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# Chapter 3

## Parallel sessions: Climate change





## 3.1 Report of outcomes from the three parallel sessions dedicated to the theme of climate change

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Among the challenges faced by food systems is that we have only one planet and we see the limits of it. There is a nutritional shock now: there are more obese than undernourished people in the world. Climate deregulation and the loss of references for climate is another challenge. The agricultural and food systems are a victim of this problem and they have to adapt. Among other factors, they have to adapt to heat tolerance, drought tolerance, flooding and to the emergence of new pests and diseases out of their original range.

We had very interesting reports about adaptation, and the role that agricultural biotechnologies can play there during the first two parallel sessions of this theme. These included use of genomic technologies to characterize wild relatives of chickpea to develop climate-resilient varieties in Ethiopia and India. Other speakers described how biotechnologies have been used, *inter alia*, to improve drought tolerance and flooding tolerance in rice as well as drought tolerance and pest resistance in maize. Presentations also covered forest trees, including how biotechnologies can be used to help them to adapt to the changing climatic conditions that the trees are likely to experience in their long lifetimes.

Aquatic animal and livestock systems also need to adapt to face the challenges of climate change. For aquatic animals, presentations showed how climate change will affect farmed fish populations and that selective breeding can be an important tool enabling them to adapt. Biotechnologies currently play an important role in diagnosis and prevention of aquatic animal diseases. Similarly in livestock, vaccines were shown to be essential tools for disease prevention. Presentations also described the role of biotechnologies in breeding animal populations that are better adapted to climate change; in understanding the genetic basis of adaptation in goats; and in producing better livestock feeds.

However, food systems also contribute to climate change. They have to mitigate those impacts, a topic that was covered in some presentations in the third parallel session held this morning. The three main greenhouse gases produced by food systems are nitrous oxide, methane and carbon dioxide. Regarding the first one, we had a talk about biological nitrification inhibition in plants to increase nitrogen use efficiency and reduce nitrous oxide emissions.

We had a very interesting talk about the types of technologies that can be used to reduce the production of enteric methane by ruminants when they digest what humans cannot digest themselves. Regarding

carbon dioxide, mostly related to deforestation and afforestation, we had a talk highlighting the importance of biodiversity in forest systems.

Beyond mitigation, agricultural and forest soils can also sequester carbon dioxide. This is an ecosystem service that agriculture can provide to mankind and we had a very stimulating talk this morning about the “4 per mil” initiative regarding how carbon sequestration by soils can at the same time increase their quality and thus food security, and mitigate greenhouse gas accumulation and thus climate change.

So, altogether, climate change is a global issue – that is what came out of these different talks. It is a global issue that must be addressed in a cross-cutting manner using all different approaches, including technological, and all different actors and must be addressed locally. A global challenge addressed locally – that is difficult! The difficulty is that we do not know the final plateau so the target is unknown – what is the climate going to be like in 50 years or so? That is one of the big issues, although we did not address it in these parallel sessions. But, we had a presentation with an economic view this morning about the equilibrium between poorer and richer areas of the globe and the importance of innovation in agriculture. End users innovate a lot and that is also the case in agriculture.

Local knowledge is very useful, and this was shown in a presentation on breeding durum wheat in Ethiopia in the third parallel session. But, when dealing with climate change, it is not always completely suited because the climate *changes* and so it is difficult to address the change with local solutions because these have been optimized for the previous situation. For instance, that is the case of chickpea. We had a talk about going back to the areas of domestication and diversification of this crop to look for more diversity etc., to address problems that the modern varieties cannot address completely now.

Another problem, especially for mitigation, is that there is no direct gain for the farmer. The fact that agriculture might make a smaller contribution to climate change is an indirect gain. It is very strong but it is long-term and indirect. There may be even a cost for the farmer. There may be a gain in some practices, such as biological nitrification inhibition, for instance, described this morning. But it is an issue that those who act are not those who benefit immediately at least. However, we heard this morning about an interesting experience in Mali where about 20 technologies related to climate change had been identified through a participatory approach and where the support of international partners could be important in applying them for the benefit of smallholders.

Agricultural biotechnology is much broader than just genetically modified organisms (GMOs). There is a lot of innovation going on. There is a lot of innovation that is on the shelf. We have to take it and put it together to address the issues. These innovations regard artificial insemination and reproductive technologies, marker-assisted breeding, fermentation and probably genome editing. We did not talk about genome editing in these parallel sessions, but it is probably very, very useful.

So, to conclude, I think the most striking point is, and there is quite a consensus, that we should not approach the problem one-by-one but in a cross-cutting manner. Probably FAO could organize this because of the breadth of its partnerships – from many different countries, fields and specialities.



FAO probably has to tackle this challenge of climate change in a silo-breaking manner somehow. Maybe having a climate change champion or something similar. Because it is very obvious that big challenges are more and more inter-connected with each other. For instance, the inter-connection between agricultural biotechnologies and agroecology is an obvious one.

### 3.2.1 **Report of the parallel session**

## **Facing the challenges of climate change: Adaptation in the crop and forestry sectors<sup>4</sup>**

Chittaranjan Kole, one of the two ‘theme leaders’ for climate change, chaired the session. He welcomed the participants and provided background information on the theme and its three parallel sessions. He also explained the objective of the session and introduced the scope of the five presentations.

Abdelbagi Ismail (International Rice Research Institute, IRRI) presented four case studies on developing rice varieties with enhanced adaptation to lowland farming systems of South Asia. The case studies addressed the following problems: 1) increasing use of direct seeding in rice production systems; 2) complete flooding (submergence); 3) drought; and 4) salinity in tropical coastal deltas. He explained that few rice accessions tolerate anaerobic conditions during germination. These accessions were identified, and molecular and physiological mechanisms associated with the tolerance were studied. Breeding lines for direct seeding tolerating anaerobic conditions have now been developed and are being evaluated at various locations in Asia. Regarding the submergence problem, the discovery of the *SUB1* quantitative trait locus (QTL) in the mid-1990s was an important turning point for breeding. *SUB1* confers tolerance of complete submergence for 10 to 18 days. Subsequently, numerous *Sub1* varieties have been developed and commercialized in several countries. He continued by noting that several drought tolerant rice accessions have been identified and crossed with high-yielding but drought-sensitive varieties. In the case of salinity, numerous tolerant accessions have also been identified over the past decades and used extensively in breeding salinity-tolerant varieties.

Yoseph Beyene (International Maize and Wheat Improvement Center, CIMMYT) presented some results of the water efficient maize for Africa (WEMA) project. He pointed out that average maize yield is low, 1.8 tonnes per hectare in sub-Saharan Africa as compared with the global average yield (4.5 tonnes/ha). Advanced conventional breeding techniques have been used to generate new high-yielding hybrids with 25 percent higher yield as compared with earlier hybrids developed in 2008. A total of 59 drought tolerant maize hybrids have been developed and recommended for commercialization in four WEMA countries (Kenya, Uganda, United Republic of Tanzania and South Africa). The project has also carried out molecular breeding which has provided two to three times higher grain yield than conventional breeding. Furthermore, the project has used transgenic approaches and tested *Bacillus thuringiensis* (Bt) maize hybrids in controlling the spotted stem borer (*Chilo partellus*) in the field and the African stem borer (*Busseola fusca*) in the laboratory with significant results.

Douglas Cook (University of California Davis) presented the work done on mapping the wild relatives of chickpea and how their germplasm could be used for breeding of climate-resilient crop varieties.

<sup>4</sup> This report was prepared by the FAO rapporteurs for the climate change theme - Jarkko Koskela, Paul Boettcher and Melba Reantoso.



A large collection of wild *Cicer* species from a representative range of natural environments has been built for characterization. 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*. A large programme of genetic crossing is being used to introduce wild genetic diversity into phenology-normalized backgrounds. The base populations involve 20 diverse wild donor accessions crossed into five cultivated elite varieties.

Ciro De Pace (University of Tuscia) provided a review of genomic approaches used for dissecting fitness traits in forest tree landscapes. He pointed out that forest ecosystems, harbouring up to 90 percent of the world's terrestrial biodiversity, continue to disappear due to deforestation and forest degradation. Climate change is altering temperature regimes, rainfall patterns, and the life cycles of pathogens that have co-evolved with forest tree hosts. To conserve forest biodiversity services and resilience in the rapidly changing world, it is necessary to understand how ecological assemblages in forest landscapes have been formed and how they respond to novel environmental conditions. He then explained how forest landscapes can be described based on 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, geo-climatic variation, and ecological processes (landscape ecology).

Sally Aitken (University of British Columbia) made a presentation on using genomics to understand and manage adaptation to climate change in forest trees. The AdapTree project in western Canada has used phenotype-environment associations, genotype-environment association and genome-wide association studies to assess climate adaptation in two economically and ecologically important conifers, lodgepole pine (*Pinus contorta*) and interior spruce (*Picea glauca*, *P. engelmannii* and their natural hybrids). Approximately one million single nucleotide polymorphisms (SNPs) were genotyped for around 23 000 genes, as well as non-coding regions, for trees from hundreds of populations in each species. Genotype-environment association analysis identified hundreds of SNPs in each species that were associated with climatic variables. The primary climatic drivers of local adaptation were low temperatures. These findings were supported by results from seedling common gardens. The 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.

After the presentations, there was a discussion moderated by the Chair. The first questions were related to the use of seawater and interaction between soil and environment in the rice production systems. It was clarified that currently rice can be irrigated with water that contains 25 percent of seawater and eventually the level of 50 percent may be possible but productivity is likely to be low. It was further explained that saline and alkaline soils create different challenges; salinity can diminish temporarily as a result of rains while alkalinity is a more permanent soil characteristic.

Concerning GMOs, it was asked whether the testing of GMOs should be done under a broader set of climatic conditions. Some noted that GMOs should be tested where they will be finally used. It was reminded that each country will ultimately make its own decisions concerning the regulation and



deployment of GMOs, and that a case-by-case approach is often the best one. It was further noted that cisgenics should also be considered as an approach for crop improvement.

It was noted that while much research has been done, it is not yet clear how much biotechnology has increased the yields of rice and maize in the hands of the farmers. It was also stressed that dissemination of technologies and germplasm for farmers is crucial for making the impact happen in the field. The speakers recognized that the impacts need to be better documented and noted that there are successful examples of deploying improved germplasm to farmers. IRRI, for example, collaborates with over 650 seed companies and non-governmental organizations (NGOs) through which the improved rice varieties have reached ten million farmers.

Some participants commented that agricultural development since the 1960s had destabilized production systems and caused erosion of genetic diversity. Several speakers emphasized that genetic diversity is used for breeding and that progress is being made. They also responded that the alleged destabilization of production systems is not true and that it is only a perception. Many speakers also stressed that it is necessary to use biotechnology as the global challenge is to feed nine billion people. It was further noted that continued research efforts are needed as the performance of crop varieties fades away over time and new pathogens and insects will always emerge.

During the discussions, it was mentioned that 2016 is the International Year of Pulses. There are some 20 000 accessions of pulses stored in different gene banks but it is unclear how many of these have been evaluated. It was noted that there is considerable duplication of the same germplasm in the gene banks so the amount of diversity is actually not that high in these collections. Furthermore, breeding programmes are often based on relatively few accessions.

The Chair concluded the session by thanking the other 'theme leader' Olivier Le Gall, the FAO officers, the three rapporteurs as well as the speakers and the participants for a lively discussion and sharing of their thoughts and experiences.



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

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The ever-increasing global demand for food makes it necessary to produce more rice from less favourable areas. These areas, however, have low productivity because of the 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 and to help meet the increasing demands for food, to combat poverty and secure sufficient food supplies.

Early floods can lead to poor crop establishment, especially in areas where direct seeding (DS) is practised. Farmers are increasingly adopting DS as the preferred method in both rainfed and irrigated rice ecosystems because of labour scarcity and reduced 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 DS in both irrigated and rainfed areas. A few rice accessions that tolerate anaerobic conditions during germination were identified and used to study molecular and physiological mechanisms associated with tolerance. A few quantitative trait loci (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 have worsened over the 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 the mid-1990s and its subsequent cloning. *SUB1* confers tolerance of complete submergence for 7–18 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 tonnes/ha, depending on the duration and depth of submergence and floodwater conditions, but with similar yields in the absence of submergence. Numerous *Sub1* varieties were developed and commercialized formally in several countries. These varieties are spreading fast in Asia since the release of the first variety in India in 2009 and are 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 modern tolerant 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 basis of tolerance. Stagnant floods reduce survival and tillering and suppresses vegetative growth leading to lower grain yield and quality. Several breeding lines were developed and are being evaluated; and mapping populations are being analysed to identify QTLs associated with tolerance for use in breeding.

Drought reduces rice yield in over 23 million ha in South 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 released recently in South 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 showing effectiveness in several genetic backgrounds and in diverse upland and lowland environments, with yield advantages of 0.5–1.5 tonnes/ha over original varieties. The effectiveness of marker-assisted backcross 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 due to increasing storm incidences and sea level rise caused by global warming. The productivity of saline soils is low, with yields averaging below 1.5 tonnes/ha, but can be doubled when salt tolerant varieties are used. Numerous tolerant donors were identified over the past few decades and used extensively 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 *Saltol* on chromosome 1. This QTL was transferred recently into several popular varieties. Additional QTLs for tolerance at both seedling and reproductive stages are being targeted to combine them with *Saltol* for higher tolerance. Ultimately, we aim to combine alleles associated with tolerance of different abiotic stresses to provide more resilient varieties for less favourable areas in Asia and Africa, to help keep up with the increasing demands for rice and to cope with climate change adversities.



### 3.2.3 Harnessing agricultural biotechnology for resilience to climate change: A lesson from water efficient maize for Africa (WEMA) project

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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 percent of the food calories to more than 4.5 billion people in 94 developing countries. Compared with 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 tonnes per hectare compared with 2.5 tonnes/ha in the Philippines, 3.1 tonnes/ha in Mexico, and 3.9 tonnes/ha in Thailand. Although several factors, including low soil nitrogen, foliar diseases, insect pests and socio-economic factors, do contribute to this low production, drought has been cited as one of the major factors that frequently limits maize production in the SSA region.

To address the problem, the WEMA project was launched in 2008 with the objective of enhancing food security in SSA 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 AATF, CIMMYT, Monsanto and five national agricultural research systems (NARS) in Kenya, Mozambique, South Africa, Uganda and United Republic of Tanzania. It is supported by the Bill and Melinda Gates Foundation, the Howard G. Buffett Foundation, and the United States Agency for International Development (USAID) for ten 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, South Africa, Uganda and United Republic of Tanzania). 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 1 600 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: ten under MARS and eight under GS. MARS and GS provided up to four 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 percent 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 1 000 fixed lines developed through molecular breeding have been tested in multilocation 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 towards commercialization in SSA.

Combined analyses of confined field trials (CFTs) of transgenic drought tolerant (DT MON87460) maize data using 34 hybrids with the same base genetics and evaluated in three WEMA countries for three or more years, showed that five traited hybrids gave 8–14 percent 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 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 laboratory in maize in Kenya (CFT I – CFT III) and in Uganda (CFT II). For example, results of CFT II in Kenya showed that 75 percent of the hybrids evaluated had significantly greater yields ranging from 26 to 113 percent with the Bt trait than without the trait. Similarly, results of CFT II in Uganda showed that all the seven Bt maize



hybrids had significantly greater yields of 49–201 percent 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 United Republic of Tanzania will commence in 2016 as approval has been obtained for testing the transgenics in confined field trials. Field testing of stacked DT and Bt commenced in South Africa in 2015, and will commence in Kenya, Mozambique, and Uganda in 2016. Widely adapted inbreds have been converted to DT and Bt traits, and will be utilized to develop transgenic products.

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

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**B**reeding 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, Kenya, Malawi, Sudan and United Republic of Tanzania) and South Asia (India, Myanmar and Pakistan), and also of importance in advanced developing economies (Turkey), and developed countries (Australia, Canada and the United States of America). 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, modelling 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 USAID 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 percent 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 twenty-first 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/modelling of trait-marker associations in nested association mapping and bi-parental populations.

A large programme of genetic crossing is being used to introduce wild genetic diversity into phenology-normalized backgrounds. The base populations involve 20 diverse wild donor accessions crossed into five cultivated elite varieties. A collection of ~8 000 segregating lineages is being increased in the field for F<sub>3</sub> seed and early generation phenotyping. In parallel, we are pursuing a programme 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 micro-organisms. For example, legumes' unique advantage of symbiotic nitrogen fixation 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 trade-offs 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 programme 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.



## 3.2.5 Genomic approaches for dissecting fitness traits in forest tree landscapes

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Forests present a wide variability among living organisms and the ecological complexes of which they are a part. Approximately 30 percent of the Earth's land surface (four billion ha in 2015) is covered by forest landscapes (FAO, 2016). The bulk of that landscape (93 percent or 3.7 billion ha in 2015) is natural forest. Most natural forests are either naturally regenerated forest (65 percent) or primary forest (the remaining 35 percent) of native species and harbour 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 the indirect effects of human activities (Steffen *et al.*, 2011). The global emission of large quantities of carbon dioxide (CO<sub>2</sub>) and other gases with "greenhouse effects" 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 temperatures, rainfall patterns, and the life cycles of pathogens which 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 defences 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-favoured 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) to measure the fitness of individual genotypes, genetic diversity, and to understand 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, e.g. the simply inherited resistance to blister rust in *Pinus lambertiana* (Kinloch, Parks and Fowler, 1970). 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 1970s, 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 environments. 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], and 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 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 the reduced representation library of a tree genome using restriction enzymes and PCR amplification of the library of fragments, speeded up genome-wide SNP identification, fine mapping, and genotyping. SNPs are used primarily in genome-wide association mapping (GWAM), also known as linkage disequilibrium mapping, to overcome limitations of pedigree-based QTL mapping by taking advantage of both linkage disequilibrium and historical recombination present within the tree species gene pool. For example, in conifers, a QTL interval spans ~15 cM (Khan and Korban, 2012). 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 phenomenon known as serotiny. The intensity of the serotiny phenotype varied in accordance to the genotype at 11 QTLs identified by GWAM which explained 50 percent 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 predator interactions have 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 the United States of America, 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 scale provides resistance to crossbills spreading cone scales apart, and increased scale thickness evolved in response to crossbill predation.



Grey squirrels (*S. griseus*) have a selective impact on western ponderosa pine by preferring seeds from cones with a high ratio of seed mass to cone mass which tends also to be small. Selection exerted by grey squirrels favoured trees with large cones and a low ratio of seed mass to cone mass, and these are the traits that characterize cones in which grey 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, suggest significant roles for the spatial scale and genomics to quantify micro-evolutionary processes in natural forest landscapes. 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, geo-climatic 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 (Díaz *et al.*, 2016). The procedure applied to geographically scattered forest landscapes sharing a common set of congeneric tree species, promises the identification of those traits and species that have successful fitness features in forestry.

Second, increased discovery of candidate genes for fitness traits: The identification of polymorphic “functional traits” within species will help to dissect traits related to fitness. Genomics 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 favoured 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 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 (Conrad and Bonello, 2016). 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. Fourier transform infrared 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. novo-ulmi*; *Quercus suber* 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 increase sharply in frequency. This prediction can be tested by determining the linkage disequilibrium decay for polymorphic SNPs in genomic regions harbouring expression QTLs and structural genes associated with the resistance phenotype and its biomarkers.

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## 3.2.6 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 programmes.

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 to which tree populations are most closely adapted.

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 heatwaves, drought

events and freezing events, and phenotype-environment associations, 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 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 are 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 such as drought hardiness, then these 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 phenotype-environment associations, 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 ~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.



### 3.3.1 *Report of the parallel session*

## **Facing the challenges of climate change: Adaptation in the livestock and fishery sectors<sup>5</sup>**

#### **Summaries of the six presentations**

Panya Sae-Lim: Climate change in all its manifestations may affect all aquaculture systems. A number of opportunities include: improved locations and geographical area, prolonged growth period and consequently fish growth rate, breeding of new-farmed species and use of spatial planning. Two main challenges were described: 1) utilizing selective breeding (e.g. rainbow trout) for species best adapted to temperature changes induced by climate change; 2) outbreaks of fish pathogens and parasites facilitated by changes in water temperature. Three adaptive strategies proposed include: 1) selection for “robustness” in aquaculture; 2) use of genetically improved species; and 3) selective breeding.

Alexandra Adams: The presentation consisted of a brief narrative regarding climate change and aquaculture; development of diagnostics tests; and vaccine development. It concluded with some final thoughts on the potential development of novel rapid diagnostic tests for laboratory and field use. While many methods for vaccine development exist they are quite difficult for parasitic diseases. Thus it will not be possible to develop vaccines against all diseases. Some challenges include understanding mucosal immunity, high cost of final product and the route from research to commercialization which can be long and expensive. Thus, alternatives to vaccines also need to be considered so that antibiotic and chemical usage does not increase. Climate change will affect the movement and spread of diseases in the aquatic environment, thus the need for relevant and rapid tests and vaccines to be in place. Continued education and training are also important – some regions of the world do not currently have wide acceptance of the use of vaccines as a fish health control method.

Paul Boettcher: For smallholder livestock keepers, climate change could be a big challenge in the future. The use of best-adapted breeds will satisfy the increased consumption of livestock products. The use of biotechnologies should be complementary to traditional technologies. Through biotechnology, e.g. artificial insemination, the livestock keepers adapt their genetic resources quicker, and will require formal selection programmes in order to increase the rate of genetic change and adaptation. Other technologies which hold promise for the future, are genomic selection (e.g. multi-marker DNA assays) and genome editing or CRISPR which introduce beneficial gene variants into the gene pool; both will rely on reproductive biotechnologies.

Ulrich Meyer: Plants are the starting point for the whole human food chain. Plant breeding and crop production play important roles. Increased production of feed with improved quality may only to a small extent be based on further expansion of agriculturally productive land. Steady increase in

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<sup>5</sup> This report was prepared by the FAO rapporteurs for the climate change theme - Jarkko Koskela, Paul Boettcher and Melba Reantos.



productivity requires specialized knowledge and depends on numerous factors to improve production systems. In this regard, the use of agricultural biotechnologies in the future will contribute to improve feed availability and quality. There are available agricultural biotechnologies used by plant breeders for genetic improvement of plant varieties, including improving the nutrient content of edible plant parts, nitrogen and water efficiency and better pest resistance, providing feed plants with lower concentrations of anti-nutritive substances, low concentration of nutritive value-determining components such as amino acids, minerals, vitamins and vitamin precursors. Biotechnology can also improve feed quality through the use of different feed additives like amino acids, enzymes and silage additives through fermentation technologies.

Jean de Foucauld: The advantages and benefits of vaccination are more widely recognized and understood now especially when comparing the actual market cost which is usually less than 1 percent of the production cost. Development of vaccines should satisfy four basic parameters: quality, reproducibility, stability and adequate cost. Quality has two aspects: producing according to acceptable standards and manufacturing according to a process allowing expression of safety, efficacy and stability. Climate change, along with other factors, triggers new and fast-moving disease patterns against which vaccines can make the difference. New vaccine technologies using genetic engineering are now really mature and already saving billions of animals every year; new ideas are ready to be implemented but more effort is needed for some key unmet needs. Development, registration and production of vaccines can be managed only by very skilled teams/companies which are not so many in the world. Vaccine registration procedures and timing might be challenging on many occasions especially when new technologies are involved and needs are urgent. Accessing customers in some markets is sometimes very difficult and unfair market competition can happen when vaccine supply is tight. A better network of veterinarians, technicians and distributors, close to the final customers are needed in many countries.

Farai Catherine Muchadeyi: Landscape genomics combines 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 potential of landscape genomics in characterizing genetic adaptation of South African indigenous goats was investigated. Goats in South Africa represents an important resource for smallholder communal farmers. The country has a highly heterogeneous livestock production landscape ranging from wet and highly fertile to dry and desert-like agroecological zones. The study highlighted the level of genetic diversity in 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 programmes.

### **Session discussion points and conclusions**

Questions raised during this session included the following: benefits, costs, affordability and accessibility, and delivery of various biotechnologies to smallholder farmers.

Biotechnology should be seen as a common good for farmers, communities and societies. The potential benefits of biotechnology (e.g. increased production, long-term protection from disease, more efficient use of resources [feed, energy and land, including marginal agricultural zones], more

efficient farming systems, better adaptation to climate change), and long-term return of investment generally outweigh the initial cost of development.

The research and development stage may be lengthy and expensive (e.g. subunit vaccines, genomic vaccines) but the final products can often be made available for use by smallholders at a price they can afford.

Breeding programmes, for example, can start at a small scale and then gradually expand. Investments may vary depending on the end goal. It is clear that having good germplasm is not sufficient. Successful breeding programmes require continuous government support, long-term sustainability and private sector investment. An integrated value chain approach is needed supported by appropriate policies and regulations, along with consideration of production technology, good management practices, better feed, good sanitary and health services, access to markets etc.

Adoption of biotechnologies, especially by smallholder farmers, will be facilitated if they are seen as meeting the needs of farmers and if they build on traditional practices and indigenous knowledge. As biotechnologies are developed, good communication and knowledge sharing between farmers and researchers is essential. This can pave the way for changing farmers' perceptions, as through science farmers may better understand the resources they have and how they may be improved. At the same time, it is important for researchers to understand the context in which the farmers are working. This improved communication and mutual understanding will contribute to research more targeted to the needs of farmers and the quicker and more extensive adoption of the research results.

Climate change poses opportunities and challenges. Selective breeding, artificial insemination, fermentation technologies for animal nutrition, use of vaccines for long-term protection against disease and for minimizing antimicrobial usage, landscape genomics – all of these can help farmers be resilient and to better adapt to climate change, thus, improving yields for better food security for the human population.



### 3.3.2 Selective breeding in aquaculture for future environments under climate change

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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 percent to meet the future global demand for aquatic foods in 2020. According to Intergovernmental Panel on Climate Change (IPCC) and FAO reports, 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.

There are major *challenges* caused by climate change.

First, 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 (G x E) is a phenomenon by which animals respond differently to changes in environment. The presence of G x E 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 G x E in growth performance of rainbow trout in different temperatures has been reported; hence, utilization of selective breeding can be advantageous for breeding rainbow trout that are best adapted to the temperature changes induced by climate change.

Second, 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. 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 percent summer mortality due to elevated water temperature, leading to AU\$1.75 million loss of profit.

To cope with the above challenges, 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.

First, 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 prioritizing robustness. Nevertheless, knowledge of, and implementation of genetic adaptation to fish breeding is limited and has not received much attention.

Second, the limited adoption of breeding programmes in aquaculture (< 10 percent) 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 with 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.

Third, 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 is a method to quantify the use of resources and emission of pollutants in the entire production chain for a product. Selective breeding for increased production is expected to enhance efficiency of resource utilization (feed, energy and land) of a production system through correlated changes in feed efficiency or shorter production period. Applications of life cycle analysis to define breeding goals that maximize production while minimizing 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 minimize the detrimental effects of climate change on aquaculture. Empirical studies are required to estimate the potential for 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 applying 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.

### 3.3.3 Development of diagnostic tools and vaccines for aquatic animals

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#### **Introduction**

Currently, aquaculture contributes approximately 50 percent 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; having relevant rapid tests in place as well as appropriate vaccines to prevent the spread of disease is therefore 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 (tropical, subtropical and temperate) and different environments (freshwater, marine and brackish water) of the world where aquaculture is practised. Aquaculture is predominantly present in tropical and subtropical climatic regions with Asia accounting for more than 80 percent 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 influencing 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 five years the pace has increased even more, as methods developed for clinical and veterinary medicine are rapidly adapted and optimized. 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 provides a review of recent advances made in pathogen detection technologies, including antibody-based, nucleic acid and nanotechnologies, 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 has 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 are 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 vaccines that differentiate between infected and vaccinated animals (DIVA vaccines) for use in fish is also 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 for 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.



### 3.3.4 Biotechnologies for animal breeding and coping with climate change

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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 8 000 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, and 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 cross-breeding 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 is the use of cross-breeding 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 (2015) indicates clearly 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 analyse the 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. Cross-breeding 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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### 3.3.5 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 food production is the threatening or already existing impact 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 GHGs during cultivation are required. In addition, the plants should have low concentrations of undesirable substances and 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 bio-availability 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 covering 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 percent for the conversion of energy into beef. It may vary, however, up to about 40 percent 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.

Increased production of feed with 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 result from an increased productivity per unit of land and 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 specialized

knowledge and depends on a variety of factors to improve 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, 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 are usually characterized according to their composition. The most important feed groups are roughages, concentrates and co-products from agriculture, food and the 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 and 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 through the sustainable use of limited natural resources, the avoidance of environmental pollution including the reduction of GHG emission, and the adaption to climate change.



### 3.3.6 Development of livestock vaccines and market access

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To follow the development of the population in the world, healthy livestock breeding systems are needed, 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 are increasingly recognized and understood, especially when comparing them with their costs which are usually less than 1 percent of the total production costs.

The purpose of this presentation is not to detail the mechanisms through which 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, the focus is on the downstream processes that make this innovation a practical and available tool for the target customers. Taking a global perspective on vaccine solutions is necessary, particularly since countries and farmers have to keep adapting to the consequences of climate change. There are currently too many cases where the solutions exist in the laboratory but cannot be applied on time in the field. Hopefully, highlighting the key success factors allowing the field application of these technological advances will help to focus the effort of all stakeholders towards success.

Vaccine innovation in the laboratory has been extremely rich since the 1980s. This led to the arrival of vaccines using these new technologies since the twenty-first century with a few notable pioneers already present in the 1990s. Some of these vaccines aim at diseases impacted by climate change like West Nile virus infection and avian influenza. More are to come, based on innovative technologies already known like vector platforms and subunit antigens, but also on newer ones like non-replicative non-inactivated virus particles. Work on other diseases like trypanosomosis and other parasitic diseases is still ongoing and proving 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 into the livestock, there are many complex steps requiring highly experienced teams, from authorities to companies. And this is the reason why it takes in some instances so long for these solutions to access their target markets.

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<sup>6</sup> Speaking on behalf of HealthforAnimals (<http://healthforanimals.org/>)



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The first of these steps 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, industrialization and finally marketing of the vaccine.

The design of the production process of the candidate vaccine should be such that it can fulfil the main goals common to all veterinary vaccines: quality, safety, efficacy and adequate cost. Quality has two aspects: producing according to acceptable standards (good manufacturing practice [GMP], United States Department of Agriculture [USDA]); manufacturing according to a process allowing expression of the main safety, efficacy and stability features singled out during the feasibility phase.

Once pilot batches have been produced satisfactorily, they are then tested according to a “regulatory” analytical and clinical programme covering, amongst other points: validation of the planned manufacturing process, shelf-life study and clinical trials to confirm the safety and efficacy claims.

Marketing authorization: a registration dossier is then prepared by gathering the data from all this work, suitable for the target markets. It is sent to the target countries with additional documentation proving that the applicant works according to acceptable standards; it is also very common that authorities from the target countries require proof that the vaccine is registered in the country of origin. This is a cause of 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 “novel technology” vaccines involve live genetically engineered product, specific procedures are needed.



Once the registration dossier has been assessed, questions have been answered and the marketing authorization granted, we are far from the end. Meanwhile, the company undergoes the industrialization 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: this is driven by different aspects including: capacity of vaccine production, vaccine supply chain, competition between “easy and difficult” markets. In many markets where these vaccines are needed, although customers are ready to pay the right price for it, there are great difficulties to establish the adequate supply chain for reaching the final customers. Some key points to solve these issues include: more veterinary product retailers, better cold chains, more trained veterinarians and vaccination technicians, better vaccination equipment, fighting counterfeit products. A tight market supply situation will lead to unfair competition between “easier-to-access” markets and the ones where it is difficult to reach the customers.

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

In conclusion, the good news is that science has already brought and will bring more solutions to current and emerging diseases, including the ones affected by climate change. But very significant effort by all stakeholders should be placed on the complex industrial, regulatory and market access tasks.



### 3.3.7 The potential of landscape genomics approaches in characterizing genetic adaptation of indigenous goat genetic resources: A South African perspective

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In most developing countries, goats make 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 are, 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 landscapes and are adapted to the agroecological zones in which they occur. Local adaptation is driven by natural selection that targets specific genomic regions. Understanding 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 unravelled 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 characterizing genetic adaptation of South African indigenous goats has therefore been investigated.



South Africa has a highly heterogeneous 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 characterized 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 were 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 agroecological 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. The majority of 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 percent), and from smallholder production systems (89.54 percent). High seroprevalence was also observed in non-descript indigenous goats (85.04 percent), adult goats (69.62 percent), in does (67.46 percent) and goats infested with ticks (85.79 percent). A logistic model showed a gradient of increasing risk for commercial meat type Savanna (odds ratio [OR] = 3.681; confidence interval [CI] = 1.335–10.149) and indigenous (OR = 3.466; CI = 1.57–7.645) compared with 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 percent of the total genetic variation. Average linkage disequilibrium ( $r^2$ ) was highest in the Tankwa ( $0.25 \pm 0.26$ ), followed by commercial breeds and lowest in the village ecotypes where it ranged from  $0.09 \pm 0.12$  to  $0.11 \pm 0.14$ . Pairwise  $F_{ST}$ , principal component analysis and the ADMIXTURE program 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 with 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.

### 3.4.1 **Report of the parallel session**

## **How can biotechnologies contribute to adaptation with mitigation co-benefits?<sup>7</sup>**

**The following are synopses of presentations given by the following speakers**

Daniel Sumner: Both science and economics specify clear linkages between agricultural and food biotechnology and climate change. Climate change may cause poor farmers in poor places to be especially vulnerable to nutritional inadequacy and potential severity of nutritional inadequacy increases for situations associated with increased variability in climate. Climate change may have positive effects in some geographical areas, which doubles the negative impact in areas subject to detrimental impacts. If those suffering refuse to use biotechnology and other changes, the impacts will be even more severe. Policies should not hinder the advantaged, but support adoption of science for the disadvantaged. Any policies must consider the unavoidable fact that over time there will be fewer farmers and more people that are only consumers.

Stephan Weise: Farmers commonly lack the information necessary to adapt, particularly as regards genetic resources. The “Seeds for Needs” initiative (11 countries) studies how agricultural biodiversity can minimize the risks associated with climate change. Ethiopia is highlighted. Productivity of staple crops is declining. Resources in the national gene bank are being studied. Geographic information system (GIS) methodology was used to screen barley and durum wheat accessions in the gene bank. Crowdsourcing was used to gather information of farmer satisfaction with distributed materials. A community seedbank was also established. Molecular studies were undertaken on durum wheat to evaluate its genetic diversity, which was shown to be particularly large relative to that from other locations. The information gathered will be used in breeding programmes.

Guntur Venkata Subbarao: The biological oxidation of ammonium to nitrate, termed nitrification, is detrimental, as nitrate is prone to pollution through leaching and to denitrification to nitrous oxide, a powerful greenhouse gas (GHG). Atmospheric nitrous oxide has increased with increased use of nitrogen fertilizer, as 70 percent of the nitrogen is lost as nitrate. Certain plants, especially tropical pasture grasses, have the natural ability to produce and release biological nitrification inhibitors to suppress nitrifier activity and soil nitrification. Rotation of pasture grasses having high biological nitrification inhibition (BNI) capacity with maize seems beneficial. Molecular studies are underway to identify markers of BNI production. Genetic exploitation of the BNI trait to produce BNI-enabled crops and pastures could be a powerful genetic mitigation technology, but everything is still in the theoretical and research stage.

Henning Steinfeld: The process of enteric fermentation in the rumen is highly beneficial for humans because it converts human-inedible plants into food and fibre, but it is also a major producer of

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<sup>7</sup> This report was prepared by the FAO rapporteurs for the climate change theme - Jarkko Koskela, Paul Boettcher and Melba Reantos.



methane, a potent GHG. Livestock produce almost 40 percent of global methane. Various approaches can be applied to decrease enteric methane, but economics do not always favour their use and technology transfer is a constraint. Biotechnologies to decrease methane output include probiotics, vaccination and genetic modification of rumen organisms. To tap the potential of biotechnology and other methane-reducing interventions, investments in technological transfer and input and product market development are required, alongside with possible emission offset incentives.

Paulo Kageyama: Molecular studies show high diversity of plants, as well as insect and micro-organism species in tropical forests. Plants have adapted to produce biochemicals to resist these potentially harmful organisms. These biochemicals could be used in agricultural systems. Conventional and organic tomato production were compared. Conventional production resulted in greater yield and economic return, with greater concentrations of pesticides. Coffee production systems combining different levels of forest tree biodiversity with coffee were compared with mono-cropping systems. Pest attacks decreased with greater plant diversity; the system with greatest economic returns was the one with a medium level of biodiversity in the coffee agroforestry system. In conclusion, maintenance of a certain level of biodiversity is beneficial.

Hervé Saint-Macary: The 4per1000 initiative seeks to use carbon sequestration in soil to offset current anthropogenic carbon dioxide emissions. 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. Research needs concern: 1) knowledge on the baseline of sequestration (or loss) of soil carbon; 2) definition and co-construction of agronomic strategies and practices at various scales (individual to collective); 3) the transfer and adoption of these strategies and the development of demonstration sites; 4) the design, experimentation and assessment of institutional arrangements and public policies that aim at promoting and rewarding relevant practices; and 5) metrics and methods for monitoring, reporting and verifying carbon sequestration.

### **The following topics were addressed and conclusions reached during the discussion period following the six presentations**

Agricultural biotechnologies currently, and will continue to, help to feed the world and help smallholders (and all farmers) to adapt to and mitigate climate change.

To achieve GHG reductions foreseen as necessary to attenuate the effects of climate change and agreed to in international agreements, all citizens and countries must contribute to climate change mitigation. This contribution will be relative rather than absolute. Poorer countries and people will almost certainly produce more GHGs as they grow economically, but will ideally emit less GHGs than industrialized countries did during similar stages of economic development. Rich countries will work to reduce their current levels of GHGs to compensate. Biotechnology can play a role in both of these instances.

Reduction of denitrification is the only logical approach to control nitrogen loss from fertilization. Other approaches, such as repeated applications of small amounts of nitrogen fertilizer are not feasible in most production systems.



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Agricultural land sequesters less carbon than forests, but techniques and approaches can be applied to limit carbon release and stabilize sequestration in agricultural systems.

Research on high biodiversity agricultural systems is inherently complex. Collecting high-quality and precise data is difficult. This fact may constrain the ability to undertake such studies and hamper the publishing and dissemination of results from studies on this technique.

Some approaches to decrease methane emissions in the dairy sector can lead to negative economic consequences, hindering their adoption. This is an example of the reality that economic incentives will need to play a significant role in mitigation approaches and application of GHG-reducing technologies.



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

**Daniel A. Sumner**

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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 GHG 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 change, 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 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 farms, while the price of food they sell may decline as productivity of their northern (or southern) competitors rises.
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, adaption to climate change, reduction of 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, it is 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.



### 3.4.3 Biodiversity: Key to helping farmers adapt to climate change

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#### The challenge

Climate change is estimated to reduce agricultural production by 2 percent every decade until 2050, with yields of major crops declining by an average of 8 percent 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 (gene banks, 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 gene bank of the Ethiopian Biodiversity Institute. 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

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<sup>8</sup> This 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.



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 gene bank using 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 multilocational trial.

The initiative included 12 villages, covering about 350 km<sup>2</sup>. To know the climatic conditions in all villages, we used sensors called iButtons<sup>®</sup> 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 seed bank. Farmers built the infrastructure and the community seed bank was 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 QTL mapping, 81 587 markers scoring 30 155 SNPs 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).

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.

### Reference

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### 3.4.4 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 ( $\text{NH}_4^+$ ) to nitrate ( $\text{NO}_3^-$ ), termed as nitrification, is carried out by two groups of soil micro-organisms – ammonia oxidizing bacteria and ammonia oxidizing archaea. Cationic- $\text{NH}_4^+$  is strongly bound to the soil and is available for crop uptake. In contrast, the anionic  $\text{NO}_3^-$  does not bind to the soil and is prone to leaching and causes pollution of water bodies. Several heterotrophic soil bacteria denitrify nitrate under anaerobic or partially anaerobic conditions, producing nitrous oxide ( $\text{N}_2\text{O}$ ), a powerful GHG with global warming potential 300 times more than carbon dioxide ( $\text{CO}_2$ ), and the third-largest contributor, after  $\text{CO}_2$  and methane, to global warming. Nitrification and denitrification are the only known biological processes that generate  $\text{N}_2\text{O}$ ; concentrations of  $\text{N}_2\text{O}$  in the atmosphere are rising since the advent of the green revolution (from 290 parts per billion in the 1960s to 320 in 2000); nearly 70 percent of global  $\text{N}_2\text{O}$  emissions come from agricultural systems.

#### Green revolution, nitrogen (N) fertilizer use and $\text{N}_2\text{O}$ emissions – the functional link

Fertilizer-responsive high-yielding wheat, rice and maize varieties largely are responsible for the green revolution, that doubled global food production (between 1960 to 2000); but global N-fertilizer consumption has increased from 10 teragrams (Tg) to 120 Tg/year 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 percent recovery of applied N by crops at present. Nearly 1.36 billion barrels of diesel energy are needed to produce 120 Tg of N-fertilizer; about 70 percent 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<sub>2</sub>O emissions will double from present levels and reach 19 Tg N<sub>2</sub>O-N per year (8.98 Gt CO<sub>2</sub> eq per year), if we carry on with business as usual.

There is an urgency to develop next-generation mitigation technologies to reduce N<sub>2</sub>O emissions from agricultural food production systems as the IPCC set a target to cut global GHG emissions by 80 percent 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<sub>2</sub>O emissions and NO<sub>3</sub><sup>-</sup> leaching.

### **Biological nitrification inhibition – A genetic-mitigation technology to curb N<sub>2</sub>O emissions from agricultural systems**

Certain plants have the natural ability to produce and release biological nitrification inhibitors 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 biological nitrification inhibitors 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<sub>3</sub> formation in soils but also reduce N<sub>2</sub>O emissions. Currently, JIRCAS in partnership with CIAT is evaluating whether biological nitrification inhibitors added from Bh root systems can improve NUE of a following maize crop in an agropastoral 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. The last four years of field evaluation suggest that maize yields have improved substantially (from 60 to 100 percent) in BNI fields compared with non-BNI fields under moderate N inputs (60 to 120 kg N/ha); N recovery and soil N retention were substantially higher in BNI fields compared with non-BNI fields, suggesting the potential value of exploiting BNI function in an agropastoral system.

In addition, JIRCAS, with participation from ICRISAT and CIMMYT, is evaluating and characterizing the BNI capacity in sorghum and wheat root systems to assess the potential for genetic exploitation of the 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 the 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 biological nitrification inhibitors with varied chemical structures and multi-modes 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 the 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 N<sub>2</sub>O emissions.

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

Low-nitrifying and low N<sub>2</sub>O-emitting agricultural production systems are important pillars to support climate-smart agriculture. Genetic mitigation technology, where BNI-enabled root systems of staple crops/pastures will become components of low N<sub>2</sub>O-emitting food production systems, should be integrated with genetic adaptation strategies to address climate change for developing climate-smart agriculture in the twenty-first century.

### **A paradigm shift is needed in nitrogen management to meet COP21 GHG emission reductions from agricultural systems**

The 21st Conference of the Parties of the United Nations Framework Convention on Climate Change (COP21) set the goal for cutting GHG emissions by 80 percent to limit global temperature increases to below 2°C by 2050. Termed the “Paris-Agreement”, this 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 N<sub>2</sub>O-neutral as well. A paradigm shift towards low-nitrifying production systems is needed; exploiting BNI function could become a powerful genetic mitigation technology to achieve the goal of reducing N<sub>2</sub>O emissions to lower the N footprint from agriculture by 2050.



### 3.4.5 Mitigation of enteric methane emissions from ruminants: The role of biotechnology

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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 micro-organisms digest carbohydrates, proteins and fibre 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, which are transformed by the ruminant tissues into animal products, along with by-products such as hydrogen ( $H_2$ ), carbon dioxide ( $CO_2$ ), ammonia ( $NH_3$ ) 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 fibre, but it is also a major producer of methane, a potent GHG. Methane ( $CH_4$ ) 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  $CO_2$ , accounting for 16 percent of global emissions. From 1750 to today, the concentration of methane in the atmosphere has increased by 150 percent (from 700 to 1 760 parts per billion). By weight,  $CH_4$  is 84 and 28 times more potent than  $CO_2$  over a 20-year and 100-year period respectively.

The agricultural sector contributes about 50 percent of the global human-induced CH<sub>4</sub> emissions, of which 78 percent are from livestock (manure and enteric fermentation). Methane from enteric fermentation is the single largest global source of anthropogenic CH<sub>4</sub>, responsible for 30 percent and 70 percent of global CH<sub>4</sub> emissions and CH<sub>4</sub> emissions from agriculture, respectively. At global level, CH<sub>4</sub> production from enteric fermentation contributes 5.5 percent (equivalent to 2.7 gigatonnes [Gt] CO<sub>2</sub> eq.) to the global anthropogenic GHG emissions. Using methane's 20-year global warming potential – a measure of the short-term climate impact of different GHGs – more than triples the share of enteric CH<sub>4</sub> to over 18 percent of global GHG, from slightly less than 6 percent at the 100-year time frame. Cattle account for 77 percent of the global enteric emissions (2.1 Gt), buffalo for 14 percent (0.37 Gt) and small ruminants (sheep and goats) for the remainder (0.26 Gt). Global enteric CH<sub>4</sub> emissions are projected to increase by 20 percent in response to growing demand between 2010 and 2030; this would add over 388 Mt CO<sub>2</sub> 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 percent of the gross dietary energy in the form of CH<sub>4</sub> depending on the quality and quantity of diet. Thus, it is essential to look for options to reduce CH<sub>4</sub> 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 CH<sub>4</sub> 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 returns at low or no cost (in the 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 with the potential both to generate relatively rapid productivity gains and economic benefits, are required.



On the other hand, the inhibition of enteric  $\text{CH}_4$  in ruminants through the use of technologies such as dietary additives have not delivered a clear and positive answer in reducing  $\text{CH}_4$  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 rely increasingly on existing and emerging biotechnological advances to produce food. Today, 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 possible emission offset incentives.



### 3.4.6 Use of biodiversity as a biotechnological tool for carbon sequestration in the tropics

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The Laboratory for the Genetics of Tree Species at the University of São Paulo, Brazil (LARGEA/USP) is studying the complex biodiversity and the genetic structure of tropical tree populations, with a view to using these on two applied projects in the field: 1) restoration of degraded riparian areas around hydroelectric dams for carbon sequestration; and 2) 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 100 times more species of insects and micro-organisms (50 000 species/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 micro-organisms, 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/USP for the past 30 years, using molecular genetic methods to determine genetic variation within and among populations, gene flow, and the 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 Climate Change (UNFCCC). The most recent PhD thesis presented by a student of LARGEA/USP within this theme addresses: “Emergy 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.

For examples from the second applied project of the laboratory, we can highlight a 2011 MSc thesis comparing, under the same ecological conditions, the cultivation of tomato by three conventional producers (using applications of pesticides and chemical fertilizers) against three smallholder farmers operating under an organic system (biodiversity surrounding the culture), without the use of industrial chemical products in Apiaí (Brazil). The final results were surprising: the productivity for the organic system was 65 percent (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 (1 000 versus 800 Brazilian real 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 pesticides. Therefore, neither the farmers nor the consumers of their products were exposed to the danger of being poisoned by the 36 applications of pesticides used by the conventional farmers during the 2.5-month cycle of the tomato culture. The essential aspect is that the tomatoes produced by the organic farmers were free of pesticides, 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. A PhD student (P. Lopes) 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: 1) high – 36 different native tree species in addition to the coffee plants; 2) medium level – 23 native tree species plus coffee; and 3) low – 12 native tree species, together with 4) 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 percent, 45.47 percent, 58.15 percent, and 88.35 percent, for the high, medium, low biodiversity, and the coffee monoculture treatments respectively. Estimates of the economic returns for the different coffee systems were respectively 1 100, 2 813, 2 250 and 1 452 Brazilian real for the agroforestry systems of high, medium and low biodiversity, and for the coffee monoculture. The best economic performance, representing a balance between biodiversity and productivity, was achieved by the second treatment, corresponding to medium biodiversity.

Final considerations:

- 1) In agriculture and silviculture in the tropics, advanced technology and the large-scale use of monocultures are destroying the biodiversity, causing increases in pests and diseases. To maintain productivity, the agroindustry has turned to more and more use of pesticides and chemical fertilizers together with the introduction of GMOs.
- 2) The adverse impacts of these production models on the environment and human health are clearly observed, including in reports commissioned by the World Health Organization

(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.

- 3) We have presented the important application of biodiversity for the maintenance of equilibrium in agroecosystems and the production of healthier food for society.



### 3.4.7 Carbon sequestration in agricultural soils: The “4 per mil” programme

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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 CO<sub>2</sub> 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 (0.4 percent) 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 Gt C (over a meaningful depth for carbon (C) sequestration, i.e. 0–40 cm), the 0.4 percent target would result in a carbon sequestration that could peak at 3.5 billion tons C per year (Gt C/year) 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 percent of the total land area) that are widespread in all biomes and in most world regions. Further, assuming that net CO<sub>2</sub> emissions from land use change could be halted, the land carbon sink that could peak in the 2030–2040s thereby substantially offsetting the current growth in atmospheric CO<sub>2</sub>.

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 is needed on: 1) knowledge on the baseline of sequestration (or loss) of soil carbon and on current soil carbon stocks; 2) the definition and co-construction of agronomic strategies and practices at various scales (individual to collective) targeting the “0.4 percent” objective; 3) the transfer and adoption of these strategies and the development of demonstration sites; 4) the design, experimentation and assessment of institutional arrangements and public policies, including financial mechanisms,

that aim at promoting and rewarding relevant practices; 5) 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 with this, the net biome productivity is 2.9 Gt. The ratio between these two values is very low and biotechnologies could be mobilized to improve them in various ways: for example, improvement of the photosynthesis process, modification of the shoot/root ratio, biomass quality monitoring, perennality of crops, improvement of knowledge on the soil-rhizosphere-plant interface.

In this presentation, these various ways will be discussed and, when relevant, the example of sorghum will be used to illustrate ongoing research and possible implementation for various environments.