INTRODUCTION

Plant height (PH) is an important quantitative trait of wheat. It affects plant lodging, harvest index, disease resistance and yield. The Rht8 as a gibberellin (GA) sensitive gene on the short arm of chromosome 2D significantly reduces plant height. Compared with Rht-B1b (Rht1) and Rht-D1b (Rht2), this semi-dwarfing gene is not associated with the GA pathway, and thus, does not reduce leaf area or coleoptile length. For this reason, Rht8 has been widely used in breeding programs worldwide, especially in moisture-limited situations where deep planting is essential. To date, a simple sequence repeat (SSR) marker Gwm261 has been the only one used for screening of Rht8, but recombinants are frequently found between Rht8 and Gwm261 because they are several map units apart. Therefore, more closely linked markers are needed for wide deployment of Rht8 in new cultivars.

OBJECTIVES

★ Identify closely linked flanking markers to Rht8
★ Validate these markers in a recombinant inbred line (RIL) population.

MATERIALS AND METHODS

- A population of 132 recombinant inbred lines (RIL) was developed from G97380A (Rht8) X G97252W (rht8)
- Genotyping-by-sequencing (GBS) was used to identify single-nucleotide polymorphisms (SNPs).
- Plant height was repeatedly evaluated for the population.
- Simple sequence repeats (SSR) markers based on reference sequence and competitive allele specific PCR (KASP) markers based on GBS SNPs were designed.
- JoinMap 4.1 was used to construct a linkage map and WinQTLCart2.5 was used for QTL mapping. R and SAS were used for data analysis.

RESULTS

- The distribution of plant height followed a normal distribution in both seasons, respectively (Fig. 1).
- A total of 2,514 single nucleotide polymorphism (SNPs) and 3 SSR (Gwm261, Xcfd53, PH2918-11) markers were constructed on linkage map. The map contains 2,238 SNPs and 3 SSRs, covering all 21 chromosomes (Fig. 2, Fig. 3).
- Marker PH2918-11 showed the largest effect on height reduction, therefore is the most closed marker to Rht8.
- Xcfd53 and PH2918-11 are the best flanking markers for Rht8, which can significantly improved selection accuracy compared to original Xgwm261 marker (Table 1).
- For high-throughput screening, flanking KASP markers were developed (Figs. 3 & 4), they are closer to Rht8 than Xgwm261, even though not as close as the two flanking SSR markers (Fig. 3).

CONCLUSION

- Two SSR markers, Xcfd53 and PH2918-11, were found to flank Rht8 at 7.3 cM apart, which are closer to Rht8 than the original marker Xgwm261. Use of these markers in breeding will significantly improve selection accuracy in developing new cultivars with Rht8.
- Several SNPs closely linked to Rht8 were converted into KASP markers, which can be used for high-throughput screening of Rht8.