# QTL mapping of pre-harvest sprouting and stripe rust resistance in wheat cultivars Danby and Tiger

Wheat yield and quality is influenced by many abiotic and biotic environmental factors. Pre-harvest sprouting (PHS) occurs when physiologically matured spikes are exposed to wet field conditions before harvest resulting in seed germination that causes significant losses in yield and end-use quality. Wheat stripe rust is one of the most important biotic factors reducing grain yield and quality. To investigate the genetic basis of wheat resistance to PHS and stripe rust and develop molecular markers for marker assisted breeding, a double haploid (DH) population, derived from two white wheat varieties Danby and Tiger, was genotyped with simple sequence repeats (SSR) markers and simple nucleotide polymorphism (SNP) markers. This DH population was also assessed for PHS and stripe rust resistance in both greenhouse and field experiments. In PHS assessments, one major resistant quantitative trait loci (QTL) was consistently detected on the short arm of chromosome 3A in three experiments and explained 21.6% to 41.0% of the phenotypic variation. This QTL is corresponding to a previously cloned gene, *TaPHS1*. A SNP in the promoter of *TaPHS1* co-segregated with PHS resistance in this mapping population. Meanwhile, two stable minor QTLs, Qphs.hwwg-3B.1 and Qphs.hwwg-5A.1, were consistently detected on the chromosome arms 3BS and 5AL in two experiments. These two minor QTLs showed significant synergistic effects with *TaPHS1* in improving PHS resistance. The same DH population was also used to investigate stripe rust resistance. Three major resistant QTLs were identified for infection type (IT) and disease severity (DS). Two of them, QYr.hwwg-2AS1 and QYr.hwwg-4BL1, identified from Danby explained up to 28.4% of the phenotypic variance (PVE) for IT and 60.5% for DS. The third one, QYr.hwwg-3BS1 identified from Tiger, had PVE values up to 14.7% for IT and 22.9% for DS. QYr.hwwg-2AS1 and QYr.hwwg-4BL1 are likely the same resistant genes reported previously on chromosome arms 2AS and 4BL. However, QYr.hwwg-3BS1 might be different from the reported gene cluster near its distal end harboring Yr57, Yr4, Yr30 and Sr2. Significant additive effects were observed among these three major QTLs in reducing IT and DS of stripe rust. In order to pyramid multiple QTLs in breeding, several user-friendly Kompetitive allele specific polymorphism (KASP) markers were successfully developed for most of the major QTLs. The major resistant QTLs and their significant interactions identified in this study together with novel flanking KASP markers developed will be useful not only for understanding genetic mechanisms of PHS and stripe rust resistance but also for marker-assisted breeding to improve these resistances by gene pyramiding.