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**Impact of gene pyramids on *Xanthomonas oryzae* pv. *oryzae* population structures—
implications for deployment of *Xa* genes**

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Previous studies of resistance gene *Xa7* suggested that *Xa7* could impact on the fitness of strains of *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) adapted to rice lines containing *Xa7*. It is not known, however, how *Xa7* in combination with other *Xa* genes may affect pathogen fitness and population structure. We tested the performance of near-isogenic lines IRBB4, IRBB5, IRBB7, IRBB21 and pyramid lines IRBB61 (*Xa4+xa5+Xa7*), IRBB62 (*Xa4+Xa7+Xa21*), and IRBB64 (*Xa4+xa5+Xa7+Xa21*) for 3 years (2002-2004) at two sites in the Philippines where *Xa7* had been exposed to local pathogen populations for 7 years. We determined the genetic diversity and virulence spectrum of the *Xoo* populations from these lines. The majority of the populations belong to Lineage C (races 3C and 9a,b,c) while a very few strains of Lineage B (race 2) were detected. The pathogen populations from single gene NILs were genetically less diverse than those collected from pyramid lines. Interestingly, the *Xoo* populations collected from 3-gene pyramids with *Xa4+xa5+Xa21* and *Xa4+Xa7+Xa21* were more diverse than those from a 4-gene pyramid containing *Xa4+xa5+Xa7+Xa21*. In the 4-gene pyramid, haplotypes C7 and C12 representing a majority of race 9b dominated the population at both sites over 2 years. Race 9b showed a continuous variation in virulence to *Xa7*, ranging from moderately to highly virulent. Strains of race 9c were highly adaptive to *Xa7* but found in lower frequency relative to those strains of 9b, suggesting a fitness cost in race 9c associated with adaptation to *Xa7*. Since *Xa7* is present in both 3- and 4-gene pyramids, the different effects of the pyramids on pathogen diversity appear to result from interaction of the *Xa* gene combinations.

In breeding programs, the common practice has been to combine single genes that have been shown effective in a region. Knowing how the gene combinations affect pathogen population structures could have predictive value on the effectiveness of the resistance gene combinations prior to deployment. With markers, it is possible to create different gene combination efficiently. In collaboration with breeders at IRRI and national program partners in Asia, we have applied markers to develop gene combinations in conventional inbreds and new plant types, and in parents of hybrid rice. Some of these lines carrying either single, two or three-gene combinations in Indonesia, the Philippines, China, India and Korea have been released as varieties or used as donors while others are in the advanced lines of testing in their breeding program.