Research Application Summary

Genetics of resistance to bacterial leaf blight in rice germplasm in Uganda

Mudingotto, P.J.[1], Tusiime, G.[1], Asea, G.[2], Rubaihayo, P.R.[1], Gibson, P.[1], Tumutegyereize, J.[1]
& Lamo, J.[2]
[1]Department of Crop Science, Makerere University, P. O. Box 7062, Kampala, Uganda
[2]National Crops Resources Research Institute, P. O. Box 7084, Kampala, Uganda
Corresponding author: mudpyani@hotmail.com

Abstract

Bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae* is one of the most serious diseases of rice worldwide. The disease causes significant losses mostly in lowland rice. This study is investigating the mode of gene action of resistance to BLB using generation mean analysis. Crosses are being done between the susceptible lines (Supa) and three resistant NILs (Nerica 1, 4 and 10) upland rice. The plants will be infected artificially using a clipping inoculation technique. Severity of bacterial leaf blight on plants will be classified basing on the length of the blighted portion of the leaves using a score chart of 1 - 9. Genetic models will be used to determine whether inheritance to BLB resistance is due to dominance, additive and/or epistatic gene interactions.

Key words: Additive effect, bacterial leaf blight, dominance effect, epistasis, heritability, rice

Résumé

La rouille bactérienne de feuille (BLB) provoquée par *Xanthomonas oryzae* pv. *oryzae* est l'une des maladies les plus sérieuses du riz dans le monde entier. La maladie cause des pertes significatives souvent dans le riz de plaine. Cette recherche étudie le mode d'action de gène de résistance à la rouille bactérienne de feuille BLB en utilisant l'analyse moyenne de génération. Des croix sont faites entre les lignées sensibles (Supa) et trois espèces de riz de montagne résistant au NILs (Nerica 1, 4 et 10). Les plantes seront infectées artificiellement en utilisant une technique d'inoculation de coupure. La sévérité de la rouille bactérienne de feuille sur des plantes sera classifiée en se basant sur la longueur de la partie enrouillée des feuilles en utilisant un diagramme de points de 1 - 9. Des modèles génétiques seront employés pour déterminer si la transmission à la résistance de BLB est due aux interactions de dominance, additives et/ou épistatiques de gène.

Mots clés: Effet additif, rouille bactérienne de feuille, effet de dominance, épistasie, héritabilité, riz

Background

Rice (*Oryza sativa* L.) is one of the major staple food crops worldwide. In Uganda, it has gained importance and is one of the popular cereals widely grown in the country. Both lowland and upland rice are grown and there has been tremendous increase in production from 123,000 MT in 2003 to 160, 000 MT in 2007 (MAAIF, 2009). Despite the importance of the crop in Uganda, its production is still below its potential mainly because of diseases. Bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae* is believed to be one of the major diseases causing high yield losses in rice. The disease has been reported in rice growing fields at Tilda-Kibimba rice scheme in Uganda (Gnanavel, pers. comm.). Recently, yellow bacteria that resemble the BLB organism have been isolated from rice seeds from eastern Uganda (Mudingotto and Mortensen, unpublished). However, limited information is available on the incidence, distribution and race diversity of BLB in Uganda.

The disease is difficult to control but a number of interventions can be employed to manage and contain it such as cultural and chemical control methods. However, some of these control measures such as the use of chemicals is costly. Therefore, the long term solution to the problem is to deploy resistant cultivars. Borines (2003) reported that the use of resistant cultivars has been the most effective and economical way of controlling bacterial leaf blight. A study is being conducted with the overall objective of developing resistant rice genotypes against BLB in Uganda.

Literature Summary

Bacterial leaf light (BLB) caused *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one the most serious diseases of rice worldwide (Agarwal *et al*., 1989; Ri *et Al.*, 2003; Chu *et al*., 2006; Niño-Liu *et al*., 2006; Swamy *et al*., 2006). The disease is widely distributed in Asia, and has been reported in Australia, Latin America, Caribbean region, North America and Malaysia. In Africa BLB has been reported mostly in West African countries of Mali, Niger and Senegal (Gonzalez *et al*., 2007). Grain yield losses due to BLB range from 10% to 60% depending on variety, severity of infection, season, and time of infection. In highly susceptible varieties, a yield loss of up to 80% is common (Lee and Khush, 2003).

Study Description

Four *(Oryza sativa)* cultivars including one susceptible landrace (Supa) from farmers and three improved and resistant varieties (Nerica 1, Nerica 4 and Nerica 10) are being used in the on-

going study. The experiments involve six generations: P_1 (susceptible parent- Supa), P_2 (resistant parent), F_1 and F_2 and backcrosses of F_1 to both parents. These generations will be planted in a randomised complete block design with four replications at the National Crops Resourses Research Institute, Namulonge in Central Uganda. This is the main research centre for rice in Uganda. In developing backcross populations parents of the respective crosses will be used as male parents and F_1 generation as the female parents. The row length will be three meters but the number of rows will vary as follows: three rows, for the non-segregating P_1, P_2, and F_1; 40 rows for F_2; and 20 rows for the BC_1 and BC_2 generations. Since the non-segregating generations represent the homogeneous population while the segregating generations represent the heterogeneous population, the sample size (i.e., the number of plants to analyze) will vary as follows: 30 plants for P_1, P_2 and F_1 generations; 400 plants for the F_2 generations; and 200 plants in the BC_1 and BC_2 generations. The traits to assess will be resistance to disease basing on the lesion length of bacterial leaf blight symptoms two weeks after inoculation of the plants. The plants will be inoculated at maximum tillering by clipping with a pair of scissors after dipping in the bacterial suspension.

The score of disease reaction on individual plants from each of the generation will be used to calculate the generation means and variances. These means and variances will be subjected to Mather's Scaling Test (Mather and Jinks, 1982), to determine the adequancy of an additive- dominant model and to test for epistasis. The level of significance for each of the scaling test will be determined by the t- values. For analysis of data, models in Genstat for generation mean analysis to determine the inheritance of resistance to BLB will be used. The first regression model (Model 1) consists of 3-parameter mean (m), additive (a) and dominance (d). The second model (Model 2) consists of the epistatic effects, [aa], [ad], [dd] in addition to the parameters in Model 1. Model 2 will be used only if a significant additive or dominant effect is detected and to determine if significant epistatic effects exist that are contributing to the significance in Model 1.

Research Application

After evaluation of 23 supas cultivars collected from farmers in Eastern Region of Uganda, one cultivar was selected basing on early maturity to be used as a susceptible parent (P1). The P1 was crossed with the 3 Nericas (resistant lines), and F_1

seed generated. The F_1 seed has been planted to raise F_2, and backcross to both parents. The study is still on-going.

Acknowledgement

References

Agarwal, P.C., Mortensen, C.N. and Mathur, S.B. 1989. Seed-borne diseases and seed health testing of rice. *CAB International Mycological Institute. Technical Bulletin* No.3. 106pp.

Borines, L., Redona, E., Porter, B., White, F., Vera Cruz, C., and Leung, H. 2003. Molecular markers for detecting bacterial blight resistance genes in maintainer lines of rice hybrids. Advances in Rice Genetics. Khush, G.S., Brar, D.S. and Hardy, B. (Eds.). IRRI. pp. 245 - 247.

Chu, Z., Fu, B., Yang, H., Xu, C., Li, Z., Sanchez, A., Park, Y.J., Zhang, J.L. and Wang, S. 2006. Targeting xa13, a recessive gene for bacterial blight resistance in rice. *Theor. Appl. Genet*. 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. *Molecular Plant-Microbe Interactions* 20 (5):534 - 546.

Lee, K.S. and Khush, G.S. 2003. Genetic analysis of resistance to bacterial blight in rice. In: Advances in Rice Genetics. Khush, G.S., Brar, D.S. and Hardy, B. (Eds.). IRRI. pp. 46 - 49.

MAAIF (Ministry of Agriculture Animal Industry and Fisheries), 2009. Uganda National Rice Development Strategy 2009 - 2018. MAAIF, Republic of Uganda.

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

Swamy, P., Panchbhai, A.N., Dodiya, P., Naik, V., Panchbhai, S.D., Zehr, U.B., Azhakanandam, K. and Char, B.R. 2006. Evaluation of bacterial blight resistance in rice lines carrying multiple resistance genes and *Xa21* transgenic lines. *Current Science* 90(6):818 - 824.