

## **SPOROPHYTIC CONTROL OF MALE FERTILITY, THE ROLE OF THE SWEET4 GENE IN BARLEY**

MICHELOTTI V.\*, ROSSI R.\*, CROSATTI C.\*, MICA E.\*, GUERRA D.\*, COLOMBO M.\*, MASIERO S.\*\*\*, RADCHUK V.\*\*\*, CATTIVELLI L.\*, BATTAGLIA R.\*

\*) CREA-Research Centre for Genomics and Bioinformatics, Via San Protaso 302, 29017 Fiorenzuola d'Arda, Italy

\*\*) Department of Biosciences, University of Milan, Via Celoria 26, 20133 Milan, Italy

\*\*\*) Heterosis, Molecular Genetics, Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung Gatersleben, Germany

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A vital process for plant growth and differentiation is represented by sugar distribution. The long-distance movement of sugar occurs from source to sink tissues; afterwards, sugar is further distributed following extra-cellular and intra-cellular pathways. Sugars are translocated through symplastic and apoplastic routes, the latter needs the activity of specific transport proteins. The SWEET (Sugar Will Eventually Exported Protein) gene family is the most recent identified group of sugar transporters in 2010 (Chen et al.). The presence of this gene family was confirmed in all the eukaryotic kingdoms, and in prokaryotes. Eukaryotic SWEET proteins are characterized by seven predicted transmembrane (TM) domains forming a pore where sugars are predicted to move following their concentration gradient.

Focusing the attention on the barley genome, we have identified 23 SWEET sequences which contained the expected TM domains; *HvSWEET* genes can be further grouped into four clades, as already observed for this gene family in different Angiosperm genomes. It was proposed that belonging to a specific clade correlates with the selectivity toward monosaccharides versus disaccharides (Eom et al., 2015).

Our group is interested in identifying genes that can be manipulated to increase specific yield components. For this reason, we focused the attention on the *HvSWEET4* (*HvSW4*) gene whose maize and rice orthologous

play an important role during the seed filling process; both these genes appeared to be recruited during domestication to enhance the hexose import into the developing endosperm (Sosso et al., 2015). To highlight the functional role of the *HvSW4* gene, we created the *sw4* mutant through genome editing in the golden promise genetic background. Interestingly, our data indicate that, in barley, the *HvSW4* gene acquired a novel function related to the sporophytic control of male fertility. Morphological analysis of mutant flowers shows that early stages of pollen maturation are affected due to lack of activity of the *HvSW4* protein, while kernel development is not altered likely due to functional redundancy with other SWEET proteins and/or other sugar transporters. Further analyses are currently ongoing to better dissect the molecular pathways influenced by the *HvSW4* activity and to identify the transcriptional regulators.