Highlights
CIAT in Africa

Application of biotechnology in bean disease management

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The Highlights series summarises research results and policy implications from the work of CIAT and its partners in Africa

Beans are notoriously susceptible to diseases, and several are responsible for significant yield and economic losses in Africa. An estimated total of 2,288,000 tons of beans are lost to diseases annually (Wortmann et al., 1998[1]). To design and assess management practices and to develop host resistance to important pathogens of beans, characterisation and understanding of their diverse structure and spatial distribution is important. Identifying some of the disease causing organisms can be difficult and slow using conventional morphological, cultural and pathogenic characteristics. For example, some species of Pythium and Fusarium are often difficult to identify due to the presence of a wide range of species in the soil. However, new biotechnological tools are fast and accurate in detecting and identifying some of these bean pathogens. CIAT and its partners are currently using some of these tools for the detection and characterisation of bean pathogens, thus improving our understanding of their diversity, distribution and role in Africa.

CIAT and its partner NARO have conducted training for African colleagues on DNA extraction methods, molecular characterisation of plant pathogens, and the use of molecular markers in crop improvement.

Characterising pathogens

To understand the diversity of Pythium species, over 206 isolates from bean root rot affected areas in Kenya, Rwanda and Uganda have been characterised by molecular methods (sequencing). A total of 38 Pythium species have been identified which include pathogens, saprophytes and biocontrol agents. Five species (*P. spinosum, P. nodosum, P. pachycaule*, *P. torulosum* and *P. salpingophorum*) were observed for the first time to be pathogenic to beans. Distribution mapping shows *P. ultimum* var *ultimum* to be the most frequently occurring species in the region.

Similar biotechnology techniques are also being used to establish the identity and relationship of Pythium species from bean and other crops. In collaboration with colleagues in CIAT Colombia, a multiplex PCR assay for six common Pythium species that are pathogenic to beans has been developed. This molecular tool is efficient in species identification, as it enables simultaneous detection and identification of several species in one assay. Molecular markers to detect and identify *Fusarium solani* f.sp *phaseoli* fungus, (which cause disease in beans), have been identified. These are used to detect and distinguish strains that infect beans from those that either infect other host crops or are saprophytes (Figure 1 overleaf).

Characterisation of the angular leaf spot organism *Phaeoisariopsis griseola,* a major foliar pathogen of beans in Africa, is based on a lengthy method using virulence of each isolate on 12 differential cultivars. However, in collaboration with colleagues in CIAT Colombia, a standardised molecular system has been developed to characterise the pathogen more efficiently. Locus-specific micro-satellite derived markers that can distinguish between different groups of *P.*

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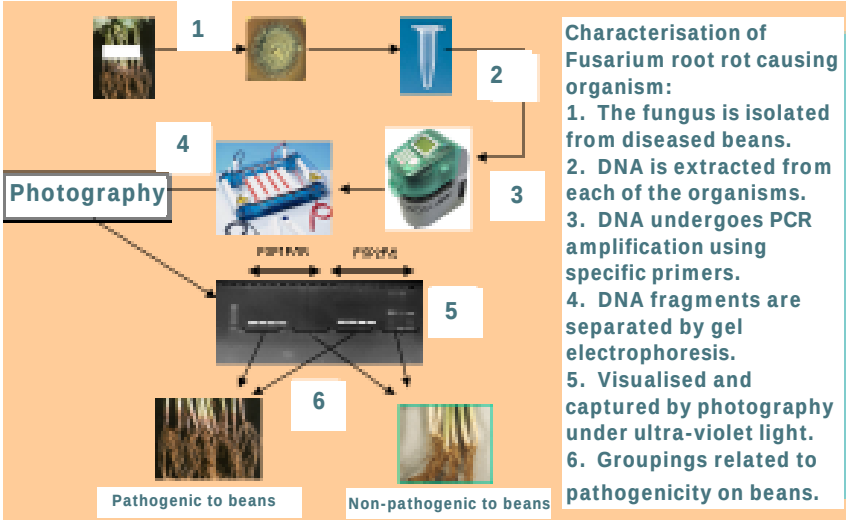

griseola, (corresponding to different gene pools) have been identified, and standardised protocols for their use developed. These markers make it faster and cheaper to accurately categorise major pathogen groups of *P. griseola* and thereafter use virulence selectively.

Tools for genetic improvement

Conventional breeding methods have been used to improve popular cultivars by transferring desired genes (by crossing) and then selecting for their presence in the progenies generated. For some simple traits, this is straightforward as it is easy to detect those off-springs with the desired traits. However, for other traits, conventional methods are difficult, lengthy and less efficient, and especially when handling multiple traits. To overcome these inherent difficulties, biotechnology tools have been developed, based on advances in plant molecular genetics and which offer novel possibilities in the genetic improvement of common bean and other crops. These tools enhance the efficiency, speed and effectiveness of developing new crop varieties. They also facilitate more precise and rapid identification of genotypes carrying certain desirable genes.

Marker-assisted selection

One of the biotechnology tools applied in bean improvement is marker-assisted selection (MAS). DNA-based markers linked to heritable traits are used to select indirectly for resistant genotypes in early generations, hence reducing the breeding process. Where applicable, MAS is fast, accurate and not influenced by climatic or other environmental factors. For example, markers linked with resistance genes against angular leaf spot disease in some genotypes (G 10474, G 10909 and Mexico 54, MAR 1) have been identified. This has facilitated the transfer of these genes and increased precision in selecting lines with angular leaf spot resistance. Markers linked to other bean diseases are also available, offering further opportunities for MAS in the transfer of resistance to well-adapted market class beans. In addition, efforts are underway at CIAT to tag genes for Pythium and Fusarium root rots of beans.

Capacity building

To improve efficiency and effectiveness of bean breeding programmes in applying modern biotechnology tools, it is crucial to build capacity of the researchers and institutions involved. Potential and capacity for utilisation of new biotechnology tools vary in different countries in eastern, central and southern Africa. However, limitations to wide application include underdeveloped infrastructure, lack of trained researchers and technicians, laboratory chemicals and equipment, and limited institutional and financial support.

Whereas, it is desirable that each national research institution acquires the minimum infrastructure to apply biotechnology tools, the reality is that for the moment this is not practical. A networking approach has been successfully used among national bean programmes in Africa where resources and responsibilities are shared, complementing efforts to overcome institutional limitations, while taking advantages of programmes with comparative advantages. A similar strategy is being put in place in the application of biotechnology tools. As capacity improves, the division of roles will gradually evolve with the use of biotechnology tools becoming more decentralised, leaving the regional facilities to carry out more specialised functions. In Uganda, NARO working in collaboration with IPGRI, CIAT and IITA has established a biotechnology centre. This facility offers an opportunity for scientists and students from the region to conduct group training attachments and postgraduate research, and is central to the application and scaling up of MAS.

For more information contact:
Robin Buruchara
r.buruchara@cgiar.org

CIAT
Africa Coordination
Kawanda Agricultural Research Institute
P.O. Box 6247
Kampala, Uganda

Phone:
+256(41)567670

Fax:
+256(41)567635

Email:
ciat-uganda@cgiar.org

Internet:
www.ciat.cgiar.org

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1. Wortmann, C.S., R.A. Kirkby, C.A. Eledu & D.J. Allen, 1998. Atlas of common bean (Phaseolus vulgaris L.) production in Africa.