

## Population structure of *Xanthomonas oryzae* pv. *oryzae*: A problem and solution within itself to combat Bacterial Blight of Rice in Eastern India

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### Abstract:

The half of the global population depends upon rice as its major staple food. Its production is threatened by a number of biotic as well as abiotic stresses. Insect pests, rodents, diseases causing pathogens (fungi, bacteria, viruses, phytoplasmas) and nematodes are the main incitants of biotic stress, either singly or in combination. During Green Revolution, the traditional agricultural strategies were replaced by modern ones. As a result, the adoption of modern high yielding semi-dwarf rice varieties along with chemical fertilizers and pesticides came to limelight compromising the resistance gene pool of the landraces. Consequently, the emergence of previously minor and unreported diseases became evident. Bacterial blight (BB), which was earlier thought to have no significant damaging effect on the crop, emerged causing up to 50% yield loss. The disease attacks the crop at all growth stages, but the typical blight symptom starts from the active tillering stage while maximum yield loss occurs in the seedling stage due to Kresak. Many resistance varieties were developed by several research institutes as well as universities and deployed for conferring resistance to BB. But the changing agroclimatic conditions, injudicious nitrogenous fertilizer application and monoculture forced the directional evolution of new prominent races (pathotypes) of the phytopathogenic causal organism of BB, *Xanthomonas oryzae* pv. *oryzae* (Xoo). There are also many reports where the resistance gene(s) is defeated by the pathogen. Since paddy is grown over a large area in the field, host resistance is the cheapest and feasible strategy for management of the disease rather than application of synthetic pesticides, antibiotics and biocontrol agents. However, thorough understanding of the pathogen population structure is the pre-requisite for resistance breeding and to formulate proper management strategy. But the most critical aspect for the development of a resistant variety is the location specific deployment of resistance gene. For this purpose, in our present study, the isolates collected from several locations and varieties were screened against differentials hosts with different resistance gene(s) to determine their virulence profile. A set of differentials/NILs (Near Isogenic Lines) developed by IRRI, Philippines have been used for pathotyping analysis. On the basis of phenotypic manifestation of the disease reaction, the Xoo isolates were further categorized into pathotypes. Our study revealed 15 pathotypes from different samples collected across the Eastern India states.

**Keywords:** Rice, bacterial blight, *Xanthomonas oryzae* pv. *oryzae*, pathotypes, virulence