Second RUFORUM Biennial Meeting 20 - 24 September 2010, Entebbe, Uganda

Research Application Summary

Inheritance of resistance to bacterial blight and implication for rice improvement in Uganda

Habarurema, I.[1], Asea, G.[2], Lamo, J.[2], Gibson, P.[1] & Edema, R.[1]
[1]Department of Crop Science, Faculty of Agriculture, Makerere University,
P. O. Box 7062 Kampala, Uganda
[2]National Crops Resources Research Institute (NaCRRI), P.O. Box 7084, Kampala, Uganda
Corresponding author: ihabarurema@yahoo.com

Abstract

Bacterial blight caused by *Xanthomonas oryzae* pv.*oryzae*, is a destructive disease of rice worldwide. Resistant varieties are the best option to avert the disease. Thirty resistance genes identified face a wide genetic diversity exhibited by the pathogen. Information on local isolates is not available and genetic mechanism for resistance harbored in Ugandan germplasm is unknown. Experimental sites were Makerere University and NaCRRI. Differential cultivars from Africa Rice were used to group Ugandan isolates. Seven parents were crossed into a half diallel to produce F_1 and F_2 progenies for determining the inheritance of resistance through inoculation. Preliminary results are reported.

Key words: Bacterial blight, inheritance, isolate, *Xanthomonas oryzae* pv. *oryzae*

Résumé

La brûlure bactérienne causée par *Xanthomonas oryzae pv.oryzae,* est une maladie destructrice du riz à l'échelle mondiale. Les variétés résistantes sont la meilleure option pour éviter la maladie. Trente gènes de résistance identifiés font face à une grande diversité génétique exposés par l'agent pathogène. L'information sur les micro-organismes locaux n'est pas disponible et le mécanisme génétique de résistance hébergé dans le matériel génétique ougandais est inconnu. Les sites expérimentaux ont été l'Université de Makerere et NaCRRI. Les différents cultivars de riz pour l'Afrique ont été utilisés pour les isolats du groupe ougandais. Sept plantes parents ont été croisées pour produire des descendants F1 et F2 pour la détermination de l'héritage de la résistance par inoculation. Les résultats préliminaires sont rapportés.

Mots clés: Brûlure bactérienne, l'héritage, isoler, *Xanthomonas oryzae pv. Oryzae*

Background

Bacterial leaf blight of rice, caused by *Xanthomonas oryzae* pv.*oryzae,* is one of the most devastating diseases of irrigated lowland and rainfed rice. It is widespread throughout several rice growing countries of Asia, Australia, America and Africa, contributing to substantial yield losses of up to 50%. Although cultural practices and chemical control have been attempted to avert the disease, the use of resistant cultivars has been proved to be more cost-effective, more sustainable and environmentally unfriendly approach affordable by rice growers. However, detailed information on pathogen diversity in Uganda is not available. Furthermore, the genetic mechanism for resistance carried by the germplasm assembled in Uganda is not yet elucidated. The current study seeks therefore to determine the nature of inheritance of resistance to bacterial blight in rice under pathogen races evolved in Ugandan environments to subsequently establish a better breeding strategy.

Literature Summary

The development of resistant cultivars is considered to be the best management option to control bacterial leaf blight in rice (Lee *et al*., 2002; Chu *et al*., 2006). Currently, twenty-one dominant and nine recessive genes resistant to bacterial blight have been identified (Chu *et al*., 2006; Niño-Liu *et al*., 2006). The resistance of rice to specific *X.oryzae* races is governed by both major and minor resistance genes. Moreover, given a high degree of genetic diversity of pathogen populations, over thirty races of isolates have been reported to have race-cultivar specificity (Niño-Liu *et al*., 2006). In this respect, breeding for resistance to bacterial blight with single resistance genes has often proved unsuccessful, as their long-term use results in the pathogen that ends up overcoming the resistance (Adhikari *et al*., 1994). Unfortunately, detailed information on Ugandan pathogen populations is not available. There is therefore a need to characterize the pathogen isolates based on pathogen-cultivar interactions that provides important information used to establish an appropriate breeding strategy (Adhikari *et al.*, 1999). The effective deployment of resistance genes in breeding programs requires also detailed information on the nature of inheritance of resistance genes. However, the genetic mechanism for resistance harbored in the germplasm assembled in Uganda is not well known, though prior studies conducted elsewhere concluded that the inheritance of resistance to bacterial blight in rice is generally controlled by single dominant or recessive genes (Gonzalez *et al.*, 2007; Lee *et al*., 2002), depending on the rice cultivars and pathogens races.

Study Description

Diseased rice seeds collected from rice growing areas in Eastern Uganda were used to obtain isolates. A single colony of each isolate was selected from peptone sucrose agar (PSA) medium and incubated at 28°C for 3 days at Biotechnology Laboratory of Makerere University. All of the isolates were inoculated to the susceptible rice cultivar IR24 to confirm their pathogenicity. Twenty differential and IR24 cultivars obtained from Africa Rice were used to characterize the virulence of *X. oryzae pv. oryzae* at National Crops Resources Research Institute (NaCRRI), Namulonge. Rice seedling of each line was planted in a nine-litre plastic bucket.

The inoculum was prepared by suspending the bacterial cells in 10 ml of sterile distilled water and adjusting by spectrophotometer to a concentration of 10^8 cells/ml. Top ten fully expanded leaves of each plant per pot were clip-inoculated with each isolate at the maximum tillering to booting stages. The experimental design was a split plot replicated twice with the rice line as main plot and the bacterial isolate as subplot.

Lesion length from the cut leaf tip was measured in centimeters (cm) 14 to 21 days after inoculation (DAI). To characterize virulence, resistance or susceptibility was assessed from the 10 inoculated leaves of each line per treatment. Disease reactions were categorized according to lesion length, where 0 to 5 cm was classified as resistant (R) and more than 5 cm as susceptible (S). The means of each treatment from the two replications were averaged to obtain the overall mean. Data on the lesion length of each cultivar-strain interaction were subjected to analysis of variance (ANOVA) using GenStat software package (GenStat, 2010). Means were separated by the least significant difference (LSD) at 5% probability level.

Furthermore, the experiments were conducted at NaCRRI-Namulonge on determining the nature of inheritance of resistance. Seven parents comprising five susceptible (IRAT 104, IRAT 216, CO 39, CT 16333(20)-CA-18-M and N-14) and two resistant (N-10 and N-4) rice varieties were crossed into a half diallel mating design to produce F_1 and F_2 progenies. The parents, F_1 and F_2 populations were challenged with the most virulent isolates and scored on a Standard Evaluation System (SES) scale. Chi-square (χ^2) test were used to compare observed R: S ratios of the F_2's to those expected from different numbers of gene and types of dominance and epistasis.

Research Application

Required germplasm comprising parental and differential lines has been assembled in Uganda. An appraisal of bacterial blight prevalence in various rice growing parts of Uganda has been performed. Bacterial leaf blight isolates have been acquired and are being stored for routine use in screening planting materials. F_1 hybrid seeds have been obtained and are being planted to produce F_2's segregating populations.

Recommendation

The disease had not been reported in Uganda before this study was undertaken. The preliminary results show that the rice bacterial blight really exists in the country. Therefore, further studies are needed to sustainably tackle the disease.

Acknowledgement

I thank the Alliance for Green Revolution in Africa (AGRA) for financial and material contributions to this study. Additional support was provided by the Regional Universities Forum for Capacity Building in Agriculture (RUFORUM), which also organized the presentation of this work in its Biennial Conference. I am very grateful to different roles played by Makerere University and National Crops Resources Research Institute (NaCRRI) staffs, especially Dr. Paul Gibson and his wife Pauline, Dr. Richard Edema, Dr. Jimmy Lamo and Dr. Godfrey Asea for facilitating and guiding this work. Africa Rice is gratefully acknowledged for supplying the seeds of differential cultivars. Many thanks go to the Institut des Sciences Agronomiques du Rwanda (ISAR) that allowed me to pursue the studies.

References

Adhikari, T.B., Mew, T.W. and Teng, P.S.1994. Phenotypic diversity of *Xanthomonas oryzae* pv. *oryzae* in Nepal. International Rice Research Institute (IRRI). Division of Plant Pathology, Manila. The Philippines. *Plant Disease* 8: 68-72.

Adhikari, T. B., Basnyat, R. C. and Mew, T. W. 1999. Virulence of *Xanthomonas oryzae* pv. *oryzae* on rice lines containing single resistance genes and gene combinations. *Plant Disease* 83:46-50.

Chu, Z., Fu, B., Yang, H., Li, C.X. Z., Sanchez, A., Park, Y. J., Zhang, J. L. B.Q. and Wang, S. 2006. Targeting Xa13, a recessive gene for bacterial blight resistance in rice. *Theoretical and Applied Genetics. Springer-Verlag 2005* 112:455-461.

Gonzalez, C., Szurek, B., Manceau, C., Mathieu T., Séré Y., and Verdier, V. 2007. Molecular and pathotypic characterization of new *Xanthomonas oryzae* strains from

West Africa. *The American Phytopathological Society* 20(5):534-546.

Lee, K. S., Rasabandith, S., Angeles, E. R., and Khush, G. S. 2002. Inheritance of resistance to bacterial blight in 21 cultivars of rice. International Rice Research Institute, Manila, Philippines.

Niño-Liu,O.D., Ronald, P.C. and Bogdanove, A.J. 2006. Xanthomonas oryzae pathovars: Model pathogens of a model crop. Pathogen profile. *Molecular Plant Pathology* 7(5):303-324.