All messages from the FAO 2013 e-mail conference on "Impacts of genomics and other ‘omics’ for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries"

[This document contains all of the 61 messages that were posted during the FAO moderated e-mail conference on "Impacts of genomics and other ‘omics’ for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries " that took place from 4 to 24 March 2013. As described in the conference Background Document, the first sequenced genomes of domesticated animals and plants were released about 10 years ago and an ever increasing number of important species have been sequenced each year since then; the genomes of several thousand micro-organisms have now been sequenced; and the knowledge generated from genomics can be applied in several different ways. With this as a background, people are asked to address two main questions in this conference:

1. What have been the impacts (positive and/or negative) so far of genomics and the other 'omics' for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?
2. What are the impacts (positive and/or negative) of genomics and other 'omics' likely to be in the near future (e.g. the next five years) for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?

By the time the conference began on 4 March 2013, a total of 471 people had subscribed themselves to the conference, which rose to 522 on 24 March when the conference finished. Of the 522 subscribers, 44 (i.e. 8%) submitted at least one message. Of the 61 messages that were posted, 36% came from people living in Asia; 28% from Europe; 13% from Latin America and the Caribbean; 10% from Africa; 8% from North America; and 5% from Oceania. The messages came from people living in 22 different countries, the greatest number coming from India (13 messages) followed by the United Kingdom (7), United States (5), Finland (4) and Nigeria (4). A total of 35 messages (i.e. 57%) were posted by people living in developing countries. Just over half of the messages came from people working in universities; a quarter came from people working in research centres, including CGIAR centres; while the remaining quarter came from people working in the private sector, for the Government or working as independent consultants.

NB: People posting messages are assumed to be speaking on their own behalf and not on behalf of their employers (unless they indicate otherwise). The conference was hosted by the FAO Biotechnology Forum and was the 19th e-mail conference hosted by the Forum since it was launched in the year 2000. The Background Document to the conference is available from the website of the Forum (http://www.fao.org/biotech/biotech-forum/). A Summary Document will also be prepared and made available from the Forum website. For further information on agricultural biotechnology, see http://www.fao.org/biotech/ (in Arabic, Chinese, English, French, Russian and Spanish).]

The Messages

Messages are numbered in order of their posting during the conference. The few messages without a number are from the Moderator.

Subject of Messages:

: Background document to the FAO e-conference on Genomics
: Welcome to the FAO e-mail conference on Genomics !
1: Genomics-based crop improvement
2: Importance of software for genomics applications
3: Re: Genomics-based crop improvement
4: Opportunities of genomics for the livestock and plant sector of the "tropics"
5: Fermentation of cysteine
6: Re: Genomics-based crop improvement
7: What have been the impacts of genomics so far...

50: Re: Establishing a global genomics/breeding forum?
51: Genomics in livestock
52: Genomics for livestock in tropical countries
53: Re: Establishing a global genomics/breeding forum?
54: Re: Establishing a global genomics/breeding forum?
55: Genomics in tropical forestry
56: Re: Genomics of crop beneficial bacteria
57: Development of mapping populations for crop species
58: Animal 'omics'
59: Omics tools versus conventional plant breeding

60: Re: Establishing a global genomics/breeding forum?
61: Genomics of rhizobacteria
: End of FAO e-mail conference on genomics

-----Original Message-----
From: Biotech-Mod3
Sent: 28 February 2013 15:38
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: Background document to the FAO e-conference on Genomics

Dear Colleagues,

Thank you for subscribing to this FAO e-mail conference on "Impacts of genomics and other ‘omics’ for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries" which begins in a few days time.

I am now sending you the Background Document to the conference.

It aims to provide information that you, as participants, will find useful for the e-mail conference. The first Section of this 10-page document provides some general background to the subject. Section 2 of the document provides an overview of the current status regarding genomics in food and agriculture. Section 3 briefly discusses some of the main ways in which the knowledge from genomics can be used. Section 4 presents some specific guidance about the topics that are to be discussed in the conference. Section 5 provides references of articles mentioned in the document, abbreviations and acknowledgements.

The document is provided below, and is also available on the FAO website at http://www.fao.org/docrep/017/aq145e/aq145e.pdf (90 KB).

I particularly encourage people to read Section 4 of the document before they begin preparing a message.

The conference begins on Monday 4 March. If any of your colleagues wish to subscribe, they should send an e-mail to listserv@listserv.fao.org with the following one line in the body of the message (leave the subject line blank):
subscribe biotech-room3-L firstname lastname

Where firstname and lastname refer to the person's first and last name. For example, if the subscriber's name is John Smith, then the line should be:
subscribe biotech-room3-L John Smith

Best regards

John

John Ruane, PhD
Moderator,
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Background document to the FAO e-mail conference on "Impacts of genomics and other 'omics' for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries"

1. Introduction

Advances in genomics, the study of all the genetic material (i.e. the genome) of an organism, have been remarkable in recent years. Publication of the first draft of the human genome in 2001 was a milestone, quickly followed by that of the first crop (rice) in 2002 and the first farm animal (chicken) in 2004. Huge technological advancements have meant that sequencing has become dramatically quicker and cheaper over time, so the genomes of many of the important crops, livestock, forest trees, aquatic animals and agricultural pests are now already sequenced or soon will be. The FAO Biotechnology Forum (http://www.fao.org/biotech/biotech-forum/) is hosting this e-mail conference to look at the impacts that genomics, and the other related 'omics', have had so far on food and agriculture in developing countries as well as their potential impacts in the near future.

Before looking at genomics in more detail, a quick overview of some basic genetic concepts can be provided [for more technical details, see FAO (2011a) or the FAO biotechnology glossary (FAO, 2001)]. All living things are made up of cells that contain genetic material called DNA, a molecule made up of a long chain of nitrogen-containing bases (of four kinds: A, C, G and T). DNA is organized as a double helix, where two DNA chains are held together through bonding of the bases, where A bonds with T and C bonds with G. Genomes can be long and 1,000 base pairs (bp) is denoted as 1 kb; 1,000 kb is denoted as 1 Mb; and 1,000 Mb as 1 Gb (i.e. 1,000,000,000 bp). For example, the size of the horse genome is about 2.7 Gb, comparable to that of most mammals, whereas that of the chicken is smaller (about 1 Gb). Compared to animals, genomes sizes in higher plants have a greater range, from about 200 Mb in the horse chestnut and 400 Mb in rice to 2.5 Gb, 12 Gb and 24 Gb in maize, broad bean and slash pine respectively (Murphy, 2011).

Only a small fraction of the genome typically codes for proteins, i.e. where the DNA is first 'transcribed' to a molecule called messenger RNA (mRNA) that is then 'translated' to protein. The remaining and major share of the DNA represents sequences that do not code for proteins and whose role is not yet clearly understood, although this is an area of intense research (The ENCODE Project Consortium, 2012). The genetic material is normally organised into sets of chromosomes (e.g. 5 pairs in Arabidopsis thaliana; 30 pairs in cattle), and the entire set is called the genome. In a diploid individual (i.e. where chromosomes are organised in pairs), there are two forms (alleles) of every gene, one from each parent. Note that the genetic material of viruses can be DNA or RNA (so they are called DNA viruses or RNA viruses respectively).

The field of genomics is still relatively young. The first genome sequence of a virus (called phi X 174, containing over 5 kb DNA) was published in 1977 and the first genome of a bacterium (a strain of Haemophilus influenzae, almost 2 Mb long) was sequenced nearly 20 years later (Fleischmann et al., 1995). The landmark human genome project began in 1990 and the draft sequence (covering about 90% of the entire 3 Gb genome) was published in 2001 and the full sequence in 2003. This project, in particular, stimulated major technological advancements in DNA sequencing and in bio-informatics (i.e. the use and organization of this kind of biological information, including development of databases, use of computers to analyse the data and integration of information from different sources), so that over time the speed of sequencing has increased rapidly while the corresponding costs have crashed.

Ten years after the draft human genome sequence was published, Lander (2011) noted that sequencing machines could read about 250 billion bases in a week, compared to about 5 million in 2000 and 25,000 in 1990 and that the cost per-base of DNA sequencing had fallen by about 100,000-fold over the decade. Thus, whereas sequencing the first human genome took over a decade and several hundred million US$, it now costs as little as 5,000 to 10,000 US$ (Hayden, 2013) and takes a few weeks. As a result, sequencing the human genome is now becoming much more accessible and the era of 'personal genomics' is beginning, although the costs and time of analyzing the sequence data still remain substantial (Soon, Hariharan and Snyder, 2013). This (r)evolution is affecting all species, not just humans, and has been made possible by so-called 'next-generation' or 'high-throughput' sequencing technologies, involving the parallel sequencing of large numbers (up to millions) of DNA molecules (Feuillet et al, 2011).

These dramatic improvements have led to a plethora of genome sequencing projects. An overview of these can be seen from the National Center for Biotechnology Information (NCBI), which hosts an important database containing, inter alia, information about genomes (http://www.ncbi.nlm.nih.gov/genome/browse/). As at 28 February 2013, the database indicates that the number of species sequenced so far includes 65 animals, 32 plants, 54 fungi and 26 protists as well as 2431 bacteria, 160 archaea and 3329 viruses. All of these completed sequences can be freely downloaded and analysed. This database, as well as others, such as the Genomes OnLine Database (GOLD, http://www.genomesonline.org), also provide information about the several thousand genome sequencing projects currently underway and which are not yet completed.

The huge investments that have been directed towards genomics are driven by the prospects of using the knowledge in several areas, particularly towards human disease diagnosis and prevention and drug development (Soon, Hariharan and Snyder, 2013). In addition, genomics is being used to assist wildlife conservation. For example, the Genome 10K project proposes to sequence the genomes of 10,000 vertebrate species, approximately one for each vertebrate genus, for this purpose (http://genome10k.soe.ucsc.edu/). It is also being used in many different areas of food and agriculture, and this is the focus of the current e-mail conference. A small idea of the enormous amount of ongoing activity in this field can be got by looking at the details of the 159 workshops held during the International Plant & Animal Genome Conference (PAG XXI) which took place in January 2013, describing advances in diverse areas ranging from aquaculture, the buffalo and cacao to rice, sugarcane and wheat rust fungi (http://pag13.mapyourshow.com/5_0/sessions/session_results.cfm?type=SessionType&SessionType=Workshops).

Sequencing the genome of an organism, and the use of bio-informatics to compare it to those of other species, or of individuals from the same species, provides important biological insights, such as the number of genes it contains; organization of its genome; identification of regions that have been strongly affected by genetic selection; and evolution of the genome over time. To find out what each of the genes do, how they are influenced by environmental factors and how they contribute to certain traits (such as growth rate or disease resistance), information on the genome can be supplemented by that from a number of other ‘omes’, including the transcriptome (i.e. all the mRNA produced by the organism), the proteome (all the protein produced by the organism) and the metabolome (all the small cellular metabolites produced by the organism during cellular metabolic reactions). In this way, information can be gathered on the outputs of the sequential biological processes in the cell whereby DNA is transcribed to mRNA which, in turn, is translated to proteins which are then used, inter alia, in cellular metabolic pathways. Study of these ‘omes’ is called genomics, transcriptomics, proteomics and metabolomics respectively. [Note that in addition to these four main ‘omics’, several other 'omic' sub-disciplines have also emerged, such as epigenomics which studies genomic-wide epigenetic modifications, like DNA methylation and histone modification, that influence which genes are turned on or off in different cells at different times without changing the DNA sequence].

Note that whereas the genome is quite stable, the levels of mRNA, proteins and metabolites can vary considerably depending on the kind of cells/tissues that are sampled (e.g. the proteins expressed in the udder cells of lactating cows will be different than in their nerve cells), on time (e.g. age of the organism) and on a wide range of environmental factors (e.g. biotic or abiotic stresses).

This Background Document aims to provide information that participants will find useful for the e-mail conference. In Section 2 a brief overview of the current status regarding genomics relevant to food and agriculture is given. Section 3 briefly discusses ways in which the knowledge from genomics can be used. Section 4 presents some specific guidance about the topics that are to be discussed in the conference. Section 5 provides references of articles mentioned in the document, abbreviations and acknowledgements. Note, for reasons of space, Sections 2 and 3 do not focus on the other ‘omics’. These are, however, increasingly being used in each of the sectors to supplement genomics information (see Lidder and Sonnino (2011) for some examples).

2. Status regarding genomics in food and agriculture

2.1 Crops

The first plant genome to be sequenced (in 2000) was Arabidopsis thaliana, a small weed of the Brassica family that is much studied as a model plant. In 2002, there was the first crop, when the draft rice genome sequence was published. By the end of 2011, the sequenced genomes included those of the cacao, cassava, cucumber, foxtail millet, grape, maize, peach, pigeonpea, potato, sorghum, soybean as well as relatives of alfalfa and strawberry (Morrell, Buckler and Ross-Ibarra, 2012). Since then, others have been added to the list, including the barley, melon, orange, tomato and watermelon genomes.

To illustrate the typical kinds of strategies used and results obtained from such genomics studies, let us look in more detail at a very recent addition to this list, the chickpea (Cicer arietinum), an important legume for food security in many developing countries (Varshney et al, 2013). In their study, they first produced a draft genome sequence of a specific chickpea variety (called CDC Frontier) using the whole genomic shotgun strategy, i.e. where the entire genome is randomly fragmented into small pieces that are sequenced, and the sequences are subsequently assembled using computational methods to produce a consensus sequence (see Feuillet et al (2011) for more details). Their genome ‘coverage’, indicating how much sequence information they had, was high, at 207x (meaning that, on average, each base was sequenced 207 times). From their sequence, they estimate, inter alia, that the chickpea genome is 738 Mb long and contains 28,269 genes (averaging 3,055 bp in length), for whom the function could be tentatively assigned in about 90% of cases. They describe the characteristics of the genome (e.g. nearly half of it consists of ‘transposable elements’, mobile pieces of DNA that can ‘jump’ around the genome) and, by comparing it with the genomes from other legume and selected non-legume species, they deduce how the chickpea genome has evolved over the past millions of years.

In the second part of their study, Varshney et al (2013) used whole genome re-sequencing (WGRS) to study the genetic diversity among 29 elite chickpea varieties from different countries. WGRS is an approach where, once a reference genome is available for a given species, genetic variation can be studied by sequencing different individuals of the species and comparing their sequences with the reference genome (Bentley, 2006). They also sequenced 61 additional chickpea accessions using another approach and analysis of the total of 90 genomes made it possible to identify over four million polymorphisms, including single nucleotide polymorphisms (SNPs) and short insertions and deletions (indels), that can be used for future genetic improvement programmes or to identify genes involved in traits of interest. By comparing the genome sequences of landraces and cultivars, they also identified specific regions of the chickpea genome that were potentially under strong genetic selection (i.e. there was a genetic or selective ‘sweep’) during domestication and breeding.

2.2 Forest trees

Compared to the crop sector, progress in genomics of forest tree species has been much slower. Contributing factors are the very large size of many tree genomes (e.g. ranging from 19 to 24 Gb in spruce and pine species) and limited funding (Neale and Kremer, 2011). The draft sequence of the black cottonwood tree (Populus trichocarpa) was the first to be published, in 2006 (see http://www.phytozome.net/poplar.php for more information). Next was the release of the draft sequence of Eucalyptus grandis in 2010 (http://www.phytozome.net/eucalyptus.php). There is, however, growing interest in this area (Neale and Kremer, 2011). The ever increasing amount of information from an expanding list of forest tree species contained in specialized tree genomics databases (such as http://dendrome.ucdavis.edu/treegenes/pubdata/summary_count.php), as well as the papers published in a special issue of the Tree Genetics & Genomics journal in June 2012 (http://link.springer.com/journal/11295/8/3/page/1), all attest to this. As the preface to this special issue notes: “our work on tree genomics is just beginning”.

2.3 Livestock

As in the crop sector, the field of genomics is very active in farm animals. During the recent FAO international technical conference on Agricultural Biotechnologies in Developing Countries (FAO, 2011b), which took place in Guadalajara, Mexico in March 2010, the Consultative Group on International Agricultural Research (CGIAR) organized two cross-sectoral sessions on genomics. They indicated that the status of genomic resources in the livestock sector might be slightly more advanced than in plants. The first livestock genome to be sequenced was the chicken (the red jungle fowl, Gallus gallus) in 2004 and since then those of the cow, horse, pig, rabbit, sheep and turkey have been released (Fan et al, 2010). The whole genome sequence of the latest addition, the goat, has just been published (Dong et al, 2013).

2.4 Aquatic animals

Following the human genome in 2001, the second vertebrate genome to be released, in 2002, was that of the pufferfish, Rugu rubripes, with a genome size of about 365 Mb. Since then, the genomes of other model fish (including the medaka and zebrafish, both model species in developmental biology, and the stickleback, a model for studies of adaptation and speciation), as well as those of important food fish, such as the Atlantic cod and Nile tilapia, have been sequenced in addition to shellfish such as the Pacific oyster. Bernardi et al (2012) report that nearly 60 fish species, including farmed fish and capture fisheries species, are currently being sequenced and an additional 100 species have been identified for sequencing in the near future.

2.5 Micro-organisms

Micro-organisms, including fungi, bacteria and viruses, make up the vast majority of organisms whose genomes have been sequenced, because of their universal importance, particularly in relation to disease, and because their genome sizes are small. Many of those sequenced have direct implications for food and agriculture, including those that cause diseases in plants and animals, are responsible for food spoilage, are used as biocontrol agents and as biofertilizers and in food fermentation processes.

To get a tiny overview of the huge diversity of these microbial genome sequencing projects, we can look at the list of a couple of hundred micro-organisms whose genomes have been sequenced in recent months (Nelson and Garrity, 2012). For bacteria, the list includes strains of Brucella abortus, a pathogen that infects livestock and humans; Cronobacter sakazakii, a pathogen associated with several outbreaks of food-borne illness; Dickeya zeae, the causal agent of rice foot rot in China; Enterobacter cloacae, which colonizes rice roots and promotes plant growth by improving plant nutrition; Geobacillus thermoglucosidans, a cause of contamination in milk processing plants; Lactococcus garvieae, found in a traditional Spanish cheese; Bifidobacterium bifidum, a probiotic microorganism that may promote health; Corynebacterium bovis, which causes mastitis in dairy cows; and a new bacteria from the Treponema genus, found in the cow rumen. The list also includes many viruses, including a number of different strains of the avian influenza virus in China; two types of bluetongue viruses, which infect ruminant animals, in China; two strains of sacbrood viruses, which infect the honeybee, in Korea; an isolate of soybean Putnam virus, which infects soybeans; and an isolate of Peste des petits ruminants virus (PPRV) from wild bharal sheep. The list also includes the filamentous fungus Aspergillus oryzae Strain 3.042, which is extensively used for the production of soy sauce and other fermented foods in China.

Metagenomics, the genomics analysis of entire microbial communities, has become increasingly important over the last decade (Relman, 2011). Environmental samples (such as soil; water from lakes, seas or wastewater treatment plants; or the contents of a rumen) are used to study the genomes of the micro-organisms they contain. An important advantage of the approach is that it is not necessary to culture the micro-organisms involved. Current figures (28 February 2013) indicate that a total of 370 metagenomics projects are ongoing or have been completed, associated with 2737 metagenome samples (http://www.genomesonline.org/cgi-bin/GOLD/metagenomic_classification.cgi).

In this Section 2, the focus has been on the status regarding whole genome sequencing projects. Note that even though a whole sequence might not yet be published for a given species, information on its genome can also be provided through other forms of genomic resources, such as ‘libraries’ of expressed sequence tags (ESTs) or bacterial artificial chromosomes (BACs) (Quinn et al, 2011). ESTs are short DNA sequences that are complementary to, and derived from, mRNA produced by the organism. BACs are vectors (i.e. DNA molecules which can replicate in a host organism, such as E. coli) that can contain large segments (up to 350 kb) of the genome.

3. Applications of genomics in food and agriculture

In this Section, a brief description is provided of some of the main ways in which the knowledge generated through genomics can be used in food and agriculture.

3.1 Genetic improvement of populations

The potential to genetically improve crop, livestock, forest tree, aquatic animal or microbial populations for specific purposes is probably the major driving force behind the use of genomics and the other ‘omics’ in food and agriculture. They allow researchers and breeders to gain direct access to knowledge about the make-up and functioning of the genetic blueprint of the population or species of interest and to use the knowledge for their genetic improvement.

There are several ways in which this can be done. For example, as illustrated by the example of Varshney et al (2013) in Section 2.1, genome sequencing leads to the identification of unprecedented numbers of molecular markers (such as SNPs) spread throughout the entire genome. Their association with genes of interest can be harnessed for genetic improvement, an approach called marker-assisted selection (see FAO (2007) for an extensive overview in the different sectors). Commercially available "SNP chips" have been developed that allow individuals to be genotyped for tens of thousands of SNP markers distributed across the genome. A number of strategies are available to use the large number of markers for genetic improvement. One strategy is the use of association mapping or genome-wide association studies (GWAS), where genome-wide marker alleles associated with the trait of interest (e.g. yield) are first identified and then, in a second step, markers with significant associations with the trait are used to predict breeding values (Hayes and Goddard, 2010). Another strategy is genomic selection where, unlike GWAS, all of the genome-wide markers are used to predict breeding values. This second strategy requires a reference (training) population of individuals that have been recorded for the trait and genotyped for the markers. Both strategies have been used in animal and plant breeding (Hayes and Goddard, 2010; Varshney et al, 2012). As an alternative to using molecular markers to predict breeding values, it has been proposed that the full genome sequence of individuals be used in the future (Hayes, Lewin and Goddard, 2013).

Genomics and the other 'omics' make it possible to identify individual genes affecting important traits and to understand how they function. This knowledge can be used for genetic improvement within the population, e.g. using marker-assisted backcrossing to transfer an important identified gene from a donor to an elite variety (Varshney et al, 2012), or to transfer the gene to another species for development of a genetically modified organism (GMO).

3.2 Characterization and management of genetic resources for food and agriculture

Domestication of plants and animals began about 10,000 years ago and studies of the timing, location and selection pressures behind the different domestication events provide valuable information about the current genetic resources for food and agriculture. Genomics has provided a whole range of new tools to explore such issues. For example, Groenen et al (2012) compared the genomes of wild and domestic pigs from Europe and Asia and their analyses indicated, firstly, that the Asian and European wild boars separated from each other roughly one million years ago and, secondly, that there was a clear distinction between European and Asian breeds, thus confirming the hypothesis that beginning about 10,000 years ago, pigs were independently domesticated in western Eurasia and East Asia.

Genomics and genomics-derived molecular markers are also playing an important role in the characterization, study and preservation of wild populations, such as capture fish and forest tree populations. For example, they have been used to estimate the effective population size (a measure of the rate of loss of genetic diversity and rate of increase in inbreeding in a population or species) of the critically endangered North Sea houting (Coregonus oxyrhynchus) and to study genetic interactions between stocked hatchery strain brown trout (Salmo trutta) and wild brown trout populations (FAO, 2008).

Metagenomics is now being used to characterize and study the diversity of different complex microbial ecosystems that are relevant to food and agriculture. For example, McSweeney and Mackie (2012) describe recent initiatives in this area to study the microbial community in the rumen.

3.3 Food and agricultural product authentication

Genomics and molecular markers derived from genome sequencing can be used to confirm the authenticity of commercially available food and agricultural products (such as timber, fish, seafood, meat, milk, fibre, vegetables or processed foods). This can involve identification at the species level or even at the within species level. For example, Wilkinson et al (2012) describe the use of a high density SNP genotyping assay (developed from SNPs identified and characterized by next generation sequencing) to authenticate pork products derived from specific British pig breeds. The use of genetic markers to identify timber species in order to curb illegal and unsustainable logging (http://www.globaltimbertrackingnetwork.org) and to recently identify horsemeat falsely sold as beef in Europe are typical applications in this area.

3.4 Pathogen detection

Knowledge of the genome sequence of specific strains of micro-organisms (see Section 2.5) makes it possible to accurately identify the agents causing food contamination as well as plant and animal diseases. The specificity involved also makes it possible to trace the source of the pathogen and to monitor its geographical and temporal spread, such as that of the highly virulent race of wheat stem rust Ug99 (http://www.fao.org/agriculture/crops/rust/stem/rust-report/stem-ug99racettksk/en/).

3.5 Vaccine development

Genomics is also used to develop vaccines to manage diseases in livestock and fish. One of the key steps in vaccine development is the identification of potential antigen candidates that may be effective in vaccines (an antigen is a molecule, usually a protein foreign to the animal, which elicits an immune response on first exposure to the immune system by stimulating the production of antibodies specific to its various antigenic determinants. During subsequent exposures, the antigen is bound and inactivated by these antibodies). As noted by OIE (2010), “the field of genomics and related areas has revolutionised the manner in which microbial antigens are identified”. Study of the host genome can also assist in vaccine development. For example, publication of the Atlantic cod genome gave new information about the genetic control of its immune system, so the authors note “our novel findings regarding the immune system will allow for more targeted vaccine development, aiding disease management and the process of domestication of Atlantic cod” (Star et al, 2011).

4. Topics to be discussed in this e-mail conference

This is the 19th e-mail conference to be hosted by the FAO Biotechnology Forum (http://www.fao.org/biotech/biotech-forum/en/) since it was launched in the year 2000. As with each conference hosted by the Forum, the focus is on applications in developing countries.

As seen in Section 2, the first sequenced genomes of domesticated animals and plants were released about 10 years ago and an ever increasing number of important species have been sequenced each year since then. Also, the genomes of several thousand micro-organisms have now been sequenced. As seen in Section 3, the knowledge generated from genomics can be applied in several different ways. In this context, the first main question to be addressed in the conference is:

4.1 What have been the impacts (positive and/or negative) so far of genomics and the other ‘omics’ for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?

In addressing this question, the specific kinds of issues that participants might wish to discuss are:

- How exactly was the knowledge derived from genomics and the other ‘omics’ used?
- What kind of impacts did they have?
- Were the impacts the same in different sectors? If not, why not?
- Were the impacts the same in different developing world regions? If not, why not?

- What products, if any, were derived from the knowledge? If products were developed, how were intellectual property rights issues dealt with (an issue discussed in the second genomics-related session at ABDC-10 (FAO, 2011b))?
- Which specific issues enabled genomics and the other ‘omics’ to have positive impacts (e.g. government policies, international collaboration, public-private partnerships, complementary infrastructure, germplasm distribution networks)?
- Which specific issues prevented them from having positive impacts (e.g. costs, intellectual property rights, the species sequenced)?
- Were the impacts influenced by the sequencing strategy (e.g. generating genome sequence data in-house in developing countries versus outsourcing this work)?
- The relative importance of genomics versus transcriptomics, proteomics, metabolomics or other ‘omics’

While the first main question looks at the past and the present, the second main question looks to the near future:

4.2 What are the impacts (positive and/or negative) of genomics and other ‘omics’ likely to be in the near future (e.g. the next five years) for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?

In addressing this question, the kind of issues that participants might wish to discuss might be:
- Whether the magnitude of their impacts is likely to be big or small, and why?
- In which food and agricultural sectors are the impacts likely to be largest?
- In which developing world regions are the impacts likely to be largest?
- What can be changed so that genomics and the other ‘omics’ can have positive impacts on food security and sustainable development in developing countries in the near future?
- The relative importance of genomics versus transcriptomics, proteomics, metabolomics or other ‘omics’ in the near future

4.3 Instructions for sending a message

Before submitting a message to the e-mail conference, participants are requested to:
a) Ensure that it addresses the topics mentioned in Section 4 above. (A specific comment: This Background Document briefly mentioned GMOs, and this may also be the case during the conference. If so, discussions in this conference should not consider the issues of whether GMOs should, or should not, be used per se; their regulation; or the attributes, positive or negative, of GMOs themselves).
b) Limit its length to a maximum of 600 words.
c) Follow the ‘Guidelines for Sending Messages’ contained at the end of the Welcome Text that participants receive when they subscribe to the conference. Among other things, the Guidelines note that participants: are assumed to be speaking on their own behalf and not on behalf of their employers (unless they indicate otherwise); should introduce themselves briefly in their first posting to the conference, providing also their full work address at the end of the message; and may not post libellous, insulting or defamatory messages or materials, or links to such materials and should exercise tolerance and respect toward other participants whose views may differ from your own.

5. References, abbreviations and acknowledgements

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ABBREVIATIONS: ABDC-10 = FAO conference on 'Agricultural Biotechnologies in Developing Countries'; BAC = Bacterial artificial chromosome; Bp = Base pairs; DNA = Deoxyribonucleic acid; EST = Expressed sequence tag; FAO = UN Food and Agriculture Organization; Gb = Gigabase pairs (1,000 Mb); GWAS = Genome-wide association studies; Indels = Insertion and deletion polymorphisms; Kb = Kilobase pairs (1,000 bp); Mb = Megabase pairs (1,000,000 bp); mRNA = Messenger RNA; RNA = Ribonucleic acid; SNPs = Single nucleotide polymorphisms; WGRS = Whole genome re-sequencing

ACKNOWLEDGEMENTS: This document was prepared by John Ruane, from the FAO Research and Extension Branch. Grateful appreciation is expressed to the following people for their comments on the document: To the external referees: Milton Kanashiro (Brazilian Agricultural Research Corporation (Embrapa), Brazil); Denis J. Murphy (University of Glamorgan, United Kingdom, http://staff.glam.ac.uk/users/184); Miguel Perez-Enciso (Centre for Research in Agricultural Genomics (CRAG), Spain, http://www.icrea.cat/Web/ScientificStaff/Miguel-Perez-Enciso-255); Raul W. Ponzoni (WorldFish, Malaysia, http://cvlist.cslive.org/EmpDetails.aspx?empNum=000557); and Rajeev Varshney (International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India http://www.icrisat.org/CEG/index.htm); as well as to Paul Boettcher (FAO Animal Genetics Resources Branch) and Andrea Sonnino (FAO Research and Extension Branch).

FAO, 28 February 2013.

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-----Original Message-----
From: Biotech-Mod3
Sent: 01 March 2013 13:57
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: Welcome to the FAO e-mail conference on Genomics !

Dear Colleagues,

Welcome to this FAO e-mail conference on "Impacts of genomics and other 'omics' for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries" !! Thank you for joining.

You can send messages now (send them to biotech-mod3@fao.org). Messages will be posted from Monday 4 March onwards while the last day for receiving messages will be Sunday 24 March 2013.

We hope that the conference will be interesting, constructive and beneficial and we encourage you to participate actively. On joining the conference, you received a Welcome Text which also contains the

Guidelines for Sending Messages. Here, we would like to briefly remind you of some of the main points about the running of the conference:

1. When sending their first message to the conference, participants should introduce themselves briefly (2-3 sentences) at the top of the message. They should also provide their full work address at the end of the message. When a message is posted, we will replace @ in the e-mail address with (at) to avoid spamming.

2. Messages should not exceed 600 words

3. People posting messages are assumed to be speaking on their own behalf and not on behalf of their employers (unless they indicate otherwise)

4. No messages will be posted with attachments. If you receive a message during the conference with an e-mail attachment, just delete it without opening the attachment.

5. Messages posted in the conference will also be made available on the web, at https://listserv.fao.org/cgi-bin/wa?A0=Biotech-Room3-L

6. The Background Document to the conference, sent by e-mail to subscribers of this conference on 28 February, sets the scene for the conference. We strongly encourage you to read it, especially Section 4 (reproduced below) which provides specific guidance about the two main questions that participants should address in the conference. The document is available at http://www.fao.org/docrep/017/aq145e/aq145e.pdf (90 KB). Contact me (at biotech-mod3@fao.org) if you want to receive the document by e-mail.

Finally, we encourage you to tell any potentially interested colleagues or contacts about this conference. A short notice is included below for this purpose.

With our sincere best wishes for a successful conference,

John

John Ruane, PhD
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Genomics in Food and Agriculture – FAO e-mail conference

From 4 to 24 March 2013 the FAO Biotechnology Forum is hosting its next e-mail conference on "Impacts of genomics and other ‘omics’ for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries". Advances in genomics, the study of all the genetic material (i.e. the genome) of an organism, have been remarkable in recent years. Publication of the first draft of the human genome in 2001 was a milestone, quickly followed by that of the first crop (rice) in 2002 and the first farm animal (chicken) in 2004. Huge technological advancements have meant that sequencing has become dramatically quicker and cheaper over time, so the genomes of many of the important crops, livestock, forest trees, aquatic animals and agricultural pests are now already sequenced or soon will be. This e-mail conference will look at the impacts that genomics, and the other related 'omics', have had so far on food and agriculture in developing countries as well as their potential impacts in the near future.

To join, send an e-mail to listserv@listserv.fao.org with the following one line in the body of the message (leave the subject line blank):
subscribe biotech-room3-L firstname lastname

The background document to the conference is available from the Forum website, at http://www.fao.org/biotech/biotech-forum/en/. For more information, contact biotech-mod3@fao.org.
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[FROM THE BACKGROUND DOCUMENT - http://www.fao.org/docrep/017/aq145e/aq145e.pdf]

4. Topics to be discussed in this e-mail conference

This is the 19th e-mail conference to be hosted by the FAO Biotechnology Forum (http://www.fao.org/biotech/biotech-forum/en/) since it was launched in the year 2000. As with each conference hosted by the Forum, the focus is on applications in developing countries.

As seen in Section 2, the first sequenced genomes of domesticated animals and plants were released about 10 years ago and an ever increasing number of important species have been sequenced each year since then. Also, the genomes of several thousand micro-organisms have now been sequenced. As seen in Section 3, the knowledge generated from genomics can be applied in several different ways. In this context, the first main question to be addressed in the conference is:

4.1 What have been the impacts (positive and/or negative) so far of genomics and the other ‘omics’ for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?

In addressing this question, the specific kinds of issues that participants might wish to discuss are:

- How exactly was the knowledge derived from genomics and the other ‘omics’ used?
- What kind of impacts did they have?
- Were the impacts the same in different sectors? If not, why not?
- Were the impacts the same in different developing world regions? If not, why not?
- What products, if any, were derived from the knowledge? If products were developed, how were intellectual property rights issues dealt with (an issue discussed in the second genomics-related session at ABDC-10 (FAO, 2011b))?
- Which specific issues enabled genomics and the other ‘omics’ to have positive impacts (e.g. government policies, international collaboration, public-private partnerships, complementary infrastructure, germplasm distribution networks)?
- Which specific issues prevented them from having positive impacts (e.g. costs, intellectual property rights, the species sequenced)?
- Were the impacts influenced by the sequencing strategy (e.g. generating genome sequence data in-house in developing countries versus outsourcing this work)?
- The relative importance of genomics versus transcriptomics, proteomics, metabolomics or other ‘omics’

While the first main question looks at the past and the present, the second main question looks to the near future:

4.2 What are the impacts (positive and/or negative) of genomics and other ‘omics’ likely to be in the near future (e.g. the next five years) for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?
In addressing this question, the kind of issues that participants might wish to discuss might be:
- Whether the magnitude of their impacts is likely to be big or small, and why?
- In which food and agricultural sectors are the impacts likely to be largest?
- In which developing world regions are the impacts likely to be largest?
- What can be changed so that genomics and the other ‘omics’ can have positive impacts on food security and sustainable development in developing countries in the near future?
- The relative importance of genomics versus transcriptomics, proteomics, metabolomics or other ‘omics’ in the near future

-----Original Message-----
From: Biotech-Mod3
Sent: 04 March 2013 16:15
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 1: Genomics-based crop improvement

[Thanks to Professor PK Gupta from India for sending in the first message of this FAO e-mail conference on the "Impacts of genomics and other ‘omics’ for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries". All messages will be numbered chronologically. If during the conference you notice that you are missing any messages, just contact me at biotech-mod3@fao.org ...Moderator].

I am Pushpendra Kumar Gupta, Emeritus Professor, Department of Genetics & Plant Breeding, CCS University, Meerut, India. At Meerut, as a group, we have been involved in crop biotechnology research for more than 20 years now. More particularly, we have been involved in the development and use of molecular markers in wheat (a cereal) and jute (a fibre crop). We have also been involved in QTL interval mapping and association studies in wheat and jute, followed by use of marker-trait associations for marker-assisted selection (MAS) for wheat breeding.

During the last 10 years, I have come across the phrase “genomics-based crop improvement”, which I have not been able to appreciate, since genomics research has not been directly used (and will not be used in future) for crop improvement, although it is relevant to crop improvement programs, since it helps us in the discovery of genes and markers, which are subsequently used for crop improvement either through the development of transgenics or using MAS. Genome sequences or transcriptomes, proteomes or metabolomes cannot be directly used for crop improvement programs, although this information may indirectly prove useful for crop improvement. Therefore, I don’t see any direct impact of genomics and other ‘omics’ research on crop improvement in developing countries. Under these circumstances, in this conference, we need to discuss if there are examples of an indirect impact of genomics and other ‘omics’ research on crop improvement. The participants should enumerate examples, if any, where this research had a direct impact. If not, we should discuss indirect impact through development of markers and discovery of genes. There are also hardly any examples where genomics or other ‘omics’ disciplines were first used for development and use of markers or for the discovery of genes, which later led to the development of improved cultivars, which can be traced back to genomics or other ‘omics’ research. If there are examples, I would myself like to be educated.

Under the above circumstances, we should give-up using the phrase “genomics-based crop improvement” (which is misleading), because crop improvement programs make use of markers, rather than genome or transcriptome sequences. These genomics and other ‘omics’ research areas generate knowledge and resources, which can then be used to develop resources that are directly used for crop improvement programs.

Notwithstanding the above, ‘whole genome resequencing’ (WGS) has been used for quantitative trait locus (QTL) interval mapping and association mapping studies, leading to identification of single nucleotide polymorphisms (SNPs), which may prove useful for crop improvement, but there are no examples where this has actually been achieved successfully. Perhaps only in future this may be done successfully. In our own laboratory, we are trying to identify wheat orthologues using available genes and sequences for traits like nitrogen/phosphorus use efficiency (NUE & PUE) and water-use efficiency (WUE), and then design polymerase chain reaction (PCR) primers for these orthologues to be used for study of polymorphism in the available wheat germplasm. This will perhaps give us markers to be used for crop improvement programs. This will be the future area of research, where genome sequences will be used for crop improvement. Also expressed sequence tag (EST) databases have already been extensively used for development of simple sequence repeat (SSR) and SNP markers in a number of crops, but this is also an indirect use of transcriptome data for crop improvement.

I would like the above issues to be addressed in this e-conference.

Professor PK Gupta
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[Orthologues, mentioned above, are genes derived from a common ancestor through vertical descent (or speciation) and can be thought of as the direct evolutionary counterpart. In contrast, paralogues are genes within the same genome that have evolved by duplication. (Source: Ensembl glossary (http://useast.ensembl.org/info/website/glossary.html) ...Moderator].

[To contribute to this conference, send your message to biotech-mod3@fao.org. For further information on this FAO Biotechnology Forum, see http://www.fao.org/biotech/biotech-forum/]

-----Original Message-----
From: Biotech-Mod3
Sent: 05 March 2013 16:25
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 2: Importance of software for genomics applications

I am Vadivel Arunachalam, Principal Scientist and Head Horticulture section and I work at the Indian Council of Agricultural Research (ICAR) at Goa centre. I worked on computational genomics and mining of genome sequences, expressed sequence tag (EST) libraries for new molecular markers (SSR, SNP, priming sites of RAPD/iSCAR). I authored a book on genomics of cultivated palms published by Elsevier. The book is a review of genomics research on palms (the plants belong to Arecaceae family). We also developed on molecular markers associated with resistance to root (wilt) disease, eriophyid mite pest in coconut. Root (wilt) is a serious disease in coconut palms of Southern India. These identified (SSR, RAPD, SNP region) markers we identified have potential in 70% accuracy of identifying the given DNA sample as resistant or susceptible.

We also developed two softwares for genomics applications:

1. Marker express 1.0 for a) locating priming sites of RAPD/ISSR primers on genome/EST sequences and b) to design in silico SCAR (iSCAR) primers. It was validated using oil palm expressed sequences and comparing with published polymorphic RAPDs (Premkrishnan, BV and V. Arunachalam. 2012. In silico RAPD priming sites in expressed sequences and iSCAR markers for oil palm. Comparative and Functional Genomics, http://www.ncbi.nlm.nih.gov/pubmed/22474414).
2. DG MAP was developed to map the primers and genes on a given genome sequence. We validated it on F locus of cucumber and found additional markers linked to F locus.

We (the authors of the software - BV Premkrishnan and myself) can help researchers to analyse the genomes using these softwares and provide the results. We also analyse few fruit and vegetable genomes and in the process of putting a database of iSCAR markers. We provide the software services only to academic (non-profit) researchers free of cost. They can explain the research problem or give details of the organism of their choice, input files of sequences to be searched and primers to be mined. Premkrishnan and I will analyse and send the output to the researchers.

Implication of these softwares in interpreting the marker-trait-gene relationship in whole genome sequencing efforts in organisms of agricultural importance is tremendous. Most of genome sequencing project aim at annotation of genes and mine for SSR, SNP regions. Quantitative trait loci (QTL) mapping experiments reveal marker-trait-gene associations in genomic regions on specific chromosomes. But the software-aided interpretation of these regions for fine mapping has important implication for population genetics/genetic improvement. Resequencing of fine mapped regions in potential populations/individuals of organisms of interest has potential in fine tuning the breeding programs.

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[ISSR, RAPD, SCAR, SNP and SSR molecular markers were mentioned above. These acronyms stand for inter simple sequence repeat (ISSR), random amplified polymorphic DNA (RAPD), sequence characterized amplified region (SCAR), simple sequence repeat (SSR, or microsatellite) and single nucleotide polymorphism (SNP). For more information on the different kinds of molecular markers, see Conference 10 of the FAO Biotechnology Forum, dedicated to "Molecular marker assisted selection as a potential tool for genetic improvement of crops, forest trees, livestock and fish in developing countries" (http://www.fao.org/biotech/biotech-forum/conference-10/en/) or the FAO book on "Marker-assisted selection: Current status, and future perspectives in crops, livestock, forestry and fish" (http://www.fao.org/docrep/010/a1120e/a1120e00.htm) ...Moderator].

-----Original Message-----
From: Biotech-Mod3
Sent: 06 March 2013 09:09
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 3: Re: Genomics-based crop improvement

I am Kedar N. Rai, working as a pearl millet breeder (using conventional breeding approaches and achieving great successes) at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. But I do try to read and follow the discussions on application aspects of genomics, and it is with this intent that I joined this e-conference.

I have read with interest the points raised by Dr. PK Gupta (Message 1) and I generally agree with him. I believe that quite a lot of basic work and validation of the results using diverse genetic backgrounds and test environments needs to be done to convince about the efficiency of genomics and other biotech tools (cost consideration not to be forgotten) in crop improvement. Its value in improving highly heritable traits controlled by few major genes cannot be doubted, although in many cases it has not been convincingly demonstrated as to why that improvement was thought un-amenable through conventional approaches: a few selected examples may not help (rather a list of successful/unsuccessful examples will be more convincing). Such things as genomic selection, proteomics, transcriptomics etc. are good researches for biological understanding, and may be useful breeding tools in quite distant future. Hope these will not end up the way research on drought tolerance mechanisms (tons of books and research/conference papers) with limited application successes went. It may be decades before these new biotech tools will find routine applications in applied plant breeding. The need for enormous increase in food production in the next 30 years is well known, and yield potential improvement remains the big challenge. These new tools for yield improvement ?--any leads having passed large-scale demonstrations with on-farm impacts?

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-----Original Message-----
From: Biotech-Mod3
Sent: 06 March 2013 11:47
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 4: Opportunities of genomics for the livestock and plant sector of the "tropics"

This is Olivier Hanotte. I am a livestock geneticist working at the University of Nottingham (UK) for the last 4 years before that I was working for the International Livestock Research Institute (ILRI), a Consultative Group on International Agricultural Research (CGIAR) institute.

In my opinion, the opportunities of genomics for the livestock and plant sector of the "tropics" is more on the new perspectives it is offering rather than new solutions to old problems. Animals and plants breeders know what they are doing. They have done it very well for centuries and will do as well for the coming generations. Genomics may help to speed up the process of breeding selection but fundamentally, it will not change the modus operandi, breeding associated to phenotypic and/or genotypic markers... It will be very helpful but no new thinking, "just" a new, very powerful tool for the same thinking.

Genomics will have a stronger impact on agricultural productivity if it can offer new solutions to our problems. We may need here a small paradigm shift in our thinking. A supermarket thinking where the buyer is the farmer, and where on the shelves we find the products: the livestock and crops genotypes, a large diversity of phenotypes to choose from. I think all the "ingredients" are here to make it work (and one of them are the biobanks). It is not going to be easy to make it work, but we have to prepare ourselves now; it is a process in the making.

In other words, when its full potential will be unleashed, genomic information will provide the missing link: the genotype barcode carrying the phenotypic information, the labeling of your product. Genomics could offer the farmers the opportunity to choose the best genotypes for livestock/plant productivity for a specific livestock productivity environment at a specific time point. Farmers will be able to buy, introduce, use, breed plant livestock genotypes knowing in advance what they will get at the end (at least with much less uncertainty).

Rather than rely on a silver bullet genotype a super crop or livestock which by definition will always require a specific production and market chain environment; genomics may offer the opportunities at last to exploit fully the diversity of our livestock and crops an important way forward for sustainable agricultural productivity.

Equally important will be tight up the agricultural genomics revolution with other ongoing technological revolutions providing increased global and local geo-spatial and environmental information.

The next question is what is the best optimum modus operandi (framework) to be developed to make it work....

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-----Original Message-----
From: Biotech-Mod3
Sent: 06 March 2013 17:30
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 5: Fermentation of cysteine

This is Jim Currie, MD of Currie Marketing. I have been involved in sales and marketing of food ingredients for 30 years although I did get a BSc Chemistry many years ago !

One of my pet projects is the production of l-cystine and L cysteine by fermentation. There is a good size market for cysteine for flavour production and as a bread additive. Most of the world supply is extracted from chicken and duck feathers and in the past from human hair. All are sources of keratin. The production of fermentation cysteine requires pure strains of bacteria and good operating procedures. The sequencing of the bacteria I understand should be much simpler and faster today and a lot cheaper. However there still seems to be problems in producing L-cysteine or the dimer cystine from fermentation. If anyone can assist or throw light on this topic please get in touch. My knowledge of biotech is limited but my knowledge of where cysteine can be sold is excellent

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-----Original Message-----
From: Biotech-Mod3
Sent: 08 March 2013 09:50
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 6: Re: Genomics-based crop improvement

This is from Drew L. Kershen, University of Oklahoma, United States.

In answer to the query in Message 3 by Dr. Rai, requesting examples (a list) of the efficiency of genomics and other biotech tools, I respond with several. Although not a scientist, I work on legal issues related to modern breeding techniques. Due to that work, I have learned some examples or citations as follows.

Insect resistance in soybeans is conditioned by 3 major genes, any of which gives resistance. Prior to the availability of genomic tools, it was not possible to tell if plants had 1, 2 or 3 of the genes because all condition for the same trait. Secondly, the wild plants with these genes have a lot of very undesirable traits. Thus, prior to the advent of genomic tools, there were 40 years of breeding attempts whereby the breeder either got the agronomic qualities back but lost the insect resistance, or vice versa. With genomic tools, such linkage drag is significantly decreased as an issue.

An example of conventional and transgenic approaches complementing each other exists for virus resistance in cassava. Conventional resistance was available for one virus, but not for the other and both techniques are needed for crop protection in the target area. (H. Vanderschuren, et al., Exploiting the combination of natural and genetically engineered resistance to cassava mosaic and cassava brown streak viruses impacting cassava production in Africa, PLoS One (Sept. 2012) 7:e45277 - http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0045277).

A specific project by Two Blades Foundation is to move a bacterial spot resistance gene from pepper into tomato. If successful, this new tomato variety would replace copper sprays for bacterial control. The solution was unamenable to conventional breeding because peppers and tomatoes do not cross. Furthermore, good natural resistance to the bacterial spot has not been found in tomato. (D.M. Horvath, et al., Transgenic resistance confers effective field level control of bacterial spot disease in tomato, PLoS One (Aug. 2012) 7:e42036 - http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0042036).

Middle-sized companies in the vegetable breeding area routinely generate tens of millions of data points annually for genotyping using molecular markers enabled by genomic sequencing and mapping. The breeding is conventional, but hugely enabled and made more cost-effective by molecular markers. Genomic sequencing is routine for major disease resistance and quality trait genes in most of these crops. The use of markers becomes so much more efficient than the traditional methods, which require screening the whole population for all of the diseases.

Some things can't be done by conventional breeding where there is a genetic glass ceiling - i.e., the needed gene does not exist in the species or its interbreeding relatives. The various virus and other disease resistance are examples. For a book that provides a goodly number of examples of this genetic glass ceiling, J. Gressel, Genetic Glass Ceiling: Transgenics for Crop Biodiversity (Johns Hopkins Univ. Press, 2008) 461 pp.

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-----Original Message-----
From: Biotech-Mod3
Sent: 08 March 2013 10:03
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 7: What have been the impacts of genomics so far...

This is from Kedar N. Rai, again.

We need to address more main question 1 (i.e. "What have been the impacts (positive and/or negative) so far of genomics and the other 'omics' for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?"). And just a few selective examples may not be so convincing. I am aware of some success stories of marker-assisted selection (MAS), but the question that those successes could have also been achieved by conventional breeding at much lower cost has not been answered (of course, the conventional approach would have taken a bit longer). Further, if a lab had achieved a particular success by genomic method, whether that lab repeatedly achieved further successes or was it a one-time shot has not been adequately addressed. These are important questions to be addressed from the viewpoint of (i) demonstrating the genomic tool power, and (ii) convince the conventional plant breeders about this power and then bring them on board to use it in their program. In doing this, the cost consideration must not be left unaddressed. I am more interested in genomic tools power in allele mining, and would like to see the outputs. Also, application of genomic sequencing in crops done quite some time ago. I have been very excited to learn about an outstanding report on yield gene in wild rice published from Cornell University. It was done more than 15 years ago. Any application of this gene and on-farm impact, considering that MAS shortens breeding time.

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-----Original Message-----
From: Biotech-Mod3
Sent: 08 March 2013 10:19
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 8: Future contribution of genomics to indigenous breeds

A message from David Steane - retired and based in Thailand. Before retirement, I lead an FAO project on 'Conservation and Use of Animal Genetic Resources in Asia' after 4-5 years in Rome HQ. Prior to that, I was Head of Animal Breeding and Genetics for the Meat & Livestock Commission in Britain for over 20 years. At present, I am a Board Director of Rare Breeds International and Honorary Adviser on Genetics and Biodiversity to the Department of Livestock Development, Thailand.

While most genomic efforts appear to be taking place in 'developed' breeds, I believe that a much greater contribution can be made by proper study of local/indigenous breeds. At present, livestock production is under great pressure to provide more product but, at the same time, to reduce its contributions to carbon emissions, water consumption, pollution and its direct competition for human foods. It is expected to do this while coping with climate change and all its consequences on the ability to produce feeds and food preferably in the locations where required. FAO has, after too long a delay, now provided a means to include crucial information alongside the data on breeds. The inclusion of Production Environment Descriptors (PEDs) is very late but nevertheless very welcome as they provide a means of using breed information in a more effective manner. Genome sequencing of such indigenous breeds would enable such data to be analysed alongside various criteria of PEDs to identify sequences which enable breeds to cope with specific conditions. Given such information, the world would be in a much better position to properly and effectively utilize the genetic diversity available and could do so as and when environmental changes such as climate, feeds available etc were better identified. Such a scheme requires global thinking, planning and support and yet most governments could manage to collect suitable samples for sequencing (some would need help in achieving the purity levels needed). The ability to sequence the different species is expanding rapidly and costs are reducing relative to the data obtained. While present efforts appear to concentrate (understandably) on more immediate returns, it is our responsibility to provide the best opportunities for the next generation in the context of food security and health. Genomics can play an important role but only if we have the right information.

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-----Original Message-----
From: Biotech-Mod3

Sent: 08 March 2013 16:30
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 9: Genomics and related omics to aquatic resources - fish resources

This is from Petros Chigwechokha, Kagoshima University, Japan.

Impacts of genomics are rather difficult to clearly isolate when it comes to aquatic resources. Genomics and its application to aquatic resources, particularly fish, still lags behind compared to other organisms. As rightly indicated in the conference background document, genomic work, most importantly, genome mapping, has been done in zebrafish (Danio rerio), medaka (Oryzias latipes) mostly because these have been widely used as model organisms for more insights into the functions of various genes that are important to human health (e.g. neuraminidase and transferase genes). Such studies have received a lot of attention by their link with human science studies (mostly diseases) and have enjoyed a lot of financial and material support. Consequently, the information generated has had an application elsewhere and not in fishes. Nile tilapia (Oreochromis niloticus) genome mapping could be isolated as the only work which has independently been conducted based on the value of the species considered. Hence, there is limited work in genomics, proteomics, metabolomics with cis-application as regards aquatic resources for such to bring out visible impacts.

In developing countries, the problem is compounded further by ‘capital intensity’ for doing work in genomics. Most developing countries have the capable human resources in genomics and related research but, unfortunately, lack necessary materials for advancing such type of research. As a result, developing countries are actually recipients of already packaged products of genomics and are themselves not generating any.

The available information has so far been used in developing molecular markers with a very wide application. Genomic and other related omics have, successfully, been used as a tool in selection for growth, spawning success, diseases resistance and other important traits, though the scale of use is very limited. Other impacts of genomics are the development of transgenic fishes, where individual labs have managed to produce such fishes but have not published the results. Genomics have also been used in development of conservation and management tools for various aquatic resources including fishes, despite the fact that this is very rare in developing countries. In general, summed up impacts are way minimal in aquatic resources if compared to the impacts in other sectors such as crops, livestock, etc.

More tangible impacts of genomics to aquatic resources in developing countries may not be available in the short-term, though the advances made in genome mapping of some fish species, most notably Oreochromis niloticus do provide some potential for more visible and tangible impacts in the near future. Unfortunately, various factors including political will, equipment and material availability, should be in place for the developing countries to achieve the desirable impacts in aquatic resources. It is a known fact that research in genomics and other omics is not cheap and scientists in developing countries can hardly afford sustaining such type of research.

Currently, I am working on molecular cloning and characterization of some genes in O. niloticus and their effects glycoconjugates and other metabolomics in an effort to develop biomarkers for various attributes in fish. The results are looking positive and I can include this as one of the impacts of genomics (though results are to be reported in the very near future). This work has directly benefited from the available whole genome sequence of O. niloticus. Unfortunately, this kind of work can only be done in laboratories which are high-tech equipped and its replication in another species and other labs especially in developing countries is unthinkable due to some of the issues herein (e.g. Malawi, where I am originally from).

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-----Original Message-----
From: Biotech-Mod3
Sent: 09 March 2013 19:15
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 10: Role of genomics in plant and livestock improvement in developing countries

My name is Uche Godfrey Okeke. I have a masters in Bioinformatics and Systems biology and a bachelors in Animal breeding and Genetics. I am currently a Bio-informatician at the DNA Sequencing and Genomics Lab, Institute of Biotech, University of Helsinki, Finland.

I must confess that I am a bit disappointed with the number of people contributing to this topic on the role of genomics in plant and livestock improvement in developing countries especially now that there is a wave of projects focusing on the application of genomic selection in many species of plants and animals across the developed world.

I am indeed very delighted as an African about this technology - Genomic selection. Genomic selection provides a way to incorporate Mendelian sampling into breeding thus allowing genomic prediction for young animals and plants. This is a sharp contrast to the age of progeny testing and several field trials required to ascertain the genetic merit of an individual. The direct consequence of this is that we in the developing world endowed with a great diversity of previously non-bred plant and animal species can start a breeding program now and be able to make fast genetic gains in a little time as compared to the time gains were made in the developed world using phenotypic breeding.

Secondly, I am also delighted (as I have always upheld this opinion) that genomic selection is a plus for food security. In Africa especially and other developing countries, the concept of food, food ingredients and nutrition differs from that of the developed world. Across regions, religions, tribes, geographical locations and so on, food and food ingredients vary greatly and even similar ones differ in their texture, taste, processing and cooking methods. This is a pointer that a niche market of food systems exist in these regions. With genomic selection, a tremendous progress can be made to develop these market niches by breeding crops and animals that satisfy the demands of these markets. Again, the main point here is that since Mendelian sampling can be utilized for breeding purposes, individuals (genotypes) with superb qualities for the support of these niche markets which previously have been discarded during breeding can be harnessed and properly utilized.

A lot of scientists, especially plant breeders, have argued that the only reason they are adopting this technology is because of the reduction in generation interval when compared to phenotypic breeding. Well, if this is the only stuff they see as gain, there its still a difference especially considering the fact that time is a key factor in breeding.

I want to point out the issue of reduced genetic variation in a population undergoing selection. The fear is that no gain will be made after some time because there is no more variation to support new gains. I want to point out an idea I have nurtured over time and which someone else shared and even had some explanations to back it up. In 2012, I was at a lecture by Professor Morris Soller (from Dept. of Genetics, Hebrew University; a lecture organised by the University of Helsinki) who coined out a phrase for this idea - selection induced genetic variation (SIGV). I gathered from this lecture that in a population under selection, genetic variation can be introduced by epistasis and recombination. It is particularly plausible to me (from my own ideas) that additive-by-additive epistasis (to any powers) and favorable recombination can combine very good genes thus developing novel gene expressions that will be superior to the average of the population. This gets more interesting if you consider the fact that some of these good genes might be pleiotropic thus offering better chances. I think we are yet to see the outcomes when breeding enabled by genomic selection starts and am pretty optimistic about this.

Finally, next generation sequencing is a wow technology. Who would have imagined a decade or two ago that people could do a mini sequencing job for a rarely known species with a low budget for the purposes of generating markers for breeding. I think a lot of achievements have been made in the field of agricultural genomics and more are coming.

My only concern is that African leaders, governments, and those in authority do not really understand the enormous potential and benefits embedded in investing in this technology especially for countries like mine (Nigeria) with a lot of human and natural resources, skill and biodiversity to make progress with this technology.

My goal with this piece is to start up a debate that will be beneficial for the implementation of genomic selection in Africa and other developing countries.

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[Epistasis is the interaction between genes at different loci, e.g. one gene suppresses the effect of another gene that is situated at a different locus. Pleiotropy is the simultaneous effect of a given gene on more than one apparently unrelated trait. The selection induced genetic variation (SIGV) hypothesis was described by Y. Eitan and M. Soller (2004. Selection induced genetic variation: A new model to explain direct and indirect effects of sixty years of commercial selection for juvenile growth rate in broiler chickens, with implications for episodes of rapid evolutionary change. In: S. Wasser (ed.). Evolutionary theory and processes: Modern horizons. Kluwer Academic Publishers, Dordrecht. p. 153–176). It argues that because of epistasis, long term selection can continuously generate part of the genetic variation required for its own continued response...Moderator].

-----Original Message-----
From: Biotech-Mod3
Sent: 09 March 2013 19:28
To: Biotech-Room3-L@LISTSERV.FAO.ORG
Subject: 11: Re: Genomics-based crop improvement

This is from Dr Chandra Sekhar Mukhopadhyay, Guru Angad Dev Veterinary and Animal Sciences University (GADVASU), India.

In reply to Dr. Drew L. Kershen (Message 6):

The replies are really impressive and hold promise. From my early inititaion in this field, I found that the molecular level solutions have always replaced the predecessor. (perhaps this is the essence of science). Now it is the time of molecular breeding with genomic selection. Can we expect that this will help the developing countries, at least to some extent. If yes, how to solve the problem of recording the proteome, at practical level, in terms of farmers' interest.

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-----Original Message-----
From: Biotech-Mod3
Sent: 10 March 2013 07:32
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 12: Omic studies in the least developed countries should have to emphasize on adaptation traits

I am Takele Taye Desta, a PhD student (Genetics) in The University of Nottingham, United Kingdom.

The majorities of a sort of omics works conducted so far in developing countries are related to genomics and in most instances these have been concentrated on genetic diversity studies. In fact dealing with genetic diversity and population structure is the entry point to work on omic disciplines. However, even these types of basic genomic works are by and large far from complete compared to the high level of genetic diversity existing in the least developed nations.

High levels of genetic improvement have been achieved for yield related traits. However, little (if any) effort has been made so far to improve genetic attributes related to hardiness. Genomic selection is a robust tool to bring genetic improvements of these kinds. In the era of alarming climate change we should have to think about robustness while developing breeds or varieties. In the meantime we also need to have deep knowledge on the efficiency of the production environments to maintain improved breeds (varieties). Genetic improvement alone may not bring magic solution if the production system is unable to support the additional genetic improvement gained.

Therefore, we need to devise an appropriate plan to exploit the wealth of adaptation traits embedded in traditional breeds through long lasting act of natural selection. This would create opportunity to introgress genes that confer hardiness (to low producing animals) to high yielding but susceptible animals. This is, however, not to say there is not any room for improvement of production traits given the large genetic variation that exists among indigenous breeds, but we need to combine yield traits with hardiness (though they are unfavourably correlated) to fit into the existing production system.

Omics require the state of art lab and computing facilities, knowledge and a carefully designed project. Therefore, all these things definitely require a substantial amount of resources which are largely beyond the capacity of most of the developing countries and hence support from developed nations is indispensable. In conclusion, we may need to develop special study protocols specifically to collect data on phenotypic traits used in association studies as the conventional type of data recording adopted in developed nations is entirely absent at smallholder farmers level.

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-----Original Message-----
From: Biotech-Mod3
Sent: 10 March 2013 07:33
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 13: Genomics for livestock improvement in developing countries

I am Abdulmojeed Yakubu, a senior lecturer in Animal Breeding and Genetics, Department of Animal Science, Faculty of Agriculture, Nasarawa State University, Keffi, Shabu-Lafia Campus, Lafia, Nigeria.

In Nigeria, while data exist on the application of genomics to improve crop production, little can be said of livestock improvement via biotechnology. In a recent lecture by Dr. I.G. Imumorin of the Department of Animal Science, Cornell University, Ithaca, "potential exists for application of biotechnology to livestock improvement in the areas of disease resistance, nutrition and reproduction". In fact, the technology of genomic selection where we select superior animals based on total genome information is a ground-breaking technology poised to transform livestock productivity in developing countries. I am quite aware that in 2010, the Federal Government of Nigeria through the Agricultural Research Council of Nigeria (ARCN) disbursed loans worth thousands of dollars to researchers to embark on cutting-edge research in livestock genomics. It is hoped that by the time the reports are submitted, the necessary organs of government charged with implementation will swing into positive action so that we can start to witness significant improvement in livestock resources in Nigeria, Sub-Saharan Africa

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-----Original Message-----
From: Biotech-Mod3
Sent: 10 March 2013 07:34
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 14: Re: Role of genomics in plant and livestock improvement in developing countries

I am Pushpendra Gupta again (I sent message 1). I like this message 10 by Uche Godfrey Okeke, and would like to submit as follows:

(1) I am also disappointed with the number of messages received (hardly 2 messages per day); what is the reason for this? I believe that not many people have read enough and therefore know enough about the role of genomic selection in crop improvement and never tried to practise it in developing countries including India, not because they don't approve of it, but because they cannot appreciate the technology yet (although the technology still suffers with difficulties of telling us which is the best prediction model; prediction models are still being suggested and it will take time to develop the best model).

(2) I also agree that most leaders, governments, and those in authority in India (like other developing countries) do not really understand the enormous potential and benefits of genomics selection and genotyping by sequencing (GBS). This is why a workshop on the use of genomics selection for wheat improvement is being organized in France in Spring/Summer of 2013. I would have personally liked such workshops on "genomics selection and other statistical genomics tools" organised in developing countries like India on a regular basis.

(3) In my message 1, I questioned a direct role of genomics for crop improvement; but genomics selection is perhaps one area, which needs to be tried and has a promise. Genomics-based genotyping and GBS for marker assisted selection and marker development could be other areas that will grow and need attention, due to the development of next generation sequencing (NGS) methods associated with dramatic reduction in the cost of sequencing.

(4) I also liked the idea of 'selection induced genetic variation' (SIGV), which is new and needs further elaboration, for those who are new to the idea of genomic selection. It is not clear how genetic variation can be introduced via epistasis and recombination; will it be recurrent selection involving cycles of selection and intermating? Uche Godfrey Okeke or somebody else may like to throw further light on this.

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-----Original Message-----
From: Biotech-Mod3
Sent: 11 March 2013 05:56
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 15: Genomics to help developing countries?

This is from Dr. Paulo Ramos, Environmental analyst from Brazil. I have been working with Agroecology and biodiversity conservation. I am now representing the Brazilian Agroecology Social Organizations as a member of the National Technical Commission for Biosafety (CTNBio).

I would like to thank everybody for sharing experiences here in this e-mail conference.

Here and there we are listening about biotech-genomic themes as a model that will help developing countries, help to put away the growing poor population's hunger threat, help with deseases like dengue, malaria and so on. But in general what we can see is that these technological improvements are taking other directions. They are at the service of others than developing countries or peasants.

I want to stress here that in Brazil about 80% of food cames from the peasant production which is not related to genomic improvements. Much of beans, fruits and vegetables does not relate to genomic achievements.

If those tools are to help famine, help the environment, help health shouldn't they promote agro-biodiversity instead of monocultures agrotoxic related like we see now. Shouldn't they promote sharing of the social-economic benefits from the wealth generated. Shouldn't they be at the service of the peasant families instead of the Big-Ag commodity companies. Shouldn't they be protecting environment and health.

We can see right now on Brazilian TV-News the amazing traffic jam where trucks get stucked in a kilometric long line to unpack their commodity grains, to fill boat holds to China, Europe or somewhere else in the world. All this grain production is related to biotech innovations of Monsanto, Syngenta, Dow AgroSciences, Bayer, Du Pont and some few others agrobusiness corporations.

We can also see right now in technical magazines the foreseen crop attack of Spodoptera frugiperda and Helicoverpa zea which are putting down the yields of maize, soy and cotton in Brazilian fields.

So, I would like to hear from the participants of this conference something that could show a distinct direction on the use of the technologies we are here to discuss about.

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-----Original Message-----
From: Biotech-Mod3
Sent: 11 March 2013 09:31
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 16: Distinguishing 3 categories of use of genomic technologies

This is from Professor John Gibson, Director of The Centre for Genetic Analysis and Applications, Armidale, Australia.

The discussion so far has covered multiple types of use of genomic technologies. I suggest that for both plants and animals it useful to distinguish three broad categories of use:

1) Use to gain information (research) that assists in the subsequent development process (e.g. characterising plant gene bank accessions or livestock breeds; assessing endemic pathogen diversity).

2) Use to develop new products (e.g. improved crop varieties; improved livestock breeds, non-genomic diagnostics, etc) that are then disseminated to aid development.

3) Use in ongoing applications in the field (e.g. genomic assisted breeding of livestock; genomic diagnostic tools)

In the case of 1 and 2, the genomic technologies are used for a discrete period of time and usually only in a single location. In case 3, long-term (ongoing) expertise and facilities are required for genomic technologies and supply chains into and back from the field are required. Comparing 1 vs 2, maintenance of genomic expertise/facilities will generally be required for much longer periods for 2 than for 1, since generation of new products generally takes longer than generation of new knowledge. As with most advanced technologies, maintenance of expertise and facilities for genomic technologies require much supporting infrastructure to be in place; establishment of genomic expertise and facilities in-country will be much easier when the need is for a discrete period of time only rather than an on-going need, where sustainability of such expertise/facilities and their operations will be difficult and expensive to ensure in many situations.

In summary, applications of genomic technology face increased challenges to sustainability as they move from categories 1), through 2) to 3) and this should be taken into account when making predictions about potential to add value to plant and livestock systems in the developing world.

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-----Original Message-----
From: Biotech-Mod3
Sent: 11 March 2013 09:36
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 17: Genome assisted selection in livestock

This is from John Gibson, again.

In the livestock world, geneticists understandably hold out hope for the application of genome assisted selection tools in developing world systems. The argument is that in most cases there is no existing genetic improvement program and genomic tools provide an alternative to the establishment of on-going recording and genetic evaluation programs. But genomic selection faces many of the same hurdles that have prevented effective genetic improvement using existing technologies. A few of these include:

A) genetic improvement is too often based on wishful thinking rather than critical assessment of farmer livelihoods, needs and demands......research geneticists have a poor track record in both developed and developing world of producing products that farmers actually want;

B) genetically improved livestock require sustainable distribution systems that among other things provide the clear incentives (price and demonstrably improved genotype) for farmers while also having a sustainable business model for the agencies/businesses operating the delivery chain;

C) need for a technically sound improvement program that is sustainable for the length of time (long) it will take to make improvement sufficiently large that the program has positive cost-benefits for the breeders undertaking the improvement and for the farmers offered the product.

In the developed world, initial excitement about genome assisted selection has been tempered by research results that have led to all genomic selection being based on enhanced relationship matrices and from these improved accuracy of estimated breeding values (EBV), and not results from genome-wide association studies. The techniques being used in developed country genetic improvement programs today are not applicable in most developing countries because they all require on-going extensive recording programs, which in most cases do not exist.

Much social-economic-genetic research is required to determine where and how genome assisted selection could deliver value in developing world livestock improvement. Without such research we can confidently predict that most money invested in genomic selection in the developing world will not result in improved livestock being used widely by farmers; just as the majority of investments in conventional genetic improvement have previously failed.

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-----Original Message-----
From: Biotech-Mod3
Sent: 11 March 2013 12:47
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 18: Re: Distinguishing 3 categories of use of genomic technologies

This is from David Jordan, Sorghum Breeder, Queensland Alliance for Agriculture and Food innovation at the University of Queensland, Brisbane, Australia.

I think John Gibson (Message 16) makes some excellent points which are equally relevant to plant breeding. In order for application of genomic selection methods to generate good returns there is a requirement for a large suite of supporting skills and infrastructure (high level of conventional plant breeding capacity, DNA extraction, data management systems, seed and DNA inventory and tracking systems, statistics, rapid generation turn around, perhaps double haploid systems etc). In many cases, these are hard or impossible to develop and maintain for sufficient time and the loss of a single capacity can prevent the system from functioning. Building and maintaining these systems is a big challenge in many developing countries. In addition, I think there are also major issues of scale. Genomic selection is not well suited to small scale breeding programs which are typical for plant breeding programs in many parts of the world. As a result, many programs lack the necessary scale to make use of the potential benefits such that resources used to develop the integrated suite skills and capacities for genomic selection would generate greater benefits if simply applied to improving conventional breeding capacity.

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-----Original Message-----
From: Biotech-Mod3
Sent: 11 March 2013 13:57
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 19: Re: Role of genomics in plant and livestock improvement in developing countries

This is Uche Godfrey Okeke, again. Greetings again to everyone and special thanks to everyone contributing in these discussions.

I am very pleased with the statement from John Gibson (Message 17) stating: " genetic improvement is too often based on wishful thinking rather than critical assessment of farmer livelihoods, needs and demands......research geneticists have a poor track record in both developed and developing world of producing products that farmers actually want".

This is exactly where the focus should be. It should be the rural community, the society and the local market niche that should tell us what to breed. If this is adhered to, then there is hope for food security. Just as Paulo Ramos (Message 15) described, regional breeding will give power to the rural people and not corporations. This is where I am very hopeful. The use of genomic selection technology promises gains in short time so that the gap we are missing in genetic improvement is filled within a short time period.

Secondly, I would like to talk more (see my Message 10) about selection-induced genetic variation (SIGV).

Lynch and Walsh (1998) in their famous book "Genetics and analysis of quantitative traits" clearly outline epistasis as one major source of genetic variation. Epistasis is simply said to be interaction of genes between loci (i.e. interaction between genes from different loci). This interaction grows with increase in the number of loci. They clearly state that epistatic interactions greatly inflate additive and dominance variances. It follows that even if epistatic effects are small, their summed effects may be very large. In fact, all genetic variation due to non-additive gene actions is by epistasis (Lynch & Walsh, 1998). For example given two loci, epistatic interactions can be additive X additive, additive X dominance or dominance X dominance. Remember that these interactions increase in power (^) with increased number of loci.

According to Eitan and Soller (2004), consider quantitative trait loci (QTLs) in a population under selection. These QTLs (or alleles or genes with effect on the complex trait) have additive or summed effect but they also exhibit strong interactions between each other from different loci (epistatic interactions). Recall that this is a population so that these QTLs are from different genetic backgrounds.

Now, this implies that a QTL or allele or gene with a minor (small) or neutral (simply understand as no effect - but no gene has a zero effect) effect in genetic background A might have a strong effect when it is transferred to another genetic background B. With this, a neutral or minor locus transforms into a QTL in a favorable genetic background. This is because it is interacting with good match QTLs from different loci (by good match I mean favorable co-adapted gene complexes which brings out the best expression from individual QTLs in these complexes).

Recall that selection fixes favorable QTLs (or alleles or genes) in a population. Now this fixation changes the genetic background of the QTLs segregating in the population. And if these backgrounds are changed, new epistatic interaction complexes are formed leading to novel gene expressions or trait values. Eitan and Soller even state that transfer of neutral alleles into new genetic backgrounds can transform these alleles into full fledged QTLs. With this, formerly neutral alleles move into additive action and these happen in an iterative manner (remember when I talked about epistasis in powers and influenced by number of participating loci) without any limit. A very interesting phrase from Eitan and Soller is that selection acts as a bootstrap (i.e. continuous sampling), continuously generating at least a part of the genetic variation required for its own continued response. Another vital point is that favorable pleiotropic effects will form desired and coordinated network of interactions that can develop into superior traits.

The key lessons are:
1. Selection introduces changes in the genetic background thereby introducing QTLs for epistatic interaction.
2. A previously neutral locus can be transformed into the most desired QTL in a different genetic background.

Now, if you think about heterosis or hybrid vigor. According to Lynch and Walsh (1998), heterosis is a result of favorable or positive dominance and additive X additive epistasis. As long as there is a build-up of favorable epistatic complexes, heterosis will occur.

I have tried to think about SIGV model as heterosis (per se) in a population under selection. As long as there is build-up of favorable epistatic complexes, there will be enough genetic variation to drive selection forward.

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-----Original Message-----
From: Biotech-Mod3
Sent: 12 March 2013 09:52
To: 'biotech-room3-L@LISTSERV.FAO.ORG'

Subject: 20: Perspectives on genomics in livestock in developing countries

This is from Mark Boggess, National Program Leader – Food Animal Production 101, Animal Production and Protection, in the United States Department of Agriculture Agricultural Research Service (USDA-ARS).

I would like to support the arguments made by Uche Godfrey Okeke and John Gibson with an additional perspective or two.

I agree that the remarkable progression of genomic theory and application is potentially providing extraordinary opportunity for small-holders and livestock industry programs in developing countries, especially when combined with next generation sequencing. I am confident that properly administered and developed there will be extraordinary progress in areas of critical need relating to food security and economic vitality.

I too agree, however, that too often the focus has been on improving genetic progress or genetic expression in a vacuum, with little consideration of the ultimate, long term impact on the farmer, the rural community or economic and environmental sustainability. A couple of points to support this perspective:

1. Starting in the 1950s in America, almost every technology, policy and regulation promoted production with extraordinary results; a 4 fold increase in corn yield, a 3+ fold increase in milk yield per lactation, incredible improvement in animal lean gain and efficiency in pork and poultry. Similar improvements were realized across virtually all of agriculture. These improvements are continuing today and will be vital to meeting the food security demands of 2050. Most of these technologies and the models which drive them have been adopted or developed around the world.

However, while the focus on production was the highest priority and has produced remarkable results, other key factors were NOT always prioritized and many not until just recently including; environmental sustainability, animal well-being (socially acceptable animal production), intellectual property (IP) and patent issues with technologies such as GMO corn, and “sun based” energy for agriculture. Priorities such as family farms or rural economic vitality were also not prioritized in the agriculture “arms race” as evidenced by the incredible reduction in farmers and farm families over the past 80 years. And, from a food security perspective this still might be the most appropriate model. However, modern North American style production agriculture – technology driven, low labor – has little application in Africa or most other developing countries which are labor rich and technology poor. In these areas we have the opportunity to promote production and food security while also considering other vital social and environmental priorities and hopefully we have learned from our mistakes.

2. Again focusing on developing countries, animal agriculture and technology; bridging the divide between the emerging technologies and application in developing countries will be a monumental challenge. Small holders and the animal industries in sub-Saharan Africa in particular, are challenged by many issues including: drought, heat, poor quality forage, lack of supplemental micro nutrients, internal and external parasites, disease and limited information/education and support programs. Additionally, many locally adapted farm animal species/genetic lines are not very productive. Being a survivor does not always mean that the animal is adapted, especially if it is not productive. On the other side of the coin, many animal breeds/lines that are highly productive in developed countries would not survive for long in Africa with these extreme challenges. Consequently, developing effective genomic programs and advancing technologies so that they have maximum impact and benefit will be difficult and will require extraordinary vision and leadership. Unlike plant systems, where a genetic mistake can be addressed with minimal human, economic or environmental impact, a mistake in an animal program might be catastrophic, particularly on a local level. Animals represent income and also provide critical animal

products, but they also represent personal wealth and physical assets for many small-holders. All of these factors must be considered and programs developed with minimal risk for the farmers and the rural community.

3. Finally, at the USDA-ARS we are currently developing a goat genome sequence/genomics project and are working in Africa with various stakeholders. As expected, the genomic program is strong and the potential is extraordinary. As stated by others, genomic technologies potentially will speed generation interval, identify valuable genes/markers/QTL, etc that will have real impact, and negate the need for pedigrees in genetic evaluation; all of which will potentially greatly increase genetic progress. And if done properly the result will be improved food security, economic vitality and animal system sustainability. The trick will be to bridge the gap between the potential for genomics and the harsh reality on the ground.

Thanks for the opportunity to contribute. I look forward to hearing the thoughts of the community.

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-----Original Message-----
From: Biotech-Mod3
Sent: 12 March 2013 09:52
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 21: Re: Genome assisted selection in livestock

From David Steane again (Message 8).

I, too, agree with John Gibson’s assessment of the situation. That is precisely why I am suggesting that the importance of genomics in the context of real contributions to sustainable agriculture depends on obtaining more comprehensive data than that used in the simplistic, naive schemes being used at the present time. The information on environmental conditions is crucial to any understanding of the genetic performance – sequencing offers an opportunity to find such links.

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-----Original Message-----
From: Biotech-Mod3
Sent: 12 March 2013 14:31

To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 22: Genomics for livestock improvement in developing countries

My name is Richard Osei-Amponsah, Lecturer of Animal Breeding and Genetics at the University of Ghana in Legon, Ghana.

I thank the organisers of this e-mail conference for the opportunity to discuss an important issue that has an impact on our efforts to attain food security.

I agree with other contributors on the potential benefits of genomics in plants and animal breeding. If a technology exists that can help us increase food production, reduce diseases and ensure that we get the best of investments from agriculture then it makes sense to utilise that technology.

I will like to know more about the impact of the genomic technologies in the developed countries (where most of the challenges indicated by Prof. John Gibson can be overcome) and why many countries are not implementing some of the results of genomics in the field.

In most of our countries the locally adapted livestock breeds still play important roles in agriculture and therefore we need to be mindful of any negative impact of genomics on the local germplasm.

In most of the developing world, the technology is still new, laboratories are non-existent or ill-equipped and the human capacity is not always available. These issues have to be addressed to gather sufficient data to sensitise all stakeholders including the livestock keepers, small scale farmers, scientists, policy makers and donors before genomics will have an impact. For instance, it will be necessary for countries to recognise the contribution of genomics to their agriculture, factor it in their breeding programmes and invest adequately in it before we can see any benefits in the field. Until then, the technology will remain in academic labs and used to develop scientific literature.

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-----Original Message-----
From: Biotech-Mod3
Sent: 12 March 2013 16:24
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 23: Re: Role of genomics in livestock improvement in developing countries

This is Gilbert Msuta, a Livestock Research Scientist at the National Livestock Research Institute in Tanzania. I am a recent graduate of Msc. Animal Science from Melbourne University, Australia, where I wrote my thesis on the Application of Bioinformatics tools to identify key candidate genes regulating residual feed intake (RFI) and other traits in dairy cattle.

I would like to thank the conference organizers for bringing us together and share this noble knowledge. I also would like to appreciate the contributions made so far.

Indeed, as far as I am concerned, I pretty much agree with what has been said and strongly believe that the use of genomics tools/technology will transform the livestock industry in developing countries. However, most of our countries (including mine, Tanzania) are yet to embrace the technology due to various challenges/factors as clearly outlined by Prof. John Gibson (Message 16) and Dr. Richard Osei-Amponsah (message 22).

But I am convinced to believe that inadequate commitment from the Governments to invest in genomic research tends to hasten the problem in developing countries. For instance, my country has currently not been able to establish a working biosciences lab in livestock research despite the presence of few trained human resources in the field. However, plans are underway to establish such facilities to realize such scientific innovations. There is therefore a need to sensitise these Governments to understand the importance of investing their financial resources cum adequate training in genomics if we are to fight against food insecurity.

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-----Original Message-----
From: Biotech-Mod3
Sent: 13 March 2013 10:11
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 24: Molecular markers, MAS and plant genetic resources

My name is Beatrix Tappeser from the German Federal Agency for Nature Conservation. I am a biologist and the head of the division GMO regulation and biosafety at the Agency.

We were interested in the use of plant genetic resources together with marker assisted breeding (instead or in addition to GMO development) and commissioned a project to researchers of the University of Kassel, Germany (Sarah Brumlop MA, Prof. Maria Finckh) to explore the potentials of marker assisted selection (MAS) in supporting agricultural biodiversity.

While historically, domestication and breeding have greatly increased agricultural biodiversity, this diversity is eroding for the past half century with increasing speed. It has been argued that some modern breeding methods, the industrialization of agriculture and especially the current legal seed regulation framework are the main causes of this erosion.

Besides their usefulness in breeding, molecular markers are potent tools for the identification and study of biodiversity. Therefore, the questions arise, if and how marker technology is or could be useful in the conservation and use of biodiversity within the current legal framework. These questions were followed up in the report "Applications and potentials of marker
assisted selection (MAS) in plant breeding" (Brumlop, S and M.R. Finckh, 2011, http://www.bfn.de/fileadmin/MDB/documents/service/Skript_298.pdf (860 KB)). The report is based on a literature survey complemented with expert interviews. It focuses on the situation in developed countries but there may be some interesting aspects also for developing countries as asked for by Richard Osei-Amponsah (Message 22).

In the interviews, all breeders consistently pointed out the big differences regarding the crop species. While MAS is not at all applied in some breeding programs, it is an important part of the breeding process in other programs. Up to now, MAS is predominantly used in hybrid breeding, especially for maize, sugar beets, canola and hybrid rye. For the other (self-pollinating) cereal crops and other minor crops, MAS is applied considerably less frequently. The main reason for this is that the decision for or against MAS is solely based on economic considerations. This growing distance between the main cash crops and minor crops like, e.g., peas or faba beans is seen as a very critical aspect.

The application of markers is seen as especially important where it can accelerate the breeding process (e.g. perennial crops) or where it allows to reach certain breeding aims which normally are very difficult or impossible to achieve (e.g. pyramiding resistance genes). It was endorsed that markers have mainly led to improvements in resistance breeding yet, with barley yellow mosaic virus (BaYMV) being the prime example. The importance of markers in resistance breeding is caused by difficulties with assessments in the field.

The respondents pointed out that MAS is still predominantly used to select for monogenic traits because markers can be developed and applied much easier for mono- or oligogenic traits with high heritability than for quantitative traits. However, in many cases (e.g. breeding for resistance) it would be far more important to have markers available for quantitative trait loci (QTLs). Research on this is mainly done in public research institutes and universities.

Another aspect of marker application is the valorization of plant genetic resources (PGR). The value of genetic resources being stored in gene banks could possibly rise through the application of markers as markers can help to reveal the presence of traits in PGR and may permit their efficient use in the improvement of crop varieties. However, some respondents pointed out that until now an increase in variability in agricultural crops through the utilization of MAS cannot be observed.

Although markers facilitate the introduction of fragments from wild species, which can be especially important in resistance breeding, molecular markers are currently hardly used to exploit PGR and/or crop wild relatives. Breeding companies investing in the exploitation of PGR normally work together with public research institutes. The participants of the interviews and of the workshop assured that pre breeding activities cannot be carried out in small and medium-sized companies. Such activities belong into the hands of public research institutes. The use of PGR poses higher risks to breeders and must therefore be carried out in public institutes - at least for the self-pollinating crops and minor crops with low economic value. Also in variety development, PGR are currently used very little. This might change, however, as backcrossing programs are becoming easier through the application of markers.

While genetically modified organisms (GMOs) are facing several legislative constraints due to biosafety concerns and bioethics questions, the introduction of varieties obtained through MAS is not meeting the same restrictions. Also the lack of public acceptance which GMOs frequently encounter is not observed with MAS. In several publications the hope is expressed that by means of MAS, products of modern biotechnology can be introduced into the market without experiencing the skepticism transgenic crops are facing worldwide. However, there are also positions claiming that MAS, as a modern biotechnology method, has to be assessed for its biosafety in exactly the same way as GMOs. The opinion that MAS could be able to replace genetic engineering completely is strongly questioned, because gene transfer across species cannot be achieved solely with MAS. Breeders clearly refuse to separate the two strategies of MAS and GMO approaches, as the decision for or against genetic engineering is often made as the case arises.

Further literature research on the topic of the loss of agricultural biodiversity showed that one of the main reasons for the loss of agricultural biodiversity lies in the legal requirement that variety registration is only possible if the variety is genetically as uniform as possible, distinguishable from others and - with the exception of hybrids - reproducible (distinctness, uniformity and stability (DUS) criteria). However, genetic uniformity within varieties makes these vulnerable to biotic and abiotic stress. In addition, in genetically uniform populations, evolutionary changes which are the basis of biodiversity development and maintenance are impossible. Evolutionary and participatory breeding approaches could help solve such problems by breeding for diversity. However, current European legislation does not allow the release of crops bred for diversity and thus hinders the maintenance of agricultural biodiversity on-farm and also participatory breeding approaches. With the help of molecular markers, it might be possible to find methods for the definition and distinction of diversified varieties, e.g. based on frequencies rather than uniformity. In addition, issues about intellectual property rights might be tackled with some innovative schemes based on open-source biology.

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-----Original Message-----
From: Biotech-Mod3
Sent: 13 March 2013 10:13
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 25: Capitalising on the possibilities of genomics

This is Professor Denis J Murphy, University of Glamorgan, United Kingdom. I previously worked with FAO on the ABDC-10 biotechnology meeting in Mexico in 2010 and in framing the crop sector background document which covered several aspects of crop genomics. More recently, I have been working on crop genomics at several levels from the use of bioinformatics to analyse next generation genome sequencing data to more applied uses of molecular marker development in crops such as oil palm.

To begin with, we need to acknowledge that even in the most scientifically advanced countries we are still at the early stages of capitalising on the immense possibilities being opened up by modern information generating technologies such as whole genome sequences, transcriptomics, metabolomics etc.

Hence, we are confronted by a mass of raw data for which in many cases our analytical tools remain less than ideal. Our task is to progress along the so-called DIKW hierarchy (data to information to knowledge to wisdom) to make practical sense of the terabytes of data that are being generated by the new technologies every week.

However, we should not let this prospect daunt us - on the contrary this is potentially one of the most exciting periods in biological science where the riches of genomes are gradually being uncovered both to deepen and enrich our understanding of nature and enable us to make more effective use of this knowledge.

It took a century from Mendel's work on genetics before it was being systematically applied in crop breeding and we have been struggling (often successfully, but not always) to apply quantitative genetics to the complex traits that regulate many key characters in our major crops.

Already there are several cases of the use of molecular markers and other genomic technologies being used successfully in developing country (DC) crops but, as several others have noted, in most cases the level of expertise and infrastructure required make it very challenging to introduce such methods to any but the most important commercially traded crops.

This would seem an ideal opportunity for DCs to form regional consortia and centres of expertise - possibly in collaboration with Northern countries and maybe also via public-private partnership (PPPs). The aim would be to ensure that current advances in genomics stand a decent chance of being applied in as many DC crops as possible.

However, these are still medium term (10yrs+) developments and in the meantime there are still huge possibilities (as others have said) for using green revolution technologies to confront the more immediate (next few years) challenges of food security especially in some regions of Africa. Both approaches are important and neither should exclude the other.

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[Regarding ABDC-10, mentioned at the beginning of the message, FAO published the 592-page proceedings in 2011, entitled "Biotechnologies for Agricultural Development", which are organized in two main sections. The first contains ten chapters with an extensive series of FAO background documents prepared before ABDC-10 took place. They focus on the current status and options for biotechnologies in developing countries in crops, livestock, forestry, fisheries/aquaculture and food processing/safety, as well as on related policy issues and options, in particular about targeting agricultural biotechnologies to the poor; enabling research and development (R&D) for agricultural biotechnologies; and ensuring access to the benefits of R&D. The second section contains five chapters dedicated to the outcomes of ABDC-10, namely the reports from 27 parallel sessions of sectoral, cross-sectoral and regional interest, most of which were organized by different intergovernmental and non-governmental organizations and regional fora; keynote presentations; and the conference report adopted by delegates in Guadalajara, Mexico, on the final day of ABDC-10. The proceedings can be freely downloaded from http://www.fao.org/docrep/014/i2300e/i2300e00.htm or contact sandra.tardioli (at) fao.org to receive a copy, providing your full postal address...Moderator]

-----Original Message-----
From: Biotech-Mod3
Sent: 13 March 2013 13:45
To: Biotech-Room3-L@LISTSERV.FAO.ORG
Subject: 26: Re: Genomics for livestock improvement in developing countries

This is Okoro, Victor Mela Ph.D, animal breeder and geneticist, Federal University of Technology, Owerri, Nigeria.

I agree with Abdulmojeed Yakubu (Message 13) where he posited that a lot has not been exploited in animal genomics in Africa, citing Dr. I.G. Imumorin in his lecture “Potential exists for application of biotechnology to livestock improvement in the areas of disease resistance, nutrition and reproduction”. Since most of our indigenous breeds are characteristically of low output and in most cases disease resistant, there is need to use genomic technologies in the improvement of these breeds in a mutual way that will also benefit the highly productive ones too. These genomic tools had been proven to speed up generation interval by identifying valuable markers/QTL etc. that will really affect and remove the need for pedigrees in genetic evaluation. Takele Taye Desta (Message 12) also reported that use of genomic technology in developing countries should have emphasis on adaptation traits; hence, the case of yield traits with hardiness, which are unfavourably correlated, can be improved with genomic studies. Genomic studies require state of art laboratories, computing facilities, knowledge and capacity as well as good and steady power supply. All these things require a substantial amount of resources which are largely beyond the capacity of most of the developing countries.

Therefore, I suggest that specific ways genomics technologies for livestock improvement in developing countries can be more generally felt are:

1. By developing an aggressive collaborative culture between developing countries’ researchers and developed countries (who have the technologies and infrastructure for such research) in order to complement each other's research findings, as this will help in the exchange of information that will be mutually beneficial to both parties, since so many genes which can enhance the adaptability of certain breeds can be discovered and utilized. This will be more apt in this period of global warming, where the environment is changing, resulting in investigation for adaptation characters to be developed.

2. This development will enhance livestock production in the area of disease resistance. We are currently developing a collaborative research with the University of Pretoria in the area of understanding how differences in genomes of indigenous and exotic breeds affect pathogenesis of pigs to African Swine Fever (ASF). A preliminary investigation in the pandemic areas has shown that indigenous breeds show resistance to this devastating disease, which can claim up to 99% mortality during an outbreak. Further research using genomic technologies can be instrumental to the development of a resistant breed which will be as productive and as hardy as both the exotic and indigenous breeds.

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-----Original Message-----
From: Biotech-Mod3
Sent: 14 March 2013 21:52
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 27: Genomics of crop beneficial bacteria

This is from Humberto Peralta, researcher at the Center for Genomic Sciences, National University of Mexico in Cuernavaca (Mexico).

Genomics can also be used to enhance yield of crops by studying the whole array of genes from beneficial microorganisms, but also by modifying specific genetic targets on them. Currently, there is a huge amount of sequenced bateria (3841 to date, http://www.genomesonline.org). There is genome information available for nitrogen fixing bacteria such as Rhizobium (bean, pea, vetch symbiont), Sinorhizobium (alfalfa symbiont), Bradyrhizobium japonicum (soy symbiont) etc. and also other plant-growth promoting rhizobacteria (PGPR) such as Herbaspirillum, Azospirillum, Azotobacter, and Frankia. Microorganisms can produce compounds to enhance root growth, incorporate nitrogen, solubilize phosphorus and potassium, cope with water stress (trehalose), biocontrol of damaging bacteria, fungi and insects, etc.

Of course, the use of these organisms must be intended to the reduction or elimination of chemical fertilizers, pesticides, insecticides, etc. in order to have a “greener” agriculture.

In the Center for Genomic Sciences (National University of Mexico), we have studied rhizobia genomes to understand the information exchange between plasmids and chromosomes, the evolution of conserved genes, the genetic keys of nitrogen fixation efficiency (comparing genomes of strains with different symbiotic abilities) and how to enhance the common bean yield. We have used an array of strategies from sequencing (firstly done here in the Center, but given the high costs of maintenance and running of the equipment, now the service is hired abroad), to transcriptomics (performed here and in collaboration with other University institutions), proteomics (done at our laboratories) and metabolomics (hired abroad).

I think that agriculture needs to be viewed as a complex system, where plants interact with inert soil elements but also with living cells. It is necessary to study the cellular processes from bacteria, fungi and plants as a whole, and in this regard the omics approach is a valuable tool.

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-----Original Message-----
From: Biotech-Mod3
Sent: 14 March 2013 22:07
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 28: Challenges and opportunities for genomics-assisted breeding in developing countries

This is Rajeev Varshney, working for two Consultative Group on International Agricultural Research (CGIAR) organizations, namely the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT, www.icrisat.org) and the Generation Challenge Programme (www.generationcp.org).

I have been following very useful discussions and submissions from a large number of colleagues. I am very excited to see contributions from both young as well as senior colleagues. It is clear from ongoing discussions that genomics has an important role in crop, forestry, livestock, fishery and agro-industry sectors. While we have success stories not only in crops, but in other sectors as well, we all realize that the majority of genomics applications in breeding (referred to as genomics-assisted breeding) happened/are happening in either developed countries or in private sectors.

Although success stories have started to come from developing countries, there are still challenges (as mentioned for instance by John Gibson in Message 17) for full realization of genomics-assisted breeding in developing countries. If we just talk about the crop sector in developing countries, quality phenotyping, infrastructure, expertise, cost on genotyping, availability of appropriate and breeders-friendly decision support tools amongst many others are still serious constraints. It is also important to mention here that genotyping (markers or sequencing based) work in developed countries and private sector is centralized or being availed through outsourcing, several colleagues in developing countries still feel that they should be able to undertake genomics-assisted breeding only if they are involved in generation of genotyping data. As sequencing and genotyping technologies are changing (evolving) continuously, I don't think that majority of national programmes in developing countries are ready to keep on buying/upgrading those machines. Economy of the scale is the other important factor when we do centralize genotyping/sequencing.

The most important aspects where we need to emphasize/invest for enhancing adoption of genomics-assisted breeding in developing countries are: (a) improve infrastructure and expertise in field-based phenotyping, (b) decision support tools (e.g. Integrated Breeding Platform https://www.integratedbreeding.net/), (c) improve expertise in making the use (instead of generation) of genotyping data, and (d) long-term investment (instead of project-based genomics-assisted breeding experiments). Some of these issues were discussed in an opinion piece published as an Open Access article we wrote in Nature Biotechnology in 2012 ('Can genomics boost productivity of orphan crops?', http://www.nature.com/nbt/journal/v30/n12/full/nbt.2440.html).

In the last, coming to decision support tools especially in the case of genomic selection for calculating genomic-estimated breeding values (GEBVs), though we may not have the perfect tools/models, we should not just wait to have the perfect tools/programme for deploying genomic selection. Of course we need to continue to improve the tools/models. Challenges are always there, (being optimistic) one should avail the existing opportunities to tackle those challenges and continue to work towards enhancing genetic gain in crop/livestock/forestry/fishery improvement programmes.

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-----Original Message-----
From: Biotech-Mod3
Sent: 15 March 2013 11:02
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 29: Re: Genomics of crop beneficial bacteria

This is Uche Godfrey Okeke again.

I strongly agree with Humberto Peralta's opinion (Message 27) on viewing agriculture as a complex system. Microbes, especially fungi and bacteria, are having profound interactions with especially the plant roots for different purposes including nutrient exchange, nutrient recycling and transfer, reduction of elements into that which can be utilized by plants, warding off pathogenic organisms, forming complex matrices for structural adaptation, aiding in plant signal transduction for adaptation in their environment and so much more.

Previously, a lot of these interactions have been skipped by breeders. It occurs to me that these elements may contribute to the Gene-by-environment (GXE) interaction that we notice in plant breeding especially. However these interactions are not easy to measure especially if they are to be included in selection indices.

Interestingly, metagenomics offers an approach to view crop production and plant-microbe interactions systematically. The next generation sequencing technologies, especially the combination of PacBio and Illumina platforms, offer an opportunity for in-depth whole metagenome sequencing allowing for a deep view of the entire microbial community interacting with a crop in the rhizosphere. *[The rhizosphere is the soil region in the immediate vicinity of growing plant roots...Moderator]*.

However as breeders, clear phenotypes is the prime interest. This has led to the concept of the microbial core (describing the taxa of organisms that occur frequently in many sequenced samples especially in the human and animal microbiomes). Most studies aiming for reduced greenhouse gases (GHG) emissions in the bovine rumen are trying to see a common microbial core implicated in less GHG emission genotypes so as to devise simpler indicators for measurement. If we imagine how complex the microbial community in the rumen is, then how complex will the rhizosphere be?

Although there is a huge challenge in trying to harmonize metagenomics experiments and especially in using them as phenotypes for breeding, I believe that this is a learning phase and things will unfold sooner or later. I am convinced that agriculture is more complex than we thought but am very optimistic especially for the applications genomics is offering. Old knowledge and new tools will be tested and as time goes by, we will understand more and more what genomics is offering us. I am very hopeful that with the genomic selection technology, different traits that have been previously neglected or under-utilized will surface again and usher in novel agricultural products that we have been sitting on for a long period of time.

In conclusion, I will strongly agree with Dr. V.M. Okoro (Message 26) that strong mutualistic collaborations are needed not just for genomic selection in the developing world, but also for same in the developed world. We are increasingly seeing that we are more linked to each other than we thought. A great pool of genotypic and phenotypic data will be needed for genetic improvement (via genomics) of different plant and livestock species existing today.

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-----Original Message-----
From: Biotech-Mod3

Sent: 15 March 2013 11:20
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 30: Young scientists from developing countries and genomics

My name is Dr. Danlami Moses Ogah. I am a lecturer in the Department of Animal Science, Nasarawa State University, Keffi, Shabu, Lafia Nigeria. My specialty is in animal breeding and genetics.

Thanks for the opportunity for me to make my input. Actually some of us young scientists from developing countries are excited in hearing and reading about application of genomics to improve production. But the majority of us have no idea about genomics, no laboratory for us to carry out researches, no funding and facilities. I solicit FAO to develop programmes that will assist scientists from Africa to learn this technology to improve the diverse resources we have

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-----Original Message-----
From: Biotech-Mod3
Sent: 15 March 2013 16:34
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 31: Genomics of tropical fruits

This is Martin Tiznado, from the Centro de Investigación en Alimentación y Desarrollo (CIAD), Hermosillo, Mexico.

Regarding "What are the impacts (positive and/or negative) of genomics and other 'omics' likely to be in the near future (e.g. the next five years) for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?":

We have been trying to work on several phenomena of tropical fruits. Currently, I am running a project to study the genes involved in the transport of lipids to the cuticle in Mango. Right now, we are facing the problem that we do not have the sequences of these genes from Mango and therefore we are walking to Mango from the tomato and Arabidopsis genomes, available in functional pages. However, it seems that the genes most likely are very different and the oligonucleotides designed based on tomato and Arabidopsis orthologs are not working properly.

Likewise, I am working on a project focusing on Avocado with scientists from Colombia and there is not too much information about the genome of this tropical fruit either. From here, I feel that in a future, it is important to start a project with the goal to sequence the genome of tropical fruits, important for our country and many Latin American countries. In this way, I hope we will be able to boost the use of genomics tools in tropical fruits. With the moderate increase of the budget for science and technology in Mexico, I hope I will be able to start this project soon.

Martín Ernesto Tiznado Hernández
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-----Original Message-----
From: Biotech-Mod3
Sent: 16 March 2013 06:02
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 32: Bridging the genomic divide

This is Tarek Yehia Soliman Kapiel, I am currently working as Assistant Professor of Plant Biotechnology, Al Baha University, Kingdom of Saudi Arabia.

I am following the important topics of the conference and the thought-provoking discussions from the 1st e-mail, and I would like to share some notes and recommendations regarding the current situation of the genomic research in developing countries.

Many researchers have concluded that genomics and related biotechnologies have a role to play in achieving five out of the eight Millennium Development Goals, the set of targets agreed by UN member states in 2000, for addressing the problems faced by poor countries by 2015. However, the researchers in most developing countries requires access to knowledge essential to reaping the benefits of genomics. Conversely, all Governments in our developing countries need to realize the potential benefits of genomics research and the genomics knowledge should be considered as a global public issue, similar to the status given to biodiversity, climate change and most global environmental issues.

Rapid progress in genome science and a glimpse into its potential applications have spurred observers to predict that biology will be the foremost science of the 21st century. Technology and resources generated by the Human Genome Project and other genomics research are already having a major impact on research across the life sciences. Some current and potential applications of genome research in developing countries may include:
(1) Molecular medicine, improved diagnosis of disease, earlier detection of genetic predispositions to disease, rational drug design, gene therapy and control systems for drugs , and pharmacogenomics "custom drugs".
(2) Microbial Genomics, new energy sources (biofuels), environmental monitoring to detect pollutants, protection from biological and chemical warfare, safe, efficient toxic waste cleanup, understanding disease vulnerabilities and revealing drug targets.
(3) Risk Assessment, assess health damage and risks caused by radiation exposure, including low-dose exposures, assess health damage and risks caused by exposure to mutagenic chemicals and cancer-causing toxins and reduce the likelihood of heritable mutations.
(4) Bioarchaeology, Anthropology, Evolution, and Human Migration study, evolution through germline mutations in lineages, study migration of different population groups based on female genetic inheritance, study mutations on the Y chromosome to trace lineage and migration of males and compare breakpoints in the evolution of mutations with ages of populations and historical events.
(5) DNA Forensics (Identification), identify potential suspects whose DNA may match evidence left at crime scenes, exonerate persons wrongly accused of crimes, identify crime and catastrophe victims, establish paternity and other family relationships, identify endangered and protected species as an aid to wildlife officials (could be used for prosecuting poachers), detect bacteria and other organisms that may

pollute air, water, soil, and food, match organ donors with recipients in transplant programs and determine pedigree for seed or livestock breeds.
(6) Agriculture, Livestock Breeding, and Bioprocessing, disease-, insect-, and drought-resistant crops, healthier, more productive, disease-resistant farm animals, more nutritious produce, biopesticides, edible vaccines incorporated into food products, new environmental cleanup uses for plants like tobacco.

Some current and potential applications of Structural and Functional Genomics in developing countries may include:
(1) Exploit the knowledge created by Human Genome Sequencing and also that of some pathogenic organisms and parasites so as to generate diagnostic and therapeutic products of special relevance for the country, mostly for dreadful diseases like malaria, HIV tuberculosis, cancer and brain disorders.
(2) Identifying genomic factors responsible for genetic disorders, development of molecular diagnostics and personalized drugs for the treatment, understanding of the biochemical pathways of the diseases leading to a safe and powerful treatment regime. Comparative genomics, functional and structural genomics, studies of single nucleotide polymorphism, proteomics, data annotation, integration and analysis.
(3) Creation of DNA polymorphism maps and databases for predictive and preventive healthcare.
(4) Creation of microarray facilities for defining the expression and functions of genes. For important crops like rice, wheat, Brassica, chickpea, a map based marker assisted technology development for precision breeding, as well as gene identification through in situ molecular hybridization.
(5) To exploit the sequence information we have to understand the specific biological functions encoded by a sequence through detailed genetic and phyenotypic analysis. For this purpose, genetic resources, e.g. mutant, isogenic lines, elite breeding lines, and high throughput facilities such as microarrays and proteomics would be developed. The programme would initially focus on selected high-priority traits such as tolerance to biotic and abiotic stresses. Bioinformatics capability for analytical and computational ability to infer gene function based on sequence information is equally essential. To enhance scientific knowledge and to discover new genes for crop improvement, a national functional genomics program is needed to make information from functional genomics studies broadly available to address practical problems.
(6) Development of new algorithms, softwares and tools for data mining and data warehousing applications especially related to human, plant and microbial genomes; establishment of small software groups and companies to develop competence for identification for useful genes; strengthening the infrastructure for supporting complex and computationally intensive problems such as protein folding and other problems in structural biology; and establish linkages with epidemiological data to discover the genetic basis of several diseases affecting certain communities in the developing countries.
(7) Exploitation of microbial genome information using strong bioinformatics machinery.
(8) To set-up dedicated network centres for developing data warehouses, data design, data mining from single and multiple databases and mirror sites to decipher the international data available in public domain to correlate the function of individual sequences.

Specific objectives of the genomic research can be summarized as follows:
(1) Developing human and financial capacities in genomic sciences.
(2) Linking developing countries with each other in the fields of research, studies, expertise, information and genomics-related matters.
(3) Sensitizing the society about the definition of genomics, its applications, benefits and dangers from a perspective that takes into consideration the ethical aspects of this technology. (4) Defining the priorities scheduled in the axes of biotechnology and that entail the use of molecular indicators, disease diagnosis, genetic engineering and genomics.
(5) Establishing a mediation role for the developing countries in matters of copyright and other arbitration fields at the international level

(6) Co-ordinating among developing countries in the field of the legislation governing biosafety (genetically modified organisms and disposal of toxic waste), and preserving biodiversity. (7) Endeavouring to develop the sector of biotechnology in the developing countries that lag behind in development to enable them to keep pace with other developed countries.
(8) Encouraging the private sector through incentives to access the field of genomics.

In his paper “Biotechnology Innovations in Developing Nations”, Jason Korenblit, BS (2006, http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3571044/) concluded that, “Biotechnology breakthroughs are coming from developing countries like China and India that are seeking a competitive edge in the world market.” The report also highlights the importance not only of transferring technology to poor countries, but also of promoting active participation in science and innovation. It concluded that the explosion of biotechnology papers and publications that is coming from nations in Asia, Africa, and Latin America in recent years is no accident, and policymakers in the international community will want to consider this fact carefully. Developing nations are working hard to close global health disparities and to reduce health inequalities with innovative products that rival the best that the Western world has to offer. The examples discussed in his paper serve to show that human ingenuity knows no borders, and that innovative developing countries are making a significant impact on the global marketplace. There are many successful instances to support the previous view, for example, Cuban researchers have developed the world's only meningitis B vaccine. Moreover, Daar points out that China licensed the world's first use of gene therapy, in order to treat naso-pharangeal cancer. In Egypt, we were facing a shortage of insulin and an overdependence on the importation of insulin from overseas. A rapid development program sponsored by the government has allowed 90 percent of Egypt’s insulin to be produced domestically and has saved millions of dollars for the national health system.

An international partnership is needed to share the benefits of genomics research and apply them to the needs of developing countries; the proposed initiative would be a network of researchers, government staff, non-governmental organisations, and citizens groups. Through it, the relative risks and benefits of new technologies could be assessed, enabling developing countries to take advantage of new genomics-based technologies.

Undoubtedly, the global partnership is needed to avoid the 'genomics divide'. What could help bridge this gap is the emerging science of initiatives and global working groups such as Global Genomic Initiative (GGI, http://www.mnh.si.edu/ggi/). GGI is a collaborative effort to create a solid foundation for genomic research through a global network of biorepositories and research organizations. The GGI will preserve and study genomic diversity and increase access to genomic information from the key branches of the Tree of Life—expanding our contribution to the preservation and knowledge of life on our planet.

Another example is the ESRC Genomics Network (EGN, http://www.genomicsnetwork.ac.uk/), which is a major investment by the Economic and Social Research Council (ESRC), dedicated to examining the development and use of the science and technologies of genomics. The activities of the EGN span the whole field of genomics, covering areas as diverse as plant and animal genetics, embryonic stem cell research, and associated health applications. The EGN spans five of the UK's leading universities, and involves over a hundred researchers, from professors to PhD students, as well as an international cast of visiting research fellows. It is one of the largest social science investments in the ESRC's current portfolio, and is growing into the largest concentration of social scientific research on genomics in the world.

The cooperation between developing countries is important, as some nations, such as China, Cuba, Brazil and India, have already made big investments in genomics and biotechnology related to health and I wish that this dream came true one day.

I solicit FAO and the distinguished participating members of this e-mail conference to initiate such a network to gather all interested researchers and scientists from the developing countries as a first step in bridging the genomic divide.

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-----Original Message-----
From: Biotech-Mod3
Sent: 16 March 2013 06:32
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 33: Past and future impacts of crop genomics in Indonesia

This is Sudarsono, from the Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural University (IPB), Bogor, Indonesia. I am a university lecturer who runs a plant molecular biology lab (PMB Lab) where a number of PhD and MSc students are conducting their thesis and dissertation researches.

Regarding the topic of discussion "what have been the impacts (positive and/or negative) so far of genomics and the other 'omics' for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?":

I can only comment on the crop aspect. My impression about the genomics and the other omics to Indonesians are as follow:

(1) At the academic and scientific level. Application of molecular markers have been employed by academics in the universities and research scientists in a number of research institutes in Indonesia. These markers have been employed to answer a number of academic questions and research exercises in a number of important crops in Indonesia.

Genomic research has just been initiated by local scientists for only one to two years ago. Therefore there has been no clear impact to the crop research yet. As an academic, I recognize the potential of genomics data for generating huge scales of molecular markers. Therefore, plant genomics and other omics data for tropical crops may have the potential to give a significantly positive impacts. However, limited availability of genomic data for tropical crops may hamper the usefulness of the genomics and other omics in developing countries such as Indonesia.

A number of major tropical crops are important sources of food, feed, and energy in Indonesia. Unfortunately, these crops may not be as important to scientists in the developed countries. Therefore, generating genomic sequences from a number of important tropical crops need to be initiated by local scientists. I have heard the success of Indian scientists in completing the chickpea genome sequence. However, more genome sequencing of tropical crops are still needed to be generated. Availability of such genomic sequences will eventually help the better understanding of the tropical crops and unlock the potential application of molecular techniques for improving them.

(2) At the farmers level, however, no direct impacts of genomics and other omics for tropical crops has been realized yet. Research and academic activities applied by research scientists and university lectures have not resulted in a significant contribution that can directly benefit Indonesian farmers in general.

However, there are a number of multi-national companies that are major producers of maize seeds and selling the seeds to Indonesian farmers. To my understanding, these companies have routinely used molecular markers in their maize breeding programs to develop desirable maize cultivars. If that is true, therefore, the Indonesian farmers as a user of the maize seeds may have actually indirectly benefited significantly by being able to access superior F1 maize hybrids cultivars.

A number of genetically engineered maize lines with herbicide tolerance and/or insect resistances have also been in the pipelines for commercial release in Indonesia. However, it may still take a couple of years before these genetically engineered maize will be available commercially. Therefore, their impact to Indonesian farmers may still be a subject of evaluation. Moreover, negative sentiments about transgenic products commercialized by multi-national companies introduced by a number of vocal non-gevernmental organization (NGO) and the "uncertain or mixed" view and policy about transgenic products between different ministries under the government of Indonesia may also potentially pose problems for commercialization of transgenic crops.

Regarding the topic of discussion "What are the impacts (positive and/or negative) of genomics and other 'omics' likely to be in the near future (e.g. the next five years) for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries?":

I would be confident that either directly or indirectly, the genomics and other omics in crops would likely give a positive impact in the near future. I believe that a number of genomic works that have been initiated in the last two years within Indonesia will actually add positive value toward understanding of a number of tropical crops. At least at the academic and scientific level, the genomic data generated within Indonesia and those produced abroad will certainly contribute significantly toward the dynamic of research activities conducted by Indonesian scientists. Similar to what has happened today, the general farmers will be indirectly benefited by the genomics and other omics through the availability of superior cultivar produced both locally and by multi-national companies.

In term of academic and scientific activities, a number of academics and research scientists have been able to generate either partial or total genome sequences and RNA seq from target crops. However, data handling and analysis of genomic sequences and RNA seq have been a major handicap. Indonesian scientists in general may need some upgrading in their competence for data handling and analysis of genomic sequences and RNA seq and for drawing useful and informative information more effectively and efficiently from such data.

Finally, I would appreciate the organizer for giving us an opportunity to participate in this e-mail conference. Although I may not be able to contribute significantly, I am learning a lot by participating in the program. Thank you.

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[Regarding RNA seq, mentioned at the end of the message: "Next generation DNA sequencing technologies are driving increasingly rapid, affordable and high resolution analyses of plant transcriptomes through sequencing of their associated cDNA populations; an analytical platform commonly referred to as RNA-sequencing (RNA-seq)" (Martin L., Fei Z, Giovannoni J, Rose JK. (2013) Catalyzing Plant Science Research with RNA-seq. Front Plant Sci 4:66). See http://www.rna-seqblog.com/ for more information on the RNA seq approach...Moderator].

-----Original Message-----
From: Biotech-Mod3
Sent: 16 March 2013 06:32
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 34: Re: Young scientists from developing countries and genomics

This is Gabriel Ataguba, from the Department of Fisheries & Aquaculture, University of Agriculture, Makurdi, Nigeria.

I quite agree with Dr Danlami Moses Ogah (Message 30). Training and equipment are the necessary tools we as young scientists in developing countries in Sub-Saharan Africa need to enable us to grasp this technology. I do research in fish breeding and genetics and I have tried to get laboratories to help me carry out basic DNA work (PCR - RAPD, AFLP) but I could not get any to get it done. We as young scientists in developing countries urgently need the support of the FAO and any other organisation that cares in funding, training and laboratories as pointed out by Dr Danlami Moses Ogah.

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-----Original Message-----
From: Biotech-Mod3
Sent: 18 March 2013 14:46
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 35: Re: Molecular markers, MAS and plant genetic resources

My name is Wayne Parrott, and I run a soybean genetics program at the University of Georgia, United States. To begin with, I want to thank the organizers of the conference.

Beatrix Tappeser (Message 24) gave a really great overview of the current state of genomic applications to breeding. Yet, although the use of marker assisted selection (MAS) is routine and widespread in a few crops, such as maize and soybean, the bottom line is that the technology is still in its infancy. I want to share my experience in soybean, and as well as where I see this technology going, because there is no reason why these developments cannot apply to other crops. Genomic breeding is evolving at an amazing speed. Furthermore, the cost of the technology is going down so rapidly, that I hope these techniques will be universally available to all crops within a decade- as long as appropriate research funding and training is in place.

MAS technology in soybean has evolved from restriction fragment length polymorphisms (RFLPs) to simple sequence repeat (SSRs) and now to single nucleotide polymorphisms (SNPs) and chips, with a greater abundance of markers and greater levels of automation at each step. We have several soybean genomes sequenced now, and their availability has made it possible to identify millions of SNP markers. In addition, 50,000 of these markers — spread every 16 centiMorgan or so apart in the genome, have been placed on a chip, making it possible to monitor the entire genome during the breeding process!

The use of recombinant inbred lines, combined with a genomic sequence, is making it possible to clone both classical monogenic traits and an ever-increasing number of quantitative trait loci (QTLs). Once the genes are identified, it is possible to develop allele-specific markers for each gene/QTL. Whereas before we had to monitor markers flanking the gene or QTL of interest, now we are starting to be able to track the gene itself. I envision that soybean DNA chips of future will be designed with allele-specific SNPs, rather than evenly spaced markers. *[Recombinant inbred lines are formed by crossing two inbred strains followed by repeated selfing or sibling mating to create a new inbred line whose genome is a mosaic of the parental genomes (from K.W. Broman. 2005. The genomes of recombinant inbred lines. Genetics, 169, 1133–1146, http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1449115/ ...Moderator].*

What does all this mean? It means that:

- Breeders can monitor multiple traits during a breeding program
- Any gene can be backcrossed in just 3 generations
- Traits with the same phenotype (e.g. disease resistance) can be stacked together
- Phenotyping for several traits can be omitted during the intermediate breeding stages
- Traits from unadapted germplasms can be deployed effectively without linkage drag

The same genomic tools that are contributing to breeding efficiency are also giving greater insights into the plant genome. Accordingly, I no longer agree with the statement in Message 24 that "in genetically uniform populations, evolutionary changes which are the basis of biodiversity development and maintenance are impossible". For example, see Rasmussen and Phillips (1997) and Fasoula and Boerma (2007). A review of the various sources of genomic variability in otherwise uniform crops can be found in Weber et al (2012).

For that matter, I do not really view genetic uniformity in any given field as a problem. First, modern cultivars are not analogous to growing a landrace across a wide area — they have a broad genetic base, with traits incorporated from dozens of parents. Secondly, the most useful place for diversity is between fields — soybeans adapted for my region don't do well in other regions. Thus, having different genetically distinct varieties for different regions ensures diversity is deployed where it does the most good. Finally, there is still a tremendous amount of diversity in old varieties, landraces, and feral relatives that has yet to be used in breeding. With genomic tools, it is becoming possible to identify this diversity and breed it into new varieties, thus increasing their genetic base and increasing the diversity between fields.

The topic of GM crops has come up in Messages 24 and 33. Although I view GMOs and genomic breeding as two different things, I agree with Message 24 that there will always be traits that MAS cannot achieve, and therefore must be moved in from other sources. Furthermore, the two approaches are complementary. Probably over 99.99% of breeding effort will be conventional, and it is conventional breeding that is used to move transgenes into dozens if not hundreds of different varieties. Ultimately, the most durable and stable quality and resistance traits are probably best achieved by stacking native genes with transgenes. Time will tell.

Finally, as DNA chips and computers play greater roles in the breeding process, the human element is irreplaceable. As has been pointed out before in this conference, traits still need to be linked to genes. And, most importantly, only a human can evaluate a cultivar's intended use and determine which are the important traits to breed for in that cultivar.

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-----Original Message-----
From: Biotech-Mod3
Sent: 19 March 2013 09:15
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 36: Progress on chickpea

This is Dele Raheem. I am a Food Scientist currently at the Arctic Centre (a multi-disciplinary centre) and part of the University of Lapland, Finland, as a visiting researcher.

It is a great opportunity to read various contributions on how these "omics" can make positive impacts in developing countries as exemplified by Message 35 by Wayne Parrott and Message 33 by Sudarsono. As more opportunity to carry out research develops in this area there are bound to be new opportunities. Research in developing countries is often hampered by challenges including funding to get access to the right equipment which retards progress.

A recent article by Varshney and colleagues describes progress made with chickpea. I quote from the abstract: "Chickpea (Cicer arietinum) is the second most widely grown legume crop after soybean, accounting for a substantial proportion of human dietary nitrogen intake and playing a crucial role in food security in developing countries. We report the ~738-Mb draft whole genome shotgun sequence of CDC Frontier, a kabuli chickpea variety, which contains an estimated 28,269 genes. Resequencing and analysis of 90 cultivated and wild genotypes from ten countries identifies targets of both breeding-associated genetic sweeps and breeding-associated balancing selection......".

As we continue to rub minds in the scientific world, the application and relevance of these technologies will continue to have positive impacts in ensuring global food security.

Finally, thanks to all the contributors and to our moderator for providing this platform.

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Varshney, R.K., Song, C., Saxena, R.K. et al. 2013. Draft genome sequence of chickpea (Cicer arietinum) provides a resource for trait improvement. Nature Biotechnology 31, 240–246. http://www.nature.com/nbt/journal/vaop/ncurrent/full/nbt.2491.html

-----Original Message-----
From: Biotech-Mod3
Sent: 19 March 2013 09:49
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 37: Access to genomics technology for developing countries

This is from Prof. Sudarsono of IPB, Bogor, Indonesia again.

I would like to add some opinions on the importance of training and more data access about the genomic sequences. I would agree with Rajeev Varshney's statement (Message 28) that we, in the developing countries may not be able to keep up with the changing technology and the cost of the genome sequencing even if it is continually going down. *[Rajeev wrote ".. several colleagues in developing countries still feel that they should be able to undertake genomics-assisted breeding only if they are involved in generation of genotyping data. As sequencing and genotyping technologies are changing (evolving) continuously, I don't think that majority of national programmes in developing countries are ready to keep on buying/upgrading those machines"...Moderator].*

In the genomic side, however, it is necessary to continue to generate more genomic data, especially for crops that are important in the developing countries. The questions remain, what are the priority crops and how are we to set the list? Who will pay for the cost of generating the data and where are they going to be stored, and in what form, might be the next questions? Last, but not least, what efficient tools are available for developing country scientists to use to fish the useful information from the generated genome sequence data, if any. The list of questions may go on and on. Therefore, I, as part of the developing country scientists interested in this new areas, may not just ask a question such as "give me an equipment and funding, and I will do the genomic sequencing."

It might be better to first have the understanding of what is the genomic sequence, how can we used it to support the breeding program, and what can I participate with if I am not a genomics expert but a plant breeder by training, a molecular biologist, or any expertise each of us have. The next thing we should want to know is where to get a helping hand if we want to do something, such as where to get the info and what specific genomic data are accessible? Of course for some of us, such a question may need follow up activities in the form of upgrading our competence through various available avenues that can be customized according to the needs. The point is, upgrading competencies of scientists from developing countries, making them aware of what genomics can do for them, and how to use the available resources are something that can be done by developed countries and probably FAO as stated by Gabriel Ataguba (Message 34) and Danlami Moses Ogah (Message 30).

I have heard that the Beijing Genomic Institute (BGI) has initiated a project to sequence the whole genome of thousands of plants and they have published a number of scientific papers about them. However, I have no idea whether the finished sequences are actually accessible to common scientists or just limited to some privileged ones.

To stress the point that was raised by Martin Tiznado (Message 31) about mango and avocado fruit, and maybe for many more tropical crops that are important for people in the tropics, the information about genomic data for these crops has been minimal. In such cases, any scientists from developing countries who are interested in working with these tropical crops will lack the supporting data and eventually have to generate the genomics data on their own. It might be important to put together human resources and interest of the developing country scientists about what crops should be selected for genome sequencing. The list may be very long but there always be a way to make a priority list of what will be done first and next. I would support the statement of Martin Tiznado that the use of genomics tools should be able to boost research of tropical fruits and also other important tropical crops.

To close my statement in this email conference, I would like to thank the organizers for inviting me and I hope that these activities will not stop after the email conference is closed. I hope that there will be many follow up activities answering some raised inquiries from participants.

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-----Original Message-----
From: Biotech-Mod3
Sent: 19 March 2013 11:53
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 38: Impact of genomics technologies so far

This is KN Rai again from ICRISAT, India.

Most of the discussions on the subject has gone on challenges and opportunities, and these are truly interesting. But the response/inputs to the first main conference question (i.e. what have been impact of genomics technologies so far) remains unaddressed and still not forthcoming, and this is vital for the breeders to appreciate the application power of these technologies and their cost effectiveness. There is no doubt in anybody's mind that these are the technologies which will be routinely applied effectively in the future, but how far away is this future (a few years or few decades from now?) when one can expect to see systematic application and impacts of these technologies rather than just a few success island stories. Most of the breeders are not appreciative of the power of genomics power when examples of successes are presented with respect to simply inherited traits (like flowering time, plant height, seed weight and disease resistance etc.), traits which have been quite ably and cost effectively improved using conventional breeding methods. To be convinced of its power, it has to be demonstrated with examples of successes for complex traits (like yield, drought tolerance, water use efficiency and several of the nutritional traits having large genotype x environment (G x E) interaction and huge field/laboratory evaluation cost) which are difficult to improve by conventional methods.

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-----Original Message-----
From: Biotech-Mod3
Sent: 20 March 2013 06:25
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 39: Two points about genomics

This is Denis Murphy again, from the University of Glamorgan, UK.

Two main points I'd like to raise:

1. About genomics in general. Together with our international colleagues, we are working on several projects aimed at the annotation of whole genome sequences in a variety of plant species from the model Arabidopsis to large commercial crops such as oil palm. We are also trying to analyze the genomes of crop pathogens, such as the fungal Ganoderma spp that infect oil palm crops.

As I stated in my previous message (nr. 25), it is very important that we do not underestimate the difficulty in moving beyond the generation of raw sequence data to extracting truly accurate and useful information/knowledge from such data. For example, although the human genome was sequenced well over a decade ago and has since been the subject of billions of dollars of research, we are still at the very early stages of exploiting it for significant medical advances. In contrast, crop and livestock genomes are still being sequenced and the amount of research funding to analyze/exploit the data is tiny compared to the biomedical sector so we must be patient.

With next generation technologies it is now relatively straightforward to get BGI or one of the many private companies to sequence a given genome. However, the analysis of such data is quite another matter. Unfortunately we have recently seen several cases where genome sequences have been published in peer-reviewed journals where the annotation/analysis is far from robust. In too many cases, relatively out dated or poorly performing bioinformatics tools are used and the result is an analysis that is at best incomplete and at worst misleading. If such a basic method as gene annotation has yet to be perfected in a way that can be used widely in the community, we are surely a long way off from direct use of such tools in many developing country (DC) crops, especially so called 'orphan crops'.

2. What is the present and future impacts of genomics? Genomics is already having a useful impact in some areas of breeding, especially in development of molecular markers. There are also other exciting tools like association genetics, targeting induced local lesions in genomes (TILLING) and phenomics that show great promise but have yet to impact much on DC crops. The small number of specific examples of genomics in practical DC applications mentioned so far in this conference underlies the fact that these are very much emerging technologies for the future. For this reason, it is essential that DC scientists and agronomists are trained in the nature and potential of genomics tools so that they can eventually apply them to their own crops in the longer term. I personally think that genomics could be a game changer in breeding – but not just yet.

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-----Original Message-----
From: Biotech-Mod3
Sent: 20 March 2013 16:46
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 40: Re: Two points about genomics

This is from Sinclair Mantell, Nakhlatec International Development Advisors, Sweden.

Denis Murphy (Message 39) should be congratulated by members of the forum for presenting very effectively the perspective and reality of the practical field-level impact of –omics in the domains of tropical livestock and crop production in low to middle income countries (notice the emphasis on production as against breeding!).

I am an agriculture/horticulture specialist with over 20 years’ expertise in application of tissue culture and genetic transformation to tropical crops, many of which are mainstay root and tuber crops like cassava and Dioscorea yams, but also several tropical fruit and tree crops with notoriously lengthy breeding cycles. Having trained in the tropical branches of the land-based sciences in the Caribbean during the 1970’s, I have been increasingly exposed during the late 1980’s and all the way through the 1990’s to the potential applications of –omics in horticulture and forestry research on tropical species. Rapidly changing developments in the field of genomics as these impact crops in low income countries is becoming challenging in view of the rapid progress being made by increasing numbers of research teams based in advanced research centres. Now away from the bench, but still supporting rural development and Higher Education, this is good and encouraging news but there remain important training and application/access implications that need attention backed up by clear strategies geared to long-term research to adoption process cycles.

The potential for -omic tools in shortening breeding cycles and targeting specific genes to generate and identify useful genetic recombination events has already been well-articulated in this conference. The current efforts and rates of advancement for instance in countries like China to incorporate drought and salt tolerance genes in rice and other cereals by gene insertion are impressive. Some edge effects of the technologies are however already in practical use and making valuable impacts in many countries.

Molecular fingerprinting of genetically uncharacterised populations of crops, and sometimes those of their wild ancestors, is generating already a wealth of useful information and guidance by which traditional clones, cultivars and varieties can be distinguished on genome diversity grounds (not by their unreliable and environmentally dependent phenotypes alone) using a variety of genetic probes based on synthesised primers homologous to partial gene sequences of the same, sister crops or even model plants like Arabidopsis. Our own experiences with distinguishing the different cultivars of cashew (Anacardium spp) and pistachio (Pistacea spp) originating from different regions of the world has led to improved breeding strategies for these crops in long term seed orchard systems in countries like Tanzania, Mozambique, Brazil and South Africa. Applications of molecular fingerprinting are not only assisting managers of seed orchard and clonal collections of tropical fruit and nut trees but also in developing better-informed genetic conservation and management strategies in fragmented forest situations, such as those experienced in the Mata Atlantica forest of Brazil close to the large urban centres like Rio de Janeiro and Sao Paulo. Using molecular fingerprinting tools to assess relative levels of gene flow between and within refuges of fragmentary forest, conservation biologists and ecologists determine whether or not a specific tree species of importance is able to regenerate and perpetuate itself efficiently in the remaining tracts of forest.

When it comes to application of information on the whole genome of a genus, actual uses will take more time to emerge for the reasons Denis Murphy has explained so eloquently. The work on the genome sequencing of eucalypts for instance (Novaes et al, 2008), is advancing well and can become more effective in identifying important regions of the genome which confer key traits, e.g. desirable wood fibre quality (to reduce need for environmentally deleterious postharvest processing in the paper industry), cold tolerance (to improve the geographical range of the genus for forestry and ornamental uses), sustainable resistance to key diseases and pests as well as many other significant traits like tree shape and incremental growth rate. The practical breakthroughs in such endeavours may well be on the near horizon.

We certainly therefore need to look to more support for training and increased facilities for these technologies to be applied in centres of expertise around the world and be mindful at the same time of not making too many premature promises as far as the genetic improvement of tropical crops and livestock is concerned.

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Reference:

Novaes E, Drost DR, Farmerie WG, Pappas GJ, Grattapaglia D, Sederoff RR, Kirst M: High-throughput gene and SNP discovery in Eucalyptus grandis, an uncharacterized genome. Bmc Genomics 2008, 9:312. http://www.biomedcentral.com/1471-2164/9/312

-----Original Message-----
From: Biotech-Mod3
Sent: 20 March 2013 17:54
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 41: Locally important crops

This is Raul O. Castillo, Director, Sugarcane Research Center of Ecuador.

I’ve been following the interesting conference on genomics and I am impressed with so many people presenting their practical views and also the number of scientists working in this issue who have gone further with gene sequencing and gene identification for several crop plants and some animal species. However, most of the research is done for the economically important crops of worldwide consumption. Minor crops of local consumption are hardly studied or included in such projects. Albeit, these crops feed millions of people living in the less developed world with increasing needs of food. After introducing this comment, let's analyze two issues:

1. Developed countries, although some of them are in economic crisis nowadays, should support research by arranging regional projects for genomic studies of these local important crops to dig in the genetic information in order to speed up the breeding processes to develop varieties suited to these environments.

Some of these crops would never be in a developed country market or part of their culinary resources; they will be mainly for local people requiring more food.

2. The need of plant breeders is evident all over the world; we have less and less students entering in schools to pursue plant breeding or animal breeding. Therefore, we should start thinking of preparing good plant/animal breeders with good knowledge and understanding of genetics (including genomics), biology and statistics in order to use the best combinations possible available today and select the best materials and release outstanding varieties for general or local consumption. In fact, the world needs more stimulated people doing research in the field to apply the knowledge released from laboratories.

In summary, we still need good plant/animal breeders in the developing world in order to use the advances of "omics" and have a sustainable use of genetic resources still available in those "centers of diversity". One big question that people have is: how much do we know of all those collections held in many gene banks? Can we sustainably use diversity from the natural reserves? The advance in genomics will certainly help us to understand and use it.

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-----Original Message-----
From: Biotech-Mod3
Sent: 21 March 2013 11:04
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 42: Partnerships in genomics

This is Sanjeev Raikar from SGS India Pvt Ltd, Hyderabad, Head Biotech Operations.

After going through a few of the messages which have mostly stressed on how and when genomics would be efficiently put to use in breeding activities especially if we were to improve the wide variety of crops mostly in our tropical developing countries.... Many views have been expressed such as lack of thorough understanding of genomics as a tool by breeding scientists in developing countries, the constant upgradation of equipments, changing methodology or protocols, the millions of dollars involved in upgradation of equipments, and above all the skill shortage in the regions to understand precisely and successfully execute the job bringing a logical conclusion to the whole exercise. In short, the question is surrounding the capability... Are the developing countries capable enough to execute such advanced work...

I feel there are many options which could address these issues. One of the options is by forging partnerships with already established entities in the field of genomics who have proved themselves through peer assessments either overseas or within the country. A partnership wherein you would be able to outsource the work at the same time get your own staff trained which would address the long term plans. Private companies such as SGS having global presence have the capabilities to invest in setting up such sophisticated high throughput facilities in providing these services. I think such kind of models would greatly help conducting the most sophisticated work in developing countries efficiently and economically which would greatly accelerate the pace of crop improvement in developing countries and should help in closing the knowledge gap. We should capitalise by implementing such kind of working model. It would also help in bringing together the different stakeholders across table which in turn would greatly facilitate the whole exercise

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-----Original Message-----
From: Biotech-Mod3
Sent: 21 March 2013 11:04
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 43: Genetic promise

This is from Adrian Dubock, Golden Rice Project Manager, and Executive Secretary to the Golden Rice Humanitarian Board.

It is good to see the excitement that the realization of genetics for improving food security generates. It is also good to see that the excitement is tempered with realistic prudence concerning where in the expected long time line to precise genetic management for useful phenotypes we are. As a case in point, I was involved with the announcement of the determination of the genome of rice by Syngenta (for whom I then worked) in about 2001 – more than a decade ago. It hasn't resulted in much yet, despite costing at the time about $30m.

Plant breeders have long induced random genetic mutation for crop breeding to release variation from which to select potentially useful phenotypes. (See http://mvgs.iaea.org).

Given all the above, I suggest that it is necessary and time for those who have previously found it difficult to embrace with enthusiasm the techniques of genetic engineering, to reassess their attitudes. And where possible to provide societal leadership in accepting the human limitations of what can be harnessed from the power of genetics currently: that is not only random mutation and subsequent selection but also genetic engineering and subsequent selection.

It will be a long time before we can do more. And the world's need is now.

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-----Original Message-----

From: Biotech-Mod3
Sent: 21 March 2013 11:05
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 44: Re: Impact of genomics technologies so far

This is Shashi Bhushan Tripathi from The Energy and Resources Institute (TERI), New Delhi, India.

I am writing in response to the point made by Dr Rai (Message 38) regarding the impact of marker-assisted selection (MAS) in plant breeding so far and my comments are from the Indian perspective only. We are working on marker-assisted breeding in several crops such as Indian mustard, Jatropha and Chilies for the past 10 years. I would like to state that the potential of MAS has not yet been realized to any level which could be considered significant. I would like to list some major causes for this from our own experience:

1. Most of the breeders in India (except few big institutes and seed companies) do not have access to marker technology. A good number of them even do not know how MAS can help in breeding. Those who work on MAS should proactively discuss with breeders to understand the requirements of breeders and to make them aware about the technology.

2. Most of the publications on marker/QTL identification are from those groups which themselves do not have the mandate of breeding and varietal development/release. Lot of effort is needed to convert the findings of a publication into a mature technologies. The current regime of "publish or perish" does not provide enough incentives to these researchers in this direction.

3. The cost economics of MAS is currently not very attractive to seed companies.

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-----Original Message-----
From: Biotech-Mod3
Sent: 21 March 2013 11:05
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 45: Re: Locally important crops

This is Rajeev Varshney (again), working for two CGIAR organizations, namely the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT, www.icrisat.org) and the Generation Challenge Programme (www.generationcp.org) and I sent Message 28.

I agree with Raul Castillo (Message 41) and support genomics research and genomics-assisted breeding for less-studied (many times called 'orphan crops') but locally important crops. But the good news is that the power of genomics technologies and collaboration can transform any so-called 'orphan crop' to

'genomics resources rich crop'. ICRISAT and its partner institute have demonstrated this in several cases. For instance, pigeonpea (Nature Biotechnology
30, 83–89; http://www.nature.com/nbt/journal/v30/n1/full/nbt.2022.html) and chickpea (Nature Biotechnology 31, 240-46. http://www.nature.com/nbt/journal/vaop/ncurrent/full/nbt.2491.html) are examples where we had only a handful of markers and few (or no) genetic map until recently but now got the draft genome sequences and molecular breeding efforts have also been initiated. Dele Raheem, in Message 36, has emphasized such efforts in the case of chickpea.

As Raul Castillo mentioned two points, I think that international collaborations (with like minded organizations/scientists) with organizations like BGI (http://www.genomics.cn/en/) because of economy of scale, can deliver genomics data at large scale in less time and less costs. However, the main question still remains (and international community needs to work) about the data analysis, interpretation and making its use in crop breeding. In this context, we need to have good (and sustainable) capacity (both human as well as infrastructure) in developing countries in addition to breeders-friendly decision support tools. In the January issue of Nature Biotechnology (30, 1172–1176; http://www.nature.com/nbt/journal/v30/n12/full/nbt.2440.html), together with some colleagues (Jean-Marcel Ribaut, Ed Buckler, Roberto Tuberosa, Antoni Rafalski and Peter Langridge), we discussed some of these issues that how genomics can improve crop productivity of so-called 'orphan' or 'less-studied' crops.

I would also like to avail of this opportunity to extend sincere thanks to FAO and especially John Ruane, Moderator, to organize such e-conferences. These conferences are very useful (without spending time and money in travel to different places) for sharing the ideas and learn from each other.

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-----Original Message-----
From: Biotech-Mod3
Sent: 21 March 2013 13:22
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 46: Property rights

This is Darmono Taniwiryono, a senior research scientist at the Indonesian Biotechnology Research Institute for Estate Crops (IBRIEC) in Bogor, Indonesia. Estate Crops cover oil palm, Hevea rubber, cacao, coffee, tea, and sugarcane. I had been the head of that institute for quite sometime, ended just recently this year. Now I become part of the Center for Agricultural Policy Studies (CAPS), based in Jakarta, Indonesia, as an Institutional Development Officer of Biotechnology Program.

When we are discussing the impact of genomics and other ‘omics’ so far and in the near future for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries, we should also look at whether any genomic and other ‘omics’ products (gene sequence, DNA markers, primers, and others) and its derivates (GMO) are readily available and easily accessible by farmers in developing countries. The essential question is: Who has the property right of genomic and other ‘omics’ products? Unfortunately, the answer is not research scientists at developing countries. If anyone wants to use it, then it should be for research purposes only. Consequently, the impacts of genomics and other ‘omics’ in developing countries could be significant only at the academic and scientific levels, and I believe that all of us still fail to bring down the impacts to the farmers level. The road to reach the heart of every human being needs (food, energy and good environment), at fast growing world population, is still far away.

Amicable law and regulation should be developed (by world body) so that research scientists from developing countries and developed countries could work together and share property rights proportionally, and receive sufficient funding for the improvement of many crops that are mostly not become the interest of research scientists in developed countries. Regulations and condition in developing countries should encourage scientists to move forwards with most of their rights in using the most current genomics and other ‘omics’ technologies without pressures from any parties for any unfounded reasons.

I am glad to be able to participate at this important world conference.

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-----Original Message-----
From: Biotech-Mod3
Sent: 22 March 2013 05:58
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 47: The status of genomics application in Iraq

I am Sahar Al-bayatti, a livestock geneticist working for the Ministry of Agriculture in Iraq, the national coordinator (NC) for animal genetic resources (AnGR) and a member of the biosafety committee working on GMO legislation for the Ministry of Environment.

First, I would like to thank the organizers of this important e-conference. I have been following the very useful discussions. It is clear from ongoing discussions that genomics has an important role in agriculture and agro-industry sectors. But this as Rajeev Varshney said (Message 28) is happening in either developed countries or in private sectors. I think it is early to talk about the impacts of the genomics and other omics in the field of agriculture and agro-industry sectors in developing countries or at least in my country Iraq. We have only a few academic researches in this field in the universities with little applications on the ground. So we can’t tell about its impact. There is a big gap between the developed and developing countries in this field. However, and talking about the future, I think it will have a great impacts especially in gene banking and genetic diversity studies.

I agree with Takele Taye Desta (Message 12) who said Omics require the state of art lab and computing facilities, which do not exist in most developing countries, also there is a shortage in knowledge in this field and a lack of specialized human resources. And I strongly agree with Richard Osei-Amponsah (Message 22) who said in the developing world this technology is still new.

I am here to emphasise on the suggestions made by Victor Okoro (Message 26), Raul Castillo (Message 41)and Sanjeev Raikar (Message 42) especially in the need for collaborative culture between developing countries researchers and developed countries (who have the technologies and infrastructure for such research) through a multinational project for genomic studies and applications.

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-----Original Message-----
From: Biotech-Mod3
Sent: 22 March 2013 06:08
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 48: Establishing a global genomics/breeding forum?

This is Denis Murphy again, from the University of Glamorgan, UK.

I greatly appreciate all the comments from colleagues throughout the world and applaud the opportunity provided by John Ruane and the team at FAO for us to communicate together in this way.

I especially welcome the comments of Adrian Dubock (Message 43) as somebody who has worked with a major biotech company (Syngenta) and currently works on the at-times controversial golden rice project. It is now 14 years since I heard Ingo Potrykus announce the successful production of golden rice at a conference in London and the variety has still to become a reality on the ground in Asia, although it now seems close to release at last. I thoroughly agree with Adrian and others in this conference that there are older technologies that still have immense potential especially for developing country crops. I still recall when as a brash young molecular biologist who was promoting 'designer crops' I was told off by breeders who told me that simplistic single gene manipulations have very limited scope in real world agriculture. Over 25 years later I think I was definitely too optimistic - but maybe they were also a little too pessimistic. For sure, techniques like quantitative genetics and pedigree breeding underpin the success of modern agriculture and these and even simpler basic methods have yet to be used systematically in many developing country crops. But we should keep focusing on the future potential of the new genomic technologies.

One suggestion that emerges from this e-mail conference is to establish some sort of actively moderated information exchange platform where there could be informal exchange of experiences, data, knowledge, and expertise on genomics and other aspects of breeding for the global community.

What would the site do? Well for a start it could be used to upload papers, reports, data, and tools such as algorithms - possibly in a similar way to sites like academia.edu where researchers can not only upload papers etc but can also ask for advice on technical problems. The site could help practitioners and policymakers stay in touch with researchers in a truly global setting. As an advisor to several official bodies in the European Union, I have been struck that even here there are many misunderstandings about genomics especially between policymakers and researchers and I am sure the same is true more globally.

The site could also serve as a useful resource more generally - for example for science journalists - as long as it was properly moderated and kept as a trustworthy repository of reliable information and informed discussion. The site would need a long term host and one obvious candidate is FAO if they were willing to take it on .....

I'm not sure about the finer details of this proposal yet and it may be completely unrealistic so I would welcome feedback (if only to say it is a crazy idea) during the last few days of this conference.

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-----Original Message-----
From: Biotech-Mod3
Sent: 22 March 2013 15:12
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 49: Re: Establishing a global genomics/breeding forum?

This is Adrian Dubock again.

I am sure I will not be the only one to support the development of the concept proposed by Denis Murphy (Message 48).

It seems that this opportunity for information sharing and creation of critical mass of capability would go some way to addressing the clearly expressed frustration of many conference participants from developing countries.

Moreover, the platform when/if established could provide a useful place to find co operators and mentors to assist developments, especially outside the 'commercially-occupied-space'.

It could be a place to advertise availability of research, and development and product adoption funds and courses for 'omics applications. (There is a good model in Platform for African - European Partnership in Agricultural Research for Development Phase II (PAEPARD II), http://dgroups.org/paepard)

Perhaps in the fullness of time it could become, in the mode of the UK's Open University, the 'Omics University'.

And as for the most appropriate founding funder........well, do we have to leave everything to Gates, FAO......?

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-----Original Message-----

From: Biotech-Mod3
Sent: 22 March 2013 15:18
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 50: Re: Establishing a global genomics/breeding forum?

This is David Steane again.

I particularly like the comments of Adrian Dubock (Message 43) and the contributions of Denis Murphy. As an animal breeder, I consider our efforts are rather more complicated than those of plant breeders. While I believe that we need much more information about the environments in which certain genotypes are normally expected to perform before we can best use the techniques, this does not mean opposition to ‘omics – simply caution that we do not get things wrong – especially as it is the farmers who suffer such mistakes. I do, however, believe that there is need for more specific requirements for evaluation of results – especially when it involves GMOs. The UK results a few years ago showing vastly different effects on insect life are a good example of the need for comprehensive evaluation – the effects were due to the changes in cultivation procedures advised for the GMO crop. Indirect effects but nevertheless very important but not reported earlier by the GMO developers although, in all fairness, they did agree to the trial and contribute towards the costs thereof.

As for Denis Murphy’s suggestion (Message 48): The forum could be of considerable value in making information more widely available. I would like to see such a facility but FAO is a governmental organization and, unfortunately, it may be difficult for FAO to get agreement to publish non-governmental data. I certainly believe that FAO should take on such a role but, for example, the animal breed data can only be submitted by the official National Coordinator which presents some limitations/potential censorship. It has taken many years (15) for FAO to get to including Production Environment Descriptors in DAD-IS (the Domestic Animal Diversity Information System, http://dad.fao.org/). It would be essential that the sort of scheme suggested by Denis gets underway quickly as there is clearly a crucial role to be played in getting information available to all - soon!.

John has done his usual excellent job as Moderator for which many thanks – I would like to think that the proposed Forum could be managed as effectively!

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-----Original Message-----
From: Biotech-Mod3
Sent: 22 March 2013 15:42
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 51: Genomics in livestock

I am Dr. A. Sudhakar, Ph.D in Animal Genetics and Breeding and presently working with the National Dairy Development Board, India.

At first I would like to thank the enablers of the e-Conference (John Ruane and the FAO team) and contributors by sharing their experiences.

I would like to highlight a few areas where knowledge of genomics is used currently:

1. The identification of the FecB mutation (major allele increasing litter size) in sheep and its association with litter size has sparked interest amongst the various stakeholders in Asia, especially India and China. Thanks to the efforts of the Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia and the Nimbkar Agricultural Research Institute (NARI), India, marker-assisted introgression of the FecB allele in local sheep breeds is lowly gaining momentum. (e.g. Garole, Nilagiri breeds). *[See the ABDC-10 proceedings for a case study on the FecB gene in India (http://www.fao.org/docrep/014/i2300e/i2300e00.htm) ...Moderator].*

2. In livestock breeds in India, genomic information is collected from all agriculturally species and breeds to assess the genetic diversity, bottlenecks to assess the need for conservation programmes. (Bargur cattle)

3. Use of any bull in artificial insemination (AI) in India requires it to be parentage tested against a panel of marker alleles and screened for genetic defects like Bovine Leukocyte Adhesion Deficiency (BLAD), Citrullenemia, Deficiency of Uridine Monophosphate Synthase (DUMPS) and Factor XI deficiency.

4. Genomic information is also used for confirmation of disease outbreaks and identifying pathogens.

5. Sexing in emu/ostrich where identifying sex of the chick is of high economic importance.

These are a few areas where I was involved either directly (1 and 3) or as an associate (2, 4 and 5) though the use of genomic information is small, either generating the required information by PCR-RFLP, SSCP or capillary sequencing.

Genomic tests based on whole genome sequencing for early identification of white spot syndrome virus in shrimp has been identified and may be available commercially soon in India. Use of genomic information for disease detection is very common among the farmers of India as the economic implications of disease outbreak in Shrimp farms are enormous.

I am sure a lot more applications are available in developing countries especially India, China and Brazil in agriculture.

Apart from these applications, new strategies for using genomic information for selection of bull calves in the near future are being evolved (use of genomic information may also negate the need for pedigree data - highlighted by Mark Boggess, Message 20). If somebody could enlighten on this it would be highly useful to animal breeders in developing countries.

Since most developing countries host most of the global livestock population providing employment opportunities for a large section of the population, the potential of genomic technologies if harnessed properly should be enormous. (In the dairy sector approximately 50 million AI is performed in India every year and with a milk production of 127 million tonnes, economic opportunities involve job opportunities for few thousand AI technicians, opportunities in logistics, dairy production, processing and marketing of semen to milk). But since use of this technology is in the nascent stages, it might take more time before the genomic information available is put into many new applications.

I also wish the suggestion by Denis Murphy (Message 48) on informal global platform for exchange of ideas, experiences would soon materialize. Since the cost of purchase of many journals involves high cost for institutions, such platforms will be very useful and hopefully FAO shall take the lead.

Further to ensure the new ideas in genomics are implemented in developing countries, FAO shall organize regional workshops/e-mail conferences with some sharing of videos in public domain, calling international experts to developing countries so that more people are exposed to technical intricacies. For example, FAO shall conduct regional conference/workshop on the need for genomic selection in species where artificial insemination are being performed to evolve strategies of implementation, creation and sharing of infrastructure for research and genotyping.

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-----Original Message-----
From: Biotech-Mod3
Sent: 22 March 2013 15:57
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 52: Genomics for livestock in tropical countries

Let me introduce myself: my name is Michel Naves, from the french Institut National de la Recherche Agronomique (INRA) and I work in animal breeding and genetics of local animal breeds in French West Indies. I am really greatly interested by this conference as I am involved in a research program on the improvement and management of the local tropical breeds, mainly on Creole cattle. Other colleagues in my team work on small ruminants and pigs. In our work, we tackle the use of genomic tools (and other -omics), for i) the identification and quantification of variability within/between breeds, ii) the link with production and adaptation traits, and iii) the mechanisms involved in adaptation.

Since very few messages concern livestock this week, I wanted to follow up the discussion on the special issues of genomics for livestock in tropical countries.

Concerning livestock, great efforts and very effective results have been obtained in dairy cattle in developed countries, and these examples raised enthusiastic hopes of a "revolution" in genetic improvement in all species and breeds, especially in tropical countries (for example, see Message 10).

Indeed, genomic selection improved the efficacy of selection in dairy cattle, in northern taurine breeds, in various points of view: time and money spent, accuracy of estimated breeding value (EBV), conservation of genetic variability,... But I think we have to pay great attention to the conditions that made this progress possible: existence of great economic interest in the milk industry and dairy cattle genetics, strong and accurate record keeping systems, large pedigree information, dense markers available across the whole genome,... And very strong limitations have also arisen, especially for the application of genomics tools for genetic evaluation, across breed, in multibreed or in crossbreeding.

I really doubt the same conditions that contribute to the development of genomic selection in dairy cattle could be easily found in developing countries. Several messages (19, 22, 23 for instance) pointed out this effective and dramatic "bottleneck" for genetic improvement of livestock in developing countries. Does that mean that we cannot afford the use of genomic tools in livestock breeding in tropical countries? I don't think so, but special organisational, methodological, and technological issues should be addressed in order to fill this gap and make possible the same transition in tropical livestock, as pointed out by John Gibson (Message 17).

In another way, generalisation of such methodology is not trivial: the technology is one thing that is easy to manage (however with a cost still unaffordable for developing country scientists) but conditions of its application have to be considered with special attention. For example, SNP chips available in cattle at the moment (9K, 54K or 777K) have a very bad coverage in tropical breeds, with about 50-60% of informative SNP in african taurine or zebu, in comparison to the 80% of informative SNP in european taurine. Next generation sequencing (NGS) technology would allow the identification of new polymorphisms in tropical breeds, and the evaluation of the variability available between breeds, but efforts in this domain are still weak however.

In tropical countries, reproductive, adaptation and resistance traits play a major role in livestock systems. Such traits are difficult to address (particularly resistance to infectious disease or drought, as an example), and may have a complex determinism (for example, tens of quantitative trait loci (QTL) for tick resistance have been cited in the literature). Genomic tools may help for their improvement, but results in this field are not yet very convincing. One difficulty is to how to identify the relationship of these traits with genetic markers, when phenotypes are not well defined, measurement is not easy, and reference population are lacking? Also the genetic background of these traits may also vary according to the breed. For example, the same SNP in the HSP70 gene is linked to higher fertility in Brahman (Rosenkrans et al, 2010), and to lower embryo heat tolerance in Holstein (Basirico et al, 2011), and I guess other examples may be found.

As far as the technology is applied with tremendous results in great dairy taurine breeds, and large breeding or technological private companies are engaged in large programs, the impact of genomic tools and especially genomic selection in local breeds, farming systems and societies in developing countries may be dramatic if not controlled by public policies, driven with common interest in mind, and advocated by highlighted advice. In particular, I am not sure we have really a good appraisal of the consequences on local genetic resources, which have a great patrimonial value. This will probably be the challenge for future research in this field, and for livestock improvement of tropical breeds.

At the present time, a lot of private efforts are developed in the market of "-omics" technology, with clear economic private interest (Message 15 gave such example in Brazil), but very sparce efforts are made in a public domain, in a "global thinking approach" as deemed by David Steane (Message 8). Some recent messages (42 and 48) call for more partnership and exchange of information on these issues and I agree with these statements, which are very important to answer such a goal for benefits of the whole human community.

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-----Original Message-----
From: Biotech-Mod3
Sent: 23 March 2013 06:39
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 53: Re: Establishing a global genomics/breeding forum?

This is Rajeev Varshney again.

I am quite excited to see the ongoing discussions by Denis Murphy (Message 48), Adrian Dubock (Message 49) and David Steane (Message 50) on establishing a global genomics/breeding forum. In fact as a part of CGIAR Generation Challenge Pragramme (GCP), GCP established the Integrated Breeding Platform (IBP) for facilitating crop breeding using advanced tools (https://www.integratedbreeding.net/). And very recently, we have established the Agricultural Genomics Network (AGN) as a part of GCP/IBP (https://www.integratedbreeding.net/agricultural-genomics). Though this portal is still under development, with an objective of making genetic research and breeding applications cost-effective by enhancing adoption of modern genomic technologies, AGN is expected to have the following three main components:

- Develop a community to discuss advances in genomics and provide critical appraisal of genomic technologies, tools and approaches

- Develop a portal that will present the information on tools, resources developed by GCP or available in the public domain either by hosting some of them, or by providing links to other existing databases and portals, and

- Broker access to economically priced large scale sequencing, construction of variety of (BAC, cDNA, fosmid) libraries, physical mapping, sequencing and re-sequencing, etc, provided by third-party service providers (e.g. BGI, JCVI, NCGR).

The current pages are the beginning of the proposed Genomic Resources Portal and will in due course be populated with appropriate information on various tools and resources - including markers, maps and QTLs. For more information, contact me or my colleagues- Manish Roorkiwal (m.roorkiwal (at) cgiar.org) or Dadu Doddamani (d. doddamani (at) cgiar.org). Colleagues interested in AGN are invited to join the AGN at http://www.linkedin.com/groups/GCPAgricultural-Genomics-Network-4919729/about?trk=anet_ug_grppro .

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-----Original Message-----
From: Biotech-Mod3
Sent: 24 March 2013 07:28
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 54: Re: Establishing a global genomics/breeding forum?

Hello, Adrian Dubock again.

Good to hear from Dr Rajeev Varshney (Message 53) about ICRISAT's plans, which seem to go some way towards what participants in this conference are asking for. One aspect which seems to be missing is "animal 'omics".

Another point: In my experience, competition keeps institutions on their toes, with benefits for speed and focus of progress. For benefit to humanity 'cooperative-competition' is to be encouraged too. So Professor Denis Murphy's idea should also be promoted.

It seems that the demand for assistance in this field in enormous, and surely the potential benefits are huge, but sustained funding and commitment will be required.

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-----Original Message-----
From: Biotech-Mod3
Sent: 24 March 2013 07:37
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 55: Genomics in tropical forestry

This is from Milton Kanashiro, Empresa Brasileira de Pesquisa Agropecuária (Embrapa), Brazil.

I am really sorry I could not enter into the Conference earlier. Working with tropical forests, focusing more on natural forest management, I do think genomics is very important tools when the level of domestication and selection is already highly developed. At this moment, molecular genetics is very important to access population diversity and the main priority is the basic and tedious job of correct species identification. In the Amazon forest, there are several commercial timber species with a very complex taxonomy puzzle to solve, which I take as the main challenge to discuss forest management and conservation, when dealing at the level of species population and its genetic diversity. Therefore, molecular tools are very important, but still there are very few and well instrumentalised laboratories in the region.

Besides the logistic of the labs, the cost of the chemicals involved in the methodologies, and the access and logistics of the region to collect material of very low density species populations, where the great majority falls on the category of rare and very rare species, to generate information on molecular data for these species become a very expensive and tremendous effort and energy involved in it.

As a consequence, there are also very few people that are highly well trained and able to deal with these methodologies, considering the size of the region and the higly diversified amount of timber species that need basic genetic diversity information.

Advanced tools and methodologies of all sorts, such as flow cytometry, near infrared spectometry, etc. would be very important to test besides the current molecular genetics applied at the moment, together with the traditional tedious and important work done by more tradition plant taxonomists, since most of the decision is primarily based on comparison of several morphological and molecular data information.

Maybe these issues are out of range of this e-mail conference, however, I thought that I should post this as a contribution to get the species identification issue into the context of use and conservation of forest genetic resources in the Amazon tropical forest and maybe this becomes as matter of concerns of a great deal of people interested in forest use and conservation, and stronger effort could be directed in this direction at the international forum level.

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-----Original Message-----
From: Biotech-Mod3
Sent: 24 March 2013 07:37
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 56: Re: Genomics of crop beneficial bacteria

This is Doris Zuñiga of the Universidad Nacional Agraria La Molina, Peru.

I am very grateful for all the contributions of scientists about the impact of genomics. I work with plant growth promoting rhizobacteria and it is significant to have the identification using the total or partial genomic of these bacteria so that they can be applied to the field for crop improvement. Yet in a few places in our country is being implemented in a limited way these bacteria as inoculants in replacement of chemical fertilizers and also for the control of phytopathogenic with good results.

Not only is it necessary to increase the knowledge of all the genomics of the microbial populations existing but also disseminate its importance to the farmers so that they can apply it in improvement of their crops within a sustainable agriculture, low-cost and environmentally friendly

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-----Original Message-----
From: Biotech-Mod3
Sent: 24 March 2013 07:48
To: biotech-room3-L@LISTSERV.FAO.ORG
Subject: 57: Development of mapping populations for crop species

This is Harjit Singh Rekhi, Professor of Crop Genetics and Breeding, University of West Indies, Trinidad and Tobago (on sabbatical leave from a Canadian Federal Agency).

I support the establishment of Global Genomics/Breeding Forum (Messages 48 - 50, 53).

To make such initiatives useful to the developing countries, in addition to other things, there would be need to provide support for development of mapping populations for the crops important to developing countries. Earlier, in Message 60 of Conference 16 of the FAO Biotechnology Forum on "Learning from the past: Successes and failures with agricultural biotechnologies in developing countries over the last 20 years" (http://www.fao.org/biotech/biotech-forum/conference-16/en/), I said:

"…….Tef (Eragrostis tef) is one of the main cereal food crops in Ethiopia, which is largely grown in Ethiopia only. Obviously, other countries may not have priority to initiate work on molecular mapping/tagging in this crop. Fortunately, breeders at the Melkassa Agricultural Research Center, Nazreth, Ethiopia could realize this need and developed recombinant inbred (RIL) populations from intraspecific and interspecific crosses. This led to development of molecular genetic map and quantitative trait locus (QTL) analysis of agronomic traits in Tef in collaboration with Cornell University, USA. In the absence of such populations conceived and developed, there would have been no molecular genetic studies in the crop of this developing country........"

This indicates the importance of providing support to the developing countries in those areas of genomics research where they do not possess capability/resources. This includes developing populations for the crops important to them. However, in crops like cassava, yam, sweet potato (for example) and other such crops which are mandated crops of the CGIAR centres and are important to developing countries, these centres can provide support.

However, good news is that developing countries like India have developed some populations for basic research useful in genetic enhancement of crops like wheat. Development of a recombinant inbred (RIL) population from a cross of Triticum boeoticum (AbAb - a diploid wild species) and Triticum monococcum (AA - a cultivated diploid wheat species) by us at the Punjab Agricultural University, India led to development of a molecular linkage map at diploid level in wheat (through Swiss funded international collaboration).

Development of similar populations involving related species of crops of interest to the developing countries would go in a long way to strengthen crop genetic enhancement in the third world.

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-----Original Message-----
From: Biotech-Mod3
Sent: 25 March 2013 17:50
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 58: Animal 'omics'

This is Acacia Alcivar-Warren from Environmental Genomics Inc, a small consulting firm in Massachusetts, USA, and an unpaid part-time volunteer at the UNA SALUD/ONE HEALTH Genomics & Epigenetics Program of the Fundación para la Conservación de la Biodiversidad Acuática y Terrestre (FUCOBI) of Ecuador.

I agree with Dr. Dubock (Message 54) that the conference is lacking on "animal 'omics'" information. On March 14, 2013, I sent a message to the AnGenMap Discussion Mailing List (http://www.animalgenome.org/community/discuss) distributed to 2365 members, some of whom are members of the National Animal Genome Research Program (NRSP-8, funded by the United States Department of Agriculture [USDA]) that include cattle, chicken, pig, sheep, aquaculture and horse. I requested that the NRSP-8 species coordinators and/or members of the list contribute to this conference by sending a short list of accomplishments with examples of practical applications to increase production for each animal species. I imagine the coordinators may be very busy at this time and they were unable to participate in this conference. Their information could have been very useful to participants from developing countries. Indeed, developed countries like the United States could also benefit from collaborating with researchers from developing countries to address emerging new zoonotic diseases and safety of imported food. For instance, by collaborating with teachers, governmental, and non-governmental organizations (NGOs) from tropical countries in Africa, Latin America and Southeast Asia, genome x environmental interactions due to climate change need to be considered in order to increase productivity of local seafood. In the US, shrimp imports alone cause an estimated ~$4 billion annual trade deficit, and collaborations with researchers from developing countries that export to the US and EU would help not only to increase production of good-quality/safe animal products short-term, but also contribute to address food security issues long-term.

I would like to make a small contribution to the issue of "animal 'omics'" by providing the web link to information on 'omics' accomplishments listed for the six animal groups included in NRSP-8, and hope the information is valuable to the conference participants: http://www.animalgenome.org/community/NRSP-8/2014-2018.proposal/ACCOMPLISHMENTS_2008-2012_revised.pdf (220 KB).

The websites for each NRSP-8 coordination group is included below, and I encourage young (and old) scientists all over the world to benefit from immediate training in bioinformatics:

Aquaculture : http://www.animalgenome.org/aquaculture/
Cattle : http://www.animalgenome.org/cattle/

Horse: http://www.uky.edu/Ag/Horsemap/
Poultry: http://poultry.mph.msu.edu/
Sheep: http://www.animalgenome.org/sheep/
Swine: http://www.animalgenome.org/pigs/
Bioinformatics: http://www.animalgenome.org/bioinfo/

Thanks to FAO for this important conference. I am hopeful that animal researchers can also be part of a "global genomics/breeding forum" as proposed for plants. As mentioned by Dr. Dubock, the potential benefits of the 'omics' field is huge, but requires sustained funding and commitment if we really want to solve long-term problems of food safety and food security for ALL.

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-----Original Message-----
From: Biotech-Mod3
Sent: 25 March 2013 17:51
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 59: Omics tools versus conventional plant breeding

I am Sathish Kumar Ponniah, plant molecular breeder working as extension specialist at the University of Arkansas at Pine Bluff, United States. I thank the moderator for the useful discussion.

I have been following the discussion for the past few weeks. I would like to thank the discussions by Beatrix Tappeser (Message 24) and Wayne Parrott (Message 35) for highlighting ‘omics’ tools that are used as plant breeding techniques in the current scenario. As we are progressing to improve plant breeding techniques, ‘omics’ tools form a very good addition to the conventional techniques. In the next-generation sequencing era, markers could solve many problems associated with single or monogenic traits (insect/pathogen damage to crops).

We need to keep on improving tools to answer the criticism raised by KN Rai (38) to solve complex traits like yield, drought tolerance, water use efficiency and nutritional traits with large genotype x environment (G x E) interaction. The cost of incorporating transformation (GMO) techniques to difficult traits could be tackled by ‘omics’ tools in the near future.

Consultative Group on International Agricultural Research (CGIAR) centers invested their money to develop various tools like iMAS (Integrated Marker-Assisted Selection System), MBP (Molecular Breeding Platform)...Similar investments in developing tools to convert these available ‘omics’ tools to breeder informed resources could be appreciated.

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-----Original Message-----
From: Biotech-Mod3
Sent: 25 March 2013 17:51
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 60: Re: Establishing a global genomics/breeding forum?

This is Denis Murphy again.

I think this has been a very useful discussion in bringing out some important genomics related issues from the wider community.

One point that I raised earlier (Message 25) was about more regional collaboration, especially in developing countries, and the establishment of larger and better resourced regional centres for genomics and related disciplines. This echoes some of the sentiments of a previous e-mail conference entitled "Learning from the past: Successes and failures with agricultural biotechnologies in developing countries over the last 20 years" which was held by the FAO Biotechnology Forum in 2009 (http://www.fao.org/biotech/biotech-forum/conference-16/en/). To quote from the report from this conference:

"Several participants suggested that increased regional and sub-regional cooperation would increase the benefits of applying biotechnologies. For sub-Saharan African, Danquah concluded that biotechnologies had failed to deliver on their promise in the past and, to change this, he highlighted the importance of education, capacity building and close collaboration between institutions and universities in sub-Saharan Africa. He also proposed the establishment of sub-regional centres of excellence and innovations in sub-Saharan Africa to train the next generation of African biotechnologists......Hash noted that for breeding programmes wishing to use molecular markers, it would be very useful if service laboratories, providing high quality and cost-effective marker data, could be established at sub-regional hubs. Agreeing with Danquah, Caesar stressed the need for capacity building and outlined the key features of a potential global biotechnology capacity building project, building on regional and sub-regional groupings of developing countries and including a comprehensive scholarship/fellowship programme for developing countries. Commenting on the many messages describing the lack of facilities and capacity for biotech R&D in developing countries, Murphy felt it might be unrealistic for each country, however small, to have its own research programme and he advocated increased collaboration with neighbouring countries and with centres in developed countries".

Obviously we are now four years on and there are few if any regional centres. Indeed I now realize that it may be unrealistic for nations, however small, to agree to fund a regional centre rather than a national one. However irrational, this is simple realpolitik. Luckily there may be another way forward and one message I am getting from the current conference is that a virtual Global Genomics/Breeding Forum might indeed be feasible both to practitioners and policymakers. I was pleasantly surprised by the information from Rajeev Varshney (Message 53) about the CGIAR initiatives and these could certainly be important resources in the future. But I also agree with Adrian Dubock (Message 54) that there are merits in a dispersed approach – after all we know that the most resilient systems, from engineering to the human body, should contain overlapping redundant components.

Therefore I favour the use of a stable long-term platform such as FAO to host such a forum. As for funding, set up costs would not be high but what is far more important is the management and curation of such a forum. Set up costs might be solicited from charities such as Gates or Rockefeller or transnational entities such as the EU. For example, I am currently involved in a bid for $1.5 million from the EU TEMPUS programme to establish a bioinformatics network including databases and collaborative training for Kazakhstan, Belarus and Russia. In the longer term the running costs should be modest and much of the work could be dispersed throughout the community – but we would need a reliable host organization and FAO seems one of the better candidates.

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-----Original Message-----
From: Biotech-Mod3
Sent: 25 March 2013 17:52
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: 61: Genomics of rhizobacteria

This is Doris Zuñiga, again.

Several researchers in Latin America have demonstrated the importance of the growth promoting plant bacteria among which are the nitrogen-fixing in various crops, the soybean crop is very important in Brasil and Argentina and pastures in Uruguay (Biofertilizantes en Iberoamérica: Una visión técnica, científica y empresarial. 2007. Edited by M.L. Izaguirre-Mayoral, C. Labandera and J. Sanjuan. 98 pages. http://www.biofag.org.ar/actividades/publicaciones/Libro-Biofag2007.pdf [2 MB]).

The genomics of these rhizobacteria allows their identification and the phylogenetic relationships among them, as well as knowing the different key genes in the processes of nitrogen fixation, solubilization of phosphate, production of hormones, genes for tolerance in conditions of stress, among others. All this is a great potential for the application of these bacteria in plants for their improvement.

Now, the inoculation of identified and selected strains in the cultivation of soya has a very large economic impact (millions of dollars per year) which means big savings for the farmer. But this is accompanied by a good implementation of legislative mechanisms to ensure good quality inoculants.

The economic impact within 5 years will be seen in other important crops (potatoes, beans, corn, among others) as there will be a greater bank of characterized strains, specific for each crop and each environment. However, it requires a larger demonstrative work with farmers and their relationship with the companies and universities.

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-----Original Message-----
From: Biotech-Mod3
Sent: 25 March 2013 17:55
To: 'biotech-room3-L@LISTSERV.FAO.ORG'
Subject: End of FAO e-mail conference on genomics

Dear Participants,

The last messages (numbers 58 to 61) have now been posted so Conference 19 of the FAO Biotechnology Forum, entitled "Impacts of genomics and other 'omics' for the crop, forestry, livestock, fishery and agro-industry sectors in developing countries", is now officially closed.

The FAO Biotechnology Forum was established in order to provide quality balanced information on agricultural biotechnologies in developing countries and to make a neutral platform available for people to exchange views and experiences on this subject. We hope that you found the conference interesting, constructive and beneficial.

The Background Document to the conference is available on the web (at http://www.fao.org/docrep/017/aq145e/aq145e.pdf - 90 KB) and all of the messages posted during the conference are available on the web, at the searchable website:
: https://listserv.fao.org/cgi-bin/wa?A0=Biotech-Room3-L . To see them sorted by date (latest on top), see https://listserv.fao.org/cgi-bin/wa?A1=ind1303&L=Biotech-Room3-L&O=D&H=0&D=1&T=1

For your interest, we can provide some figures about participation in this 3-week long conference. The number of conference subscribers rose from 471 people on 4 March 2013 when the conference began to 522 on 24 March when the conference finished. Just one person unsubscribed during the conference. Of the 522 subscribers, 44 (i.e. 8%) submitted at least one message. Of the 61 messages that were posted, 36% came from people living in Asia; 28% from Europe; 13% from Latin America and the Caribbean; 10% from Africa; 8% from North America; and 5% from Oceania. The messages came from people living in 22 different countries, the greatest number coming from India (13 messages) followed by the United Kingdom (7), United States (5), Finland (4) and Nigeria (4). A total of 35 messages (i.e. 57%) were posted by people living in developing countries. Just over half of the messages came from people working in universities; a quarter came from people working in research centres, including CGIAR centres; while the remaining quarter came from people working in the private sector, for the Government or working as independent consultants.

I would like to conclude by thanking all of you who participated actively in this conference. My impression is that a large number of people joined this conference to learn and to get an updated overview about this fascinating and fast moving area. So, a big thanks to those of you who made it possible by dedicating your time and effort to sharing your knowledge, ideas, experiences and viewpoints with the rest of us.

With best wishes

John

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