

What we know about vernalization process in wheat

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A transition from vegetative to reproductive stage is a crucial step in the plant development. Some plants have to undergo a few weeks of cold treatment – vernalization. Bread wheat (*Triticum aestivum* L., $2n = 6x = 42$), is one of the most cultivated crops worldwide and occurs in two growth habits: a spring type and winter type. Winter wheat varieties are characteristic for their vernalization requirement for transition from vegetative to reproductive phase. To date, four genes controlling this process are known, denominated as *VRN1*, *VRN2*, *VRN3* and *VRN4*. An allelic variability in the *VRN-1* gene is associated with large differences in flowering time and thus fast adaptability of wheat to diverse locations. These changes are linked with variation at the DNA sequence level (rearrangements in the promoter region and the first intron) and also with copy number variation (CNV) of the genes. In addition, epigenetic modifications like DNA methylation and histone modifications are associated with the gene expression and triggering of flowering. We focused on the role Polycomb repressive complex 2 (PRC2) in vernalization process. Here, we describe individual components of these complexes in bread wheat for the first time. *In silico* identification of PRC1 and PRC2 subunits in hexaploid wheat was supported by gene expression data from RNAseq. Moreover, we are studying influence of different sequence motives of *VRN-1* gene and promoter to determine the most critical region for vernalization requirement. New molecular tools could contribute to better understanding of molecular mechanism of this important biological process.

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