

Anthocyanin pigmentation in wheat and barley: identification of genes controlling the trait and their allelic diversity

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Anthocyanins play important role in plant-environment interactions including protection of plant against stress. Due to convincing data on their health benefit, there is steady tendency to increase anthocyanin content in food. Particular attention in this aspect is paid to breeding new varieties of cereals with high anthocyanins content in grain that is not possible without knowledge of genetic control of its biosynthesis, diversity of the pigmentation patterns and sources of valuable genes. In wheat and barley, the pigments can be accumulated in pericarp and aleurone, imparting, respectively, purple and blue color to grain, as well as in vegetative parts of plant. Here we identified the full sets of genes encoding flavonoid biosynthesis MBW regulatory complexes that activate anthocyanin synthesis in tissue-specific fashion in wheat and barley. Using sets of near-isogenic lines differing by pigmentation we revealed features of anthocyanin biosynthesis regulation in the two related species. Although the metabolic pathway is universal, there are differences among species in regulation of structural genes encoding enzymes of the pathway. In addition, we noted that wheat and barley genotypes differ by the presence of pigmentation and its intensity that we assume to be caused by allelic diversity of regulatory genes. Studying accessions of different Triticeae tribe species from VIR collection, we found that dominant alleles of some genes determining anthocyanin pigmentation are widely distributed among the accessions investigated (eg. *TaCI* and *HvAnt1*, controlling red color of coleoptile and leaf sheath, respectively), whereas some of them are rare and have local origin (eg. *TaMyc1*, determining in conjunction with *TaCI* purple color of grain).

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