Wang\_Li\_Abstract

Biotic stress session 2024 ISRFGC

Receptor-ligand interactions in the rice blast system revealed by AlphaFold protein structure prediction

**Li Wang****1**, Yulin Jia1, Aron Osakina1,2, Kenneth M. Olsen2, Yixiao Huang1, Melissa H. Jia1, Sathish Ponniah3, Rodrigo Pedrozo1, Camila Nicolli4, Jeremy D. Edwards1

1USDA ARS Dale Bumpers National Rice Research Center, Stuttgart, AR72160

2Washington University in St Louis, St Louis, MO 63130

3University of Arkansas at Pine Bluff, Pine Bluff, AR71601

4University of Arkansas Rice Research and Extension Center, Stuttgart, AR 72160

Email: Li.Wang@usda.gov

Rice blast, caused by the fungus *Magnaporthe oryzae*, is a significant threat to rice production worldwide. Over the years, numerous researchers have identified more than 100 resistance (*R*) genes that provide some level of defense against this disease. A key aspect of plant innate immunity involves the recognition of pathogen avirulence (*AVR*) gene products by products of corresponding resistance (*R*) genes, often following a gene-for-gene model. This makes it essential to identify the corresponding *AVR* genes to fully understand the mechanisms of resistance. However, for most identified *R* genes, their interacting *AVR* genes remain unknown, and traditional biological experiments to discover these *AVR* genes are time-consuming, labor-intensive, and challenging. In contrast, Artificial Intelligence (AI)-based approaches, like the recent advancements in protein structure prediction by AlphaFold, offer significant advantages in this area. In this study, we present our progress in using AlphaFold to predict interactions between *R* genes and *AVR* genes, potentially paving the way for more targeted and effective strategies in rice blast resistance breeding.