

Sources of genes for crop improvement by biotechnology. C. VERA CRUZ (1), G. Carrillo (1), K. Webb (1,2), I. Oña (1), S. Begum (1), P. Goodwin (3), J. Wu (1), L. Bin (1), N. Sugiyama (1), B. Jianfa (2), J. Leach (4), and H. Leung (1). (1) IRRI, DAPO Box 7777, Metro Manila Philippines; (2) Kansas State University, Manhattan, KS; (3) University of Guelph, Guelph, N1G 2W1, Canada; (4) Colorado State University, Fort Collins, CO. *Phytopathology* 95:S132. Publication no. P-2005-0082-SSA.

Disease resistance (R) genes from economically important crops have become available for biotechnologists. However, a large collection of genes for use in crop improvement that are demonstrated to clearly confer the desired phenotype is lacking. A few NBS-LRR genes conferring qualitative R and other defense response (DR) genes involved in quantitative R have been cloned and used in crops to achieve durable broad-spectrum resistance (DBSR). Although successful, some genes conferring qualitative R may not always be durable. We used rice-*Xanthomonas oryzae* pv. *oryzae* (*Xoo*) system to identify R genes predicted to be durable by understanding adaptation and evolution in the pathogen population. As *Xoo* evolved to overcome single genes, combinations of durable R genes have been employed to enhance the level of resistance to multiple pathogen races. To further enrich the sources of DR genes for crop improvement, we established and continue to build upon a collection of candidate genes that may account for DBSR against bacterial and fungal pathogens based on homology to genes known or suspected to play a role in defense using biochemical/physiological studies in rice and other plants, chromosomal position in relation to disease resistance QTL, altered gene expression under pathogen challenge, and altered phenotypes in mutant lines. We are validating functions of novel DBSR genes for use in biotechnology programs.

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