Research Application Summary

Introgressing resistance to *Fusarium* root rot in selected farmer preferred Andean bean genotypes from Meso-American line and mapping of associated resistance quantitative trait loci

Kamfwa, K.[1], Okori, P.[2], Mwala, M.[1] & Mukankusi, C.[3]
[1]School of Agricultural Sciences, University of Zambia, P. O. Box 32379, Lusaka, Zambia
[2]Faculty of Agriculture, Makerere University, P. O. Box 7062, Kampala, Uganda
[3]Central internacional de Agricultura Tropical (CIAT), P. O. Box 6247, Kampala, Uganda
Corresponding author: kelvinkamfwa@yahoo.co.uk

Abstract

Two populations of beans *(Phaseolus vulgaris)* from K20 x MLB-49-89A and K132 x MLB-49-89A were assessed for resistance to *Fusarium solani f.sp. phaseoli*. Additionally, 35 SSR markers were screened for polymorphisism in the parents. The results showed that improvement of Andean varieties for resistance to *Fusarium* root rot was possible using American line MLB-49-89A. The SSR study identified a major QTL for resistance to *Fusarium solani f.sp. phaseoli.*

Key words: *Fusarium solani f.sp. phaseoli*, MLB-49-89A, *Phaseolus vulgaris,* QTL

Résumé

Deux populations des haricots *(Phaseolus vulgaris)* de K20 x MLB-49-89A et K132 x MLB-49-89A ont été évaluées pour la résistance à *Fusarium solani f.sp. phaseoli*. En plus, 35 marqueurs de SSR ont été examinés pour le polymorphisme dans les parents. Les résultats ont prouvé que l'amélioration des variétés andines pour la résistance à la putréfaction de racine de *Fusarium* était possible en utilisant la Ligne Américaine MLB-49-89A. L'étude de SSR a identifié un QTL important pour la résistance à *Fusarium solani f.sp. phaseoli*.

Mots clés: *Fusarium solani f.sp. phaseoli*, MLB-49-89A, *Phaseolus vulgaris,* QTL

Background

The common bean (*Phaseolus vulgaris* L.) is a major protein source in the diet of many low-income populations worldwide. Its production is however constrained by root rots. Bean root rots have been reported to occur in most bean fields throughout the world. In Uganda, bean root rot caused by *Fusarium solani* is one of the major constraints to bean production. The use of resistant varieties is probably the most effective control measure against *Fusarium* root rot, especially for small-scale farmers with limited access to fungicides (Abawi *et al*., 2006). Sources

of resistance to *Fusarium* root rot exist in common beans, including in Africa. Most of the developed and identified resistant genotypes are either late-maturing and small or black-seeded, with a climbing growth habit. None of the commercial Andean bean varieties currently grown in Uganda is resistant to this pathogen. Genetic resistance to *Fusarium* root rot is polygenic and is strongly influenced by environmental factors (Román-Avilés and Kelly, 2005). Response to selection for quantitative traits, such as root rot resistance, is slow due to the genetic complexity of the trait and the difficulty in evaluating resistance. Indirect selection for *Fusarium* root rot resistance based on genetic markers linked to the quantitative trait loci (QTL) for resistance would facilitate speedy improvement, given the limitations of field selection, which is expensive, not consistent across environments and requires destructive sampling. The overall objective of this study was to develop approaches based on quantitative trait loci for improving resistance in common beans to *Fusarium* root rot. The specific objectives were: (i) to confirm the usefulness of a Meso-american source (MLB 49-89A) in transferring resistance to *Fusarium solani* f.sp. *phaseoli* into locally adapted Andean types (K20 and K132); and (ii) to identify quantitative trait loci that condition resistance to *Fusarium* root rot in common beans.

Study Description

Two populations of 90 and 78 $F_{4:5}$ recombinant lines from K20 x MLB-49-89A and K132 x MLB-49-89A respectively, were used to confirm the usefulness of MLB 49-89A in transferring resistance to *Fusarium* root rot into locally adapted Andean types (K20 and K132). Both K20 and K132 are susceptible to *Fusarium* root rot, while MLB-49-89A is resistant. The two populations and their parents were evaluated for resistance to *Fusarium* root rot in a screen house. In addition, a mapping study for resistance locus was conducted.

Research Application

The K20 x MLB-49-89A population was skewed toward resistance while K132 x MLB-49-89A was skewed toward susceptibility. These results show differences in parental effects of K20 and K132 on the resistance to *Fusarium* root rot. Such differences suggest that K20 possesses one or more genes that interact in an epistatic manner with two or more resistance loci in MLB-49-89A. In contrast, K132 probably lacks the beneficial allele that is present in K20, or has an alternate allele that enhances susceptibility. The frequency distributions for both populations were bimodal, suggesting that a major gene was involved in resistance. A number of lines that had very good

resistance levels to *Fusarium* root rot were identified from both populations. Both the narrow and broad sense heritabilities obtained for K132 x MLB-48-89A in this study were very high (h^2_B=0.99; h^2_N=0.98). Heritability estimates in K20 x MLB-48-89A population were also high (h^2_B=0.86; h^2_N=0.81). The heritability estimates obtained in this study and in previous studies by Mukankusi (2007) indicate that improvement of the Andean varieties for resistance to *Fusarium* root rot using the Meso-american line MLB-49-89A should be possible.

For the mapping study a total of 35 SSR markers were screened for polymorphism in the parents. Fifteen of the 35 SSR markers were polymorphic, representing 42% of the tested SSR markers. Twelve of the SSR markers gave clearly distinguishable bands and were therefore used for analysis. A mapping population of 62 $F_{4:5}$ recombinant inbred lines of K132 x MLB 49-89A was used for identifying quantitative trait loci conditioning resistance to *Fusarium* root. Using single marker analysis, two SSR markers that were closely linked to each other (PVBR87 and PVBR109) were significantly associated with *Fusarium* root scores (p<0.0001) in K132 x MLB-49-89A population. Another SSR marker, PVBR255, showed significant effects on *Fusarium* root rot scores, but at a reduced significance level (p<0.05). The other nine SSR markers showed no significant effects. Composite interval mapping detected a major QTL in K132 x MLB-49-89A population between PVBR87 and PVBR109 with a LOD score of 6.1 and coefficient of determination (R^2) of 34% and did not assign independent significance to the distantly-liked marker, PVBR255. Therefore, only one QTL was detected in the present study, but it is a major QTL, as indicated by the large R^2. The two markers associated with the QTL (PVBR87 and PVBR109) are found on linkage group B3 of the common bean core map, close to the region where resistance to root rots, anthracnose, common bacterial blight and bacterial brown spot have been previously mapped. Only four SSRs (PVBR87, PVBR109, BM156 and BM172) were used in the K20 x MLB 49-89A population because of resource constraints. PVBR87 and PVBR109 that were significantly associated with *Fusarium* root rot resistance in K132 x MLB-49-89A population, also showed significant associations ($R^2 = 14\%$, $P < 0.001$) in the K20 x MLB-49-89A population. This is a confirmation of the presence of a QTL identified on linkage group B3 close to these two markers in the K132 x MLB-49-89A population. The

association of this major QTL with resistance in both populations suggests that this QTL may be useful more broadly.

This study has shown that it would be easier to improve K20 than K132 for *Fusarium* root rot resistance when using MLB-49-89A as a source of resistance. Also, the detection of a major QTL for resistance to *Fusarium* in this study provides good prospects for using QTL—based approaches to introgress resistance to *Fusarium* root rot from Meso-american genotypes into locally adapted Andean bean genotypes.

Recommendations

There is need to determine whether this QTL is also present in different sources of resistance and whether the two associated SSR markers are useable for marker-assisted selection in a wider range of materials. Fine-resolution mapping should also be done to establish whether the QTL identified in this study is indeed a single QTL.

Acknowledgement

References

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