

Unravelling the genetics of disease resistance and agronomic traits of spring triticale using wheat and rye genomic resources

Triticale is an important small grain cereal crop which suffers severe yield, grade and end-use quality losses due to *Fusarium* head blight (FHB) and ergot (ERG) diseases predominantly caused by the fungal pathogens *Fusarium graminearum* (*Fg*) and *Claviceps purpurea*, respectively. Where losses to kernel weight can be up to 30–70% and 5–10% due to FHB and ERG, respectively, the contamination of grains by *Fg*-produced mycotoxin deoxynivalenol (DON) and poisonous alkaloids containing ERG sclerotia (compact masses of fungal mycelium) are of foremost concern due to their harmful effects on human and animal health. The lack of understanding about the genetic makeup of different traits e.g. ability to resist diseases such as FHB and ERG, and some other traits that often showed association with these diseases e.g. grain protein content (GPC), test weight (TWT), yield (YLD), plant height (PHT) and lodging (LDG) in spring triticale is still a major hindrance for its breeding. This can partly be attributed to unavailability of genome sequence and high-throughput marker system for triticale. One solution for these can be utilization of wheat and rye genomic resources developed in recent past.

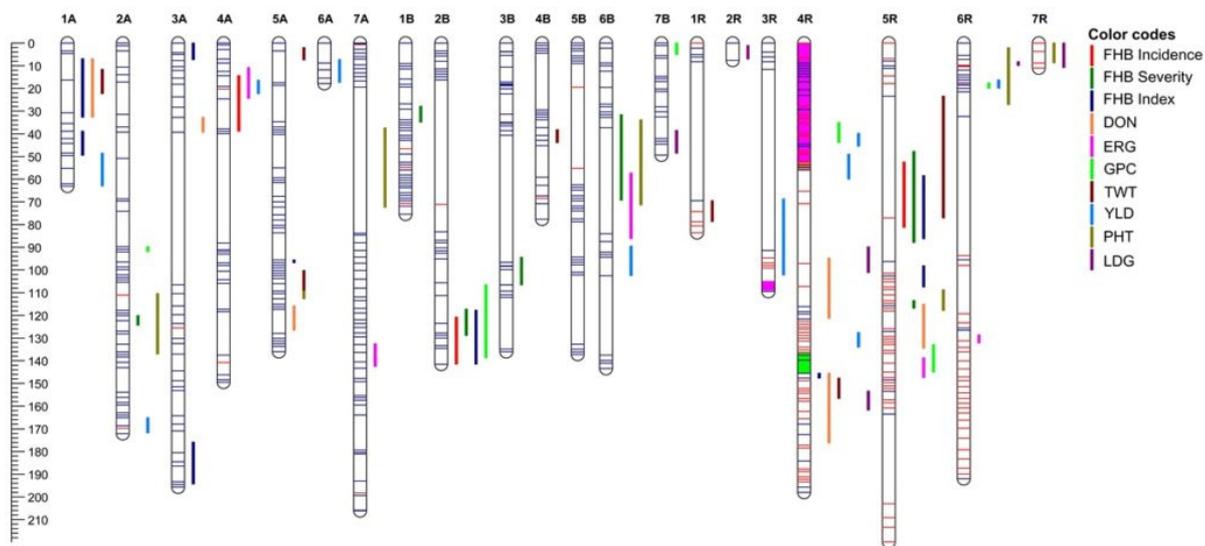


Fig. 1. TMP16315/AC Ultima spring triticale genetic map. The twenty-one linkage groups (LGs; seven from each of three triticale genomes A, B and R) are labeled as 1A to 7R. A scale ruler for marker positions (in cM) are shown on the left side of the chart. Unique loci (all the single nucleotide polymorphism or SNP markers that co-segregated among doubled haploid lines and mapped at same location on a LG were considered as single marker or unique locus) are represented by horizontal lines of either dark blue or red color on LGs. Dark blue and red colors represent loci largely dominated by SNPs derived from the wheat genomes A/B/D and the rye genome R, respectively. Colored LG blocks indicates genomic rearrangements or interchanged/translocated fragment from a different chr (4R: red, 6R: pink, 7R: green, and mosaic of triticeae chr groups 1, 2, 4, 5, 6 and 7: brown). The quantitative trait loci (QTL) for different traits are shown on the right side of respective LGs as different color bars. Color codes for different traits associated with QTLs are shown on the right side of the chart.

Therefore, we utilized >100 thousand wheat and rye genome single nucleotide polymorphism (SNP) markers for DNA profiling of 93 double haploid (DH) lines produced from a cross between Canadian spring triticale cultivar AC Ultima and an uncharacterized spring triticale line TMP16315 using microspore culture, a tissue culture method. DHs were also characterized for different traits in replicated trials at multiple locations.

Utilizing DNA profile of DHs, a high-density SNP genetic map comprising 5274 markers mapped on all 21 chromosomes (chrs) belonging to three triticale genomes A, B and R with a map density of 0.48 cM/SNP was generated (Fig. 1). This map also showed genomic rearrangements such as interchanged/translocated fragment between wheat and rye genome chrs (Fig. 1). The map and the trait values were incorporated together, and several new genomic signatures, called quantitative trait loci (QTLs) and some epistasis interactions (QTL x QTL) were identified (Dhariwal et al. 2018). Together, 20 major QTLs were identified for resistances to FHB and ERG, along with other major and minor QTLs for other traits. Identified QTLs included both specific (such as a QTL on chr 3A for reduced DON) and co-localized/pleiotropic QTLs (such as ERG resistance QTLs on chrs 4A and 5R that were associated with YLD and GPC, respectively). Presence of pleiotropic QTLs with favorable alleles from different parents such as one on chr 4A for ERG and YLD suggested a possible trade-off between stress and developmental pathway genes and can be explained by the plant's balance mechanism for growth and defense. However, at some co-localized QTL regions, such as a chr 5R QTL for reduced FHB and PHT, the favorable alleles were contributed by same parent. These QTLs represents rare variants and can efficiently be used for breeding triticale without any disadvantageous outcomes to improve >1 traits simultaneously using marker-assisted selection. Conversely, both parents contributed favorable QTLs (such as GPC QTLs on chrs 2B and 4R were contributed by TMP16315 and AC Ultima, respectively) and identified QTLs expressed either across environments (such as all FHB incidence QTLs) or in a specific environment (such as an FHB index QTL on chr 2B).

This study provides new insights into the genetic makeup of resistances to FHB and ERG, and other agronomic traits in triticale. Particularly, resources generated in this study, including the high-density SNP map and QTLs for different traits will facilitate rapid transfer of these genomic signatures into desirable lines. The SNP map also promises a starting platform for comparative mapping with wheat and rye, and map-based cloning of genes.

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Publication

[High Density Single Nucleotide Polymorphism \(SNP\) Mapping and Quantitative Trait Loci \(QTL\) Analysis in a Biparental Spring Triticale Population Localized Major and Minor Effect Fusarium Head Blight Resistance and Associated Traits QTL.](#)

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