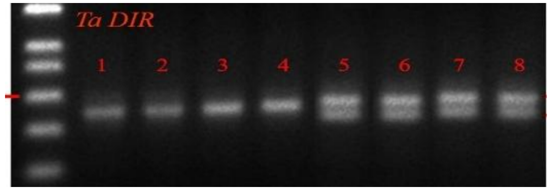
A loss-of-function of the dirigent gene *TaDIR-B1* improves resistance to Fusarium crown rot in wheat

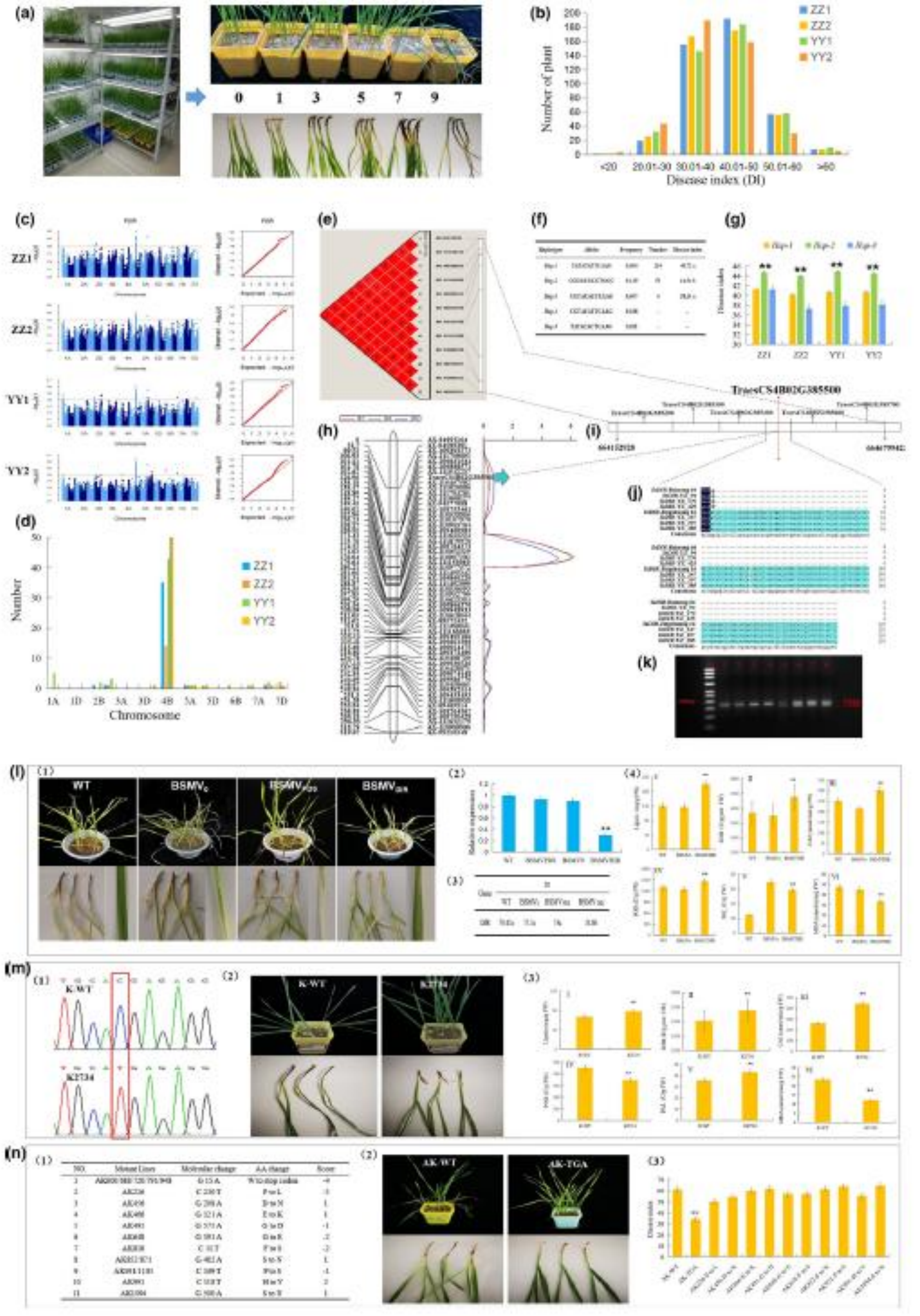
Xia Yang[1], Shaobin Zhong[2], Qijun Zhang[2], Yan Ren[1], Congwei Sun[1] and Feng Chen[1,*]

[1]Agronomy College/National Key Laboratory of Wheat and Maize Crop Science/CIMMYT-China (Henan) Joint Center of Wheat and Maize, Henan Agricultural University, Zhengzhou, China

[2]Department of Plant Pathology, North Dakota State University, Fargo, ND, USA

Breeding marker

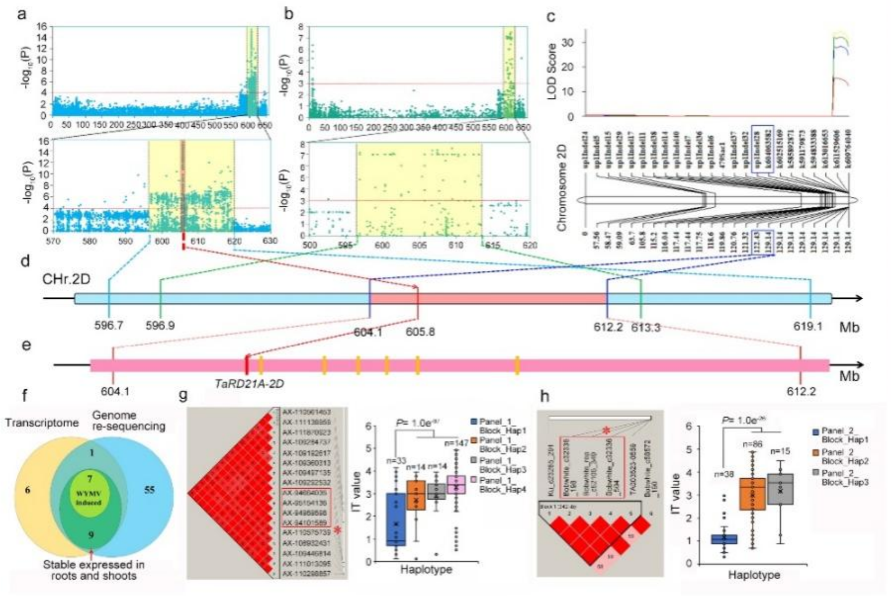


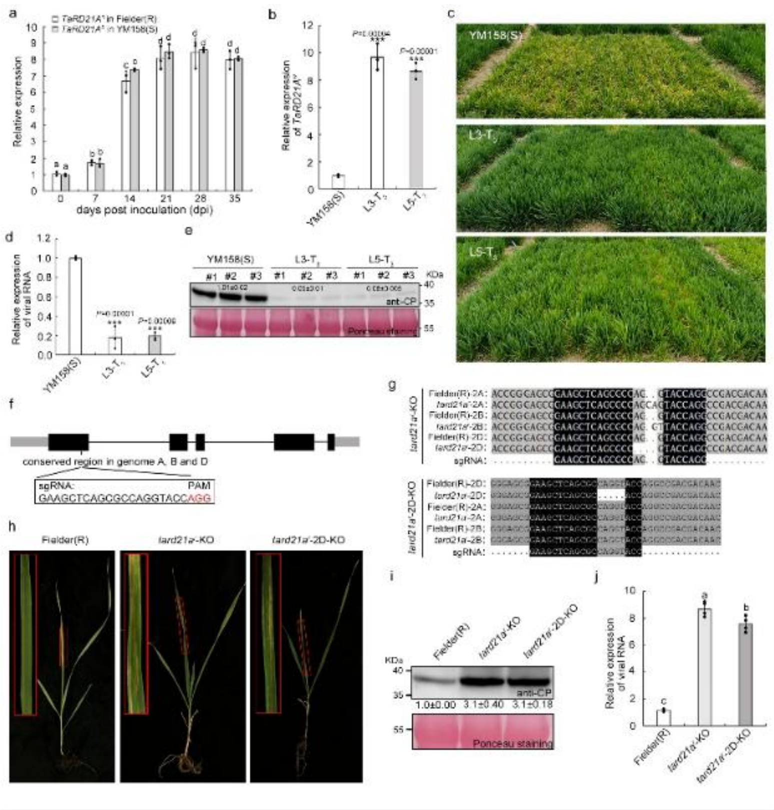


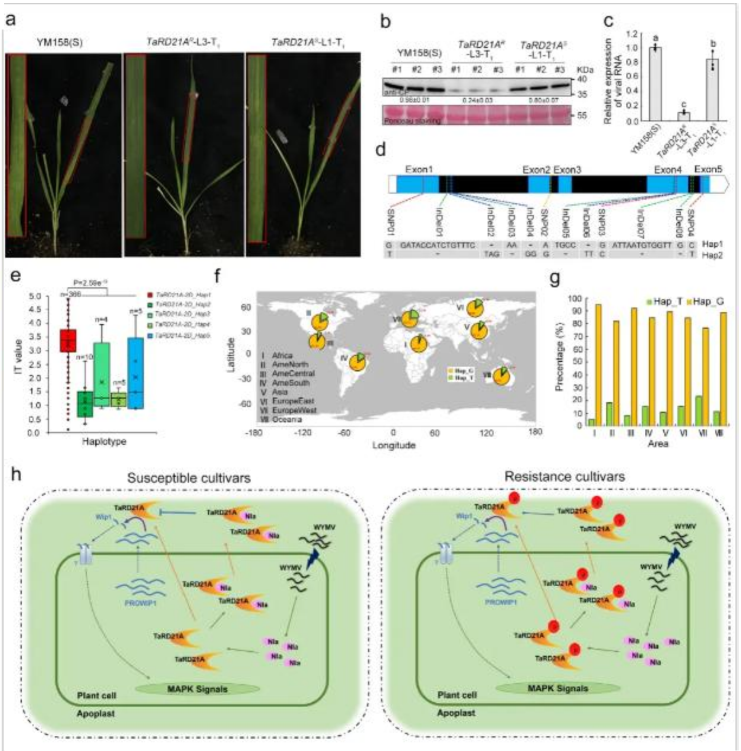
5) Clone a WYMV (wheat yellow mosaic virus) regulatory gene *TaRD21a*

GWAS+QTL: Clone TaRD21a regulating WYMV resistance by releasing small peptide

In collaboration with the team of Jianping Chen in Ningbo University



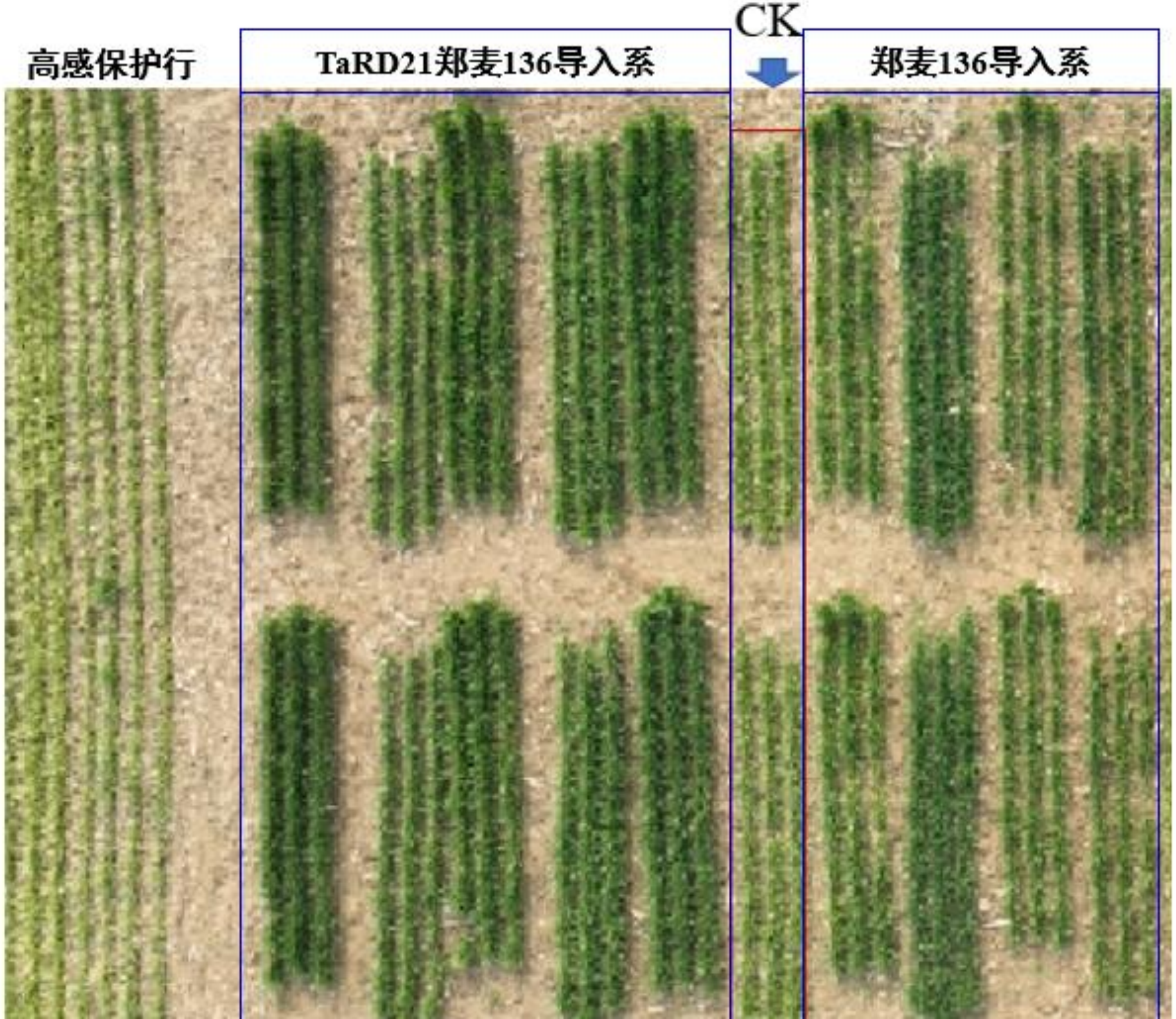




Nature Communications, **2023, 14: 7773**

TaRD21a was transferred to Henan Molecular Breeding Institute with the price of 1 million Yuan

***TaRD21a*-introgressed lines showed stable WYMV resistance in field**



6) Clone a WYMV-sensitive gene *TaMTB* (*methyltransferase B*)

GWAS+QTL: *TaMTB* could be recruited by WYMV to accelerate infection

In collaboration with the team of Jianping Chen in Ningbo University

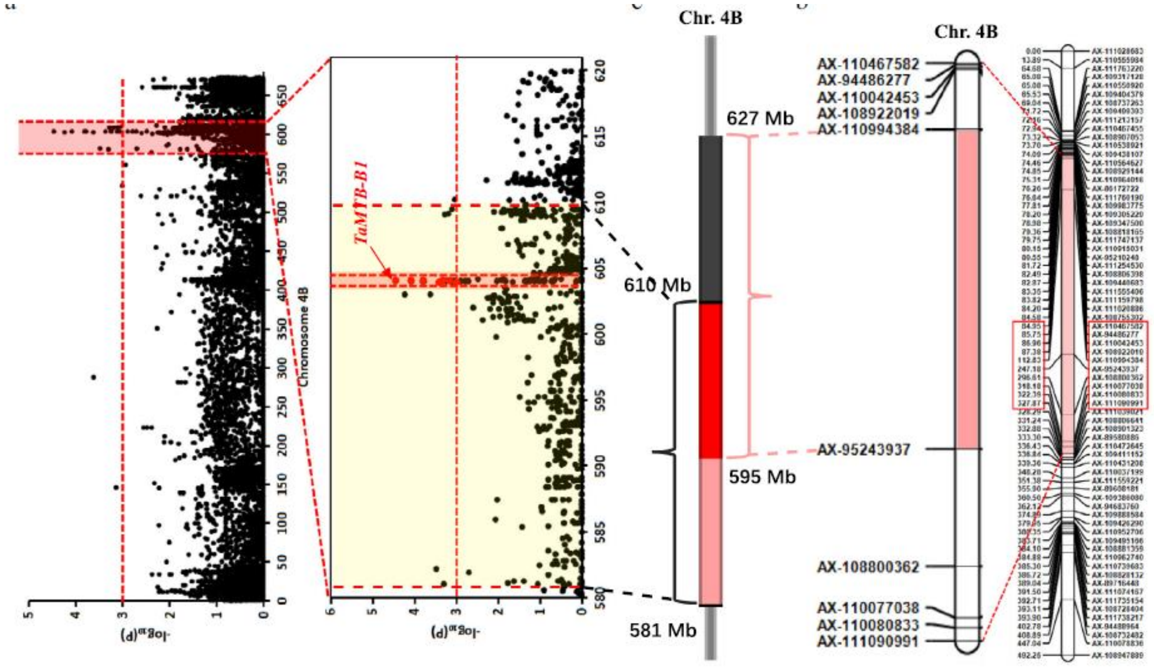


Fig. 1 The qWYM.hau-4B was co-located by GWAS and QTL

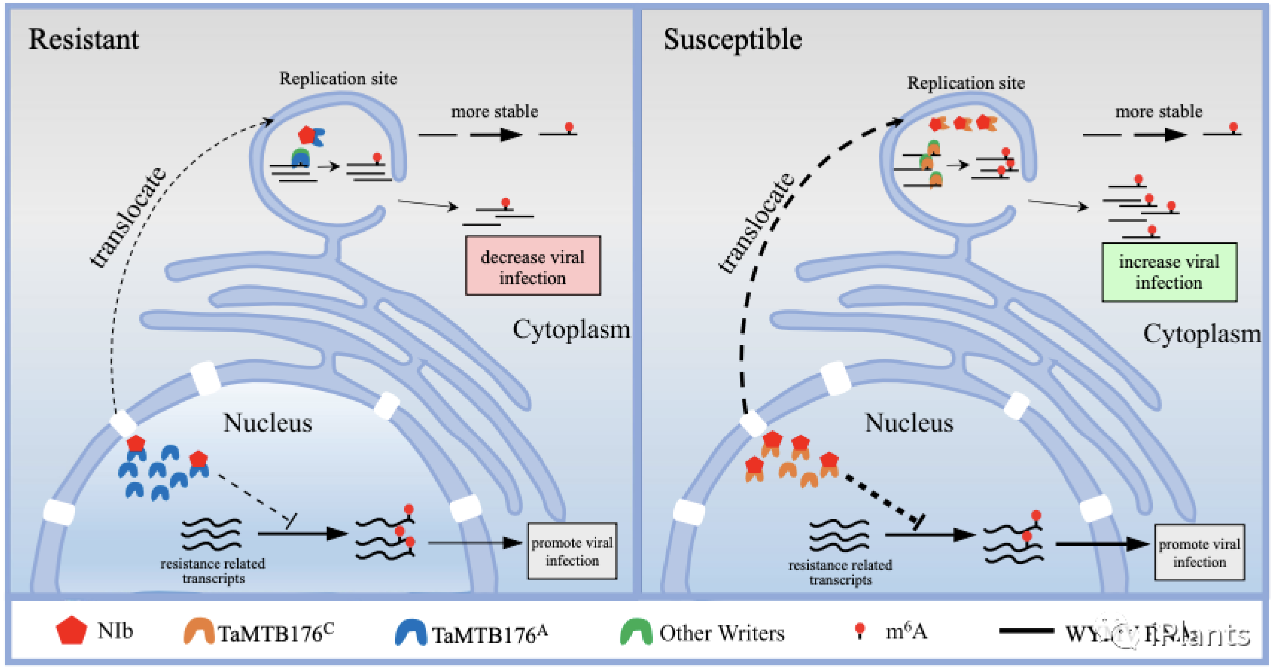
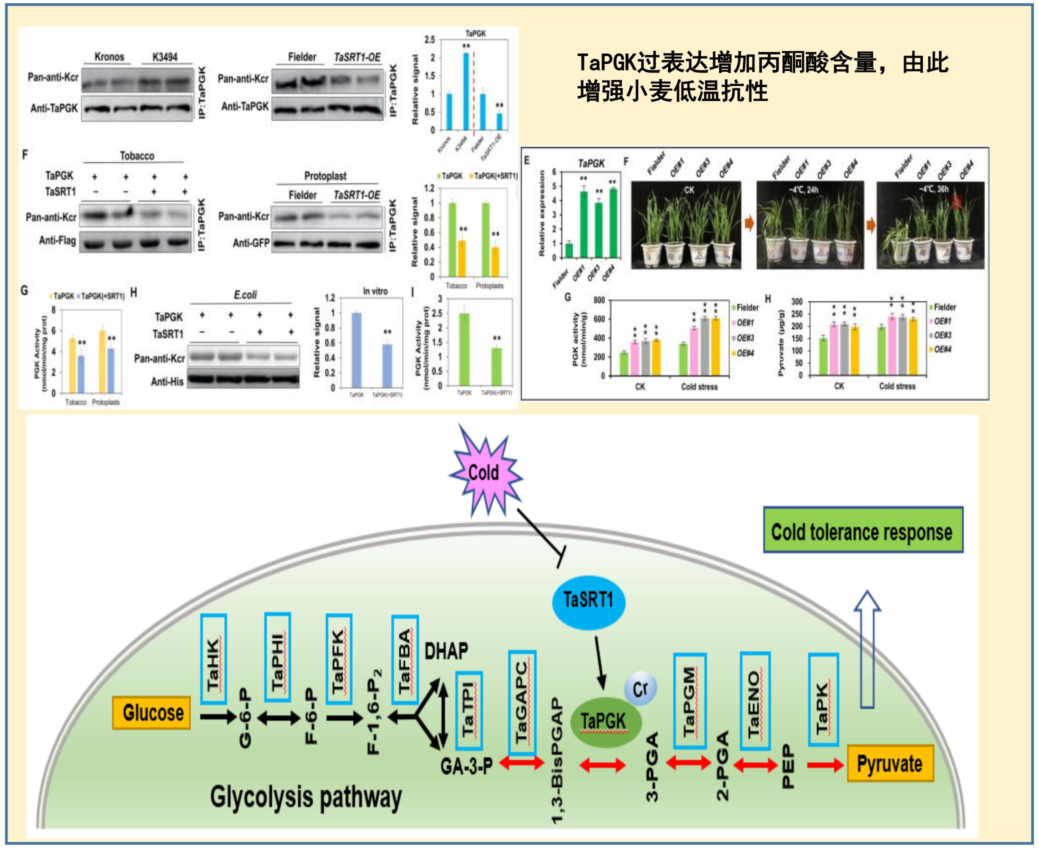


Fig.2 Model for N6-methyladenosine RNA modification promotes viral genomic RNA stability and infection.

Nature Communications, 2022, 13(1):6576

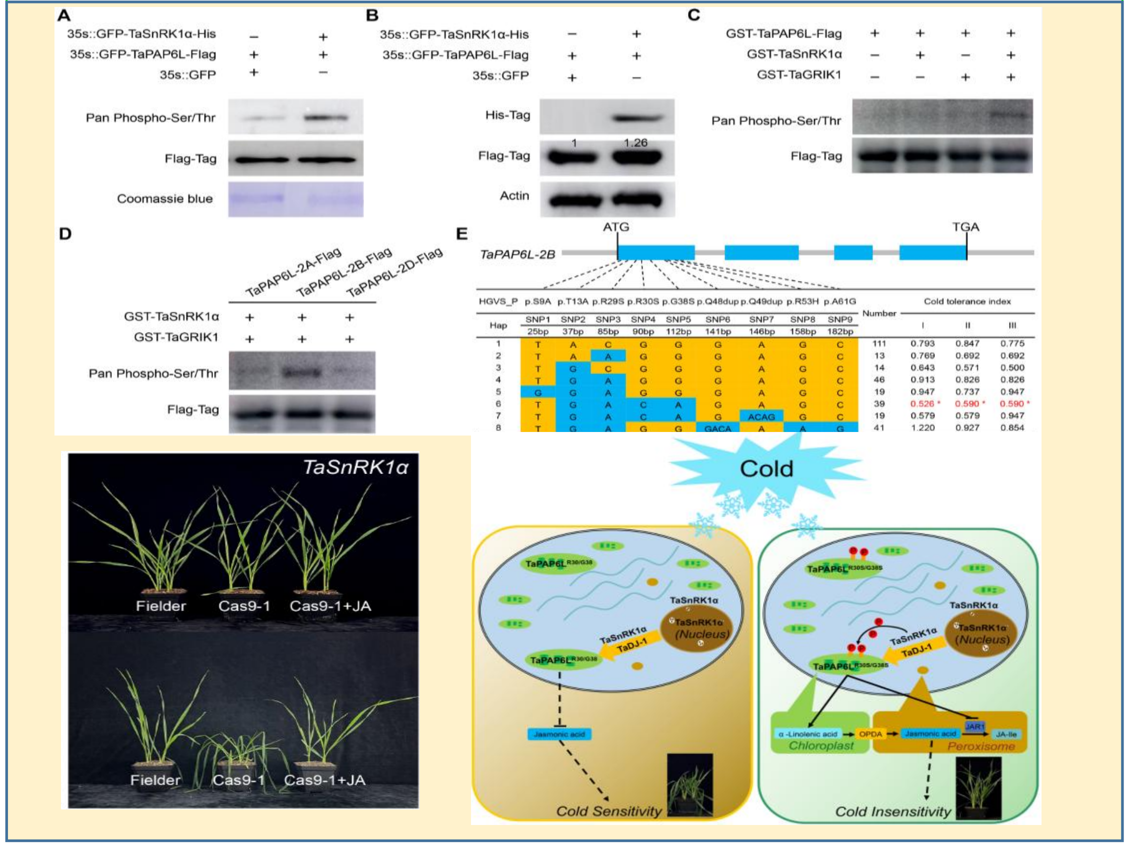
7) Identification of TaPGK and TaSnrK1a regulating wheat cold tolerance

- **Clone a cold tolerance gene TaPGK by multi-omics**
- **TaSRT1 decrotonylates TaPGK to change pyruvate content, finally increasing wheat cold**



Science Advances, 2023, 9(19):eadg1012

- **GWAS+RNA-seq: *TaSnrK1a***
- **TaSnrK1a phosphorylates TaPAP6L to promote jasmonic acid, finally increasing wheat cold**



Advanced Science, 2023, 10(31): 2303478

8) Identification of yield-related genes in wheat

GWAS+QTL: *TaGL1* regulates grain length by changing JA content

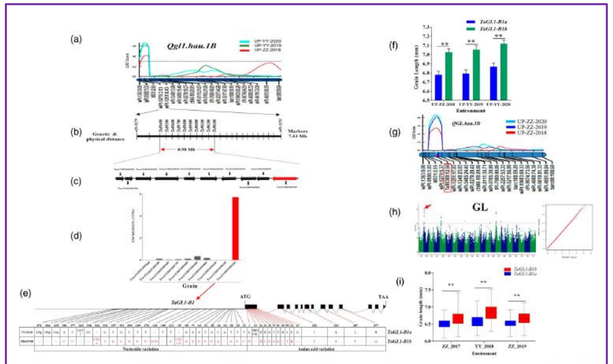


Figure 1 Identification and association of *TaGL1-B1* with grain length in wheat. (a) Linkage map of the *Qgl1.hau.1B* locus for grain length in the UC1110/PI610750 recombinant inbred lines (RIL) population. Horizontal dotted line represents a limit of detection (LOD) threshold value of 3.0. (b) Fine mapping of

Plant Biotechnology Journal

Plant Biotechnology Journal (2023) **21**, pp. 979–989 doi: 10.1111/pbi.14009

Identification of *TaGL1-B1* gene controlling grain length through regulation of jasmonic acid in common wheat

Mohsin Niaz, Lingran Zhang, Guoguo Lv, Huiting Hu, Xi Yang, Yongzhen Cheng, Yueting Zheng, Bingyang Zhang, Xiangning Yan, Aye Htun, Lei Zhao, Congwei Sun, Ning Zhang, Yan Ren and Feng Chen*

National Key Laboratory of Wheat and Maize Crop Science, CIMMYT-China Wheat and Maize Joint Research Center, Agronomy College, Henan Agricultural University, Zhengzhou, China

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GWAS+QTL: *TaHST1* controls tiller angle by regulating auxin content

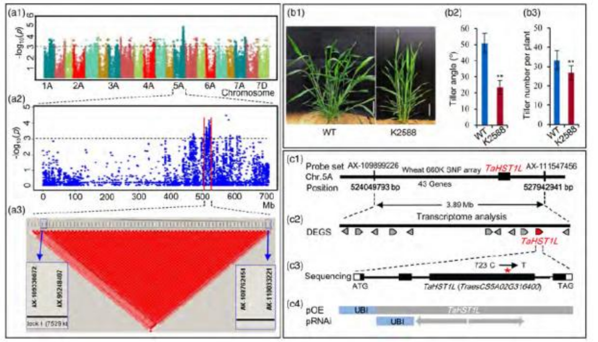

Figure 1 Physical mapping and identification of *TaHST1L*. (a1) Manhattan plot for the wheat tiller angle identified by GWAS. (a2) Local Manhattan plot of chromosome 5A. (a3) LD heatmap surrounding the peak on 5A. (b1) Phenotype of WT and K2588 at the jointing stage. Scale bar = 10 cm. (b2, b3)

Plant Biotechnology Journal

Plant Biotechnology Journal (2023) **21**, pp. 122–135 doi: 10.1111/pbi.13930

A *HST1-like* gene controls tiller angle through regulating endogenous auxin in common wheat

Lei Zhao[†], Yueting Zheng[†], Ying Wang, Shasha Wang, Tongzhu Wang, Canguan Wang, Yue Chen, Kunpu Zhang, Ning Zhang, Zhongdong Dong and Feng Chen*

National Key Laboratory of Wheat and Maize Crop Science / CIMMYT-China Wheat and Maize Joint Research Center /Agronomy College, Henan Agricultural University, Zhengzhou, China

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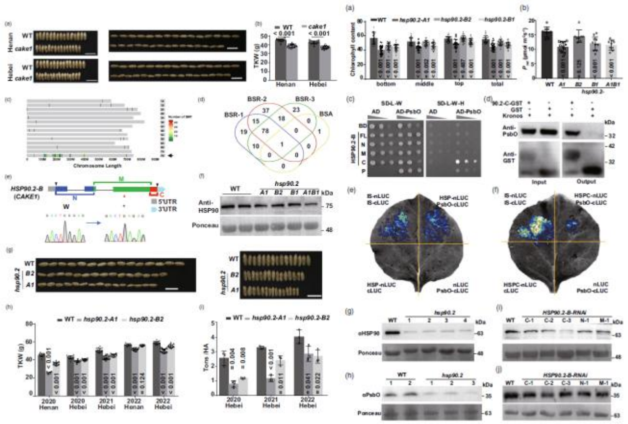
GWAS+EMS-mutants: *HSP90.2* control grain weight by promoting CO_2 assimilation rate



Plant Biotechnology Journal

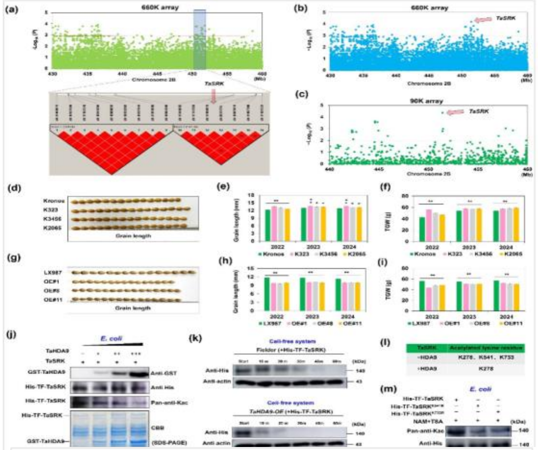
Plant Biotechnology Journal (2023), pp. 1–11 doi: 10.1111/pbi.14032

HSP90.2 promotes CO_2 assimilation rate, grain weight and yield in wheat

Yan Yan[1,2], Meng-Lu Wang[1], Yue-Ting Guo[1,3], Ci-Hang Ding[1,3], Ke-Xin Niu[1,3], Xiao-Ming Li[1,3], Congwei Sun[2], Zhongdong Dong[2], Dangqun Cui[2], Awais Rasheed[4], Chenyang Hao[5], Xueyong Zhang[5], Ganggang Guo[6], Zhongfu Ni[1], Qixin Sun[1], Feng Chen[2,]* and Jin-Ying Gou(缑金营)[1,3,]*

[1]*Key Laboratory of Crop Heterosis and Utilization (MOE) and Beijing Key Laboratory of Crop Genetic Improvement, China Agricultural University, Beijing, China*
[2]*CIMMYT-China Wheat and Maize Joint Research Center/National Key Laboratory of Wheat and Maize Crop Science/College of Agronomy, Henan Agricultural University, Zhengzhou, China*
[3]*MOE Engineering Research Center of Gene Technology, School of Life Sciences, Fudan University, Shanghai, China*
[4]*Plant Sciences, Quaid-i-Azam University, Islamabad, Pakistan*

GWAS+RNA-seq: TaHDA9-TaSRK controls grain length by mediating TaPsbO involving in photosystem



ELSEVIER

Science Bulletin

Available online 15 April 2025

In Press, Journal Pre-proof ⓘ What's this?

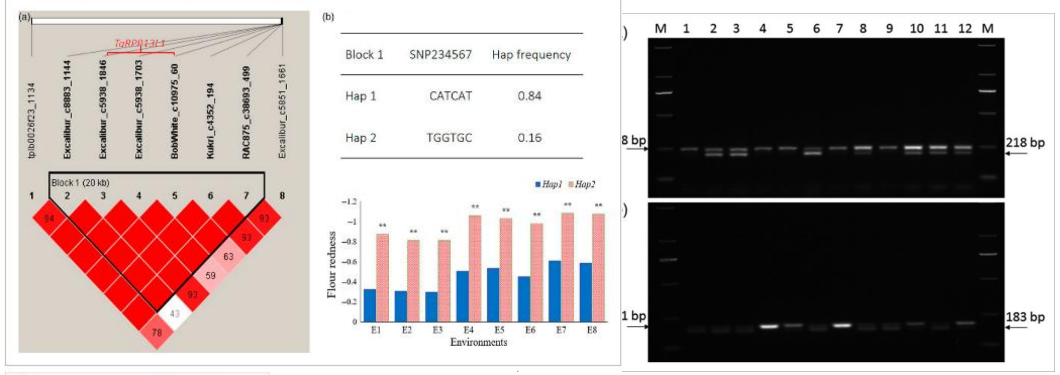
Short Communication

A lectin receptor-like kinase TaSRK that is deacetylated by TaHDA9 regulates wheat grain length by mediating the Photosystem II protein TaPsbO

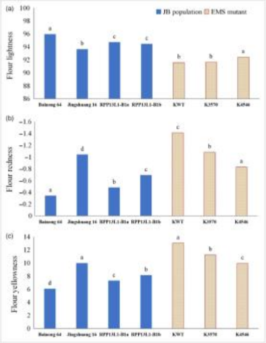
Ning Zhang [1], Songgang Li [1], Zhipeng Sun, Jingjing Dai, Shuyu Zhang, Daiying Chen, Lei Zhao, Aolin Jia, Feng Chen ✉

9) Identification of wheat quality-related genes

GWAS+QTL: *TaRPPl3L* controls flour color by regulating flour redness (a*)



Block 1	SNP234567	Hap frequency
Hap 1	CATCAT	0.84
Hap 2	TGGTGC	0.16




Plant Biotechnology Journal
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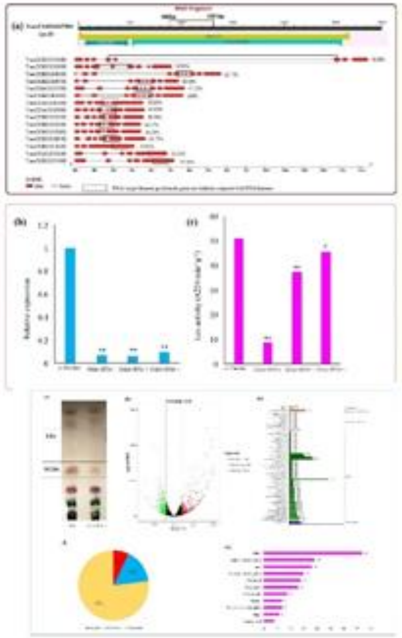
Research Article | Open Access

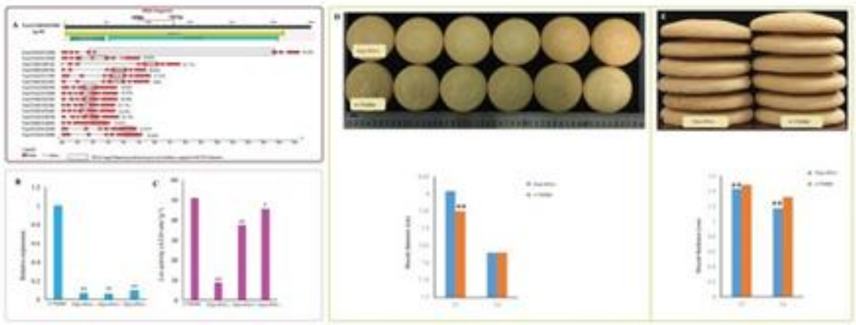
Genome-wide association study of six quality traits reveals the association of the *TaRPP13L1* gene with flour colour in Chinese bread wheat

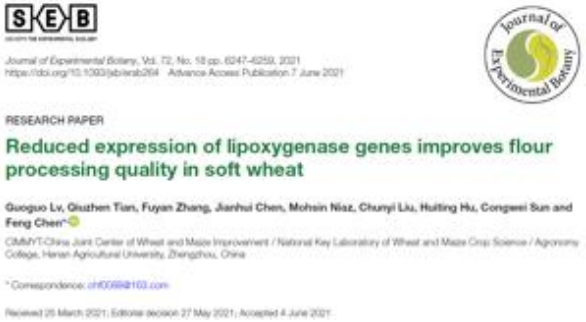
Jianhui Chen, Fuyan Zhang, Chunjiang Zhao, Guoguo Lv, Congwei Sun, Yubo Pan, Xinyu Guo, Feng Chen

First published: 08 April 2019 | https://doi.org/10.1111/pbi.13126 | Citations: 50

GWAS+QTL: *TaLPX4* controls dough stability time to regulate cookie quality






SEB
Journal of Experimental Botany, Vol. 72, No. 18 pp. 6247–6259, 2021
https://doi.org/10.1093/jxb/erab264 Advance Access Publication 7 June 2021

RESEARCH PAPER

Reduced expression of lipoxygenase genes improves flour processing quality in soft wheat

Guoguo Lv, Qiuzhen Tian, Fuyan Zhang, Jianhui Chen, Mohsin Niaz, Chunyi Liu, Huiting Hu, Congwei Sun and Feng Chen*
CIMMYT-China Joint Center of Wheat and Maize Improvement / National Key Laboratory of Wheat and Maize Crop Science / Agronomy College, Henan Agricultural University, Zhengzhou, China
* Correspondence: chf0088@163.com

Received 25 March 2021; Editorial decision 27 May 2021; Accepted 4 June 2021

Wheat molecular breeding

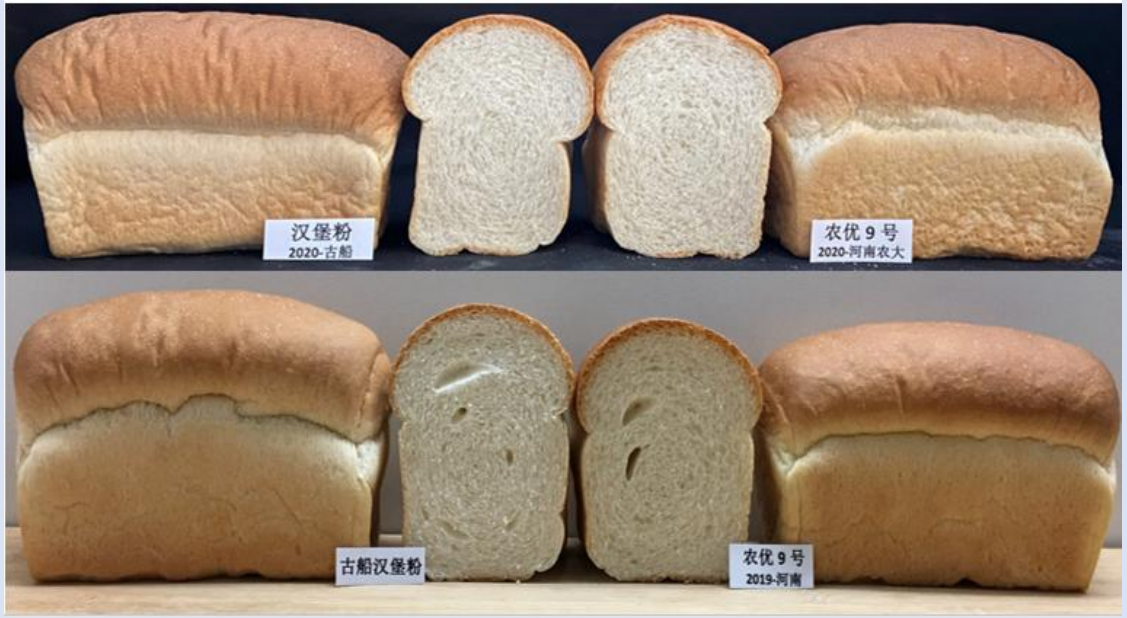
Yunong 268

Released by Henan Province Seed Station in 2023；

Parents: Yanzhan 1 You/AM108

Charac.: Weak Springness, high quality and yield

Marker： *TaSD1, TaDIR*



Yunong 269

Released by Henan Province Seed Station in 2023

Parents: Xinmai26/Zhoumai22

Charac： Semi-winterness, high quality

Marker： *TaSD1*

Performance of Yunong268 in field of Yuanyang

Good quality (high Zinc, 46.7mg/kg) and high yield

4. Acknowledgement

Wheat gene chip

- CEO Zhongxu Chen (陈中旭), Chengdu Tiancheng Future Sci&Tech Co. Ltd. (成都天成未来科技有限公司)

Soil-borne disease

- Prof. Jianping Chen (陈剑平院士) and Jian Yang (羊健教授)，Ningbo University
- Prof. Xing Wang Deng(邓兴旺院士)，Peking University
- Pawan Singh, Xinyao He, CIMMYT
- …