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Adult plant development in triticale (x *Triticosecale* Wittmack) is controlled by dynamic genetic patterns of regulation

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Abstract

Triticale is a man-made wheat-rye hybrid, considered a promising crop due to its genetic variation for several traits of agronomic importance. In particular, many of the relevant traits are classified as dynamic because they exhibit variations in their expression over time. The use of approaches that only evaluate a single time point can lead to having simplified conclusions of the underlying genetic architecture of the trait. Würschum et al. (2014) used triticale as model crop to investigate the genetic patterns of regulation and phenotypic plasticity in adult plant development. A large mapping population of 647 doubled haploid lines derived from four families was evaluated at three time points corresponding to the developmental stages of visible awns (DS1), late flowering (DS2) and early dough development (DS3). All the DH lines were phenotyped using a partially replicated experimental design at two locations and two years. Genome-wide association mapping was performed to identify main effects and epistatic quantitative trait loci (QTL) in each phenological point of interest. The results showed that 29, 14 and 14 markers were significantly associated with DS1, DS2 and DS3, and 73.9%, 52.1% and 57.4% of the total genotypic variance was explained respectively. Some of the identified QTL are present in the three time points, while others were only associated with a developmental stage in particular. Few epistatic QTL for all three time points were identified. This indicates that epistatic interactions are a component of the genetic architecture underlying the triticale adult plant development. This study demonstrated that development during the reproductive phase is controlled by a dynamic pattern of genetic regulation in triticale. The development of better strategies and phenotyping platforms will be very useful in the future to study genetic control in dynamic traits in cereals.