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Inheritance of Resistance to Brown Spot Disease in Upland Rice in Uganda

Abstract

Brown spot disease, caused by *Bipolaris oryzae*, is a biotic threat to rice production in Uganda. The disease is responsible for significant economic losses as it results in loss of both grain quality and yield. Cultural and chemical control measures have been used to reduce the severity of the disease and increase the growth and yield of rice, but breeding resistant varieties to brown spot is the most cost effective measure for disease management.

In this study, field trials and screen house experiments were conducted at the National Crops Resources Research Institute (NaCRRRI) – Namulonge, Uganda during 2013/2014 with the objective of identifying new sources of resistance to brown spot. A hundred germplasm were screened for brown spot disease resistance under rain-fed conditions in the field using an alpha lattice design and replicated twice. Plants were artificially inoculated with the disease pathogen and disease scored at 15, 30, 45 and 60 days after inoculation. The inheritance of resistance to brown spot disease was investigated through the nine-parent full diallel mating design. The F₁ progenies were advanced to F₂, and then F₂'s together with parents were evaluated against brown spot disease when the panicle had fully emerged. Second filial (F₂) generation progenies of specific crosses were also characterized for their segregation patterns.

There was significant variation for brown spot resistance among genotypes tested. Among the hundred tested rice lines, eighteen lines were rated as highly resistant, fifty one resistant, twenty seven as moderately resistant and four lines were susceptible. The effects of both general combining ability (GCA) and specific combining ability (SCA) were significant, indicating that both additive and non-additive effects respectively, were important in determining resistance to brown spot. The preponderance of GCA effects ($2\sigma^2_{gca} / (2\sigma^2_{gca} + \sigma^2_{sca}) = 0.29$) suggests that non-additive genetic effects were predominant compared to additive genetic effects. The broad sense coefficient of genetic determination (BS-CGD) was 0.83, indicating that most of the variability was genetically controlled. Narrow sense coefficient of genetic determination (NS-CGD) was low (0.24), indicating that non-additive effects were more influential than additive effects.

Reciprocal effects were significant, suggesting that cytoplasmic genes effects played a role in modifying brown spot resistance. Care should, thus be taken when selecting the female parents during hybridization, as it has been observed the maternal effects plays a role in conditioning the resistance. The segregation patterns within specific crosses suggested that brown spot resistance could be explained by the presence of one or two dominant genes.

The resistant lines thus identified may be brought forward and involved in a rice breeding program for the development of brown spot resistant lines. These results further suggest that a breeding program based on planned crossing would be effective for improving the resistance to brown spot in rice varieties adapted in Uganda.