

THE MIRNA397A/LACCASE REGULATORY MODULE CONTROL KERNEL SIZE AND SHAPE IN BARLEY

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Working on the functional role of selected miRNAs, we have initially identified the barley miR397a and demonstrated in vitro, through 5'RNA Ligase-Mediated RACE, and in vivo, through ectopic expression, that *HvLac12* is a major target of miR397a in barley. Beside a clear down-regulation of *Lac12*, the ectopic expression of miR397a led to an increased seed length suggesting that the miR397a-laccase module may represent a strategy to increase seed size. Laccases (LACs) are multicopper-containing enzymes potentially involved in the polymerization of phenolic compounds like lignin and evidence, in rice, suggest that *Lac* genes play a role in the determination of the final seed dimensions. We have therefore induced mutation in *HvLac12* to reproduce with genome editing the phenotype highlighted in the ectopic expression of of miR397a. Plant carrying knockout mutations in the second multicopper domain of *HvLac12* led to a novel phenotype associated to larger leaves, longer kernels and delayed flowering time.

Taken together our data suggest that miR397a controls kernel size, some development-related traits and, in turn negatively regulates the abundance of the *lac12* gene. The functional characterization of key genes acting in this pathway pave the way for gene manipulation in the perspective of boosting yield potential in cereals.

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