

QTL validation in introgression line populations of common wheat

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Project Rational

- Wheat is the staple food for 35% world population, usually suffers drought stress in the arid and semi-arid areas.
- Rainfed wheat of more than 6 667 000 ha is grown in China.
- Developing DT cultivars by MAS is an efficient way to stabilize wheat production and alleviate food insecurity.
- Challenge for MAS is that majority of QTLs involved significant additive and epistatic effects interact with genetic backgrounds.
- Large sets of DT introgression lines (ILs) with elite Chinese wheat backgrounds are available.

Objectives

- To introduce MAS into conventional breeding programs and establish wheat molecular breeding networks for DT improvement.
- To develop a large-scale DT screening platform and select DT accessions.
- To establish a sharing platform of techniques and information to serve the wheat molecular breeding in DT cultivars.

Activities

- To integrate MAS tools into conventional breeding program and select stable DT introgression lines (ILs) carrying target genes/markers.
- To phenotype and genotype the ILs with the elite Chinese wheat genetic backgrounds in diverse environments and select DT ILs.
- To exchange the information, technology and methodology associated with the DT molecular breeding, promote interactions among regions, build the capacity of wheat modern breeding in China.

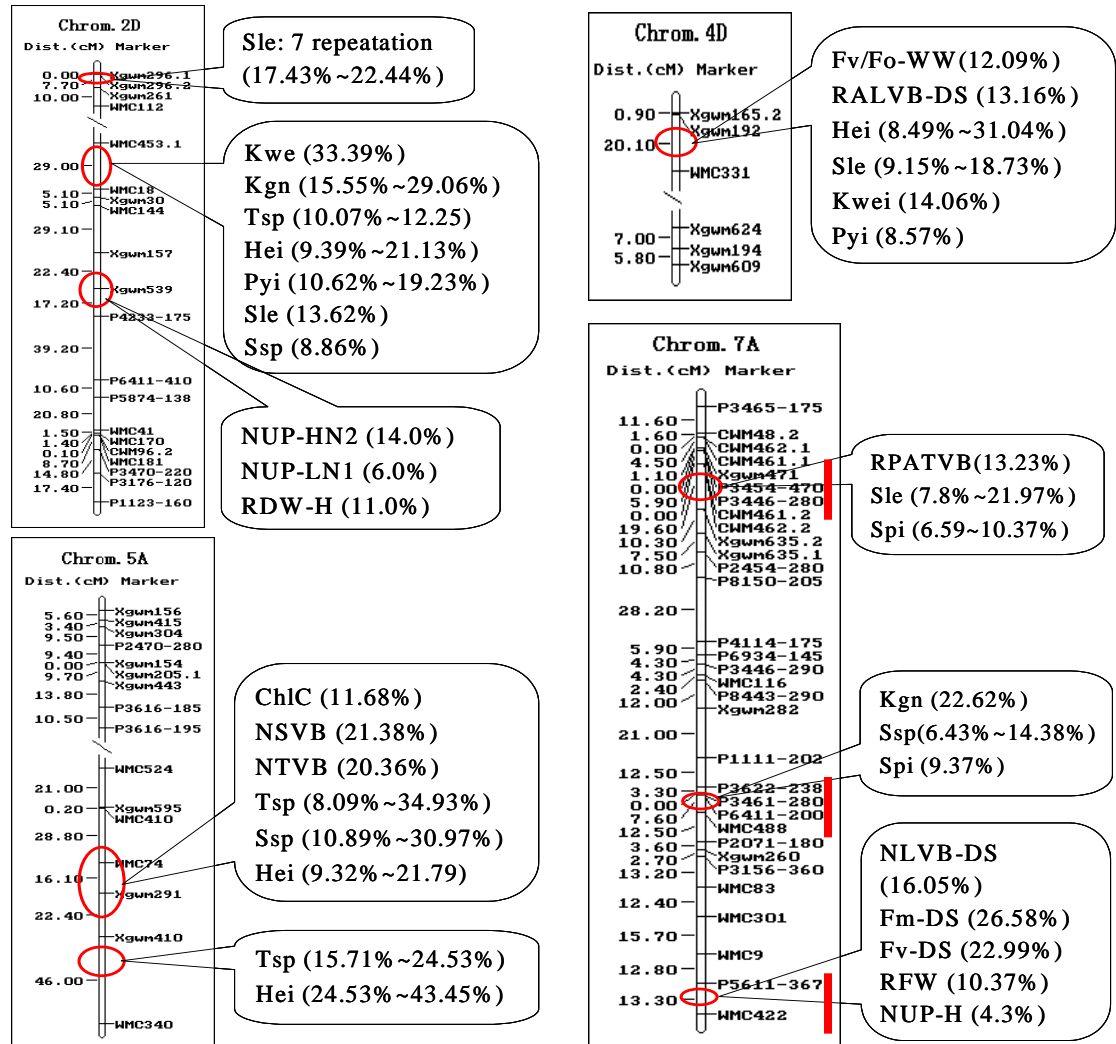
Integrated mapping of QTLs for drought tolerance in common wheat



↑ Hanxuan 10 DH Lines
↑ Lumai 14

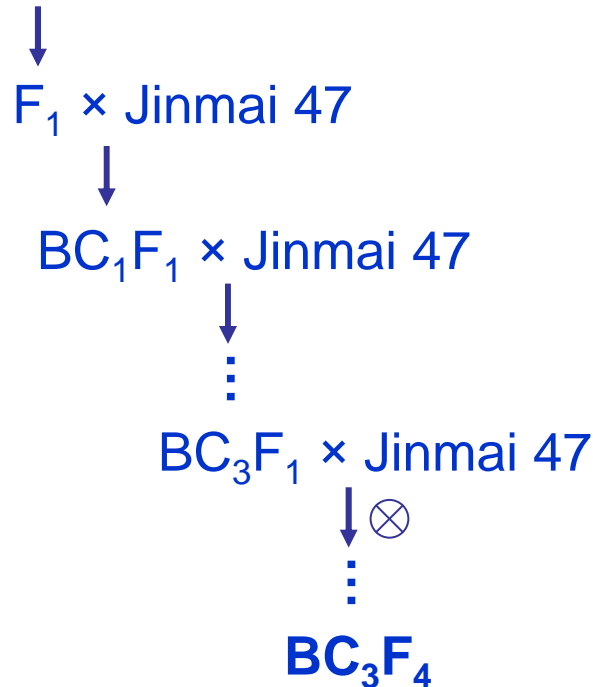
Hanxuan 10 DT variety grown under rainfed condition in semi-arid region

Lumai 14 High yield potential variety grown under irrigated condition



Validation of putative QTLs in ILs

Jinmai 47 × Donor parents



Donor parents

Gaoyou 504

Lumai 14

Shaanyou 225

Xiaoyan

Zhongyou 9507

Pandas

Salgamma

Trait: yield components, photosynthetic characteristics, developmental dynamics of plant height

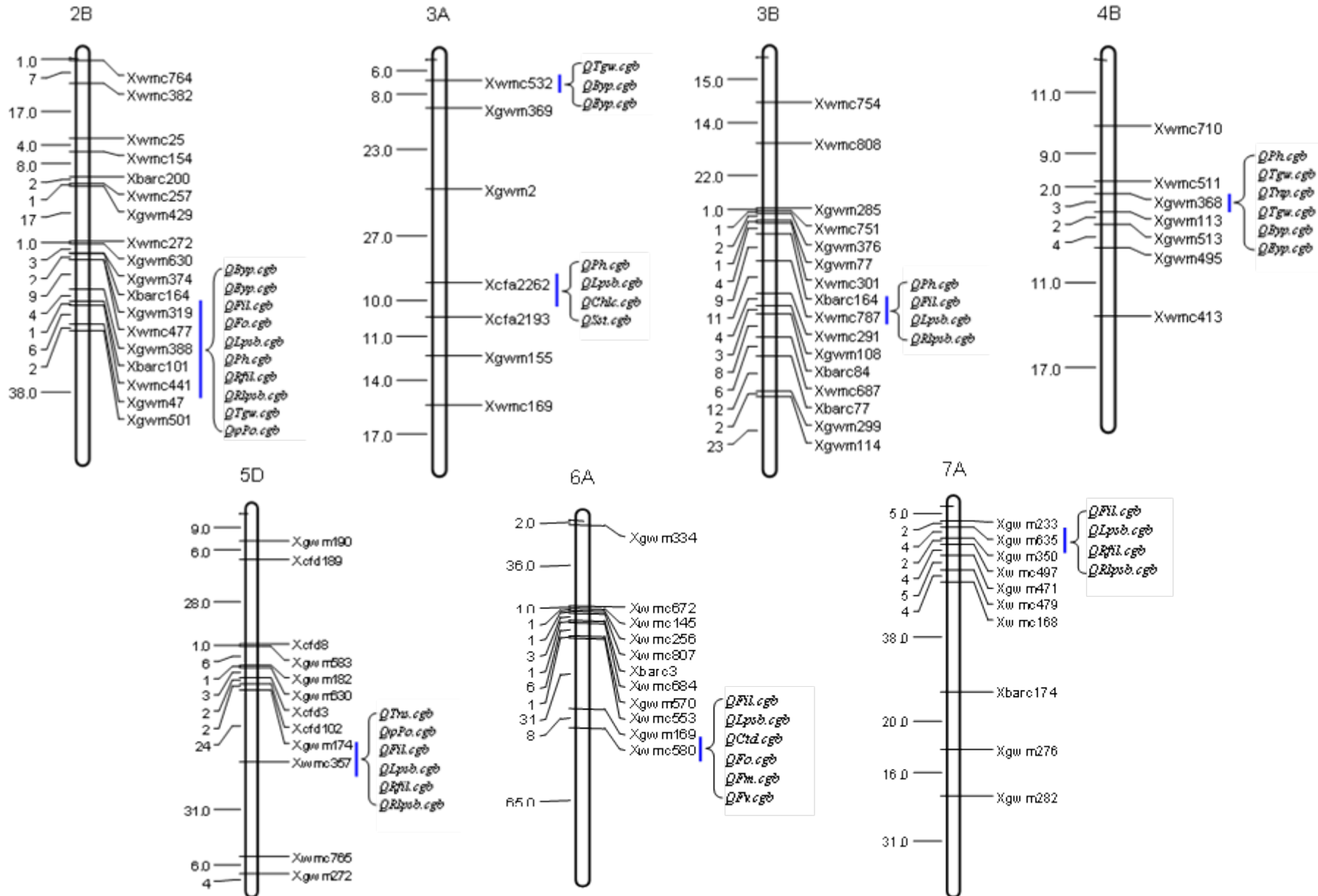
Analysis method: Chi-square (X^2) test ($P < 0.005$)
One-way ANOVA ($P < 0.01$)

Marker assisted selection for DT ILs derived from recurrent parent Jinmai 47

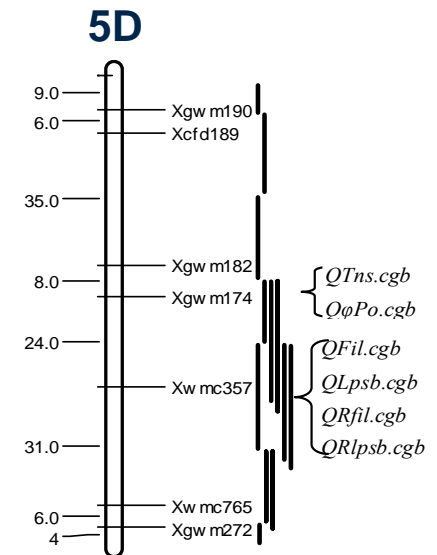
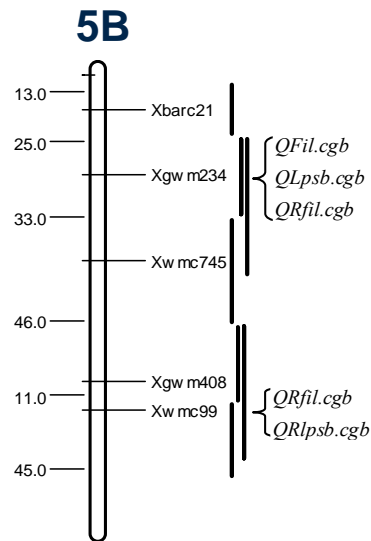
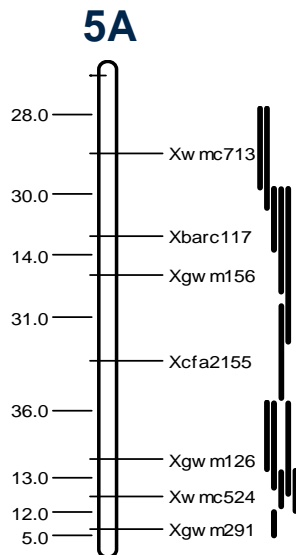
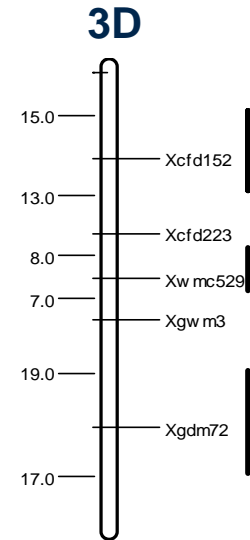
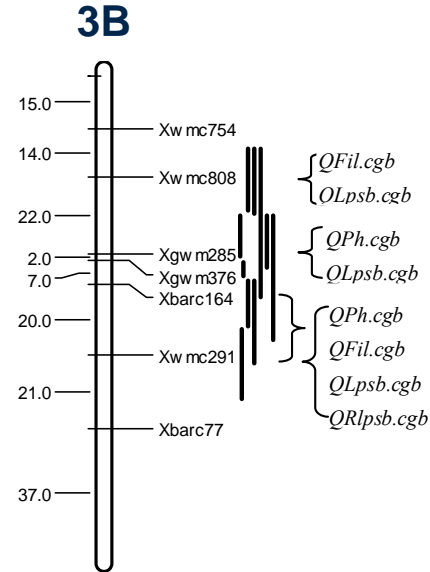
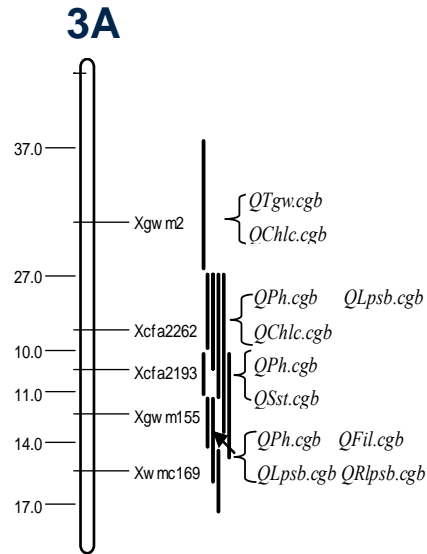
Donor parent	No. of IL	No. of polymorphic SSR marker
Lumai 14	148	137
Salgemma	150	116
Gaoyou 504	25 selected lines	37
Shaanyou 225	25 selected lines	50
Xiaoyan 54	25 selected lines	52
Zhongyou 9507	25 selected lines	55
Pandas	25 selected lines	54

25 selected lines: 15 lines are the best, 10 are the reverse lines with target traits.

QTL hot regions validated in ILs



Identification of introgressed segments and QTLs related to DT in ILs derived from Jinmai 47 and Lumai 14



QTLs validated in ILs

- Total of ten QTL hot regions for target traits identified from DHLs were selected for validation in seven IL populations.
- Eight QTL hot regions were consistent with that detected in the DHLs on chromosome 2B, 3A, 3B, 4B, 5D, 6A and 7A in all seven ILs.
 - More than half of the QTL flanking markers differed from that in DHLs.
 - Seven QTL hot regions identified in the DHLs were only confirmed in one or several IL populations.
- Fourteen QTLs were validated in two IL populations derived from donor parents Lumai 14 and Salgemma.
 - Nine QTLs controlling yield components, *Xgwm268* on 1B, *Xwmc272*, *Xwmc477* and *Xgwm388* on 2B, *Xwmc41* on 2D, *Xgwm368* and *Xgwm513* on 4B, *Xgwm297* and *Xpsp3033* on 7B.
 - Five QTLs for developmental dynamics of plant height, *Xgwm501* on 2B, *Xcfd116* on 2D, *Xwmc291* on 3B, *Xgwm368* on 4B and *Xgwm371* on 5B.

Drought-tolerant ILs with the elite Chinese wheat genetic backgrounds selected by phenotype

Recipient	Donor parent	IL generation	DT ILs
Jinmai 47	Chinese cultivar	BC ₃ F ₂ - BC ₃ F ₅	52
	European cultivar	BC ₃ F ₄	14
Jinmai 54	Chinese cultivar	BC ₃ F ₂ - BC ₃ F ₅	35
	European cultivar	BC ₃ F ₄	12
Lumai 14	Chinese cultivar	BC ₃ F ₃ - BC ₃ F ₅	23
Yumai 18	Chinese cultivar	BC ₃ F ₂ - BC ₃ F ₄	20

- 156 DT ILs were selected by phenotype.
- Among them, 23 ILs were selected by genotyping and phenotyping.
- DT line JL28 has been recommended to the pre-yield trial in Shaanxi.

Product delivery and impact on users

- DT ILs were distributed to
 - GCP partners for multi-environment evaluation and breeding utilization
 - Breeders for utilization
- MARS techniques
- DT phenotyping techniques



Linkage with other projects

- Field evaluation of wheat-barley introgression lines under different water regimes (GCP SP3: G4007.23)
 - DT phenotyping of wheat-barley ILs
- Breeding for drought tolerance with known gene information (GCP SP3: G4008.04)
 - QTL analysis and MAB modeling design

Summary

Results of last year:

- Seven ILs were genotyped with 50-137 putative DT SSR markers.
- Eight DT QTL hot regions on chromosome were validated in seven ILs.
- Nine QTLs for yield components, and five for developmental dynamics of plant height were validated.
- Total of 156 DT ILs were selected by phenotype, among them, 23 were selected by genotyping.

Plan for next years:

- To validate DT QTLs in nine IL populations.
- To select 30-40 DT ILs based on genotyping and phenotyping.
- To deliver DT ILs to the breeders for breeding utilization.
- To exchange information and technology among breeders and geneticists for building the capacity of wheat molecular breeding.