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TEMASEK LIFESCIENCES LABORATORY

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The Auditorium (Level 1)

Hosted by: Dr YIN Zhongchao

Genome Editing for Host Resistance to Bacterial Blight of Rice

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Professor YANG Bing got his Bsc and MS from Southwest Forestry University, China and thereafter he went to Kansas State University to pursue his PhD studies and postdoctoral training. Currently, he is a Professor with University of Missouri, Columbia and his research focuses include the study of the development and utilization of genome editing technologies in rice and other crop plants including maize, wheat, sorghum, and soybean; and the study of host/bacterium interaction by using bacterial blight of rice as a model and engineering disease resistance.

Modified CRISPR (clustered regularly interspaced short palindromic repeats) systems, comprising single guide RNAs (sgRNAs) and Cas9 endonucleases, and TALENs (TAL effector nucleases) have emerged as potent biotechnological tools for both basic and applied research. The most promising utilization of both Cas9/sgRNA and TALENs is for targeted genome editing, precise genetic alterations within any genome of interest, as demonstrated in a plethora of organisms including several crop plants. My presentation describes development and application of these two technologies to generate heritable genome modifications in rice. TALENs and CRISPR/Cas9 were employed to generate stable, heritable mutations in TAL effector binding elements within the promoters of the three S genes targeted by multiple native TAL effectors of essential virulence of pathogen *Xanthomonas oryzae* pv. oryzae (Xoo). Xoo causes the devastating rice bacterial blight in Asia and Africa. The resulting promoter alterations in rice result in loss of inducibility of disease genes by the cognate TAL effectors and concomitantly loss of disease susceptibility (or gain of resistance) to pathogen. The TALEN gene constructs can be genetically segregated out in some modified plants. We also modified the Cas9/sgRNA system suitable for targeted gene mutagenesis in rice. Transgenic lines of T0 generation carrying site-specific mutations were produced at frequency as high as 100% in rice. The results demonstrate the feasibility of using genome editing tools for targeted genetic changes for crop improvement and also raise the prospect of producing genetically modified plants without a trace of “foreign” DNA left in the genome.

Recent Publications:

1. Shan S., Mavrodiev E. V., Li R., Zhang Z., Hauser B. A., Soltis P. S., Soltis D. E., and Yang B. (2018) Application of CRISPR/Cas9 to *Tragopogon* (Asteraceae), an evolutionary model for the study of polyploidy. **Molecular Ecology Resources**, in press.
2. Jungil Yang, Dangping Luo, Bing Yang, Wolf Frommer and Joon-Seob Eom 2018 SWEET11 and 15 as key players in seed filling in rice. ***New Phytologist***. 218(2):604-615.
3. Margaret Bezrutczyk, Thomas Hartwig, Marc Horshman, Si Nian Char, Jinliang Yang, Bing Yang, Wolf Frommer and Davide Sosso 2018 Impared phloem loading in zmsweet13a,b,c sucrose transporter triple knock-out mutants in *Zea mays*. ***New Phytologist***. 218(2):594-603.