Bayesian Factorial Design as a Tool in the Identification of Rice Blast Resistance Sources

Mello, R.N.; Morais Júnior, O.P.; Abreu, A.G.; Borba, T.C.O.

Embrapa Arroz e Feijão, PO Box 179, Santo Antônio de Goiás, GO, 75375-000, Brazil. E-mail: raquel.mello@embrapa.br

Rice germplasm banks have many promising sources of resistance to pathogens. However, identification of resistant genotypes is often arduous, notably when the host-pathogen relationship is complex as in rice blast. In addition, selection of representative *Magnaporthe oryzae* isolates to adequately identify sources of broad-spectrum resistance is challenging. To overcome these obstacles, data from pathogenicity assays were analyzed as a factorial design, where the pairwise combination comprised rice genotypes and blast isolates. Using this methodology, we aimed to access information about host resistance. A set of 91 rice genotypes consisting of inbred lines and traditional varieties, from Brazil and abroad, adapted to irrigated and rainfed systems, was challenged by 40 *M. oryzae* isolates, collected from 12 distinct varieties in commercial fields in eight Brazilian States. Using a randomized block design with three replications, eight trials were performed in greenhouse, combining 45 genotypes (and the susceptible control BRS Primavera) with 10 isolates. Seeds were sown in peaty soil in plastic trays and plants were grown until the three leaf stage. For each genotype, 12 to 15 seeds were sown, representing the experimental unit. Seedlings were inoculated by spraying 5×10^3 conidia/ml water suspension. Inoculated plants were incubated in a humid chamber at 22-25°C for 48h then moved to an 80% humidity environment. Symptoms were scored seven days after inoculation, using the standard 0-9 rating scale. Due to the loss of experimental plots, final analysis was carried out with 83 genotypes and 33 isolates. To obtain the general reaction ability (GRA), reaction data were analyzed with joint analysis by a Bayesian factorial model. Both groups (genotypes and isolates) were considered as random effects. To adjust block and trial effects, the susceptible control BRS Primavera was evaluated in all trials. A previous theoretical simulation study showed that factorial design is an efficient methodology to assess host-pathogen interaction and identify resistant genotypes. The present study proved the method is suitable to identify promising sources of resistance. Thirty-one out of 83 rice genotypes displayed significant negative estimations for GRA, based on a 95% credible interval, implying on potential host resistance. The most resistant genotypes identified in this study were C79-272-4-1-2-3-10; BRS Biguá; and EMPASC 104. Several previous studies in both greenhouse and field conditions showed that in fact these genotypes displayed resistance against multiple isolates. Bayesian factorial design proved to be powerful to identify potential sources of resistance. Genome-wide association study (GWAS) is in progress in order to determine the genetic basis of these genotypes resistance and further use in breeding.

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ABSTRACTS