Genetic regulation of tillering.

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The activity of the shoot apical and axillary meristems largely determines above ground plant architecture. In wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.), tillers develop from axillary meristems in the leaf axil. The number of vigorous tillers with spikes determines the overall grain yield. The overall objectives of this work are to understand the genetics of tillering in the Triticeae. In barley, we have characterized the low-tillering mutants *uniculm2* (*cul2*), *uniculm4* (*cul4*), *low number of tillers* (*lnt*), and *absent lower laterals* (*als*). We used histological approaches to examine the morphology of axillary meristems in the mutants. RNA profiling was used to identify candidate genes for the mutants and physiological processes that are unique to the mutants. Our double-mutant analysis indicates that at least two pathways are involved in tillering. We also identified and characterized a *suppressor of uniculm2* (*suc2*) mutant that, in combination with c*ul2*, exhibits tillering. In wheat, we developed transgenic wheat expressing the maize *teosinte branched1* (*tb1*) gene. These plants exhibit reduced tiller and spike number, an increase in the number of spikelets and leaves, and a reduction in height compared to wildtype control plants. These results demonstrate that overexpression of the maize *tb1* gene results in reduced tillering in wheat. Decreased tiller number in the transgenic wheat plants is due to the restriction of the outgrowth of the tiller buds. Increased expression of the *tb1* gene in maize, rice, and *Arabidopsis* also results in plants that exhibit reduced branching, indicating that increased expression of *tb1* is a general mechanism that plants use to repress branching.

Genetic regulation of developmental phases in winter wheat.

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The orderly development and growth of winter wheat through its life cycle can be dissected into several phases based on morphological, physiological, or agronomic traits. In the present study, the developmental process was characterized at three stages, initial internode length at stem elongation, heading date, and physiological maturity. These traits were mapped in a population of recombinant inbred lines (RILs) generated from a cross between two winter wheat cultivars, Jagger and 2174. The variation in the developmental process was found to be controlled by three major QTL, each tightly associated with a known flowering gene, *VRN-A1* on chromosome 5A, *PPD-D1* on chromosome 2D, and *VRN-D3* on chromosome 7D. On the basis of the average contributions of these candidate genes for QTL to the total phenotypic variation (R^2) over three years, *VRN-A1*, *PPD-D1*, and *VRN-D3* were found to have the most significant effect on stem elongation, heading date, and physiological maturity, respectively, and all of them also had durable effects on other developmental traits characterized at different stages. Whereas the Jagger *VRN-A1* and *VRN-D3* alleles promoted the developmental process, the Jagger *VRN-D1* allele delayed the developmental process due to its sensitivity to photoperiod. No direct interactions were found between these genes, but the combination of their alleles and effect durations determined various developmental phases in winter wheat.