QTL validation in introgression lines of common wheat

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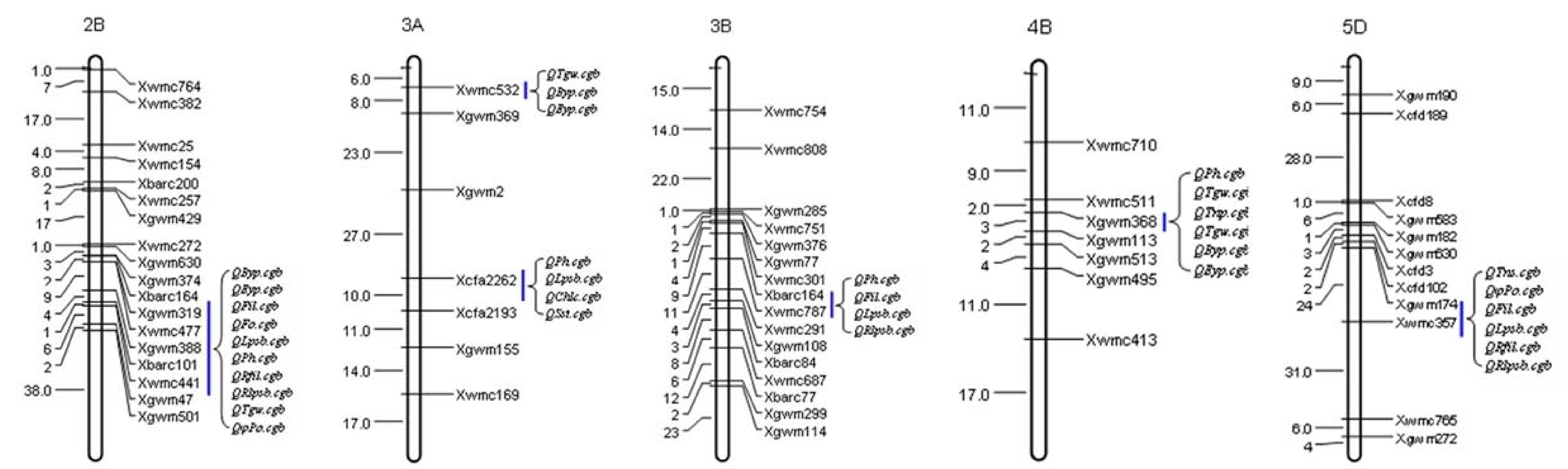
Theme 3: Marker Development and Breeding Applications

One of the challenges for marker assisted selection (MAS) is that majority of QTLs involved significant additive and epistatic effects with the interactions of QTLs and genetic backgrounds, which badly impact the MAS effect. Seven introgression line (IL) populations (BC_3F_4) derived from a common recurrent parent Jinmai 47, an elite Chinese common wheat cultivar, and seven donor parents, including five Chinese drought-tolerant cultivars Gaoyou 504, Lumai 14, Shaanyou 225, Xiaoyan 54 and Zhongyou 9507, and two European cultivars Pandas and Salgemma with drought tolerance (DT) and good quality were used to validate the DT QTLs identified from a doubled haploid (DH) population, which was derived from a cross of two Chinese common wheat cultivars Hanxuan 10 and Lumai 14. A total of eight QTL hot regions for yield components, photosynthetic physiological characteristics and developmental dynamics of plant height were detected on chromosome 2B, 3A, 3B, 4B, 5D, 6A and 7A in all seven ILs, respectively (Figure 1). All eight chromosome regions were consistent with that detected in the DH population, but more than half of the QTL flanking markers differed from that in DH, and moreover, most QTL hot regions identified in the DH population could be only confirmed in one or several IL populations. The QTL hot regions shared by multi-populations with different genetic backgrounds maybe more helpful for using MAS in wheat molecular breeding.



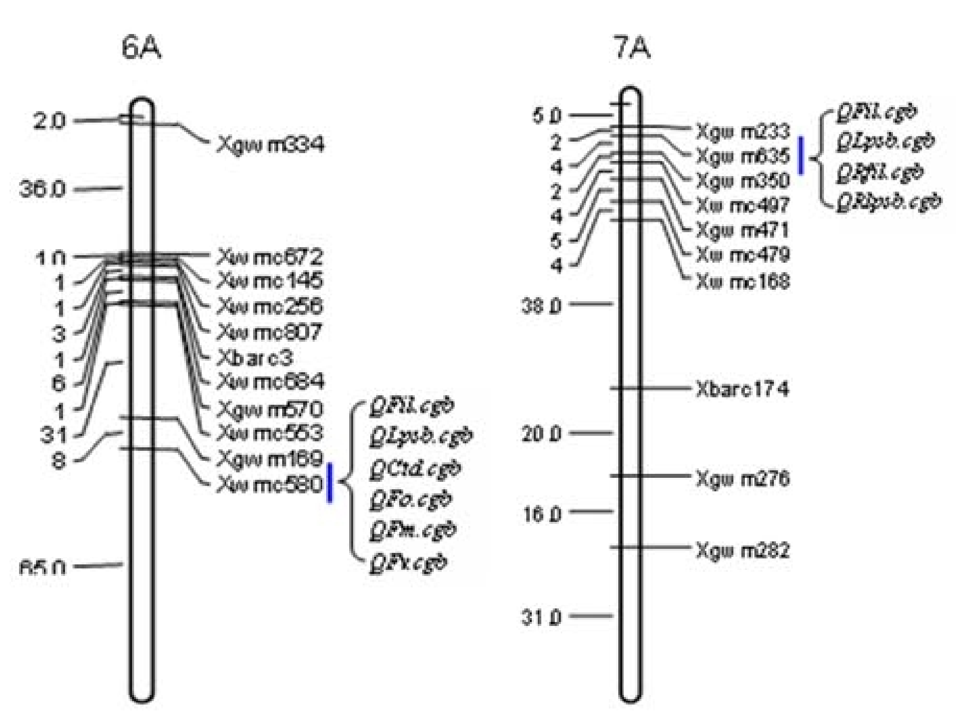


Figure 1 Distribution of eight QTL clusters on chromosomes, which were identified in seven ILs and consistent with that detected in the DH population.

Table 1 Marker assisted selection for BC_3F_4 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	57
Shaanyou 225	25 selected lines	50
Xiaoyan 54	25 selected lines	52
Zhongyou 9507	25 selected lines	55
Pandas	25 selected lines	54

Conclusion: Seven introgression line populations derived from a recurrent parent Jinmai 47 were genotyped with 50 ~ 137 DT QTL candidate SSR markers. Total of 23 DT ILs have been selected based on the genotype and phenotype evaluations.