Use of Yeast Two-hybrid to Dissect Kinase-mediated Signaling in Rice

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Identification of protein-protein interactions has proven to be valuable in understanding protein function. The rice genome is predicted to encode 1429 protein kinases, the majority of which have unknown function. We have developed a cost-effective yeast two-hybrid system using rolling circle amplification. By using this system, we have generated a protein interaction map for 140 representative rice kinases. The map contains 303 interactions among 250 proteins. The data provides a basis for further functional analysis of a large number of kinases and their interactors, and for deciphering kinase-mediated signaling networks in rice and other plant species.