

Paper presented at the International Rice Congress 2023 from October 16-19 in Manila, Philippines.

## **The evolution and dispersal of bacterial blight pathogen in Asia**

Ian Quibod <sup>1</sup> , Hanna Nguyen <sup>1</sup> , Dale Pinili <sup>1</sup> , Genelou Atienza-Grande <sup>1</sup> , Ricardo Oliva <sup>2</sup> , Van Schepler-Luu <sup>1</sup>

*1 International Rice Research Institute. 2 World Vegetable center, Shanhua, Taiwan*

Agricultural ecosystems have played a key role in the evolutionary trajectories of plant pathogens. Rice-based environments have been a breeding ground of pathogen evolution, thus, it is imperative to understand the genetic diversity and evolutionary potential of the pathogen across different time points. In this study, we examined the diversification of bacteria by analyzing the genomes of *Xanthomonas oryzae* pv. *oryzae* (Xoo), the causal agent of rice bacterial blight, collected from various Asian countries. Our analysis revealed the existence of three primary lineages of Xoo, which can be further categorized into twelve distinct modern populations (AXoo1-AXoo12), each with its own unique genetic composition. Furthermore, we observed variations in the composition of TAL and non-TAL effectors in each population, which could potentially be linked to different host phenotypes. By employing Bayesian phylogenetic analysis, we were able to predict the possible migration and spread patterns of certain Xoo populations across different geographical regions in Asia. Among the populations, AXoo1 displayed the highest level of diversity and is considered the oldest population, exhibiting a greater proportion of genetic variation compared to other populations. Two populations, namely AXoo9 and AXoo12, showed high levels of recombination and are currently expanding their presence, leading to recent outbreaks in rice fields across Asia. Our findings highlight the effectiveness of a population genomic approach in predicting the evolutionary trajectory and dispersal patterns of bacterial pathogens affecting rice cultivation.

© By the International Rice Research Institute (IRRI) and is licensed for use under Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International (CC BY-NC-SA 4.0)