

A GENE DUPLICATION AT THE BLP LOCUS IS ASSOCIATED WITH THE BLACK GRAIN PHENOTYPE IN BARLEY

GUERRA D.*, DELBONO S.*, MASCHER M.***, STEIN N.***, CATTIVELLI L.*, TONDELLI A.*

*) CREA, Centro di Ricerca Genomica e Bioinformatica, 29017 Fiorenzuola d'Arda, Italy

**) Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), 06466 Gatersleben, Germany

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Barley is the most important cereal crop in terms of ecological area occupied, therefore it represents a useful source of genetic diversity for adaptive traits. For instance, the black colour of barley grains, caused by the accumulation of melanin in the pericarp and husk cells, may have evolved because of environmental adaptation to abiotic and biotic stresses such as high UV radiation, high temperatures and fusarium head blight. By exploiting whole exome sequencing data from a collection of barley landraces of different origins, the black lemma and pericarp (*Blp*) locus responsible of the black grain phenotype was mapped at gene-resolution level on chromosome 1H and a gene coding for a Purple Acid Phosphatase (PAP) has been proposed as the best candidate for the trait. Mining exome reads for heterozygous calls and depth of coverage at the locus, a duplication of the *PAP* gene has been observed in black grain genotypes, suggesting a possible neofunctionalization, in agreement with the dominant inheritance of the locus. The *PAP* duplication was further confirmed by exploiting the recently released barley pan-genome and by developing paralog-specific genomic and expression assays. Moreover, a link between the black grain genotypes and their geographic origins in Ethiopian and Tibetan plateau has been noticed; accumulating more melanin in the grain might be considered an adaptive advantage in environments where UV incidence is higher. Other than representing a significant improvement on the genetic mapping of *Blp*, our study is a nice example on the integration of genetic and genomic resources for the identification of structural variants responsible of interesting phenotypes.