Bean Root Rot Management in Africa

R. Buruchara, G. Mahuku, C. Gichuru, C. Mukankusi, S. Buah, A. Male, S. Sebuliba and C. Acam
Centro Internacional de Agricultura Tropical, Pan Africa Bean Research Alliance , P.O. Box 6247, Kampala Uganda.

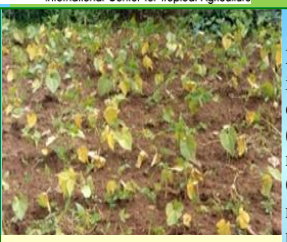


Figure 1. A bean field infected by root rot

Introduction

Bean root rot diseases are a relatively recent problem in east and Central Africa that is increasing in importance . They are caused by a number of soil-borne pathogens that occur singly or as a complex of two or more organisms resulting in considerable yield losses (221,000 m/tones / year) (Wortmann 1998). Basing on spatial distribution, damage and effect on yield, *Pythium* spp are more frequently associated with severe outbreaks. Others include *Fusarium* and *Rhizoctonia* spp. Occurrence and severity of the diseases are high in areas that are densely populated, land size is reducing and is intensively used resulting in the decline in soil fertility and a build-up of soil pathogen inoculum. Yield losses of up to 70% have been reported in Rwanda and when susceptible varieties are grown under ideal disease conditions. The diseases are manifested as seed rot, damping-off, root rot and plant yellowing (Fig 1 and 2).



Figure 2. Root rot symptoms on bean roots

To curb the effects of these diseases, efforts have been made to: 1) characterize the types and distribution of root rot causing pathogens, 2) identify sources of resistance, 3) improve resistance in preferred genotypes, 4) identify other non-varietal management technologies which can be used in an integrated manner. Below we highlight key results from these efforts.

Characterization of bean root rot pathogens

Over 100 species have been reported in the genus Pythium. We made efforts to characterize the types, relative importance and distribution of key bean root rot pathogens in affected areas in Kenya, Rwanda and Uganda. This involved surveys, isolation (in specific media), cultural and molecular (RFLPs and sequencing) techniques.

Results:

✓ Novel rapid and reliable diagnostic tools for identifying, and differentiating *Fusarium* and *Pythium* species were developed, including multiplex PCR techniques for positive identification of the main *Pythium* species.

✓ Little or no molecular variation was observed within groups of pathogenic and non-pathogenic isolates of *Fusarium solani* fsp *phaseoli* (FSP) . *P*athogen-specific PCR primers were developed.

✓ A total of 38 Pythium species were identified by sequencing the ITS region of about 480 isolates. Eleven were pathogenic to beans and included: *P. spinosum, P. nodosum, P. pachycaule, P. torulosum, P. salpingophorum, P. aphanidermatum, P. irregulare, P. graminicola, P. echinulatum, P. ultimum* and *P. paroecandrum. (Table 1).*

✓Species distribution maps were developed for Uganda, Kenya and Rwanda . *P. ultimum* var *ultimum* is the most prevalent species.

✓These species are now being used in selecting for and deploying *Pythium* resistance in preferred backgrounds.

Table 1. Pathogenic *Pythium* spp characterized in the region

	Isolates			
Pathogenic Species	Uganda	Kenya	Rwanda	**Total**
P. ultimum	**17**	**9**	**23**	**50**
P. aphanidermatum	**1**		**1**	**2**
P. irregulare		**9**	**1**	**10**
P. myriotylum		**1**	**1**	**2**
P. torulosum	**8**	**11**	**10**	**29**
P. salpingophorum	**12**	**1**	**4**	**17**
P. spinosum	**7**	**1**	**7**	**15**
P. pachycaule	**3**			**3**
P. graminicola		**7**		**7**
P. nodosum	**2**			**2**
P. paroecandrum		**3**	**3**	**6**

Varietal Improvement

A strategy considered effective in root rot management is the use of integrated approach with a strong component of resistant varieties. To design resistant gene deployment (in bean types preferred by resource-poor small holder farmers), strategies that are long lasting are dependent on identification of useful genes and a good understanding of the host-pathogen interactions. Based on the characterization of the pathogens described above, we evaluated (using artificial screening and at hotspots) a wide range of germplasm to identify sources of resistance. We also determined the nature and mode of inheritance of resistance and initiated efforts to improve resistance in popular but susceptible varieties.



Figure 3. Reaction of AND 1062, RWR 719 and susceptible CAL 96 and LRK 33-1 following inoculation with *P. ultimum*

Results:

✓ About 70 lines were identified as resistant following evaluations of over 6000 germplasm to form a root rot nursery.

✓ A number of elite sources of resistance (to most pathogenic species of Pythium and at several hot spots and farmer participatory evaluations) and potentially valuable lines included RWR 719, MLB-49-89A, AND1062, AND 1055 and SCAM 80CM/15.

✓ MLB-49-89A, Vuninkingi (G685), G4795, RWR 719 and G2333 were the best sources of resistance to Fusarium root rot.

✓ Farmer participatory variety selection has led to growing or release of a number of root rot resistant varieties in Kenya (RWR 719, SCAM 80CM/15, MLB-49-89A), Ethiopia (RWR 719), DR Congo (MLB-49-89A), Rwanda (MLB-49-89A, SCAM 80CM/15) and Uganda (RWR 1946 and RWR 2075).

✓ Resistance in 5 genotypes (RWR 719, MLB-49-89A, SCAM-80 CM/15, AND 1055 & AND 1062) to Pythium root rot were shown to be simply inherited and conditioned by single dominant genes. RWR 719 seems to have 2 resistant genes. Resistance to Fusarium root rot was shown to be complexly inherited and conditioned by 3-9 additive genes.

✓ Crosses have been made to create several populations designed to transfer resistance of Pythium and Fusarium root rots into a number of locally adapted commercial but susceptible cultivars and selections are being made.

Development of Markers and Application MAS in Varietal Improvement

To facilitate rapid and effective transfer of Pythium root rot resistance genes, molecular markers were developed and application of MAS implemented for certain traits.

✓ Three SSR markers that are linked to the resistance genes in RWR719 (2 markers) and AND 1062 (1 marker) were identified.

✓ The RAPD markers linked to the Pythium root rot resistance gene in RWR719, MLB-49-89A and AND 1069 have been validated and may be used for marker assisted selection.

✓ Only one SCAR marker, PYAA19, in RWR 719 proved useful and is routinely used in marker assisted selection at CIAT Kawanda, Uganda.

✓ In addition, great strides have been made in the application of molecular markers in bean improvement with ALS, BCMV, BCMNV and anthracnose.

✓ There are efforts to facilitate and enhance capacity of NARS partners to integrate and apply MAS.

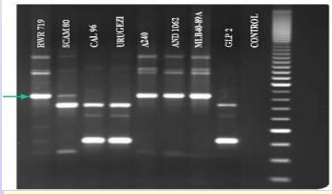


Figure 4. An agarose gel showing amplification of the RWR719 SCAR on different bean genotypes. Arrows indicates the band associated with resistance

Integrated Pest and Disease Management (IPDM)

✓ In addition to varietal improvement, potentially useful cultural methods have been evaluated using participatory approaches and selected as integral components of IPDM. These include soil fertility improvement options using different types of organic amendments (FYM, compost and green manures).

✓ In epidemiological studies, a number of *Pythium* species associated with crops grown together with beans were found to be pathogenic on beans, sorghum and peas. This confirmed that these crops are alternative host of *Pythium* species that are pathogenic to beans and possibly play a role in prevalence, survival and inoculum level Pythium species in the soil. This is should be an important consideration in developing management strategies.

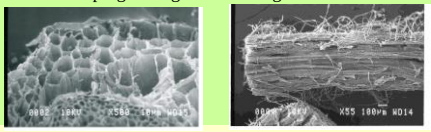


Figure 5. Scanning electron micrographs of sorghum tissue: non-inoculated (left) and 8 days after planting with in *P. utlimum* soil

We acknowledge with thanks:

- PABRA Partners
- CIAT
- Financial support by the Rockefeller Foundation, DFID, CIDA and SDC

Improved Beans for the Developing World