

***Ant13* encodes the WD40 regulatory factor controlling anthocyanin and proanthocyanidin synthesis in barley (*Hordeum vulgare* L.)**

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Proanthocyanidins (PAs) are polymeric flavonoid compounds that accumulate in the seed coat of barley grains. Despite the important role of PAs in seed dormancy, their absence in barley grain is a valuable agricultural trait. In particular, their ability to bind proteins negatively affect nutrient uptake and weight gain in poultry and cause colloidal haze in beer. Therefore, identification of recessive alleles of the genes that control synthesis of PAs in barley with the least effect on growth and development is an important task in breeding PA-free barley cultivars. Analyses of PAs in grains of two hundred varieties from the GenAgro collection (ICG SB RAS, Novosibirsk) did not reveal any PA-free cultivars. Hence, artificially induced barley mutants with lesion in anthocyanin and/or proanthocyanidin biosynthesis can be considered as the only source of recessive alleles of the PAs synthesis genes. Such collection, consisting of 766 individual mutants, is maintained at NordGen (Alnarp, Sweden). In the current study, molecular functions of the *Ant13* locus and its effect on plant growth and development were determined. Phenotyping of the mutants for *Ant13* locus confirmed that they do not contain PAs in the grains and anthocyanins in leaf sheaths. Further, they were characterized by similar germination rates compared to the parental cultivar Foma but had decreased rate of root and shoot growth. Co-localization of the *Ant13* locus, mapped to chromosome 6HL, with the gene that encodes for the WD40 protein suggested this gene as a candidate for *Ant13*. The gene was transcriptionally active in seedling roots, seedling shoots, leaves, and developing grains. Sequencing of the *WD40* gene in a set of allelic mutants *ant13.13*, *ant13.152*, *ant13.222*, *ant13.2010*, *ant13.2011* revealed single nucleotide nonsense and missense mutations in this gene disrupting the function of the WD40 protein. The data obtained showed that the gene has pleiotropic functions in flavonoid biosynthesis and plant development.

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