

R4D Review



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Editors

Lava Kumar and Katherine Lopez

Production team

Copy editor: Rose Umelo

Creative production: Godson Bright

Adegboyega Juba, and Clement Ono-Raphael

Editorial board

Robert Asiedu, David Chikoye, and Victor Manyong

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Cover: Research worker in IITA's maize field collecting tassels for hand pollination. Photo by C. Ono-Raphael.

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IITA at 45: 1967 to 2012 and beyond...

This year, IITA marks its 45th year of service to the African farmers and national agricultural systems.

In 1962, two years after the Ford and Rockefeller Foundations helped launch the International Rice Research Institute (IRRI, Los Baños, the Philippines), both Foundations began discussing the possibility of establishing centers concerned with improving the yield and quality of tropical food crops other than rice. Thus, was the idea of an institute that would conduct research in the tropics of sub-Saharan Africa conceived by IITA's founders¹.

The Institute was established in July 1967, as the first major African link in an integrated network of international agricultural research centers located throughout the developing regions of the world.

IITA is under the umbrella of the CGIAR, a global research partnership that unites 15 organizations engaged in research for sustainable development for a food secure future that carries out research in collaboration with hundreds of partner organizations.

Funding for IITA came initially from the Ford and Rockefeller Foundations, and the land for the headquarters in Ibadan was allotted by the Government of the Federal Republic of Nigeria.

Currently, the Institute is one of the world's leading research partners in finding solutions for hunger, malnutrition, and poverty. IITA's award-winning research for development (R4D) addresses the development needs of the poor and vulnerable in the tropics.

Together with scores of partners, IITA is contributing to enhance crop quality and productivity, reduce producer and consumer risks, and generate wealth from agriculture.

For the last 45 years, IITA has delivered over 70% of the impact from the CGIAR in sub-Saharan Africa. The Institute has achieved this by focusing on key tropical food crops, such as banana and plantain, cassava, cowpea, maize, soybean, yam, and tree and vegetable crops.

For the next decade, IITA plans to raise over 20 million people out of poverty while simultaneously making available over 25 million hectares of farm lands for agricultural production. This is important as demand for food in the midst of the rising population and limited natural resources will remain as important challenges.

IITA will tackle these challenges by pursuing high quality research that improves food security, increases the profitability of foods and other agricultural products, and helps national entities to expand agricultural growth.

With the help of partners and other stakeholders, IITA endeavors to continue to improve the lives of the poor in the region through R4D.



IITA logo used until 2002 (left); current logo (right)

¹Excerpts taken from Ortiz, R. 2004. IITA: 40 yeas after. Historical account for the Handbook of IITA Board of Trustees. IITA Report. 36 pp.

EDITOR'S NOTE

Mind the gap...

IITA was established in 1967 to increase and improve food crop production, and soil and crop management for sustainable agricultural development. The Institute has become integral to the quest by sub-Saharan Africa (SSA) to attain food and income security. Multi pronged approaches, in partnership with national and international organizations, on natural resource management and the genetic improvement of staple crops in the humid tropics and tropical savannas have led to the development of high-yielding varieties. These have resilience to counter multiple biotic and abiotic threats, and new technologies have been established for crop protection and sustainable natural resource management. Since its establishment, the institute has become a pacesetter in agricultural development in SSA.

This issue commemorates the 45th anniversary of IITA. It focuses on the successes, challenges, and prospects of the genetic improvement programs which have been the cornerstone of IITA's success in improving food crop production in SSA. These innovations in genetic improvement, together with supportive policies and training, have dramatically improved crop productivity and lifted millions out of poverty.

However, achieving self-sufficiency in food production and reducing poverty

still remain as intractable problems in many countries here. There are many reasons for this situation. Inadequate economic and political systems, conflict, adverse weather, lack of crop production support mechanisms, inadequate funds for research and development, inefficient marketing structures, and a limited pool of trained scientists are key factors for the poor performance of the agriculture sector in SSA¹.

Many governments are embarking on initiatives to establish agriculture as a commercially viable entity to produce enough food and create opportunities for employment. However, institutional reforms are also required to establish sound technical capacity, infrastructure, and enabling policies for the benefit of technological innovations to be fully realized and to facilitate farmers' access to inputs and markets.

Governments are urged to show greater commitment to invest in reforms that can foster the establishment of a strong and sustainable agricultural system. This is essential to cater to the demands from economic growth and the rapid rise in population (set to double by 2050²) and to develop the adaptive capacity needed to cope with risks from climate change. Without these, the current situation can only worsen and increase the levels of hunger and poverty.

¹Joubert, G.D. 2007. Trends in Africa's crop production and the way forward on research and development. African Crop Science Proceedings 8: 5–7.

²Eastwood, R. and M. Lipton. 2011. Demographic transition in sub-Saharan Africa: how big will the economic dividend be? Population Studies 65: 9–35.

"Countries need strong leadership to introduce changes in implementing agricultural development programs."

Dr Nteranya Sanginga, Director General, IITA



NEWS

Boosting yam productivity in Ghana and Nigeria

IITA and partners recently launched the Yam Improvement for Income and Food Security in West Africa (YIIFSWA) project, supported by a US\$12 million grant from the Bill & Melinda Gates Foundation.

The project aims to boost yam productivity and double the incomes of three million yam small-holder farmers in West Africa. It will focus on increasing yields through better seed yam supply and improving markets for this underground, edible tuber.

A key priority of the project is to ensure that affordable higher-yielding pest- and disease-free seed yam are available to farmers, along with storage and handling technologies that can reduce postharvest loss. The project will also develop a host of new yam varieties that can address the challenges in yam production.



Yam market, Nigeria. Photo by IITA.

The project has major emphasis on training and capacity development of farmers and farmers' organizations, and improvement of linkages of small-holder farmers to markets where a strong and steady demand for seed and ware yam allow them to realize the economic benefits of increased productivity.

IITA leads the 5-year project in collaboration with the national organizations of Ghana and Nigeria, the UK's Natural Resources Institute (NRI), the Alliance for a Green Revolution in Africa (AGRA), and Catholic Relief Services (CRS).

For more information, visit www.iita.org/web/yiifswa.

Pro-vitamin A cassava released

Three pro-vitamin A cassava varieties released in December 2011 were launched recently by the Nigerian government. IITA, in partnership with the National Root Crops Research Institute, Nigeria, developed these varieties using traditional breeding methods in a HarvestPlusfunded project.

The varieties were released by the National Variety Release Committee of Nigeria as UMUCASS 36, UMUCASS 37, and UMUCASS 38; and are recognized as IITA genotypes TMS 01/1368, TMS 01/1412, and TMS 01/1371. The project works with national partners and the private sector to ensure that the pro-vitamin A-rich varieties reach resource-poor farmers. The consumption of pro-vitamin A cassava could help Nigeria reduce economic losses in gross domestic product estimated at about \$1.5 billion. Most importantly, it will also improve the nutrition of women and children who are the most vulnerable.

In developing countries, vitamin A deficiency remains a major bottleneck to improved nutrition with approximately 250,000 to 500,000 malnourished children going blind each year, half of whom die within a year of becoming blind. The prevalence of night blindness due to vitamin A deficiency is also high among pregnant women in many developing countries.

The yellow root color of the vitamin A-rich varieties is the product of over 20 years of breeding efforts for improved nutritional quality. Other partners in this biofortification work include the International Center for Tropical Agriculture (CIAT) and the Brazilian Agricultural Research Corporation (Embrapa).

Multi-CGIAR center initiative launched

The African Development Bank (AfDB) has approved a US\$63.24 million fund package for the implementation of a 5-year, multi-CGIAR center project dubbed "Support to Agricultural Research for Development of Strategic Crops in Africa" (SARD-SC).

SARD-SC is a research, science, and technology development initiative aimed at enhancing the productivity and income derived from cassava, maize, rice, and wheat—four of the six commodities that African heads of states, through the Comprehensive African Agricultural Development Program, have defined as strategic crops for Africa.

The project will be coimplemented by three Africa-based CGIAR centers: IITA, Africa Rice Center, and the International Center for Agricultural Research in the Dry Areas. IITA is also the executing agency of the project. Another CGIAR center, the International Food Policy Research Institute, provides support to the other centers.

The SARD-SC allows for the first time ever in a single project—a continental coverage of the food security challenges in Africa.

The project's goal is to enhance food and nutrition security and contribute to poverty reduction in the Bank's low-income regional member countries by working across the full value chain of each crop and addressing both food costs and employment creation. Through its value chain approach, SARD-SC will also contribute to crop-livestock integration. Its target beneficiaries are farmers and consumers, farmers' groups including youth and women, policymakers, private sector operators, marketers/traders, transporters, small-scale agricultural machinery manufacturers, and institutions.

Plant Virology Symposium slated in 2013

IITA will host the 12th Plant Virus Symposium (http://www.iita.org/IPVE) to be held on 28 January-1 February 2013, in Arusha, Tanzania. The theme is Evolution, Ecology, and Control of Plant Viruses. The symposium, held

under the auspices of the International Committee on Plant Virus Epidemiology (www.isppweb.org/ICPVE/) of the International Society of Plant Pathology, provides a forum for the exchange of latest knowledge on emergence, epidemiology, and control of native and new encounter viruses.

The symposium will hold a special Africa focus session to develop a strategy to combat emerging and re-emerging plant virus diseases in sub-Saharan Africa.

Registration and abstract submission are ongoing; late abstract submissions will be until 31 October 2012; abstract acceptance notification will be done by 15 November 2012.

For more information, send an e-mail to: iita-ipve@ cgiar.org or contact Lava Kumar (L.kumar@cgiar. org), IITA.



FEATURES

During the past 45 years, the genetic improvement programs of IITA and its partners have made spectacular progress in developing high-yielding crop varieties that offered best-bet solutions to major production constraints, such as, cassava mosaic, maize streak, *Striga*, soybean rust, insect pests, and even drought. These have led to dramatic increases in the production of cassava, maize, soybean, cowpea, and yam in sub-Saharan Africa that have directly contributed to increases in food availability and indirectly to improvements in national economies. This section presents the status, progress, and achievements, and also outlines future work on crop improvement by genetic enhancement in IITA's six crops.

Maize genetic improvement for enhanced productivity gains in West and Central Africa

Abebe Menkir (a.menkir@cgiar.org), Baffour Badu-Apraku, and Sam Ajala

Maize is an important food security and income-generating crop for millions of people in West and Central Africa (WCA). Maize breeding at IITA was initiated around 1970. Using as base materials two composites created from diverse sources in Nigeria under a West African project supported by the Scientific and Technical Research Committee of the

Organization for African Unity, breeders at IITA formed several broadbased populations and improved them through recurrent selection. The main research focus at that time was the development of open-pollinated maize varieties (OPVs) with resistance to diseases. and adapted to the humid forest and moist savannas of WCA. The products generated from this research were

channelled to research and development partners for further testing, multiplication, and dissemination in various countries in the subregion.

The widespread outbreak of the maize streak virus (MSV) disease in the late 1970s prompted IITA to develop two resistant populations. These were crossed to high-yielding

A. Menkir, B. Badu-Apraku, and S. Ajala are Maize Breeders, IITA, Ibadan, Nigeria.

and broad-based germplasm from the International Maize and Wheat Improvement Center, eastern and southern Africa, the temperate zone, central and south America, Thailand, DECALB, and other sources to create populations and varieties resistant to MSV. IITA has supplied MSV-resistant inbred lines, OPVs, hybrids, and populations to partners within and outside WCA through diverse delivery pathways for more than 25 years. Direct use of MSV-resistant maize germplasm that also had resistance to southern leaf rust, southern leaf blight, downy mildew, and leaf spot has been recorded in several countries in Africa.

The significant breakthrough in the development and release of highyielding extra-early, early, intermediate, and late-maturing varieties with resistance to leaf rust, leaf blight, and leaf spot has caused a phenomenal increase in maize production in WCA, notably in Bénin, Burkina Faso, Cameroon, Chad, The Gambia, Guinea, Ghana, Mali, Nigeria, Senegal, and Togo. Further expansion in

production has also occurred in many countries in this subregion because of the adoption of extra-early maturing improved varieties identified from regional trials coordinated by the Semi-Arid Food Grain Research and Development (SAFGRAD) and the West and Central Africa Collaborative

Maize Research Network (WECAMAN).

The development of extra-early maturing varieties enabled production to expand into new areas, especially to the Sudan savannas where the short rainy season hitherto had precluded maize cultivation. The highest growth in maize area, yield, and



Maize streak virus disease causes severe stunting and extreme yield reduction in maize. Creating Maize streak virus-resistant varieties is one of the major successes of IITA's maize breeding program. Source: L. Kumar.

production in sub-Saharan Africa since 1961 occurred in WCA. These productivity gains, achieved through farmers' adoption of improved varieties in the 1980s, were driven by the suitability of the cultivars to the major production environments, the availability of inexpensive fertilizer and extension services, as well as favorable government policies that encouraged the use of these technologies.

In a recent impact assessment study conducted in nine countries, the number of varieties annually released in WCA had increased from fewer than one in 1970s to 12 in the late 1990s. The availability of such high-yielding and adapted varieties resulted in a 2% annual increase in land area planted to maize and a 3.5% annual increase in grain yield from 1971 to 2005. Among the varieties released from 1998 to 2005 in the nine

countries, 67% were derived from IITA's maize germplasm. Of the 4 million ha planted to improved maize in these countries, about 43% of the area was planted to varieties derived from IITA's germplasm. The joint IITA-NARS investment in maize research in the nine countries had lifted an average of 1.6 million people out of poverty annually from 1980 to 2004.

While working with diverse partners to promote the



IITA maize breeders in action, maize breeding program. Source: L. Kumar.

dissemination of maize varieties in the various countries, IITA realized that the major constraint to the adoption of improved varieties in WCA was the absence of an effective seed production and delivery system. To promote the establishment of indigenous private seed companies, IITA embarked on the development of hybrids in 1979 with financial support from the Federal Government of Nigeria and the active participation of Nigerian scientists. This led to the release of the first generation of hybrids in 1983, with a spill-over effect of the establishment of seed companies in Nigeria for marketing hybrid maize seeds. The official announcement of IITA's maize OPVs and hybrids in the catalogs of indigenous seed companies in Nigeria provide further evidence of the adoption, deployment, and commercialization of IITA-bred varieties and hybrids.

In recent years,
IITA has also made
significant progress
in the development
of a large number of
maize inbred lines,
OPVs and hybrids with
resistance to Striga



Maize production in Saminaka area in Kaduna State, Nigeria. Photo by A. Menkir.

hermonthica, stem borers, and aflatoxin contamination, with tolerance for drought, efficient nitrogen use, and enhanced contents of lysine, tryptophan, and provitamin A. We have the first generation of extra-early, early, intermediate, and latematuring OPVs and hybrids that combine drought tolerance with resistance to S. hermonthica developed under the Drought Tolerant Maize for Africa Project and supplied to partners for testing through regional trials. The number of droughttolerant OPVs identified from these trials and released for production since 2007 were 7 in Bénin Republic, 5 in Ghana, 3 in Mali, and 13 in Nigeria.

On the other hand, only one droughttolerant hybrid selected in Mali and six drought-tolerant hybrids selected in Nigeria were released for production. Furthermore, three varieties with high lysine and tryptophan content, two varieties resistant to S. hermonthica, two varieties that are nitrogen use efficient, a stem borer-resistant variety, two yellow and two white hybrids were released from 2008 to 2011 in Nigeria.

To accelerate the release and commercialization of hybrids with different maturity classes, high yield potential, combining resistance to *Striga* and drought tolerance, and other

desirable traits in different countries in WCA, IITA has supplied parental lines of promising hybrids to private seed companies for further testing, production, and commercialization. The institute has also trained technical and management staff of seed companies to strengthen their human capacity to produce and market hybrid maize.

In addition, IITA has promoted community-based seed production schemes through its work with WECAMAN and more recently with diverse partners to make improved seeds

available to farmers in countries where the private sector is less developed and in areas with limited access to markets.

Despite the impressive strides that have been made so far, continued investment in maize productivity research still remains critical to sustain agricultural growth, food security, improved nutritional quality, and safe harvests. Considering the predominance of the crop in diverse farming systems, heterogeneous landscapes, and the diets of millions of people in WCA, enhanced yield gains

have the potential to further expand production in WCA, thus contributing to bridging the gap between food supply and demand in the region, because research has led to and will continue to deliver excellent results.

Increased investment not only in research but also in strengthening the private seed sector will still be needed to promote the rapid turnover of maize hybrids on farmers' fields that help to achieve higher yield gains to support improved farming in WCA.



IITA maize breeding trial. Photo by IITA.

A success tale on improving two legume crops in Africa

Ousmane Boukar (o.boukar@cgiar.org), Tahirou Abdoulaye, Manuele Tamó, Hesham Agrama, Hailu Tefera, Christian Fatokun, and Steve Boahen

Cowpea and soybean are cultivated by poor and middle-income farmers as a sole crop or as intercrop with maize and other cereals for their protein-rich grains which are consumed in different forms. The haulms from plant residues and the dry pod walls of both crops are good sources of quality fodder for livestock.

The two crops contribute substantially to sustain crop production through their ability to fix atmospheric nitrogen, some of which is left behind in the soil after harvesting for subsequent crops. IITA and its partners have been involved in improving legume production systems for several decades. An overview of these efforts is presented in this article.

Cowpea

Cowpea—indigenous to sub-Saharan Africa (SSA), is grown on about 14 million ha worldwide, with over 84% of this area in SSA. Between 1985 and 2007, the rate of growth was 4.5% in land area planted to cowpea, 4.5% in grain yields/ha, and 5.9% in quantity of cowpea produced. These data indicate

that the increase in the quantity of grain produced over the period resulted mainly from an expansion in the land area and less from an improved yield/unit area. In well-managed experimental stations, yields of up to 2 t/ha can be obtained but globally the average yield is about 450 kg/ha.



Improved cowpea varieties being tested in a field trial. Photo by L. Kumar.

O. Boukar, Cowpea Breeder; T. Abdoulaye, Socioeconomist, IITA, Ibadan, Nigeria; M. Tamó, Legume Entomologist, IITA, Benin; H. Agrama and H. Tefera, Soybean Breeders, IITA, Malawi; C. Fatokun, Cowpea Breeder, IITA, Ibadan, Nigeria; S. Boahen, Legume Specialist/Agronomist, IITA, Mozambique.

Several abiotic and biotic factors keep the productivity of cowpea low in African farmers' fields. Notable among these are drought, poor soil fertility, inappropriate agronomic practices, an array of fungal, viral, and bacterial diseases, and parasitic flowering plants (Striga and Alectra). Cowpea is particularly susceptible to infestation by several insects with devastating effects on plants in the field and seeds in storage.

Efforts in genetic improvement have been and are still being made to develop varieties with resistance to these various yieldlimiting factors and in various research institutions across SSA, IITA, and other advanced research institutions. Cowpea breeders from these various institutions meet regularly to share information and exchange ideas on the way forward.

Elite lines generated from IITA's breeding nurseries are shared with interested colleagues from the national research institutions who evaluate these at their stations and in farmers' fields. Those

that perform well are recommended for release in the respective countries. For example, in Mali, a cowpea line IT99K-499-35 was recently adopted by many farmers in the Segou area and because of its superior performance and resistance to *Striga*, given a local name, Jinguiya which means `hope'.

Under the Tropical Legumes II (TL II) project, several new cowpea varieties [IT97K-499-35 (in 2008), IT89KD-288 and IT89KD-391 (in 2009), IT99K-573-1-1 and IT99K-573-2-1 (in 2011)] were released in Nigeria. Regional trials are being conduced for two cowpea lines (IT97K-1122 and IT00K-1263) identified through farmers' participatory selection as part of the TL II project in Tanzania to facilitate their official release. In 2011, three IITA cowpea lines (IT97K-1069-6, IT00K-1263, and IT82E-16) were released in Mozambique; and IT99K-494-6 was released by Bunda College in Malawi as an *Alectra*-resistant variety in 2011.

Research on integrated pest management (IPM) for cowpea has resulted in the development and deployment of biopesticides including the use of entomopathogenic organisms combined with botanicals, and biological control agents such as hymenopteran parasitoids which attack and feed on some of the cowpea pests. An example is the mixture of a specific entomopathogenic virus capable of infecting and killing the legume pod borer Maruca vitrata with aqueous formulations of neem oil. This has proved to be as effective as the use of conventional insecticidal sprays. With regard to biological control, a small parasitic wasp which attacks the flower bud thrips, another major pest of flowering cowpea, has been introduced and established in most of Bénin and parts of Ghana, It has been reported to reduce the thrips population on wild alternative host plants by up to 40%.

The development of improved cowpea varieties has so



Legume scientists in a disease resistance screening trial. Photo by L. Kumar.

far depended on conventional breeding methods. However, efforts are being made to apply molecular breeding tools to cowpea improvement. Fairly saturated genetic linkage maps of cowpea have been produced in several laboratories. The linkage maps have been used for the detection of DNA markers associated with resistance/tolerance to Striga, drought, macrophomina, and bacterial blight, and seed characteristics such as size. A few of the markers have been converted to user-friendly markers which will make them

readily available for breeders in the national systems. Molecular markers are contributing to progress in variety development.

IITA is collaborating with Purdue University, USA, in implementing the Purdue Improved Cowpea Storage (PICS) project on the hermetic storage of cowpea grain in Nigeria, Bénin, Togo, and Cameroon. From 2008 to 2010, IITA and its partners disseminated hermetic triple-layer bags for storage in more than 13,500 villages in the cowpea-producing areas of Nigeria, Cameroon, Togo, and Bénin. This project

addresses one of the most important constraints to cowpea production which is grain damage in storage, Furthermore, by not using any type of chemical, this hermetic storage method is protecting farming families and consumers from accidents from the mishandling of and poisoning by the chemicals used in cowpea storage. To date, farmers have purchased more than 30,000 PICS bags in these countries.

IITA is also collaborating in an adoption study that will provide information about the reach of the

technology. Another study on analysis of the supply chain of the PICS bags in the same four countries will help to improve the farmers' access to the PICS bags through a better distribution network.

Soybean

Soybean is a fairly new crop in SSA and has few biotic constraints. Fewer than 400 ha were planted to soybean in SSA during the 1980s but this exceeded the 1-million ha mark by 2007. Grain yield/ ha increased from about 900 kg/ha in the 1980s to >1000 kg/ ha between 2005 and 2007. Initially most varieties grown in parts of SSA had the problem of seed longevity. Farmers could not store seeds successfully from one cropping season to the next. This problem has now been

solved so that seeds of the newly developed over a longer period. Another constraint to soybean production was pod shattering, which resulted in seeds being lost in the field. Farmers could not leave their before harvesting without losing some of the grain. The varieties that have been developed at IITA have tolerance to pod shattering, and resistance to rust-a fungus (Phakopsora savanna agroecology. Some genotypes of sovbean are noted for their abilities to reduce the seed bank can cause serious damage to cereal

varieties remain viable crop to dry in the field pachyrhizi) that causes significant yield losses, especially in the moist of Striga hermonthica, a parasitic weed which crops.



Improved soybean varieties. Photo by IITA.

Several elite lines from IITA's breeding nursery have been evaluated in many countries in SSA and found to perform well in farmers' fields. Some of these have been recommended for release in the different countries. For example, rustresistant TGx1835-10E and TGx1987-62F have been released in Nigeria; TGx1740-2F was released in Malawi; TGx-1485-1D, TGx1740-2F, TGx1904-6F, TGx1908-8F, and TGx1937-1F were released in Mozambique in 2011. These were the first batch of varieties ever released in Mozambique. The development of improved varieties also involved farmers' participation in selection, which made it possible for farmers to have some knowledge on performance of the lines being selected, thus facilitating rapid adoption and dissemination. IITA, in collaboration with Laval University in Canada, completed genotypic [using single nucleotide polymorphism (SNP) markers] and phentotypic characterization of 300 soybean genotypes for rust resistance and symbiotic performance.

In addition to efforts on genetic improvement of soybean, major emphasis has been placed on promoting and using soybean to encourage consumption, and thus create markets for farmers to sell their produce. Recipes were developed to promote the use of soybean arain for food. This promotional activity was necessary because the crop was new in many parts of the region and people were not familiar with how it could be best used as food. Vegetable oil millers were also encouraged to accept soybean as a raw material from where good quality oil could be extracted.

Legumes fix atmospheric nitrogen in their root nodules through the symbiotic association between the crop and rhizobium, a free-living soil bacterium. Legume seeds are inoculated with the rhizobium before sowing to increase the number of rhizobium available to the plant for infection and nodule formation, and subsequently enhance the quantity of the nitrogen fixed. Soybean is one such crop that requires rhizobium inoculation

if a good crop is to be established on soils with no existing rhizobia or inadequate number if rhizobia.

At IITA, some soybean varieties have been developed which are capable of fixing atmospheric nitrogen using the native rhizobium present in the soil. These varieties which require no inoculation before sowing are characterized by promiscuous nodulation. Growing such varieties will save the farmers some expense and the time needed to purchase the inoculants with which the seeds are treated.

Conclusions

Decades of collaborative research efforts on genetic improvement of these two important legume crops involving scientists in the national agricultural research systems of different countries in SSA, IITA, and advanced research institutions in Europe and North America have resulted in the development and promotion of different improved varieties to meet the preferences of farmers and consumers. Improved varieties

developed through this partnership have been released in over 70 countries around the world, which signifies the success of this partnership for legume crop improvement.

Further efforts will focus on use of innovative approaches to pyramid pest and disease resistance genes into improved lines and varieties; application of molecular markers to rapidly introduce genes for simply inherited desirable traits into popular varieties; and genetic modification using recombinant DNA technology to produce insectresistant cowpea varieties (Bacillus thuringiensis or Bt cowpea for resistance to the *Maruca* pod borer). Efforts will be continued to address diseases, such as the need to develop improved cowpea and sovbean lines with combined resistance to different fungal, bacterial, and viral pathogens. The factors that influence tolerance to drought in cowpea require further elucidation, as this would facilitate progress in developing new varieties with enhanced drought tolerance.

Breeding superior banana/ plantain hybrids

Jim Lorenzen (j.lorenzen@cgiar.org)

Banana (the term includes plantain in this article, *Musa* species), is a major staple crop in Africa. Although it originated in Asia and was introduced to Africa long ago, it has become more important as a food security crop in its new home in Africa than in its region of origin. From its early domestication in Southeast Asia and the islands extending toward Australia, banana spread to Africa before recorded history. Archaeological evidence suggests that it reached Central Africa several millennia ago.

The main types of cooking banana in Africa include plantain (AAB genome), East African Highland Banana (EAHB, AAA genome), and a wide range of other types including sweet dessert banana (AAA or AAB genome), starchy but sweet roasting or brewing banana (ABB genome), and a number of other types. The "genome" refers to the portion of the chromosomes that come from one of the progenitor species of banana, Musa acuminata (A genome) or Musa balbisiana (B genome). However, most banana production in sub-Saharan Africa (SSA) consists of the East Africa Highland type or plantains, two sets of varieties with very limited genetic diversity in either. This lack of genetic diversity is a serious concern. About 60% of African

production occurs in Uganda and its immediate neighbor countries (Tanzania, Rwanda, Kenya, D.R. Congo; also including Burundi).

Since banana production is yearround, it serves as a buffering bridge crop to provide food in times of scarcity between cereal harvests. As a long-lived clonal crop, it (like cassava) also can serve as a famine-avoidance crop because it is less susceptible than annual crops



Pollination of banana flowers, Photo by L. Kumar.

J. Lorenzen, Banana Breeder, IITA, Tanzania.

to catastrophic failure in the event of unseasonable drought and can act as a survival crop during cereal crop failure. Banana also provides important ecological functions for sustainable agriculture by reducing erosion in sloping highland agriculture, and recycling nutrients through the crop residue returned to the soil in each production cycle. In some locations banana leaves and cut stems are an important fodder component in the livestock sector, providing some fodder even during the dry season.

Production constraints

While precolonial banana production may have been relatively stable, pests and diseases introduced into Africa in the last century have destabilized production in some areas. Some important introduced diseases and pests include black leaf streak (also known as Black Sigatoka), Banana bunchy top virus (BBTV), burrowing nematode, banana weevil, and Fusarium wilt. More recently, banana Xanthomonas wilt (BXW) has emerged as an important bacterial disease that apparently originated in Ethiopia and caused a major disease epidemic in much of East Africa in the last decade. Breeding for resistance to these diseases and pests provided the initial motivation for IITA and partners to initiate breeding in Africa.

Banana breeding history

Although early efforts to breed banana using modern breeding concepts were initiated by British scientists in the Caribbean about 80 years ago, even today the world has only about seven significant banana breeding programs. IITA initiated a plantain breeding program at the Onne High Rainfall research station

in southeast Nigeria in the 1980s as a new epidemic disease, Black leaf streak, arrived in the region. This program made relatively rapid progress, identified fertile plantain varieties to cross to wild sources of resistance, optimized and implemented embryo rescue as a means of boosting germination from <1% to 5-30%, and produced resistant high-yielding hybrids by the early 1990s. Realizing that the bigger portion of African banana production was in highland East Africa and also threatened by black leaf streak, in 1995, IITA initiated a banana breeding program in Uganda in collaboration with the National Agricultural Research Organization (NARO). Working together, scientists identified fertile EAHB varieties, produced resistant high-yielding tetraploid hybrids to serve as parents, and initiated a program to produce resistant highyielding triploid hybrids that were more likely to remain seedless.

Banana breeding process

Although most of the world eats banana, few realize that wild banana are full of hard seeds and domestication resulted in the seedless fruits that we now eat. Most varieties are triploids (have 3) sets of each chromosome), which are both more productive and more likely to remain sterile and seedless. However, some edible varieties retain a bit of residual fertility and will set a few seeds if pollinated with a strong source of viable pollen. Banana breeders serve as surrogates to natural pollinators (bats), climb ladders in the early morning to collect male flowers, and carry them and the ladders over to the intended female plants to hand-pollinate female flowers. The flowers open



Manual pollination of banana flowers. Photo by IITA.

sequentially each day, so each floral bunch is pollinated daily for a week. While many pollinations produce no seeds, some produce a few and a very few produce many seeds. Unfortunately, due to the complex background of domesticated banana, most seeds will not germinate on their own. Therefore breeding programs extract embryos from surface-sterilized seeds and germinate them in test tubes in nutritious media, from which they can later be transplanted to sterile soil, hardened, and eventually planted in the field. Triploid hybrids are evaluated as potential new varieties, while diploid (2 sets of chromosomes) and tetraploid (4 sets) hybrids are evaluated as potential improved parents.

Progress

The original plantain hybrids, as well as superior hybrids developed later, are currently being tested for agronomic performance, yield, and consumer acceptability in a number of countries in West and Central Africa, including Nigeria, Cameroon, Ghana, and Coté d'Ivoire. In the meantime, IITA's original East African partner in banana breeding, NARO, has grown to be one of the largest banana research programs in the world, with internationally recognized capacity in several disciplines. Fittingly, in 2010 NARO became the first national program in Africa to officially release a banana variety bred in Africa. Kabana6 (nicknamed Kiwangaazi) is a highyielding variety with resistance to black leaf streak and partial resistance to nematodes and weevils. More encouragingly, newer selections likely to be more acceptable to Ugandan consumers are "in the pipeline," and procedures are now in place to move some jointly developed NARO-IITA hybrids to countries where their cooked texture and appearance fit the traditional variety "type" better than they do the "matooke" variety type of Uganda. A couple of promising hybrids are finding acceptability in Burundi and eastern D.R. Congo, and hopefully will also be released as varieties. IITA recently opened a second East African breeding site near Arusha, Tanzania, a country with a broader range of environments and irrigation opportunities, potentially better to breed widely adapted varieties and providing the opportunity to screen more systematically for drought tolerance.

Other aspects

To support the breeding program, other genetics studies are being conducted, including development of populations for molecular mapping studies, mapping genes controlling important traits, manipulating ploidy to try to create fertility in "sterile" lines, developing molecular "tools" to make breeding more efficient, and investigating gene expression in response to drought. IITA has excellent capacity for screening for resistance to pests and diseases.

The entire banana improvement program depends on collaborative relationships, both within IITA and from a range of partners within Africa and in other continents. The pending release of the reference genome sequence from La recherche agronomique pour le développement (CIRAD)/ Genoscope in France should greatly

accelerate genetics research on banana and its relatives. In light of the challenges of breeding and the lack of good sources of resistance for two important pathogens (BXW and BBTV), IITA is also investing in biotechnology approaches to banana improvement, with promising signs of resistance in early laboratory, screenhouse, and confined field trials (companion article by Tripathi on page 58).

Challenges

While encouraging progress is being made, banana breeding is challenging, slow, and expensive. Low fertility, poor seed set, and low germination rates mean that it is difficult to produce large numbers of progeny to evaluate. Banana plants are large, so evaluation plots are likewise large and expensive, and plants require up to 3 years to progress through two fruiting cycles. Much of the background



Physical measurements of banana fruits. Photo by IITA.

genetics underlying key traits have yet to be properly investigated, so the list of research opportunities to make breeding more efficient and productive is long. Musa is one of the major crops in the world for which wild relatives have yet to be systematically collected, so access to wild species for breeding for more resistant or more nutritious hybrids is problematic. Unfortunately, the global gene pool with the resistance and quality genes for future breeders remains at risk. Hopefully arrangements can be made for collection expeditions in the center of origin (Southeast Asia) in the near future while wild Musa still remain.

Future

Although banana has been a neglected crop in terms of research investment and scientists' effort in many countries, key decision makers are beginning to realize the essential role of banana/ plantain in food security, enhanced livelihoods, and resilient agricultural systems for Africa. The potential to breed superior hybrids has been demonstrated, and there are numerous opportunities for improving both the process and the product, and for realizing impact from already developed hybrids. The future for banana crop improvement looks promising.

16th Triennial Symposium





International Society for Tropical Root Crops

Symposium Secretariat, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria E-mail: istrc2012abeokuta@yahoo.com Tel: +2348034046873, +2348033469882

Background

The 16th Triennial Symposium of the International Society for Tropical Root Crops (ISTRC) will be held at the Federal University of Agriculture, Abeokuta (FUNAAB), Ogun State, Nigeria, 23–28 September 2012.

About the Symposium

Tropical roots crops are essential to meeting global food security and sustaining the livelihoods of many millions of people. Climate change provides both opportunities and challenges for attaining the potential contribution of tropical roots for sustainable human development. Strategies need to be developed to address key issues in productivity, crop plant-soil/water/energy resources management, and postharvest utilization as food and feed, nutritional and health value addition, and trade and commercialization, so that the role of tropical roots in ensuring sustainable development can be enhanced. The symposium provides an opportunity for experts from around the world to meet and address this agenda.

Theme: The Roots (and Tubers) of Development and Climate Change

Subthemes

- 1. Policies favorable to enhancing the contribution of RTCs to development
- 2. Global scenario on production, utilization and marketing of root and tuber crops
- 3. Progress in science and technology for enhancing the contribution of tropical root crops to development
- Applying new scientific and technical knowledge on RTCs to contribute to development

Cassava improvement in the era of "agrigenomics": the road to next-generation breeding

Ismail Yusuf Rabbi (i.rabbi@cgiar.org), Melaku Gedil, Morag Ferguson, and Peter Kulakow

In the last 45 years, IITA has played a pivotal role in the genetic improvement of cassava for resourcepoor farmers in sub-. Saharan Africa (SSA). More than 400 varieties have been developed that are not only high yielding but also resistant to diseases and pests. Many of these improved varieties have been extensively deployed in SSA and have helped to avert humanitarian crises caused by the viral disease pandemics that devastated local landraces in East and Central Africa.

The cassava breeding program in Ibadan has a collection of more than 750 elite cassava clones representing current and historical materials accumulated over the last 45 years. These materials, referred to as the genetic gain

collection (GGC), are accompanied by extensive field evaluation (phenotypic) data. In addition, the active breeding collection contains over 1000 African landraces and more than 400 new advanced breeding clones that are also accompanied by phenotypic data, including observations of disease and pest resistance, plant architecture, flowering ability, and performance in storage root yield.



Pro-vitamin A 'yellow root' cassava developed by the IITA cassava breeding program. Photo by IITA.

I. Rabbi, Postdoctoral Fellow (Molecular Genetics); M. Gedil, Head, Bioscience Center, IITA, Ibadan, Nigeria; M. Ferguson, Molecular Geneticist, IITA, Nairobi, Kenya; and P. Kulakow, Cassava Breeder, IITA, Ibadan, Nigeria.

The most recent success of the conventional cassava breeding program culminated in the release of three vitamin A cassava varieties by the Government of Nigeria. These varieties (IITA TMS I011368, IITA TMS I011371, and IITA TMS I011412) were first cloned from seedlings in Ibadan in 2001 and have been subjected to extensive field testing throughout Nigeria. While almost all cassava in Nigeria are currently white fleshed, vitamin A cassava produces yellowfleshed roots with nutritionally significant concentrations of

carotenoids that produce vitamin A in the human body when consumed as yellow gari or fufu. In cooperation with HarvestPlus, IITA and partners will distribute vitamin A cassava planting materials to more than 25,000 farmers in 2013. New yellowfleshed genotypes in the pipeline promise continued improvement in pro-vitamin A content, yield, and dry matter in the coming vears.

As the vitamin A cassava illustrates, the genetic improvement of cassava has mostly been achieved through

conventional breeding methods based on phenotypic selection. The only known direct application of molecular markers in cassava breeding is selection for resistance to cassava mosaic disease and cassava green mite. Recent advances and a reduction in the cost of the nextgeneration sequencing technologies now promise to usher in a new era for cassava breeding that will combine the success. of conventional hybridization, selection, and multilocational vield trials with the latest advances in genomic resources.

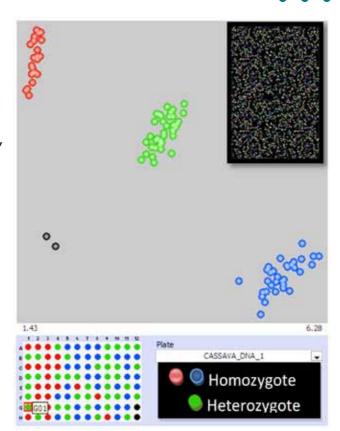


Preparation of cassava DNA for genotyping by sequencing. Photo by IITA.

Setting the stage for "next-generation cassava breeding"

Cognizant of the potential of marker technologies to improve the efficiency and effectiveness of cassava breeding, IITA, in collaboration with partners, embarked on the development and deployment of molecular markers1. With the recent accumulation of genomic resources in cassava research, including the first full cassava genome sequence2, our emphasis at IITA has shifted towards the application of these resources in molecular breedina3.

One recent achievement is the identification and validation of nearly 1500 single nucleotide polymorphism (SNP) markers through an international collaboration led by IITA's geneticist, Morag Ferguson⁴. These SNPs have been converted to a highly parallel hybridization-based genotyping system that has been shared with the international cassava research community through partnership with the Generation Challenge Program (GCP).



An example of an SNP genotyping data plotted with KBioscience's SNPviewer software. Inset: raw SNP genotyping data from Illumina's GoldenGate®assay.

In addition, the first SNP-based genetic linkage map of cassava has been developed by IITA in collaboration with Heneriko Kulembeka of the Agricultural Research Institute (ARI), Ukiriguru, Tanzania. A linkage map is analogous to landmarks (SNP markers in this case) placed along chromosomes that

quide researchers to genes or genomic regions controlling traits of interest. Such a linkage map is an indispensable tool for marker-assisted selection (MAS). SNP and SSR markers have also been applied to uncover quantitative trait loci (QTL) associated with resistance to cassava brown streak disease (CBSD)—which is ravaging cassava

production in Eastern and Southern Africa—in a collaboration between IITA, CIAT, and ARI-Tanzania.

Another dramatic development in cassava genomics is the recently completed sequencing of the cassava genome through the partnership of the US Department of Energy's Joint Genome Institute and 454 Life Sciences².

Genotyping-bysequencing

The progress in nextgeneration technologies has drastically reduced the costs of DNA sequencing so that genotyping-bysequencing (GBS) is now feasible for species such as cassava, ushering in a new era of agricultural genomics5. This will revolutionize the application of genomic tools for cassava improvement. GBS involves the cutting of genomic DNA into short pieces at specific locations using a restriction enzyme. The ends of these pieces are sequenced using techniques that allow sequencing of many samples at the same time. The beauty of this method is the use of adaptors containing barcodes (unique tags) that are enzymatically

joined to the digested DNA fragments, enabling simultaneous sequencing or multiplexing of up to 384 samples in one sequencing reaction. This economy of scale greatly reduces the cost of processing each individual DNA to less than \$10/ sample. Approximately 200,000 markers can be identified and mapped in a very short time. With this powerful tool, breeders may conduct genomicsbased research that was inconceivable a couple of years ago. Some of the exciting new research applications include polymorphism discovery, high-density genotyping for QTL detection and fine mapping, genome-wide association studies, genomic selection, improving reference genome assembly, and kinship estimation.

High-density QTL mapping and fine mapping

In the past, a limitation for QTL mapping was the number of markers on a genetic linkage map. With new SNP-based technologies this is no longer a limitation. This allows for fine mapping of QTLs so long as a sufficient number of individuals in the mapping population

can be developed. IITA, in collaboration with national partners [ARI-Tanzania and National Crops Resources Research Institute (NaCRRI), Uganda], is using SNPs to discover QTLs associated with sources of tolerance for CBSD.

The next frontier for cassava genomics

Using the genotyping by sequencing approach, scientists from IITA and Cornell University, USA, are currently genotyping more than 2000 accessions of cassava, including released varieties, advanced breeding lines, and landraces from Africa. This is a pilot study of genomic selection funded by the Bill & Melinda Gates Foundation to explore the potential for using the IITA breeding collection, including genetic gain, local germplasm, and current advanced breeding lines, as the base population to begin genomic selection for West Africa. The IITA breeding collection has been extensively characterized in many locations and over many years.

The convergence of high-density SNP data and extensive phenotypic data in

IITA's cassava collection sets the stage for the implementation of genome-wide association studies (GWAS) and genomic selection (GS) in breeding. The aim of GWAS is to pinpoint the genetic polymorphisms underlying agriculturally important traits. In GWAS, the whole genome is scanned for significant marker-trait associations, using a sample of individuals from the germplasm collections, such as a breeder's collection. This approach of "allele mining" overcomes the limitations of traditional gene mapping by (a) providing higher resolution, (b) uncovering more genetic variants from broad germplasm, and most importantly, (c) creating the possibility of exploiting historical phenotypic data for future advances in breeding cassava.

GS is a breeding strategy that seeks to predict phenotypes from high-density genotypic data alone, using a statistical model based on both phenotypic and genotypic information from a "training population". For cassava, phenotyping is the slowest and most expensive phase of the

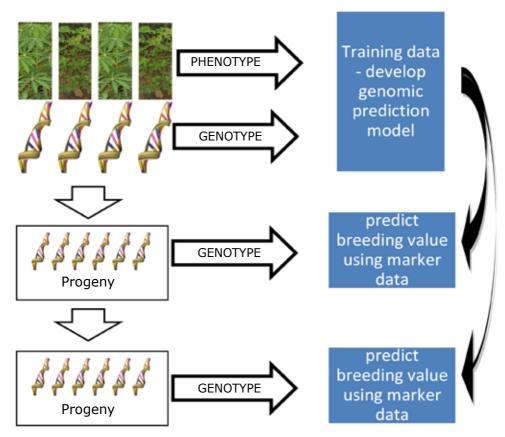


Preparation of gari, the most popular food product from cassava, made from yellow root cassava. Photo by IITA.

crop's breeding cycle because of the crop's low multiplication ratio of between 5 and 10 cuttings/plant. Thus, it takes several cycles of propagation (up to 6 years) to carry out a proper multilocational field trial evaluation. The implementation of GS at the seedling stage should: (a) dramatically reduce the length of the breeding cycle, (b) increase the number/ unit time of crosses and selections, and (c) increase the number of seedlings that could be accurately evaluated. The reduced breeding cycle means that the "engine of evolution," i.e., recombination and selection, can

proceed at a rate that is three times as fast as phenotypic-based selection, while saving resources.

In conclusion, cassava breeding in IITA is being redefined, thanks to the increasing availability and deployment of genomic resources. Combining these resources with IITA's long-standing conventional breeding pipeline means that the best days of cassava improvement lie ahead. These efforts will ultimately satisfy the increasing need for more healthy and nutritious food produced in environmentally sustainable ways.



A schema of genomic selection (GS) processes, starting from phenotyping and genotyping of the training population and selection of parental candidates via genomic estimated breeding value (GEBV)-based selection. Note that selection model improvement can be performed iteratively as new phenotype and marker data accumulate.

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Yam breeding at IITA: achievements, challenges, and prospects

Antonio Lopez-Montes (a.lopez-montes@cgiar.org), Ranjana Bhattacharjee, and Gezahegn Tessema

Yam—an integral part of the West African food system

Yam (*Dioscorea* spp.) is a multispecies, clonally propagated crop cultivated for its starchy tubers. About 10 species are widely cultivated around the world, but only *D. rotundata*, *D. alata*, and *D. cayenensis* are the most widely cultivated species in West Africa, accounting for 93% of the global yam production. Since inception, IITA R4D efforts have focused on developing new varieties of yam with desired agronomic and quality traits and to improve yam-based cropping systems.

Largest collection of yam genetic resources

IITA maintains the largest world collection of yam, accounting for over 3,000 accessions mainly of West African origin. The collection represents eight species: D. rotundata (67%), D. alata (25%), D. dumetorum (1.6%), D. cayenensis (2%), D. bulbifera (2%), D. mangenotiana (0.25%), D. esculenta (0.7%), and D. praehensilis (0.3%). The passport data and characterization information on these accessions are maintained in databases accessible at http://genebank.iita. org/. On request, these germplasm



Novel vertical sacs method for seed yam production using vine cuttings.
Photo by L. Kumar.

A. Lopez-Montes, Yam Breeder; R. Bhattacharjee, Molecular Geneticist; G. Tessema, Associate Professional Officer, IITA, Ibadan, Nigeria.

accessions are distributed following Standard Material Transfer Agreements (SMTA). As in many other crops, the request for gene bank accessions has been low for use in national and international yam improvement programs. Of a total of 3170 accessions, only 1077 accessions have been distributed in the last 10 years.

To increase the use of yam germplasm, which are a wealth of rare alleles for target traits, a core collection (391 accessions) was established in 2006 representing 75% of genetic diversity of the entire collection using data on 99 morphological descriptors and country of origin. The germplasm collection is being genotyped using 18 DNA-based markers. Presently, research efforts are under way in collaboration with CIRAD for cryopreservation, using liquid nitrogen, to reduce the cost of maintenance of such a large collection. Efforts to improve yam germplasm conservation and use will be continued under the framework of the CGIAR Research Program (CRP) on Roots, Tubers and Bananas (RTB) for Food Security and Income. As part of this program efforts will be made to (a) optimize ex situ and in situ vam conservation methodologies; (b) increase coverage of yam gene pools; (c) evaluate, genotype, and phenotype yam collections for important traits; (d) enrich databases with information on yam collections and make it freely accessible to users; and (e) improve procedures for safe exchange of RTB genetic resources.

Making the difference

IITA's yam breeding program has mainly focused on clonal selection

from landraces and hybridization of elite clones of *D. alata* and *D.* rotundata. Conventional breeding efforts in yam have resulted in substantial achievements leading to release of high-yielding and disease-resistant cultivars. For instance, through collaborative evaluation of IITA-derived breeding lines with national research institutes (National Root Crop Research Institute, Umudike, Nigeria, and the Crops Research Institute, Ghana), 10 varieties of D. rotundata (10 during 2001-2009 in Nigeria and 1 in 2007 in Ghana) and 5 varieties of *D. alata* (during 2008-2009 in Nigeria) were released. More lines are in the pipeline to be released by these institutions in Nigeria and Ghana, and also in Benin, Burkina Faso, Côte d'Ivoire, Sierra Leone, Togo, and Liberia. The released varieties have multiple pest and disease resistance, wide adaptability, and good organoleptic attributes.

Some work has also been carried out in interspecific hybridization, but it is faced with a lot of challenges, including cross-compatibility and synchronization of flowering. For instance, D. rotundata can be crossed to D. cayenensis, but crossing either of the two to D. alata has not been successful. Research effort in interspecific hybridization has been geared towards the genetic improvement of yam, primarily on D. rotundata, D. cayenensis, and D. alata by transferring complementary traits from one to the other, e.g., higher carotenoid in *D. cayenensis* transferred to *D. rotundata* by interspecific hybridization.

Besides success in hybridization, efforts of the breeding program



Researchers in accelerated yam breeding trial plot. Photo by L. Kumar.

resulted in identification of resistance to nematodes (D. dumetorum), fungi and viruses (D. alata and D. rotundata); selection of germplasm for their response to soil nutrients and nutrients use efficiency; physicochemical characterization of D. alata for food quality, sensory evaluation of 'amala' (yam flour paste) and pasting characteristics of fresh yam as indicators of textural quality in major food products. Studies are ongoing to determine the variation in nutrient retention during processing of yam into food products; characterization of tuber micronutrient density, specifically for iron, zinc, total carotenoids, ascorbic acid (vitamin C), phytate, and tannin content. Traits, such as photoperiod response, flowering, and dormancy are also being studied in D. rotundata.

The future thrust will be on reducing the breeding period required to

develop improved varieties with consumer-preferred traits, as well as increased participation of stakeholders for improved efficiency and impact of the yam breeding program. Developing participatory value chain strategy will set priorities not only for research and development but also for a consistent value chain articulation and low risk models to link farmers to markets. Yam for food security, food industry (flour, pasta, noodles, pancakes etc.), and pharmacology (drugs, cosmetics) needs prioritized by stakeholders will drive the development of new varieties, that are high yielding, resistant to diseases and pests, and with good adaptability to specific production systems, low fertility soils, and dry environments. GIS-based characterization of yam production systems, yam growth models and genome sequencing will provide strategic knowledge for the success of the yam breeding program.

Rapid and high-ratio seed yam propagation systems will support the variety development and dissemination efforts to breeders and other stakeholders. The implementation of the new scheme is expected to reduce the time to develop and recommend new varieties from 9 to 3.5 years and facilitate rapid release of consumer-preferred varieties by the national programs.

Genomic resources for yam improvement

Research on biotechnology of yam includes tissue culture, genetic transformation, and development and use of molecular markers. However, no genetically modified yam has been produced so far although this approach could be used to transfer resistance to virus and anthracnose diseases into popular commercial varieties. Progress on yam genomics and transformation is covered in Bhattacharjee et al. (next page).

Future prospects

Review of constraints in yam production in West Africa identified the high cost of planting material, high labor costs, poor soil fertility, low yield potential of local varieties, pests and diseases (on-farm and in storage), and shortage of quality seed yam of popular landraces and released varieties as major limitations. To overcome these challenges, in the next five years

under the CRP-RTB framework, yam breeding efforts will focus on (a) development of new breeding tools and strategies, (b) trait capture and gene discovery, (c) pre-breeding for new traits, (d) development of new varieties incorporating consumer-preferred characters, and (e) aligning research with farmer and end-user priorities.

These efforts will be supported by the ongoing R4D programs on developing efficient phenotyping protocols for nutrient use efficiency, moisture stress tolerance and biotic stresses in different yam species; regeneration protocol for transformation of various species (D. rotundata, D. alata, and D. cavenensis); methods for efficient interspecific hybridization among D. alata, D. rotundata, D. bulbifera, D. cayenensis, and D. dumetorum; establishment of marker-assisted breeding platform; techniques for rapid propagation of high quality seed yam; protocol for double haploids from yam microspores; and adoption of stakeholder participatory approaches in development and release of new varieties. Ongoing efforts to strengthen seed yam systems for ensuring sustainable production and supply of quality seed yam in West Africa, and communication and promotional strategies for the dissemination of breeding materials and improved varieties underpin the success of these efforts.



Genomics for transforming yam breeding

Ranjana Bhattacharjee (r.bhattacharjee@cgiar.org), Melaku Gedil, and Antonio Lopez-Montes

Breeding challenges in yam

Yam (*Dioscorea* spp.), a multi-species, polyploidy, and vegetatively propagated crop, is an economically important staple food for more than 300 million people in West Africa, Asia, Oceania, and the Caribbean. The five major yam-producing countries in West Africa (Bénin, Côte d'Ivoire, Ghana, Nigeria, and Togo) account for 93% of worldwide production. *Dioscorea rotundata* and *D. alata* are the species most commonly cultivated

in West Africa¹. The genetic improvement of yam is faced with several constraints, including the long growth cycle (about 8 months or more), dioecy, plants that flower poorly or not at all, polyploidy, vegetative propagation, heterozygous genetic background, and poor knowledge about the genetics of the crop². Progress has been made in breeding to develop F1 full-sib mapping populations from crossing male and female parents of *D. rotundata* for traits



Strategizing genomics for precision breeding. Photo by L. Kumar.

R. Bhattacharjee, Molecular Geneticist; M. Gedil, Head, Bioscience Center; A. Lopez-Montes, Yam Breeder, IITA, Ibadan, Nigeria.

such as multiple tuber production, improved cooking quality, and virus disease resistance; and of *D. alata* for resistance to anthracnose, improved cooking quality, and reduced tuber oxidation³. These are valuable sources of populations for genetic analysis in yam for its improvement.

Current status of yam genomics

There is no convenient model system for yam genomics. In recent years, some progress has been made in the development of molecular markers to assess their potential for germplasm characterization and phylogenetic studies in *D. rotundata-cayenensis* and their wild progenitors, such as D. abyssinica and D. prahensilis. Two framework linkage maps were constructed using D. alata that included 338 AFLP markers on 20 linkage groups with a total map length of 1055 cM; and D. rotundata in which 107 AFLP markers were mapped on 12 linkage groups (585 cM) for the male and 13 linkage groups (700 cM) for the female. Three quantitative trait loci (QTLs) on the male and one QTL on the female were identified for resistance to yam mosaic virus (YMV). Similarly, one AFLP marker was found to be associated with anthracnose resistance on linkage group 2, explaining about 10% of the total phenotypic variance.

Another linkage map was generated for *D. alata* based on 508 AFLP markers that covered a total length of 1233 cM on 20 linkage groups, accounting for about 65% of the entire genome. Genes conferring resistance to YMV have been identified in *D. rotundata* and to anthracnose in *D. alata* by the successful use of bulked segregant analysis (BSA). Two RAPD markers,

OPW18850 and OPX15850, closely linked in coupling phase with the dominant YMV-resistance locus Ymv-1 were identified. Similarly, two RAPD markers, OPI171700 and OPE6950, closely linked in coupling phase with anthracnose resistance gene, *Dcg-1*, were identified².

Enriching the repertoire of molecular markers

In an effort to develop additional genomics resources, IITA was involved in sequencing ESTs from a cDNA library constructed from floral tissue. However, the first several hundred sequences were predominantly housekeeping genes. Recently, in a collaborative project with University of Virginia through USAID-Linkage funds, several thousand ESTs were generated using cDNA libraries from yam leaf tissues challenged with Colletotrichum gloeosporioides, the fungal pathogen responsible for yam anthracnose disease. This resulted in the identification of >800,000 EST sequences, from which about 1152 EST-SSRs were generated in *D. alata* for use in a yam improvement program. Although AFLP markers have been used for generating linkage maps so far, efforts are under way to saturate the maps with these EST-SSRs to identify the genomic regions associated with resistance to anthracnose disease.

DNA barcoding

Species identification in the genus *Dioscorea* has remained a challenge when active domestication is continuing in several parts of West Africa. Research on DNA barcoding is under way using chloroplast markers (rbcL, matK, and trnH-psbA) to understand the phylogenetic relationship between different species and also



Designing molecular markers using a bioinformatics platform. Photo by A. Alonge.

to get an insight into the ongoing domestication process.

Whole genome sequencing

Important considerations for the whole genome sequencing of yam include the genome size, ploidy level, and availability of homozygous clones. Estimation of the genome sizes of various Dioscorea species showed widely variable figures: *D. alata* and *D.* rotundata have genome sizes of about 800 mega base pairs (Mbp). Recently, an initiative was launched at IITA in collaboration with the Japan International Research Center for Agricultural Sciences (JIRCAS) to complete the whole genome sequencing of D. rotundata. Preliminary data yielded reasonable sequences. Further work is in progress to generate additional sequence data from the BAC library to facilitate the assembly of the genome which will culminate in

producing the first draft genome sequence of *Dioscorea* species. Additional genomic information produced by resequencing several breeding materials and a parallel project in transcriptome analysis are poised to result in the discovery of a large number of molecular markers and help in the annotation of the genome.

Transcriptome analysis

In contrast to the genome sequence, which is fixed and uniform in all cells of a particular organism, transcriptome refers to the study of the total set of transcripts (expressed genes) in a given cell/tissue at a particular developmental stage or external environmental condition that could influence the physiology of the cell/tissue. IITA, in collaboration with USDA-Agricultural Research Service, Stoneville, embarked on RNAseq, the latest revolutionary tool for

transcriptome profiling, based on differential gene expression for anthracnose disease. One of the expected outcomes of this project is to enrich the genomic resources available for yam improvement, including the discovery of SNPs. The latest informatics and statistical methods will be applied to saturate the available linkage map and high resolution mapping of the QTL(s) for anthracnose resistance in different genetic backgrounds.

Genotyping-by-sequencing

With advances in the next generation technologies, the costs of DNA sequencing have come down to such an extent that genotyping-by-sequencing (GBS) is now possible in almost all crops. IITA has recognized the potential of such innovative techniques in accelerating the breeding of clonally propagated crops, such as yam. Hence, in an ongoing USAID-Linkage project, a diverse panel of *D. alata* genotypes, including parents of available mapping population progenies segregating for anthracnose disease will be genotyped by sequencing to identify a large set of SNPs and determine the divergence among the parents.

Conclusions

To meet the steadily increasing demand, the viable approach is to adopt the innovative plant breeding strategies for yam that

integrate the latest innovations in molecular technologies with conventional breeding practices. As efforts are under way to obtain the complete genome sequences and the development of additional genomic resources, the groundwork for deploying yam molecular breeding has been laid. With the availability of new genomic markers and GBS, it would be possible to fingerprint yam germplasm to identify duplicates/mislabeled accessions, to conduct diversity analysis and association mapping. As the genus *Dioscorea* contains several other useful species, comparative genomic tools can be used to transfer or deduce genetic and genomic information in other species.

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Cassava: Overcoming Challenges of Global Climatic Change

June 18-22, 2012 Speke Resort & Conference Centre, Kampala, Uganda

A 'Green Revolution' in the West African cocoa belt

Jim Gockowski (j.gockowski@cgiar.org), Ranjana Bhattacharjee, Richard Asare, and Sander Muilerman

Over two-thirds of global cocoa production comes from small farms carved out of the humid forests of Côte d'Ivoire, Ghana, Nigeria, and Cameroon in West Africa, Cacao in West Africa was introduced in the late 1800s and the production of cocoa was, and still remains, largely a small-holder enterprise. Today, the large majority of West African cocoa farmers are aging and struggling with aging tree stocks on depleted soils that exhibit low and declining yields. In contrast, the rapid expansion of intensified cocoa production systems through the High Tech Program (HTP) of the Ghana Cocoa Marketing Board (Cocobod) over the last 10 years has resulted in productivity gains that appear to rival those of wheat during the Indian Green Revolution (Fig. 1).

Over the last 10 years, IITA and various stakeholders in the cocoa belt have been developing cocoa innovations and sharing knowledge through the Sustainable Tree Crops Program (STCP). The HTP is credited for having demonstrated the technical feasibility of a Green Revolution in the Ghanaian farm sector.

Structural overview of a Brown Revolution

Recent STCP studies attribute impressive yield gains over the

last 10 years to a combination of factors. A three-fold increase in the global price of cocoa that occurred simultaneously with the establishment of Cocobod and the reform of producer price policy resulted in much higher producer prices as compared to the previous decade. Higher farm-gate prices combined with Cocobod subsidies on fertilizers and pesticides greatly improved the profitability of input use. In less than 10 years, fertilizer use in the Western Region of Ghana rose from less than 6% to over 80% of cocoa farmers. The increased use of fertilizer was the largest estimated factor that



Red-podded cocoa. Photo by IITA.

J. Gockowski, Agricultural Economist, IITA, Ghana; R. Bhattacharjee, Molecular Geneticist, IITA, Ibadan, Nigeria; R. Asare, Cocoa Agroforester; S. Muilerman, Associate Professional Officer, IITA, Ghana.

contributed to productivity gains in the sector. Improved farmer access to fertilizers resulted from the liberalization of internal cocoa marketing. As a result of this reform, private licensed buying companies were allowed to compete for the purchase of the farmers' dried cocoa. The ensuing competition was not in terms of the farm-gate price paid (Cocobod sets a pan-territorial producer price) but rather in the supply of inputs including fertilizers to farmers. These inputs are most often provided as an in-kind loan linked to the future sale of the farmers' cocoa to the buyer. Another important factor underlying the productivity gains explained in Figure 1 has been the intensified control of cocoa pests and diseases achieved by the US\$40 million in annual expenditures of the Cocoa Disease and Pest Control (CODAPEC) program.

Other innovations such as cocoa hybrids developed by the Cocoa Research Institute of Ghana (CRIG) were estimated to be four times more productive than locally selected planting materials but were only planted on a small proportion of farms. Likewise, farmer field school (FFS) training was received by only a small proportion of farmers but the mean output was 52% higher among those farmers as compared to those who did not receive such training, all other things being equal.

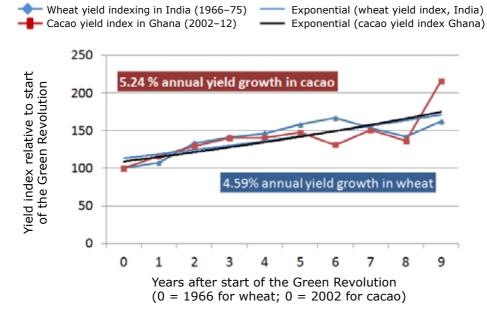


Figure 1. A comparison of yield growth per hectare during the initial phases of the Indian Green Revolution in wheat (1966 to 1975) and the Ghanaian Green Revolution in cocoa (2002 to 2011). Data source: FAOSTAT production statistics accessed online 16 February 2012.



Research will help bring about a Brown Revolution in West Africa. Photo by IITA.

In the light of these findings, cocoa productivity growth in Ghana can further increase by continued increases in fertilizer use and intensified pest and disease control, particularly outside the Western region. There is also much to be gained from improving farmer access to hybrid planting materials and to scaling up participatory farmer training approaches.

Among the lessons drawn from the first 10 years of the cocoa Brown Revolution are the critical importance of (1) a government-supported vision for the subsector; (2) supportive producer price policy; (3) affordable and unproblematic access to inputs; (4) profitable technologies; and (5) farmer training. As seen in Ghana, research has a critical role in developing and sustaining profitable technologies and in generating knowledge that small-holders are able and willing to act upon.

Agenda for sustainable intensification in West and Central Africa

Limited access of farmers to extension, fertilizers, and improved planting materials were among the major technical constraints revealed by a 2001/2002 baseline survey of the cocoa sector conducted by the STCP. While progress has been made in Ghana, there still remain the principal constraints to the achievement of a Brown Revolution across West Africa.

Improving access to improved planting material

Improving farmers' access to highquality planting material has been the focus of the STCP-supported African Cocoa Breeders Working Group (ACBWG) since 2003. The working group collaborated with cocoa breeding programs of the US Department of Agriculture and Mars, and received regional backstopping and training from

STCP tools for the rehabilitation of West African cocoa farms

Cacao tree stocks in West Africa are mainly established from seeds procured from farmers' fields. This planting material lacks the disease tolerance and yield potential of the hybrid seed. Productivity is also affected by the old age of West Africa's tree stock. Replacing and rehabilitating the tree stocks of West Africa is fundamental to the achievement and long-run sustainability of a cocoa Brown Revolution.

The STCP has developed a Planting, Replanting and Diversification (PRD) training package to provide farmers the knowledge and technical skills needed to rehabilitate old cocoa farms or reclaim degraded areas using hybrids. However, a major constraint to hybrid adoption is a lack of access to hybrid seeds. To overcome this constraint, STCP introduced a Seed Brokerage System (SBS) for the collective acquisition of hybrid seeds by farmer field school groups from government production units. An initial evaluation of 375 randomly selected trainees revealed that the mean participant had successfully established 0.4 ha of hybrid cocoa seedling with an 81% seedling survival rate after two dry seasons. Approximately half of the surveyed trainees had replanted old farms while half had established new farms on degraded fallow land. The SBS also brokered timber seedlings for farmers desiring to include high-value timber (Terminalia ivorensis and *T. superb*) as permanent shade in their production system. The mean participant reported the successful establishment of 12 timber seedlings which is equivalent to 30 trees per hectare. Farmers favored the SBS innovation and are seeking its continuance.

IITA. The ACBWG has characterized cocoa germplasm from farmers' fields and research stations which has contributed to an understanding of the genetic diversity in West African cocoa germplasm. The study revealed mislabeling of cocoa germplasm in breeder collections and confirmed the low adoption of improved materials by the farmers in West Africa. The working group is currently using molecular breeding approaches to rapidly develop superior true-to-type genotypes with disease resistance and improved horticultural traits.

The delivery of existing improved planting materials to farmers remains a key constraint in West Africa. The low adoption of improved planting materials was thought to be due to poor

awareness about the benefits of growing improved planting materials and high transaction costs in acquiring these materials. To address these constraints. the ACBWG joined the African Cocoa Initiative (ACI) of the World Cocoa Foundation (WCF) to demonstrate the performance of improved planting materials and best agricultural practices under farmers' field conditions and design and test innovative approaches that will increase adoption of improved germplasm. IITA provides technical support to the ACBWG in molecular breeding, develops training materials pertaining to replanting and rehabilitation of old and unproductive tree stocks, and provides assistance with seed brokerage systems developed and tested in Ghana by the STCP.

Integrated crop, pest, and disease management

The increased use of fertilizers and the intensified control of capsid insects by small-holders were the major factors underlying the productivity growth of the Ghanaian cocoa sector. The tonnage of granular fertilizer applied on cocoa rose from essentially zero in 2000/2001 to 130,000 t in 2009/2010. There is a need to develop diagnostic protocols for assessing nutrient balances, pest and disease pressure, yields, and economic returns that will lead to more profitable fertilizer and treatment recommendations tailored to the specificities of the farmers' local environment. IITA has developed such a protocol for the coffee-banana systems of Eastern Africa and proposes adapting this diagnostic to the cocoa sectors in Nigeria and Cameroon. Major economic losses are also caused by capsid insects, black pod fungal disease, and cocoa swollen shoot virus disease. An integrated program of soil, pest, and disease management research is required to keep these constraints under control.

Extension

The STCP farmer field school program was designed and developed by scientists from IITA and the national research systems of Ghana, Côte d'Ivoire, Nigeria, and Cameroon to address the extension constraint in 2003. Since then, more than 150,000 cocoa farmers have participated in FFS training. On average, the productivity gains following training have ranged from 15 to over 50% depending on the locality. The task, however, is not complete; evolution in knowledge and knowledge

delivery technologies requires a continual effort to update and adapt extension approaches.

Conclusions

The technical and economic feasibility of Brown Revolution technology in the cocoa sector has been demonstrated. However, the long-run sustainability of the institutions and enterprises engaged in the generation and delivery of these technologies among all small-holder farmers is still an area of concern. Without bottom line profitability, small-holders will forgo inputs and revert to environmentally destructive practices which mine soil nutrients, result in unabated pest and disease losses, and lead to unnecessary deforestation. Research has a fundamental role to play in maintaining the profitability of these technologies.



Training of trainers for cocoa farmers in Ghana. Photo by IITA.

IITA through the years



Bird's eye view of IITA, circa 1980s. Photo by IITA.



View of IITA campus, circa 1990s. Photo by IITA.



F.F. Hill, the Administration Building, also known as Building 500, circa 1977. Photo by IITA.



F.F. Hill, the Administration Building, also known as Building 500, 2012. Photo by IITA.

BEST PRACTICE

Partnerships as relationships for agricultural development

Krishnamurthy Sriramesh (k.sriramesh@massey.ac.nz)

Humans and organizations have to depend on others for optimal existence to work effectively to achieve their goals. However, the significance of such interdependencies is often overlooked because of the tendency to take for granted partnerships, relationships, and communication in the organizational context. These key areas are often ignored, being labeled as "soft science".

Each partnership has three broad phases: initiation, management, and exit. Entering into a partnership,

whether at the personal or the organizational level, should be done with care and a level of informed thinking that should include how the partnership will also be terminated. If partnerships are entered into in haste or without much groundwork, there is a high probability that they will lead to failures, and often result in loss of reputation as well. Especially when one does not have the luxury of time to assess potential partners, relying on previous experiences of working with a partner (and an assessment of the strengths and weaknesses of the partner) is a very good

What is partnership?

In organizational contexts, the term "partnership" usually means the legal/contractual association between two or more entrepreneurs. The word "partner" originated from parcenter –a legal term meaning "joint heir." In the fourteenth century, the emphasis on "partner" shifted away from this legal orientation because of the similarity to "part" (part of). Webster's dictionary still puts the contractual relationship of the word partner first and only then mentions "a cooperative relationship between people or groups who agree to share responsibility for achieving some specific goal." This non-legal definition is most useful for discussing partnerships in agriculture for development. Using the term "partner" to refer to the various human elements involved in the long chain of agriculture for development helps us counter such conventional wisdom and assists in moving science closer to the common man.

K. Sriramesh, Professor, College of Business, Massey University, Wellington, New Zealand.



Building a coalition of public-public and public-private partnership for the promotion of 40% cassava flour in bread. Photo by IITA.

foundation with greater potential for success. Therefore, personal as well as institutional "memory" is crucial to success in choosing the right partner. So also is harnessing the strengths of a partner (while avoiding weaknesses) for maximum harmony and symbiosis.

Types of partnership

As relationships, three types of partnerships can be discerned: exchange, communal, and exploitive. An exchange relationship is one of pure barter where material or even information may be exchanged often among strangers as seen between a buyer and salesperson. Communal relationships often occur between partners who have known each other and thereby care for each other at a deeper level. The exchanges in a communal relationship can often be for altruistic purposes where one partner derives gratification by making the other happy, successful, comfortable, etc. Exploitive partnerships are indicative of parasitic tendencies from one

partner often exploiting the goodness (kindness) of the other. Knowledge of the characteristics, strengths, and weaknesses of partners is vital to managing partnerships for increased harmony and efficacy.

Ingredients of good partnership

There are other key ingredients that help to develop/identify good partners. Foremost is the element of trust. Every good partnership is built on trust. When trust is lost, partners become suspicious to the point of being paranoid and that leads to a breakdown of the relationship. Transparency and open communication help to build trust. A reasonable argument can be made that it is impossible to build and maintain trust without effective (twoway) communication among partners. Mutuality of control (sharing control in the partnership) is another key ingredient of good partnerships. When control is not mutually shared, this often leads to exploitive partnerships and that is certainly not a healthy relationship. Commitment is another

key element of a good partnership. Every partnership is built around attaining certain goals and objectives. Unless every partner involved has adequate, or nearly equal, commitment to those goals and the ways by which to reach them, there can be no synergy in that partnership. Commitment to harmony within the partnership is equally vital and when both are present, a partnership is bound to flourish, leading to exponential outputs. Finally, satisfaction is a vital ingredient of a good partnership. Unless all partners are satisfied with the various elements of the partnership (process, output, and outcome), there is bound to be discord, ultimately leading to a breakdown in the partnership.

Considerations for good partnerships There are several elements that help in cultivating good partnerships:

Partnership is a mission of IITA

IITA works in partnership with national, regional, and international research institutes, national governments, civil society organizations, and the private sector to conduct research and ensure that research results benefit agriculture growth and development, particularly in sub-Saharan Africa. During the course of 45 years, IITA has partnered with over 800 different organizations all around the world to advance pro-poor research programs. IITA recognizes that close collaboration with partner organizations is essential for the optimum use of resources, knowledge, technologies, access to cutting-edge science and technologies, mutual learning and for making a positive impact on the livelihoods of poor farmers.

(a) access: when partners share access to each other and their networks of information and influence, there is harmony in the partnership; (b) disclosure and openness: unless both partners are equally open, the more "closed" partner is more likely to exploit the openness of the more "open' and sharing partner; (c) share mutual networks: good partners help one another's integration into individual networks, thereby enhancing one another's outreach and influence; (d) shared interests and shared tasks: overlapping interests obviously bring partners closer together whether in personal or professional settings; similarly, sharing similar tasks (and thereby goals and objectives) also leads to closer partnerships; and (e) continuing dialog: frequent communication between partners is a sure way of building good partnerships. In addition, dialog helps to reduce tensions in partnerships before these become irreparable.

Intra-organizational partnership matters

It is important for organizations to recognize that partners internal to the organization (employees) are just as, if not more, important than partners outside the organization. Internal partners are often taken for granted, a sure recipe for a weak organizational culture that breeds rumors, discord, and low morale. Involving internal stakeholders in governance is vitally important as it drives employees to feel they have invested in the organization and thereby elicits greater loyalty, commitment, and satisfaction in the partnership. Finally, it would not be hyperbole if one were to state that organizations neglect relationship building at their peril.

TOOL BOX

Afla-ELISA: A simple and lowcost quantitative test for the estimation of aflatoxins

Lava Kumar (L.kumar@cgiar.org) and R. Bandyopadhyay



Aflatoxin testing using Afla-ELISA. Source: L. Kumar

Aflatoxins threaten human and animal health

Aflatoxins are the hepatotoxic and carcinogenic secondary metabolites produced by Aspergillus flavus and A. prasiticus. They are common contaminants in several staple crops,

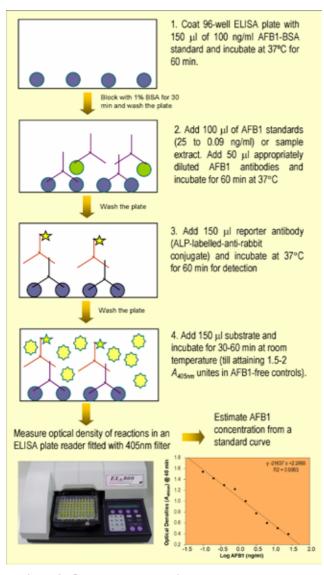
such as maize and groundnut, produced in the tropics and subtropics. Aflatoxins are a group of four toxins: aflatoxin B1 (AFB1), AFB2, AFG1, and AFG2. A metabolite of aflatoxins, namely AFM1, is detected in milk. Aflatoxin contamination in

foods is considered to be unavoidable, as the causative fungi are ubiquitous in the tropical parts of the world. However, fungal infestation and toxin contamination are unpredictable and depend on certain environmental conditions. Aflatoxin exposure in humans and animals results from the consumption of aflatoxincontaminated foods and feeds.

Regulations check aflatoxin contamination

Stringent food safety regulations are enforced in most countries to prevent use of aflatoxincontaminated foods and feeds. These programs are executed through a monitoring process by testing all commodities for aflatoxins and rejection of those with toxin levels exceeding the tolerable limits [ranges

L. Kumar, Head of Germplasm Health Unit and Virologist; R. Bandyopadhyay, Plant Pathologist, IITA, Ibadan, Nigeria.



Outline of Afla-ELISA testing scheme. Source: L Kumar.

between 2–20 parts per billion (ppb), depending on the type of toxin and country¹]. Heavy infestation of fungi results in moldy products which can be physically sorted. However, aflatoxins per se are invisible and leave no visual clues of their presence in the contaminated products. Aflatoxins

can be found even in commodities that show no apparent signs of fungal infestation. This situation poses a serious challenge to monitoring aflatoxin contamination, which depends on aflatoxinmonitoring tools.

Aflatoxin control relies on monitoring tools Monitoring for aflatoxins has become integral to effective measures to control aflatoxins in foods and feeds. A variety of aflatoxin monitoring tools are available to detect and quantify aflatoxin levels2. **Quantitative** estimation is most critical as decisions are based on aflatoxin levels in the commodity. Products with aflatoxin levels within the permissible range are allowed in trade and those with exceeding levels are rejected1.

Despite the availability of a wide variety of diagnostic tools for monitoring aflatoxins, their use in most of the developing countries is limited by high cost, difficulties with importation, and lack of appropriate laboratory facilities and well-trained staff. Among the many types of aflatoxin-monitoring tools, antibody-based

methods were proven to be relatively easy for developing countries to adopt.

Convenient option

At IITA, we developed an enzyme-linked immunosorbent assay (ELISA) named Afla-ELISA, for quantitative estimation of aflatoxins. Very high titered rabbit polyclonal antibodies for AFB1 were produced. These antibodies have an end-point titer of 1:512,000 (v/v) against 100 ng/mL AFB1-BSA standard; they are highly specific to AFB1 and also react with ABF2, AFG1, and AFG2. They were used to develop Afla-FLISA based on the

principle of indirect competitive ELISA for quantitative estimation of aflatoxins. This assay has a lowest detection limit of 0.09 ng/mL, and a recovery of 98±10% in maize.

Afla-ELISA is simple to perform, offers sensitive detection. and is convenient for adoption in sub-Saharan Africa. This test is suitable for routine aflatoxin surveillance in crops and commodities, and offers a low-cost alternative to official monitoring methods. It offers a sustainable solution to the problem of ever-increasing demand for monitoring programs related to

food safety and trade, and has the potential to enhance aflatoxin monitoring capacity in sub-Saharan Africa. To contribute to capacity development, training workshops have been organized on monitoring for mycotoxins and application of Afla-ELISA.

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Prototype Afla-ELISA kit—a quantitative serological assay for the estimation of total aflatoxins in maize and other commodities, using 96-well microtiter plates. Up to 20 samples can be tested in each 96-well plate at a cost of US\$4 per sample. Source: L Kumar.

Who's who

Nteranya Sanginga:

Science can solve agricultural problems

Nteranya Sanginga, the seventh Director General of IITA, talks about his journey to becoming the top man of one of the biggest international agricultural researchfor-development institutions in Africa, and some of Africa's most pressing issues regarding agriculture and food security in this interview with Jeffrey Oliver of the Communication Office.



Sanginga is an African of Congolese origin who comes from a very modest family. I studied science and then agriculture because I believed in it. Farming during my younger days made me realize that studying agriculture would help to contribute to solving problems in Africa, and everybody has "experimented" with the use of agriculture to address issues such as food security, health, or poverty. I strongly believe that science can help to alleviate some of these problems.

What motivated you to become DG?

The motivation comes from my passage through IITA. I was a student in IITA. I did my PhD here. I was very much encouraged and impressed with the diversity of our scientists from all



over the world—Asia, America, Africa. I saw them working on diversity, and I felt that I could contribute to that. I led a team which was composed of scientists from many places and we made a very good contribution. From there I started to develop my quality of leadership, and I was hoping (and also dreading) that one day I could lead this institution. So here we are.

You started as a student at IITA and now you are the DG. How would you describe your journey?

I think it has been an exciting journey with a lot of challenges and opportunities as well. As a student, my biggest challenge was language, since I came from a Francophone country. When I arrived for my PhD at IITA, I could not speak a word of English. My first contact with a scientist here was with a

microbiologist, Dr Ayanaba, and this was very challenging because he could not speak French and I could not speak English. But after 6 months, I gave my first seminar in English in the Conference Center in the presence of the DG. I distinctly remember the day that I got a scholarship because of the work that I had presented. After finishing my PhD, I went to work at the International Atomic Energy Agency in Vienna, At that time I didn't think that I would ever come back to IITA. On IITA's twenty-fifth anniversary, I won an award which I came to collect and I delivered a paper in the presence of the Board of Trustees and IITA's scientists. Then DG Dr Stifel convinced me that I should come back. So I came back to IITA as a scientist for 14 years where I led the Savanna program. When Hartmann, my predecessor as DG, came, I helped him set up his

strategy. In 2002, I got the position of TSBF director. I thought that was the end of my association with IITA. But after 8 years as director, dealing with the same problems, I thought I was qualified to take on the leadership of IITA when the DG position was announced. Hence, here I am.

As DG, what are your priority thrusts and why?

My first priority is to bring back research (to make new contributions to agricultural development, environmental protection, and food security). Having seen how our research moved toward development for almost 2 decades, and for good reason, because of the position of donors to push for the use of technology and products, I want to make sure that research is backed by strong science in the areas of crop improvement, plant health,



Dr N. Sanginga interacting with facilities management staff of IITA. Photo by IITA.

and natural resources management (NRM); to make sure we are thinking about the next 20 years, instead of talking about what is happening now. I see the role of IITA as being very proactive in solving the problems of the future—those that would come in the next 20 years. The second priority is capacity building. This is a neglected area and I want to bring it back. Hence, one of my first decisions was to create a directorate of partnership and capacity building.

We are a research-for-development institution. How should IITA balance these two elements (research and development)?

We have to put research in a position that alleviates constraints to development, so the research we are doing has to be relevant and must address development needs, not just research done for the sake of research. We need to strengthen our linkages with partners who can translate our research outputs to outcomes for alleviating poverty, NRM, degradation, food security, and malnutrition in Africa.

Let us talk about the new CGIAR research programs (CRP). How is IITA positioned with regard to these new CRPs?

We are the first center to align all our research programs to these new CRPs. IITA was created to be an institution that addresses integrated agricultural systems in the humid tropics. We are therefore happy that IITA is leading the CRP on Humidtropics. This CRP is an umbrella for all other CRPs which are components of the systems, including be commodity programs, such as maize, cassava, banana, which could provide the institutional framework for socioeconomic studies, markets, policies, and NRM. So our programs are naturally and very much aligned

to the CRPs; I believe that IITA will make a major impact on reaching the system-level outcomes in the new CRP.

Climate change has emerged as a major challenge to food security. How is IITA positioning itself to address this issue?

IITA's work for the past 30 years or so on crop improvement and breeding for resistance to biotic and abiotic constraints, such as drought or waterlogging, for example, all address the climate change issue. IITA was the first center that worked on farming systems in terms of adaptation to mitigate the effects of climate change. We are a part of the CRP on climate change where we will continue to contribute to aspects of adaptation and mitigation. IITA also has a lot to offer, especially in the future, in dealing with the problems from diseases and pests due to climate change. These are known to be very severe in Africa. IITA is probably among the better equipped CGIAR centers in terms of human resources to tackle that problem; we are proud to have the strongest biocontrol group in the system. Mitigation of climate change effect is integral to all our programs.

What is your take on the food security situation in Africa in the light of changing climate and increasing population? What do you see as IITA's role in securing food especially for the poor?

Africa has a huge expanse of arable land but the key to success is to intensify all the cropping systems in Africa. That is basically the framework that IITA is using to solve most of the problems of food security—using the intensification of cropping systems and building the capacity to scale up some of our successful technologies and products.

What should governments in Africa consider when investing in science and technology, especially in agricultural research? What is IITA's role in strengthening this?

IITA should have a very strong relationship with the host country, not only Nigeria but all the other countries where we work in Africa, especially in Tanzania, DRC, and Zambia. The major problems in most countries are low yields of major crops and poor capacity because of the low investment in agriculture. I advise countries to implement the Maputo declaration and invest more than 10% of the GDP in agriculture to overcome these problems. Countries should put high priority on investing in people at all levels, strengthening scientists, extension agencies, and farmers. I believe the government should back policies that allow private sector involvement in agriculture. Of course, countries need strong leadership to introduce changes in implementing agricultural development programs.

This year IITA celebrates its 45th anniversary and you are in a unique position to take IITA to its golden jubilee, 50 years. What is your general vision for the Institute?

IITA is the center of excellence for agricultural development in Africa. It will continue to play this role and I anticipate that it will become the global center for R4D in the humid tropics. I would like to see IITA leading efforts in the intensification of agriculture in the next 20 years. I would like IITA to be at the helm of the agriculture revolution in Africa, just as CIMMYT has been to Latin America and IRRI to Asia for the last 2-3 decades. I want IITA to lead this effort and enable other centers to achieve that goal. I would like IITA to double its resources financially and in terms of human resources to achieve this goal.

What will be the main challenges in realizing that vision?

The main challenge will be changing the mindsets of people not only in Africa but in IITA as well. People in IITA should believe that it is possible. If that mindset changes to one of people fighting hunger through research and everybody is motivated, I think this will be achieved. My challenge is to convince people that all together in 10 years we will be able to do that.

What is your message to IITA staff?

Please believe in what you are doing. Believe that you are doing unique research, that in this continent, everybody is counting on you to deliver science to help agricultural intensification to happen. And when that happens, the food increase in this continent is really possible. Believe that you can make this possible and that will be a major contribution.



Dr N. Sanginga inspecting an experiment in IITA, Ibadan. Photo by L. Kumar.

LOOKING IN

Valerie Bemo: Major breakthroughs in African agriculture require collaboration

Valerie Bemo (MD, MPH) is a native of Cameroon. She is a senior program officer in the Bill & Melinda Gates Foundation's Global Development Special Initiatives. Before joining the Foundation, she held various roles at the International Rescue Committee, most recently serving as senior technical advisor for health in the Democratic Republic of Congo and West Africa. She also worked with various NGOs and had extensive involvement in Aceh, Indonesia, Côte d'Ivoire, Sierra Leone, Mauritania, Kenya, and Chad. Dr Bemo received her medical degree from the University of Côte d'Ivoire, her epidemiology diploma from the University of Paris, and her MPH from Madrid Autonome University.

Tell us about yourself.

Born in Cameroon and educated in Cameroon, Côte d'Ivoire, France, and Spain, I have spent the last 15 years working on community development at the district and national level in Africa, Asia, and Europe. My professional and personal time is devoted to various organizations that impact health and development on a global scale.



Please describe your work at the Foundation. What are your goals?

My role as a Senior Regional Adviser (SRA) for West Africa is to help the Foundation's Agricultural Development team to establish and maintain relationships with key stakeholders that would lead to a greater impact of the Foundation's investments in the region. Our initial countries are Mali, Ghana, Burkina Faso, and Nigeria. The work involves:

- Ground-truthing country context and developing country strategy
- Providing a voice from the region to the foundation's Seattle headquarters
- Building partnership and understanding donor/partner context and landscape
- Providing social and cultural context
- Enhancing impact by influencing and shaping investments in coordination with foundation stakeholders.

What new agricultural initiatives is the Foundation undertaking in West Africa & Central Africa?

The Agricultural Development team at the Foundation has restructured their strategy. Our priority is for small-scale farmers and rural economies to thrive. We are now using a value chain approach, focusing on productivity improvements and the reduction of postharvest losses in specific staple crops and livestock, working closely with the governments of these countries and engaging stakeholders to get a complete sense of their agricultural work and plans. We are especially keen to work in areas that overlap with our strategy to achieve maximum leverage and address any major gaps that are impeding sustainable productivity growth in these value chains.

What are some of your challenges at work? What are the exciting highlights?

One of the key challenges to our involvement in the region is security. Violence and civil unrest, and unpredictability surrounding policies/politics in the region slow our momentum and disrupt plans.

The major highlight we have seen so far is that governments and existing players in the region are very welcoming. They are very willing to work with us and in most cases they see us not just as donors, but as thought partners.

What are some successful initiatives in agriculture and development in the region and their impacts?

It will take time to dramatically improve the productivity of small-scale farmers in the region, and it is too early for us to claim success in our own investments. This will require initiatives and collaboration from stakeholders. For instance, we believe that strong market incentives and a vibrant private sector involvement in agriculture are two very important factors for agriculture to thrive. The ultimate impact is to lift as many people out of poverty as possible, so focusing on the needs of the poorest farm families is also necessary.

As a partner, how would you describe the collaboration with IITA?

The partnership with IITA has been very good. With IITA's work in some of the same priority crops and value chains, this collaboration may become even stronger. We are optimistic that our collaboration in the context of our new strategy will bring good results in Nigeria, and in the region as a whole.

What are some of the areas that IITA should focus more?

IITA priorities have been set out in the context of the reform of the

international agricultural research centers, and we support that reform and those priorities.

How important is partnership in the African context? How could the collaboration among the various stakeholders be more effective? Collaboration among all stakeholders in Africa will be very crucial for Africa to be able to tap into the incredible potential and increased agricultural productivity.

Any major breakthroughs in agriculture in the region will require collaboration from upstream research and development, to downstream adoption and scaling. It will require governments working with farmers, research institutions, private sector players and NGOs. Every group has the potential for making an important contribution, and a great variety of skills and resources are needed. We are optimistic that these critical

players will achieve a new level of collaboration and sharing, leading to more efficiency and effectiveness.

What is your dream for African agriculture and development?
My dream for Africa is to see Africans leading the strategies and efforts to reduce poverty and to see the population, especially women and children, have access to basic health, education, clean drinking water and to be able to feed themselves. These will ultimately lead the people of Africa to

having healthy and productive lives.

I fully share the Foundation's "impatient optimist" vision for African agriculture development, that is to see productivity for 30 million farming households increase by 170% by 2030, with the ultimate goal of a 40% reduction in the \$1/day poverty rate in the region. It is a big goal that will require not just our effort but that of all the major stakeholders, including IITA.



Dr V. Bemo on a mission in Makindu. Photo from Bill & Melinda Gates Foundation.

FRONTIERS

Modern biotechnologies have dramatically reshaped the crop improvement research during the past decade. Biotechniques have become indispensable for efficient and effective development of new knowledge, processes, and products. IITA's biotechnology, strategized as three major themes—genomics, transgenics, and diagnostics, is directed toward the genetic improvement of staple food crops of Africa, such as cooking-banana, plantain, cassava, yam, and cowpea. This section provides some insights and progress in this program.

Leveraging "agrigenomics" for crop improvement

Melaku Gedil (m.gedil@cgiar.org) and Ismail Rabbi

Harnessing state-of-the art genomics technologies

The potential application of "Omics" technology, as demonstrated by the steadily growing impact of biosciences, in alleviating the multitude of constraints in agricultural production is rapidly becoming a reality with the advent of next-generation DNA sequencing and genotyping technologies, high throughput (HTP) metabolomics and transcriptomics, informatics, and decision-making tools. These technologies, together with rapidly evolving bio-computational tools, are accelerating the discovery of genes and closely linked molecular markers underlying important traits. This has lead to the rapid accumulation of genomic

resources necessary for devising an efficient and effective breeding strategy geared toward the faster development of varieties.

The state-of-the-art technologies including the next-generation sequencing (NGS) for genome and transcriptome analysis, as well as genotyping-by-sequencing (GBS) are being adopted in R4D programs at IITA. For instance, the NGS through outsourcing and multi-partner collaboration; the RNAseq for HTP expression study in cassava: the Illumina's Golden Gate Assay for HTP single nucleotide polymorphism (SNP) genotyping in cassava, soybean, and maize as well as GBS in maize and cassava. Data generated by these techniques

M. Gedil, Head, Bioscience Center; I. Rabbi, Postdoctoral Fellow (Molecular Genetics), IITA, Ibadan, Nigeria.

are being applied for markerassisted recurrent selection (MARS) of drought-tolerant maize, and genome selection (GS) for highyielding, disease-resistant cassava.

Development of an integrated molecular breeding platform

The new technologies, however, are very data-intensive and demand advanced computational and communication technologies and infrastructure for data acquisition, analysis, and management. For the effective integration of genomics technologies in our breeding schemes, we are building capacity (connectivity to the internet, the necessary hardware/software, and skilled personpower) to acquire, store, and analyze terabytes of data.

The Generation Challenge Program (GCP) of the CGIAR is developing an integrated breeding platform (IBP) to build a comprehensive and integrated crop information system enabling linkages among molecular, phenotypic, and pedigree data. The maize version of International Crop Information System (ICIS), dubbed International Maize Information System (IMIS), has been expanded to include all pedigrees of IITA maize under the Drought Tolerant Maize for Africa (DTMA) project. It has some functionality in terms of molecular data storage but this is limited and we are now generating data sets of hundreds of thousands of markers per line that require different storage solutions. The GCP is consulting with other initiatives such as iPlant and DArT and is working on collaboratively creating solutions for the needs of several user-cases including DTMA. Tropical Legumes (TL)-I, and TL-II projects. In the IBP initiative, IITA

is the leading crop center to host the main web-accessible databases of cassava, cowpea, yam, and soybean. The form and functionality of the databases are still a work in progress although activities are ongoing in the application of current versions of ICIS to cassava, yam, and cowpea.

In view of the IBP initiative, we are developing a bioinformatics capacity to (a) manage the newly generated genomic resources of IITA's research crops, particularly those clonally propagated, (b) use the genomic resources in the public sector for soybean and maize, (c) use comparative genomics techniques for other African orphan crops of high importance, such as cassava, yam, and cowpea, and (d) create a bioinformatics center of excellence to train and provide access for African research scientists.

HTP by genotyping and informatics support tools

The increasing affordability of the NGS technologies has shifted critical consideration from genotyping to phenotyping. According to leading experts, it is now cheaper to genotype than to phenotype a plant. Quality phenotypic data are essential for the interpretation and use of the deluge of genomic data to identify the changes in DNA sequences that influence important traits. The fact that priority agronomic traits are complex and polygenic and interact with the environment necessitates conducting extensive and precise multi-environment evaluations of candidate breeding materials (over several years and in several locations). Therefore, there is a need to invest in precision phenotyping of traits and data capture (from electronic sample tracking to non-invasive HTP) through the use of hand-held devices such as barcode readers and near-infrared spectroscopy. Efforts are being made to develop rapid and accurate phenotyping protocols to integrate with genomic tools in establishing breeding schemes at IITA.

A wide array of techniques and tools is being deployed to associate molecular markers with desirable phenotypic traits. Associated markers can be used to accelerate germplasm enhancement via MARS, marker-assisted backcrossing

for the introgression of disease resistance and other simple traits, hence bypassing the necessity of evaluating breeding materials in the field; MARS for rapid cycle population improvement in biparental crosses based on genomic estimated breeding value; and GS based on a model developed with a training population to select untested samples.

Our efforts to harness the unparalleled scientific progress in the fields of genomics and bioinformatics are expected to find solutions to the recalcitrant problems confronting small-holder farmers in sub-Saharan Africa.



Researchers in IITA's Bioscience Center. Photo by L. Kumar.

Transgenics in crop improvement research at IITA

Leena Tripathi (I.tripathi@cgiar.org)



Harvested bunch of transgenic bananas, Kampala, Uganda. Photo by L. Tripathi.

Biotechnology has opened unprecedented avenues for exploring biological systems. Transgenics is one of the key techniques particularly useful for the genetic improvement of crops that are not amenable to conventional breeding, such as those that are vegetatively propagated. In IITA, transgenic technologies are being used for improving banana/plantain (*Musa sp.*), cassava (*Manihot esculenta*), and yam (*Dioscorea sp.*).

Genetic transformation platform

An efficient protocol for plant regeneration and transformation is a prerequisite for the successful use of transgenic technologies. Despite the technical difficulties in transforming monocot species, efficient transformation protocols that are embryogenic cell suspension based and Agrobacterium mediated have been established for many cultivars of banana/plantain. This system, however, is a lengthy process and cultivar dependent. Therefore, a transformation protocol using meristematic tissues was also established which is rapid and genotype independent. These protocols have paved a way for the genetic manipulation of banana/plantain by incorporating agronomically important traits such as those conferring resistance

L. Tripathi, Biotechnologist, IITA, Nairobi, Kenya.

to diseases or pests as well as tolerance to abiotic stress factors.

Agrobacterium-mediated transformation protocols for three popular cassava varieties preferred by African farmers were established through somatic embryogenesis. A regeneration and transformation protocol is also established for yam (Dioscorea rotundata and D. alata) using nodal explants, but transformation efficiency needs to be improved. A transformation protocol using somatic embryogenic callus for yam is under development.

Development of disease- and pestresistant transgenic crops

Banana Xanthomonas wilt (BXW), caused by the bacterium Xanthomonas campestris pv. musacearum (Xcm), is the most devastating disease of banana in the Great Lakes region of Africa. In the absence of natural host plant resistance, IITA, in partnership with NARO-Uganda and the African Agricultural Technology Foundation, has developed transgenic banana by constitutively expressing the Hypersensitive Response Assisting Protein (*Hrap*) or plant ferredoxinlike protein (Pflp) gene from sweet pepper (Capsicum annuum). The transgenic plants have exhibited strong resistance to BXW in the laboratory and screenhouse tests. The best 65 resistant lines were planted in a confined field trial at the National Agricultural Research Laboratories (NARL), Kawanda, Uganda, for further evaluation.

Based on results from mother plants and their first ration plants, 12 lines were identified that show absolute resistance. The plant phenotype and the bunch weight and size of transgenic lines are

similar to those of nontransgenic plants. These lines will be further tested in a multilocation trial in Uganda. They will be evaluated for environmental and food safety in compliance with Uganda's biosafety regulations, risk assessment and management, and procedures for seed registration and release, and are expected to be released to farmers in 2017.

Cassava brown streak disease (CBSD) has emerged as the biggest threat to cassava cultivation in Fast Africa. As known sources of resistance are difficult to introgress by conventional methods into the cultivars that farmers prefer, the integration of resistance traits via transgenics holds a significant potential to address CBSD. Of the available transgenic approaches, RNA silencing is a very promising strategy that has been successfully employed to control viral diseases. IITA, in collaboration with Donald Danforth Plant Science Centre (DDPSC), USA, is developing CBSDresistant cassava for East Africa.

Nematodes pose severe production constraints, with losses estimated at about 20% worldwide. Locally, however, losses of 40% or more occur frequently, particularly in areas prone to tropical storms that topple the banana plants, IITA, in collaboration with the University of Leeds, UK, has generated transgenic plantain using maize cystatin that limits the digestion of dietary protein by nematodes, synthetic peptide that disrupts chemoreception, or both of these traits. These lines expressing the transgenes were challenged in a replicated screenhouse trial with a mixed population of the banana nematodes, Radopholus similis and Helicotylenchus multicinctus.

Many lines were significantly resistant to nematodes compared with nontransgenic controls. The promising transgenic lines showing high resistance will be planted in confined fields in Uganda for further evaluation in mid-2012.

Transgenic technologies for abiotic stress tolerance

Cassava roots undergo rapid deterioration within 24-48 hours after harvest, the socalled postharvest physiological deterioration (PPD), which renders the roots unpalatable and unmarketable. IITA, in collaboration with the Swiss Federal Institute of Technology (ETH) Zurich, is developing cassava tolerant of PPD through the modification of ROS (reactive oxygen species) scavenging systems. The potential is being assessed of various ROS production and scavenging enzymes, such as superoxide dismutase, dehydroascorbate reductase, nucleoside diphosphate kinase 2, and abscisic acid

responsive element-binding protein 9 genes, to reduce the oxidative stress and the extent of PPD in transgenic cassava plants.

Future road map

Efforts at IITA over the last 10 years to establish transformation protocols for all the IITA crops have been paying off and have led to the establishment of a genetic transformation platform for cassava, banana/plantain, and yam-the three most important food crops in sub-Saharan Africa. These technologies have contributed to significant advances in incorporating resistance to pests and diseases in banana and cassava. Some of these technologies have the potential to offer additional benefits. For instance, the transgenic technology to control Xanthomonas wilt may also provide an effective control of other bacterial diseases of banana (Moko, blood, and bugtok diseases), and of bacterial blight in other crops such as cassava and cowpea.



Transgenic technologies provide a platform for controlling diseases in banana, cassava, and cowpea. Photo by IITA.

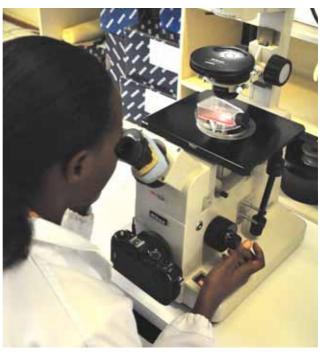
Molecular diagnostic tools for plant health protection

Lava Kumar (L.kumar@cgiar.org)

Molecular tools in disease diagnosis

Rapid advancements in biotechnologies have led to the development of a myriad of molecular diagnostic tools in the past decade1. These tools, either based on the properties of nucleic acid (DNA or RNA) or proteins of the target agents, have improved the efficacy, accuracy, and speed of detection and identification of disease-causing agents and characterization of the diversity of pathogens and pests.

Most popular protein detection methods depend on antigenantibody interactions. Polyclonal or monoclonal antibodies produced against the proteins of interest are used as probes to detect the target proteins by techniques such as enzyme-linked immunosorbent assay (ELISA), Western immunoblotting, dot immunobinding assav, and several variants of these techniques. Meanwhile, nucleic



Researcher observing mouse hybridoma cell lines under microscope in the Virology and Molecular Diagnostics Unit, IITA, Ibadan, Nigeria. Photo by IITA.

acid-based diagnostic tools are based on the hybridization of homologous nucleotides, size of the DNA fragments generated by restriction enzyme treatment, order of nucleotide arrangement, or a combination of more than one of these

approaches. Polymerase chain reaction (PCR), developed in the mid-1980s, has led to the development of several new and simplified techniques, fast established as a mainstay of applied molecular biology and molecular diagnostics.

Platform for developing molecular diagnostics

The objective of the molecular diagnostics research in IITA is to develop tools and technologies for better understanding, diagnosis, and monitoring of biological systems. This program emphasizes the development of simple and accurate tools and procedures for rapid identification of pathogens and pests affecting the food and horticultural crops in sub-Saharan Africa (SSA). Both protein and nucleic-acid based diagnostic tools have been developed against target agents (viruses, fungi, bacteria, phytoplasma, insect pests, and mycotoxins). These tools are critical to several programs on crop improvement and crop protection, including evaluation of germplasm for host resistance, breeding for pest and disease resistance, surveillance surveys, and monitoring programs.

ELISA-based diagnostics are preferred for the identification of plant viruses. It is simple, reliable, cost-effective, and easy to adopt in minimally-equipped labs. Backed with facilities for purifying proteins, and production of polyclonal

and monoclonal antibodies, ELISAbased diagnostics were established for about 20 economically important viruses affecting IITA's mandate crops in SSA (e.g., Maize streak virus, cassava mosaic begomoviruses, Cowpea mottle virus, Southern bean mosaic virus, and more). Antibodies were also produced against nonviral targets such as mycotoxins. Polyclonal antibodies produced against aflatoxin B1 were used to develop the 'Afla-ELISA' test for quantitative estimation of aflatoxins in maize and other commodities (see article on page 45). Monoclonal antibodies are usually produced for discriminating closely related virus species or strains (e.g., African cassava mosaic virus and East African cassava mosaic virus). The production of monoclonal antibodies is expensive and tedious, but it offers the advantage of perpetual production of antibodies from mouse hybridoma cell lines. Because of this, IITA has placed increasing emphasis on producing monoclonals for all important pathogens.

PCR-based diagnostics are developed as an alternative tool or to overcome the limitations of ELISA in detecting viroids, viral satellites, and to discriminate strains and closely related species. Oligonucleotide primers have been developed based on the genomic data generated from our research programs and those available in the public database for the specific detection of targets in PCR assays. Procedures were also established to simplify PCR application. For instance, a procedure established for direct detection of viruses in leaf sap bypasses the need for nucleic extraction2. Emphasis is placed on the development of multiplex PCR assays for the simultaneous detection of more than one virus in a single reaction. A multiplex PCR method has been developed for the simultaneous detection of African cassava mosaic virus and East African cassava mosaic likeviruses responsible for cassava mosaic disease in SSA2. This test was further improved to detect cassava brown streak viruses that have emerged as a major threat to cassava in East Africa, thereby making it a one-stop test for detecting all the major viruses infecting cassava in SSA.

Similar efforts are being devised to detect all viruses infecting yam. Real-time PCR using TagmanTM probes are being developed to quantify virus concentrations within the plants to characterize host response to virus inoculation. Presently, specific and generic diagnostic tools for the detection of almost all the pathogens that affect major food staples in SSA have been established at IITA.

Pathogen diversity and DNA barcodes

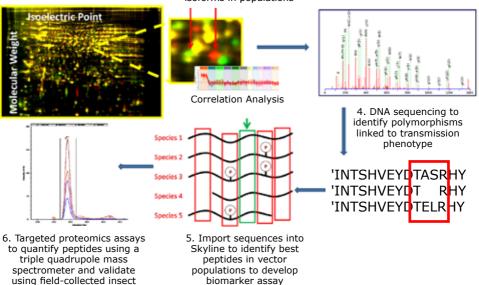
Detailed knowledge of pathogen diversity is a prerequisite to developing unambiguous diagnostic tools. Pathogen populations are characterized by sequencing the specific genes and the data generated is used to interpret origin and spread of the pathogen, taxonomy, and phylogeny. For diversity assessment, gene targets are selected based on the pathogen that comprise, ribosomal Internal Transcribed Sequence (ITS), mitochondrial cytochrome oxidase-I (COI), histone, virus coat protein, etc. This approach has been used for assessing the diversity of Colletotrichum

aloeosporioides responsible for anthracnose of yam, Cercospora spp. causing gray leaf spot of maize, cassava brown streak virus, banana bunchy top virus, and several other agents. Information generated from these studies have provided valuable clues to understand the origin and drivers of spread, identification of previously uncharacterized pathogens3,4 and identification of unique markers known as "DNA barcodes" for use as genetic markers for identifying pathogens and pests5.

1. DIGE quantification

samples

 Statistics to find isoforms linked to transmission and all other isoforms in populations 3. Protein identification



Workflow in development of protein biomarkers. Source M. Cilia, Cornell University

Biomarkers for insect vectors

Recently a new initiative was started in collaboration with Cornell University to identify protein biomarkers to rapidly identify variation in vectoring potential of aphid and whitefly vector populations. Diagnostic tools developed in this program will aid in better understanding the virus-vector interactions, disease epidemiology, and improved management of insect vector-borne virus diseases.

Training in application of molecular diagnostics

In addition to technology development, efforts are made to transfer technology, products, and skills to stakeholders in national research and extension services. This is done through collaborative activities and organization of training courses at regular intervals in collaboration with national organizations such as the Nigerian Institute of Science Laboratory Technology. During the training courses, specific emphasis is placed on the application of diagnostics in monitoring and surveillance programs. Standard diagnostic protocols are compiled into a cookbook style laboratory manual⁶ and distributed during the training courses.

End note

Molecular diagnostics development programs in IITA consider the latest knowledge and state-of-theart technologies in establishing simple and robust tools that are relevant to endusers, are low-cost, and conducive for adoption in minimally equipped labs. We are adding new tools, such as, loop-mediated isothermal amplification reaction (LAMP) assay and deep sequencing approaches to broaden the knowledge on pathogens occurring in our mandate crops to increase the repertoire of available tools.

Molecular diagnostic tools are routinely used in germplasm indexing, phenotypic evaluation of germplasm, disease surveillance, and monitoring programs in SSA. They are also used in collecting baseline information and monitoring shifts in pathogen and pest dynamics due to changes in agricultural systems and climate change effect. These tools are already proving useful in rapid detection and identification of new and emerging pathogens

and pests [e.g., Paracoccus marginatus (papaya mealybug) in Nigeria; Phytophthora colocasiae causing taro leaf blight in Nigeria and Ghana; 16srII group phytoplasma responsible for witches' broom disease of soybean in Southern Africa; and Banana bunchy top virus in Benin].

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The R4D Review has six sections:

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Headquarters: IITA, PMB 5320, Ibadan, Nigeria Mailing address: IITA, Carolyn House, 26 Dingwall Road, Croydon CR9 3EE, UK Telephone: (234 2) 751 7472, (1 201) 633 6094





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