

Summaries of presentations: Opening plenary session and parallel sessions

FAO International Symposium on
“The Role of Agricultural Biotechnologies in Sustainable Food Systems and Nutrition”
15- 17 February, 2016

The international symposium will explore how the application of science and technology, particularly agricultural biotechnologies, can benefit smallholders in developing sustainable food systems and improving nutrition in the context of climate change. The symposium takes a multisectoral approach, covering the crop, livestock, forestry and fishery sectors. It also aims to cover the wide spectrum of available biotechnologies, including microbial food fermentation, tissue culture in plants, reproductive technologies in livestock, use of molecular markers, genetic modification and other technologies.

The symposium takes place over two and a half days, with keynote speakers addressing the opening plenary session on 15 February. A high-level ministerial segment will take place on 16 February. Three parallel sessions will also be held each day and the symposium will close on 17 February 2016 with a final plenary session where outcomes from the parallel sessions will be reported.

All parallel session speakers and opening plenary speakers have been asked to provide a 2 page summary (1000 words) of their presentation. **This document provides these summaries.**

The agenda for the keynote speeches and parallel sessions is provided below with hyperlinks to each speaker’s summary. If a summary is available, the name of the speaker will be in blue text. **CTRL+ Click** on the author’s name to go directly to their summary. At the end of each summary there is another hyperlink to return to the top of the document.

This document will be updated to include new speaker summaries. Please see the symposium website (<http://www.fao.org/about/meetings/agribiotechs-symposium/en/>) for the latest version.

49 out of a total 51 summaries are now provided

Monday 15th February 2016**09.30-12.30: Plenary Session, Green Room**

Welcome address by **José Graziano da Silva**, Director-General, FAO, Rome, Italy

Keynote addresses:

1. *The state of knowledge in biotechnology*, by **Louise Fresco**, President, Executive Board of Wageningen UR, Wageningen, the Netherlands
2. *Towards ending the misplaced global debate on biotechnology*, by **Gebisa Ejeta**, Distinguished Professor, Purdue University, West Lafayette, United States of America
3. *Biotechnologies in action in Brazil*, by **Mauricio Lopes**, Empresa Brasileira de Pesquisa Agropecuária, Brasília, Brazil
4. *Breakthroughs in resource productivity*, by **Gunter Pauli**, Founder, Zero Emissions Research and Initiatives Network, Japan

14.00-17.00: Parallel Sessions

Sheikh Zayed Centre	Red Room	Green Room
1.1 Facing the challenges of climate change: Adaptation in the crop and forestry sectors	2.1 Improving productivity through enhanced resource use efficiency	3.1 Social and economic impacts of agricultural biotechnologies for smallholders: Taking stock of the evidence and prioritizing future assessments
Chair: Chittaranjan Kole Jacob School of Biotechnology & Bioengineering, Allahabad, India	Chair: Sergio Feingold Instituto Nacional de Tecnologia Agropecuaria, Buenos Aires, Argentina	Chair: Sachin Chaturvedi Research and Information System for Developing Countries, New Delhi, India
<i>Introductory Remarks (5')</i> Chittaranjan Kole	Co-chair: Thuy Nguyen BioSciences Research Division, Melbourne, Australia	Co-chair: Eduardo Trigo Ministry of Science, Technology and Productive Innovation, Buenos Aires, Argentina
1.1.1 Abdelbagi Ismail <i>Developing rice varieties with enhanced adaptation to lowland farming systems: Case studies from South Asia (20')</i>	<i>Introductory Remarks (5')</i> Thuy Nguyen	<i>Introductory Remarks (5')</i> Sachin Chaturvedi <i>Introductory Remarks (5')</i> Eduardo Trigo
1.1.2 Yoseph Beyene <i>Harnessing agricultural biotechnology for resilience to climate change: A lesson from water efficient maize for Africa project (20')</i>	2.1.1 Sibin Yu <i>Resource use efficiency in crops: "Green Super Rice" to increase water and nitrogen use efficiency of rice (25')</i>	<i>Introductory Remarks (5')</i> David Spielman <i>Evidence-based policy-making: The role of impact assessment studies and their implications for agricultural biotechnologies (25')</i>
1.1.3 Douglas Cook <i>Molecular breeding in legumes for resource-poor farmers: Chickpea for Ethiopia and India (20')</i>	2.1.2 Sean Mayes <i>Resource use efficiency in vegetables: Application of molecular breeding to bambara groundnut, an underutilised crop for low-input agriculture (25')</i>	3.1.1 Andrea Sonnino <i>Lessons learned from case studies of applying biotechnologies for smallholders (15')</i>
1.1.4 Ciro De Pace <i>Genomic approaches for dissecting fitness traits in forest tree landscapes (20')</i>	2.1.3 David Penman <i>Resource use efficiency in fish: Application of biotechnology in genetic improvement in tropical aquaculture (25')</i>	3.1.2 Jikun Huang <i>Evidence at work: Country experience in the use of evidence in policy-making on agricultural biotechnologies (15')</i>
1.1.5 Sally Aitken <i>Use of genomics for understanding and improving adaptation to climate change in forest trees (20')</i>	2.1.4 Denis Mujibi <i>Resource use efficiency in livestock: Bridging the biotechnology-livestock productivity gap in East Africa</i>	3.1.3 Narayan Hegde <i>Factors that determine whether biotechnologies can have positive impacts on the livelihoods of smallholders: Examples from India (15')</i>
<i>Discussion (70')</i> moderated by Chittaranjan Kole	2.1.5 Judy Loo <i>Resource use efficiency in forestry: Utilisation of tree genetic resources (25')</i>	<i>Discussion (95')</i> moderated by Eduardo Trigo
<i>Closing Remarks (5')</i> Chittaranjan Kole	<i>Discussion (45')</i> moderated by Dominic Glover Institute of Development Studies, Brighton, United Kingdom	<i>Closing Remarks (5')</i> Sachin Chaturvedi
<i>Closing Remarks (5')</i> Chittaranjan Kole	<i>Closing Remarks (5')</i> Sergio Feingold	

February 18, 2016
Tuesday 16th February 2016

09.30-12.30: Parallel Sessions

Sheikh Zayed Centre	Red Room	Green Room
1.2 Facing the challenges of climate change: Adaptation in the livestock and fishery sectors	2.2 Post production value addition and food safety (2 sub-sessions)	3.2 Public policies, strategies and regulations on agricultural biotechnologies
Chair: Shadrack Moephuli Agricultural Research Council, Pretoria, South Africa Co-chair: Thuy Nguyen BioSciences Research Division, Melbourne, Australia	Chair sub-session 1: Sergio Feingold Instituto Nacional de Tecnología Agropecuaria, Buenos Aires, Argentina Chair sub-session 2: Delia Grace International Livestock Research Institute, Nairobi, Kenya	Chair: Vimlendra Sharan
<i>Introductory Remarks (5')</i> Thuy Nguyen	Sub-session 1: Enhancing value in the post-production phase <i>Introductory Remarks (5')</i> Sergio Feingold	<i>Introductory Remarks (5')</i> Vimlendra Sharan
1.2.1 Panya Sae-Lim <i>Fish breeding for future environments under climate change (20')</i>	2.2a.1 Cavaba Srinivas Prasad <i>Use of feed additives generated through fermentation technologies for livestock feed (20')</i>	3.2.1 Rodrigo Sara <i>The role of intellectual property rights in enabling or impeding the application of agricultural biotechnologies, with special reference to developing country agriculture (15')</i>
1.2.2 Sandra Adams <i>Development of diagnostic tools and vaccines for aquatic animals (20')</i>	2.2a.2 Eric van de Weg <i>Use of biotechnologies to increase the storability and shelf life of fruit (20')</i>	3.2.2 Adrienne Massey <i>Regulation and intellectual property of agricultural biotechnologies: Perspectives from the private sector (15')</i>
1.2.3 Paul Boettcher <i>Biotechnologies for animal breeding and coping with climate change (20')</i>	2.2a.3 Howard-Yana Shapiro <i>Applying agricultural biotechnology tools and capabilities to enhance food security and nutrition from local food crops to stimulate sustainable income opportunities for small holder farmers to reduce poverty. (20')</i>	3.2.3 Guy Kastler <i>Regulation and intellectual property of agricultural biotechnologies: Perspectives from the civil society (15')</i>
1.2.4 Ulrich Meyer <i>Use of biotechnologies to improve feed quantity and quality: Adaptation to the changing climate from the animal nutrition perspective (20')</i>	<i>Discussion (20') and sub-session closing remarks (5') moderated by Sergio Feingold</i>	
	Sub-session 2: Using biotechnologies to ensure the safety of food <i>Introductory Remarks (5')</i> Delia Grace	
1.2.5 Jean de Foucauld <i>Livestock vaccines: development and market access</i>	2.2b.1 Kohei Makita <i>Traditional milk fermentation as a potential tool for sustainable improvement of food safety' (20')</i>	3.2.4 Eduardo Trigo <i>The challenges of developing national policies and regulations for agricultural biotechnologies: Reflections from cumulative experience (15')</i>
1.2.6 Farai Muchadeyi <i>A landscape genomics approach in unravelling adaptive genetic diversity in goats: A case study of South Africa (20')</i>	2.2b.2 Ranjit Bandyopadhyay <i>Aflasafe: a case study for aflatoxin reduction in crops (20')</i>	3.2.5 Dominic Glover <i>How to ensure that policies, strategies and regulations on agricultural biotechnologies act to benefit smallholders (15')</i>
<i>Discussion (50') moderated by Shadrack Moephuli</i>	2.2b.3 Flábio Ribeiro de Araújo <i>Diagnostic tools to detect pathogens causing tuberculosis in cattle and prevent their transmission through dairy products to humans (20')</i>	<i>Discussion (80') moderated by Vimlendra Sharan</i>
<i>Closing remarks (5')</i> Shadrack Moephuli	<i>Discussion (20') and sub-session closing remarks (5') moderated by Delia Grace</i>	<i>Closing remarks (5')</i> Vimlendra Sharan

09.00-12.00: Parallel Sessions

Sheikh Zayed Centre	Red Room	Green Room
1.3 How can biotechnologies contribute to adaptation with mitigation co-benefits?	2.3 Nutrition and food quality	3.3 Investing in biotechnology solutions through capacity development and partnerships
Chair: Olivier le Gall Institut National de la Recherche Agronomique, Auzeville-Tolosane, France	Chair: Maggie Gill Consultative Group for International Agricultural Research and University of Aberdeen, Aberdeen, United Kingdom	Chair: Kongming Wu Chinese Academy of Agricultural Sciences, Beijing, China
<i>Introductory remarks (5')</i> Olivier le Gall	<i>Introductory remarks (5')</i> Maggie Gill	<i>Introductory remarks (5')</i> Kongming Wu
1.3.1 Daniel Sumner <i>Agricultural biotechnology and the economics of food security and climate change mitigation (25')</i>	<i>Introductory remarks (5')</i> Maggie Gill	3.3.1 Helen Altshul <i>Biosciences capacity building in Africa: Lessons learned from Biosciences eastern and central Africa (BecA) (15')</i>
1.3.2 Stephan Weise <i>Bioversity, key to helping farmers adapt to climate change (15')</i>	2.3.1 Anna Lartey <i>Our food, our diet, our health: Where do we go from here?</i>	3.3.2 Denis Murphy <i>Case studies of public-private partnerships in agricultural biotechnologies: Lessons learned (15')</i>
1.3.3 Guntur Venkata Subbarao <i>Biological nitrification inhibition (BNI) in plants: Implications for nitrogen-use efficiency and nitrous oxide emissions from agricultural systems (15')</i>	2.3.2 Melissa Fitzgerald <i>Application of biotechnologies in improving the quality of rice and wheat. (20')</i>	3.3.3 Sarah Evanega <i>Building Partnerships, Empowering Champions: The example of the Cornell Alliance for Science (15')</i>
1.3.4 Henning Steinfeld <i>Mitigation of enteric methane emissions from ruminant animals (15')</i>	2.3.3 Howarth Bouis <i>Biofortification of Staple Food Crops: Justification, Progress, and Future Activities. (20')</i>	3.3.4 Riccardo Aleandri <i>North-south/west-east cooperation in agricultural biotechnologies: Some lessons from Italy. (15')</i>
1.3.5 Paulo Kageyama <i>Use of biodiversity as a biotechnological tool for carbon sequestration in the tropics (15')</i>	2.3.4 Albert Tacon <i>Fish for all: role of biotechnology in improving nutrition (20')</i>	3.3.5 Sachin Chaturvedi <i>Case studies of south-south collaboration in agricultural biotechnologies: Lessons learned (15')</i>
1.3.6 Hervé Saint Macary <i>Carbon sequestration in agricultural soils: The "4 per mil" program (15')</i>	<i>Discussion (80') moderated by</i> Maggie Gill	
<i>Discussion (70') moderated by</i> Olivier le Gall	<i>Closing remarks (5')</i> Maggie Gill	
<i>Closing Remarks (5')</i> Olivier le Gall		<i>Discussion (95') moderated by</i> Courtney Paisley , Young Professionals for Agricultural Development (YPARD), Rome, Italy
		<i>Closing Remarks (5')</i> Kongming Wu

Monday 15 February
09.30-12.30 Plenary Session, Green Room

Opening plenary addresses:

Welcome address by José Graziano da Silva, Director-General, FAO, Rome, Italy

Dear Ministers;
Excellencies;
Honourable keynote speakers;
Distinguished delegates;
Representatives from Civil Society, Private Sector, Research Institutions, Academia;
Ladies and gentlemen;

Welcome to this International Symposium on "The Role of Agricultural Biotechnologies in Sustainable Food Systems and Nutrition".

I am delighted to see representatives of governments, civil society and private sector, as well as eminent experts, opinion leaders, research organizations, cooperatives and development partners, gathered here at FAO for this 3 days event.

Thank you for coming in order to share your views, experiences and lessons learned on such an important issue.

As you all know, we have many challenges ahead by 2030 to eradicate hunger, improve nutrition and make food systems more sustainable.

And these challenges are surrounded by uncertainties and complexities, especially in the context of a changing climate.

We are constantly facing new and unexpected situations that emerge as a national, regional or global threat. The Zika Virus, in the health sector, is just an example of such unexpected scenarios.

It reminds me of the words of Lord Keynes, which I quote: *"There is no scientific basis on which to form any calculable probability. We simply do not know what may happen"*.

I am afraid that the challenges posed by climate change to the world food security should be considered under this keynesian perspective. Because we simple do not know much about what has been called the "new normality", in order to make calculations on the most probable scenario in the coming years.

The huge amount of information and sometimes mere speculation circulating today increase the uncertainties even more.

Professor Bertrand Hervieu has recently addressed this issue in Paris. Let me quote:

"The events we are experiencing refer to the obvious uncertainty of the course of history and the complexity of the world."

These uncertainty and complexity are enhanced by the immediacy of information, which leads to fragmentation, preventing any development of perspectives, explanations and understandings of the world and of the time we live in.

You can be sure, said Professor Hervieu, that the year 2016 will be at least as uncertain and complex as 2015 was.

So, let us wish for each other the intellectual strength and courage to penetrate this complexity, and, if possible, to control it. Let us not give up to the hardships of our times. Let's try to master them".

Ladies and gentlemen,

I am using these words to highlight the importance of considering every possible solution to achieve world food security for all in the years to come.

We must count on a broad portfolio of tools and approaches to eradicate hunger, fight every form of malnutrition and achieve sustainable agriculture in the context of climate change.

As a neutral forum, FAO has been promoting debates, dialogues and exchange of information in order to enhance our knowledge of these tools and approaches.

We held an international symposium on agroecology in 2014.

We helped launch the Global Alliance on Climate Smart Agriculture in the same year.

And we have just released a new edition of "Save and Grow in Practice", FAO's model of ecosystem-based agriculture.

Now it is time to discuss and analyse what agricultural biotechnologies has to offer.

This symposium aims at showing the many possibilities and benefits of applying biotechnology in the agricultural sectors, including crops, livestock, forest and fisheries.

Showing, for instance, how it can help to transition to an agricultural production that relies on fewer inputs with less negative environmental impacts.

And, ladies and gentlemen, let me state this loud and clear: this symposium is not only about Genetically Modified Organisms. Agricultural biotechnologies are much broader than GMOs.

Biotechnology gives us options and improves our capacity to act and respond in many different areas. We will address fermentation processes, bio-fertilizers, artificial insemination, the production of vaccines, disease diagnostics, just to name a few.

I look forward to hearing stories on how biotechnologies can accelerate the development of improved and locally adapted crop varieties. And can permit the rapid diagnosis of diseases and pests. We want also to investigate and give examples of how modern biotechnology can be compatible with principles of agroecological approaches.

Knowledge and innovation are also key to address complex challenges:

- Knowledge and innovation that are grounded on sound evidence and science;
- That leads to better integrating different concerns and perspectives of women and men of all ages;

- That can facilitate transfer of technologies and practices, and promote collaboration, including through South-South cooperation.

Ladies and gentlemen,

We cannot lose sight of the fact that biotechnology, knowledge and innovation must be available, accessible and applicable to family farmers. Otherwise, they will have a limited impact.

We must find means to remove the barriers that prevent their availability to family farmers.

They are responsible for the largest proportion of the food we eat.

I hope we will be able to identify new, better and innovative ways to make agricultural biotechnologies accessible to those who could benefit most.

Ladies and gentlemen,

The Symposium is planned around three main themes:

- Climate change impacts;
- Sustainable food systems and nutrition; and
- People, policies, institutions and communities

We will have a high-level segment where government representatives shall express and exchange their views.

There will be also a special student interactive session to provide an opportunity for the young generation to interact.

The symposium will be webcast live on the FAO homepage. That enables everybody, especially those not present in Rome, to follow the proceedings.

This event is another critical step to our efforts in order to reach zero hunger, improve nutrition and promote sustainable food systems.

I thank the members of the Advisory Panel who worked very hard with FAO in developing the programme.

Once more, thank you all for coming and participating in this symposium. I wish you fruitful debates and a successful event.

Thank you for your attention.

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Keynote Address 1: The state of the art and current dilemmas of biotechnology for poor producers and consumers

Louise O. Fresco, Wageningen University and Research, The Netherlands

Since the dawn of agriculture humans have modified, in a direct or indirect way, the genetic constitution of plants, animals, insects, bacteria and viruses to feed themselves and improve their wellbeing. As a result, only a few present day crops or domestic animals still resemble their ancestors. To restore useful lost traits, cross-breeding with wild ancestors is – if at all possible – a tedious task. Improvements in crops and animals were based initially on rather random visual selection and trial and error, also affecting lower life forms such as pathogens and beneficial species in agricultural systems.

From the 19th century onwards, more systematic approaches of breeding and agricultural processes became based on statistics and an understanding of the biological and chemical determinants of productivity. The discovery of DNA - the blueprint of heritable traits - in the 1950s and advances in molecular biology in the 1970s paved the way for the breakthrough of biotechnology in the 1990s. The term biotechnology designates a toolbox of many diverse molecular and genetic techniques allowing the ever more precise characterization of the genetics of specific traits and the full genome of useful species. Biotechnology does not equal genetic modification (GM) but genetically modified organisms can result from the application of biotechnology. However, public opinion often considers them identical.

Today, the genome sequences of some of the most important staple crops, fruits, vegetables, domestic animals and some fish have been determined and work is in progress for many more, allowing a more focused/targeted identification of important genes. This work is largely publicly funded research or joint public-private partnerships, even though relevant gene constructs may be patented. This provides insights into the genetics of traits and their transferability. Genetic modification has already allowed the insertion of traits from wild ancestors or unrelated species to remarkable effects, especially in the area of pathogen resistance, with *Bacillus thuringiensis* is the most widely used transfer mechanism. The latest molecular-genetic techniques, in combination with advanced bioinformatics, such as gene silencing, splicing and editing make it possible to change the genome at specific locations through which desired traits are obtained without the adding of foreign genes/DNA. Technically speaking these do not result in GMOs, although this is still under consideration from a legal point of view in some countries. These technologies have also sparked vast applications outside plant and animal breeding, in vaccine production, food processing and safety testing. In other words, genetically modified organisms are only one of the many outcomes of biotechnology applications. To use a simple analogy: if GM was like the MS-Dos of the first computers, new techniques like CRISPR/Cas9 resemble windows 10 and supercomputing.

The first GM-crops, planted 20 years ago, provided herbicide resistance for large-scale zero-tillage systems particularly in feed crops. Biotechnology and GM have rarely been targeted explicitly at poor farmers and consumers, although efforts in enhanced vitamin and mineral contents have been stepped up, and small farmers benefited from increased production. Further work on drought tolerance, digestive and processing qualities and enhanced bio-based products, taste, shelf life, open new avenues for farmers and consumers. New relevant applications of biotechnology are emerging in maintaining biodiversity through embryo rescue and advanced gene banks, reduction of greenhouse gases from agriculture through feed characteristics and ruminant bacteria, or the sexing of chicken embryos.

Like nearly all forms of breeding, biotechnology and GM are not inherently biased against small farmers or poor consumers. Numerous concerns have been expressed about the risks of biotechnology and GM for human, animal and ecosystem health, as well as the exclusivity of the materials. Such social and political concerns must be taken

seriously, even if there is no evidence of such negative effects. Many new traits acquired in this way such as nutritional quality, disease resistance, adaptation to stress are scale-neutral. Vaccines and food processing applications underscore this point. The price of new breeding stock is generally not an overriding factor for small producers, nor is the dependency on commercial seed, as this is already common in nearly all parts of the world with hybrid seeds and improved animals breeds. Nevertheless, small farmers will only benefit if their mode of production is upgraded to a resilient, resource-efficient system.

However, issues of intellectual property rights and regulations may present considerable hurdles to allow biotechnology and GM to benefit poor farmers and consumers. Because of the controversy and lack of understanding of the nature of biotechnology most countries have imposed cumbersome regulatory systems with concomitant delays in approval procedures, particularly in the EU. Furthermore, the long opposition between patenting systems and breeders rights has resulted in a stalemate. A delicate balance must be struck between the need to compensate companies for R&D investments and the need to keep access open for further improvements. It would seem that breeders' rights systems, in contrast to patenting, allow and support farmer-to-farmer exchange among smallholders and work by local breeding companies and avoid painful court cases against inadvertent farmers using GM-seed. The greatest benefit of new biotechnology techniques such as CRISPR is that cultivars or breeds can be tailor-made more easily to specific small farmer conditions because the selection process is much faster and broad adaption is not necessary to achieve commercial success. Current regulations, however, add years to biotechnology based breeding programs, and more regulation means that private and public breeders have to aim for broadly adapted dominant applications such as cereals, resulting in a potential bias against poor farmers and orphan crops, breeds and processes. Hence the resolution of intellectual property rights and biosafety regulatory regimes is one of the priorities to provide full benefits of new biotechnology to the poor. Ironically, the same advances in genetic characterization that are under scrutiny will help traceability, labeling and determination of authenticity of products and processes, permitting to assuage potential conflicts with organic agriculture and consumer fears about lack of choice.

The bottom-line is that biotechnology is both a continuation of traditional and classical breeding as well as a qualitative and quantitative step towards high precision methods to increase the performance of biological species and processes that are relevant to the supply of food, feed, fibers, pharmaceuticals and flowers to mankind and that potentially allow poor farmers and consumers to reap the benefits of the advancement of science.

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Keynote address 3: Towards ending the misplaced global debate on biotechnology

*Gebisa Ejeta, Purdue University
FAO Biotechnology Symposium, Rome, Italy
February 15, 2016*

Summary of Presentation

Over the last 30 years, significant investments of resources, energy, and intellect, have been invested to advance and expand the development and use of products of biotechnology to benefit agriculture worldwide. The discovery of the double-helix structure of deoxyribonucleic acid (DNA) by Watson and Crick in 1953, and the Utility Patent Act of 1985 that replaced the Plant Variety Protection Act of 1970 were catalytic in providing the impetus for this ambitious investment by major chemical companies that ventured into the seed market. The discovery of the DNA inspired the ambition, and the patent act suggested solid protection to potential investments by the private sector. Impressive gains were made in the development and deployment of new biotechnology products, catalyzed by the unprecedented levels of financing from the private sector, particularly in the United States. The private industry saw opportunities and invested heavily. There were public investments as well, though that was disproportionately smaller. These combined investments yielded advances in several fields of agricultural biotechnology, such as molecular biology, molecular genetics, genetics, genetic engineering, marker assisted breeding, and more recently in genomics. In the early years, the most dramatic advent came from the field of genetic engineering in the creation of transgenic crops, where through recombinant DNA technology, a gene or genes from one organism are introduced to the genome of another plant, sometimes across different species, genera or kingdom.

The first successful commercial release of transgenic products was made in 1996. The release and launch of GMOs was made with great fanfare in the commercial seed and farming industry that is sustained to this day. Genetic engineering and its derivative commercial products of insect resistant and/or herbicide resistant corn, cotton, soybean, and canola, have altered the face of agriculture in the last 20 years, particularly in the Americas. By all accounts, they have been a great market success, benefitting farmers and the private industry that invested in the roll out of these technologies. Unfortunately, from the beginning, genetic engineering (GE) technology and its products have been hounded by fierce debate around the world. These debates centered on a few critical issues, including the potential adverse effects of GM crops on the environment, human health, as well as the value of the technology in addressing the food needs of the world, or if they benefitted the poor. Though the questions raised were sound and reasonable, the spirit in which they were discussed and how long these GMO debates lingered made them appear irrational, unfortunate, and misplaced.

That strong sentiments would consistently be expressed against GMOs, even in the face of overwhelming evidences that showed no adverse effects on humans, animals, and the environment, made the sustained debate appear and feel very **irrational**. Accusations and condemnations increased in spite of reports of repeated negative results from several experiments conducted in different geographies. The debate also became an **unfortunate** saga, created by the confusion around the terms assigned to distinguish the technology. In the euphoria that ensued the scientific breakthrough that reported new transgenic crops, the industry took a miscalculated risk, by choosing to label the new transgenic products, '*genetically modified organisms (GMOs)*' to seemingly draw attention to the great power and novelty of the new transgenic products. The label was unfortunate as it was advanced to mean genetically engineered, but implicated the broader disciplines of biotechnology, molecular biology, even modern science, or all other manipulations that result in genetic modifications to create new crop

types, including plant breeding. The debate about biotechnology for smallholder farmers in particular has been an utterly *misplaced* debate. It was a misplaced debate because it sadly focused on the products and not on the science and the technology employed. It hovered over the fate of currently available commercial GMO products of Bt (*Bacillus thuringiensis*) and HR (herbicide resistant) corn and cotton. It needed to be on whether the science of genetic engineering was used to solve important agricultural problems, and what was needed to give it the chance to do so.

As the fierce debate on GMOs continued, farm areas planted to these technologies expanded significantly. It is estimated that over 180 million hectares of GE crops are grown annually, but greater than 90% of that acreage is in the Americas. (75 M in the US, 90M in the S America and Canada; and 15M in china, India, and others. Conservative estimates of the current market value of GE crops stands at around \$20 billion, growing at > 12% annually, and is expected to grow to over \$35 billion by 2020. The current state of biotechnology is a mixed bag, as on one hand, over 20 years after the first commercial launch of the technology the global agriculture industry is only marketing products based on the very same two primary genetic events (Bt and HR). Jointly, these two traits inserted in four high volume market commodities of cotton, corn, canola, and soybeans, provide crops protection against several insects and a mighty herbicide, glyphosate. Although a few other traits have been introduced to a handful of forage (sugar beets and alfalfa), and horticultural crops (papaya, squash, and eggplants), neither the market value nor the acreage of these crops has been significant, however. On the other hand, the science of biotechnology has advanced immensely in the last 25 years. In spite of diminished public funding of science and applied biotechnology research in recent decades advances have been made in molecular biology, genetic engineering, in genetics and genomics, as well as in commercial plant breeding.

New and powerful genetic engineering (GE) technologies have recently emerged, with 'Whole Genome Sequencing, Genome editing, RNA interference, Synthetic biology' where, once approved, each has the potential to be directed to impacting an expanded set of crop traits. These technologies, potentially, could address the many constraints of agriculture and could readily be applied to vital crops of the poor. However, the ethical considerations of the new biotechnologies could be stronger, particularly with gene editing where the natural genome of an organism is edited (fixed or cleansed off its limitations) through very precise genetic engineering procedures, allowing the new cleansed up version to be passed on to unsuspecting future generations of plants, animals, and humans. The currently available commercial transgenic crops have not penetrated the grain market in developing countries, because they just didn't fit the need in many regards. The potential of genetic engineering or the broader area of biotechnology in addressing critical problems of the poor is immense. Unfortunately the current GE products have done wonders for the seed industry and big farmers of the western world, but very little for the poor. More is needed to address hunger and poverty in poor nations. Increased public research investment in biotechnology would help. Similarly, more is needed to align better the interest of the poor with that of our agricultural industry. The presentation will describe lessons learned from past experiences and challenges with available GE crop commodities, the current state of developments in new biotechnology, and what the future holds for programmatic and institutional adjustments and interventions needed to offer greater opportunity for generating appropriate agricultural biotechnology tools for solving some of the most acute problems of agriculture in poor nations.

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Keynote address 3: Biotechnologies in Action in Brazil

*Mauricio Antonio Lopes, PhD,
President, Brazilian Agricultural Research Corporation – Embrapa
Read on his behalf by Pedro Machado, PhD*



Brazil is one of the largest countries in the world, with an extensive surface of continuous land, a large supply of fresh water, abundant solar energy, and a rich biodiversity. The wide range of climatic conditions, from temperate to tropical, together with advanced capacity in technology development, allowed considerable diversification of agricultural systems, making the country one of the world's largest producers of food, feed, fibers and renewable fuels. Brazil is today an acknowledged leader in generation and implementation of modern tropical agricultural technology. Responding to increasing concerns over agriculture's footprint on its natural resource base, the agricultural research system in Brazil has taken important leaps, in a short period of time, towards development of innovations for increasingly safer and sustainable agricultural systems. The country is a leader in crop management based on minimum and no tillage systems, which significantly helps decrease erosion and improve general soil quality and groundwater recharge. Biological nitrogen use, through inoculation techniques with nitrogen fixing bacteria, has led to a significant decrease in the amount of chemical fertilizers applied to crops such as soybean. This, in turn, has significantly reduced environmental impacts such as water resources contamination with nitrates or other harmful elements. Over the last decades, plant breeding programs have allowed development of cropping systems to a wide variety of environmental conditions in the country. This has been achieved by incorporating adaptation to different latitudes, increased efficiency in phosphorus and nitrogen use, as well as resistance and tolerance to biotic stresses, that are especially severe in tropical regions. The country is now investing in sustainable farming intensification, incorporating integrated crop-livestock and crop-livestock-forest systems. These and many other innovations incorporated by Brazilian agriculture allowed increased resource use efficiency, higher productivity and more efficient use of land, reducing drastically the environmental costs of farming.

Despite these advances, the challenges arising from global warming, the consequent climatic extremes, and an increasing world population make sustainable food production a key issue for the next decades. To maintain productivity and sustainability of agricultural systems, it is crucial to be alert, informed and acquainted with new technologies and practices that could change production and consumption concepts, standards and paradigms. Scientific revolutions are happening in various fields of knowledge, in biology with genomics, in physics and chemistry with nanotechnology, in information and communication technology, with innovations that increase our ability to respond to risks and challenges. In recent years, biology has produced tremendous advances, which allow us to broaden our understanding of complex mechanisms in plants, animals and microorganisms. New biotechnologies are already impacting agricultural diversification, specialization and value aggregation, allowing increased productivity, safety and improved food quality. Using advanced biotechnologies in agriculture to confront the challenges ahead is strategic not only for Brazil, but for the world.

In the past decade, Brazil has become the second largest user of genetically modified (GM) crops, with an area greater than 42 million hectares during the last crop season (2014/15). As of July 2015, there are 45 GM events approved for commercial cultivation in Brazil, of which 25 events for corn, 12 for cotton, six for soybeans, one for dry edible beans, and, most recently one for eucalyptus. GM events with herbicide tolerance traits lead the adoption rate with 65 percent of the total area planted followed by insect resistance with 19 percent and stacked genes with 16 percent. The adoption of biotechnology products in agriculture definitively helped the country to reach its current production level, even with the late adoption of genetically modified (GM) crops, due to a "non-official moratorium" caused by legal disputes from 1998 to 2005. Only after the implementation of the new Biosafety Law was the use of GM plants officially endorsed in a trustable legal framework, essential for the stability of any economic sector. Several public

and private, national and foreign institutions conduct research and development in Brazil to produce GM plants with several agronomic traits and/or characteristics that add value to agricultural products. The majority of GM crops being grown in Brazil are soybeans, corn and cotton, all belonging to the first generation of transgenic plants, which are insect and/or herbicide tolerant. As is the case in the rest of the world, the biggest share of GM crops being produced commercially in Brazil were developed by private companies. However, the local research community has the capabilities to prospect genes of interest, to run “*proof concept*” of novel genetic engineering strategies, test it in controlled and real field conditions and take the developed product to the market. Research institutes, universities and the Brazilian Agricultural Research Corporation (Embrapa) have been developing various GM plants with different traits of interest. Embrapa developed and deregulated the first GM bean (*Phaseolus vulgaris*) with resistance to the golden mosaic virus to be produced commercially in Brazil, and, in a joint venture with the German company BASF, developed and deregulated an herbicide-resistant soybean. The new variety, which has resistance to imidazolinone herbicides, was released commercially in the 2015/16 growing season under the trade name “Cultivance.” In addition to soybean, corn and cotton, various other GM crops are being tested in advanced development stages in field conditions in Brazil. Rice, passion fruit, eucalyptus, cowpea and sugarcane are examples of species being tested in actual field conditions for different traits such as yield improvement, drought tolerance, fungus resistance, oil quality and wood density. It is undeniable that there was a rapid increase in the utilization of genetic engineering technologies in the Brazilian agriculture after the new Biosafety Law, in 2005. The unification of laws, rules and guidelines by all agencies involved in the Biosafety legislation framework allowed, undoubtedly, the rescue of the confidence by investors, researchers, private/public institutions, and by all other stakeholders involved in the agrifood and agroindustry sectors.

Brazil is also investing in biotechnologies that can connect its agricultural system to the nascent bioeconomy. The growth of the bio-based economy can generate multiple opportunities for economic growth and creation of new jobs, including in rural areas. Among the major routes considered are the metabolic processes of organisms (plants, animals and micro-organisms) with focus on the production of substances and materials of high value, targeted to multiple uses (chemical and biochemical, medical, pharmaceutical, nutritional, energy, etc.). Biomass and bio-refinery technologies are being developed and special attention is being given to research in molecular biology, multiple “*omics*” sciences, nanotechnology, and information technology, among others, to meet the demands for production of sustainable energy, chemicals and new bio-based materials.

In summary, the current, general feeling in Brazil is that there is no way back in the use of biotechnology in agriculture if we want to improve food production and food quality and address the challenges of food security and low-carbon sustainable development.

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Keynote address 4: Breakthroughs in resource productivity

Prof. Gunter Pauli, Founder of ZERI, Chairman of Novamont SpA (Italy)

www.zeri.org www.TheBlueEconomy.org

@MyBlueEconomy on Twitter

Written on January 21, 2016



The quest for food security goes hand in hand with the need to produce and consume within our planetary boundaries. There is an urgent need to respond to the basic needs of all on Earth, while there is an equal emergency to shift towards healthier nutrition. The combination of food security, sustainable farming and health concerns forces the world to embrace innovations. These will be social, technological and organizational. It is clear that one technology will not offer a complete solution. Any response to the challenges we face today will require a cluster of responses that will evolve over time. While we know that more of the same will not produce better results, we should establish a few basic principles that guide us in our search for breakthroughs.

Core Principles

Since 1994, the ZERI foundations developed a network of scientists who collectively think beyond the obvious. Our search for solutions originally to be presented at COP3 in Kyoto in 1997 were all inspired by "how nature evolves from scarcity to abundance", and started from the observation that the only species on earth capable of producing something no one desires is the human species. Nature continuously cascades matter, energy and nutrition, and every member contributes to the best of its capabilities. The concept of unemployment does not exist in ecosystems. It is against this idealistic framework that ZERI engaged in the design of business models that increase resource efficiency while generating more food and nutrition than we ever imagined before, solely using locally available resources.

Coffee Chemistry

While many embark on programs to solve the food challenge that rely on splitting and manipulating genes, we often ignore that our present farming and consumption model is extremely wasteful. Do we realize that a cup of coffee only contains 0.2% of the biomass of the red cherries harvested? The process of fermenting, drying, roasting, grinding and brewing leads to the ingestion of a minute fraction of the 10 million tons of coffee produced worldwide, and the disposal of nearly everything else. This understanding has given rise to the "coffee chemistry", including the farming of mushrooms on post-harvest, post-industrial and post-consumer coffee biomass, the use of the spent substrate enriched with amino-acids as animal feed, the use of fine coffee particles as an odor control, UV-protector and even hydrogen storage system. The logic of coffee can be applied to tea and dozen other crops. The bundling of innovations not only allow for the substitution of toxic chemicals, it generates income and jobs.

The Design of Biorefineries

Recent cases demonstrate that the generation of 500 times more nutrition, from the same coffee harvest, and the creation of 300 times more value from readily available biomass is not an exception. Over the past 20 years the partners of the ZERI Foundation created dozens of cases which are now scaling up as demonstrated by the 3,000 farms that combine coffee and mushrooms. The design of biorefineries offers more insights into the dynamics food and chemistry. The critical success factor is the availability of feedstock. The case of Novamont in Sardinia demonstrates that the processing of thistles, a weed that grows prolifically on abandoned farm land, can respond to multiple needs in society, while offering a new perspective to farming. Thistles are harvested, processed as oil or sugars from cellulose, then converted into a portfolio of biochemicals including polymers for

plastic bags, elastomers for rubber gloves, herbicides, lubricants, and the waste can be processed into animal feed.

3D Sea Farming

The portfolio of innovative business models is not limited to farming on land. The introduction of 3D sea farming, combining the cultivation of seaweeds, mussels, scallops, oysters, fish, crabs and lobsters has demonstrated to be a highly effective way of reviving the healthy production of seafood in a controlled environment that secures a diverse output ranging from food, animal feed, ingredients for cosmetics, pharmaceuticals, and a waste converted to fertilizers. This farming system requires no inputs like fresh water, pesticides or fertilizers, on the contrary, this technique - which is considered the permaculture of the sea - alkalizes the sea, regenerates biodiversity and helps shift the diet towards a much healthier one.

Fishing with Air Bubbles

There is a need to dramatically shift our production systems if we are to respond to the basic needs of all. One of the most profound changes is fishing and fish farming. The age of nets, hooks and cages are over. The conversion of sardines to salmon feed is absurd at a time we need to double food output. The ZERI Foundation has focused on the design of fishing techniques that rely on air bubbles, inspired by the way dolphins and whales catch their prey. This leads to a redesign of fishing vessels and techniques. All female fishes with eggs are released into the sea securing future generations with ample supply of wild catch. Indeed, the only reason that fish farming is perceived as more productive than fishing is because fishermen indiscriminately kill females with eggs, which turns farming into a productive solution.

Time has come to innovate, and encourage innovators to take another degree of freedom in their minds, ensuring that disruptive innovations scale fast. This not only generates jobs, it turns the productivity logic on its head. After all a 3D fish farm generate 2 jobs per hectare on the sea, which require 25 lines at a total cost of \$7,500 generating 600,000 shell fish and 75 tons of seaweed per hectare per year, leading to an intensive economic engine. After all this is the Blue Economy: more value, less investment costs, more output and an increased number of jobs. We may even get healthier in the process.

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Monday 15 February
14.00-17.00 Parallel Sessions

Session 1.1: Facing the challenges of climate change: Adaptation in the crop and forestry sectors

1.1.1 Developing rice varieties with enhanced adaptation to lowland farming systems: Case studies from South Asia

Abdelbagi M. Ismail, U. S. Singh, D. Platten, E. Septiningsih R. K. Singh, A. Kumar, D. J. Mackill
International Rice Research Institute

The ever increasing global demands for food makes it necessary to produce more rice from less favorable areas. These areas, however, had low productivity because of prevalence of abiotic stresses like floods, drought and excess salt, the effects of which are becoming progressively more severe because of climate change. Recent scientific advances are providing opportunities to fast track breeding of tolerant rice varieties that maintain their productivity under these conditions, to help meet the increasing demands for food, to combat poverty and secure sufficient food supply.

Early floods can lead to poor crop establishment, especially in areas where direct seeding (DS) is practiced. Farmers are increasingly adopting direct seeding as the preferred method, both in rainfed and irrigated rice ecosystems, because of labor scarcity and expense. However, large scale-adoption of DS requires rice varieties that can germinate in flooded or waterlogged soils, as rice is extremely sensitive to flooding during germination and early seedling growth. Developing high yielding varieties that can withstand such conditions can accelerate the adoption of direct seeding in both irrigated and rainfed areas. Few rice accessions that tolerate anaerobic conditions during germination (AG) were identified and used to study molecular and physiological mechanisms associated with tolerance. Few QTLs were mapped and one cloned. Breeding lines with tolerance under field conditions were developed and are being evaluated at various locations in Asia.

Complete flooding (submergence) is constraining rice production in over 16 million ha of rainfed lowlands in Asia and large areas in Africa, and its effects are worsening over recent past; leading to concomitant poverty and food insecurity in the heavily populated flood-prone areas. Significant progress was made in developing tolerant varieties through conventional and molecular breeding approaches. An important turning point in breeding for this ecosystem was the discovery of the *SUB1* QTL in mid 1990s and its subsequent cloning. *SUB1* confers tolerance of complete submergence for 7 to 18 days, with no undesirable consequences, and is effective at almost all growth stages. Its usefulness was validated in farmers' fields with yield advantages of 1 to over 3 t ha⁻¹, depending on the duration and depth of submergence and floodwater conditions, but with similar yields in absence of submergence. Numerous *Sub1* varieties were developed and formally commercialized in several countries. These varieties are spreading fast in Asia since the release of the first variety in India in 2009; currently grown by about 4 million farmers in over 2.5 million ha. Further research is targeting additional QTLs to strengthen *SUB1* and to combine it with tolerance of other abiotic stresses.

Longer-term stagnant flood (SF) causes severe reductions in yield, and farmers in affected areas are mostly using traditional varieties that are partially tolerant but have low yield and grain quality because tolerant modern varieties are not widely available. We identified several landraces and elite lines with reasonable tolerance of SF, and some of them were used to study the bases of tolerance. Stagnant floods reduce survival and tillering, suppress vegetative growth leading to lower grain yield and quality. Several breeding lines were developed and

are being evaluated; and mapping populations are being analyzed to identify QTLs associated with tolerance for use in breeding.

Drought reduces rice yield in over 23 million ha in S. Asia. Significant genetic variability for yield under drought in rice led to the search for major QTLs for grain yield. Several tolerant donors were identified and crossed with high yielding but drought sensitive varieties, and several drought tolerant varieties were recently released in S. Asia, demonstrating significant impacts on rice productivity in drought affected areas. Numerous mapping populations were developed over the past decade and 14 large effect QTLs were identified, seven of them showed effectiveness in several genetic backgrounds and in diverse upland and lowland environments, with yield advantages of 0.5 to 1.5 t ha⁻¹ over original varieties. The effectiveness of marker-assisted backcross (MABC) breeding for improving drought tolerance in rice was demonstrated, with the recent release of the first variety, IR64-drought in 2014.

Salinity limits rice productivity in large irrigated and rainfed areas, particularly in tropical coastal deltas where rice dominates the cropping systems. These areas are most vulnerable, as being reflected in increasing storm incidences and sea level rise caused by global warming. The productivity of saline soils is low, with yields averaging below 1.5 t ha⁻¹, but can be doubled when salt tolerant varieties were used. Numerous tolerant donors were identified over the past few decades and extensively used in breeding tolerant varieties. Some of these new varieties were recently released, with large yield gains in affected areas. QTLs associated with tolerance were identified; the largest of which is *Salto1* on chromosome 1. This QTL was recently transferred into several popular varieties. Additional QTLs for tolerance at both seedling and reproductive stage are being targeted to combine them with *Salto1* for higher tolerance. Ultimately we aim to combine alleles associated with tolerance of different abiotic stresses to provide more resilient varieties for less favorable areas in Asia and Africa, to help keep up with the increasing demands for rice and to cope with climate change adversities.

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1.1.2 Harnessing Agricultural Biotechnology for Resilience to Climate Change: A Lesson from Water Efficient Maize for Africa Project (WEMA)

Yoseph Beyene¹, Kiru Pillay², Kassa Semagn¹, Stephen Mugo¹, Sylvester Oikeh³, Amsal Tarekegne¹, Kingstone Mashingaidze⁴, Murenga Mwimali⁵, Godfrey Asea⁶, Alois Kullaya⁷, Pedro Fato⁸, Barbara, Meisel², Francis Nangayo³ and Prasanna BM.¹

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Maize is among the most important food crops in the world and, together with rice and wheat, provides at least 30% of the food calories to more than 4.5 billion people in 94 developing countries. Compared to other regions, maize yield is extremely variable in sub-Saharan Africa (SSA), though maize is the most important staple food for more than 300 million people. For example, between 2005 and 2008 the average maize yield was estimated at 1.8 tons per hectare (t/ha) compared to 2.5 t/ha in the Philippines, 3.1 t/ha in Mexico, and 3.9 t/ha in Thailand. Although several factors including low soil nitrogen, foliar diseases, insect-pests and socio-economic factors do contribute for this low production, drought has been cited as one of the major factors that frequently limit maize production in the SSA region. To address the problem, the WEMA project was launched in 2008 with the objectives of enhancing food security in sub-Saharan Africa through developing and deploying drought tolerant and insect-pest protected maize, developed using conventional breeding, molecular breeding and transgenic biotechnology approaches. The WEMA project is a public-private partnership among African Agricultural Technology Foundation (AATF), International Maize and Wheat Improvement Center (CIMMYT), Monsanto Company and five National Agricultural Research Systems (NARS) of Kenya, Uganda, Mozambique, Tanzania and South Africa; supported by the Bill and Melinda Gates Foundation (BMGF), the Howard G. Buffett Foundation (HGBF), and the United States Agency for International Development (USAID) for 10 years (Phase I 2008-2013, Phase II 2014-2017). This presentation highlights the achievements, challenges, and lessons learnt from the project.

Advanced conventional pedigree breeding techniques, using managed drought stress selection environments and a large testing network (60 sites), are used to generate stable high-yielding hybrids. In a typical year, WEMA scientists evaluated 30,000 inbred lines and 15,000 hybrids, many of them grown under managed drought stress and optimum-moisture environments. To date, 26,000 doubled haploids (DH) lines have been developed by CIMMYT and Monsanto from crosses of Monsanto, CIMMYT and NARS inbred lines. The development and use of DH lines has increased rates of genetic gain and empowered NARS breeders who were able to access DH lines for the first time. New germplasm combinations using temperate germplasm introgressed into tropical germplasm are producing elite hybrids with high yield potential. Since 2008, WEMA partners have used DH technology and pedigree breeding to develop 59 drought tolerant hybrids recommended for commercialization in four WEMA countries (Kenya, Uganda, Tanzania and South Africa). Currently, 23 seed companies have been engaged through sub-licensing to produce and market the released WEMA hybrids. Overall, 35 drought tolerant hybrids are in on-farm demonstrations and five hybrids are in commercial production in four countries with projected production of 1600 tons of certified seed in 2016.

To facilitate the development and use of improved tropical maize germplasm, the project adopted several approaches for breeding for drought-stress tolerance including Marker-Assisted-Recurrent Selection (MARS),

Genomic selection (GS), and pedigree selection. The project scientists conducted the largest genomics-assisted breeding work that includes analysis of the efficiency of MARS and GS over pedigree-based selection in tropical maize. Genetic gain studies have been completed for 18 tropical populations: 10 under MARS; 8 under GS. MARS and GS provided up to 4 times higher grain yield than pedigree-based selection, without significantly affecting plant height and anthesis date in most populations. Also, hybrids developed through MARS produced 19% higher grain-yield than the commercial-checks. The high genetic gain of hybrids developed using molecular breeding was highly remarkable considering that the commercial-checks used for the studies were the best available in the region. In addition, more than 1000 fixed lines developed through molecular breeding have been tested in multi-location trials. This improved germplasm will facilitate a flow of drought tolerant hybrids for several years to come. Several hybrids derived using lines developed through molecular breeding are currently under national performance trials, a step for commercialization in SSA.

Combined analyses of confined field trials of transgenic drought tolerant (DT MON87460) maize data using 34 hybrids with same base genetics evaluated in three WEMA countries for three or more years, showed that five traited hybrids gave 8–14% greater yield than the non-traited versions, indicating a strong positive gene effect with ample scope for selection and breeding in germplasm of similar genetic background as these hybrids. MON87460 was approved for commercialization in South Africa in May 2015. In 2011 the transgenic *Bacillus thuringiensis* (*Bt*) event MON810 was added to the transgenic component of the Project and provides insect-pest resistance to all the WEMA countries except South Africa. For South Africa a second transgene, MON89034, coding for a different protein, has been added and is already approved for commercialization. Existing regulatory systems supported the testing of MON810 transgene in Kenya and Uganda and the efficacy of single trait events has been demonstrated. Efficacy trials were carried out on *Bt* MON810 in controlling the spotted stem borer (*Chilo partellus*) in the field and the African stem borer (*Busseola fusca*) in the lab in maize in Kenya (CFT I – CFT III) and in Uganda (CFT II). Results of CFT II in Kenya showed that 75% of the hybrids evaluated had significantly greater yield ranging from 26–113% with the *Bt* trait than without the trait. Results of CFT II in Uganda similarly showed that all the seven *Bt* maize hybrids had significantly greater yield of 49–201% due to the *Bt* trait compared with the non-traited hybrids. Full deregulation of the MON810 transgene is likely to occur in Kenya and Uganda in 2016. Field testing of transgenics in Mozambique and Tanzania will commence in 2016 as approval for testing the transgenics in confined field trials has been obtained. Field testing of stacked DT and Bt commenced in South Africa in 2015, and will commence in Kenya, Uganda and Mozambique in 2016. Widely adapted inbreds have been converted to DT and *Bt* traits, and will be utilized to develop transgenic products.

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1.1.3 Molecular breeding in legumes for resource-poor farmers: Chickpea for Ethiopia and India

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Breeding for climate resilience as well as other high value traits in pulse legumes will be greatly accelerated if we can expand the range of adaptations accessible to breeders. We address this need in chickpea, the world's second most important pulse legume, by harnessing the capacity of chickpea's wild relatives to survive in harsh environments. Chickpea is a global commodity of critical importance to food security in low income, food deficit countries of sub-Saharan Africa (Ethiopia, Malawi, Sudan, Kenya and Tanzania) and South Asia (India, Myanmar, and Pakistan), and also of importance in advanced developing economies (Turkey), and developed countries (USA, Australia and Canada). Effective use of wild germplasm in chickpea improvement requires new and systematic surveys of genotypes from natural environments, identification of adaptive alleles to environmental extremes, and incorporation of the diversity of wild alleles into phenology-normalized backgrounds for trait analysis and breeding.

Achieving these objectives requires a close marriage of cutting-edge science (e.g., genomics, modeling and high-throughput precision phenotyping), with appropriately structured pre-breeding and breeding activities. The current project involves multiple donor agencies in several countries, built around a core Feed the Future grant from the US Agency for International Development that is focused on chickpea improvement for Ethiopia and India.

Chickpea (*Cicer arietinum*), like most cultivated crops, has exceedingly narrow genetic and phenotypic diversity. Whole genome sequencing reveals a remarkably strong domestication bottleneck through which ~95% of genomic variation was lost from modern elite cultivars. This has profound implications for breeding of climate-resilient crop varieties. The dearth of adaptive variation likely limits our ability to both adapt the crop to a scenario of changing environments and to expand the cultivation of domesticated species into environments beyond those under which historical domestication occurred. Thus breeding only within cultivated germplasm is likely to have diminishing returns, raising an urgent need for new sources of diversity.

Wild species are a key but underutilized resource for crop improvement and harnessing their potential represents a primary challenge for 21st century agriculture. The challenge, which is the explicit focus of numerous international efforts under the Global Crop Diversity Trust (one of our sponsors), is particularly acute in the developing world where extreme climatic conditions, marginal soils and reduced inputs limit productivity, create increased risk, and diminish livelihoods through reduced income and malnutrition. The impact of a properly implemented and well-utilized resource of wild germplasm would extend beyond the developing world, because many of the crop phenotypes of importance in the developing world (e.g., tolerance to heat and drought, reduced dependence on inputs [e.g., nitrogen, phosphate, pesticides, water], and increased seed nutrient density) are also key to meeting the global demands for crops that incorporate traits for climate-resilience, increased sustainability, and increased nutritional value.

The potential for genetic gains from use of wild crop relatives is well documented. Nevertheless, wild crop relatives of chickpea have been used sparingly and in an ad hoc manner in chickpea improvement. Among the impediments to the use of wild material is the dramatic phenological difference between wild and cultivated forms, in particular with respect to flowering time. Phenological differences complicate crossing and preclude the ability to systematically evaluate wild alleles in an agricultural context. Moreover, traditional approaches of genetic crossing and phenotypic assessment are laborious, severely limiting the scale at which studies can be undertaken.

With these challenges in mind, we have built and are characterizing a large and systematic collection of wild *Cicer* species from a representative range of natural environments, including gradients in rainfall, temperature, soil chemistry and altitude. Genomic technologies have been used to characterize genetic diversity among ~1,100 accessions and to nominate particular plant accessions as targets of pre-breeding, phenotyping and breeding. Three de novo whole genome assemblies have been produced to provide reference genomes for cultivated *Cicer arietinum*, wild *C. reticulatum* and wild *C. echinospermum*. The remaining accessions are being sequenced under a prioritized, hierarchical strategy of high, medium and low read depths to facilitate allele and trait discovery using a combination of computation of genomic features and phenotyping/modeling of trait-marker associations in nested association mapping and bi-parental populations.

A large program of genetic crossing is being used to introduce wild genetic diversity into phenology-normalized backgrounds. The base populations involve twenty diverse wild donor accessions crossed into five cultivated elite varieties. A collection of ~8,000 segregating lineages are being increased in the field for F3 seed and early generation phenotyping. In parallel, we are pursuing a program of intercrossing to increase recombination and genotyping to normalize flowering time and plant architecture. The resulting populations are expected to exhibit relatively uniform phenology and thus be suitable for large-scale phenotyping, which we are beginning using a combination of automated field platforms, greenhouses and controlled environment chambers. Initial climate resilience traits under analysis include those related to drought, heat and cold tolerance.

Abiotic stress in chickpea is inextricably tied to both beneficial and pathogenic microorganisms. For example, legumes' unique advantage of symbiotic nitrogen is strongly impacted by abiotic stress, and thus developing plant varieties and bacteria symbiont genotypes that maintain symbiosis under stressful conditions is an additional objective. Similarly, the agronomic cycle in chickpea is driven by tradeoffs between abiotic stress and plant disease. Planting of chickpea is delayed until after the rainy season ends, because moisture promotes soil seedling disease and foliar *Ascochyta* blight. Conversely planting or maturing too late exposes the crop to terminal drought, heat stress and *Fusarium* wilt, leading us to initiate efforts on targeted plant disease phenotypes. Finally, the importance of microbial communities (the "microbiome") in promoting the health and stability of both animal and plant systems is increasingly recognized, though it remains poorly understood. We have initiated a program to understand the dynamics of chickpea's microbiome, with the long-term objective of developing microbial treatments to mitigate abiotic stress, nutrient deficiency and plant disease.

The outcomes of this project are intended to be high-yielding, climate-resilient chickpea varieties within the context of user-preferred traits: seed quality and nutrient density, reduced inputs due to climate resilient nitrogen fixation, and biotic stress resistance among them. We have a clear focus on research-for-development, with all upstream activities (i.e., germplasm collection, genomics and population development) predicated on the need to facilitate downstream phenotyping and breeding activities. In the course of this work we aim to identify and introduce newly collected wild alleles into diverse high performing elite cultivars that increase crop productivity, food and nutritional security for smallholder farmers.

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1.1.4 Genomic approaches for dissecting fitness traits in forest tree landscapes

Ciro De Pace

Forests present such a wide variability among living organisms and the ecological complexes of which they are a part. Approximately 30% of the Earth's land surface (4 billion ha in 2015) is covered by **forest landscapes** (FAO global forest resource assessment). The bulk of that landscape (93 % or 3.7 billion ha in 2015) is **natural forest**. Most natural forests are either **naturally regenerated forest** (65%) or **primary forest** (the remaining 35 %) of native species and harbor up to 90 percent of the world's terrestrial biodiversity where there are no clearly visible indications of disturbance of the ecological processes by direct human-related activities. However, natural forests continue to disappear at an alarming rate as a result of disturbance and degradation of the ecological processes, fragmentation, and other stressors that can be linked to [indirect effect of human activities](#). The global emission of large quantities of carbon dioxide (CO₂) and other gases with 'greenhouse effect' in the air can disturb the energy balance at the Earth's surface and the intensity of weather events. Globalization and climate change can alter seasonal air temperature, rainfall patterns, and the life cycles of pathogens that have co-evolved with forest tree hosts and facilitate the spread of non-native and invasive pathogens to areas where native tree species lack specific defenses against them.

To meet the challenge of conserving forest biodiversity, services and resilience in this rapidly changing world, it is necessary to understand how ecological assemblages in a forest landscape have formed and respond to novel environmental factors. Darwin provided some key ideas for understanding the fate of ecosystems. He stated that species "favoured by any slight change of climate" will increase in numbers, whereas other, less-favored species "must decrease". Darwin clearly believed that the 'natural selection' process explains the increase in frequency of individuals carrying adaptive alleles as well as why individuals or species are adapted to their environments.

The Modern Synthesis of Mendelian **genetics** with Darwinian evolution, developed in the 1930s and 1940s, provided the conceptual framework for a basic population genetics model ([reviewed in Provine 2001](#)) for measuring fitness of individual genotypes, genetic diversity, and understanding its change paths when mutation, migration–gene flow, genetic drift and natural selection evolutionary forces act in ecosystems. **Examples of fitness-related traits displaying Mendelian inheritance**, are known for forest tree species (i.e. [the simply inherited resistance to blister rust in *Pinus lambertiana*](#)). However, the majority of traits of both economic and ecological significance in forest trees are complex including life history traits (i.e. generation length, mating system, pollination mechanism, fecundity, seed dispersal, growth rate) and resistance to abiotic stresses.

Since the early 1970's, biochemical markers identified by electrophoretic techniques have been used in the first attempt to dissect, at the molecular level, the fitness components of forest trees in homogeneous environment. Those markers of the nuclear or organellar genome were limited in number and soon revealed, with few exceptions, their adaptive-neutrality. On the other hand, they helped in making inferences on demographic patterns and colonization dynamics in several conifers, European oaks and *Castanea sativa*, but rarely (*Fagus sylvatica* and *Pinus sylvestris*) elucidated fitness components in tree populations. Similar limitations affected early genetic DNA markers (Restriction Fragment Length Polymorphism, RFLP; Random Amplified Polymorphic DNA, RAPD; Amplified Fragment Length Polymorphism, AFLP; Simple Sequence Repeats, SSR), which were difficult to reproduce (RAPD) or expensive to detect (RFLP, AFLP, SSR).

The recent development of next-generation sequencing platforms has helped to revolutionize population genetics by providing rich databases for Single Nucleotide Polymorphism (SNP) genetic markers. SNPs are generated from resequencing candidate genes for the phenotype of interest in a small (<100) panel of individual trees of model species and from expressed sequence tag (EST) sequencing projects. Recently, *de novo* multiplexing sequencing

of reduced representation library of a tree genome using restriction enzymes and PCR amplification of the library of fragments, speed-up genome –wide (GW) SNP identification, fine mapping, and genotyping. SNPs are used primarily in GW association mapping (GWAM), also known as linkage disequilibrium (LD) mapping, to overcome limitations of pedigree-based quantitative trait loci (QTL) mapping by taking advantage of both LD and historical recombination present within the tree species gene pool. For example, in conifers, a [QTL interval](#) spans ~15 cM. This suggests that the majority of identified QTLs, particularly those with minor to moderate effects, are specific to the mapping population and without fine-mapping are of limited utility in metapopulation genetic studies. GWAM has the potential to identify the genetic architecture of traits when candidate genes for the phenotype of interest are unavailable. It has been used to map genetic regions affecting the release of seeds over a long period of time in response to an environmental trigger (i.e. wildfire), a phenomena known as serotiny. The intensity of the serotiny phenotype varied in accordance to the genotype at 11 QTLs identified by GWAM which explained 50% of the phenotypic variation in serotiny in three populations of lodgepole pines (*Pinus contorta*). Much of that variation was related to geographically variable natural selection arising from fire frequency and seed predation. Forest-tree species and seed-predators interactions has been documented in a wide variety of systems, including *Greya* moths and the *Lithophragma* woodland plants they pollinate and oviposit in, and crossbill finches (*Loxia*) preying on the seeds of lodgepole pine.

The most clear example of geographic variation in species assemblage that cause difference in forest tree fitness and direction of disruptive selection involve competition between squirrels (*Sciurus* sp.) and crossbills (*Loxia curvirostra*) for *Pinus ponderosa* cone-seeds. *S. aberti* squirrel feed mainly on the inner bark of ponderosa pine twigs found on the Rocky Mountains in USA, and exert selection on resin characteristics but not directly on cone structure. In the absence of *S. aberti* squirrel, captive crossbills had significantly longer seed extraction times when feeding on cones. But cone scales provide resistance to crossbills spreading cone scales apart, and increased scale thickness evolved in response to crossbill predation. Gray squirrels (*S. griseus*) have a selective impact on western ponderosa pine by preferring seeds from cones with high ratio of seed mass to cone mass which tend also to be small. Selection exerted by gray squirrels favored trees with large cones and a low ratio of seed mass to cone mass, and these are the traits that characterize cones in which gray squirrels are present and crossbill finches absent. Significant quadratic relationships exist between standardized relative tree fitness and size-related traits.

The above examples on variation patterns of serotiny and cone size related to geographical differentiation of the intensity and trend of ecological processes and natural selection, suggested a significant role of the spatial scale and genomics to quantify microevolutionary processes in natural forest landscape. Conceptually, the forest landscape may be seen as layers of landscapes whether they describe fitness (fitness landscape), genome architecture (landscape genomics), the spatial distribution of environmental variables and population genetics parameters (Landscape genetics), and the relationships between spatial patterns, geoclimatic variations, and ecological processes (landscape ecology). Integration of spatially explicit ecological analyses and genomic approaches will result in more comprehensive sampling of ecological landscapes providing a more diverse set of inferences regarding fitness landscapes.

Perhaps, the broadest implication of the work on serotiny is thus the focus on phenotypes measured in natural populations in the light of their fitness, genomic, and ecological landscapes. This directly complements and extends the work performed in natural forest tree populations, common garden experimentation in the field, and growth chamber comparison of forest regeneration materials, which is where precise estimates of heritability and genetic effects can be obtained. When such experimentation is coupled with genomics and integrated with emerging infrared technologies, the first metaphorical and geographically based fitness landscapes may indeed be covered by trees.

Future directions for forest tree genomics and forest fitness landscape research will take advantage of the rapid advances in ‘-omics’ technologies. Three priority research areas for genomic research in trees can be highlighted.

First, identification of “functional” traits targeted by natural selection.

The informativeness of high-throughput phenotyping technologies in test plantations and laboratory environments may be increased when “functional traits” affecting fitness are evaluated. [Recently](#), it has been demonstrated that principal component analysis of plant traits with ecological meaning (i.e. adult plant height, dry mass per unit of fresh stem volume, leaf dry mass accounting for investment in xylem tissue per unit leaf area, and diaspore mass) in forest tree communities reveals patterns of functional-trait variation that allow one species to survive natural selection, physiological challenges and competitive exclusion. The procedure applied to geographically scattered forest landscapes sharing a common set of congeneric tree species, promise the identification of those traits and species that have successful fitness features in forestry.

Second, increase discovery of candidate genes for fitness traits.

The identification of polymorphic “functional traits” within species, will help dissecting traits related to fitness. Genomic research directed towards finding the candidate genes coding for the polymorphic “functional traits”, will provide the population genetic parameters to measure and predict evolutionary changes in forests disturbed by stressors affecting those traits. For example, climate explained meaningful proportions of variation in leaf and xylem traits across the globe. In arid habitats, natural selection has favored strategies that increase certain “functional” expressions such as the embolism resistance of xylem, investment in xylem tissue per unit leaf area, as well as the density of xylem tissue. It is likely that genes for these same traits could confer drought resistance in forest tree species and help adaptation under global warming.

Fourier-transform infrared (FTIR) spectroscopy, a chemical fingerprinting technique of the metabolome, [has been used](#) to identify *Quercus agrifolia* plants resistant to *Phytophthora ramorum*, the causal agent of sudden oak death prior to infection. Concentrations of quercetin flavonol and ellagic acid phenolic dilactone were found to be highly significant biomarkers of resistance. Therefore, chemical fingerprinting can be used to identify resistance in a natural population of forest trees prior to infection with a pathogen. GWAM and expression analysis of genes involved in the biosynthetic pathways of biomarkers will provide information on candidate genes to be followed in the fitness landscape for increased adaptation to diseases in forestry. FT-IR spectroscopy may be a useful approach for dissecting traits affecting fitness under directional selection due to biotic stressors and to manage forests impacted by sudden oak death, as well as in other situations (*U. minor* following infection with *O. novoulmi*; *Quercussuber* roots following infection with the pathogen *Phytophthora cinnamomi*; *Pinus pinaster* after inoculation with the pathogen *Fusarium circinatum*) where emerging or existing forest pests and diseases are of concern.

Third, deep genomics to explore the fitness landscape.

Deep genomic surveys may be used to explore the metaphoric fitness landscape for alleles at the candidate genes discovered by chemical fingerprinting and involved in biotic and abiotic stress resistance in forest trees. Usually, those resistances, as for antibiotic resistance in prokaryotes, carry a fitness cost that must be overcome in order for resistance to persist over the long term. Functional defects associated with resistance mutations may be compensated by mutations at other genes that overcome the cost of resistance. Compensatory mutations are expected to be rare relative to generally beneficial mutations that increase fitness, irrespective of resistance trait. If the cost of resistance is large, compensatory mutations will sharply increase in frequency. This prediction can be tested by determining the LD decay for polymorphic SNP in genomic regions harboring expression QTLs and structural genes associated to the resistance phenotype and its biomarkers.

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1.1.5 Using genomics to understand and manage adaptation to climate change in forest trees

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Introduction

Forest geneticists have long recognized that natural populations of forest trees differ genetically for adaptive traits along climatic gradients. Such patterns were first documented centuries ago for temperate tree species in provenance trials; common garden experiments containing trees grown from seed collected in different locations. These observations led to forestry practices and policies supporting the use of local populations as seed sources for reforestation and as base populations for breeding programs.

Strong and mounting evidence of the effects of anthropogenic climate change on the health of forests globally has resulted in a stronger imperative to manage adaptation to climate in reforestation, better matching genotypes with new climates. Tree populations are lagging behind their historic climatic conditions as climates shift. In a stable climate, forest geneticists need to define the geographic areas over which populations did not differ much in climate adaptation, but for new climates, they need to understand the specific tree traits that vary with climate, and the specific climatic factors that tree populations are most closely adapted to.

Traditional field-based provenance trials can be valuable for predicting the effects of climate change on long-term health and productivity, but they have limitations. They often do not sample a wide enough range of populations, and are often not planted on sufficiently variable sites to predict responses to projected climate change. The sampling designs often do not allow for the decomposition of climatic variation into seasonal temperature and moisture regimes to determine the effects of average or extreme climate on reforestation risks. Finally, phenotyping in field trials is often limited to survival and growth, with assessment of heat, cold or drought stress-related traits not feasible. Both genomic methods and short-term seedling common garden experiments generate information on genetic variation in climate adaptation more quickly than long-term provenance trials, and provide different types of information.

Seedling common garden experiments

Seedling common garden experiments in controlled environment growth chambers, greenhouses, or outdoors can be used to characterize responses to climate-related stresses such as heat waves, drought events, and freezing events, and phenotype-environment associations (PEA), correlations between traits and climatic variables. Seedlings can be particularly sensitive to extreme climate events. Phenological traits such as the timing of active growth (e.g., bud break timing) and dormancy (e.g., terminal shoot bud set timing) can be phenotyped. Samples of seedlings can be used for artificial freeze tests or for assessing water-use efficiency through stable carbon isotope ratios. Allocation of biomass to roots versus shoots can also be assessed through destructive sampling.

Genomic methods for detecting and managing climate-related adaptation

SNP genotyping methods: The most common type of genomic marker is a single nucleotide polymorphism (SNP). SNPs can be generated for many anonymous locations within the genome through using methods such as genotyping-by-sequencing and Restriction site Associated DNA Sequencing (RADseq). These methods are relatively inexpensive, but can lead to uneven data coverage among individuals and greater bioinformatic challenges than some other methods. Targeted sequence capture yields higher-quality SNP datasets for known genes but requires more resources. Once SNPs and their flanking regions are identified, they can be used to design SNP genotyping arrays if sufficient demand exists for such tools.

Genotype-environment association (GEA) analysis:

GEA are correlations between the frequency of individual SNPs and environmental factors associated with provenances such as climatic variables. Population structure and demographic history can lead to false-positive associations, and so must be accounted for in analyses. GEA methods have several advantages. First, phenotypic data is not required to detect patterns of local adaptation to climate among populations, instead variation in DNA can be directly used. As a result, they can detect patterns of adaptation associated with traits that have not been phenotyped (e.g., variation in response to biotic factors or age-related traits). Finally, they can identify the particular aspects of climate that are most important, e.g., specific temperature and precipitation variables that are associated with the strongest patterns of adaptation.

Genome-wide association studies (GWAS): GWAS approaches test relationships between genotypes and adaptive phenotypes. Like GEA, this approach also controls for population structure. If SNPs can be identified that are associated with key adaptive traits, e.g., drought hardiness, then those could be used either to screen populations for assisted gene flow, or to screen genotypes within breeding populations for climate resilience.

Experience from the AdapTree Project

The AdapTree Project in western Canada has used PEA, GEA and GWAS methods to assess climate adaptation in two widespread, economically and ecologically important conifers; lodgepole pine (*Pinus contorta*) and interior spruce (*Picea glauca*, *P. engelmannii*, and their natural hybrids). Approximately one million SNPs were genotyped for around 23,000 genes, as well as non-coding regions, for trees from hundreds of populations in each species. GEA analysis identified hundreds of SNPs in each species that were associated with climatic variables (after population structure was taken into account), and there was considerable overlap in patterns of local adaptation and in some genes involved between the two species. The primary climatic drivers of local adaptation were low temperatures, with fewer SNPs associated with precipitation or with high temperatures. These results were supported by results from seedling common gardens, where cold injury in artificial freeze tests had the strongest geographic patterns of variation of all traits, and was correlated with low temperature-related climatic variables. Heat and drought stress-related traits showed relatively little variation among populations. These results suggest that assisted migration and assisted gene flow could be used to translocate more productive warm-adapted genotypes from milder climates to colder locations as climates warm, and that this should not increase the risk of drought injury relative to using local seed sources. However, care should be taken to avoid translocations that would substantially increase the risk of cold injury to young seedlings. This project has also evaluated the extent and nature of climate adaptation in natural versus breeding populations in order to design climate-based seed transfer strategies for selected genotypes.

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Monday 15 February 14.00-17.00 Parallel Sessions

Session 2.1: Improving productivity through enhanced resource use efficiency

2.1.1 “Green Super Rice” to be resource saving and environment friendly

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Sustainable crop production is of predominant concern for food security. The global demand for crop production is expected to double by 2050 as the growing world population is estimated to be over 9.6 billion. This forecast would require the global increase of crop yield to be around 1.5% per year, which is a massive challenge in the face of climate change and diminishing resources. Increasing crop production to meet the demand must be achieved in a sustainable manner from less land and fewer inputs including great reduction of pesticides, fertilizers, water and other resources.

Rice is the main staple food for more than half of the world’s population, particularly in Asia where 90% of rice is consumed. In the past half century, the increase of rice production has made great contributions to global food security. However, crop production with high-yield cultivars requires high-inputs of nutrient, water and labor. For example, China has been in recent years consuming 55-60 million tons of chemical fertilizers annually, which accounts for more than one third of total fertilizers consumed globally. China has also been consuming 31% of the total pesticides produced worldwide. In addition, irrigation water is used annually in agriculture accounting for 70.4% of the total water consumption in China, of which 70% is used for rice production alone. Excessive uses of fertilizers, insecticides, and water have resulted in severe problems such as the deterioration of soil, water and environment, as well as the decline of crop productivity. To achieve continuous enhancement of crop production in a sustainable manner, Chinese scientists proposed the notion for “Green Super Rice” (GSR) with the key words of “less input, more production and better environment”, as the goal for agricultural research and crop improvement.

GSR aims to produce more rice of good quality to meet the consumers’ demands with promoted resource use efficiency and resilience to climate change in crop production. GSR focuses on promoting resource saving and environment friendly in rice production, while still achieving yield increase and quality improvement. Thus, the new varieties should possess the following characteristic: resistance to major insects and diseases in various rice producing regions, improved nutrient-use efficiency, and resistance to drought and other stresses in areas needed. Furthermore, GSR is not only a variety with the above desirable traits, but it also advocates an efficient and environment-friendly crop management. Labor saving, mechanization and less intensive field management in crop production are now emerging as necessary with the rapid urbanization in China. Such changes require the GSR varieties to have those traits suitable for labor-saving and mechanized crop cultivation.

In the past decade, on the basis of the GSR concept and breeding strategies, we have made tremendous achievements in development and adoption of GSR in rice production in China. For the development of GSR, a combination of strategies has been formulated by integrating germplasm, genomic resources, molecular technology, traditional and genomic breeding with target traits of insect and disease resistances, nitrogen (N) and phosphorus (P) nutrient efficiency, drought tolerance, good quality and high yield. With the rapid advances in

functional genomics, a large number of genes identified so far have provided a rich source for developing GSR cultivars. For examples, several genes related to root growth are currently available for developing N- and P-nutrient use efficient rice. Many genes for drought tolerance hold promise for the development of water-use efficient cultivars. Accumulation of these desired genes by genomic design and marker-assisted or genome-based selection would result in progressive improvement of the rice varieties, eventually leading to GSR.

Currently, the Chinese government has launched the mega-project of GSR with the goal to benefit billion farmers and to boost rice productivity by 8% in the target regions with 30% less input. A national network for the GSR project has been established and it comprises more than 360 scientists from 21 research institutions, 4 universities and 2 seed companies with the strongest expertise in rice breeding and genetic research in China. By using the GSR strategies, the GSR network team has developed thousands of pre-breeding lines with resistance to major insects and diseases, improved drought tolerance, high N- and P-use efficiencies, and other desirable traits in many elite rice genetic backgrounds. The first version of the GSR cultivars with stacked favorable genes has accelerated in recent years. Several hundred varieties with the green traits have been tested in many regions of China as well as in other countries. Almost one hundred GSR varieties are now widely demonstrated across various rice-growing ecological areas in China, where they are helping farmers produce more rice using less input of pesticide, fertilizer and water, and thus increase the income. So far about fifty first-version GSR cultivars have been releasing by national or provincial Crop Variety Approval Committee. Utilization of these cultivars will result in increased rice productivity with much reduced inputs to ensure a great sustainability of rice production. With an international collaborative project supported by the Bill and Melinda Gates Foundation and the Ministry of Science and Technology of China, GSR practices have also spread to other countries in Asia and Africa. Some developed varieties are now being trialed and demonstrated in African and Southeast Asian.

The GSR development and demonstration has set up a successful model with its significance for sustainable agricultural production. The notion of GSR has influenced the prioritization of research direction and changes in agricultural policies in China. Further activities are underway including determination of key traits for GSR in each target region or country, integration of platform of green genes and pre-breeding lines for developing GSR, procedures for evaluating and releasing GSR varieties in targeting countries, establishment of efficient crop management for the development and adoption of GSR varieties, and capability building for widely application and dissemination of the GSR technologies in agricultural production.

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2.1.2 Resource use efficiency in vegetables: Application of molecular breeding to bambara groundnut, an underutilised crop for low-input agriculture

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Intensive agriculture will continue to help provide food and nutritional security. High inputs of nitrogen, growth regulators, irrigation, mechanisation and monoculture of yield-selected genotypes has a valid role for the future. Nevertheless, multiple drivers have forced a partial re-think, with efforts underway to reintroduce resource use efficiency traits into major crops, while maintaining yields. Progress is being made at the pre-breeding level with the introduction of exotic germplasm from ancestors and relatives of current major crops. However, re-engineering 'resilience' into major crops still leaves food and nutritional security vulnerable from abiotic and biotic stresses associated with extensive and intensive monoculture. In marginal environments often found in the global South (where subsistence farming still produces the majority of the world's food) inputs, infrastructure and finance are often not available for high input, high return farming, while degraded soils may not support such agricultural systems.

A complementary approach is to evaluate the potential of many of the minor and underutilised crop species which have been grown under low input agricultural systems for millennia. Such traits and crops may have potential to support agricultural resilience in the face of climate change. In addition there is some evidence that the dietary nutritional value of such crops can be greater than many of the comparator major crops. However, underutilised crops often suffer from a range of factors which limit their potential. Often very little breeding work has been carried out, the pollination systems of the plants are poorly understood and relatively simple genetic problems remain unsolved. Yet, breeding 'elite' cultivars (if that is the aim) is unlikely to be the critical step towards further uptake of underutilised crops. Farmer requirements and preferences, the existence of markets, value added products, validated nutritional data and sustainable agricultural systems to grow these species in, are all required and their lack can significantly limit progress. Moreover, given that it is estimated that around 7,000 species of plants have been used at some point by humankind, a critical question is how to choose the crops that should be the focus of future efforts? A sensible approach is to identify crops which already have outstanding trait values, whether for drought tolerance, nutritional content or another characteristic which makes these species potentially valuable. Even in their 'unimproved' state such crops have some potential to complement, or in some circumstances replace, major crops and are likely to exhibit good resource use efficiency after many centuries of selection in low input systems.

Crops For the Future (CFF) is the world's first research centre with a specific focus on underutilised and minor crops for food, feed, fuel and industrial uses. Based next to the University of Nottingham Malaysia Campus near Kuala Lumpur, Malaysia, it has adopted a Research Value Chain approach, which requires disciplinary input from across the range of academic subjects which impact the growth and use of a crop; from biotechnology to socio-economics.

BamYIELD (www.bamyield.org) is a programme within CFF which is focused on using Bambara groundnut as an exemplar crop, with the lessons learned in this species being tested in other species. Bambara groundnut (*Vigna*

subterranea (L) Verdc) is an African drought tolerant legume which is widely grown in sub-Saharan Africa by subsistence and small-scale farmers. As a legume, it also contributes nitrogen to the agricultural system and non-animal protein to the human diet. We are beginning to apply these approaches in winged bean (*Psophocarpus tetragonolobus*), *Amaranthus* ssp. and Proso millet (*Panicum miliaceum*).

Biotechnology and Crop Genetics

We have developed and used markers to assess pollen transfer, genetic diversity of accessions and for quality control as we develop breeding lines and carry out field work. We concluded that seed from a single plant represents an inbred line. With the International Institute for Tropical Agriculture (IITA) we are developing an extensive collection of lines (500) with genotypes which will be available world-wide to researchers and farmer groups. Working with DArT Pty Ltd., a Genotype-by-Sequence (GBS) marker system has allowed us to map the order of markers on the chromosomes of bambara groundnut. Using this approach we have bred lower sensitivity to long day lengths into a number of lines, which can be an issue for pod filling, for testing in 2016 in UK, Tunisia and South Africa. The markers also allow us to compare marker and gene positions in related species, such as common bean, which has been far more extensively studied. A coordinated effort to supply germplasm for the African Orphan Crop Consortium (AOCC) through BamNetwork (www.bambaragroundnut.org) will ensure that the sequenced genomes are linked to known genetic lines available worldwide.

Breeding and agronomy

Matching the genotype to the environment is a critical aspect of introducing new crops to new environments. An ITPGRFA-FAO Benefit Sharing Fund 3rd round grant will allow common protocols and a core of common genotypes to be trialled with local material in Ghana, Nigeria, Indonesia and Malaysia. This will generate robust data on the environmental influence on nutritional and processing traits. By including the major crop equivalents (peanut, 'cowpea') in the trials we will also produce robust data to determine under what circumstances it makes sense to grow the underutilised crop, rather than the major crop. The network of field partners will also be used for selection and breeding work alongside collaborations with seed companies in Southeast Asia and Africa.

Meteorology and Ecophysiology

Given the predictions of climate change, it is also important to understand how any introduction of a new crop is likely to be impacted by climatic change over time, as well as to know that it is suitable for planting now. Based on trial data from Gaborone (Botswana) we predicted that bambara groundnut has potential in Malaysia, both today and also in the future. We are now generating a comparable set of data in Malaysia alongside actually selecting genotypes within Malaysian field environments, to allow validation of the models. This approach can be applied worldwide.

Nutrition and Bioproducts

Many underutilised crops are held back by a lack of nutritional and processing knowledge and how to produce value added products. These can limit a crop to remaining purely a commodity. We have developed a number of potential products, including vacuum fried and extruded products, soy-replacement drinks and supplemented wheat flour (which has a better balance of amino acids than either wheat or bambara groundnut flour alone). We are working (non-exclusively) with a major manufacturer in Southeast Asia to develop the supply chain needed for large scale supply of raw materials for such products, with the potential to expand approaches to multiple countries.

Social, economic and policy.

Ultimately, the development of underutilised crops must contribute to social and economic benefits for producing communities. Currently many of these communities are made up of subsistence farmers growing crops in small scale low input farming systems, with limited resources, little leverage over the supply chain and a very limited

ability to effectively markets and/or capture added value which could come from the processing of the raw materials. PhD work currently underway in Tanzania is directly addressing the question of devising appropriate economic metrics for underutilised crops employing bambara groundnut as an exemplar. Further projects are being undertaken with partners in Ghana, Nigeria and Indonesia CFF to develop and test approaches to increasing our general understanding of the current role of bambara groundnut in smallholder systems and evaluating its current and potential contribution to smallholder welfare.

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2.1.3 Resource Use Efficiency: Applications of Biotechnology in Genetic Improvement in Tropical Aquaculture

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Aquaculture is the most rapidly growing food production sector, but modern aquaculture has a short history, of about 40-50 years. Many aquatic species are farmed [541 are reported in FAO production statistics) and others are being tested on a pilot scale level; several are becoming major global aquaculture species, while some have fallen out of use. Among the dominant fish groups in world aquaculture are the tilapias and carps, which are mostly farmed in tropical and subtropical regions. Catfishes have also seen rapid recent growth in production. Seaweeds, clams and oysters are dominant groups in tropical marine aquaculture.

Several biotechnologies have been developed that have potential to assist genetic improvement and resource use efficiency in aquaculture. These include: chromosome set and sex ratio manipulation to overcome problems with differential growth of the sexes, early maturation and reproduction before harvest; DNA markers, linkage mapping and quantitative trait loci (QTLs) are useful in tracking pedigree and identifying genetically superior individuals; cryopreservation can assist with gene banking, storage and transport, and assessing genetic gain; and genetic modification allows for targeted genetic improvement based on the function of specific genes.

The first group (chromosome set and sex ratio manipulation) are appropriate for species-specific problems rather than having generic application for long term genetic improvement. Thus, there is very little need for such techniques in most large carp species, which reach harvest size before maturation and show relatively little sexual dimorphism at this stage. However, in tilapias, the second ranking group in world aquaculture by production volume, maturation and reproduction before harvest constitute a significant problem in most farming environments. Energy is wasted in reproduction and the resultant fry compete with the originally stocked fish, leading to wasted resources and reduced market prices due to lower harvest sizes. The most commonly used way to overcome this is by dietary treatment of fry with 17 α -methyltestosterone (MT), although this is banned in some countries. Triploidy, induced through the application of pressure or temperature shocks to newly fertilised eggs, renders most females sterile and prevents males from producing functional sperm, and has been shown to result in increased yields in experimental trials. However, it is not feasible to use this in commercial tilapia hatcheries due to their reproductive biology: females spawn small batches of eggs frequently and asynchronously, making it impossible to obtain large quantities of unfertilised eggs to induce triploidy. The production of genetically male tilapia (from crosses between YY males and XX females) has been commercialised on a small scale, but the management of this is complex, partly due to several generations of breeding to produce large numbers of YY males and partly due to the complexity of sex determination in tilapia. The recent discovery of a master sex-determining gene (*amhy*) may help to overcome these problems through the application of marker-assisted selection (MAS). Other species in which these techniques have potential include the African catfish (triploidy to reduce female egg mass at harvest), giant freshwater prawn (all-male production to take advantage of faster growth rate) and oysters (triploidy to reduce maturation and allow all-year marketing).

The second group (DNA markers, linkage mapping and QTLs) are linked to the rapidly developing science of genomics. The genomes of several important aquaculture species (including the Nile tilapia) have been sequenced in the last few years, and more are underway. Polymorphic DNA markers (microsatellites and more recently single nucleotide polymorphisms, SNPs) have been used in studying the structure of the wild populations of many species (aquaculture still relies on wild fish as broodstock and in some cases for juveniles), for parentage

assignment (can be achieved from communally reared mixed families, particularly important in mass spawning species and also to allow communal rearing of families in breeding programmes to reduce environmental effects on selected traits), and in the development of QTL mapping and MAS in aquaculture species. While high-value, high-latitude species have led the way in the application of such techniques (the first QTL to be applied in commercial breeding programmes in aquaculture was one for resistance to infectious pancreatic necrosis, a viral disease of Atlantic salmon; this only happened a few years ago), the potential for the application of DNA markers and MAS in tropical aquaculture species is there and starting to be realised.

Unlike mammals and many plants, gene banking in fish is currently only possible for sperm. The inability to cryopreserve eggs and/or embryos is a serious limitation. However, sperm cryopreservation has been used for gene banking at the start of several breeding programmes, as a tool in assessing genetic gain (progeny from the current generation of selection can be compared to crosses between eggs from current generation females and cryopreserved sperm from earlier generation males), and as a way of transferring genetic material between aquaculture programmes. Cryopreservation has not, however, found large-scale use in routine seed production. Genetic modification in fish was first achieved in the 1980s in China, but progress towards use in aquaculture has been limited due to the negative image of GM animals for consumption. Recently, the US Food and Drug Administration approved a long-running application by AquaBounty for Atlantic salmon with modified growth hormone expression. These fish are produced in a hatchery in Canada and currently grown on in tanks in Panama to reduce risk of impact from accidental escapes. This case may act as watershed for other potential applications, although public acceptance remains in doubt and is likely to vary from country to country. These GM fish were produced by microinjection of many copies of the DNA construct into fertilised eggs, with random integration of a very low proportion, often creating mosaic insertion patterns. The recent emergence of highly targeted gene editing offers the potential for more accurate genetic modification, which is now being realised at an experimental level.

Although the current impact of biotechnology in genetic improvement in tropical aquaculture is limited, the increasing level of application in temperate aquaculture, the development of breeding programmes for tropical species, current research on tropical aquatic species and the decreasing costs of sequencing and genotyping all indicate increasing impact on production. As will be outlined in the presentation, it is to be expected that this will improve the efficiency of resource use.

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2.1.4 Resource use efficiency in livestock: Bridging the biotechnology-livestock productivity gap in East Africa

Denis Mujibi

Introduction

Africa's indigenous cattle populations are the backbone of the continent's livestock industry, providing sources of income, nutrition and livelihoods to millions of people in marginal areas. However, unit productivity of these animals lags behind most other regions of the world. Recent studies predict significant contraction of mixed farming systems, which represent the majority of food producers in sub-Saharan Africa. Changes in the growing length, disease vector habitat as well as water distribution and availability, require that sustainable intensification of livestock productivity, be given priority.

Biotechnology, and specifically genetic improvement can play a significant role in increasing productivity of livestock in Africa. There is a wealth of information and tools available for such improvement, but they have been poorly utilized for most livestock species because of lack of infrastructure, high initial investment and the long time required for impacts to be made. We present 3 case studies that illustrate our efforts in applying genetic tools in improving livestock productivity in Africa.

Identification of appropriate crossbreeding levels for smallholder dairy enterprises

The use of crossbred animals continue to be the basis of most dairy enterprises in Eastern Africa. However, the indiscriminate crossbreeding practiced in these systems produces highly admixed animals resulting in huge differences in productivity. Additionally, since the breed composition is unknown, there is often a mismatch between production environment and animal breed type, a situation which cannot sustain the growth and expansion of the local dairy sector.

We have recently applied SNP markers in order to match breed composition with production environment for smallholder dairy cows. The results indicate that there is an optimal level for crossbreeding beyond which increased upgrading to exotic breeds does not result in additional yields. In high input smallholder production systems, higher grade exotic breeds would be ideal to maximize returns. However, for mid and lower input systems, high grade crossbred do not perform any different from lower grade crosses. In these systems, the overriding considerations would be the percentage of exotic genes that an animal harbors, which needs to be balanced against the unfavorable effect of lower survival and higher disease incidence.

There are opportunities to identify bulls that sire more adapted offspring that produce higher yields. We intend to develop genomic tools that allow mass profiling of animals to identify and propagate tropically adapted high yielding cows.

Unveiling the genetic basis of African swine fever virus tolerance

Diseases are responsible for enormous productivity losses in Africa. In hotspots where several livestock and zoonotic diseases are endemic, the net effect of disease can be very large, especially when disease control systems are poor. African swine fever (ASF) is a viral hemorrhagic disease of pigs (*Sus scrofa*) that results in complete mortality of infected animals. The disease is endemic in Africa and Sardinia where it is largely restricted. Spread of the disease into major pork producing regions of the world could lead to massive losses to farmers. There is anecdotal evidence that indigenous pigs in Africa are less susceptible to African swine fever virus (ASFv) infection compared to improved international breeds. Apparently healthy pigs have tested positive for the virus or viral antibodies, without clinical symptoms for the disease. However, the determinants of this tolerance are not known.

We used genome-wide SNP markers to investigate the genomic structure of indigenous and improved international breeds in comparison to wild pigs. Wild pigs are resistant to ASF. Results indicate that village pigs that tested negative for ASFv have significantly higher indigenous ('African') ancestry (54% and above) compared to those testing positive, which had higher proportions of international commercial breeds. This has significant implications in disease surveillance and diagnosis of infection status. A genome wide scan detected several regions having signals that indicate preferential selection for genes within those regions. These results point to a possible underlying genetic control to ASF tolerance.

The understanding of the genetic basis for ASFv tolerance will be a great boost in the management of ASF.

Harnessing fecundity in Goats

Goats play an important role as a source of meat and income for large numbers of African families. The biology of the goat, particularly its small size (10 – 80kg), short generation interval (15 months), prolificacy (up to 5 live births possible) and short age to market makes it a very attractive prospect for many households, and especially for women and youth. Owing to it being one of the hardiest animals that is adapted to a host of harsh environments, the goat has been integrated into the social fabric of Africa. The goat's dominance and distribution is testament to the high regard it receives.

The specific genes underlying the capacity of the goat to easily adapt to diverse agro-ecologies are poorly understood. Current efforts are trying to reverse this lack of knowledge, and activities targeting genomics of disease and adaptation are already underway. One of the research projects underway is looking at improved fecundity in goats. Given the nature of goat production systems, reproduction equals production. Success of the enterprise depends on the number of kids raised, weaned and sold.

The West African dwarf goats are extremely fecund. Super does that produce multiple kids have been observed, with twins and triplets being quite common. We are studying the genetic determinants underlying this trait with the aim of increasing the utility of high prolificacy. We intend to produce a marker panel applicable in a Marker Assisted Selection framework to identify bucks that sire does that produce more triplets and quadruplets. Access to highly fecund super does will not only increase incomes for families, but also improve household nutritional status.

Conclusion

Despite the promise that biotechnology presents, there are still many challenges to be contended with, including the high cost of genomic tools, markers systems that are biased towards exotic breeds and the lack of phenotypes to aid in associating performance in smallholder systems with genomic determinants. These limit the application, utility and potential benefits accruable from use of genomic tools.

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Monday 15 February
14.00-17.00 Parallel Sessions

Session 3.1: Social and economic impacts of agricultural biotechnologies for smallholders: Taking stock of the evidence and prioritizing future assessments

3.1.1 Evidence-based policymaking: The role of impact assessment studies and their implications for agricultural biotechnologies

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Summary prepared for Parallel Session 3.1 on: “Social and economic impacts of agricultural biotechnologies for smallholders: Taking stock of the evidence and prioritizing future assessments”, FAO symposium on ‘The role of agricultural biotechnologies in sustainable food systems and nutrition’, Rome, 15–17 February 2016

Recent decades have seen an exciting increase in new tools and products that could accelerate the application of biotechnology to agriculture in developing countries. From genetic diagnostics, tissue culture, genetic modification and genome editing, to reproductive and vaccine technologies, nanotechnology, and synthetic biology—all of these technologies have the potential to increase the availability of and access to quality foods in developing countries and to improve the livelihoods of the rural and urban poor. In fact, scientists, businesses, governments, and civil society organizations are already exploring technologies that increase crop and livestock yields, decrease production costs, reduce susceptibility to environmental stresses, and improve the nutritional content of food crops.

The agricultural and economic impacts of several technologies in this broad category of biotechnology—for example, genetically modified insect-resistant Bt cotton and maize—have already been the subject of extensive scrutiny at the farm, household, and market levels. A large number of rigorous studies of these technologies find significant cost savings, yield improvements, and reductions in pesticide exposure for farmers, including many who operate small and poorly resourced farms.

There is also a range of innovative technologies—for example, tools that improve the efficacy and efficiency of plant breeding, livestock vaccine development, or the propagation of planting materials—that have yet to receive much scrutiny. This is partly because these technologies are upstream process innovations that address scientific discovery and product development, rather than downstream product innovations that more immediately affect smallholders’ farming practices and rural livelihoods. Nonetheless, we know these technologies play an equally important role in accelerating progress in the agricultural and life sciences.

Looking to the future, it will be important to continuously gather evidence about the full range of biotechnology tools and products in order to better inform policy design by developing-country governments and other actors in the global food and agriculture system. Well-informed, evidence-based policy design relies on rational, systematic decisionmaking to shape social, economic, and scientific choices made by the state. Of course,

evidence-based policy design does not occur in a vacuum. Careful attention must be given to the nature of evidence used in policymaking, how it is integrated into the policymaking process, and the role of other influences on decisionmaking. There is, however, general recognition that the use of rigorous evidence is essential to sound policymaking, particularly when the issues at stake concern agricultural growth, economic development, and poverty reduction in developing countries.

Traditionally, published papers from the biophysical sciences have set the standard for credible and rigorous evidence. They evaluate new applications of biotechnology under carefully controlled conditions of a laboratory experiment or field trial. Yet this body of evidence is far from complete, which is why economists and social scientists are also asked to explore the costs, benefits, and trade-offs of these applications under real-world conditions—where weather and price risk play a critical role, where individual and household characteristics are essential considerations, and where individual preferences, expectations, and beliefs can further shape social and economic impacts. While their findings often support results from the biophysical sciences, they can also add nuance to the picture, or even call into question the best of good laboratory science.

Two types of evidence on the social, environmental, and economic impacts of biotechnologies are increasingly needed to strengthen the evidence base around which public policies—laws and legislation, rules and regulations, public investments and expenditures, taxes and subsidies, and trade and investment regimes—are designed. The first is forward-looking evaluation, or the construction of ex ante scenarios that explore the societal, economic, and environmental gains and losses associated with a particular biotechnology application or policy design relative to appropriate counterfactual scenarios. For example, a forward-looking analysis can be used to identify the varied impacts of a new labor-saving crop technology for large farmers, smallholders, and landless laborers. It can also be used to understand the productivity losses associated with regulatory delays and uncertainty that impede the release of new biotechnology research tools to scientists or new biotechnology products to farmers. Rigorous foresight analysis of the impacts of both technologies and policies allows policymakers to consider their policy options from a more informed position, particularly at high levels of aggregation—global, national, or landscape.

The second type of evidence relies on insights into the choices that farmers, firms, consumers, and governments make with respect to biotechnology. Here, the science of individual and household decisionmaking has advanced considerably in recent decades. Economists and social scientists have access to more rigorous experimental designs and long-term panel data that allow them to identify complex causal—not just correlated—relationships between technology or policy interventions on the one hand, and productivity, sustainability, and welfare outcomes on the other. Moreover, a growing convergence among disciplines that study the behavioral dimensions of decisionmaking is increasing our understanding of how individuals make choices about new technologies, how they value competing choices, and how they learn about these technologies and choices over time.

These same scholars are applying increasingly sophisticated tools of analysis to the study of how the interactions between firms in the market for innovation in agriculture can influence the availability and price of new

biotechnologies for farmers and consumers, and how government interventions in those markets can help or hinder innovation processes around biotechnology.

More rigorous evidence on these micro-level dimensions not only improves the accuracy of our forward-looking analyses, but also helps us better identify what works under real-world conditions. Ultimately, this combination of real-world evidence and forward-looking analysis translates into insights about biotechnology applications at the landscape, national, or global scale, taking into account both patterns of technological change and social, environmental, and economic impacts. When combined with historical perspectives and qualitative insights from stakeholders, these analyses and insights can provide the critical evidence needed for developing countries to improve the policy, regulatory, and investment choices that influence the development and introduction of biotechnology applications. Greater commitment to the use of science-based evidence in policymaking can, in turn, help overcome ideology and advance the technological opportunities available to the world's 500 million farmers and 7 billion consumers.

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3.1.2 Lessons learned from case studies of applying biotechnologies for smallholders

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Jim Dargie, Former Director, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, Vienna, Austria

John Ruane, FAO, Rome, Italy

Summary

FAO promoted the study of 19 cases, in which biotechnologies were applied to serve the needs of smallholders in developing countries. The case studies, selected after an open call for proposals, were prepared by scientists directly involved in the initiatives who were asked to describe the background, achievements, obstacles/challenges encountered, factors for success (or failure), impacts and lessons learned from their case study. The cases covered different world regions, production systems, species and underlying socio-economic conditions in the crop (seven case studies), livestock (seven) and aquaculture/fisheries (five) sectors. Apart from one on West Africa, the studies focused on a specific initiative within a single country. More details on the different case studies are provided in Ruane *et al.* (2013).

A wide range of biotechnologies was used in the case studies, including some of the traditional methods, such as fermentation and artificial insemination, as well as several advanced techniques involving sophisticated DNA and genetic analyses. Genetically modified organisms (GMO) applications were not included because of the highly polarised debate they normally engender. By dominating the debate, this has prevented serious consideration to be given to the potential contributions that the many non-GMO biotechnologies can make to sustainable development and food security (Ruane and Sonnino, 2011). Most of the case studies involved application of a single biotechnology in a single crop, livestock or fish species, with the objective of overcoming biological and technological constraints to increase productivity, improve people's livelihoods, tackle diseases and pests, expand market opportunities through diversification and value addition, and to conserve genetic resources.

The case studies yielded many varied and valuable outputs, in terms of the scientific and technical knowledge, capacities and products. While not all cases provided evidence of widespread adoption by farmers, some biotechnologies were adopted on a large scale. For example a new high yielding and downy mildew resistant hybrid of pearl millet, developed in partnership by the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Indian agricultural universities and British research institutes, was released in 2005. By 2011, cultivation of this variety had spread to almost 900,000 hectares (ha) in northern India, bringing greater food security to about two million people. In rice, the International Rice Research Institute (IRRI) and Indian research institutes released in 2009 the Swarna-Sub1 variety, highly tolerant to submergence and lodging. In flood-affected areas, it was able to produce 1-3 tonnes per hectare more than other previously grown varieties. During the 2012 wet season, Swarna-Sub1 was cultivated by over three million farmers, covering over one million ha. In aquaculture, the Jian carp, developed in China by within-family genetic selection and gynogenesis (a reproductive technology resulting in all-female carp offspring which have received genetic material only from their mothers), is now grown on about 160,000 farms and is responsible for over 50 per cent of the total common carp production in the country.

The rate of adoption indicated in other case studies was less wide but nonetheless meaningful to the farming communities concerned. For example, a community-based foundation provides production-related veterinary services, including artificial insemination, to around 3,000 smallholder dairy cattle farmers in Bangladesh. The initiative increased milk production and farmers' income and generated employment.

From all the case studies, ten general and interrelated lessons have been drawn which can be used to inform and

assist policy-makers when deciding on potential interventions involving biotechnologies for smallholders in developing countries. These are:

1. Commitment by national and/or state governments was critical for improving the productivity of smallholder enterprises and the livelihoods of smallholder farmers.
2. Financial support from bilateral and multilateral donors and international agencies was indispensable for supplementing national efforts.
3. International and national partnerships were vital for achieving results, particularly for translating research outputs into field outcomes and impacts. The case studies provided numerous examples of successful partnerships within the public sector, between public and private sector entities, and involving NGOs and community-based approaches.
4. Long-term national investments in both human capital and infrastructure for science and technology were critical components of the recipe. The case studies involved continuous agricultural research efforts that extended over 15 to 40 years.
5. Biotechnology approaches did not work in a vacuum, but were introduced into both the research mix and farmers' fields through appropriate integration with other sources of science-based and traditional knowledge.
6. The diffusion of genetic resources, techniques and know-how across national and continental boundaries was an essential ingredient of most case studies.
7. Intellectual property issues did not constrain research or the production or use of biotechnology innovations in the case studies examined here.
8. Products generated through the biotechnologies described did not need to conform to new biosafety or food safety regulations or standards. Without entering into the merits of such regulatory issues, this clearly represents an advantage for the development and use of products from the biotechnologies described in these case studies over those developed using genetic modification.
9. Some case studies demonstrated clearly that development projects involving smallholder farm production systems can be dynamic and risk-prone. Stakeholders need to be aware, and anticipate, that the system may evolve quickly because of issues like changes in plant or animal disease dynamics or changes in farmer and consumer preferences.
10. Planning, monitoring and evaluation of biotechnology applications were weak and should be strengthened. Most of the studies provided no information concerning the costs or benefits (in terms of production, productivity or financial returns) or changes in livelihoods. To improve both the planning and management of future projects, these aspects should be given much higher priority.

These case studies demonstrate that despite the complexities of smallholder farmer production systems, agricultural biotechnologies can indeed represent powerful tools to benefit smallholder farmers given the appropriate conditions and enabling environment.

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3.1.3 Impacts of Agricultural Biotechnology and Policies: China's Experience

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Facing enormous constraints in natural resources, China's ability to feed its growing population with rising income is impressive. Per capita water availability is only one fourth of world average and arable land accounts for only 8% of world total, but China supported over 20% of the world's population and had been a net food exporter before the middle 2000s. However, total food demand growth has surpassed production growth thereafter, which resulted in a fall of overall food self-sufficient to 96% in 2014. Most imports have been soybeans and feed grains (e.g., maize and other coarse grain) for livestock production.

China's food import is expected to rise as demand growth is expected to exceed production growth for many agricultural commodities in the future. In the past, increased food production has been at the expensive of sustainable development. Recent rising cost of production due to rising wage has resulted in less competitive of China's agriculture in the global market. Under these backgrounds, China has been looking for all potential measures to increase its agricultural production at more sustainable ways.

Among many efforts, biotech is considered as one of major tools by the national leaders to boosting China's agricultural productivity and ensuring the national food security. After China initiated its agricultural biotech program in the middle 1980s, public investment was doubled within every 4 years during the late 1990s and the middle 2000s. Since 2008, Chinese R&D on genetically modified (GM) crops and animals has been further spurred by \$3.8 billion of new funding from the National GM Variety Development Special Program (GMSP) for the period of 2008-2020. By 2010, there were more than 13,000 researchers work on agricultural biotech, including GM plants, animals and microorganisms. By 2015, a number of GM crops have been issued the production safety certificates though major GM crops have not been approved for commercialization.

Bt cotton is one of the most successful cases of GM technologies in China. After its commercialization in 1997, about 7.1 million small farmers adopted Bt cotton by 2009, and now Bt cotton accounted for more than 85% total cotton area in China. Our empirical studies show that the impacts of Bt cotton have been impressive. On the average, Bt cotton increased cotton yield by 9.6%, reduced pesticide use by 34 kg/ha, reduced labour input by 41 days/ha, and despite of higher seed cost, net profit increased by 1857 RBM (or about USD 225) per hectare. Our surveys of randomly selected farm households in the experimental villages show that the households cultivated Bt rice, when compared to household cultivating non-GM rice, small and poor farm households also benefit significantly from GM rice adoption by both higher crop yields and reduced use of pesticides. Moreover, both Bt cotton and Bt rice also contributed to improved health of farmers by reducing the probability of farmers suffering pesticide-related incidences of morbidity during crop growing season.

The model simulations further show that economic-wide impacts of GM crops are substantial. Annual gain from Bt cotton and Bt rice reached USD 1.1 billion and USD 4.2 billion, respectively, which already exceeds total investment in agricultural GM R&D in China. Moreover the commercialization of GM crops will significantly increase China's maize and other food production and therefore raise food and feed self-sufficient levels in the future.

However, the rising debate on the safety of GM food has largely changed the consumers' attitudes toward GM food in China. Our surveys show that the percentage of urban consumers who perceived such food as unsafe for consumption increased by more than 30% in the period of 2002–2012. Major shifts have been occurred after 2010, one year after China issued the biosafety certificate of production for Bt rice and Phytase maize. The

public concerns on GM food obviously have affected China's policy on the GM tech commercialization after the late 2000s. However, given the significant socioeconomic impacts of GM technologies, China has reemphasized the roles of biotech in ensuring the nation's food security in recent years. The national leaders have decided to take the three step development strategy: moving from non-food (e.g., fiber) to indirect food (e.g., feed), and finally to direct food (e.g., rice and wheat). Under this new strategy, China is expected to commercialize its GM maize in very near future.

The presentation ends with four remarks: 1) China has invested significantly in GM technology, and the progress has been impressive; 2) China has also gained significantly from Bt cotton commercialization, and will gain much more from the commercialization of other major GM crops such as maize and rice; 3) GM technologies will play more important roles in improving agri. productivity, ensuring food security, and improving farmers' welfare; and 4) recent policy to facilitate commercialization of GM maize is encouraging and will also have important implications to global biotech development and global trade in the future.

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3.1.4 Socio-Economic Impact of Agricultural Biotechnologies for Small Holders in India

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Biotechnology for Improving Agricultural Production

Application of biotechnology in Indian agriculture gained prominence with the cultivation of transgenic *bacillus thuringiensis* toxin (BT) producing cotton crop in 2002. Since then, India has taken the lead in exploring the potential of biotechnology on various fronts. The biotechnology programme in agriculture includes; molecular mapping of genes of important plants, marker genes for selection of quality traits, development of transgenic crops, tissue culture for plant propagation, bio-fertilisers, bio-pesticides, vermicomposting, biodegradation of wastes and toxic substances and mushroom production. With regard to transgenic crops, the objectives of breeding new genetically modified (GM) crops were increased in crop yield, improvement in product quality, increased nutritional values, reduction in biotic stress, tolerance to abiotic stress such as drought, frost, heat, salinity, herbicide, and production of plant-based pharmaceuticals.

When the genetically modified BT hybrid cotton was introduced in 2002, 55,000 farmers cultivated it on 30,000 ha. There was an initial setback because of certain concerns such as low yield, non-resistance against sucking pests and high cost of inputs. With the rectification of these problems, BT cotton was widely accepted across the country. In 2014, 7.5 million farmers were engaged in cultivation of BT Cotton on 11.6 million ha, covering 96% of the total area under cotton production, using 1,100 varieties and more than 50% of them were small land holders. Indian cotton production increased from 13 million bales in 2002 to 40 million bales in 2014 enhancing the income of farmers from 300% to 400%. Since the cultivation of BT cotton, BT cotton seed oil and BT cotton seed cakes have entered the food chain in India. In 2007, the Government of India allowed the import of glyphosate tolerant genetically modified soybean oil and canola oil to meet the growing demand for edible oils. Presently, India ranks fourth among GM crop producing countries in the world.

In spite of phenomenal progress in GM cotton production, India has been very hesitant in introducing other GM crops, mainly due to failure to exhibit resistance against all pests, low crop yield, high cost of seeds, heavy dependence on seed companies, lack of mechanism to monitor safety measures and assess risk, inadequate bio-safety studies, monopoly of a few MNCs and lack of transparency. However, with the change in the Government in 2014, 11 new crops have been approved for field trials. These include corn, rice, mustard, wheat, sugarcane, groundnut, brinjal, okra, cabbage, cauliflower and tomato for insect resistance, herbicide tolerance, stress resistance, drought resistance, enrichment of nutrients, vitamin, sugar, proteins, etc. Large number of public and private research institutions have taken up studies on identification of marker-assisted genes, development of new transgenic crops and varieties.

Tissue culture is another important programme becoming popular and commercially viable in India for rapid propagation of superior plants, elimination of viral diseases, germplasm storage, inducing desirable, heritable changes, incorporate potentially useful genes, somatic hybridization and regeneration of transgenic plants through transfer of genes into protoplasts. Presently, India is producing over 150 million plantlets every year particularly for cultivating horticulture, aromatic, medicinal and forestry crops. Tissue cultured plants are very well accepted by small farmers due to assured quality and timely guidance to adopt good production practices.

Use of biofertilisers and biopesticides are also becoming popular during the last two decades. During 2012-13, over 0.5 million tons of biofertilisers were produced while the potential is 2.5 million tons a year. Presently, the biofertilisers under commercial production are Rhizobium, Azotobacter, Azospirillum, Herbspirillum, Azolla and Blue Green Algae species for nitrogen fixing, Pseudomonas and Bacillus species for phosphate solubilisation,

Frateriia species for potash solubilisation and Vesicular Arbuscular Mycorrhizae (VAM) for micro-nutrient supply. Commercial production of biopesticides has also been undertaken by the private sector for crop protection. These include biofungicides and nematodes apart from a wide range of botanicals. These products have been very well accepted by farmers because of low cost, easy availability and safety, while ensuring effective control.

Biotechnology for Animal Husbandry

India has been successful in clonal propagation of buffaloes. However, the major research focus is on genomic studies of Indian cattle and buffaloes to identify genes for economic traits such as heat/cold tolerance, disease resistance, calving interval, milk yield, high protein and fat, etc. and marker added selection for productivity enhancement. Use of embryos for bull production, karyotyping for screening of cattle against genetic disorders and use of sexed semen for producing female milk animals are the other initiatives in animal production. Selection of thermo-stable microbial strains for production of efficient diagnostics and vaccines is another area of priority. Technologies have been developed for efficient recycling of dung and bio-waste through vermicomposting and biogas production using efficient microbes, which benefit small farmers who represent 87% of land holders in India.

Studies on identification and introduction of bacteria which can suppress methane production in rumen, to improve feed efficiency, while reducing the emission of greenhouse gases, need greater attention.

Conclusion

Biotechnology sector in India is generating an annual income of \$4 billion with Agricultural Biotechnology having a share of 14%. With the change in the policy to grow GM crops, agricultural biotechnology is bound to have a major role on food security and rural prosperity in India.

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Tuesday 16 February
09.30-12.30 Parallel Sessions

Session 1.2 Facing the challenges of climate change: Adaptation in the livestock and fishery sectors

1.2.1 Selective breeding in aquaculture for future environments under climate change

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SUMMARY

Aquaculture is the fastest growing food production sector that contributes significantly to global food security. Based on FAO reports, aquaculture production has to increase by 42.9% to meet the future global demand for aquatic foods in 2020. According to the reports by IPCC and FAO, climate change may result in global warming, sea level rise, changes of ocean productivity, freshwater shortage, and more frequent extreme climate events. Consequently, climate change may affect aquaculture to various extents depending on climatic zones, geographical areas (inland or coastal), type of aquaculture systems, and species farmed. Climate change may introduce opportunities as well as several challenges:

Opportunities may arise at certain locations and geographical areas; for instance, a rise of temperature may prolong growth period, increase fish growth rate, allow new and more efficient farming systems, and new-farmed species. Spatial planning will enable the identification of locations with optimal conditions for farming.

Challenges; There are two major challenges caused by climate change.

Firstly, the current fish material, adapted to the prevailing environmental conditions, may be suboptimal under future conditions. Similarly, breeding programmes selecting for genotypes with current superior performance, may not be the optimal genotypes in the future. Genotype-by-environment interaction (GxE) is a phenomenon by which animals respond differently to changes in environment. The presence of GxE indicates that there is genetic variation in environmental sensitivity and it is possible to select for fish that can adapt to the changing environments. For instance, rainbow trout (*Oncorhynchus mykiss*), a very popular farmed salmonid worldwide, has a narrow optimal temperature range. Strong GxE in growth performance of rainbow trout in different temperatures has been reported; hence, utilisation of selective breeding can be advantageous for breeding rainbow trout that are best adapted to the temperature changes induced by climate change.

Secondly, climate change may facilitate outbreaks of existing pathogens or parasites. Moreover, change in water temperature may promote dispersal of new diseases. Disease prevalence increases with physical stress, e.g., that associated with a change in temperature, due to reduction in host resistance and increasing growth of pathogens. Many diseases of farmed fish can potentially become a greater problem at higher temperatures. Thus, mortality rates will increase and production from aquaculture will reduce. In Australia, farmed abalone (*Haliotis laevis*) has experienced 25% summer mortality due to elevated water temperature, leading to AU\$1.75 million loss of profit.

To cope with the challenges above, adaptive measures must be addressed through both a reduction of environmental impacts from greenhouse gas (GHG) emissions and selective breeding strategies.

Adaptive strategies. Three major adaptive strategies are identified:

1. Fish species are often poikilothermic, and may therefore be particularly vulnerable to temperature changes. This will make low sensitivity to temperature more important for fish than for livestock and other terrestrial species. Hence, general “robustness” will become a key trait in aquaculture, whereby fish will be less vulnerable to current and new diseases and parasites while at the same time thriving in a wider range of temperatures. Breeding goals may change toward prioritising robustness. Nevertheless, knowledge of, and implementation of genetic adaptation to fish breeding is limited and has not received much attention.
2. The limited adoption of breeding programmes in aquaculture (<10%) is a major concern. Aquaculture based on wild stocks that are not adapted to the farm environment, or farmed animals from breeding programmes without proper selection and/or control of inbreeding, will lead to poor performance and survival compared to genetically improved or well-managed stocks. This implies low aquaculture production and inefficient use of resources for feed and land. Consequently, a higher carbon footprint with a negative impact on climate change per kg fish produced is expected. Aquaculture should use genetically improved and robust species not suffering from inbreeding depression. This will imply using fish materials from well-managed selective breeding programmes with proper breeding goals and a controlled rate of inbreeding. Policy makers should provide incentives and public support to boost selective breeding programmes in aquaculture for more robust fish tolerating climatic changes.
3. Although aquatic organisms do not emit GHGs as ruminants do, aquaculture activities, such as input power, transport, and feed production contribute to GHG emissions. Life cycle analysis (LCA) is a method to quantify the use of resources and emission of pollutants of the entire production chain for a product. Selective breeding for increased production is expected to enhance efficiency of resource utilisation (feed, energy and land) of a production system, through correlated changes in feed efficiency or shorter production period. Applications of LCA to define breeding goals that maximise production while minimising environmental impacts can be one solution, as already demonstrated in African catfish.

Conclusions.

Climate change poses opportunities and challenges to aquaculture production. Selective breeding is a long-term, cost-effective strategy that can best minimise the detrimental effects of climate change on aquaculture. Empirical studies are required to estimate the potential of increasing robustness of fish by selection methods. Applying selective breeding to develop robust animals will become more important under climate change, and dissemination of genetically improved stocks will in-turn efficiently increase aquaculture production and reduce environmental load, including GHG-emissions. Established selective breeding programmes are a prerequisite to apply genomic information for further genetic improvement of aquaculture production. Hence, stakeholders should support the adoption and development of selective breeding by disseminating genetically improved materials and knowledge of selective breeding at all levels of the aquaculture sector worldwide, to ensure food security for the growing human population under climate change.

Keywords: aquaculture, climate change, environmental sensitivity, genotype-by-environment interaction, selective breeding

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1.2.2 Development of Diagnostic Tools and Vaccines for Aquatic Animals

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SUMMARY

Introduction

Currently aquaculture contributes approximately 50% of global food fish consumption. Disease, however, is still regarded as a major constraint to aquaculture production. Control of disease is complex and relies on a combination of pathogen detection, disease diagnosis, treatment, prevention and general health management. Speed of pathogen detection is crucial to prevent the spread of disease. Clearly climate change will affect the movement and spread of diseases in the aquatic environment, thus having relevant rapid tests in place as well as appropriate vaccines to prevent the spread of disease is vital for the future sustainability of aquaculture.

Climate Change and Aquaculture

There is concern that climate change may increase the risk of disease to aquaculture through alterations in the distribution, prevalence and virulence of pathogens (bacteria, viruses, fungi and parasites) and changes in the susceptibility of the host species. The impact of climate change will vary across the distinct climatic regions (topical, sub-tropical and temperate) and different environments (freshwater, marine and brackish water) of the world where aquaculture is practiced. Aquaculture is predominantly present in tropical and sub-tropical climatic regions with Asia accounting for more than 80% of global aquaculture production, and some key aquatic diseases in Asia have been identified as potentially climate sensitive. Global warming, rise in sea level, changes in ocean productivity and circulation pattern, water stress, changes in monsoon patterns and occurrence of extreme weather events are all features of climate change that are likely to impact on aquaculture species. Any increase and/or decrease in temperature of their aquatic habitat will have a significant influence on their body metabolism and this could include influence susceptibility/resistance to disease. Depending on the climatic zone the impacts on aquaculture could be both positive and negative.

Development of Rapid Diagnostic Tests

There has been significant progress in the development of rapid pathogen detection methods for aquaculture over many years, and in the last 5 years the pace has increased even more, as methods developed for clinical and veterinary medicine are rapidly adapted and optimised. Pathogen detection methods for use in aquaculture need to be robust yet sensitive, as well as affordable and requirements will depend on whether methods are to be performed in the laboratory or in the field. This presentation will provide a review of recent advances made in pathogen detection technologies, including antibody-based, nucleic acid and nano-technologies, taking into consideration the limitations of both existing and novel methods, and how applicable some of the new methods are to aquaculture.

Fish Vaccine Development

The number of fish vaccines commercially available have grown in recent years but there are still numerous diseases where no vaccines are available, or cases where existing vaccines do not perform well. The most crucial step in developing an effective vaccine is identification of 'potentially' protective antigens and confirming their protective response in the host species by efficacy testing. The most effective approach taken depends on the type of pathogen and the final end use envisaged for the vaccine (e.g. cost, fish species, and immersion *versus* injection vaccination). Technologies such as recombinant and DNA vaccines are powerful tools for future vaccine development as these enable the separation of potential protective antigens from suppressive ones. These are being developed because the simpler approach of using inactivated whole cell vaccines did not succeed for many

important diseases, and attempts at attenuated vaccines in general have not been encouraged from a safety point of view. A number of case studies will be presented, such as identifying isolates from given serotypes to include in traditional whole cell vaccines and describing technologies for the identification of specific antigens for recombinant or peptide vaccines. The potential of developing DIVA vaccines for use in fish will also be discussed, where a vaccine is developed in tandem with a diagnostic test to differentiate vaccinated from infected animals.

Final Thoughts and Conclusions

Climate change will affect the movement and spread of diseases in the aquatic environment, thus having relevant rapid tests in place as well as appropriate vaccines to prevent the spread of disease is vital for the future sustainability of aquaculture. It will, however, not be possible to develop effective vaccines against all diseases, and in some cases vaccines may be considered too expensive to use. Thus alternatives to vaccines also need to be considered so that antibiotic and chemical usage does not increase. Continued education and training is also important in combating the future effects of climate change on aquaculture with regard to disease as some regions of the world do not currently have wide acceptance of the use of vaccines as a fish health control method.

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1.2.3 Biotechnologies for animal breeding and coping with climate change

Paul Boettcher and Grégoire Leroy, FAO

Climate has historically played an important role in the development of animal genetic diversity. The origins of most livestock species can be traced to a few domestication centres across the world. Over the recent millennia, as humans migrated away from these centres, they took their livestock with them and created new breeds, leading to a set of markedly diverse populations that now numbers more than 8000 breeds.

Each of these breeds has been adapted to the demands of its local conditions, whether those demands were environmental, markets-based or cultural. The individual animals best suited for a given situation were naturally or formally selected to have more offspring and the gene variants associated with survival became more common, providing the biological basis for different breeds. Where market forces allowed it, such as in Europe and North America, livestock keepers controlled the environment so that economic drivers and formal selection influenced survival more than climatic conditions. In most of the world, however, differences in temperature, rainfall, endemic diseases and feed resources have been the main factors determining the characteristics of specific breeds.

Over the decades, the forces guiding the formation of breeds have been pretty stable. The same collection of favourable gene variants has tended to be maintained across the years, meaning that most breeds have continued to be viable, particularly from the biological standpoint, without much outside intervention. Internal genetic adjustments to environmental changes could be made within the natural generation intervals of the species.

That situation seems bound to change, however. According to some forecasts, the future changes expected to the climate may occur too fast to allow livestock populations to keep up within their natural reproductive rhythm. In developing countries, the capital required to invest in housing and other infrastructure to control the environment may not be sufficient to allow this option, especially for smallholders. Moreover, for many breeds, especially traditional local breeds, increasing demands for livestock products and competition for resources predicate that traits associated with productivity will also merit stronger attention than in the past, putting increased pressure on breeds' capability to adapt. To account for all these forces, formal selection programmes will be desperately needed.

Biotechnologies, reproductive biotechnologies in particular, can play a key role in allowing animal genetic resources to meet the demands of the future, including climate change. Artificial insemination (AI) is an especially powerful tool for this objective. The genetic gains made through formal selection programmes are achieved by obtaining multiple offspring from the best males and obtaining few, if any, offspring from the inferior males. For most livestock species, males can naturally mate with 20 to 50 females per year. AI affords males the possibility to mate with hundreds and even thousands of females, greatly increasing the genetic progress if males can be selected accurately. When few can be chosen from among many, chances also increase that the males used for breeding can be genetically superior not only for traits favouring survival in continually more difficult climatic conditions, but also for increased output and production efficiency. AI is especially beneficial for smallholders, as truly superior males are statistically rare. The probability to produce such an outlier from a small group of breeding animals is extremely scant. For smallholders, AI also provides access to a wider gene pool and eliminates costs of raising male animals. AI also allows access by smallholders to the benefits of other technologies, such as genomics and sexed semen, although the potential benefits of these technologies depend on the situation. Embryo transfer is a biotechnology that allows females to have more offspring, but it is much less powerful and more costly than AI and practically out of reach for smallholders.

If climatic changes are too fast or breeds lack the genetic diversity to adapt through biotechnology-enhanced selection, new sources of variation, via crossbreeding or breed-replacement may be necessary. In general, climate change is not expected to render many environments inhospitable for livestock, but rather simply different and often harsher. The new climate in one location will often resemble the past climate in another. Thus, in theory,

genetic resources formerly adapted to one area can simply be moved to a new location that matches their potential. Moving of live animals is very costly, however, and may involve strict veterinary regulations, if national borders are crossed. AI can be also be a powerful tool in dealing with this situation. Semen can be moved long distances much more quickly and simply, less expensively and in much greater quantities than can live animals. Furthermore, unless animals are being imported to restock after a climate-related disaster, the genes of the incoming population are the primary resource of interest, not the animals themselves.

In general, climate change is not likely to be so fast that complete breed replacement is necessary. The original breed is also likely to have particular characteristics and provide locally-demanded services that are not available in alternative breeds. Therefore, a scenario more likely than breed replacement the use of crossbreeding to gradually introduce characteristics of the non-local breed through a process called “adaptive introgression”. In this process, AI would be used to introduce the adaptively favourable gene variants from the outside breed and several generations of selection would follow to increase the frequency of these favourable genes, while keeping the desired characteristics of the original breed. Used with AI, genomic biotechnologies also have the potential to enhance such a strategy, by increasing the efficiency of introduction of genes known to be associated with adaptation to a given environmental constraint or with increased productivity.

The methods proposed here will clearly alter the genetic constitution of the populations in question, risking or even promoting the loss of valuable genetic resources. Conservation should therefore be implemented in concert with any such actions. Reproductive biotechnologies would be a cornerstone of such activities, combined with cryogenic biotechnologies to preserve material in gene banks. Semen is the most common material stored in gene banks, but embryo-related technologies can be more economically justifiable in cryoconservation than in genetic improvement or selective adaptation programmes.

Unfortunately, major obstacles exist in the implementation of AI and other reproductive technologies for the adaptation to climate change, especially for smallholders and developing countries. These biotechnologies will only be effective when complemented with the application of other simpler technologies. Biotechnological interventions can only be successful if applied in the context of a formal breeding programme. FAO has recently released the Second Report on the State of the World’s Genetic Resources, which clearly indicates that many countries have a significant deficit in the capacity to apply such programmes. Although most countries indicate they have access to AI and related biotechnologies, few developing countries report having the basic elements of breeding programmes, such as animal identification, performance recording and genetic evaluation systems needed to identify the best animals. Without these basic tools, application of AI will not only be ineffective, it will needlessly and dangerously reduce the genetic diversity. Information is the basis for effective breeding programmes and tends to be severely lacking.

The utilization of reproductive biotechnologies for distribution of genetic material also requires substantial infrastructure. Information systems are needed to collect, collate and analyze data upon which to base selection. Storage and wide-scale distribution of semen requires a continuous and affordable source of liquid nitrogen, a resource that is exceedingly rare in many countries with large number of smallholder livestock keepers. Crossbreeding requires knowledge and the proper inputs to support husbandry of the new genotypes.

In conclusion, a changing climate is simply an additional obstacle confronting smallholders in breeding animals to support sustainable livestock production. Biotechnologies, particularly AI, have great potential for this challenge. However, the implementation of biotechnologies is input-intensive and their full power can only be harnessed when complemented with traditional technologies. Support for livestock development must approach livestock genetic improvement by considering adaptation as a single trait in a holistic objective that includes increased productivity, enhanced efficiency and maintenance of genetic diversity.

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1.2.4 Use of biotechnologies to improve feed quantity and quality: adaptation to the changing climate from the animal nutrition perspective

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Achieving food security is one of the most important challenges with a view to the future and taking into account the continued increase of the world's population. An additional major challenge for the food production is the threatening future or already existing impacts of climate change. Increased extreme weather events like hurricanes, heavy rainfall, flooding, heat waves and drought are likely to occur in different regions of the world and may affect both the growth conditions of cereal and forage crops and livestock production.

Plants can be regarded as the starting point for the whole human food chain. Therefore, to achieve food security plant breeding and crop production play an important role. High yields of highly digestible phytogetic biomass produced with low external inputs of non-renewable resources and low emissions of greenhouse gases during cultivation are required. In addition, the plants should show a low concentration of undesirable substances and a high resistance against biotic and abiotic stressors including the ability of adaptation to potential impacts of climate change.

Food of animal origin is characterized by a high bioavailability of most nutrients and is a source of some important trace elements and vitamins. The consumption of meat, fish, milk, eggs and other protein and energy sources may contribute substantially to cover the human requirements for amino acids and energy. A rapid increase in the demand for food of animal origin is expected in the foreseeable future. In this context it should be noted that the conversion of energy and protein from feed into food of animal origin is relatively low with about 3% for the conversion of energy into beef. It may vary, however, up to about 40% for the conversion of energy into milk and of protein into chicken meat. As a result, the production of livestock feed must grow disproportionately higher to meet the growing demand.

An increased production of feed with an improved quality may only to a small extent be based on the further expansion of agriculturally productive land. The major part of the necessary additional livestock feed should be the result of an increased productivity per unit of land and of reduced post-harvest losses. This approach appears applicable throughout the world and could be of particular relevance for smallholders in developing countries. A steady increase in productivity requires a specialized knowledge and depends on a variety of factors to improve the production systems. In this regard, agricultural biotechnologies play an important role.

Agricultural biotechnologies represent a number of technological applications used in food and agriculture. Some of these technologies are used by plant breeders for the genetic improvement of plant varieties. This includes amongst others the improvement of the nutrient content of edible plant parts, higher nitrogen and water efficiency and better pest resistance. In addition, the adaptation of plants to the expected adverse impacts of climate change represents a particular challenge.

Feeds usually are characterized according to their composition. The most important feed groups are roughages, concentrates and co-products from agriculture, food and biofuel industry. Feeds from these different groups contain various concentrations of crude nutrients, but also further desired and undesired substances. An additional objective of plant breeding which may be achieved by the use of agricultural biotechnologies is

providing feed plants with for example lower concentrations of anti-nutritive substances, low concentrations of substances that influence availability of nutrients such as lignin, phytate, enzyme inhibitors, tannins and plants with a higher concentration of nutritive value-determining components such as amino acids, minerals, vitamins and vitamin precursors.

Feed additives are used to supplement feed with essential or non-essential substances in order to increase the nutrient digestibility of the diets or to cover the demand of the animals. Therefore, the impact of biotechnologies to improve feed quality also includes the use of different feed additives like amino acids, enzymes and silage additives which are partly produced by fermentation technologies based on biotechnological applications.

In conclusion, it can be stated that the use of agricultural biotechnologies to improve feed quantity and quality may contribute to solving the important global challenge of food security in consideration of the sustainable use of limited natural resources, the avoidance of environmental pollution including the reduction of greenhouse gas emission and the adaption to climate change.

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1.2.5 Development of livestock vaccines and market access

Jean de Foucauld, Ceva Santé Animale, speaking on behalf of HealthforAnimals

Summary of presentation given on February 15, 2016, at the FAO symposium on *The Role of Agricultural Biotechnologies in Sustainable Food Systems and Nutrition* in the session:

To follow the development of the population in the world, healthy livestock breeding systems are needed, allowing sparing the resources needed to feed the animals, increasing the value they represent for many farmers and feeding more people. In this, vaccines have a critical role to play. The advantages and benefits of vaccination is more and more recognised and understood, especially when comparing them to their costs which are usually less than 1% of the production costs.

The purpose of this presentation is not to detail the mechanisms how new or existing diseases are linked to climate changes as this is already well documented. After mentioning a few examples on how innovation can fight these diseases, we would like to focus on the downstream processes that make this innovation a practical and available tool to the target customers. Looking at the global perspective on vaccine solutions is necessary, but even more so when countries and farmers have to keep adapting to the consequences of climate change. There are currently too many cases where the solutions exists in the laboratory but cannot be applied on time in the field. Hopefully highlighting the key success factors allowing the field application of these technology advances will help focusing the effort of all stakeholders towards success.

Vaccine innovation in the laboratory has been extremely rich since the 80's. This led to the arrival of vaccines using these new technologies since the years 2000 with a few notable pioneers already present in the 90's. Some of these vaccines aim at diseases impacted by climate change like West Nile virus infection, avian influenza... More are to come, based on innovative technology already known like vector platforms and sub-unit antigens, but also on newer ones like vaccines based on non-replicative, non-inactivated virus particle. The work for other diseases like Trypanosomosis and other parasitical diseases is still ongoing and prove to be quite difficult. Research effort should continuously be encouraged in these fields.

Thanks to all this high standard research work, proofs of concept for candidate vaccines are usually well established. But from successful research to the dose being injected to the livestock, there are many complex steps requiring highly experienced teams and companies. And this is the reason why it takes so long to see these solutions accessing their target markets. The first one is vaccine development. It consists of establishing the manufacturing process, validating it, and testing the vaccine for its shelf life, safety and efficacy. This step is followed by the registration process, industrialisation and finally marketing of the vaccine.

The design of the production process of the candidate vaccine should be so it can fulfil four main goals common to all veterinary vaccines: quality, reproducibility, stability and adequate cost. Quality has two aspects: producing according to acceptable standards (GMP, USDA); manufacturing according to a process allowing expressing the main safety, efficacy, stability features singled out during the feasibility phase. Once pilot batches have been produced satisfactorily, then they are tested according to a 'regulatory' analytical and clinical program covering all sorts of aspects: validation of the planned manufacturing process, shelf life study and clinical trials to confirm the safety and efficacy claims.

Marketing authorisation: a registration dossier is then prepared gathering the data from all this work, suitable for the target markets. It is sent to the target countries with additional documents proving that the applicant works according to acceptable standards; it is also very common that authorities from the target countries require a proof that the vaccine is registered in the country of origin. This is a cause for great concern when a company decides to develop a vaccine for which there is no market in the country/region where manufacturing takes place. Solutions are possible but this is not accepted everywhere. Moreover, when 'new technology' vaccines involves live genetically engineered product, specific procedures are needed.

Once the registration dossier has been assessed, questions have been answered and the marketing authorisation granted, we are far from the end. The company has then to complete the industrialisation process to ensure that what was planned in development happens in the industrial world, meeting quality and price targets.

Last but not least, market access: it is driven by different aspects, amongst them: capacity of vaccine production, vaccine supply chain, competition between 'easy and difficult' markets...

In many markets where these vaccines are needed and where customers are ready to pay to right price for it, there are great difficulties to establish the right supply chain for reaching the final customers. Some key points can be listed to solve these issues: more veterinary retailers, better cold chain, more trained veterinarians and vaccination technicians, better vaccination equipment, fighting counterfeit products...

A tight market supply situation will lead to an unfair competition between 'easier' access markets and the ones where it is difficult to reach the customers.

Looking at the extraordinary development of 'new technology' vaccines and the increasing needs for livestock vaccines everywhere in the world, it is a strategic goal for governments, global organisations, pharmaceutical companies and their associations like HealthforAnimals, to help increasing supply of vaccines and improving market access in regions where it is not satisfactory. Initiatives are taken in this direction with some successes, involving charitable organisations, companies and HealthforAnimals in Africa and on the Indian subcontinent. More ambitious projects are needed to find ways to expand manufacturing capacities, to harmonise regulatory barriers, to train more veterinarians and vaccination technicians, to work on supply chain issues...

In conclusions, the good news is that science already brought and will bring more solutions to expanding diseases, including the ones affected by climate changes. But very significant effort of all stakeholders should put on the complex industrial, regulatory and market access tasks.

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1.2.6 The potential of landscape genomics approaches in characterising genetic adaptation of indigenous goat genetic resources: A South African Perspective

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Summary

In most developing countries, goats play a significant contribution to poverty alleviation and improving household food security and livelihoods of many smallholder farmers in marginal areas. Several goat ecotypes have been historically described as adapted to the harsh environmental conditions and low input production systems. In South Africa, the ecotypes are the main genetic resource in the development of the current commercial meat-type Boer, Savanna, and Kalahari Red breeds. The genetic diversity and relations of the South African goat populations is however not fully understood. Communal and feral goats thrive under a host of harsh environmental, climatic and nutritional conditions, and numerous impediments to gene flow. They are characterized by non-descript and hyper-variable production systems as well as heterogeneity in phenotypic and genotypic landscape and are adapted to the agro-ecological zones in which they occur. Local adaptation is driven by natural selection that target specific genomic regions. The genetic mechanisms underlying local adaptation in these marginal populations is crucial for goat improvement strategies and conservation of adapted genetic resources. However, the exact genomic architecture of these goat populations remains unknown and the effect of natural and/or artificial selection on the diversity is not fully understood. Until recently, demographic, production and evolutionary events that impact on the local adaptation of indigenous goats have not been fully unraveled in South Africa and worldwide.

Landscape genomics combines the phenotypic and genotypic information as well as data on the local environment of spatially referenced individuals or populations across different landscapes to identify genomic regions that are involved in local adaptation. The hypothesis behind landscape genomics is that certain alleles and genotypes are adapted to a specific environment that is defined by climatic conditions, disease and disease pathogens, and feed availability profiles, which are referred to as the environmental/production landscape. Only markers that show higher genetic differentiation and subsequently skew allele frequencies related to environmental variation are targeted for genomic association analysis. Landscape genomics has found use in studying indigenous livestock populations that are raised in low input production systems where record keeping is limited and populations are highly fragmented thereby complicating use of conventional genome-wide association studies. The potential of landscape genomics in characterising genetic adaptation of South African indigenous goats has therefore been investigated.

South Africa has a highly heterogenous livestock production landscape that ranges from wet and highly fertile to dry and desert like agroecological zones. The first step of analysis surveyed the goat production systems in the different provinces and characterised the management systems and production challenges faced by farmers in raising their animals. Morphological traits linked to genetic differentiation of goat populations by farming communities where investigated. The goat production system is mainly scavenging with limited interventions provided by farmers. Goats were therefore exposed to the full variability of nutritional, climatic conditions and disease challenges that differed amongst agro-ecological zones. Qualitative traits such as characteristics of coat, horn, ears, and wattles were recorded for village goats. The analysis clustered populations into well-defined

groupings. Heartwater is endemic to most parts of South Africa, and livestock farmed in these regions are constantly under threat from this disease. Majority of the indigenous goat populations are raised for subsistence production in rural areas and tick control is less frequent and erratic unlike in the commercial sector. The study identified and quantified the effects of geographic regions, and animal- and production system- associated risk factors for *E. ruminantium*. It also explored the relationship between these risk factors and prevalence of heartwater in South African goats. Highest seroprevalence for antibodies to *E. ruminantium* was observed in goats from endemic regions (76.09%), and from smallholder production systems (89.54%). High seroprevalence was also observed in non-descript indigenous goats (85.04%), adult goat (69.62%), in does (67.46%) and goats infested with ticks (85.79%). A logistic model showed a gradient of increasing risk for commercial meat type Savanna (OR= 3.681; CI= 1.335-10.149) and indigenous (OR= 3.466; CI= 1.57-7.645) compared to Boer goats and for goats from the smallholder production system (OR=2.582; CI=1.182-5.639) and those with ticks (OR=3.587; CI=2.105-6.112). Results from this study showed that *E. ruminantium* infections were prevalent but were widely and unevenly distributed throughout South Africa.

An investigation into the genetic diversity, population structure and breed relations of the goat populations was undertaken. The three locally developed meat type breeds of the Boer (n= 33), Savanna (n = 31), and Kalahari Red (n =40), a feral breed of Tankwa (n =25), and unimproved non-descript village ecotypes (n =110) from four goat-producing provinces of the Eastern Cape, Kwazulu-Natal, Limpopo, and North West were genotyped using the Illumina Goat 50K SNP Bead Chip assay. Within individual variation accounted for approximately 91.69% of the total genetic variation. Average linkage disequilibrium (r^2) was highest in the Tankwa (0.25 ± 0.26), followed by commercial breeds (0.25 ± 0.26), and lowest in the village ecotypes where it ranged from 0.09 ± 0.12 and 0.11 ± 0.14 . Pairwise F_{ST} , Principle Component Analysis and ADMIXTURE identified Tankwa as a genetically distinct population and supported clustering of the populations according to breed affiliation and production system. Genome-wide F_{ST} identified 101 SNPs potentially under positive selection in the Tankwa compared to the farmed goat populations. This study highlighted the high level of genetic diversity in the South African indigenous goats as well as the utility of the genome-wide SNP marker panels in genetic studies of these populations with potential use in identification of gene loci under selection that could be used in genetic improvement programs.

Key words: Goat genetic resources; genomic tools; genetic adaptation; smallholder farming

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Tuesday 16 February
09.30-12.30 Parallel Sessions

Session 2.2 Post production value addition and food safety (2 sub-sessions)

2.2a: Enhancing value in the post-production phase

2.2a.1 Use of feed additives generated through fermentation technologies for livestock feed

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The primary aim of the livestock industry is to produce safe and quality animal products after due contemplation of consumer awareness, public health, ethical issues and the environment. Feed additives occupy a significant niche amongst the list of scientific interventions that guided the enhancement of livestock production for meeting the growing demands for animal products by the global population. However application of some of those feed additives such as antibiotics raised grave concerns to both animal industry as well as public health. As a result, several countries have already imposed ban on addition of antibiotics in feed. This emphasizes the need to develop an alternate strategy to enhance the nutrient mobilization towards achieving higher productivity and/or quality. Evidently, feed additives sourced through fermentation technologies seem to be the front runner to cater to the new and emerging challenges of the livestock sector.

In simplified terms “feed additives” are defined as non-nutritive ingredients that selectively stimulate the growth or enhance the performances (quality/ quantity) of animals through improvement of nutrient utilization and its uptake. Presently, feed additives are also advocated for maintenance of the health of animals. The use of feed additives is much greater in poultry and pig production than in ruminants. One of the simpler ways of producing feed additives is through microbial fermentation. The feed additives generated through microbial fermentation technologies could be broadly classified into prebiotic, probiotic, enzymes, yeast embedded minerals and amino acids.

Prebiotic

Prebiotic is a non-digestible bioactive molecule that beneficially affects the host by selectively stimulating the growth and or activity of one or a limited number of bacteria in the gastrointestinal tract of an animal. Although most feed additives target only one or a limited number of functions, the prebiotic targets a range of different physiological functions such as increase in gut health, mineral absorption, immune stimulation and pathogen exclusion, and decrease in cholesterol.

Commercially available prebiotics are inulin, fructooligosaccharides, galactooligosaccharides, mannanoligosaccharides, xylooligosaccharides, etc. Supplementation of prebiotics in the diet of poultry and swine enhanced the population of beneficial gut microflora followed by decreased pathogenic microflora in addition to improved mineral absorption, immunity and growth performance. As the demand of prebiotics is increasing, researchers around the world are enriching the ‘Nutraceutical Basket’ with newer ones and attempts to use agricultural residues like straws, coconut husk and grasses for production of prebiotics is gaining importance.

Probiotic

A probiotic is defined as a “live microorganism which, when administered in adequate amounts, confers a health benefit on the host”. The beneficial effects of probiotics are manifested by regulation of intestinal microbial homeostasis, stabilization of the gastrointestinal barrier function, secretion of bacteriocin and immunomodulatory effect. The probiotic organism may originate either from a prokaryote (bacteria) or eukaryote (yeasts) cell. The bacterial probiotic are Lactobacillus, Enterococcus, Bacillus, Streptococcus spp. among others. In the eukaryotic class of probiotic, the important genera are Saccharomyces, Kluyveromyces and Aspergillus. Among the several species of yeasts, *Saccharomyces boulardi* is a commonly used probiotic in both ruminant and non-ruminant species. Administration of Lactobacillus based probiotic reduced the population of *Salmonella enteridis* in challenged broiler chicks. Daily dosing of piglets with *Enterococcus faecium* as a probiotic supplement reduced the incidence of diarrhea and improved daily weight gains.

Enzymes

The rearing of animals and the use of enzymes have been a distinct part of human life for many thousands of years but it is only recently that their use is increasing due to drastic reduction in the cost of enzyme production. The major enzymes that are being commonly used in animal feeds are broadly classified into four categories namely (i) fiber degrading enzymes, (ii) protein degrading enzymes, (iii) starch degrading enzymes and (iv) phytic acid degrading enzymes. As the name implies, each enzyme can specifically act on a particular substrate and ensure benefits to the animals either by unlocking the energy, by releasing amino acids, by complementing an animal's own enzyme activities or by releasing nutrients from unbreakable linkages such as phosphorus from phytate using phytase. Phytate removal by phytase also enhances the availability of minerals to animals.

Yeast embedded micronutrients

Chromium (Cr) and Selenium (Se) have been found to be essential for ruminants as well as monogastrics due to their anti-oxidation properties. They also improve immunity and reduce thermal stress. However the inorganic form of these minerals is less bioavailable and use of organic chromium and selenium in the form of Cr-yeast and Se-yeast is being extensively studied due to their enhanced bioavailability. Cr-Yeast has been found to not only improve immunity but also reduce cholesterol content in eggs. Se-yeast supplementation in poultry during peak summer reduced the ill effects of thermal stress and improved the anti-oxidant status.

Amino acid production through fermentation

Inefficient utilization of absorbed protein in ruminants and monogastrics can lead to high nitrogen (N) losses. Matching the animal's dietary amino acid with their biological needs minimizes N excretion to the environment. Providing the essential amino acids (lysine, methionine, threonine, and glutamic acid) would help in reducing the protein content in the feed leading to better utilization of nutrients, less wastage of nitrogen and reduced diet cost.

Use of feed additives is limited in the smallholder ruminant production systems because their effects are not consistent. Also high cost prohibits their use. However their use in smallholder poultry and pig production system is higher. Future research to better understand the conditions under which they produce consistent, long-term and higher effects would enhance their use in animal diets.

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2.2a.2 Use of biotechnologies to increase the storability and shelf life of fruit.

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Storability and shelf life are major determinants for the economic value of fruit and determine the risk for loss of produce due to decay. Extended storability and shelf life supports the delivery and consumption of high quality fruit during a longer time period, thus improving market prices (avoiding dumping prices due to over-supply), food availability, income, job opportunities and economic sustainability of especially small producers.

Improved storability and shelf life have been successfully addressed through the breeding of new, well adapted cultivars in a series of crops following classical breeding approaches. New biotechnology techniques that recently became available may further accelerate the coming available of new cultivars, especially for tropical crops for which little breeding activity is currently going on.

For the application of biotechnology in breeding, climacteric fruit especially may have potential. In climacteric fruit, ripening is accompanied by a burst of ethylene production and respiration. The produced ethylene stimulates the ripening. Being a gas, ethylene from a ripe fruit can also stimulate the ripening of other (unripe) fruit (e.g. at the household level, a ripe banana may be wrapped together with unripe mangoes). Tomatoes, apples, bananas, mango, peach, and avocado and melon, among others, are climacteric. Non-climacteric fruit like citrus, grape, watermelon and strawberries do not show ethylene and respiration bursts and do not need ethylene for ripening.

In view of storability, shelf life, and transport over long distances to e.g. export markets, climacteric fruit is harvested unripe: the earlier harvested, the better the storability. Later, close to point of sale ripening is forced by the external application of ethylene. This is common practice for crops like banana, mango and avocado. However, the early harvesting of unripe fruit has negative drawbacks on flavor attributes including texture, juiciness, sweetness and aroma. When harvested too unripe, the fruit will never become as tasty as a tree-ripened fruit.

Thanks to breeding and biotechnology, the shelf life of tomatoes has been extended from 7 days to more than a month. Freshly picked apples have a shelf life of two to four weeks, depending on the cultivar. Apples can be stored for another 2 weeks up to four months under temperature controlled conditions, and even up to 13 months when also the atmosphere in the cold room is controlled (Low oxygen, high CO₂). This variation in storability results from variation in the genetic composition of cultivars. More precisely, it is based on natural variants of a very limited number of genes that are involved in the ethylene production or ethylene perception pathway, or in the production of specific cell-wall degrading enzymes. In tomato, natural variants of 3 specific genes are involved. Taste of tomato is 'repaired' by enhancing other taste related pathways. In apple, seven of such genes are involved which slow down ripening without giving in on taste.

Classical breeding approaches include the search for the desired trait in wild germplasm or the raise of the desired trait through the creation of gene variations through, for instance, radiation. Next, these new sources are used in crosses to raise new progenies, the best of which are selected and released as cultivar. Through time, diagnostic molecular markers have been developed that supported the breeding: they allowed to more efficiently trace the progenies with the desired trait.

Classical GM approaches have led to the approval of a limited number of GM-cultivars in melon and tomato which targeted storability and shelf life. They were introduced between 1992 and 1999 and none of them are on the market anymore. Besides lack of public acceptance, the techniques of that time were still that crude that too many

other traits may have been affected negatively. Other fruit crops for which GM-cultivars have been approved are apple (2015), eggplant (2013), plum (2007) and papaya (1998), all of which except plum are in commercial production. That of plum is deliberately held in stock till an outbreak of Plum Pox Virus would show up in the USA.

Recently, new biotechnologies came up that are now turning out to be true game changers. They allow one to remove or change just a few nucleotides of a gene in a very precise way. Such minor changes in e.g. an ethylene gene, may have major effects on ethylene production and hence on storability and transportability, especially when applied on the promoter region of such a gene. This is because each promoter region has several on/off switches that determine the activity of the gene in a tissue and a time-specific manner. In principle, this would allow to hamper or delay the production of ethylene of just that fruit that is close to maturation. At that time, the fruit is not only sensitive to external ethylene applications, but is also ready to produce all the specific components that give it its delicious taste. Moreover, in the near future modifications brought about through this new procedure may not fall under GM regulation.

These technologies may offer great opportunities for crops like mango and banana, which are not easy to improve through classical breeding approaches. Small growers may be the first to benefit, through immediate extended periods of sale, whereas large scale export production will follow once production volume allows. Still it may take 15-20 years from application to marketable fruit because of the various successive stages in production that have to be passed, from the actual application of this technology (y1-3), to the cultivation of small in-vitro plantlets to fruit producing trees (y3-6), selection of the best performing new plants (y6-8), multiplication of the few initial copies of these best plants to ten-thousands of trees, completion of the IP and admission procedures (y9-12), plantation of orchards (y13), and first production of fruit (y15).

An excellent overview on new biotechnology and breeding techniques can be found in the brochure “Opportunities of New Breeding Techniques”, which is available for free at <http://edepot.wur.nl/357723>

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2.2b: Using biotechnologies to ensure the safety of food

2.2b.1 Traditional milk fermentation as a potential tool for sustainable improvement of food safety

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Abstract

Every year, 1.5 million people die due to diarrhea, and animal source foods are important source of food borne diseases (FBDs). FBDs include non-diarrheal serious zoonoses such as brucellosis and tuberculosis. Large proportion of FBDs occurs in developing countries where informal markets dominate in food supply, and improvement of food safety through implementation of public services is challenge in the settings. The authors of this abstract conducted a study on this subject. The objectives of the study were twofold: to prove that participatory risk assessment can be applied to informally-marketed foods, and to assess the risk of staphylococcal poisoning through consumption of raw milk and home-made yoghurt in Debre Zeit, Ethiopia. Staphylococcal food poisoning is one of the most common FBD in the world, and is caused by ingestion of staphylococcal enterotoxin (SE) produced in food by certain strains of *Staphylococcus aureus*. *S. aureus* starts producing enterotoxin in milk when the population density reaches about $10^{6.5}$ cfu/ml and thereafter the amount of SE increase linearly with time. A small amount of SE; 100-200ng, can cause illness. The intoxication is characterized by the sudden onset of nausea, vomiting, abdominal cramps, and diarrhea. The optimum pH for *S. aureus* growth is 7 and the minimum pH is reported to be 4.9. In the paper based on this study, contribution of traditional milk fermentation to food safety found by the risk assessment is described.

The study sites were urban and peri-urban areas of Debre Zeit, Ethiopia. Rapid urban appraisals were combined with conventional interviews to identify and quantify formal and informal milk value chains and to collect information on consumers' food preparation and consumption behavior. Milk was sampled in 170 dairy farms and five milk collection centers and microbiological tests were conducted. Published data on milk fermentation in Ethiopia was used to estimate the time when pH becomes lower than 4.9 after milking, to model the stop of growth of *S. aureus*. A published mathematical growth model of *S. aureus* was used to model the competition between SE production by *S. aureus* reaching $10^{6.5}$ cfu/ml, and stop of bacterial growth due to traditional milk fermentation reaching low pH. The growth of *S. aureus* was dependent on initial bacterial population in milk, temperature (storage of milk in room or refrigerator), and length of storage time for milk consumption. A system from production to consumption was stochastically modelled in @Risk, and Monte Carlo simulation was run for 10,000 iterations. Sensitivity analysis for all the uncertainty parameters was run for 1,000 iterations.

Prevalence of *S. aureus* in five milk collection centers (72%, 18/25) was significantly higher than in bulk milk samples at dairy farms (43.5%, 74/170, $\chi^2 = 5.99$, $df = 1$, $p = 0.014$). No dairy farmers boiled milk for sale. Consumption of raw or fermented milk was common, and there was no significant difference in the probability of boiling between farmers (68.2%, 116/170) and consumers (64.0%, 16/25, $\chi^2 = 0.038$, $df = 1$, $p = 0.85$). The annual incidence rate of staphylococcal poisoning was estimated to be 20.0 (90% CI: 13.9-26.9) per 1,000 people. When the effect of fermentation was removed from the model, the annual incidence rate increased to 315.8 (90% CI: 224.3-422.9) per 1,000 people, showing the importance of traditional food preparation methods in risk mitigation;

traditional milk fermentation reduced the risk by 93.7%. Sensitivity analysis found two very sensitive factors: initial population of *S. aureus* and storage temperature of milk.

Improving the safety of milk and dairy products could be achieved through supporting appropriate traditional food preparation and consumption where an industrial risk mitigation system is not feasible. For example, provision of good strains of fermentation bacteria to farmers and consumers can be highly effective and sustainable intervention for food safety. In the industrialized settings, communication to avoid mixed use of refrigerator and natural fermentation of raw milk may be necessary. Improvement of milk hygiene was another important factor to reduce the illness.

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2.2b.2 Aflasafe: a case study for aflatoxin reduction in crops

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Food quality and safety issues resulting from aflatoxin contamination are significant obstacles for improving nutrition and agricultural production while linking smallholder farmers to markets. Aflatoxin exposure is frequent and widespread in most African countries where the key staples maize and groundnuts are particularly vulnerable to aflatoxin contamination. Aflatoxin poses a significant public health risk in many tropical developing countries and is also a barrier to the growth of domestic, regional and international markets for food and feed. The most documented health impact of chronic exposure to aflatoxins is liver cancer. Broader health effects such as child stunting and immune suppression with higher rates of illness have also been associated with aflatoxin exposure. Aflatoxin contaminated feed decreases livestock productivity. Aflatoxin contamination has also led to the destruction of hundreds of thousands of tons of grains, contributing to huge losses of much-needed income, food, and trade with health and food security consequences.

An innovative scientific solution in the form of a natural biocontrol has been developed by USDA-ARS. This breakthrough technology, already in wide use in the United States, reduces aflatoxins during both crop development and post-harvest storage, and throughout the value chain. Atoxigenic-strain-based biological control is a natural, non-toxic technology that utilizes the ability of native atoxigenic (incapable of producing aflatoxins) *Aspergillus flavus* to naturally out-compete their aflatoxin-producing cousins. IITA and partners have successfully adapted this competitive displacement technology for use on maize and groundnut in various African countries using native micro-flora, developing biocontrol products called Aflasafe. We describe progress made with development of biocontrol of aflatoxins in Africa, the current status, and prospects for further scaling-up in maize and groundnut value chains.

Field testing of country-specific Aflasafe products in Burkina Faso, Kenya, Nigeria, Senegal, The Gambia and Zambia for several years has produced extremely positive results in reducing aflatoxin contamination of maize and groundnut consistently by 80% to 90%, and even as high as 99%. The biocontrol strains carry over through the value chain, discouraging contamination in storage and transport even when conditions favor fungal growth. Positive influences of atoxigenic strain applications carry over between crops and provide multi-year benefits. A single application of atoxigenic strains may benefit not only the treated crop but also rotation crops and second season crops that miss a treatment. Additionally, because fungi can spread, as the safety of fungal communities within treated fields improves, so does the safety of fungal communities in areas neighboring treated fields. The excellent efficacy of biocontrol in reducing aflatoxin in these countries has led to the expansion of the program to other countries in the East (Burundi, Rwanda, Tanzania and Uganda), West (Ghana) and Southern (Malawi, Mozambique and Zambia) Africa.

To make the biocontrol product available to farmers and other end-users, a manufacturing plant (capacity 5 tons/hour) has begun to produce Aflasafe in Nigeria. A small-scale modular manufacturing plant is under construction in Kenya. A model for creating sustainable market demand for Aflasafe in maize value chain is being piloted under the AgResults Aflasafe Initiative in Nigeria where farmers have purchased Aflasafe to treat about 30,000 ha of maize crop (application time: 2-3 weeks before crop flowering; application rate: 10 kg/ha; cost of product: \$12 to \$18.75/ha). Farmer groups that treated maize crop with Aflasafe sold grains at 13-15% premium to food and feed processing industries. These farmers also retained a portion of the treated crop for home consumption thereby improving safety of food for their families. The Kenyan government is providing a Kenyan Aflasafe product to smallholder farmers to treat almost 23,000 ha in aflatoxin-prone areas as a public good in the interest of public health and to improve marketability of maize grains. Initial results are very encouraging—all the maize harvested from several hundred hectares of treated maize crops in the Government's food security initiative in Hola/Bura/Galana irrigation scheme met the stringent European Union standard (4 parts per billion). A Senegalese agribusiness firm provided 20 tons of Aflasafe to its contract growers in 2014 and 2015 to improve the safety and marketability of groundnuts procured from the farmers.

Smallholder farmers harvest, store and consume home-grown crops. The deployment of Aflasafe can profoundly improve safety of food of smallholder farm families and reduce postharvest losses since the technology dramatically reduces the source of contamination in the field before harvest, during storage and until maize/groundnut is consumed. Reduced crop contamination could translate into improved food security and better access to domestic, regional and international markets that pay premium for aflatoxin standard abiding maize and groundnuts. Scaling-up of biocontrol has also the potential to revitalize exports and to increase smallholder farmers' opportunities to access premium export markets where aflatoxin-safe grain is a prerequisite for trade. For realizing health and income improvements, the biocontrol technology must be scaled up to reach the various players in the maize and groundnut value chains by developing sustainable product manufacturing and delivery mechanisms. Several challenges remain for scaling up. To address these challenges, the next phase of Aflasafe development is geared towards technology transfer to the private or public sector (as per situational analysis) and commercialization of the product in 11 countries.



Figure: The manufacturing plant of Aflasafe, a biocontrol product for aflatoxin mitigation, located at the IITA campus in Ibadan, Nigeria.

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2.2b.3 Diagnostic tools to detect pathogens causing tuberculosis in cattle and prevent their transmission through dairy products to humans

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Mycobacterial species that cause tuberculosis in humans and animals belong to the *Mycobacterium tuberculosis* complex (MTBC), including: *M. tuberculosis*, *M. africanum* and *M. canettii*, which are mainly human pathogens; *M. bovis* and *M. caprae*, which are mainly ruminant pathogens; *M. microti*, a pathogen of small rodents; *M. pinnipedii*, from marine mammals; *M. mungi*, from mongooses; and *M. orygis*, from oryx.

Members of the MTBC have been associated to foodborne transmission to man. The consumption of contaminated raw dairy products has been recognized as a major cause of transmission of *M. bovis* to humans, generally associated with the development of extra pulmonary TB. Another MTBC species that infects man is *M. caprae*. Although the transmission to man by raw dairy products has not been proven formally for *M. caprae*, the relatedness of the pathogens and the epidemiological settings suggest that this is probably the case.

Current bovine tuberculosis (bTB) eradication programs are based on a screening and slaughter policy, using mainly the intradermal tuberculin test, which detects the cell-mediated immunity (CMI) to the injection of purified protein derivative (PPD), a mixture of proteins prepared after a heat-treatment and lysis of *M. bovis* AN5 (bovine PPD) and *M. avium* D4ER or TB56. Single Intradermal Tuberculin Test (SITT) and Caudal Fold Tuberculin Test (CFTT) both use bovine tuberculin, while the Comparative Intradermal Tuberculin Test (CITT) uses both bovine and avian PPD. The CITT is used to differentiate between animals infected with *M. bovis* and those responding to bovine tuberculin as a result of exposure to other mycobacteria.

Advantages of the intradermal tuberculin tests and reasons for its wide use are low cost, low logistical demands, and a well-documented use. Limitations include difficulties in administration and interpretation of results, need for a second-step visit, low degree of standardization and imperfect test accuracy. False-negative reactions are also a concern, since infected cattle may remain on herds. In Brazil, there is strong evidence of resurgence of bTB in accredited-free herds due to infected cattle not responsive on CITT. Also, when results of intradermal tests are inconclusive, it is necessary to wait at least 60 days before repeating the SITT or applying a CITT. This mandatory interval requires cattle to be kept in quarantine, and it increases the risk of spreading the disease to herd mates and potentially to humans.

The Interferon-gamma (IFN- γ) assay also detects the CMI on TB-infected cattle. In this test, sensitized lymphocytes from infected cattle are incubated *in vitro* for 16-24 hour with PPD and the release IFN- γ is detected with a sandwich ELISA that uses two monoclonal antibodies to bovine gamma-interferon. In animals that are difficult or dangerous to handle, the advantage of the IFN- γ test over the skin test is that the animals need be captured only once. Another advantage is that there there is since lymphocyte stimulation is done *in vitro*, it is not necessary to wait 60-90 days to repeat the test when the initial test is inconclusive.

Bovine tuberculosis is an infection that triggers predominantly CMI during early and intermediate phases of the infection. Therefore, main diagnostic techniques used worldwide in eradication programs are based on the detection of the CMI: intradermal tests and interferon-gamma (IFN- γ) assay. As the disease progresses, there is a

decrease of CMI and the development of serological responses. The importance of antibodies for the diagnosis of bovine tuberculosis has been debated because of the variable sensitivity (18-73%) reached with serological assays in preliminary studies, although high specificity has been observed (88-96%).

Recent studies have re-established the interest in serological assays as diagnostic tests to detect false-negative animals in the intradermal tests and the IFN- γ assay. In animals with experimental infection, serological response has been shown to increase after performing intradermal tests (anamnestic effect), leading to an improvement of the sensitivity of these techniques. The serological response varies depending on the different antigens. Embrapa has developed an ELISA for detection of *M. bovis* antibodies based on a fusion recombinant antigen with the hydrophilic domains of ESAT-6, MPB70 and MPB83 proteins. This ELISA has been used to detect infected animals, missed by the CITT.

In Brazil, the control of bTB is regulated by the Brazilian National Program for the Control and Eradication of Animal Brucellosis and Tuberculosis (PNCEBT). These regulations involve the slaughter of cattle with positive reactions to the intradermal tuberculin test (ante-mortem diagnosis) and the inspection of carcasses for gross lesions in abattoirs (post-mortem diagnosis). However, there is an increasing pressure from beef markets for a definitive diagnosis of tuberculosis in cattle exhibiting lesions compatible with tuberculosis (LCT). Since 2012, the Brazilian Ministry of Agriculture, Livestock and Food Supply (MAPA) determined that farms with cases of bovine/bubaline tuberculosis cannot export beef to the Customs Union of Belarus, Kazakhstan, and Russia. All lots of animals from a farm with suspicious animals are sequestered and the LCT are submitted to an official laboratory for etiological diagnosis.

The culture is considered to be the “gold standard” and definitive test for the confirmation of bovine tuberculosis. However, the microbiological diagnosis of *M. bovis* is an extremely slow procedure which may take as long as 2 to 3 months. Additional 2 to 3 weeks are required for the biochemical identification of isolates. Therefore, the need for more rapid diagnostic systems is evident. Molecular diagnostic systems, particularly those based on real-time PCR technology, are faster.

A nested-PCR technique was developed by our research group, that showed a clinical sensitivity value of 76.0% with tissue samples from animals that exhibited positive results in the CITT, as well as from those with lesions compatible with tuberculosis that rendered positive cultures. A clinical specificity value of 100% was detected with tissue samples from animals with CITT negative results, with no visible lesions and negative cultures. Nested-PCR allowed the identification of *M. bovis* in tissues with a performance that was similar or superior to the culture. Individual results from the nested-PCR were obtained in a short period of time (2 days), in contrast with the culture, which took up to 90 days.

It is a priority to improve and simplify diagnosis of bTB. The excretion of mycobacteria in milk is intermittent, and up to 30% of infected cows uses to eliminate it by milk. Because milk samples are very easy to collect, a new strategy based on PCR in bulk tank has been developed in INTA, in order to detect herds infected with *M. bovis*. The Touch Down (TD) modification program of PCR was used to amplify IS6110, since sensitivity increases significantly when compared to conventional PCR. In individual milk samples, 55% of PPD positive cows shown to be positive and 95% of PPD negative cows were negative to TD-IS6110, respectively. Besides, in infected herds, 47% of samples were positive, whereas in herds with official free of tuberculosis certification (TFC) 62% were negative and 38% were positive by TD-IS6110 PCR, respectively. TD-IS6110 PCR in bulk tank could be used as a vigilance strategy for negative skin test in herds with official TFC, since the negative predictive value was 95%. This method has been incorporated since 2012 in the Plan of Control and Eradication of Tuberculosis of Santa Fe province, Argentina, which produces 41% of the total milk production of the country.

To the extent that programs for the eradication of bTB advance, more effective genotyping techniques are required, in order to trace back the remaining outbreaks. A research group, which involves Embrapa Gad de Corte, INTA, Universidade Federal de Mato Grosso do Sul, LANAGRO-MG, Instituto Biológico and Universidade de São Paulo, has been working on the sequencing of genomes of South American strains of *M. bovis*, and comparing with genomes from US, in a conjunction with the ARS/USDA. These studies will give us a better understanding of bTB and the relationship to specific phenotypes of all strains investigated, and also will generate important data for local epidemiological studies.

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Tuesday 16 February
09.30-12.30 Parallel Sessions

Session 3.2 Public policies, strategies and regulations on agricultural biotechnologies

3.2.1 The role of IP rights in enabling or impeding the application of agricultural biotechnologies in a developing country context

Rodrigo Sara

International legal framework for IPRs

Intellectual property rights (IPRs) bestow on the owner the right to control commercial exploitation of the projected subject matter for a specified period of time. Different forms of IPRs exist such as copyright, patents, trademarks and plant variety protection (PVPs), with each having different requirements. The exclusionary rights conferred by IPRs are typically justified in economic and policy terms as being essential to reward innovation which would otherwise not occur in the absence of such rights.

The WTO Agreement on Trade Related Aspect of Intellectual Property Rights (TRIPS) sets down minimum standards for protecting of IPRs which signatory countries are required to implement through national legislation. With 162 signatories TRIPS-driven harmonization facilitates global trade across industries in which IPRs operate as the common bedrock across industries driving innovation and diffusion of technologies in the developed and developing countries alike. Patents and PVPs in particular are considered to be key drivers of innovations in agricultural biotechnology as they allow recoupment of the substantial investment in research required to develop a novel inventions and plant varieties.

IPRs impeding the diffusion of agricultural biotechnologies

The use of IPRs in an agricultural biotechnology context are not without controversy, particularly in a developing country context. Critics claim that far from facilitating access and diffusion, the increasing fragmentation of IP ownership from upstream agricultural research inputs and production technologies to downstream improved plant varieties and agricultural inputs for use in cropping systems collectively raise barriers to access and impede dissemination. This proliferation of IPRs also increases the threat of infringement such that in a developing country context IPRs are often accused of favoring the market expansion interests of corporations at the expense of farmers and consumers. Criticisms concerning IPR-related issues are also broad and include, for example, conflicts with farmers' traditional practices of reusing seed, excessively broad patent claims, patentability of genetic materials and plant varieties, uncertainty regarding the scope of research use, high transaction costs, pricing of improved varieties as a result of licensing of IPRs, and appropriation of traditional knowledge and sovereign genetic resources. IPRs in agricultural biotechnology create a complex landscape to navigate and while there is certainly substance in many of the critiques raised, in many instances it is not IPRs per se that impede diffusion of agricultural biotechnologies in developing countries. Often confounding issues are involved such as institutional familiarity with IPRs, increased transactions costs, and regulatory/stewardship challenges.

The presentation will draw examples from CGIAR to contrast the role of IPRs with these confounding factors as an impediment to diffusion.

IPRs enabling the diffusion of agricultural biotechnologies

Global harmonization and strengthening of IP protection in recent decades has been credited with attracting an increase in private sector investment in agriculture-related research and development, and a surge in innovation leading to improved plant varieties, agricultural chemicals and production technologies. Agricultural biotechnologies have transformative potential in a developing country context and an effective IPR framework not only encourages home grown innovation, it also provides a framework for catalyzing technology transfer. Permissive licensing of IPRs play an important role in the local adaptation and diffusion of agricultural biotechnologies and the presentation will draw examples from CGIAR to highlight IPRs as an enabler for diffusion.

Developments concerning IPR related issues and diffusion of agricultural biotechnologies

Future developments concerning a number of IPR-related issues and trends have the potential to effect the diffusion of agricultural biotechnologies. These include the following and will be covered in the presentation if time permits:

- humanitarian licensing and the rise of “open access” frameworks;
- increased patent activity and the potential for patent thickets/pools;
- the expiration of patents for GM traits and the potential for a generics market;
- Prior Informed Consent and Mutually Agreed Terms associated with access and use of genetic resources under the Nagoya Protocol (potential for reach through for commercialization);
- differentiated regulatory approach for transgenic and cis-genic technologies;
- increasing concentration of the agricultural biotechnology market

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3.2.2 Biotech Policy: The Need for Historical Perspective and Context

Adrienne Massey

Presentation Summary

The issues most people consider to be problems of “ag biotech” are not unique to ag biotech but, instead, are inseparable from all forms of agricultural production. Whether the issues are socio-economic, legal or biological, if modern biotechnology and “GMOs” disappeared from the agricultural landscape today, the issues and problems would remain with us. This presentation will focus on one of those issues: intellectual property protection for plants.

One unique issue associated with ag biotech, however, is the pre-market regulatory approval of genetically engineered crops. In the U.S. this form of regulation is added to the post-market regulatory oversight that covers all new plant varieties. A pre-market regulatory approval process has significant impacts on the types of crops that are developed, and it also limits the entities developing crops to those with sufficient resources. The opportunity costs associated with NOT developing certain crops will vary from one country to the next.

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3.23 FAO must support peasants' selection and condemn the seizure of cropped biodiversity by patented genes

Guy Kastler, La Via Campesina

To deal with biotechnologies, it is legitimate for FAO to call upon those using them in research and industry. It is however not legitimate at all that FAO almost exclusively relies on those protagonists when it comes to discussions on public policies and food policies, considering that a great number of farmers and civil society organisations opposed to the uncontrolled use of those technologies are not invited to make presentations, or marginally through the invitation I received. I suggest you do take into consideration the public position those organisations have released.

Transgenic plants have not met expectations. Most of them have been modified to tolerate herbicides. It has led to resistant weeds emerging, an exponential use of herbicides being more and more toxic with sanitary and environmental impacts of which farmers, their families and rural people are the first victims. Other transgenic plants produce insecticide molecules which also lead to resistant insects emerging and an already known agronomic failure. First victims are once again farmers having lost their harvests, often despite an additional use of chemical toxic insecticides. Genetic technologies used to produce those plants have generated many unintentional and unintended effects the industry is desperately trying to hide. The most obvious ones have been loss of crops or of products quality. The cotton sector in Burkina Faso have lost its rank on the market after having conquered it so hardly thanks to the quality of its fibre, a quality which has suddenly disappeared after genetically modified organism (GMO) adoption: what's the point to increase yields if harvests can't be sold? Once again, small farmers are the first victims when the industries, even though they are accountable for such disasters, simply claim they cannot explain what occurred.

Transgenic seeds will keep on being of no interest for food security. Their cost, as one of the required inputs, make them suitable for the sole market of industrial crops for rich countries' need of feed and fuel, and for the emerging economy of biomass which confiscates agricultural lands for non-food use. Industry show no interest in subsistence crops which provide three-quarters of food available on earth. Small farmers producing this food do not have the funds to buy GMOs and the required inputs for cropping them. GMOs only aim at taking over their lands to replace them by industrial monocultures for export.

Every time they are authorised, transgenic plants replace the huge cropped biodiversity coming from centuries of farmer's selection by a few patented varieties. Patented genes are moving from one field to another because of the wind, insects, agricultural tools... which carry pollen and grains. They contaminate peasants' seeds which then become counterfeit of industries' patents. In less than 20 years, 89% of maize and 94% of soybeans in the USA have become patented GMOs. This violation of farmer's rights forbidding them to use seeds coming from their harvests also prevents them from adapting their crops to climate changes. Those changes are not linear. By the time of seedling, no one knows what the weather will be like. It's useless to have a gene for drought resistance during tornados or exceptional flooding years and vice-versa. Resilience of crops facing worsening violence of climate shocks depends in the first place on their genetic diversity and local adaptation, not on one new gene or another patented in a laboratory. Only the peasants' selection in the fields, working with seeds coming from local harvests, contributes to this adaptation. No solution can exist without them. Patents present in all GMOs are an inappropriate solution because they forbid peasants' selection. Facing consumers' rejection of GMOs, industries have come up with new techniques of genetic modification and are now willing to have them escaping GMO regulations. Those genetic engineering techniques aim at modifying *in vitro* the genes of cropped plants' cells. They undoubtedly produce living modified organisms as defined by the Cartagena protocol. Under the pretext that some of those techniques leave no trace of the genetic material

introduced in the cells to modify their genome, the industry is willing to have those plants not qualified as GMO in order to escape the international rules of the Cartagena protocol and the mandatory labelling, risk assessment and follow up as imposed by many national regulations. It therefore tries to modify the GMO definition in order to reduce it to the insertion of recombinant DNA found in the final product. It is totally unacceptable that FAO endorses in its own publications this obvious violation of the only accepted international definition of GMOs given by the Cartagena Protocol.

This new move from industry is all the more perverse that it allows the industry to patent genes without distinguishing them from naturally occurring genes in peasants' seeds and in seeds stored in gene banks. The entire cropped biodiversity available is this way being brought under the control of a few multinationals owning the biggest patent portfolios. Peasants and small breeders cannot know if seeds they're using contain patented genes or not in order to protect themselves from those. This legal uncertainty speeds up on one hand the extreme concentration of the seed industry, allowing three multinational companies to control more than half of the international seeds trade and, on the other hand the disappearance of the huge diversity of peasants' seeds preserved and renewed each year by peasants in their fields. By making free the access to the information of genetic sequences of the entire phylogenetic resources of the Multilateral System of the ITPGRFA, Divseek program violates the mandatory requirement for prior consent and sharing of benefits, supporting this new biopiracy. ITPGRFA's complicity by collaborating with this program is an unacceptable betrayal of millions of peasants' trust who provided their seeds.

Via Campesina and civil society organisations supporting it expect FAO to immediately put an end to this new biopiracy and to any kind of support of genetic modification technologies which only aim at allowing a few multinationals to patent and take over existing cropped biodiversity. On the contrary, FAO must support peasants' organisations and researchers which are involved in collaborative peasants' selection programs for food sovereignty and peasants' agroecology.

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3.2.4 The challenges of developing national policies and regulations for agricultural biotechnologies: Reflections from cumulative experiences

Eduardo J. Trigo, Director, Grupo CEO S.A., Buenos Aires, Argentina

Biotechnology is transforming the processes and the products of agricultural research, as well as the institutional and economic environment of agricultural technology development and innovation systems. Advances in the biological sciences are producing quantum leaps in our knowledge about the way plants and animals grow and synthesize useful products, as well as the scientists' ability to transform them. In response to this many developing countries have moved to design and implement promotional policies aimed at promoting the use of the new concepts both as research tools and at the level of specific production situations. Countries as diverse as Nicaragua, Paraguay, Jamaica, the Dominican Republic, Brazil, Colombia and Mexico in Latin America and the Caribbean; Namibia, Zambia, and South Africa in Africa; and Sri Lanka, Malaysia and India in Asia, among others have defined strategies and component policies to promote biotechnology based activities and moved to create specific regulatory mechanisms, particularly concerning biosafety. Biotechnology has also been the base of many international cooperation initiatives linking developed and developing countries, as well as involving different kinds of south-south cooperation approaches.

Looking in retrospect these efforts do not seem to have been very successful. Even though it is true that developing countries make up most of the list of the top ten performers in terms of the adoption of GMO crops – the best known of the products of biotechnology – the fact is that biotech is not a widely used tool within the toolkit of agricultural research, and consequently great opportunities are being lost in terms of capturing the potential benefits of the new technologies for sustainable development, improving nutrition, and addressing the challenges of climate change among other issues. Explaining poor performance is not an easy task. In part, the issue is wider than biotechnology and many of the same aspects can be pointed in reference to conventional agricultural research as well as science and technology policies in general. However, it is important to highlight that biotechnological approaches evolve in an institutional environment that is very different to that of conventional agricultural research, and many of the shortcomings identified could be linked to a poor recognition of what this environment looks like, and the consequent failure to effectively reflect it in the policies designed.

The increased convergence between biological and other sciences, higher investment requirements, the higher profile of intellectual property and biosafety issues, the changed role of the private sector both in the development of the technologies and the technology delivery systems, are all aspects that should be clearly present in an effective policy development process. Clearly there are no recipes to follow for effective policy making but given the characteristics of the present processes and limitations developing countries have to address a few comments can contribute to more effective policy development in the future. A first issue is the need to make agricultural research and technological policy an integral part of the country's general science and technology policy, and discuss biotech related issues within that framework. A second aspect – more related to a better recognition of biotech-based right to information processes – would be moving to decomposing the policy space in policies and instruments addressing issues dealing with access to knowledge and technologies, and instruments dealing with the utilization of the technologies in specific production systems could be a good way to improve existing approaches.

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3.2.5 Ensuring that policies, strategies and regulations on agricultural biotechnologies benefit smallholders

*Dominic Glover, Research Fellow, Institute of Development Studies (IDS), Brighton, UK
February 2016*

Why consider the impacts of biotechnology on small-scale farmers? Isn't small-scale farming a relic of the past? Some policy makers and academics argue that small-scale farmers need either to take a 'step up' in their farming operations – intensify, enlarge, commercialise and become more productive – or 'step out' of farming altogether. According to this view, the major policy challenge in relation to smallholder farming is to find pathways out of agriculture for most of its practitioners, and pathways to large-scale agriculture for the few.

This is a debatable point. What is certain is that, today, many millions of rural people still depend heavily on agriculture for their livelihoods and food security. Agriculture can be a motor of economic growth and development in the wider economy. Moreover, times have changed since the days when industry was absorbing millions of unskilled workers. In the future there will be concerns not only about food security but about employment.

Meanwhile, many families with roots in rural areas exhibit a strong desire to keep hold of their land as a buffer against economic insecurity and a source of resilience. And farm-based rural livelihoods are diversifying to include off-farm and non-farm sources of income and livelihoods. So small-scale and family farm operations are unlikely to disappear overnight, if at all. So focusing policy on the needs and interests of small-scale farmers remains vital.

There is no structural reason for thinking that small farms cannot absorb or benefit from modern agricultural biotechnologies. Key questions for development policy and strategy include: What types of biotechnologies will be suitable and appropriate for small-scale farms? And how can the benefits for this sector be maximised and the risks minimised?

The first observation is that both the design of the technology and the context of deployment matter. The best policy, strategy or regulation to support the interests of small-scale farmers will be different for different types of technologies and for different communities or circumstances. There should not be a standard prescription for every situation. However, taking this into account I can offer some general suggestions. Most of these would apply equally to all kinds of farming technologies, not just biotechnologies, or transgenic crops and livestock.

A good start is to think about an effective *process* for developing policies, strategies and regulations. In particular, it is advisable to consult groups likely to be affected (beneficially or adversely) by the technologies in question. This is one reason why Article 23 of the Cartagena Protocol on Biosafety stipulates that signatories should take steps to inform and involve the public in decision-making; but it is particularly important to involve those stakeholders who are directly implicated in technological change, such as small-scale farmers.

It is well to ask some key questions, such as:

- Who is expected to deploy or practise this technology? For example, will it be used by an individual farmer him/herself, or by a specialist acting on his/her behalf (such as an extensionist, consultant or field technician)? Or will adoption of this technology require cooperation across a community of farmers? Answers to these questions can help decision makers to develop impact strategies and design extension programmes.
- What behaviours or practices are envisaged if this technology is introduced, and which might be eliminated or changed? Who might be affected, positively or negatively, by such changes? Answers to

these questions will help to identify key intervention points and the stakeholders who need to be involved in decision making.

- What material inputs, equipment or tools may be needed in order to take full advantage of the technology? For example, does the new biotechnology depend on additional supplies of fertiliser or water? If so, are these resources readily available? Small-scale producers often farm in unfavourable environments, where desirable inputs are unavailable or inaccessible.
- What information, knowledge or skills are required to make the most of the new technology? Who will supply the necessary information and how will farmers be supported to acquire new knowledge and skills they may need to benefit from the technology or avoid possible negative impacts?
- In many cases the deployment of new technology implies a redistribution of power, income, employment or other assets. Who are likely to be the winners and losers from this new technology? How might the potential losses be mitigated or how might losers be compensated? Or can policy ensure that the benefits are more evenly distributed?

Policy- and decision makers can take several concrete steps to support the uptake of beneficial modern biotechnologies by small-scale farmers. Some key priorities should be:

- Ensuring that the extension and marketing of biotechnologies is done in ways that are effective, clear, transparent, accountable and well-targeted towards small-scale producers.
- Ensuring that modern biotechnologies are accessible to small-scale farmers – i.e. affordable (low or moderate prices), locally available (effective distribution and delivery), and readily understood and usable by small-scale farmers (accompanied by clear and useful information).
- Ensuring that short-term and long-term, individual and societal benefits and risks are weighed and distributed fairly and transparently.

Policy makers can learn from mistakes that have been made in the past. For example, we know now that it is helpful if new technologies are *recognisable* and *trialable*, that is:

- Technologies can be distinguished from other technologies, inputs etc., both on the farm and in the market. This might be due to the technology's effects or because it is properly labelled. It is important to eliminate fraudulent misrepresentation so that farmers can be confident they are using the technology they need.
- Technologies are introduced at a moderate pace, which allows farmers the time necessary to familiarise themselves with the technology, try it out, observe how it works and understand how to get the best from it.
- Technologies are accompanied by clear and usable information, training and other support.

Learning from mistakes does not happen automatically, however. Decision makers need systems for gathering lessons that can serve to inform improved policies into the future, from implementing agencies, extension services and field technicians and farmers.

These guidelines are especially important in the case of seed technologies (e.g. transgenic seeds or treated seeds) which might not be easily identifiable in the field or in the market.

A more challenging proposition is that genetic material, including transgenics, for example, should be made available to small-scale farmers in forms that are unencumbered by intellectual property restrictions, so that they can be decomposed and reconstructed to suit the farmers' own local requirements. Small-scale farmers have managed genetic material in their seed portfolios for many generations; allowing them to do so in future

could be an effective way to ensure that useful traits are incorporated into locally adapted germplasm quickly and effectively.

This might be a controversial proposal because it confronts the interests of IP owners, who wish to control who may use new genetic material, and also because it might create special difficulties for the stewardship and monitoring of genetically modified organisms in the environment. Assessing biosafety risks in advance would be vitally important (including short and long-term effects on human, animal and plant health, crop and natural biodiversity, impacts on non-target organisms, and so on).

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Wednesday 17 February 09.00-12.00 Parallel Sessions

1.3 How can biotechnologies contribute to adaptation with mitigation co-benefits?

1.3.1 Economics of agricultural biotechnology, food and nutritional security, and climate change adaptation and mitigation

*Daniel A. Sumner**

Climate change is a natural concern as we explore the broad theme of “The Role of Agricultural Biotechnologies in Sustainable Food Systems and Nutrition.” Both science and economics specify clear linkages between agricultural and food biotechnology and climate change. One natural question is: How can biotechnologies contribute to adaptation to anticipated and realized climate change? A second is: How can biotechnology, which may be adopted in part to help adapt to climate change, also help reduce the greenhouse gas emissions that drive climate change? Thus, how can biotechnology reduce the rate and extent of climate change? Within these broad questions, I focus on some economics of how agricultural biotechnology is likely to affect food and nutritional security in the context of climate change adaptation and mitigation.

This presentation examines economic issues surrounding relevant science and technology, including incentives for and consequences of adoption of technology by farmers. Regulation of and incentives for investments in science of biotechnology and impacts of incentives for use of biotechnology related especially to food demand. That is consumer information and perception affect market derived demand for biotechnology as they affect demand for food produced using modern scientific tools.

Economics considers costs to reach goals, and here the goals of sustainable food systems and sustainable nutrition security are paramount. Economics of adaptation to climate changes, adaptation to climate change policies, and the economics of agricultural and food system contributions to the rate of climate change and mitigation all affect the roles of biotechnology in farming and the rest of the food system.

Nutritional security requires attention to food production and distribution. But economics focuses attention on incomes of the poor relative to the price of nutritious food, where we define income inclusively to mean command over resources needed to access food. We define the price of food inclusively to mean the resources that must be sacrificed to acquire and consume a nutritious diet. In this context security is necessarily refers to stochastic distributions and nutritional security is tied to the probability of satisfying nutritional criteria, typically for those at the lower end of the nutrition adequacy distribution in a population.

Main economic points of the presentation

1. Climate change may cause poor farmers in poor places to be especially vulnerable to nutritional inadequacy. Many of the poor of the world are farmers and global warming threatens to reduce their productivity and hence reduce their incomes and lower their production of and access to food.
2. Climate change that causes increased variability of weather outcomes (a less clear implication of climate change models and evidence) increases vulnerability and the probability of periodic severe nutritional inadequacy.

3. Climate change will likely improve productivity in some places, and models and evidence suggest that farm productivity may rise more in places with already wealthy and highly productive farms. If that happens farmers in poor regions (often nearer the equator) are doubly disadvantaged. Their own productivity may deteriorate, so they produce less food from their own farm, while the price of food they sell may decline as productivity of their Northern (or Southern) competitors rise.
4. Biotechnology has much to offer for both poor and rich farmers, and especially poor consumers, but only if it is allowed to play its role in improving productivity and allowing more benign environmental outcomes. That is, adaptation to climate change, reduction of greenhouse gas (GHG) emissions, and responses to GHG and other environmental incentives and constraints can all be enhanced by drawing on the most effective science available.
5. However, if the rich accept biotechnology while the farmers in poor places reject biotechnology, the poor will be triply disadvantaged by climate change as they struggle to sustainably achieve nutritional security.
6. The goal and promise of more and better agricultural science is that fewer resources are required to make more food available and accessible to the poor. If prices fall because of more productivity on rich farms, but farmers in poor regions do not have matching productivity gains, they lose again. They lose not just from climate change, but also because richer farmers adapt better to the challenges and opportunities of climate change and climate change regulations and incentives.
7. The policy implication is not to block science for rich farms. Rather is it to remove constraints and enhance incentives for the development and adoption of science and technology applicable to vulnerable farms and farmers in poor regions that are likely to face larger challenges from climate change in any case.
8. Finally, we should remember that a central consequence of successful agricultural development is almost always fewer farms and farmers. Thus, agricultural success means more people who are not farmers, but rather are purely food consumers who gain from lower farm prices. They have better diets and more secure nutritional outcomes as a result of larger food supplies no matter what the source.

**Daniel Sumner is the Director of the University of California Agricultural Issues Center and the Frank H. Buck, Jr. Distinguished Professor in the Department of Agricultural and Resource Economics, UC, Davis.*

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1.3.2 Biodiversity: key to helping farmers adapt to climate change

Carlo Fadda, Gloria Otieno, Stephan Weise
*Bioversity International*¹

The challenge

Climate change is estimated to reduce agricultural production by 2% every decade until 2050, with yields of major crops declining by an average of 8% in Africa and South Asia (IPCC, 2014). As extreme weather events become more frequent and unpredictable, smallholder farming communities will continue to be the hardest hit. Diversification of crops and varieties is one way to give farmers more options to cope with the effects of climate change. But farmers do not always have the information or planting material to choose what diversity best suits their conditions. How can we tap into the vast genetic diversity that exists in different countries to address farmer needs in a timely manner?

Bioversity International's 'Seeds for Needs' initiative works with more than 20,000 smallholder farmers in 11 countries to research how agricultural biodiversity can minimize the risks associated with climate change. Our focus is on deploying existing diversity to farmers from wherever it is found (genebanks, plant breeding programmes, farmers' own fields). The farmers are directly involved in the process.

Research highlights – Seeds for Needs in Ethiopia

Production systems in Ethiopia are largely dominated by cereals: barley, teff, durum and bread wheat are some of the most important crops, and are key to achieve food security. Yet, due to climatic changes the productivity of these crops is declining. Farmers need solutions now, and might not be able to wait until breeders have gone through the long process of crop improvement.

The traits farmers need could be found in the vast genetic diversity conserved at the national genebank of the Ethiopian Biodiversity Institute (EBI). The aim of the initiative is to identify landraces of durum wheat and barley with the potential to adapt to changing climatic conditions, and make them available to farmers and breeders. We developed an approach in which farmers and scientists work together, integrating scientific knowledge with farmers' knowledge and needs, to help farmers in their effort to adapt to climate change, and contribute to improve their food security and livelihoods.

After screening barley and durum wheat accessions in the genebank using a Geographic Information System (GIS) methodology, we selected the varieties that could grow well in different climatic conditions in three regions. We then asked farmers to evaluate the selected varieties using a participatory approach. The key challenge was to link, in a scientifically-sound way, two different sets of information: the detailed agronomic and morphological data of the varieties, with the farmers' preferences. This information could be of great interest to breeders, who could better target their efforts to meet farmers' needs. Linking these sets of information helped us further narrow down the number of varieties for farmers to test under their own conditions. To better understand the linkage between climatic conditions, performance and preference of varieties, we wanted to cover the broadest possible geographic areas and have as many farmers as possible to test the seeds. Hence we used a crowdsourcing approach that allowed us to easily reach farmers and get their feedback. In the crowdsourcing approach, farmers receive three varieties to blind test from a portfolio of 20 and one control variety. These mini trials allow us to involve more farmers than a typical multi-locational trial.

The initiative included 12 villages, covering about 350 km². To know the climatic conditions in all villages, we used sensors called iButtons[®] that monitor temperature and humidity eight times/day. In each village, we installed a plot where all the varieties used in the trial are planted together, so farmers can observe and evaluate the diversity. By combining weather data with the performance of the varieties, we were able to link farmers'

feedback with scientific data. Once farmers have an understanding of how different varieties perform, they need to have access to this diversity, which is not commercially available. Consulting with farmers, we identified a sustainable solution to overcome this challenge: the creation of a community seedbank. Farmers built the infrastructure and the community seedbank opened in May 2014.

As one of the main climate stresses faced by farmers is drought, we concentrated our efforts on identifying drought-resistant varieties. Several varieties that are more resistant to drought than the one commercially released by breeders with the same goal were already identified.

Meanwhile, we conducted a study at the genetic level for the durum wheat accessions, to have a better understanding of the genetic diversity we are using. This analysis revealed that we introduced new valuable genetic traits for climate change adaptation to farmers. Most importantly, we are trying to identify where the traits preferred by farmers are located in the genome.

We evaluated hundreds of domesticated, locally adapted varieties (landraces) of durum wheat - many identified and conserved by local farmers - and performed detailed genetic characterizations at the molecular level. More specifically, we tested, through quantitative trait loci (QTL) mapping, 81 587 markers scoring 30 155 single nucleotide polymorphisms and used them to survey the diversity, structure, and genome-specific variation in the panel. We showed the uniqueness of the Ethiopian germplasm using a siding collection of Mediterranean durum wheat accessions. We phenotyped the Ethiopian panel for ten agronomic traits in two highly diversified Ethiopian environments for two consecutive years and used this information to conduct a genome-wide association study. We identified several loci underpinning agronomic traits of interest, both confirming loci already reported and describing new promising genomic regions. We discovered that the variety in outwardly expressed traits such as plant growth, morphology, resistance to pests and productivity correlated specifically with diversity at the genome level. The results indicate an especially high level of genetic diversity for Ethiopian durum wheat compared with durum wheat cultivated elsewhere, suggesting that it could provide an important, as yet unexplored source of durum wheat diversity (Mengistu *et al.* 2016)².

This information is also useful for a breeding programme being conducted by the Sirinka Agricultural Research Station in Ethiopia, aiming at creating new lines using the best material identified by scientists and farmers.

¹This work is done within the framework of the Climate Change Agriculture and Food security CGIAR Program and in partnership with: Institute of Life Sciences, Scuola Superiore Sant'Anna, Pisa, Italy; Department of Dryland Crop and Horticultural Sciences, Mekelle University, Ethiopia; Sirinka Agricultural Research Center, Sirinka, Ethiopia; Amhara Regional Agricultural Research Institute, Ethiopia; Ethiopian Biodiversity Institute, Ethiopia; and Department of Agricultural Sciences, University of Bologna, Bologna, Italy

² Mengistu, D.K., Kidane, Y.G., Catellani, M., Frascaroli, E., Fadda, C., P_e, M.E. and Dell'Acqua, M. (2016) High-density molecular characterization and association mapping in Ethiopian durum wheat landraces reveals high diversity and potential for wheat breeding. *Plant Biotechnol. J.*, doi: 10.1111/pbi.12538

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1.3.3 Biological Nitrification Inhibition (BNI) in Plants- Implications for Improving Nitrogen-Use Efficiency and Reducing Nitrous Oxide Emissions from Agricultural Systems

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The biological oxidation of ammonium (NH_4^+) to nitrate (NO_3^-), termed as nitrification, carried out by two groups of soil microorganisms - ammonia oxidizing bacteria and ammonia oxidizing archaea. Cationic- NH_4^+ is strongly bound to the soil and is available for crop uptake. In contrast, the anionic- NO_3^- does not bind to the soil and is prone to leaching and cause pollution of water-bodies. Several heterotrophic soil bacteria denitrify nitrate under anaerobic or partially anaerobic conditions, produce nitrous oxide (N_2O), a powerful greenhouse-gas (GHG) with global warming potential 300 times more than CO_2 , and the third-largest contributor, after CO_2 and methane to global warming. Nitrification and denitrification are the only known biological processes that generate N_2O ; concentrations of N_2O in atmosphere are raising since the advent of Green Revolution (from 290 ppb in 1960s to 320 ppb in 2000); nearly 70% of global N_2O emissions come from agricultural systems.

Green Revolution, Nitrogen fertilizer use, and N_2O emissions - the functional link

Fertilizer-responsive high-yielding wheat, rice and maize varieties largely are responsible for Green Revolution, that doubled global food production (between 1960 to 2000); but global N-fertilizer consumption has increased from 10Tg to 120 Tg yr^{-1} during this period. A 12-fold increase in N-fertilizer consumption for a two-fold increase in global food production led to a dramatic decline in nitrogen-use efficiency (NUE; kg of grain produced per kg of N-fertilizer applied), reaching <30% recovery of applied-N by crops at present. Nearly 1.36 billion barrels of diesel-energy is needed to produce 120 Tg of N-fertilizer; about 70% of N-fertilizer applied to agricultural systems is lost to nitrate leaching and denitrification; the economic cost from the lost N-fertilizer is estimated at US\$ 90 billion annually. Global N-fertilizer consumption will reach 300 Tg by 2050 and global N_2O emissions will double from present levels and reach 19 Tg $\text{N}_2\text{O-N yr}^{-1}$ (8.98 Gt CO_2 eq yr^{-1}), if we carry on with the business as usual. There is an urgency to develop next-generation mitigation-technologies to reduce N_2O emissions from agricultural food-production systems as IPCC set a target to cut global GHG emissions by 80% by 2050. Controlling soil nitrification is thus critical to reverse the present trend in declining NUE by improving N-retention and reducing N-leakage from N_2O emissions and NO_3^- leaching.

Biological Nitrification Inhibition (BNI) - A genetic-mitigation technology to curb N_2O emissions from agricultural systems

Certain plants have the natural ability to produce and release biological nitrification inhibitors (BNIs) to suppress nitrifier-activity and soil-nitrification, a plant-function, termed 'biological nitrification inhibition' (BNI). Tropical pasture grasses such as *Brachiaria humidicola* (Bh) have the strongest BNI-capacity and release 'brachialactone' a powerful nitrification inhibitor from roots. Our initial estimations suggest that sufficient BNIs can be produced and added from Bh-root-systems (from root-exudation and from root-turnover) that can potentially reduce soil-nitrification. This hypothesis was field-tested where it was demonstrated that Bh-pastures not only suppress nitrifier-activity and NO_3^- formation in soils but also reduce N_2O emissions. Currently, JIRCAS in partnership with

CIAT is evaluating whether BNIs added from Bh-root systems can improve NUE of a following maize crop in an agro-pastoral system. We tested the hypothesis that a reduced soil-nitrifier activity from a high-BNI-capacity Bh-pasture grass can improve N-recovery thereby improving NUE of a follow-up non-BNI maize crop. Last four-years of field evaluation suggest that maize yields have improved substantially (from 60 to 100%) in BNI-fields compared to non-BNI-fields under moderate-N inputs (60 to 120 kg N ha⁻¹); N-recovery and soil-N-retention were substantially higher in BNI-fields compared to non-BNI fields, suggesting the potential value of exploiting BNI-function in an agro-pastoral system. In addition, we (JIRCAS with participation from ICRISAT and CIMMYT) are evaluating and characterizing the BNI-capacity in sorghum and wheat root-systems to assess the potential for genetic-exploitation of BNI-trait in major staple food crops. Sorgoleone, a powerful hydrophobic BNI-compound is exuded from roots and contributes to the BNI-capacity in sorghum. Current research is focused on identification of molecular markers linked to sorgoleone-release-trait for deploying high-BNI-capacity into next-generation sorghum varieties. Cultivated wheat lacks adequate BNI-capacity in their root systems and current efforts are directed towards introducing high-BNI-capacity from one of its wild relatives (*Leymus racemosus*), using chromosome-engineering techniques. As plant root-systems produce a cocktail of BNIs with varied chemical structures and multi-mode of inhibitory action on *Nitrosomonas* (the nitrifying soil bacteria), exploiting BNI-function (using both genetic- and agronomic- strategies) may be more effective than using chemical nitrification inhibitors to control soil-nitrifier-activity. Genetic exploitation of BNI-trait to produce BNI-enabled crops and pastures could be a powerful genetic-mitigation technology for the Next-Green-Revolution that must improve NUE and reduce N₂O emissions.

Low-nitrifying food production systems are critical components of climate-smart agriculture

Low-nitrifying and low-N₂O emitting agricultural production systems are one of the important pillars to support climate-smart agriculture. Genetic-mitigation technology, where BNI-enabled root systems of staple crops/pastures will become components of low-N₂O-emitting food-production systems, and it should be integrated with genetic-adaptation strategies to address climate change for developing climate-smart agriculture in 21st Century.

A paradigm shift is needed in nitrogen management to meet COP-21 GHG emission reductions from agricultural systems

COP-21 set the goal for cutting GHG emissions by 80% to limit global temperature raise to below 2°C by 2050, termed as 'Paris-Agreement' and created a climate fund of US\$ 100 billion per year, operational from 2020 to facilitate development of novel mitigation-technologies that are carbon-neutral, and N₂O-neutral as well. A paradigm shift towards low-nitrifying production systems are needed; exploiting BNI-function could become a powerful genetic-mitigation technology to achieve the goal of reducing N₂O emissions to lower the N-foot-print from agriculture by 2050.

Prepared as a short-article for publication in FAO proceedings on Climate Change Symposium (Feb. 15-16, 2016 at FAO Hq in Rome, Italy)

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1.3.4 Mitigation of enteric methane emissions from ruminants: The role of biotechnology

Henning Steinfeld, Food and Agriculture Organization of the United Nations

Carolyn I. Opio, Food and Agriculture Organization of the United Nations

Animal biotechnology has been practiced in one form or another since the beginning of the domestication of animals. Many of the classically used tools such as nutrition, reproduction, animal breeding and genetics have played an important role in the proliferation of desirable and economically important traits that have enabled ruminants to respond to human demand for food.

Modern livestock production has relied on biotechnology for the development of improved feedstuffs and feed ingredients, vaccines, high quality genetics, and improved reproduction traits, disease diagnosis – all aspects that have combined to improve the sector's contribution to global food supply.

The domestication of ruminants represents one of the earliest forms of human application of biotechnology to produce food. This has been made possible through the process of enteric fermentation that takes place in the rumen - the site where rumen microorganisms digest carbohydrates, proteins, and fiber under anaerobic conditions.

Ruminants and microbes have evolved together, filling a niche based on the conversion of complex plant carbohydrates to energy that is beneficial to both the host animal and the microbial population in the rumen. The production of ruminant products, such as milk and meat depends on the microbial fermentation of feed into products such as microbial protein and volatile fatty acids (VFA), which are transformed by the ruminant tissues into animal product, along with by-products such as hydrogen (H₂), carbon dioxide (CO₂), ammonia and heat. This microbial transformation in the rumen allows ruminant species such as cattle, buffalo, sheep, and goats, to use fibrous feeds for production.

The process of enteric fermentation in the rumen is thus highly beneficial for humans because it converts low quality, coarse and fibrous plants into food and fiber, but it is also a major producer of methane, a potent greenhouse gas. Methane (CH₄) production is a natural and inevitable outcome of the fermentation process that prevents the accumulation of the hydrogen end product released by rumen microbes during the fermentation of feeds.

Methane emissions are the second largest cause of global warming after carbon dioxide (CO₂), accounting for 16% of global emissions. From 1750 to today, the concentration of methane in the atmosphere has increased by 150% (from 700 to 1760 parts per billion). By weight, methane is 84 and 28 times more potent than CO₂ over a 20-year and 100-year period, respectively.

The agriculture sector contributes about 50% of the global human-induced CH₄ emissions of which 78% are from livestock (manure and enteric fermentation). Methane from enteric fermentation is the single largest global source of anthropogenic CH₄, responsible for 30% and 70% of global methane emission and CH₄ emissions from agriculture, respectively. At global level, methane production from enteric fermentation contribute 5.5% (equivalent to 2.7 Gt CO₂ eq.) to the global anthropogenic GHG emissions. Using methane's 20-year GWP – a measure of the short-term climate impact of different GHGs – more than triples the share of enteric methane to over 18% of global GHG, from slightly less than 6% at the 100-year timeframe. Cattle account for 77% of the global enteric emissions (2.1 Gt), buffalo for 14% (0.37Gt) and small ruminants (sheep and goats) for the remainder (0.26 Gt). Global enteric CH₄ emissions are projected to increase by 20% in response to growing demand between 2010 and 2030; this would add over 388 MtCO₂ eq. in 2030.

Methane production through enteric fermentation is not only of global concern for its contribution to global warming, but also for its wastage of feed energy, an inefficiency that limits the production performance of ruminants. As a result of this process, ruminants lose between 2-12% of the gross dietary energy in the form of methane, depending on the quality and quantity of diet. Thus, it is essential to look for options to reduce CH₄ emissions through improving feed conversion efficiency, which also translates into economic benefits for millions of producers dependent on ruminant production for their livelihoods.

In the last few decades, there has been a rapid growth of knowledge in the functioning of the rumen as well as research into mitigation technologies to reduce the enteric CH₄ emissions from ruminants. Several options are available ranging from nutritional strategies (such as feed processing to enhance digestibility, inclusion of concentrates in diets, improving the quality of forages), to the use of feed additives (ionophores, organic acids, fats and oils, plant extracts), and to modern technologies such as defaunation, immunization, genetic modification of rumen micro-organisms, conventional and advanced (molecular genetics) plant and animal breeding.

Currently, nutritional strategies and interventions focusing on the optimization of feed rations are some of the most developed and readily available for immediate application in the field. These are often low-cost, low-risk, low-tech, resilience-enhancing and provide productivity gains. Nevertheless, despite the obvious benefits, these technologies have been adopted much more slowly. In low input – low output systems, ruminants are usually reared because they do not necessarily require resource ownership as they often depend on free access and communally-owned grazing resources, while providing high return at low or no cost (in form of milk, meat, draught power, manure, etc.) relative to other investment options. In addition, several other factors restrict action on enteric fermentation including the heterogeneity of management practices, the cost of mitigation and inherent price volatility of options dependent on diet manipulation.

For systems operating at very low levels of efficiency, many of the nutritional strategies outlined involve employment of existing technology. With such strategies, the main constraint is technology transfer, diffusion and deployment. Policies that aim at incentivization of technologies with a high to intermediate level of scientific certainty and have the potential both to generate relatively rapid productivity gains and economic benefits, are required.

On the other hand, the inhibition of enteric CH₄ in ruminants through the use of technologies such as dietary additives have not delivered a clear and positive answer in reducing CH₄ emissions in ruminants, highlighting the difficulties in their application. Many of these strategies still require further research to allow application. The scope to use specific dietary additives in ruminants is much greater in developed regions than in the developing world because of cost, applicability (i.e. it is much easier to administer products to animals in confined systems than in free ranging or nomadic systems). In addition to this, the high upfront cost and the knowledge gaps surrounding their impacts remain major obstacles.

Finally, there are many novel and advanced biotechnologies in their early stages of development, such as the use of probiotics, vaccination and genetic modification of the rumen. For these technologies, further research and development is needed before they can be widely employed. The potential applications of biotechnology in ruminant production are endless. With the current challenges facing the sector, it is possible to envisage a future where livestock production will increasingly rely even more on existing and emerging biotechnological advances to produce food. Today, techniques of modern and advanced biotechnologies are a reality and are rapidly finding their way into research and development. Consequently, there are high expectations about the developments in biotechnology and the potential benefits it can offer in enhancing productivity, improving livelihoods while protecting the environment. To tap this potential, investments in technological transfer and input and product market development are required, alongside with possible emission offset incentives.

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1.3.5 Biodiversity as a Biotechnological Tool for Carbon Sequestration and Healthier Food Production in Smallholder Communities in the Tropics – Brazil

Professor Paulo Kageyama. ESALQ, Univ. São Paulo. Brazil

The Laboratory for the Genetics of Tree Species (LARGEA), at the University of São Paulo, Brazil, is studying the complex biodiversity and the genetic structure of tropical tree populations, viewing to use these main concepts on two applied projects in the field: i) restoration of degraded riparian areas around hydroelectric dams for carbon sequestration; and ii) agroforestry systems with high biodiversity for smallholder farmers, protecting the system against pests and diseases, and producing healthy food.

Basic research using molecular genetics is showing that there are around 500 plant species per hectare in tropical forests (Atlantic Forest), with one hundred times more species of insects and microorganisms (50,000 spp/ha). The majority of these organisms are normally enemies to plants and can eat them. Why is the biodiversity so high? The plants in these natural forests have evolved to be protected against insects and microorganisms, producing secondary chemical compounds to survive in nature, and this can be used as a biotechnological tool in the construction of agroecosystems.

The genetic structure of the Atlantic Tropical Forest in Brazil has been studied by LARGEA, University of São Paulo, for the past 30 years, using molecular genetic methods to determine genetic variation within and among populations, gene flow, and breeding systems of more than 50 representative tree species of natural tropical forests. This basic information is very important for a deep understanding of the biodiversity of natural tropical forests, and input for restoration and agroforestry system projects.

The two main applied projects of LARGEA/USP are using biodiversity as the basis. In the first project, trees of 100 different species were planted to give a biodiversity of 100 tree species per hectare in a restoration project for degraded riparian areas, in cooperation with hydroelectric companies in the State of São Paulo, Brazil. In the second, the project was in association with the “Landless Movement” of Brazil, the most well-organized smallholder communities, developing agroforestry systems with high biodiversity, for producing healthier food. The main result of the restoration project of LARGEA/USP was the planting of 500 hectares per year (during a period of 30 years) with the previously mentioned biodiversity (100 tree species/ha) for Carbon Sequestration. This project was under the UN Framework Convention on Climatic Change (UNFCCC). The most recent PhD thesis presented by a student of LARGEA/USP within this theme addresses: “Energy evaluation of ecological restoration around hydroelectric dams in Pontal – Brazil.” This thesis presents an evaluation, through effects on the same parameters of nature and economics, of 26 years of restoration under the same planting methodology.

To separate out examples from the second applied project of the laboratory, we can highlight an MSc thesis comparing, under the same ecological conditions, the cultivation of tomato by three conventional producers (using applications of agrottoxics and chemical fertilizers) against three smallholder farmers operating under an organic system (biodiversity surrounding the culture), without the use of industrial chemical products. The final results were surprising: the productivity for the organic system was 65% (130 boxes of 20 kg of tomatoes per 1,000 plants) of that for the conventional system (200 boxes per 1,000 plants), while the economic returns to the farmers under the two systems were about the same (R\$ 1,000 reais *versus* R\$ 800 reais per 1,000 plants, for the conventional and organic farmers, respectively). The most important aspect to highlight is that the smallholder farmers did not use agrottoxics; therefore, neither the farmers nor the consumers of their products were exposed to the danger of being poisoned by the 36 applications of agrottoxics used by the conventional farmers during the 2.5 month cycle of the tomato culture (Tomas and Kageyama, 2011). The essential aspect is that the tomatoes produced by the organic farmers were free of agrottoxics, and represented healthier food. The project illustrates

the use of biodiversity as a biotechnological tool for the production of healthier food by smallholders within settlements of agrarian reform in Brazil.

The second example of an Agroforestry System studied in our laboratory is coffee cultivation. The PhD student (P. Lopes, 2014) has presented a thesis comparing coffee cultivation under different levels of native tree biodiversity with monocultures of coffee in settlements in Pontal do Paranapanema, Brazil. Three levels of biodiversity were used in the coffee agroforestry systems: i) high - 36 different native tree species in addition to the coffee plants, ii) medium level - 23 native tree species plus coffee, and iii) low - 12 native tree species, together with iv) the control - pure monoculture of coffee. The results supported the hypothesis that attacks on the coffee plants by the most important pest in the region, *Leucoptera coffeella* - the so-called “bicho mineiro”, could be reduced by adopting an agroforestry system with biodiversity provided by native tree species. The average levels of attack, expressed as percentages, observed for the different coffee agroforestry systems were: 31.24%, 45.47%, 58.15%, and 88.35%, for the high, medium, low biodiversity and the coffee monoculture treatments, respectively. The estimates of the economic return for the different coffee systems were: R\$ 1,100.00, R\$ 2,813.00, R\$ 2,250.00 and R\$ 1,452.00, for the agroforestry systems of high, medium, low biodiversity, and the coffee monoculture, respectively. The best economic performance, representing a balance between biodiversity and productivity, was achieved by the second treatment, corresponding to medium biodiversity.

Final Considerations: i) In Agriculture and Silviculture in the tropics, advanced technology and the large-scale use of monoculture are destroying the biodiversity, causing increases in pests and diseases. To maintain productivity, the agroindustry has turned to more and more use of agrottoxics and chemical fertilizers, aggregated with the introduction of GMOs; ii) The adverse impacts of these production models on the environment and human health are clearly observed, including in reports commissioned by the WHO. In contrast, smallholder farmers have adopted agroforestry systems for the production of healthier food, avoiding the use and high costs of dangerous industrial chemical products; iii) We have presented the important application of biodiversity for the maintenance of equilibrium in agroecosystems and the production of healthier food for society.

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1.3.6 Carbon sequestration in agricultural soils : the « 4 per mil » program

Authors : Hervé Saint-Macary (Cirad), David Pot (Cirad), Jean-Francois Soussana (INRA), Jean-Luc Chotte (IRD)

Summary

The proposal, made by the French authorities ahead of COP21, to store annually four per mil of the soil organic carbon stock to offset current anthropogenic CO₂ emissions is now part of the Lima-Paris agenda for action (LPAA) and it is confronted to state-of-the art scientific understanding.

The adoption of best agronomic and forestry practices can allow a significant carbon sequestration rate, reaching locally up to 4 per mil (4‰) of the soil organic carbon stock for some of the documented examples. However, these examples are unevenly distributed with, in particular, little data for tropical soils. Assuming a global soil organic carbon stock of ca. 820 GtC (over a meaningful depth for carbon sequestration, i.e. 0-40 cm), the 4‰ target would result in a carbon sequestration that could peak at 3.5 billion tons C per year (Gt C/ yr) when considering soils from all biomes.

A rise in global soil carbon sequestration could be obtained through a large increase in global net primary productivity partly obtained by restoring degraded lands (ca. 24% of the total land area) that are widespread in all biomes and in most world regions. Further assuming that net CO₂ emissions from land use change could be halted, the land carbon sink that could peak in the 2030-2040's thereby substantially offsetting the current growth in atmospheric CO₂.

Positive impacts of increasing carbon contents of soils on food security and ecosystem services can be anticipated, including increased biomass production for bioenergy, reduction in erodibility as well as climate change adaptation, thereby contributing to sustainable development goals. The additional soil organic carbon stock would need to be preserved until the end of the century - and as far as possible beyond - through a combination of soil conservation practices and of land adaptation to climate change.

Research needs concern: a) Knowledge on the baseline of sequestration (or loss) of soil carbon and on current soil carbon stocks; b) The definition and co-construction of agronomic strategies and practices at various scales (individual to collective) targeting the '4 ‰' objective; c) The transfer and adoption of these strategies and the development of demonstration sites; c) The design, experimentation and assessment of institutional arrangements and public policies, including financial mechanisms, that aim at promoting and rewarding relevant practices d) Metrics and methods for monitoring, reporting and verifying carbon sequestration, if possible on the basis of a net-net accounting.

As mentioned an increase in the global net productivity is one way to achieve the goal. However the final sequestration of carbon is determined by the net biome productivity. Estimations are that the global primary production of carbon is 123 GT of C per year; compared to this the Net biome productivity is 2.9 GT. The ratio between this two values is very low and biotechnologies could be mobilized to improve them in various ways: improvement of the photosynthesis process, modification of the shoot : root ratio, biomass quality monitoring, pereniality of crops, improvement of the soil-rhizosphere-plant interface knowledge.

In this presentation, these various ways will be discussed and, when relevant, the example of sorghum, will be used to illustrate on going researches and possible implementations for various environments.

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Wednesday 17 February
09.00-12.00 Parallel Sessions

2.3 Nutrition and food quality

2.3.1 Our Foods, Our Diets, Our Health: Where do we go from here

Anna Lartey

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By 2050, the world's population is expected to increase to about 9 billion and this is expected to call for a 60% increase in food production. For developing countries where the bulk of the population growth will occur, food production needs will increase by 100% from current levels. Increase in cereal production will far out-weigh other food crops. The production of fruits, vegetables and pulses over the past 5 years has increased little. While the price of staple foods are dropping, the price of non-staple foods such as fruits and vegetables, pulses and animal source foods are increasing. Under the circumstance, for poor households it is cheaper to meet food needs on staple foods, even if less nutritious, than to use scarce resources on the more expensive non-staple foods.

Many developing countries are going through the nutrition transition characterised by improved economic conditions, but increased consumption of highly processed foods high in fat, sugar and salt. As economic conditions improve, many countries are moving into a state of the double burden of malnutrition- a situation where undernutrition including micronutrient deficiency co-exist with overweight and obesity. The food environment is changing globally. Access to healthy diets affordable to the majority of the population is becoming an issue. The consequence is the slow progress made in addressing malnutrition. Although significant progress has been made in reducing hunger from over 1 billion people affected in 1990-1992 to under 800 million in 2015, the progress made in reducing stunting, and micronutrient deficiency has been slow. Micronutrient deficiency affects about 30% of the world's population. Anaemia, a major contributor to maternal death affects over 500 million women of reproductive age. The other side of malnutrition has crept up on us. About 1.9 billion are overweight or obese, this is about 30% of the global population. The economic burden of obesity and its associated non-communicable diseases is estimated to be \$2.0 trillion, comparable to that of armed conflicts and smoking (\$2.1 trillion each). Not surprising, concerns about broken food systems dominates the discourse around our diets.

The 2nd International conference on Nutrition (ICN2) hosted by FAO and WHO in November 2014, drew the world's attention to actions needed to promote sustainable food systems. Among these are: the need to review national policies and investments and integrate nutrition objectives into food and agriculture policy, programme design and implementation to enable healthy diets (Rec # 8); strengthen local food production and processing, especially by small holder and family farmers, giving special attention to women's empowerment, while recognizing that efficient and effective trade is key to achieving nutrition objective (Rec #9); promote the diversification of crops including underutilized traditional crops, more production of fruits and vegetables, and appropriate production of animal-source products as needed, applying sustainable food production and natural resource management practices (Rec #10); improve storage, preservation, transport and distribution technologies and infrastructure to reduce seasonal food insecurity, food and nutrient loss and waste (Rec # 11); establish and strengthen institutions, policies, programmes and services to enhance the resilience of the food supply (Rec #12); develop, adopt and adapt, where appropriate, international guidelines on healthy diets (Rec# 13); encourage gradual reduction of saturated fat, sugar and salt and trans fat from foods and beverages to prevent excessive intake by consumers

and improve nutrient content of foods needed (Rec # 14); explore voluntary instruments- to promote healthy diets (Rec# 15); establish food and nutrient-based standards to make healthy diet accessible (Rec # 16).

The knowledge and technology to tackle the current nutritional and food systems problems exist. One of such tools is biotechnology. This tool can be used to enhance human nutrition by making foods more available and by enhancing the nutritional content of foods. There are many examples where modern biotechnology has been used to improve the nutrient content of food such as orange-flesh sweet potatoes, iron and zinc rich millet, vitamin A rich Cassava. Biotechnology in the form of fermentation has been employed in traditional cultures to transform food and prolong shelf life. Modern science has opened up a wide range of techniques for the application of biotechnology to agriculture and nutrition. The evidence around the potential of biotechnology to improve nutrition has built up. It is up to us to use it well to our advantage.

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2.3.2 Application of Biotechnologies to Improve the Quality of Rice and Wheat

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Background

Rice and wheat account for most of the global grain harvest, and together these two grains supply around half of all calories consumed by the entire human population. Human consumption accounts for 85% of all rice produced and 72% of wheat produced, illustrating (i) the importance of these two crops for human sustenance; and (ii) the need to ensure that production is able to overcome future challenges.

Current trends of population growth, middle class expansion, and climate change have consequences for crop improvement programs and agricultural production into the future. Social science also informs us that as developing countries undergo economic transition, the demand for high quality food will increase. High quality can include physical appearance, sensory quality and nutritional traits. Breeding programs have already embraced the challenge of developing new high-yielding varieties adapted to new climates, and scientists are searching for the genes and physiological pathways that lead to crops reaching and exceeding yield potential and maintaining this yield under stress. However, with demand for quality increasing, success of a new variety of any cereal is more likely to be measured by consumer acceptance of the food derived from the harvested grain, rather than adoption by farmers of the plant and its suite of agronomic traits.

Biotechnology

“Climate change, Urbanisation, Biotechnology. Those three narratives still taking shape, are developing a long arc likely to dominate this century.”

Stewart Brand 2011.

Biotechnology applies scientific and engineering principles to living organisms in order to produce products and services of value to society. Biotechnology encompasses features from many different disciplines such as chemistry, mathematics, physics, engineering, microbiology, and genetics. It can drive transformational changes for agricultural production, food security, and nutrition security for our future generations. Much biotechnological research reveals genes with important functions, and biotechnology enables those genes to be mobilised into different varieties either through conventional breeding and marker-assisted selection, or through more rapid techniques, such as genetic transformation or the newer technique of genome editing. Transformation leads to the insertion of a gene into the DNA of another variety or organism, and genome editing refers to the insertion, deletion or replacement of DNA within the genome of an organism.

Equipping the genome of rice or wheat with a valuable gene by either transformation or genome editing is a translational outcome of biotechnology research because it places the research outcome into farmers' fields for maintaining yield and therefore income, and then if the new gene increases the nutritional content of the grains, then the value is found in the diets of people with chronic micronutrient deficiency or those with Type II diabetes. Currently the nutritional traits being investigated are for micronutrients of beta carotene, zinc, and folate in rice grain, and in both rice and wheat iron and carbohydrates with low digestibility for diabetics. Not all consumers

accept that value can be derived from using the tools of biotechnology to modify the genome of animals or plants that are intended to be food. This is powerfully illustrated by the destruction of field trials of plants genetically modified to express traits for health and nutrition, which means that it will take a lot longer to place these nutritionally beneficial foods into the food bowls of the people most affected by these chronic nutritional conditions. In order to avoid such devastating impact in the future, it is important to (i) understand what drives the fear, and (ii) initiate a dialogue supported by science to explain the value of equipping plants with a valuable gene when evolution did not.

As with improving plants with genes for agronomic traits, a new variety is unlikely to be accepted with a nutritional trait unless it also meets quality traits for the cooked rice or the processed wheat.

Using biotechnology to discover genes for quality

The expansion of middle classes is most strongly seen in the rice-consuming countries of Asia. One of the quality traits of rice that all consumers rate important is fragrance, and this is demonstrated by the cost of fragrant rice in all markets. The compound giving fragrance is 2 acetyl-1-pyrroline (2AP) and the gene leading to the presence of the compound is known. Both jasmine and basmati rice contain 2AP, and no other compounds have been identified that combine with 2AP to give the characteristic jasmine or basmati aroma, and no genes have been discovered that lead to different amounts of 2AP.

Using metabolomic profiling and sensory evaluation, we have identified a number of compounds that determine the high quality jasmine fragrance, compounds that associate negatively with fragrance, genetic regions (QTLs) for several compounds, and three QTLs that associate with the concentration of 2AP. Using different tools of biotechnology, these QTLs can be delivered as markers to breeding programs to enable them to use conventional breeding with genetic selection. Using that pathway, breeders must keep track of the new QTLs as well as the host of other agronomic and quality traits, so a new, highly fragrant variety will take many years to reach a market. If consumers can be persuaded to accept genetic engineering technologies, and Brand's long arc can be shortened, a new, highly fragrant version of currently accepted varieties could be fast-tracked to market by editing the genomes to insert or replace the genes required for high fragrance for the many rice consumers that value fragrance highly, and for the new varieties with nutritional benefit.

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2.3.3 Biofortification of Staple Food Crops: Justification, Progress, and Future Activities

Howarth E. Bouis
February 17, 2016

An estimated 2 billion people in the developing world suffer from the effects of micronutrient malnutrition, caused primarily by poor quality diets which are characterized by high food staple (e.g. rice) intakes. Inadequate intakes of essential vitamins and minerals lower disease resistance, increases mortality, compromise cognitive development, stunt growth, and lower work productivity. Preschool children and mothers of reproductive age are most vulnerable due to their higher requirements.

The density of minerals and vitamins in food staples eaten widely by the poor may be increased either through conventional plant breeding or through use of transgenic techniques, a process known as **biofortification**. For example, HarvestPlus seeks to develop and distribute varieties of food staples (rice, wheat, maize, cassava, pearl millet, beans, sweetpotato) which are high in iron, zinc, and provitamin A through an interdisciplinary, global alliance of scientific institutions and implementing agencies in developing and developed countries.

Biofortified crops offer a **rural-based** intervention that, by design, initially reach these more remote populations, which comprise a majority of the undernourished in many countries, and then extend to urban populations as production surpluses are marketed. In this way, biofortification complements fortification and supplementation programs, which work best in centralized urban areas and then reach into rural areas only in areas with good infrastructure. Initial investments in agricultural research at a central location can generate high recurrent benefits at low cost as adapted biofortified varieties become available in country after country across time at low recurrent costs.

In broad terms, three things must happen for biofortification to be successful. First, the breeding must be successful – high nutrient density must be combined with high yields and high profitability. Second, efficacy must be demonstrated – the micronutrient status of human subjects must be shown to improve when consuming the biofortified varieties as normally consumed. Thus, sufficient nutrients must be retained in processing and cooking and these nutrients must be sufficiently bioavailable. Third, the biofortified crops must be adopted by farmers and consumed by those suffering from micronutrient malnutrition.

First greeted with skepticism by plant breeders who worried that adding micronutrients would reduce yield, it has now been demonstrated conclusively that these high mineral and vitamin traits can be combined with high yields and high profits. More than 15 million people in 30 developing countries are already growing and eating biofortified foods, and the number continues to grow rapidly. Ex ante and ex post cost-effectiveness analyses have been conducted for several micronutrient-crop-country-crop combinations. Cost-effectiveness of biofortification interventions has also been compared to other micronutrient interventions within several countries. All of these analyses indicate that biofortification is highly cost effective and has the potential to engender significant reduction in micronutrient deficiencies.

Peer-reviewed published data demonstrate that these nutritious foods improve nutritional status and reduce disease incidence and duration. For example, a study in Mozambican children (Jones & De Brauw, 2015) who ate biofortified vitamin A-rich sweet potatoes showed an impressive 42% reduction in the incidence of diarrhea in children under five, and a 52% reduction in children under three. The same study showed a reduction in the duration of diarrhea among children who fell ill – 10% in under-fives and 25% in under-threes. These were comparisons between children in intervention villages four years after orange sweet potato was first introduced and two years after all extension activities were discontinued, as compared with children in control villages where white sweet potato was continued to be grown.

To date all released biofortified crops have been developed using conventional plant breeding techniques. However, transgenic techniques are very powerful tools for adding vitamins and minerals to food staples. Transgenic biofortified crops could be of great benefit in reducing mineral and vitamin deficiencies if political barriers to their development and release could be overcome.

The example of Golden Rice is well-known. Milled rice contains no provitamin A. Potrykus and Beyer have demonstrated that transgenic techniques can result in high levels of provitamin A in milled rice (Ye et al 2000).

Likewise recently Trijatmiko et. al. (2016) have demonstrated that high levels of both iron and zinc can be added to milled rice using transgenic techniques. Substituting this biofortified transgenic rice one-for-one for non-biofortified rice on any given day would result in an additional 30% of the Estimated Average Requirement (EAR) of iron in the diet and, at the same time, an additional 60% of the EAR of zinc.

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2.3.4 Fish matters: role of biotechnology in improving nutrition

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Aquaculture has been the world's most rapidly growing food sector for over a quarter of century, with total global production (includes all farmed aquatic plants and animals) increasing over nine-fold from 10.2 million tonnes in 1984 to a new record high of 97.2 million tonnes in 2013. Valued at over US \$157 billion, global aquaculture production has been growing at an average annual rate of 8.1% per year since 1984, compared with 0.66% per year for total capture fisheries landings, and 2.6% per year for terrestrial meat production over the same period. Moreover, with over 95.2% of total global aquaculture production being produced within developing countries, aquaculture is viewed as an important weapon in the global fight against hunger and malnutrition as a much needed provider of high quality food and essential dietary nutrients.

According to FAO agricultural biotechnology includes "Any technological application that uses biological systems, living organisms, or derivatives thereof, to make or modify products or processes for specific use". For the purposes of this paper agricultural biotechnology is used here to include those activities related to improving nutrition, including the improved nutrition of the aquaculture feeds used for the production of farmed aquatic species, the reduction of potential environmental impacts of aquaculture feeds, and the improvement of the nutritional content of aquaculture produce for direct human consumption.

The paper presents examples of microbially produced feed additives commonly used within commercially formulated aquaculture feeds (total global production currently estimated at about 42 million tonnes), including microbially produced dietary essential amino acids (lysine, threonine, tryptophan), dietary enzymes (proteases, phytases, complex carbohydrate digesting enzymes), vitamins (vitamins B₁₂, riboflavin), trace minerals (selenium yeast, zinc yeast, chromium yeast, iodine), carotenoid pigments (algae produced astaxanthin), nucleotides and immune enhancers (derived from bacteria and/or yeast), organic acids, and probiotics.

Particular emphasis was given to the use of microbially produced phytases to increase the utilization of indigestible plant based phytates, and by so doing reducing phosphorus excretion and pollution to the aquatic environment. Similarly, the important role played by the microbially produced essential amino acids lysine and threonine (these two amino acids usually being the second and third limiting amino acids in most aquaculture feeds) within compound aquafeeds has helped the aquaculture feed industry move away from its reliance on fishmeal with alternative more sustainable feed ingredient sources.

In addition to feed additives, agricultural biotechnologies have recently placed particular effort to the mass production of microbial biomass for use as dietary fishmeal replacers (including yeast and bacterial single cell proteins) and/or as a source of long-chain polyunsaturated fatty acids (algal DHA). The paper also discusses the traditional and current use of fermentation technologies for the conservation of small lower-value fish (from a marketing viewpoint) within most Asian countries, including the common production of fish sauces for food seasoning, and the more recent trend toward the fortification of farmed fish produce with supplemental nutrients for the benefit of consumers prior to harvesting, including long-chain omega-3 polyunsaturated fatty acids and essential trace minerals.

Finally, particular emphasis was given to the fact that aquatic food products represent one of the world's most nutritious and healthy food sources. Thus, according to the FAO/WHO Joint Expert Consultation on the risks and benefits of fish consumption, there is convincing evidence that: 1) fish consumption reduces the risk of death from

coronary heart disease and that fish consumption by women reduces the risk of sub-optimal neurodevelopment in their offspring; 2) fish consumption may reduce the risk of multiple other adverse health outcomes, including ischaemic stroke, non-fatal coronary heart disease events, congestive heart failure, atrial fibrillation, cognitive decline, depression, anxiety and inflammatory diseases, and 3) fish consumption may provide a greater nutritional impact than the sum of the health benefits of the individual nutrients consumed separately.

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3.3 Investing in biotechnology solutions through capacity development and partnerships

3.3.1 Biosciences capacity building in Africa: lessons learned from the Biosciences eastern and central Africa – International Livestock Research Institute (BecA-ILRI) Hub

Helen Altshul

Background

The need to harness biosciences-based innovations to capitalize on agriculture's potential underpinned the vision of the African Union/New Partnership for Africa's Development (AU/NEPAD) Africa Biosciences Initiative (ABI). The ABI aimed to create four regional biosciences "centers for excellence" across the continent:

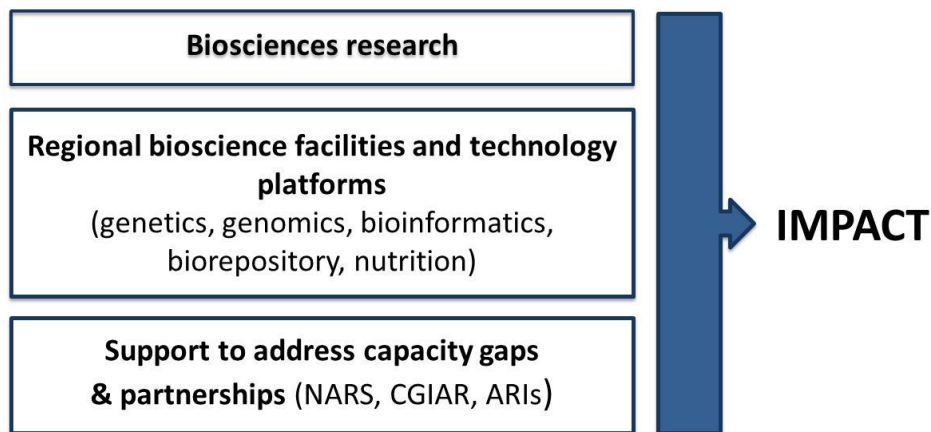
- NABNet (North African Biosciences Network) for Northern African countries;
- WABNet (West African Biosciences Network) for ECOWAS countries;
- SANBio (Southern African Network for Biosciences) for southern African countries;
- BecA-ILRI Hub for countries in eastern and central Africa - Burundi, Cameroon, Central African Republic, Congo Brazzaville, Democratic Republic of Congo, Equatorial Guinea, Eritrea, Ethiopia, Gabon, Kenya, Madagascar, Rwanda, Sao Tome and Principe, Somalia, South Sudan, Sudan, Tanzania, Uganda. The BecA-ILRI Hub was established in 2002 when ILRI agreed with NEPAD to host the Hub at its headquarters in Nairobi, Kenya due to its interest in supporting agricultural research in the region through facilitation of access to modern research infrastructure by scientists in Africa.

The need for the BecA-ILRI Hub

- Biosciences are one of the major engines of global growth not just in agriculture but also in human health, environmental conservation and industrial processes.
- Africa lags behind in biosciences due to low human capacity and limited facilities.
- The main driver of the BecA-ILRI Hub is to support and mentor African scientists in the application of biosciences in food security and agricultural development. The platform hosts and supports the work of scientists from African National Agricultural Research Systems (NARS), ILRI, other CGIAR centers and CGIAR Research Programs (CRPs), international institutions and the private sector.

Key program pillars

The BecA-ILRI Hub consists of a state of the art suite of shared biosciences platforms that make the best technologies available to the African (and international) scientific community to address national, regional and continental priorities.



The outputs of research, technologies and capacity building combine to achieve (developmental) impacts at the beneficiary level e.g. increased productivity or improved food safety. The BecA-ILRI Hub's vision is that by contributing to stronger national agricultural research systems, the livelihoods of millions of resource poor people in Africa will be improved through advances in agricultural bioscience.

Capacity building at the BecA-ILRI Hub

Capacity building is conducted via four streams.

1. Africa Biosciences Challenge Fund (ABCF) Research Fellowships, an essential driver of the BecA-ILRI Hub, which seeks to strengthen the capacity of individual scientists and NARS institutions to deliver on their national research mandates:
 - Research projects of 3-12 months;
 - African NARS-affiliated scientists;
 - Fit with BecA-ILRI Hub priority research themes:
 - Crop improvement;
 - Food safety and nutrition;
 - Livestock productivity;
 - Climate change mitigation;
 - Under-utilized crop/animal species.
 - Training workshops:
 - Introductory molecular biology and bioinformatics;
 - Introductory lab management and equipment operations;
 - Advanced genomics and bioinformatics;
 - Scientific research paper writing;
 - Animal quantitative genetics and genomics.
 - Institutional capacity strengthening:
 - Technical assistance with lab design/management, equipment installation and procurement, training of engineers and lab technicians;
 - Support with resource mobilization;
 - Connections to networks e.g. suppliers of reagents and lab equipment;
 - Customized training workshops at NARS institutions;
 - Brokering partnerships for research, training and resource mobilization.

- Mobilizing capacities for joint action:
 - Joint NARS actions for multi-country/multi-disciplinary research.

Capacity building achievements

- Increased awareness of BecA-ILRI Hub;
- Regional impact of the ABCF on the NARS;
- >15 research papers published and >40 in preparation;
- Informing private sector, policy and local government;
- ABCF contribution to downstream impact;
- Strong endorsement of the ABCF Fellowship scheme by stakeholders - Evaluation in 2014 found 96% of stakeholders believe that the BecA-ILRI Hub builds the capacity of individuals and institutions to harness the latest bioscience technologies to improve agriculture in Africa;
- 4 Communities of Practice at nascent stages - chicken genetics (4 countries); fish genetics (3 countries); striga resistance (4 countries); taro improvement 4 countries).

Strategic partnerships

Through strategic collaborations with international advanced research institutions, the BecA-ILRI Hub has set the stage for African sub-regional organizations, universities and research institutions to benefit from relevant high-end basic research.

Challenges

- High demand for fellowships and training courses;
- Diversity of African research and capacity building landscape - some NARS are well resourced and others are less so. This has led to a decision to focus for the next few years up to 2018 on engaging NARS in what the BecA-ILRI Hub calls “Stage Two” countries (where we have made substantial investments, matched by investments from NARS): Burkina Faso, Cameroon, Ethiopia, Ghana, Kenya, Rwanda, Senegal, Tanzania and Uganda;
- Few applications from some countries;
- Few applications from women scientists;
- Limited investment by African governments.

Lessons learned

- Mentorship is a key cross-cutting mechanism in the capacity building process;
- A strictly competitive process for ABCF Fellowships may not achieve strategic objectives;
- Need to engage National Councils for Science and Technology to provide return-to-home institution grants;
- Need to encourage NARS to provide increased co-funding of lab users and ABCF Fellows;
- Collaboration with other capacity building programs helps to magnify impacts e.g. AWARD (African Women in Agricultural Research and Development) & IFS (International Foundation for Science).

Way forward

The development of an African-led R&D agenda that responds to market drivers and supports the transformation of agriculture as a driver of economic growth in the countries of Africa is being articulated

by the African Union and its partners, including AU/NEPAD, Forum for Agricultural Research in Africa (FARA) and other Pan African, regional and national bodies, in the public and private sectors. Being aware of and responding to new priorities and new opportunities will keep the BecA-ILRI Hub relevant as well as responsive to the emergence of agriculture as a profitable enterprise in growing African economies.

The BecA-ILRI Hub faculty will be expanded to include as adjunct appointees more senior bio-scientists working with African NARS and universities as well as those with advanced research institutes and international research institutes. This expanded faculty will enable a broader and deeper range of capacity strengthening programs to be conducted at the BecA-ILRI Hub and a larger number of young African scientists to be mentored in their research by more experienced African and international scientists.

Ensuring the availability of “state of the art” technology platforms, across a wide range of modern biotechnologies is an important part of the BecA-ILRI Hub’s role as a shared research platform that is a “center for excellence” for biosciences in Africa. These technology platforms serve multiple partners and research consortia that are addressing African agricultural issues. As bioscience is a rapidly evolving field, these technology platforms will need to be continually updated to stay relevant.

The BecA-ILRI Hub is accessible but not always affordable for some scientists working in national research institutes and universities across Africa. Restricted core support from international investors will be needed to underwrite some of the fixed and capital costs. Mobilizing additional financial resources will also be required to fund more ABCF fellowships for African scientists. Affordability can also be increased by forming new partnerships with African governments and regional bodies, such as Association for Strengthening Agricultural Research in Eastern and Central Africa (ASARECA); Conseil Ouest et Centre Africain pour la Recherche et le Développement Agricoles/ West and Central African Council for Agricultural Research and Development (CORAF/WECARD); and Regional Universities Forum for Capacity Building in Agriculture (RUFORUM), to support tailored capacity strengthening programs for particular countries/regions.

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3.3.2 Case studies of public-private partnerships in agricultural biotechnologies: Lessons learned

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Introduction

Public-private partnerships (PPPs) have played vital roles in much of the progress of modern agriculture, from the creation and dissemination of hybrid maize in the early 20th century to the Green Revolution of the 1960s and beyond. However, during most of the 20th century, much of the leadership in organization and innovation in agricultural systems in industrialized countries was provided by powerful public bodies, such as the USDA and land-grant universities in the USA. This public sector dominance was much reduced after the 1980s as many state entities were privatized and/or suffered funding reductions. The process coincided with the growth of a dynamic, increasingly globalized agbiotech sector, originally based on agrochemical companies that diversified into bio-based areas including crop breeding and livestock management. As we move through the 21st century, future innovations and their implementation will require ever closer partnerships (i.e. PPPs) between public entities (including state organizations, research institutes, universities, extension bodies etc) and an increasingly diverse private sector that includes multinationals, SMEs, NGOs, citizen groups, retailers, small farmers etc.

Such PPPs are especially important in enabling smallholders to contribute to the nature and implementation of modern biotech-derived crops, most of which have hitherto addressed the needs of larger commercial farmers and agribusiness interests. These PPPs tend to be highly dynamic as the nature of the various partners constantly changes, the technologies advance, and fresh challenges arise, such as climatic change and (possibly related) newly emerging threats including pests and diseases. Because PPPs involve so many players and can occur at all scales from single farmers to globe-spanning international partnerships, it is difficult to describe them fully in such a brief presentation. Instead, three selected PPP examples relating to smallholders will be described in some detail in order to derive some lessons for future policymaking.

Case studies

1. Brinjal in Bangladesh: breaking the impasse on GM crop acceptance?

While there have been several examples of widespread smallholder adoption of GM cash crops, most notably Bt cotton, several promising subsistence GM crop candidates have faced lengthy delays. However, in 2013 Bangladesh approved Bt brinjal/eggplant for planting after a rapid approval process. In 2014 commercialization was initiated via a PPP when a total of 120 farmers planted 12 hectares. This followed strong political support from the government, with leadership from Ministry of Agriculture, and close collaboration with farmer groups and private sector breeders. This approval by Bangladesh is important in that it has broken the impasse experienced in trying to gain approval for commercialization of Bt brinjal that blocked its introduction in India and the Philippines. It also serves as a possible model for other small poor countries.

Two other developing countries in Asia, Vietnam and Indonesia, also approved cultivation of GM crops in 2014 for commercialization in 2015. Vietnam approved Bt maize and Indonesia approved a drought tolerant sugarcane for food, whilst approval for feed is pending; 50 hectares of sugarcane were planted in 2014 for planned commercialization in 2015. In 2014, it is estimated that approximately 18 million farmers grew GM crops, about 90%, or 16.5 million, were small farmers in developing countries. In addition to economic gains, farmers benefited enormously from at least a 50% reduction in the number of insecticide applications, thereby reducing farmer exposure to insecticides, and importantly contributed to a more sustainable environment and better quality of life. All of these GM crops were introduced via PPPs.

2. EMBRAPA in Brazil: PPP-led GM crop development

EMBRAPA is the major public agricultural R&D organization in Brazil with an annual budget of US\$1 billion and has been especially active in fostering PPPs in ag-biotech. EMBRAPA is one of the few public bodies to have developed and commercialized GM crops that are grown by farmers ranging from smallholders to large international combines. In 2014, Brazil commercially planted GM soybeans with insect resistance and herbicide tolerance on 5.2 million hectares, up substantially from 2.2 million hectares in 2013. In 2015, EMBRAPA gained approval to commercialize its GM virus resistant bean, planned for 2016, plus a novel herbicide tolerant soybean, which it developed via a PPP with BASF (this variety is currently awaiting EU import approval prior to planned commercialization in 2016). EMBRAPA is also developing GM folate-fortified lettuce and drought resistant sugarcane. EMBRAPA is an example of a large state enterprise that has taken the lead in innovative biotech crop development with PPP engagement, which has been primarily commercially focused but with increasing trickle-down to smallholders.

3. Emergence of ag-biotech PPPs in Africa

Over the past decade there has been a range of PPP ventures in Africa that have focused on both GM and non-GM crops aimed at smallholders. For example, Cameroon, Egypt, Ghana, Kenya, Malawi, Nigeria, and Uganda have conducted field trials on the following broad range of staple and orphan crops: rice, maize, wheat, sorghum, bananas, cassava, and sweet potato. The Water Efficient Maize for Africa (WEMA) is a major PPP that is expected to deliver its first GM drought tolerant maize with Bt insect resistance in South Africa as early as 2017, followed by Kenya and Uganda, and then by Mozambique and Tanzania, subject to regulatory approval. Over the past two years there has been a distinct improvement in state engagement with biotech related PPPs in much of Africa.

Future lessons

The major lessons from recent PPP experiences are that success is dependent on a full commitment by host countries, appropriate regulatory systems, and the sustained participation of all partners, especially smallholders, over the entire duration of what can be complex and long term ventures. Such lessons are especially important given recent developments in ag-biotech. During the last few years, and especially in 2015, there has been a veritable revolution in genetic technologies with the development of gene editing methods such as CRISPR and TALENs. In terms of crop breeding, this means that it will soon be possible to progress from the random insertion of single or small numbers of genes into a genome (as in traditional GM) to the highly precise insertion into a defined location of large numbers of genes, chromosome segments or pseudo-segments encoding entire metabolic pathways into virtually any plant species.

These new technologies will make current GM methods (and their regulation) obsolete and there are already calls that organisms altered by gene editing should not be characterized as GMOs. Gene editing can considerably widen the range of traits (especially smallholder relevant traits in hitherto orphan crops) to be altered much more rapidly and cheaply than was hitherto possible. This provides a golden opportunity for the emergence of a new generation of PPPs aimed specifically at improving smallholder agriculture as we face up to increasing food security challenges across the world.

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3.3.3 Building Partnerships, Empowering Champions: The Case of the Cornell Alliance for Science

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We face a global challenge of ensuring access to safe, nutritious food for an unprecedented population, while simultaneously seeking to minimize agriculture's negative impact on the environment. Innovations in the field, such as the tools of genetic engineering, should help us address this challenge.

Many promising products generated using the tools of genetic engineering are in the late stages of development and testing. Public sector institutions, including universities and national agricultural research programs, have played an important role in the development of these products. In many cases, scientists in the developing world not only lead these projects, but their farmers are the intended beneficiaries. In order for these products to reach their intended beneficiaries and to have impact on increasing access to a safe, sustainably produced food supply in the face of an increasingly erratic climate, the proper enabling environment must be established.

Private foundations have demonstrated their willingness to make higher-risk investments to ensure these technologies do not bypass the poor. The Bill & Melinda Gates Foundation has invested across diverse areas of the biotechnology ecosystem to ensure its impact, making significant investments in the research and the development of products that will address the biotic and abiotic constraints that some of the world's most vulnerable farmers face. In addition, they have invested in programs to help foster an effective regulatory environment. The Gates Foundation invests in capacity building to address the dearth of voices in the community that can help lead the debates around agricultural biotechnology and help to bring a rational, evidence-based voice to the global conversation around it. The Cornell Alliance for Science is one such initiative.

Founded in 2014 with a grant from the Foundation, the "Alliance" is addressing this challenge by building an international network of concerned scientists, farmers, and humanitarian organizations working to restore the place of science in food policy decisions. The organization works to ensure that scientists have access to the tools they need to innovate for the grand environmental and food security challenges we face today; the organization also works to give voice to farmers—regardless of where they live—who need access to the advances of science to help them provide the world with a safe, stable, and environmentally sustainable food supply.

Hunger, poverty, malnutrition, and sustainable agricultural growth problems impact less developed countries more than others. Solutions such as biotechnology are often inaccessible to those who need them most. In the global biotechnology discussion, opponent activists continue to spread misinformation, obstructing the voices of those who would benefit most. Stakeholders around the world now must face the ambitious task of fostering constructive public dialogue and policy that employs biotechnology as a tool to help solve global challenges.

Recognizing this, the Alliance has three primary objectives:

Our first goal is to build a globally coordinated alliance of individuals and organizations who share our mission of promoting access to scientific innovation as a means of enhancing food security, improving environmental sustainability, and raising the quality of life globally.

We believe that as a coordinated community, this global alliance will have a much stronger voice for science that can favorably shift the global conversation around biotechnology. We want to serve as a platform where individuals and organizations can lend their voices to advocate for science-based decision-making and encourage

global coordination of a proactive pro-science community. Just over a year into our initiative, we have engaged over 6200 Science Allies in 109 countries.

It is our hope that we can engage not only “likely” allies who already cohabit our shared “echo chamber,” but also the “unlikely allies.” These are the people who share our core values around access to safe, sustainably produced, and nutritious food, but who maintain a healthy skepticism of the technology.

Our second goal (and the focus of the oral presentation) is to strengthen the global network we are building through innovative training programs in forward leaning, strategic communications. The Alliance uses a people-focused, metrics-driven approach to train and support knowledgeable, empowered champions to build effective communications strategies in their own country contexts.

We host two types of training programs: The Global Leadership Fellows Program, a twelve week, Cornell University certificate program designed to equip and empower emerging leaders who will advance our shared mission for a more enabling environment for the adoption of biotechnology globally. The twelve week program, held August through November on the Cornell University campus in Ithaca, NY, combines modules on strategic planning and grassroots organizing, training on digital and traditional communications tools, exposure to global thought leaders, weekly colloquia, and field trips. Through this program we host and build the capacity of 25 Fellows from approximately seven to ten countries.

Additionally, in a series of week-long “short courses” held regionally around the world, we work with the Global Leadership Fellows to strengthen their networks through courses in strategic communications planning and grassroots organizing.

Global Leadership Fellows come from diverse backgrounds — from communications specialists working at National Agriculture Research programs, to organizers at NGOs, religious leaders, scientists and others. Upon completion of the program the Fellows are members of a growing collaborative international cohort of forward-leaning communicators uniquely equipped to promote evidence-based decision making around global issues such as food security, environmental sustainability, and agricultural growth and to ensure that the tools of science—tools like biotechnology—do not bypass the poor.

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3.3.4 North-south/west-east cooperation in agricultural biotechnologies:

Some lessons from Italy and China in buffalo

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Summary

A case of applied solutions through capacity development and partnerships will be illustrated in the sector of buffalo production between Italy and China. The operative steps in the process of capacity development and the accomplishments in terms of partnership will be illustrated. These steps will be focused on existing difficulties and possible solutions in the buffalo breeding sector of mutual interest for both countries through complementary use of different biotechnologies. The set of operational steps could also be fitted to buffalo improvement programs in different countries of the Southeast Asian region.

Buffalo in the world:

The world buffalo population is estimated to amount to be about 195 million, spread over more than 40 countries. 189.79 million (97.2%) buffaloes are in Asia (FAO, 2011) where India has 112.9 million (approximately 57.8% of the total world buffalo population), followed by Pakistan (16.2%) and China (12%). Buffaloes provide more than 10% of the world milk supply; their milk has a higher fat, lactose, and protein content than cow milk. In the domestic water buffalo (*Bubalus bubalis*), we find two subspecies, fertile inter se: the river buffalo which is the predominant type in India, West Asia, America and Europe and the swamp buffalo which is found more frequently in Southeast Asia and China. The two subspecies differ in morphology, behaviour, and chromosome number. In fact the river buffalo has $2n=50$ chromosomes and the swamp buffalo has $2n=48$ chromosomes.

River buffalo:

The population of river buffalo is estimated to amount about 158 million animals. River buffalo breeds have become mainly dairy animals and among those Mediterranean, Murrah, and Nili-Ravi are the most productive breeds for milk yield. The Italian Mediterranean breed undergoes a well-established recording system, supporting since the early 90's an official breeding program for the genetic improvement of dairy traits. The Italian Mediterranean buffalo breed is a small population compared to Asian buffalo populations, representing 0.19% only of the world buffalo population. However it is the largest "active population" in the world. In fact about 54,000 Mediterranean buffaloes in more than 300 herds are currently recorded in Italy. This recorded population is used to run a national genetic improvement program allowing progeny testing of at least 5 young bulls every year. Currently more than 20 proven bulls are producing semen for freezing in Italy. The Murrah buffalo is mainly found in Indian sub-continent. Murrah has widely spread to other parts of Asia and in the world and it has been broadly used as an improver breed. The population size is over 6 million (FAO, 2005). The Nili-Ravi buffalo is mainly farmed in Pakistan, however it is also present in India. The population size is of about 6.5 million (FAO, 2005). The three dairy river buffalo breeds present differences in dairy performance. Currently the Italian Mediterranean breed shows the highest milk yield production per day compared to Murrah and Nili-Ravi breeds. Additional important traits to be compared are: body weight, age at first calving and calving interval. For all these traits the Mediterranean breed has the most suitable phenotypic values for a dairy buffalo type. In particular it is important to underline the smaller body size of the Mediterranean breed, about 20% and 10% smaller than Murrah and Nili-Ravi, respectively. That means that Mediterranean buffaloes need less energy for body maintenance.

Swamp buffalo:

The population of swamp buffalo is estimated to amount about 37.16 million, representing 19% of the world total population (FAO, 2011). The history of swamp buffaloes is rooted in the traditional agriculture based on small

holdings, in fact they play a major role in the practices and economic income of small farmers. These buffaloes are easy to raise, the costs involved in raising them are low, and they can make full use of low quality local forage. They may be used for the cultivation of crops and for rice field preparation, and their dung is used as soil fertilizer so reducing expenditure on chemical fertilizer and preserving the environment. Swamp buffaloes are smaller than water buffaloes and they are very poor in milk production, the average milk yield ranges from 1.0 to 1.5 kg per head per day over 270 to 305 days lactation.

Buffalo breeding and greenhouse gas (GHG) mitigation:

Methane (CH₄) emission from enteric fermentation is a major source of agricultural GHG emissions. Enteric fermentation from ruminants is the largest single source of CH₄ total emissions. The world buffalo population of 195 million significantly contributes to such CH₄ emissions. It is well known that the following actions can mitigate the total GHG emissions from ruminants per unit of milk and/or meat produced: a) increasing productive and improving reproductive traits in a given population and b) improving feeding strategies in a given herd. Both of these goals could be achieved by suitable buffalo breeding and buffalo herd management programs. Increasing the efficiency of production can reduce the total number of animals needed to produce a fixed level of output. In the world buffalo population room exists for such improvement and modern genetic improvement technologies should be more largely adopted.

Use of biotechnologies to improve buffalo milk production in China:

In China 23 million swamp buffalo are farmed and about 1 million swamp buffalo have been mostly crossed with Murrah and Nili Ravi river buffalo to produce milk. Cross breeding has improved milk production in first generation but, in the long term, crossing alone will not improve milk yield in the Chinese buffalo population. CREA has proposed a 5-year project based on three applied biotechnologies: a) using artificial insemination (AI) to replace a subpopulation of the swamp crosses with Mediterranean buffalo; b) using genotyping technology to improve milk and meat production traits and to reduce methane emissions from buffalo population and c) establishing nucleus herds of Mediterranean buffalo of higher production level and optimized management.

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3.3.5 South-South Collaborations in Agricultural Biotechnology: Lessons Learned

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South-South Collaboration (SSC) is an important mechanism in technology development, transfer and diffusion. Thanks to the support of the respective governments, with massive investments in R&D, many developing nations have developed home grown technologies in agricultural biotechnology. They may range from tissue culture to development of GMOs and gene stacking.

A study by Research and Information System for Developing Countries (RIS) on biotechnology capacity in the Asia-Pacific region showed that while many countries remained in the low ends of agricultural biotechnologies, some have moved rapidly to high end technology. The picture in Africa and Latin America is no different. In Africa agricultural biotechnology has taken roots in few countries such as South Africa while in many countries it is in initial stages. Similarly in Latin America while countries like Argentina, Brazil and Mexico have applied this technology rapidly, despite controversies, in many countries it is in the initial stages. Another important concern in agricultural biotechnologies is that of biosafety and many developing nations have ratified Cartagena Protocol on Biosafety. In fact countries with very limited activities in agricultural biotechnologies have ratified the Protocol and hence are bound by it.

For effective utilization of agricultural biotechnology, it is essential that the countries have a functional innovation system in the agricultural sector. This is important for technology adoption and further development of agricultural biotechnology.

Work by RIS has resulted in a paper examining three case studies where South-South Cooperation has helped move upward on the trajectory. The areas captured are of (1) Cooperation for Capacity Building in Biosafety Management (2) India-Bangladesh Cooperation for Bt Brinjal and (3) Cooperation for Primary Biotechnology. The paper concludes that in the long run SSC in agricultural biotechnology should be based on an integrated approach that includes product development along with capacity building. The groupings like IBSA and BRICS can play an important role as they can engage in SSC as a group complementing each other's strengths. As the countries in these groups have the capacity to develop GM and non GM boutique of technologies in agricultural biotechnology, they can jointly promote SSC projects in this field.

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