



Food and Agriculture Organization
of the United Nations

Meeting Report

Application of genome sequencing for sustainable agriculture and food security

**Side event of the 25th Session of the Committee
on Agriculture (COAG)**

30 September 2016

Food and Agriculture Organization of the United Nations
Rome, Italy

Executive Summary

The Food and Agriculture Organization of the United Nations (FAO) and the joint division of FAO and the International Atomic Energy Agency (IAEA) held a side event on “application of genome sequencing for sustainable agriculture and food security” on 30 September 2016 during the 25th session of Committee on Agriculture (COAG) at FAO headquarters in Rome, Italy. Genome sequencing has the power to revolutionize food security and sustainable agriculture including food safety, animal, plant and public health, reducing the risks from disease outbreaks and improving agriculture through effective plant and animal breeding. While several industrialized countries advance with the technology, application in developing countries is limited. The side event provided a forum for Members to discuss benefits, drawbacks, policy implications and challenges in genome sequencing that call for global actions. During the event, the panelists explained to the audience about the relevant work carried out by their respective units and divisions and discussed the impact and potential implications of the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity (CBD). The meeting was opened by Mr Ren Wang who emphasized on the benefits of international discussion of the topic and relevant global data sharing and Ms Renata Clarke provided the summary of the discussions to close the meeting. Presenters and panellists included Ms Masami Takeuchi, Ms Gwenaelle Dauphin, Mr Francisco Lopez, Mr Kathiravan Periasamy and Mr Daniel Manzella. The event was attended by more than 50 COAG participants and FAO staff.

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Acknowledgement

FAO would like to express its appreciation to all the side event participants for their valuable inputs. The side event was organized by FAO and administered by Masami Takeuchi under the overall guidance of Renata Clarke. FAO would like to thank all the speakers and participants who shared the perspectives on the topic and provided insights on the relevance to FAO’s work and impact for developing countries. The meeting report was prepared by Amrutha Anandaraman (Intern) and finalized by Masami Takeuchi.

Acronyms

ABS	Access and Benefit Sharing
AGAG	Animal Genetic Resources
AGAH	Animal Production and Health
AGDT	International Treaty on Plant Genetic Resources for Food and Agriculture
AGFF	Food Safety and Quality Unit
CBD	Convention on Biological Diversity
DDNC	Commission on Genetic Resources for Food and Agriculture
DNA	Deoxyribonucleic Acid
EMPRES-AH	Emergency Prevention System for Animal Health
FAO	Food and Agriculture Organization of the United Nations
IAEA	International Atomic Energy Agency
IT	Information Technology
MAT	Mutually Agreed Terms
OIE	World Organisation for Animal Health
PCR	Polymerase Chain Reaction
PIC	Prior Informed Consent
SARS	Severe Acute Respiratory Syndrome
WGS	Whole Genome Sequencing
WHO	World Health Organization

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Side event of the 25th session of Committee on Agriculture (COAG)
Application of genome sequencing for sustainable agriculture and food security
30 September 2016, FAO Headquarters, Rome, Italy



1. Introduction

On 30 September 2016, the Food and Agriculture Organization of the United Nations (FAO) and the Joint division of FAO and the International Atomic Energy Agency (IAEA) organized a side event to the 25th session of Committee on Agriculture (COAG) at the FAO headquarters in Rome, Italy, entitled “application of genome sequencing for sustainable agriculture and food security”. The side event provided a forum for Members to discuss benefits, drawbacks, policy implications and challenges in genome sequencing that call for global actions. Experts from various FAO divisions presented the relevance of genome sequencing for developed and developing countries, the input and impact of the technology for animal health, the relevance of the use of the technology to the Nagoya protocol, and approaches applied to improve food and agriculture using nuclear and related technologies. The final meeting agenda is provided in the Annex. All presentation materials are available at <http://www.slideshare.net/FAOoftheUN/tag/wgs>. The recording of the event is available at <http://www.fao.org/webcast/home/en/item/4197/icode/>. The event was attended by more than 50 COAG participants and FAO staff.

2. Opening remarks by Ren Wang



Mr Ren Wang, Assistant Director-General of the Agriculture and Consumer Protection Department (ADG) welcomed the Members on behalf of FAO. Genome Sequencing is a novel technique developing at a fast pace and the amount of data produced is enormous. Mr Wang emphasized the importance of discussing the potentially useful applications in food and agriculture and making the data available on public domain, which would help future generations to revolutionize plant and animal breeding, food safety, and prevent the outbreak of diseases. He provided a number of examples of the applications of genome sequencing in the different sectors, such as the sequencing of the Severe Acute Respiratory Syndrome (SARS) virus in China and the sequencing of orphan crops by

the African Orphan Crops consortium. Mr Wang explained that to understand the diseases and pathogens, having a blueprint is not enough but it is important to understand how to interpret the data to generate usable information. He also expressed FAO's interest in proactively engaging in the facilitation of international discussions on this issue.

Mr Wang then explained FAO's commitment to a broader agenda and objectives to be achieved using genome sequencing technology, which is the main purpose of why experts from food safety, animal health, animal genetic resources, and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) come together to discuss the application of the technology in their sectors and the surrounding issues that need to be addressed. He reminded the audience that other than the technical issues, one must keep in mind the key peripheral issues including legal issues not to mention intellectual property rights and the regulatory issues that come along with the generation of the large amount of data. Thus, this side event would be a good opportunity to obtain a basic understanding of not only the technical implications or the technical side but also the policy implications so that both benefits and challenges can be identified in order to call for global actions. Mr Wang recalled the International Symposium on "the role of Agricultural Biotechnologies in Sustainable Food Systems and Nutrition"¹ held at FAO in early 2016, where there were discussions on the development of regulatory aspects and the management of global governance of technologies including the genome sequencing techniques. Mr Wang expressed the need to convene such dialogues in the future and thanked the participants.

3. Genome sequencing in food and agriculture by Masami Takeuchi



Ms Masami Takeuchi, Food Safety Officer of the Food Safety and Quality Unit (AGFF) first explained the basics of the technology including the mechanisms of genome sequencing and the layout of the obtained sequenced data, while at the same time, she reminded the audience that the main purpose of the side event is to highlight the issues surrounding the technology and not the technology itself. Ms Takeuchi pointed out the rapid advancements in the field of genome sequencing and that a single discovery in the field of genetics could lead to thousands of discoveries which will benefit mankind. The new sequencing machines have been rapidly

developed both in terms of the functions and the speed with several companies competing to produce faster and more efficient machines. The cost of these machines and the relevant running costs have drastically reduced over the past decade and one sequencing run now costs only about 200 US dollars. There has been a tremendous improvement in the Information Technology (IT) capacity and functions as well which have enabled the ease of data storage and transfer.

Ms Takeuchi spoke about the relevance of the technology to food safety. Using traditional sub typing methods, multiple target detection tests have to be used to detect and identify the multiple pathogens in contaminated food. With genome sequencing techniques, one run can detect multiple pathogens. During the technical meeting on the Impact of Whole Genome Sequencing on Food

¹ Based on the outcomes of the 2010 FAO international technical conference on Agricultural Biotechnologies for Developing Countries, FAO acted as a neutral broker and convened the symposium to examine how the application of science and technology, particularly agricultural biotechnologies, can be of benefit to smallholders in developing sustainable food systems and improving nutrition in the context of climate change. The investments required and other issues related to the acquisition and use of these technologies were also addressed. More information about the symposium can be found at: <http://www.fao.org/about/meetings/agribiotechs-symposium/en/>

safety management², held in May 2016 at the FAO headquarters, around 175 participants gathered from 50 countries, with half of them being developing countries, to discuss the concerns, views and implications of using the technology in their countries. Through this meeting, it was clear that even if sequencing knowledge is transferred to the developing countries, these efforts remain futile if there are no genomes to sequence in the first place. Thus priorities of countries and the preliminary readiness assessment needs to be carried out.

Genome sequencing is significantly relevant to FAO and various units are actively involved in the work of WGS:

- Commission on Genetic Resources for Food and Agriculture (DDNC);
- Animal Genetic Resources (AGAG)
 - Molecular genetic characterization of animal genetic resources (for biodiversity and production);
- International Treaty on Plant Genetic Resources for Food and Agriculture (AGDT)
 - Global information system for plant genetic resources (for biodiversity and production);
- Animal Health Service (AGAH)
 - Genome sequencing of pathogens (microorganisms) for animal diseases detection and prevention;
- Food Safety and Quality (AGFF)
 - Genome sequencing of foodborne pathogens (microorganisms) for detection, source-tracking and disease prevention;
- Joint FAO/IAEA Division (AGE)
 - Sequencing approaches to improve food and agriculture using nuclear and related technologies.

Members of the World Health Organization (WHO) recommended WHO to fully utilize the technology to combat diseases like Ebola and Zika viruses, and facilitate immediate sharing of such sequenced data for public good. The World Organisation for Animal Health (OIE) has adopted the technology to be considered for their standard setting activities and database development. Various socio-economic, ethical and legal issues have been emerging – in particular on the topic of international (or bilateral/multilateral) data-sharing.

Though various initiatives exist, Ms Takeuchi explained to the audience that some misperception of the technology for food safety varies among different countries. While some countries, especially the developing countries consider that they are not at all ready to even consider applying this new technology, thinking this is too advanced and possibly too expensive, some other countries immediately consider that this technology must be the solution to all the problems they have in the area of food safety. There are several countries that are urged to use WGS for regulatory activities and other countries that feel the need to build their capacity and resources before considering the use of the technology. However, the reality remains that more than several industrialized countries have applied WGS in their governmental activities for regulatory purposes in food and animal borne disease control and prevention. Genome sequencing is already being used for food inspection including imports and exports. Global databases exist to collecting and sharing information in various formats. Ms Takeuchi highlighted the impact and implications on developing countries and flagged that the knowledge gap between the developed and the developing countries is widening.

²The [Technical Meeting](#) on the impact of Whole Genome Sequencing (WGS) for food safety management was held at the headquarters of the Food and Agriculture Organization of the United Nations (FAO), Rome, Italy on 23- 25 May 2016 and provided an overview of the Technical Paper entitled “[Applications of Whole Genome Sequencing in food safety management](#)” developed by FAO in collaboration with WHO and discussed benefits and potential drawbacks of WGS, considerations for developing countries and key needs on global actions and potential roles of international organizations. More information can be found at: <http://www.fao.org/food/food-safety-quality/a-z-index/wgs/wgs-food-safety/en/>

In conclusion, Ms Takeuchi stated that since FAO is a Member-driven organization, all activities conducted by FAO are in response to the official requests by FAO Members. The positive outcome of this system is the prioritization of activities for the different countries. On the other hand, requests on new technological development may be delayed and countries may fall behind rapid advancement of the technology. Since several issues around data sharing exist, she believes that harmonization is critical and accessibility and equal opportunity should be ensured for all. FAO can facilitate the creation of networks between Members and existing initiatives and databases while also providing capacity development assistance. Ms Takeuchi stressed that proactive planning and actions are key.

4. Genome sequencing for animal health – input and impact by Gwenaëlle Dauphin



Ms Gwenaëlle Dauphin, Coordinator of the Animal Health Service (AGAH), stated that most of the genome sequencing related work in the Department of Animal Health and Production (AGA) at the FAO is targeted to viruses. Though the genetic material of viruses may be very short since they are intracellular parasites, these organisms change rapidly and thus continuous and quick monitoring of their genetic features is essential. Ms Dauphin explained that sequencing of live organisms has greatly increased over the past 10 years, as shown by a graph describing the exponential growth in the number of available sequences of genomes in GenBank.

Ms Dauphin spoke about the basic requirements to conduct genome sequencing in a laboratory which include a Polymerase Chain Reaction (PCR) machine, reagents, a functional laboratory and technical skills. Once the PCR is complete, the sample is placed in a sequencer and then the sequence is analysed by alignment with different sequences and checking the genetic relatedness between viruses using a phylogenetic tree or looking at mutations of interest. The obtained scientific results are then deposited in open-access databases and often referenced in scientific papers. She explained that the AGAH service along with the FAO/IAEA joint division are responsible in supplying PCR reagents, PCR machines, building or strengthening laboratory facilities and training of laboratory staff on molecular biology testing, sequencing, bio informatics and use of databases, including sequence deposition. The units also assist countries in data analysis and provide open-access software to align and analyse sequences.

There is an FAO reference centre for bioinformatics that develops and maintains databases and informs FAO on future directions in this field. There are also FAO reference centres designated for various animal diseases or groups of diseases which also use sequencing and are particularly helpful for developing countries with training, confirmatory testing, protocol validation and mentoring. The AGAH service also invests efforts to work with database developers, especially secondary databases which are pathogen specific and easier to use. AGAH has also developed linkages between some of these secondary sequence databases and the global animal health platform (EMPRES-i, for Emergency Prevention System for Animal Health). FAO provides assistance in the following practical activities:

- a) Monitoring virus distribution. Molecular epidemiology enables to monitor genetic groups of viruses and their possible jump into new species or new geographical areas;
- b) Monitoring virus genetic evolution, especially for influenza and for pandemic preparedness;
- c) Monitoring vaccine matching for animals and zoonotic diseases. The veterinary sector contributes to the gathering of information required for the selection of influenza human vaccines led by WHO.

Whole genome sequencing provides a clear added value for a more in-depth knowledge on viruses: deeper phylogenetic analysis, better design of diagnostic assays and easier differentiation of virus genotypes.

Ms Dauphin elucidated two countries where sequencing capacities built under FAO projects have a significant impact on the control of Highly Pathogenic H5N1:

- a) In Indonesia, which is an endemic country, H5N1 influenza viruses are monitored by a national influenza network established through FAO support. The Influenza Virus Monitoring Network has benefitted from increased capacity for PCR testing and sequencing, harmonized testing protocols, and an IT platform that enabled laboratory technicians to upload data and conduct analyses with national genetic and antigenic data related to circulating influenza viruses. This network has streamlined the process for decision making, especially for the development and registration of new influenza vaccines.
- b) Egypt, another endemic country, has reported around 3,500 poultry H5N1 outbreaks in 2006. Mostly thanks to FAO support, virus sequences have been generated and deposited to the public domain for half of these outbreaks, which is a very good ratio. Thus capacities for PCR and sequencing have been strengthened in the national laboratories. For several years, Egyptian scientists in the veterinary sector characterized influenza viruses, deposited sequences to the public domain on their own and produced high quality scientific papers.

Ms Dauphin also flagged the importance of molecular biology and sequence data in the control and prevention of animal and zoonotic diseases. Sequencing is used for all pathogens and the use of sequencing is expanding. Thus, there is a high demand for training of personnel from Member Countries for this technology. The real challenge lies in the continuous update of the skills due to the rapid evolution of the technology. With respect to data sharing, Ms Dauphin reiterated that sharing of sequences is of utmost importance. There are various barriers to sharing samples with reference laboratories and sequences with the public domain, including cultural, technical, political and legal barriers. Ms Dauphin also touched upon the Nagoya protocol which she believes will have a major impact on data sharing and material transfer, with the hope that it does not increase the already existing complexities which would make handling animal health emergencies difficult.

5. Protecting plant biodiversity: The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), genome sequencing and the relevance to the Nagoya protocol by Francisco Lopez



Mr Francisco Lopez, Technical Officer of ITPGRFA (AGDT), began his presentation by informing that the Treaty entered into force in 2004. It is an international access and benefit sharing (ABS) instrument with 140 Contracting Parties. Bolivia and the United States of America have announced that they will join the Treaty soon. The Treaty's objectives are "the conservation and sustainable use of plant genetic resources for food and agriculture and the fair and equitable sharing of the benefits arising out of their use, in harmony with the Convention on Biological Diversity (CBD), for sustainable agriculture and food security".

Mr Lopez mentioned the interdependence of all countries with regard to plant genetic resources for food and agriculture as well as their special nature and importance for achieving food security worldwide. It is also a key legal and operational instrument for the sustainable development of agriculture in the context of poverty alleviation and climate change. Thus, both the ITPGRFA and

the FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) are relevant policy fora at an international level. He compared the access to the genetic resources under the CBD and its Nagoya protocol with the ITPGRFA. The Nagoya Protocol requires Prior Informed Consent (PIC) from the provider for the development of Mutually Agreed Terms (MAT) regarding the conditions of use and the benefit sharing option. On the other side, the International Treaty applies to a subset of plants, to the plant genetic resources for food and agriculture (PGRFA). In this context, as the Treaty sets up a multilateral system and uses the Standard Material Transfer Agreement (SMTA) it really facilitates the exchanges. Up to the end of September 2016, the Multilateral System included 1.5 million accessions of PGRFA and the Governing Body had received reports of 3.2 million PGRFA transferred since January 2007.

Mr Lopez indicated that in the context of the Treaty, genomics is one type of non-confidential information related to PGRFA. He indicated that the community has indicated the need to link phenotypic, genotypic and geographic data with passport information. Gene banks cannot become just PGRFA museums. It is key connecting genomics and other information to add value to the PGRFA and further facilitate plant breeding and the benefits for the PGRFA development chain. Under the Treaty, there is an obligation to make available to the recipient all scientific information and non-confidential, like characterization and evaluation data. He indicated that every scientific community exchanging material and information needs clear transfer rules. Plant breeders should be supported to use genome sequencing technology and that their behaviour should be understood. Mr Lopez also advised conciliating access to genetic resources with fair benefit sharing, particularly with farmers in developing countries.

Mr Lopez highlighted the benefits of developing and implementing coherent policy guidance and rules for users of plant material for both the ITPGRFA and Nagoya. He stressed that a global dialogue between science and policy makers to identify the impact of new developments will help in reviewing and understanding the impact of genomics and phenomics on existing rules and mechanisms. FAO has demonstrated over the years to be a neutral policy forum and has accumulated valuable experiences in the plant sector which could be relevant to other sectors.

6. Capacity building on sequencing approaches to improve food and agriculture using nuclear and related technologies by Kathiravan Periasamy (FAO/IAEA)



Mr Kathiravan Periasamy, from the Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture (AGE), spoke about the active technical support provided to Members of FAO and IAEA on sequencing and related technologies. The FAO/IAEA laboratories under the Joint Division are directly involved in building capacities and transfer of technology related to genome sequencing on five major thematic areas: animal production and health, plant breeding and genetics, food and environment protection, insect pest control and soil and water management.

Mr Periasamy explained about the increasingly important role genome technology plays in livestock improvement for increased productivity, conservation of domestic animal diversity, molecular diagnostics for animal and crop health, improved vaccines against transboundary animal diseases, mutation breeding for crop improvement, food traceability, authenticity and safety. He also provided examples in the plant, animal sector and food sectors where significant impact has been achieved in highly industrialized production systems using these technologies:

- Revolution in dairy cattle breeding improvement for milk production: The sequencing of the livestock genomes has led to the discovery of genome wide Deoxyribonucleic Acid (DNA)

markers which in turn paved way for the development of DNA chips enabling genomic selection in dairy cattle. These DNA chips with thousands of markers across the genomes are now used to estimate the breeding value of a bull for milk production on the day of its birth. Unlike the traditional progeny testing method that takes 6-8 years to obtain the first breeding value of a bull, genomic selection technology has reduced the generation interval and doubled the rate of genetic gain per year for milk productivity. This technology is also relatively cheaper and economical and helps breed organizations to screen large number of bulls for selection and breeding.

- Genome sequencing for mutation breeding and crop improvement: Irradiation technologies have been used to induce mutations and derive new varieties of crops with special characteristics like salt tolerance, drought and disease resistance and so forth. Genome sequencing technologies are extremely helpful in optimizing mutation induction in crops and development of mutant markers for rapid improvement of farmer-preferred varieties and landraces.
- Technologies for Food Traceability, Authenticity and Safety: DNA Barcoding has been traditionally used to trace the origin of food. WGS has proved not only to increase the efficiency of detecting food fraud, but also offers the advantage of non-targeted screening of food samples for microbial contamination.

Although the technology has been implemented in various sectors in different countries, Mr Periasamy highlighted the fact that the developing countries are yet to capitalize on the advantages of genomic technologies. He also discussed the gaps and challenges that limit the implementation of these technologies in developing countries as follows:

- High cost of establishing and maintaining sequencing/genotyping facility; Low quality of outsourcing services
- Lack of low cost genomic tools (e.g. low cost all species DNA array for livestock) appropriate for local production systems
- Lack of skilled personnel and limited access to tools for bioinformatics analysis of genomic data
- Lack of database tools for storage and management of high throughput genomic data
- Limited access to internet

Mr Periasamy presented the efforts put forth by the FAO/IAEA laboratories to address these challenges in developing countries. Member states are assisted to set up laboratories, install equipment and implement DNA based technologies related to animal production, animal health, mutation plant breeding and food traceability, authenticity and safety. The laboratories are providing individual fellowship training and organize group training courses to scientists and professionals from member state laboratories to improve their capacities on genome sequencing technologies applied to food and agriculture. The Joint Division also conducts field support missions and onsite demonstrations on the use of this technology as well as bioinformatics analysis of the genomic data. In conclusion, Mr Periasamy stated that in order to move ahead with the technology and to fill the widening gap between industrialized and developing countries, support from national governments through increased investments in genomic and agriculture biotechnologies is indispensable.

7. Panel discussion on the benefit, impact and implication of the Nagoya Protocol



The panel discussion was facilitated by Masami Takeuchi (AGFF). She first gave the floor to Mr Daniele Manzella (AGDT) who briefed the audience about the Nagoya Protocol. The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the CBD is an international legally binding agreement, in force and with a current membership of 78 state parties. Mr Manzella reviewed the different positions expressed by governments and stakeholders as to whether the provisions of the Protocol on scope, utilization and PIC and MAT may apply to data generated from genetic material, and utilized for research. Mr Manzella referred to the need to consider national applicable legislation. He discussed the various concerns, views and coping strategies in response to the Protocol from the various sectors of the society. In his views, the Protocol is considerably influencing the researchers' perceptions and the institutions and norms that govern their activities. Further possible work by FAO in the area of the Nagoya Protocol could include stimulation of self-governance and adaptation patterns, and multilateral dialogue to reinforce research commons.

Ms Takeuchi expressed the common concerns shared among experts in the area of food safety about the use of the protocol. She elucidated a scenario where a food product, produced in Country A, is consumed by a person from Country B, and falls ill due to the consumption of the particular food product. The person is diagnosed in Country C, where a strain is identified pertaining to the contamination of the food produced in Country A. In this case, the ownership of this data remains a topic of discussion still as the provisions for such scenarios have not yet been made by the Nagoya Protocol. Ms Dauphin agreed with Ms Takeuchi on this issue and stated that the animal health sector could face similar situations. Another concern expressed by Ms Dauphin was about the delay for treatment in emergencies when people are infected with viruses of animal origin. The delay and the complex paper work might dissuade people for sample sharing.

Mr Lopez stated that there is an obligation to have clear and transparent rules in all the sectors for data sharing. Through the various presentations, it is evident that FAO has accumulated experience in implementing sequencing technologies and facilitating the collaboration of databases. Keen attention must be paid to the evolution of science to avoid complex situations in the future.

8. Closing remarks by Renata Clarke



Ms Renata Clarke, Senior Food Safety and Quality Officer of the Food Safety and Quality Unit (AGFF), stated that the purpose of the side event was to place the topic of genome sequencing in the spot light in the context of FAO's work. She thanked the speakers for the interesting overviews in the various domains of food and agriculture. She stated that it is evident that genome sequencing is a powerful technology, but on the other hand, it is also clear that further initiatives and efforts need to be made to realise its full potential. Ms Clarke believes that the partnership will aid in staying abreast with the technology to guide the evolution of the technology while keeping in mind that all the countries are benefitted and not just the technology advanced. Therefore FAO intends to keep working across the departments and divisions and in partnership with sister organizations and with Member countries.

Annex: Agenda of the side event

Side event of the 25th session of Committee on Agriculture (COAG)
Application of genome sequencing for sustainable agriculture and food security
30 September 2016, FAO Headquarters, Rome, Italy

Time	Item	Speaker
13.00 – 13.10	Welcome Remarks	Ren Wang
13.10 – 13.30	Genome sequencing in food and agriculture: What it is, how relevant it is to developing countries, and why we are discussing this now	Masami Takeuchi (AGFF)
13.30 – 13.40	Genome sequencing for animal health – input and impact, Examples from Egypt and Indonesia	Gwenaelle Dauphin (AGAH)
13.40 – 13.50	Protecting plant biodiversity: ITPGRFA, genome sequencing and the relevance to the Nagoya Protocol	Francisco Lopez (AGDT)
13.50 – 14.00	Capacity building on sequencing approaches to improve food and agriculture using nuclear and related technologies	Periasamy Kathiravan (AGE)
14.00 – 14.25	Panel discussion on the benefit, impact and implication of the Nagoya protocol	All
14.25 – 14.30	Closing Remarks	Renata Clarke (AGFF)