Proceedings of the LXIV SIGA Annual Congress Online, 14/16 September, 2021 ISBN: **978-88-944843-2-8**

Poster Communication Abstract - 1.39

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

barley, black lemma and pericarp, structural variation

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 for heterozygous calls and depth of coverage at the locus, a reads 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 be considered an adaptive advantage in environments where UV might 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.