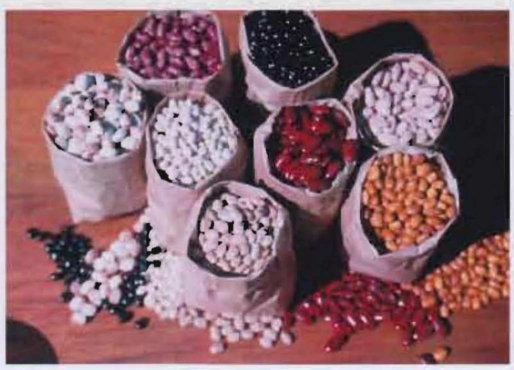
University of Hohenheim

Institute of Plant Physiology and Biotechnology

Prof. Dr. Andreas Schaller

Characterization of pathogenic variation in *Colletotrichum lindemuthianum*, the causal organism of anthracnose of common bean (*Phaseolus vulgaris* L.) in South Africa, resistance screening of local germplasm, and evaluation of existing molecular markers



Diploma thesis submitted by

Peter Muth

Faculty of Natural Sciences

Supervised by Dr. Merion M. Liebenberg, ARC GCI

Hohenheim, October 2008

This work was financially supported by the Eiselen Foundation Ulm

Submitted for publication in the Annual Report of the Bean Improvement Cooperative 2009, Vol. 52, on 6th March 2009. http://www.css.msu.edu/bic/Reports.cfm

Resistance of dry bean to South African races of *Colletotrichum lindemuthianum*

Peter Muth[1] and Merion M. Liebenberg[2]
[1]Institut für Physiologie und Biotechnologie der Pflanzen, Universität Hohenheim, 70593 Stuttgart, Germany.
pierrecourage@gmx.de
[2]ARC-Grain Crops Institute, Private Bag X 1251, Potchefstroom 2520, South Africa

INTRODUCTION

Anthracnose, caused by the fungus *Colletotrichum lindemuthianum*, is an important disease of the common bean in South Africa. Although the disease is well controlled by an efficient disease-free seed scheme, many subsistence and small-scale farmers, as well as some commercial farmers, keep back some of their own crop as seed for the next season. Infected seed gives rise to infected seedlings, and the disease can be particularly aggressive under cool, wet conditions, causing serious yield and quality losses. Popular local cultivars are all susceptible to at least one race, and some are highly susceptible to several races. The aim of the present study was to update the knowledge of local races of the pathogen and to identify suitable sources of resistance as donor parents for a directed resistance breeding programme.

MATERIALS AND METHODS

Diseased material was collected from main production areas in South Africa and 13 single-conidium isolates were made. These were spray-inoculated on the international set of 12 differential bean lines (Michelite, Michigan DRK, Perry Marrow, Cornell 49242, Widusa, Kaboon, Mexico 222, PI 207262, TO, TU and AB 136) with a concentration of $1.2 \cdot 10^6$ conidia·ml^{-1}. Disease severity rating was done seven days after inoculation (which included four days incubation in a dew chamber) using the standard 1 to 9 scale (Van Schoonhoven and Pastor-Corrales, 1987). Results were subjected to cluster analysis by UPGMA and principle co-ordinates analysis (PCoA). The races identified were used to screen local cultivars and potential sources of resistance.

RESULTS

Races 3, 65, 80, 81, 83, 81/593 (Koch, 1996); and 3, 6, 81, 323, 390, 593 (Mohammed, 2003) had been previously identified in South Africa. In this study, five races, with the binary codes 7, 81, 83, 89 and 263, were identified. Three of these, namely races 7, 89 and 263, had not been previously collected in South Africa. The differential G 2333 (with anthracnose resistance genes *Co-4²*, *Co-5* and *Co-7*) was resistant to all South African races, as was AB 136 (*Co-6* & *co-8*) and Kaboon (*Co-1²*). Ratings for Kaboon were generally somewhat higher than for AB 136 and G 2333, and races virulent on Kaboon (Leakey & Simbwa-Bunnya, 1972, Uganda, and Alzate-Marin & Sartorato, 2004, Brazil), as well as Kaboon and AB 136 (Mohammed, 2003, Ethiopia) have been reported. The resistance genes in AB 136 and Kaboon, in particular the single gene *Co-1²*, should therefore not be solely relied on but be used in gene pyramiding with additional resistance genes. It is also possible that all South African races have not yet been collected.

For the present study, cluster analysis, supplemented by the PCoA, indicated two groups of races, namely 7 & 263, and 81, 83, & 89. Races 7 & 263 were generally virulent on large seeded material of Andean origin, and races 81, 83 and 89 were generally virulent on small seeded material of Middle-American (MA) origin.

Germplasm accessions also clustered into two main groups, namely those of MA origin or with resistance genes of MA origin, and those of Andean origin. Within these two main groups, subgroups indicated resistance to zero, one or several races. This information can be used to select genotypes with complementary resistances.

Although, due to moderate reactions, the distinction between races 7 and 263 was not very clear, the South African small seeded cultivar Teebus differentiated these two races clearly. Two isolates were designated as race 83, although ratings for Michigan DRK differed from moderately susceptible to susceptible and for Cornell 49242 and Kaboon from resistant to moderately resistant. These two isolates were clearly differentiated into two different races by the large seeded local cultivars Jenny and RS-4 (Table 1). These results indicate that Teebus, Jenny and RS-4 may contain genes or gene combinations that are not represented in the standard differential set.

CONCLUSIONS

It is clear that, although cultivars of Andean origin are by far the most commonly planted types in South Africa and in Africa generally, races of both Andean and MA origin are prevalent in the region. Although no single gene can be relied upon to give resistance to all local anthracnose races, suitable resistance sources are available. Some germplasm accessions that contain more than one resistance gene have high levels of resistance to all reported SA races, and some local cultivars have complementary resistance, in particular the more resistant accessions from the Andean and MA gene pools (Table 1).

Table 1: Potential sources of resistance to South African races of *C. lindemuthianum*

Cultivar	Seed type	Origin	Resistance gene(s)	Race 7	81	83a	83b	89	263
Most local A types	Large	A		S	R	R(S)	S	R	S
Most local MA types	Small	MA		R	S	S	S	S	R
Kaboon	Crème	A	*Co-1²*	R	R	R	MR	R	R
PAN 146 (Sani)	Cranberry	A (MA)	Unknown	R	S	S	-	S	R
OPS RS-4	Cranberry	A (MA)	Unknown	S	R	R	S	R	S
RH4-1308C-3-B3	DRK	A (MA)	*Co-4², Co-1?, Co-2?*	R	R	R	-	R	R
Huron	Small White	MA (A)	*Co-2*	R	R	MS	R	MS	R
Ouro Negro	Small Black	MA	*Co-10*	R	S	R	R	MS	R

A: Andean, MA: Middle American, R: resistant, S: susceptible, MR/S: moderately resistant/susceptible

ACKNOWLEDGEMENTS

Financial support by the EISELEN foundation, Ulm, Germany, receipt of the line RH4-1308C-3-B3 from Dr. PN Miklas, USDA, Prosser, and advice on the culture of *C. lindemuthianum* by Dr. S. Koch, ARC-PPRI, Pretoria are acknowledged.

REFERENCES

Alzate-Marin, A.L. & Sartorato, A., 2004. Analysis of the Pathogenic Variability of *Colletotrichum lindemuthianum* in Brazil. Ann. Rept. Bean Improv. Coop. 47: 241-242.

Koch, S. 1996. *Colletotrichum* spp. on Dry Beans and Lupines in South Africa. Ph.D. thesis, University of Pretoria, South Africa.

Leakey, C.L.A & Simbwa-Bunnya, M., 1972. Races of *Colletotrichum lindemuthianum* and Implications for Dry Bean Breeding in Uganda. Ann. Appl. Biol., 70: 25-34.

Mohammed, 2003. Biology and Control of Bean Anthracnose in Ethopia. Ph.D. thesis, Department of Plant sciences, University of the Free State, South Africa.

Van Schoonhoven, A & Pastor-Corrales, MA. 1987. Standard System for the Evaluation of Bean Germplasm, CIAT, Cali, Colombia