

Research Application Summary

Prevalence of bean anthracnose in Zambia and diversity of *Colletotrichum lindemuthianum* in Southern Africa

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Abstract

Prevalence of bean anthracnose, caused by *Colletotrichum lindemuthianum* was assessed in four agro-ecologies in Zambia. Subsequently, fungal isolates were tested for race specifically involving race differentials and DNA analysis using Simple Sequence Repeats (SSRs) and Random Amplified Microsatellites (RMMs). The disease was highly prevalent and severe in the wetter agro-ecology of Kasama and 17 pathotypes were found.

Key words: *Colletotrichum lindemuthianum*, *Phaseolus vulgaris*, Southern Africa, Zambia

Résumé

La prédominance de l'antracnose de haricot, provoquée par *Colletotrichum lindemuthianum* a été évaluée dans quatre zones agro-écologiques en Zambie. Plus tard, des isolés champignons ont été examinés pour la race impliquant spécifiquement des différences de race et l'analyse d'ADN en utilisant des répétitions d'ordre simples (SSRs) et des Microsatellites amplifiés aléatoires (RMMs). La maladie était fortement répandue et grave dans la zone agro-écologique plus humide de Kasama et 17 pathotypes ont été trouvés.

Mots clés: *Colletotrichum lindemuthianum*, *Phaseolus vulgaris*, Afrique australe, Zambie

Background

Phaseolus bean is a major staple food in the Southern African region where it is the second most important source of dietary protein and the third most important source of calories. It is a relatively cheap protein source, especially for resource constrained households in sub-Saharan Africa. However, full realisation of its benefits is hindered by many biotic and abiotic constraints, especially anthracnose disease caused by the fungus *Colletotrichum lindemuthianum*. This pathogen can cause total yield loss, if not controlled (Pastor-Corrales, 2005). At least ten resistance genes from the standard set of CIAT differential cultivars (Kelly and Vallejo, 2004) are being deployed in various

combinations to manage the pathogen. To do this effectively requires knowledge of the incidence and severity of the disease as well as the population structure and variability of the pathogen in the target locality. This information is largely lacking in Zambia and most of Southern Africa. Therefore this study assessed incidence and severity of anthracnose in Zambia and variability of *C. lindemuthianum* in Southern Africa.

Literature Summary

Bean anthracnose is one of the major bean production constraints in Southern Africa (SABRN, 2005) and many tropical regions of the world (Pastor-Corales, 2005). Various methods have been used to manage the disease but the use of host resistance remains the most efficient and environmentally friendly approach (Gonçalves-Vidigal *et al.*, 2007). However, effective use of host resistance in disease management depends on a clear understanding of the pathogen-host interaction. This partly requires establishing the diversity that exists in the pathogen population. This diversity is best measured by use of DNA analysis and response of the pathogen population on a set of resistance genes (Mc Donald, 1997; Okori *et al.*, 2004). The variability existing in a population aids in establishing the potential of the pathogen to evolve as well as in the choice of resistance genes to deploy.

Study Description

Bean anthracnose disease samples were collected from four districts (Kasama, Mbala, Solwezi and Kabwe), representing the main bean-growing areas of Zambia. A hierarchical strategy was used during sampling from each agro-ecology, districts within agro-ecologies and fields within each district. Incidence and severity were scored for each sampled field. Disease samples were similarly collected from Malawi, Southern Tanzania and South Africa. Incidence and severity data were subjected to analysis of variance using GENSTAT (Payne, 2007 or Lawes, for Discovery). DNA analysis was done using Simple Sequence Repeats (SSRs) and Random Amplified Microsatellites (RAMs). Analysis of molecular variation and phenetic analysis were done using Arlequin (ver 2.000) and Treecon (ver 1.3b) software, respectively. Additionally, 20 isolates were tested against the standard set of CIAT anthracnose race differentials.

Findings

Incidence and severity of anthracnose were highest in the cool, humid and high rainfall regions of Kasama, followed by Mansa and Solwezi, with the low rainfall region (Kabwe) having the least. Analysis of molecular variance (AMOVA) revealed high

levels of genetic variation ($F_{ST} = 0.29$), indicating that *C. lindemuthianum* was very diverse in Southern Africa and thus had a high potential to evolve and overcome resistance genes (MC Donald and Linde, 2002). Genetic differentiation ($F_{ST} = 0.20$) was evident between isolates from different locations. Phenetic analysis separated isolates into groups that were geographically defined. This suggests presence of local populations. Out of the 20 isolates tested 17 pathotypes were realised, revealing high levels of physiological diversity. This indicated presence of new and more virulent strains than was previously reported in Zambia (Zulu, 2005). Differential cultivars PI 207262 and Tu each succumbed to only one isolate. These cultivars carry resistance genes *Co 4³* and *Co 9* (PI 207262) and *Co 5* (Tu) (Kelly and Vallejo, 2004), suggesting that pyramiding these genes could be important in the management of bean anthracnose in Southern Africa.

Research Application

The results of this study indicate that wet and humid areas of Zambia have high potential for anthracnose epidemics, and should thus be targets for resistance breeding efforts. Due to the high diversity of *C. lindemuthianum* in Southern Africa, resistance breeding should target pyramiding major resistance genes. More specifically, the combined deployment of resistance genes *Co 4³* and *Co 9* and *Co 5* could provide a genotype that would offer resistance to a wide range of pathotypes.

Recommendations

There should be continued monitoring of *C. lindemuthianum* populations particularly in the cool humid high rainfall regions of Zambia due to the pathogen's high potential to evolve. Pyramiding of resistance genes *Co 4³*, *Co 9* and *Co 5* should be carried out.

Acknowledgement

This research was funded by The Regional Universities Forum for Capacity Building in Agriculture (RUFORUM) and hosted by Makerere University. We also thank Uyole Agricultural Research Institute (Tanzania), Chitedze Research Station-Lilongwe, (Malawi), Grain Crop Institute (South Africa) and University of Zambia for their collaboration.

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