13th International Wheat Genetics Symposium 23rd-28th April 2017, Tulln / Austria

Genetic and Epigenetic Controls of Heat Tolerance in Wheat

Mingming Xin

China Agricultural University

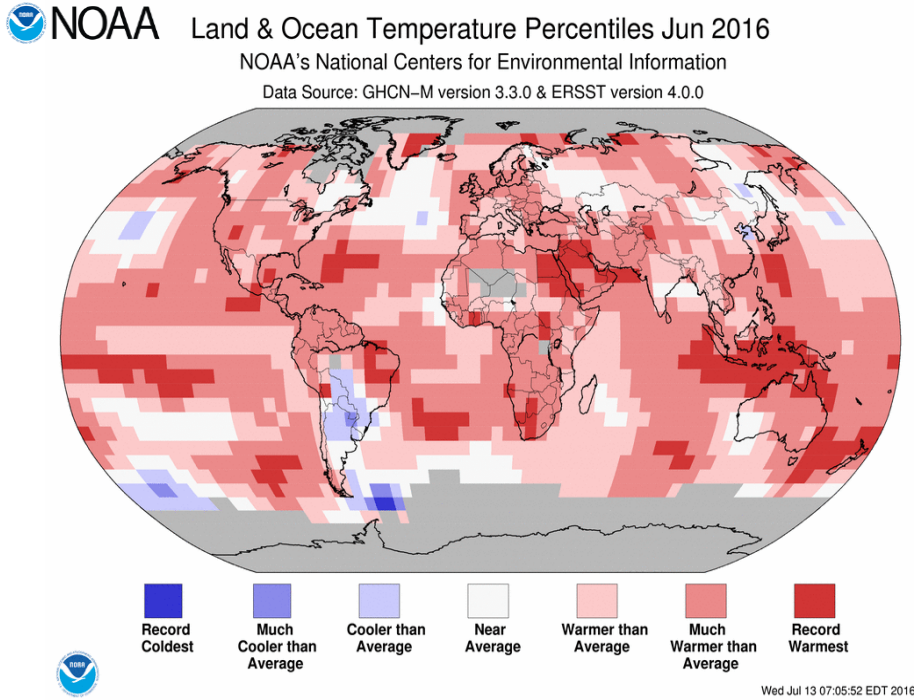
mingmingxin@cau.edu.cn

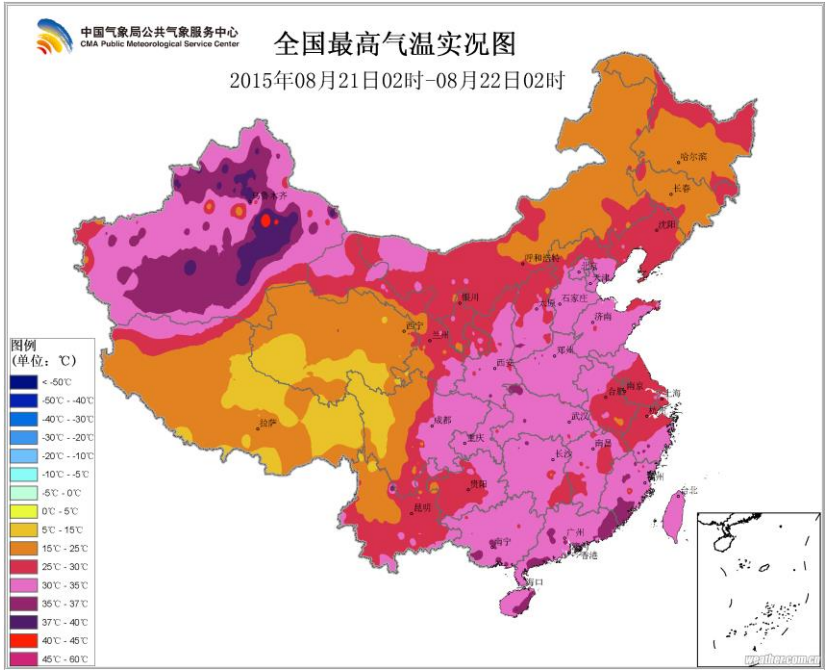
Outline

- Climate Change threaten wheat production
- Genetic Diversity and GWAS
- Genetic Dissection of Heat tolerance
- Epigenetic Control of Heat Tolerance
- Breeding for Heat Tolerance

1. Climate Change Threaten Wheat Production

- The global average temperature increases, extreme hot weather frequently occurs





- The global warming climate puts the food supplies at risk over the next decade

KEY MESSAGES

1. **CLIMATE CHANGE ALREADY AFFECTS AGRICULTURE AND FOOD SECURITY** and, without urgent action, will put millions of people at risk of hunger and poverty.

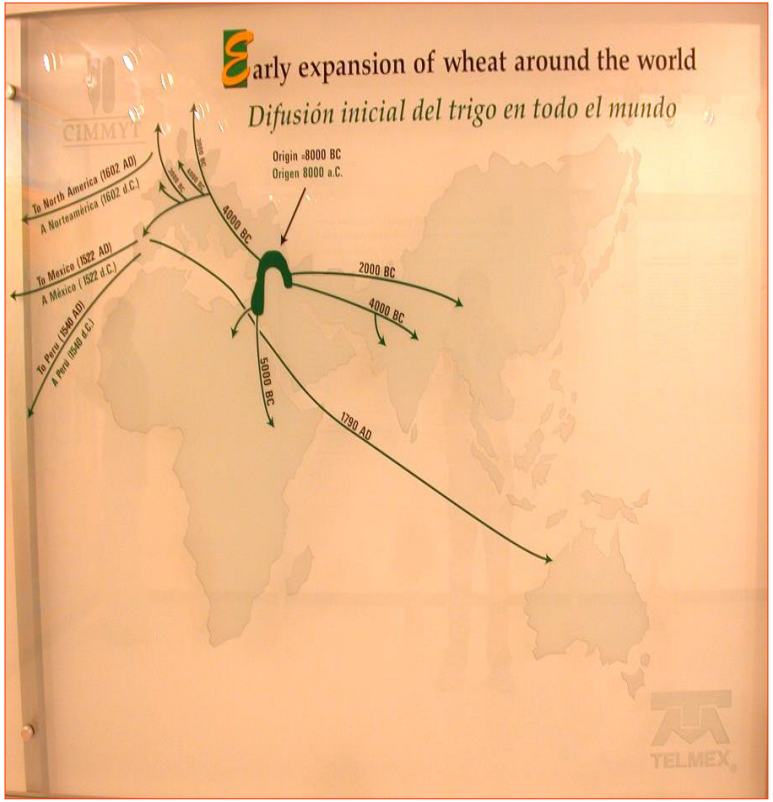
2. While **IMPACTS ON AGRICULTURAL YIELDS AND LIVELIHOODS** will vary across countries and regions, they will become increasingly adverse over time and potentially catastrophic in some areas.

3. **LIMITING GLOBAL TEMPERATURE INCREASES TO 1.5 °C ABOVE PRE-INDUSTRIAL LEVELS** would significantly reduce the risks and impacts of climate change.

4. **DEEP TRANSFORMATIONS IN AGRICULTURE AND FOOD SYSTEMS**, from pre-production to consumption, are needed in order to maximize the co-benefits of climate change adaptation and mitigation efforts.

5. **THE AGRICULTURE SECTORS HAVE POTENTIAL TO LIMIT THEIR GREENHOUSE GAS EMISSIONS**, but ensuring future food security requires a primary focus on adaptation.

- Global Wheat production is estimated to fall by 6% for each centigrade of further temperature increase



RESEARCH HIGHLIGHTS
Selections from the scientific literature

266 | NATURE | VOL 511 | 17 JULY 2014

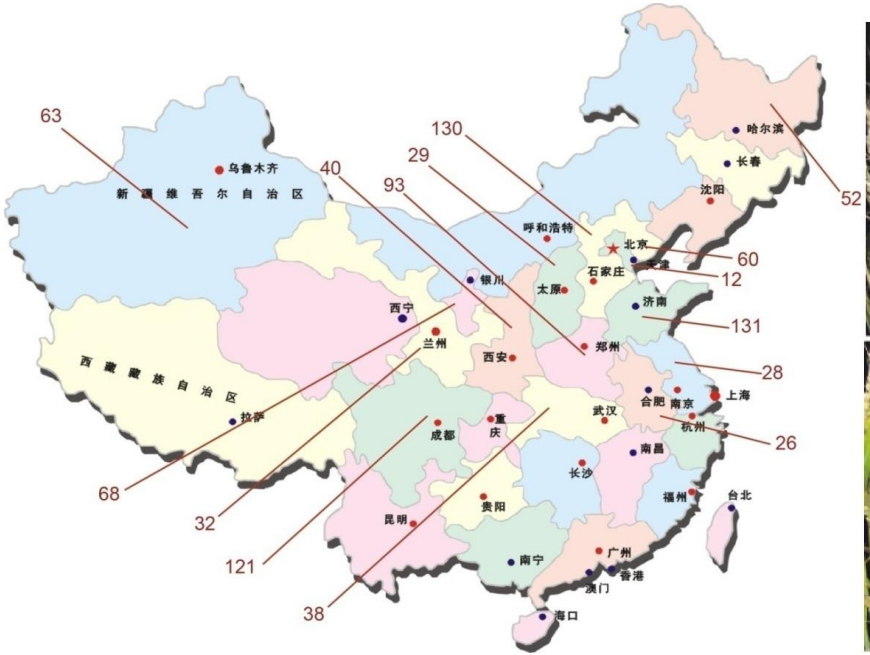
AGRICULTURE

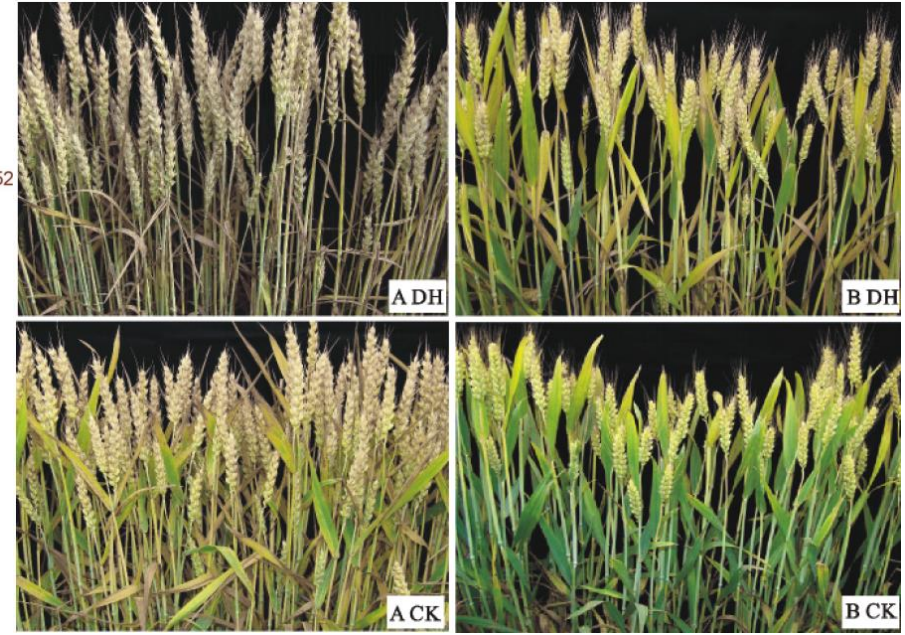
Global warming could hurt crops

(*Asseng et al., 2015, Nature Climate Change*； *Ray et al., 2015, Nature Communication*)

2. Genetic diversity and GWAS

2.1. Collection of Wheat Germplasms

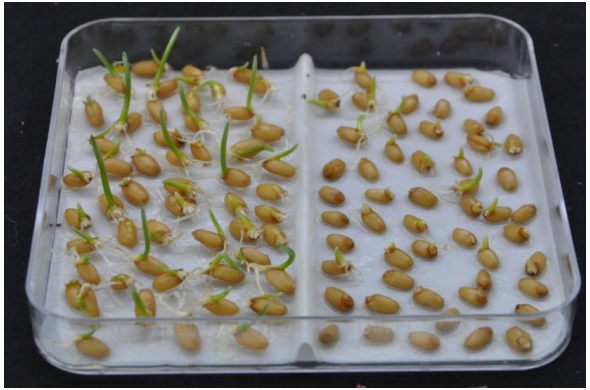




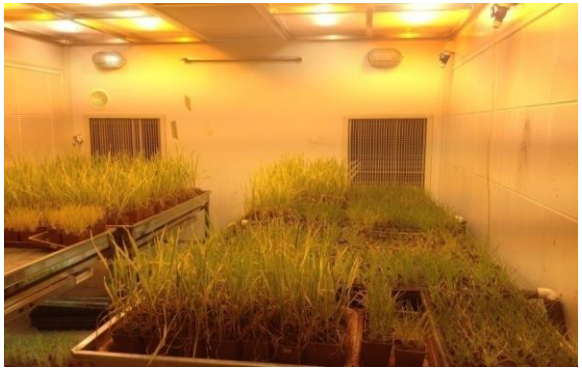
1353 wheat germplasms were collected all over China including wheat cultivars, isonucleus-alloplasmic lines, synthetic wheat, substitution lines, translocation lines and introgression lines

2.2 Phenotyping

1) Evaluation of heat tolerance through seed germination



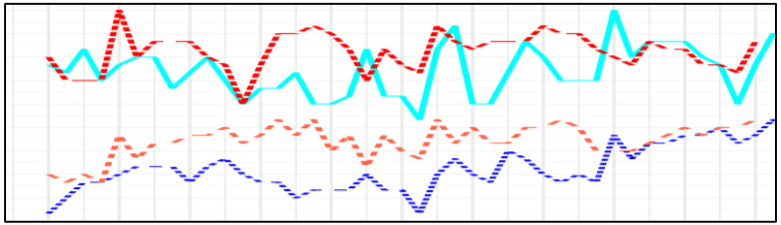
2) Assessment in greenhouse/ growth chamber

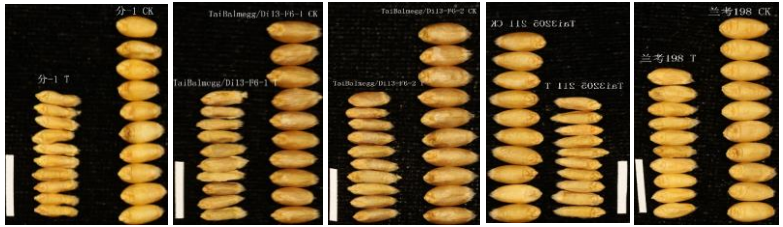


3) Evaluation of heat tolerance in plastic tunnel

4) Field evaluation with delayed sowing time

Phenotype for plastic tunnel evaluation

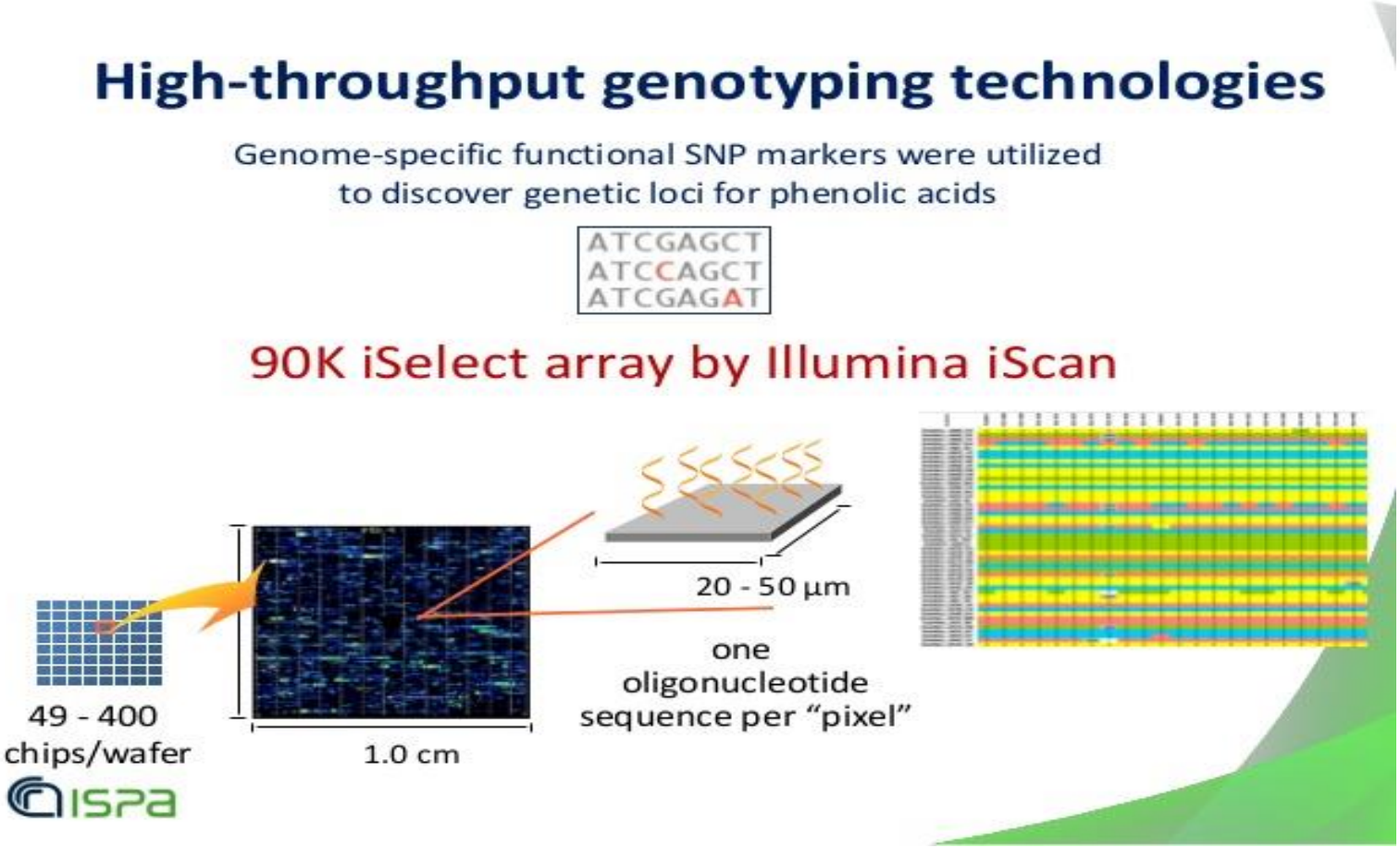




Phenotyping data for field evaluation

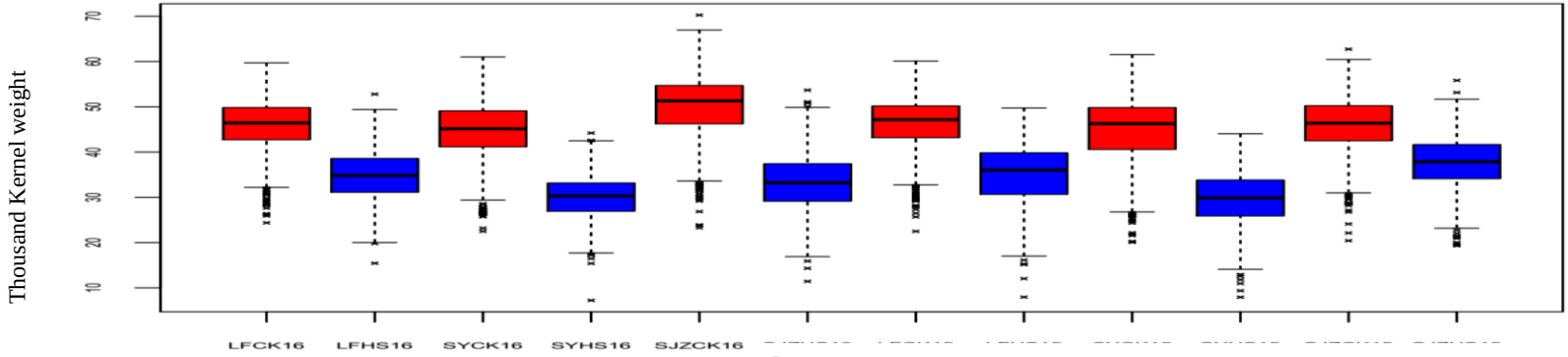
	Tolerant HSI<0.5	Medium T 0.5<HSI<1	Medium S 1<HSI<1.5	Susceptible HSI>1.5
Shijiazhuang	126（17.8%）	251（35.4%）	228（32.2%）	104（14.6%）
Linfeng	115（16.7%）	309（44.9%）	156（22.7%）	108（15.7%）
Sanyuan	135 （18.8%）	266（37.2%）	225（31.4%）	90 （12.6%）

2.2 Genotyping

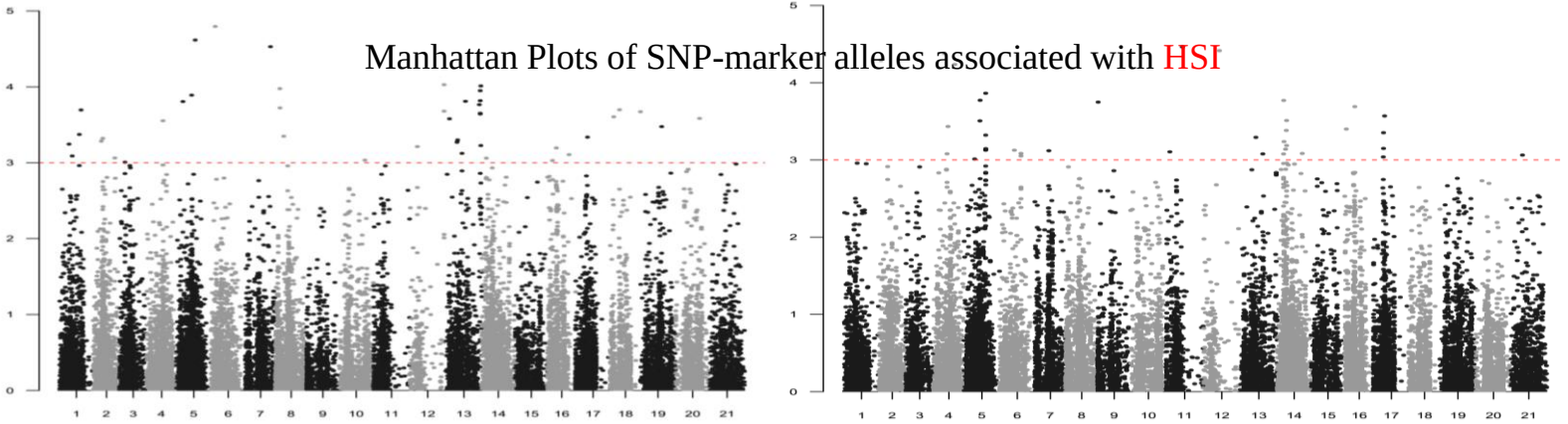


2.3 GWAS Analysis

Box plot for TKW before and after heat stress



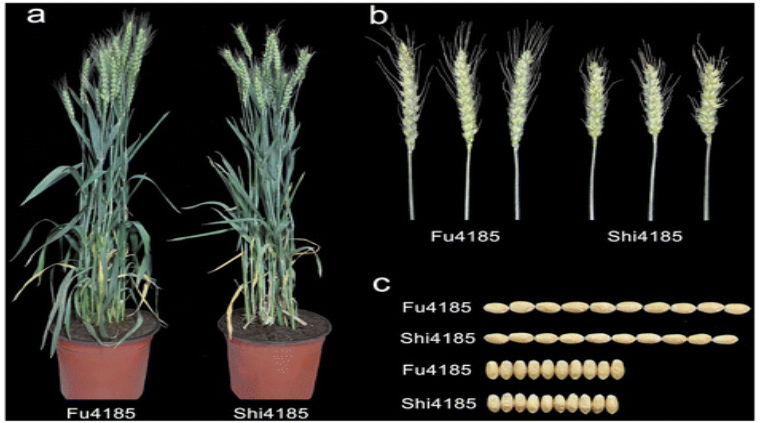
Manhattan Plots of SNP-marker alleles associated with HSI

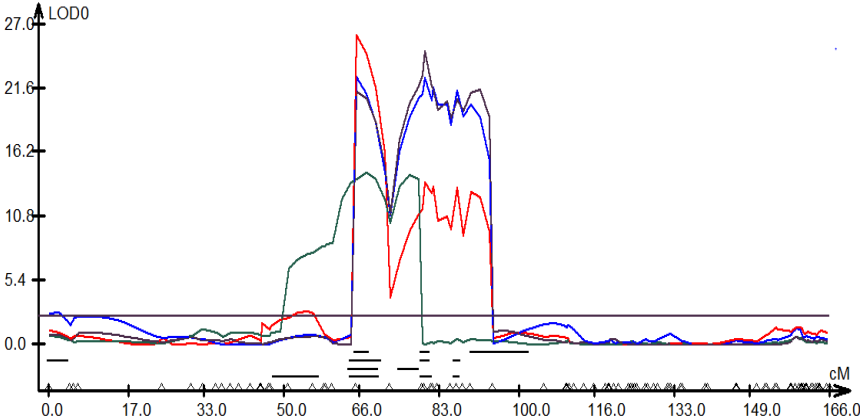


The overlapped heat tolerance associated QTLs were mapped to 2B, 5A, 5B

3. Genetic Dissection of Heat tolerance

➢ En-stable QTL Mapping for TKW in DH population

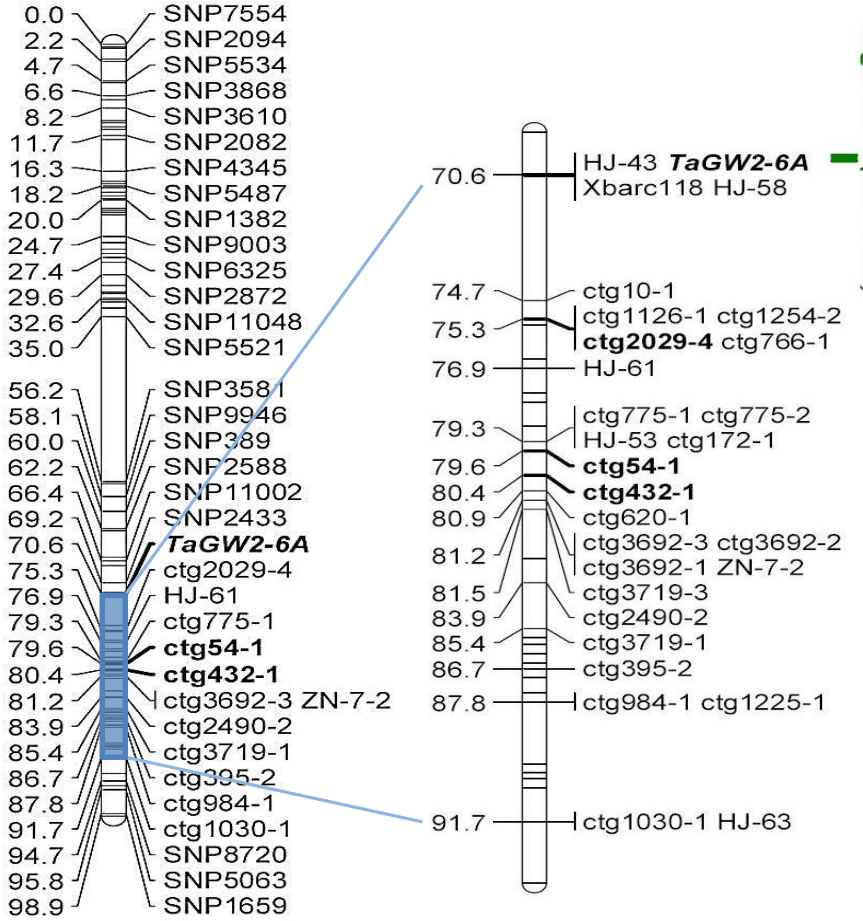


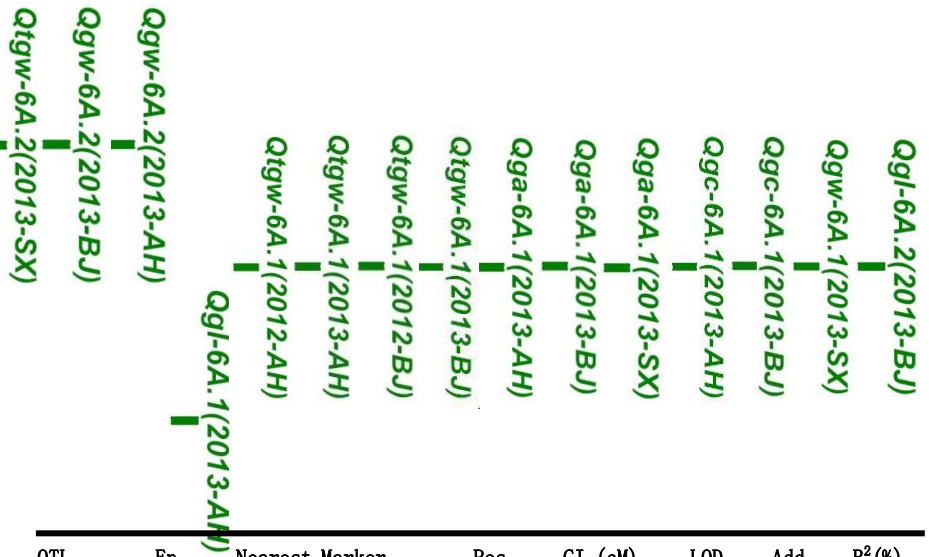


Environment	Sowing season	Shi4185	Fu4185
BJ-2011	Autumn	36.01 ± 0.86	42.82 ± 0.75**
HB-2012	Autumn	33.51 ± 1.29	37.14 ± 1.10*
SX-2012	Autumn	32.23 ± 1.26	39.44 ± 0.70**
BJ-2014	Spring	33.76 ± 1.09	38.79 ± 1.20**
SX-2014	Spring	29.90 ± 1.10	36.61 ± 1.41**

Cheng et al., 2015, *BMC Genetics*

En-stable QTL Mapping for TKW in RIL population



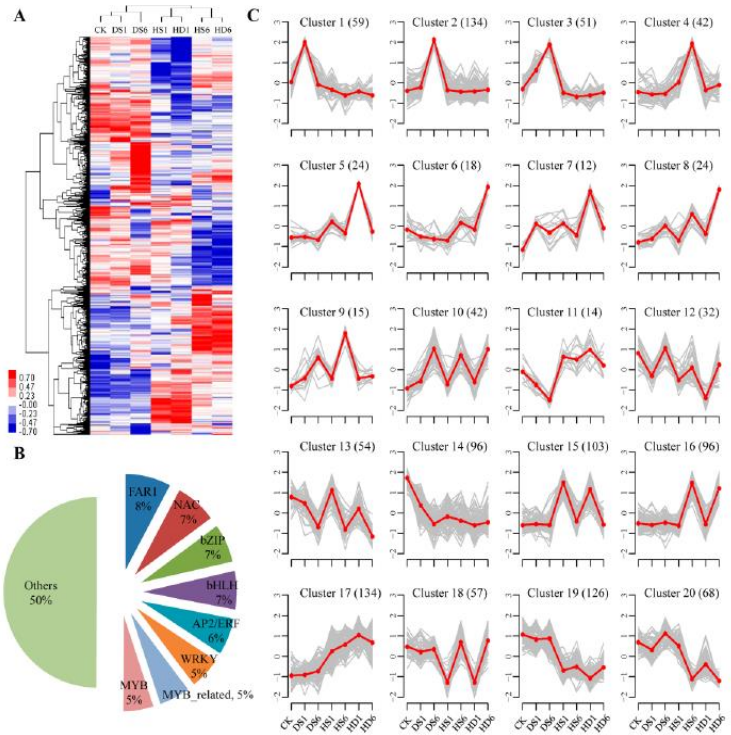


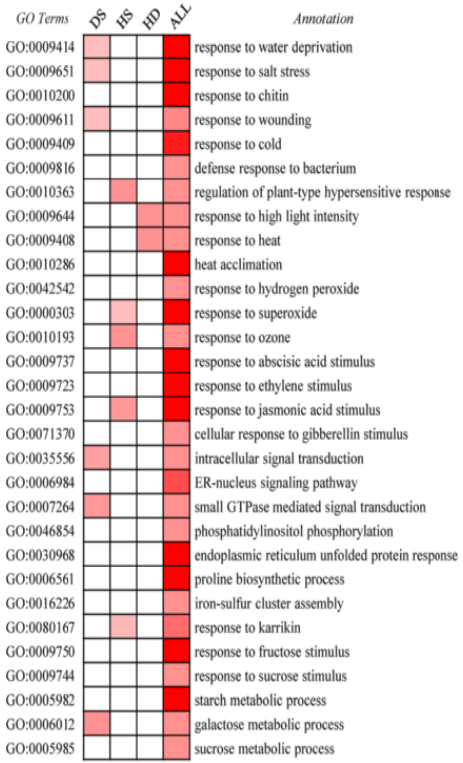
QTL	En.	Nearest Marker	Pos.	CI (cM)	LOD	Add	R^2(%)
QTgw-1	LFW	IACX1298	69.20	69.1-70.2	7.98	1.54	12.17
QTgw-1	BLUP	IACX1298	69.20	69.0-70.6	7.18	0.83	9.32
QTgw-2	LFW	Ra_c29420_237	75.50	74.9-76.9	9.80	1.68	14.62
QTgw-2	BLUP	Ra_c29420_237	75.50	74.9-76.9	8.34	0.89	10.68
QTgw-3	SYW	ctg432-1	80.40	79.3-81.2	4.55	1.09	6.71
QTgw-3	BJW	BS00082211_51	81.50	81.2-82.6	8.15	3.80	13.97
QTgw-4	SYW	Kukri_c14906_220	87.00	86.7-90.5	3.34	0.93	5.00
QTgw-4	BLUP	Kukri_c669_259	90.30	90.1-90.5	3.62	0.60	4.91

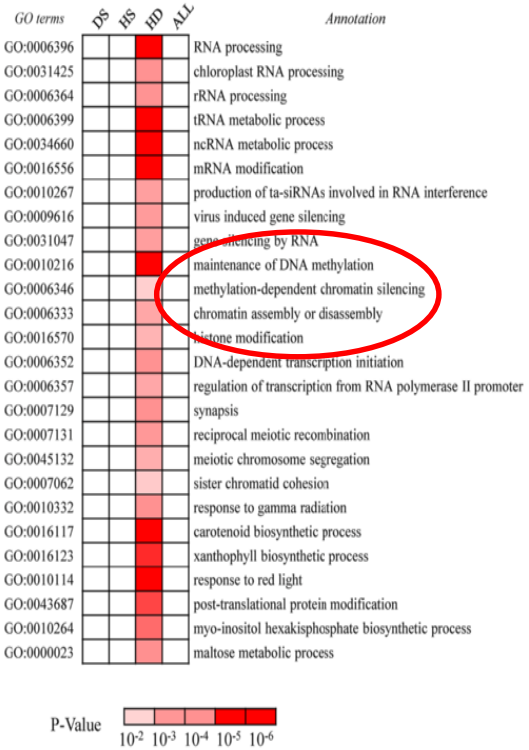
Zhai et al., Submitted to *New Phytologist*

4. Epigenetic Control of Heat Tolerance

- Transcriptome analysis showed epigenetic pathway involved in the regulation of heat stress response

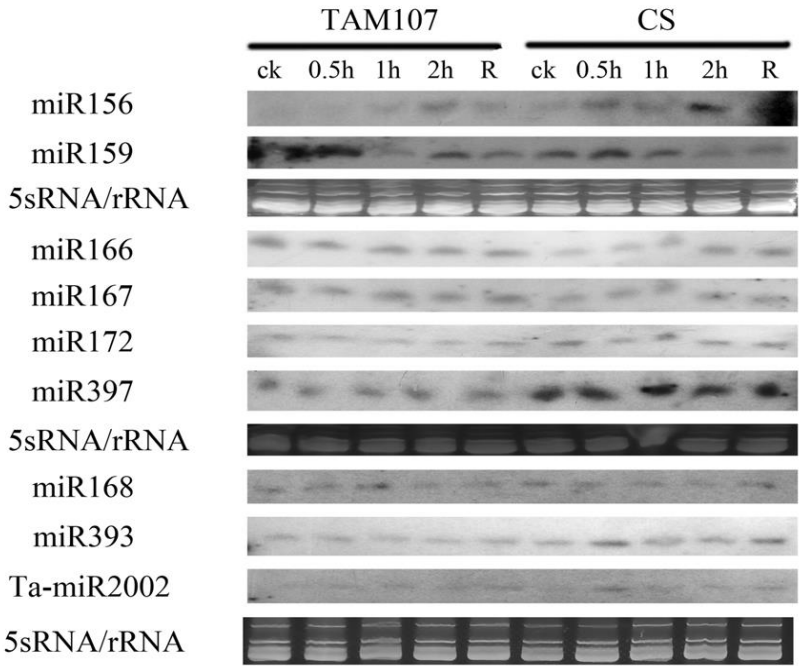


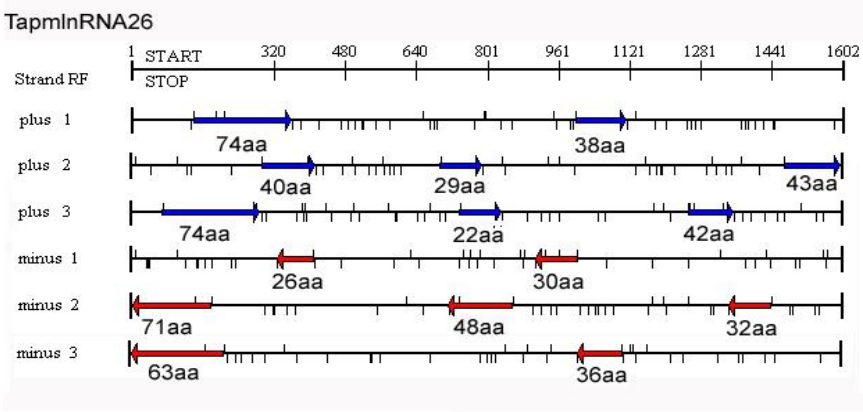


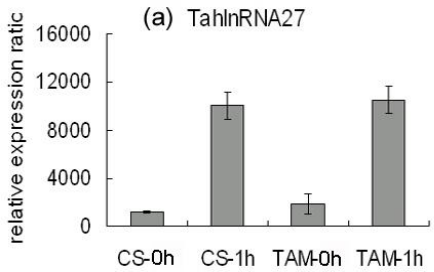


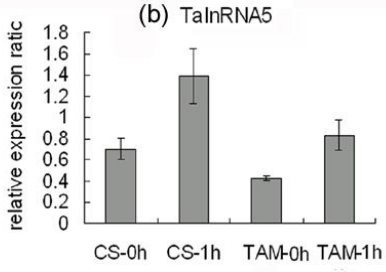
Qin et al., 2008, *BMC Genomics* Liu et al., 2015, *BMC Plant Biology*

MiRNAs and lncRNAs play an important role in response to heat stresses





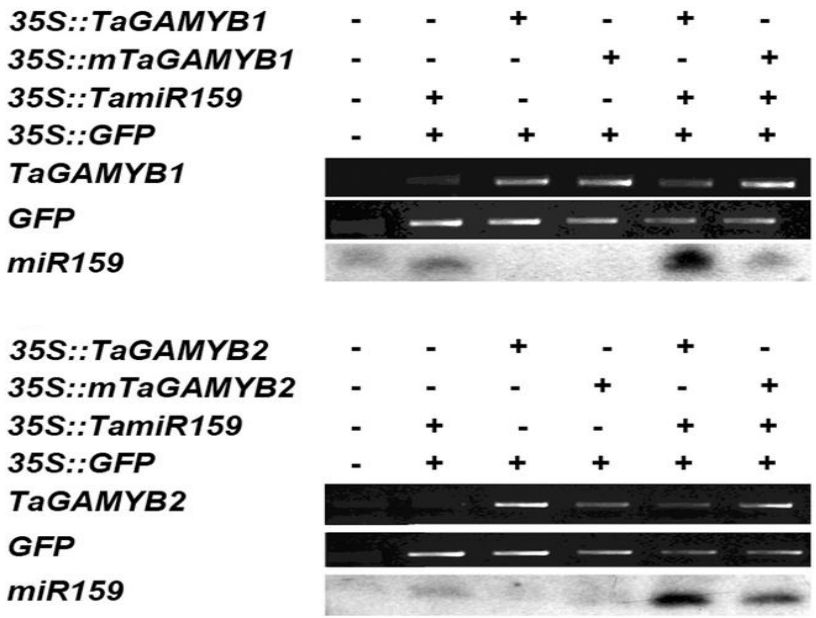


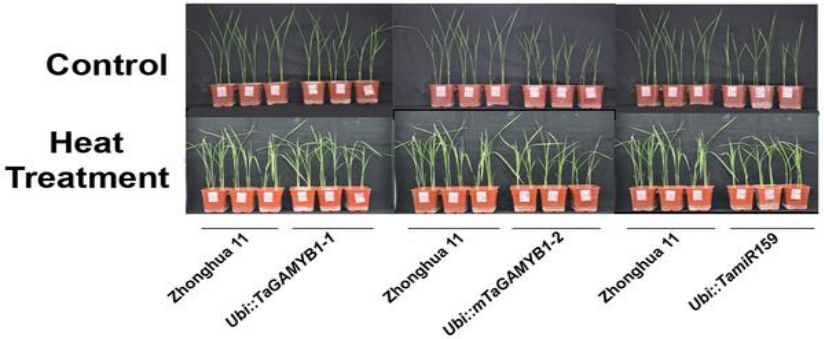


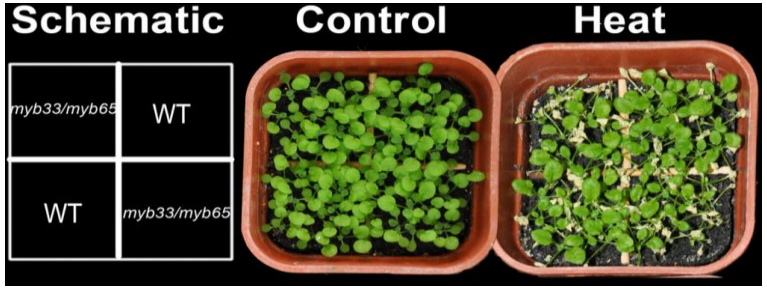
We reported 12 miRNAs and 77 lncRNAs with varied expression patterns under heat stress in wheat by using small RNA transcriptome and SBS sequencing.

Xin et el., 2010, BMC Plant Biol. *Xin et el., 2011, BMC Plant Biol.*

➢ *TamiR159* directed wheat *TaGAMYB* cleavage and involved in heat response



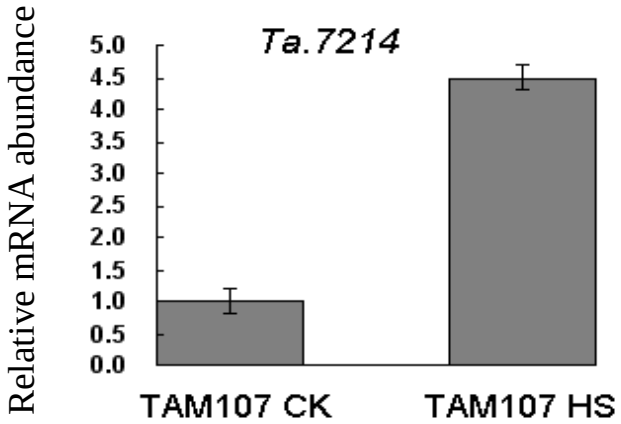


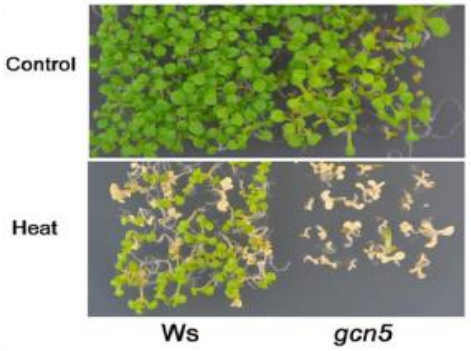


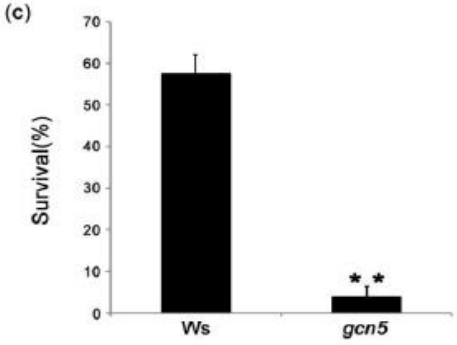
TamiR159 overexpression rice lines were more sensitive to heat stress compared to the wild type, indicating that the downregulation of *TamiR159* in wheat after heat stress might participate in a heat stress-related signaling pathway, in turn contributing to heat stress tolerance. Additionally, double mutation of miR159 targets in Arabidopsis is more sensitive to heat stress.

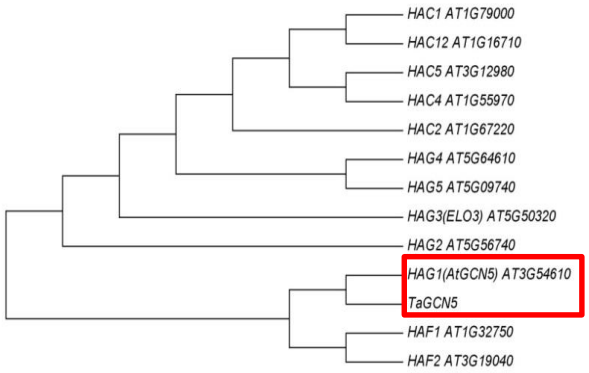
Wang et al., PLOS ONE, 2012

➢ Histone acetyltransferase *TaGCN5* contributes to heat tolerance



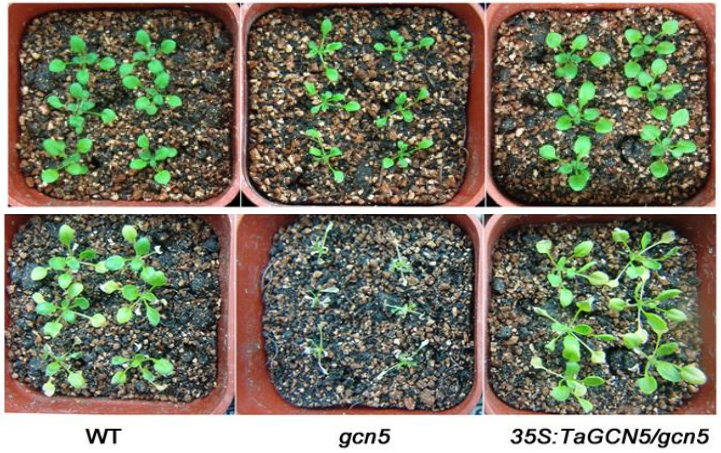




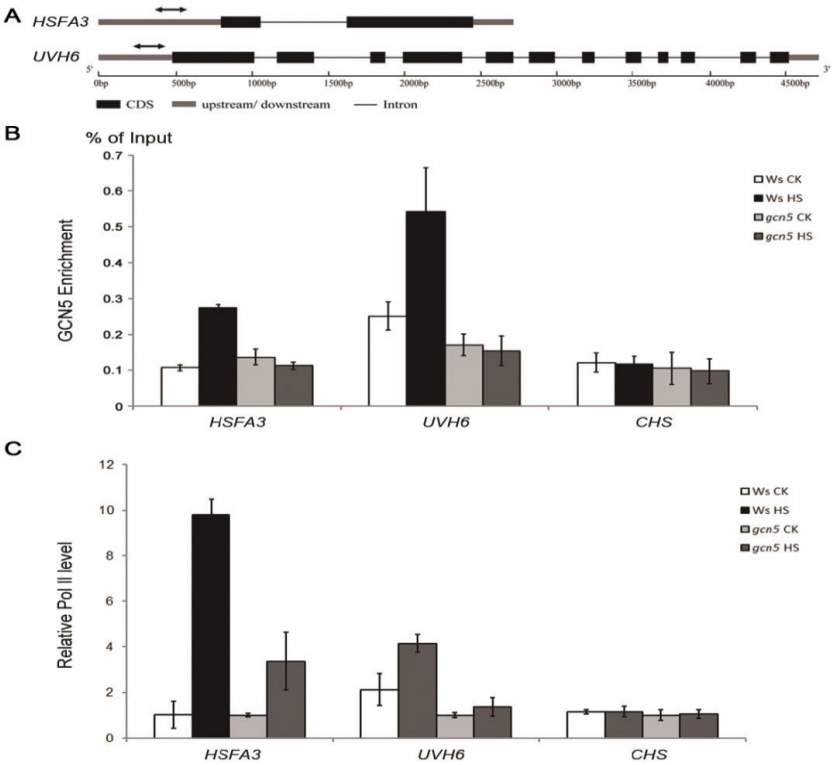


Control (22°C 12d)

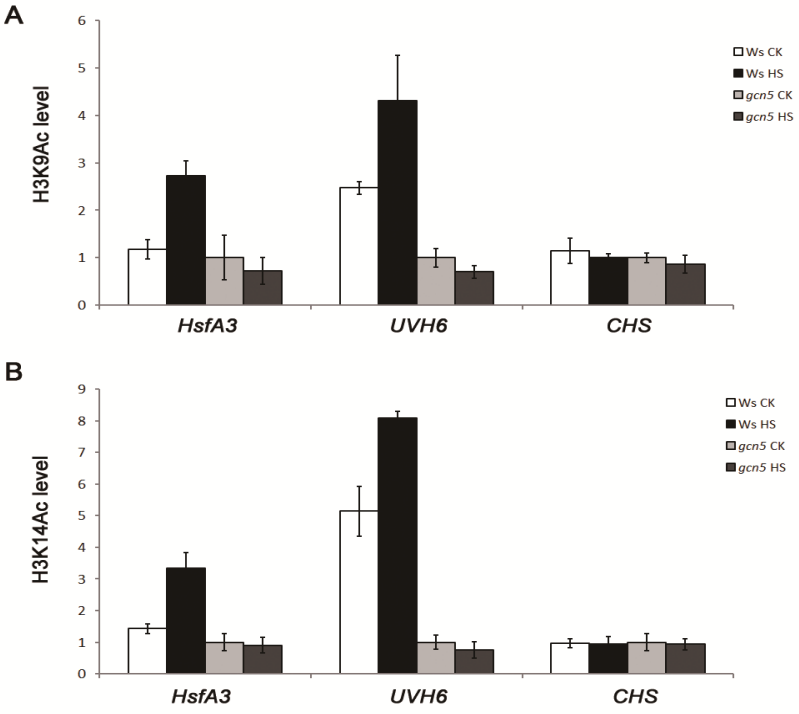
Heat stress (22°C 10d, 45°C 2h, then 22°C 2d)



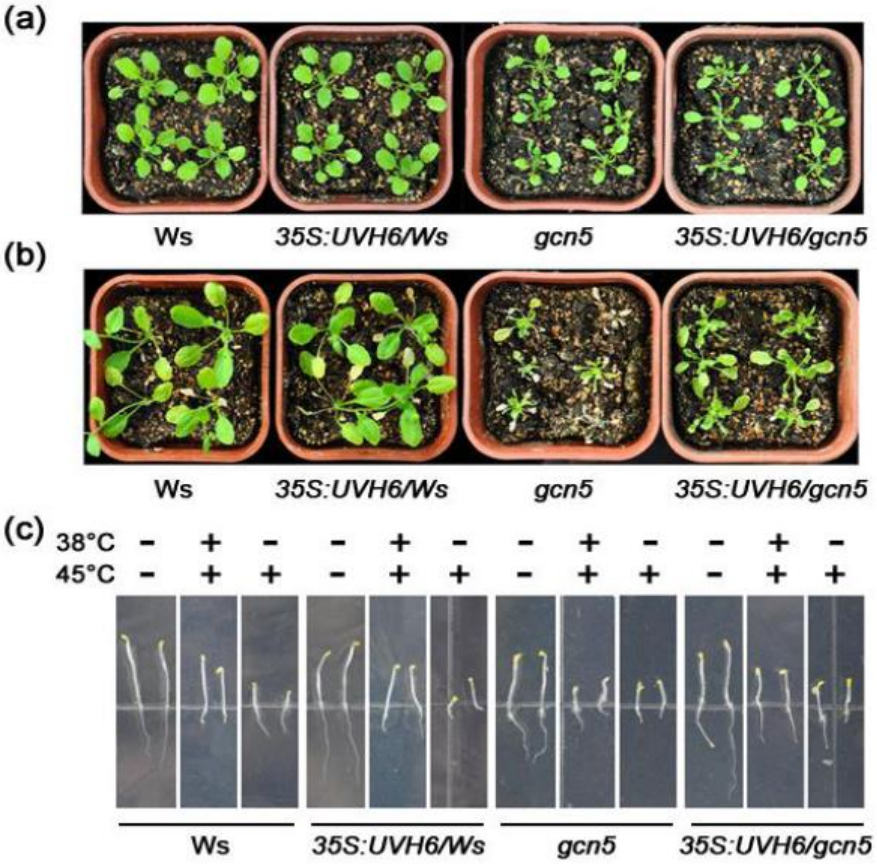
GCN5 enrichment analysis in promoter of *HSFA3* and *UVH6* genes

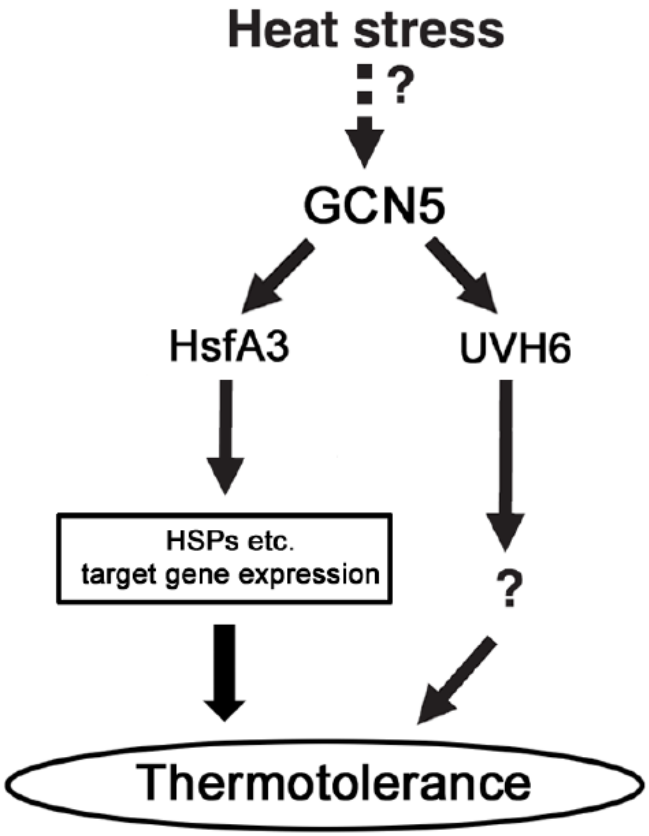


H3K9 and H3K14 acetylation states of the *HSFA3* and *UVH6* genes in wild type and *gcn5* mutant seedlings before and after HS



- Overexpression of *UVH6* in *gcn5* mutation background partially recover their phenotype under heat stress condition





Hu, et al, 2016, Plant Journal

5. Breeding for Improved Heat Tolerance in Wheat

Nongda211	Nongda3214
Nongda212	Nongda3251
Nongda318	Nongda3432
Nongda399	Nongda3488
Nongda408	Nongda3659
Nongda417	Nongda3677
Nongda1108	Nongda5181
Nongda2423	Nongda5182

Since 2004, we have registered 14 wheat cultivars with heat-tolerance

Acknowledgement

中国農業大學

Prof. Qixin Sun
Prof. Zhongfu Ni
Prof. Huiru Peng
Prof. Mingshan You
Prof. Yingyin Yao
Dr. Zhaorong Hu
Dr. Weilong Guo

CIMMYT
International Maize and Wheat Improvement Center

Prof. Matthew Reynolds

西北农林科技大学
Northwest A&F University

Dr. Rui Zhang
Dr. Manshuang Liu
Dr. Zhenshan Liu
Dr. Yu Wang

973 国家重点基础研究发展计划 www.973.gov.cn

中华人民共和国科学技术
The Ministry of Science and Technology of the People's Republic of

National Natural Science Foundation of China