

IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF KEY GENES INFLUENCING YIELD POTENTIAL IN BARLEY

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Food security is today one of the main urgencies that policy and science must ensure to the world population and plant scientists are involved in the identification of novel sustainable routes to boost crop yield. In this frame, we are working on the identification of key genes controlling fertility and kernel formation in barley, two factors that participate in the determination of yield potential. The movement of sugars from the source to the sink tissues impacts many aspects of plant growth. Studying the role of selected SWEET (Sugar Will Eventually be Exported Transporters) genes in barley we found that male fertility is linked to the activity of the HvSW4 gene. The development of the hvsw4 mutant through genome editing, together with its morphological and molecular characterization, allowed us to dissect specific aspects of anther and pollen formation. Furthermore, preliminary data indicate that the HvSW4 gene might play a role in shaping spike architecture influencing the number of lateral spikelets. Kernel development is a further step that determines yield potential. In particular, the trade-off between kernel size and kernel number represents a difficult obstacle to overcome. Focusing the attention on the functional role of selected miRNA genes we have identified two pathways that control kernel size and shape. Our data suggest that kernel size is controlled by the activity of the miR397a and miR396 genes that in turn negatively regulate the abundance of the LAC12 and GRF4 transcripts. Laccases (LACs) are multicopper-containing enzymes potentially involved in the polymerization of phenolic compounds like lignin. GRF4 (Growth Regulating Factor 4) is part of a transcription factor family involved in regulating cell cycle and organ shape. Strong evidences in rice suggest that GRF and

LAC genes are fundamental for final seed dimensions. Gene editing and over-expression of these genes represent the first step to better dissect the molecular pathways controlling seed size in barley. Taken together our data present different molecular pathways controlling fertility and kernel traits in barley, the functional characterization of key genes acting in these pathways put the basis for gene manipulation in the perspective of boosting yield potential in cereals.

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