IPA1 promotes high yield and resistance to rice blast disease

With supports from the National Natural Science Foundation of China, National Key Research and Development Program of China, and Program for New Century Excellent Talents in University from the Ministry of Education in China, the research team led by Prof. Chen XueWei (陈学伟) at the Rice Research Institute, Sichuan Agricultural University, and Prof. Li JiaYang (李家洋) at the State Key Laboratory of Plant Genomics and National Center for Plant Gene Research, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, uncovered that Ideal Plant Architeture1 (IPA1) could promote both yield and immunity in rice, which was published in *Science* (2018, 361: 1026—1028).

Activation of the plant immune response often penalizes yield. However, breeding practice has selected crop varieties with high yield and high resistance to diseases. Therefore, it is of great interest to explore the mechanism of the balance between yield and resistance. Although several reports have shown that some genes are involved in regulation of the balance between yield and immunity, no gene was reported to promote both of these two competing biological processes.

The SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (SPL) family transcription factor IPA1 (also known as SPL14) conditions an ideal plant architecture with reduced tiller number, increased panicle branch number and size, and enhanced lodging resistance. A genome-wide study on IPA1 binding sites revealed that IPA1 could target "GTAC" and "TGGGCC/G" motifs in rice plants. These findings were published in *Nature Genetics* (2010, 42: 541—544) and *Plant Cell* (2013, 25: 3743—3759).

In our study, rice plants carrying the *ipa*1-1*D* allele, which carries a mutation abolishing the inhibition by miR156 resulting in elevated amounts of IPA1 RNA and protein, produce yields >10% higher than wild type rice. Surprisingly, rice plants with increased expression of *IPA*1 show enhanced resistance to *M. oryzae*; furthermore, plants carrying the *ipa*1-1*D* allele enhance yield to an even higher extent compared to wild type when under blast disease pressure than under no blast pressure. Therefore, IPA1 promotes rice resistance to *M. oryzae* in addition to high yield. They built a model for IPA1 action on promotion of both yield and immunity based on our findings. In this model (Figure), the phosphorylation state of IPA1 is an important switch between growth for yield and immunity for disease resistance. Without *M. oryzae* infection, non-phosphorylated IPA1 targets the downstream genes with GTAC site to promote panicle development resulting in high yield. Upon pathogen attack, IPA1 rapidly becomes phosphorylated at Ser163. Phosphorylated IPA1 preferentially binds to the TGGGCC site in the *WRKY*45 promoter to promote expression of *WRKY*45 leading to enhanced disease resistance. More interestingly, IPA1 returns to the de-phosphorylated state within 48 hours post infection to sustain plant growth and development avoiding the yield penalty caused by constitutive phosphorylation of IPA1. This discovery clearly shows how one single protein, like IPA1, promotes two competing processes, such as yield and immunity, and provides new insights into the mechanisms underlying the balance between yield and immunity.

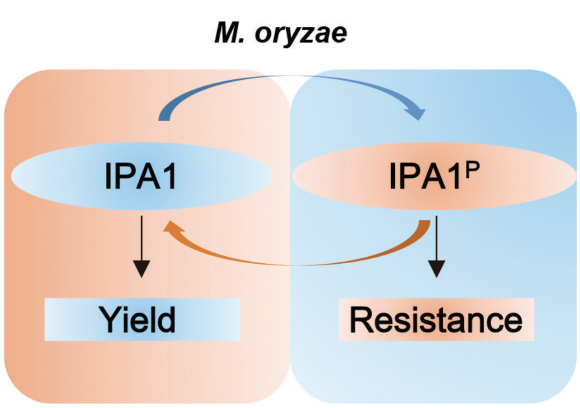

Figure A working model for IPA1 to promote both yield and disease resistance in rice.