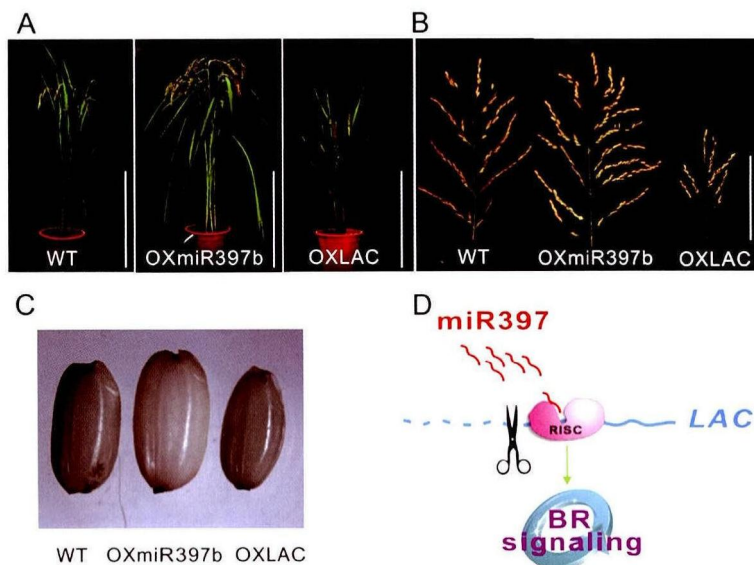


A microRNA-miR397 boosts rice grain yield



Rice yield is a complex trait that is directly associated with grain size, panicle number and the number of grains per panicle. Although several genes have been identified to regulate these traits, our knowledge of the molecular networks that control rice yield is still limited. Exploring new genes that modulate these traits would help us better understanding the relevant molecular mechanisms and would also facilitate the breeding of new varieties with increased yields. Funded by a key project of the National Natural Science Foundation of China and the Ph. D. Programs Foundation of Ministry of

Education of China, Professor Chen Yueqin from the School of Life Science, Sun Yat-sun University and her colleagues have found a microRNA, miR397, positively regulating rice grain yield, and the genetically modified rice plants with higher miR397 expression level could yield up to 25% more grains than normal rice plants (Figure A). This work has recently been published in *Nature Biotechnology* (2013, 31(9): 848- 852). This is the first report that an miRNA positively controls plant seed size and grain yield and the finding is of great importance for both theoretical research and potential applications.

MicroRNAs (miRNAs), a class of abundant small noncoding RNAs, have been identified as important regulators of gene expression in both plants and animals and are involved in many aspects of plant development and metabolism. The Prof. Chen's group has found that miR397, which is highly expressed in the young panicles and grains of rice, is associated with increased grain size, more rice panicle branching, and higher grain productivity (Figure B and C). As comments by F1000 and Nature China Highlights, this finding is interesting as it is the first time that the increased rice yield is shown to be achieved through the manipulation of a small non-coding RNA.

More importantly, the study revealed that miR397 increases grain yield through down-regulating the expression of OsLAC, a laccase-like protein. LACs belong to the polyphenol oxidase family with various spatial-temporal modes and functions, and are broadly accepted to participate in the metabolism of lignin. However, no report on the relationship between LACs and grain yield was available yet. The study unraveled the mechanism that miR397 directly down-regulates OsLAC and affects the brassinosteroids (BRs) sensitivity of rice plant, which in turn increases grain yield (Figure D). BRs are a class of polyhydroxysteroids that have been recognized as a sixth class of plant hormones, and reported to play an important role in regulating rice grain yield. The findings revealed a novel and important function of laccase family. As miR397 is highly conserved in different crops species, it also provides a new gene resource for increasing grain yield in other cereal crops.