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A NEW ANTHOCYANIN REGULATORY C1 GENE IN DURUM WHEAT GENOME, AS POSSIBLE CANDIDATE FOR PP-B1

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Anthocyanins constitute the largest and probably the most important group of water-soluble natural pigments with health-promoting effects. In wheat grains, these compounds are mainly localized in different bran layers, conferring black, purple, blue or red tones.

Nowadays, the existence of genotypes with different grain colors represents a highly valuable source for adding health benefits to derived end-products. Due to the importance of these pigments, the genetic basis of their accumulation has been recently studied in wheat grains. Three main loci have been mapped on chromosomes of the homoeologous groups 2 and 7. The *Pp3* (*Purple pericarp 3*) homoeallele has been mapped to chromosome 2A both in bread (*T. aestivum* L., 2n = 6x = 42) and durum (*Triticum durum* Desf., 2n = 4x = 28) wheat, whereas another one has been positioned on chromosomes 7B (*Pp-B1*) and 7D (*Pp-D1*) in durum and bread wheat, respectively. In durum wheat, although these loci have been mapped through molecular markers, the causative genes are still unknown. To uncover this aspect, an F7:8 recombinant inbred line population (RIL) derived from two

durum wheat parents with different anthocyanin grain content was used for quantitative trait loci (QTL) mapping. A total of three major QTLs were identified on chromosomes 2A, 3A and 7B (LOD values ranged from 6- to 14) and explained the highest phenotypic variation (> 50%). Taking advantage of the reference genome of the cv. Svevo (v1.0) and the latest insights regarding the functional role of *Pp3* and *Pp1* in regulating the transcription of the anthocyanin biosynthesis genes, a *de-novo* annotation of a member belonging to the *MYB* subfamily, located on the short arm of chromosome 7B, is reported as possible candidate for *Pp-B1*. The *MYB* is highly similar to Anthocyanin Regulatory C1 proteins of different plant species; these latter are supposed to be responsible for the activation of anthocyanin biosynthesis genes. By investigating the promoter region of the candidate gene, significant differences were highlighted between the two RIL parents. Structural genes of the anthocyanin pathway such as *Dihydroflavonol-4-reductase* (*DFR*), *Cinnamoyl-CoA reductase* (*CCR*) and *Flavonoid-3-O-glucosyltransferase* (*UFGT*) were also identified within the major QTLs. Further studies are on-ongoing to functionally validate both the candidate *MYB* gene and the other structural genes involved in the accumulation of anthocyanins in grain pericarp. The expected results could open new opportunities for future genome editing approaches, including possible modifications in the promoter region.