Summary document of the FAO e-mail conference: "The role of biotechnology for the characterisation and conservation of crop, forest, animal and fishery genetic resources in developing countries"

Executive Summary

Characterisation and conservation of genetic resources of crops, forest trees, livestock and aquatic species are important for all countries, but particularly for developing countries whose economies depend heavily on these sectors, and where genetic resources are often threatened. A number of biotechnology tools are available that can help in characterisation and conservation of such genetic resources, ranging from relatively cheap and uncomplicated technologies to sophisticated, resource-demanding ones. In each of the crop, forestry, animal and fishery sectors, albeit to different degrees, biotechnology tools are currently being applied in developing countries for these purposes and numerous examples of the wide range of applications were provided during this FAO e-mail conference. Of the different biotechnologies, most discussions were about molecular markers, in particular their use for characterisation of genetic resources, where issues such as the advantages or disadvantages of different marker systems and the proposal to develop a universal molecular marker database were debated. In situations involving potential use of marker and non-marker information, such as development of a core collection of plant genebank accessions or prioritisation of animal breeds for conservation purposes, there was general consensus that decisions should not be based on marker information alone and that other factors, such as morphology and agronomic performance, should also be considered. The merits of several in vitro techniques, including tissue culture, cryopreservation and DNA storage, were considered with a view to conservation of genetic resources, where e.g. DNA banks for plants were seen as potentially complementing but not replacing seed banks, at least in the near future. The ability to apply these biotechnologies in developing countries is currently limited by the lack of sufficient funds, human capacity and adequate infrastructure. The importance of human resource capacity building was highlighted. There was a general call for greater collaboration among researchers and practitioners, particularly at the regional level, to reduce costs and pool limited resources, and between developed and developing country institutions. A role was seen for international organisations, including FAO, and the centres of the Consultative Group on International Agricultural Research (CGIAR), in coordinating these collaborative efforts and in supporting these capacity building activities.

1. Introduction

The theme of the 13th e-mail conference of the FAO Biotechnology Forum, which took place between 6 June and 4 July 2005, was "The role of biotechnology for the characterisation and conservation of crop, forest, animal and fishery genetic resources in developing countries". As for all other conferences of this Forum, a Background Document was prepared and posted before the conference began. The document gave an overview of the current status of genetic resources in the different food and agricultural sectors; a description of relevant biotechnologies (such as molecular markers, cryopreservation and reproductive technologies); and a discussion of some potential factors that may influence applications of biotechnology in developing countries in this area.

This Summary Document represents a concise account of the principal issues and opinions received from contributors to the conference. Specific messages are referenced in the document using participants' surnames and the message number. All messages can be read at the Archives of Conference 13. About 650 people subscribed to the conference and 127 e-mail messages were posted from people living in 38 different countries; over 60% of messages were from developing countries. The majority of messages came from people working in research organisations, including centres of the CGIAR, and universities.
Most participants directed their messages to issues in one of the crop, forestry, animal or fishery sectors, with greatest attention given to crops and animals. Some also addressed cross-sectoral issues such as resource availability and constraints and international collaboration. In Section 2 of this document, the main issues discussed during the conference are summarised. Section 3 provides information on participation and Section 4 represents a list of names and countries of those who sent referenced messages.

2. Main themes discussed

2.1 Current applications and potential of biotechnology in the different sectors

Most of the messages addressed the current situation and potential of using biotechnology tools for characterisation and conservation of genetic resources in one of the individual sectors (crop, forestry, animal or fishery). Although each sector has its specificities, some of the discussions were also very relevant for other sectors.

2.1.1 Crop genetic resources

The potential importance of biotechnology for locally-important crop genetic resources was raised right at the beginning of the conference. Nkhoma (1), describing activities at the Southern African Development Community Plant Genetic Resources Centre (SPGRC) in Zambia, noted that while their programme had succeeded fairly well with common cereals and legumes, they were in some cases unable to work on indigenous crops, for example when difficult to cultivate, which were locally useful and on which nobody else was working. He said that biotechnology facilities would help them to tackle these problems. He also reported that the SPGRC collections were only characterised using agronomic and morphological data, although molecular markers would be helpful to allow removal of duplicate accessions. The usefulness of applying biotechnology to genetic diversity studies of less common crops was reported by Infante (8), who described their results in Venezuela where they found genetic variability in clonally reproduced henequen and cocuy following analysis with molecular markers. This had implications for conservation because clonally reproduced species were assumed to be of uniform genetic constitution. Morphological data were also gathered and analysed which supported the molecular data.

Kisha (6) noted that molecular markers are now an accepted and widely used tool for measuring genetic diversity, where "molecular marker technology can be used to characterize the extent of diversity within a collection and for the development of collection management strategies, which may include establishment of core collections, identification of redundancies or contamination, guidance for future collection efforts, and identification of gaps of ancestral crop relatives. Additionally, analysis of world-wide genetic diversity can identify areas suited for the establishment of in-situ conservation sites". Ndjiondjop (41) reported that recent studies with molecular markers based on repetitive DNA sequences had provided useful information on genetic diversity present in rice, Oryza glaberrima. Previous studies, using isozyme and restriction fragment length polymorphism (RFLP) markers, had failed to identify as many polymorphisms although considerable variation for many morphological and agronomic traits had been recorded. The microsatellite marker information will be used to develop the core collection of O. glaberrima accessions in the Africa Rice Center (WARDA) genebank. Also regarding core collections, Huaman (38) said that "molecular markers are the most valuable source to get data on genetic diversity of a given crop or plant species" but added that when selecting a core collection, other factors, such as eco-geographical data, disease and pest reaction and morphological diversity, had to be taken into account. Ghamkhar (28) suggested that molecular markers should be "definitely employed as the best technique for screening of genetic diversity but they must also be double checked by morphological data to make certain there is no major loss in our breeding and/or core collection development programs".

Molecular marker data were considered to be only one aspect of characterisation (Huaman, 38), but one that would be of greater use were a universal molecular marker database to exist (Kisha, 6). He noted that in the current situation, few, if any, plant genetic diversity studies can be directly compared or compiled; that marker data can be lost or forgotten after publication; and that studies of genetic diversity are usually limited to a few accessions or accessions from a limited area of interest. The development of such a database was supported by several participants, including Vijay (18), who urged, however, that consideration should be given to selection of a set of universally reliable and
reproducible markers; to consensus on the outcome from different markers; and to standardisation of methodologies, including the mode of analysis. In this context, both De Vicente (26) and Ford-Lloyd (30) mentioned an initiative by the International Plant Genetic Resources Institute to define community standards for documenting information about genetic markers so that researchers can generate and exchange genetic marker data that are standardised and replicable. Barker (24) noted that a large number of molecular markers were already available in the public domain, but to assemble a universal database would require considerable effort and it was hard to see any single country willing to invest in such a project. He did envisage, however, that it would be easier to establish databases on a single species basis. Kisha (51, 103) expanded on his original proposal, describing how the database would need to be curated and why a core set of primers would be useful to make studies comparable. Sales (19) noted that some microsatellite databases already exist and Ghamkhar (28) mentioned some web-based databases, mostly for cereals. R. Jones (54) hoped that a global marker database might also include data for key fish and crustacean species.

Kisha (51) also commented on the relative usefulness of different types of molecular markers, arguing that amplified fragment length polymorphism (AFLP) markers can cover a large area of the genome with less cost than simple sequence repeat (SSR) markers, also known as microsatellites. Ghamkhar (28, 80) proposed that inter-simple sequence repeats (ISSR) techniques were also cheap and efficient, and Varshney (43) supported using single nucleotide polymorphism (SNP) markers for characterisation, while acknowledging their high cost and the relative paucity of species for which markers currently existed. In a similar vein, Ghamkhar (53) suggested that SNPs might be useful in well-studied crops like wheat and maize but not for less common crops because of the sequencing work required to get the markers. Warburton (42) described experiences in using SSR markers to study molecular diversity in maize among several laboratories and highlighted problems of comparison and reproducibility among laboratories even when using the same protocols and platforms for genotyping. She said that the possibility of combining datasets if laboratories used different techniques was "virtually non-existent" and that there were problems of repeatability with some other kinds of markers as well. Varshney (43) had had similar experiences and suggested that expressed sequence tag (EST)-derived SSR markers showed higher reproducibility than genomic SSR markers. Krishna (88), supported by Buso (93), felt that all molecular marker data were nevertheless useful and, even though random amplified polymorphic DNA (RAPD) and AFLP markers might have some problems with reproducibility (highlighted by Vijay (79)), they also had advantages (highlighted by Muchugi (77)).

Dulieu (95) also compared different markers systems with respect to the reproducibility of their results, noting that some markers, such as microsatellites, were more reliable than others but required more preliminary research, and suggested that biotechnology companies should be encouraged to produce kits for the most important species, following the example of human DNA fingerprinting kits which are used universally. De Vicente (26) noted that as part of the CGIAR Generation Challenge Program, microsatellite kits were being put together which they hoped to have available in the near future. Dulieu (95) also pointed out that many of the molecular markers revealed differences between populations that were not highly correlated with performance or phenotypic characters. Gupta (44) suggested that if molecular markers were to be used for genetic diversity analysis, they should be functional markers rather than random genomic markers. He (44, 87) also reported that they got different results from genetic distance analyses of bread wheat when different kinds of markers (SSR, AFLP or selective amplification of microsatellite polymorphic loci (SAMPL)) were used, suggesting that the best estimate of diversity might be got from data on large numbers of morphological traits. Kisha (88) wrote that it would be useful to compare at least two different marker systems for agreement in the resulting relationships. Ghamkhar (118) agreed that there can be inconsistencies between results obtained with different sets of molecular and morphological data, concluding "more molecular techniques/data, more resolution or better results".

The merits of tissue culture as a means of genetic resource conservation were discussed by several participants (e.g. Muchugi, 68). Lin (2) suggested that tissue culture and other forms of micropropagation were useful tools for the conservation and multiplication of plant species, noting that low-cost options were also available. Cummins (9), however, felt that because of somaclonal variation (i.e. mutations that occur spontaneously in tissue culture), tissue culture was not a good way of conserving local genetic material. Muralidharan (22) agreed and favoured use of slow-growing shoot culture. He suggested also that molecular markers could be used to study the extent of somaclonal variation in slow-growing or cryopreserved cultures. Lin (21) reported that improved protocols for in vitro conservation, developed for a range of species, could overcome the potential
problems of somaclonal variation and that in vitro conservation was useful, particularly for plants that
do not produce seeds or that produce seeds of limited viability. Ford-Lloyd (30) pointed out that in
vitro conservation was being used to support genetic conservation, despite genetic instability, as it
represented a better option than the currently available alternatives.

There were several responses to a question from Muralidharan (22) regarding the potential of DNA as
a means of long-term conservation of genetic material. Wang (32) pointed out that germplasm
conservation as pure DNA was already a reality in some countries, which was supplemented by
concrete examples in later messages (Ghamkhar, 38, 48; Widjaja, 40; Vijay, 47). De Vicente (46)
reported results from a 2004 worldwide survey on plant genetic resources DNA banking activities
showing that 20% of the 243 institutions that replied to the questionnaire kept DNA as a genetic
resource. Although noting that both DNA banks and seed banks have advantages and disadvantages,
Ghamkhar (34), suggested that seed banks were currently preferable to DNA banks as e.g.
contamination was more immediately apparent and morphological screening and maintenance were
easier. Vijay (47) agreed with Ghamkhar (34) and described the major limitations he saw to use of
DNA banks, suggesting they could complement, but not replace, seed banks, at least in the near
future.

Dulieu (96) preferred phage genomic libraries over DNA banks for genetic resource conservation
because they are easier to prepare and maintain. However, he warned against using more technology
to counter effects of misuses of technology (mainly the destruction of traditional agricultural
systems), a point echoed in a different context by Magalhães (72), supported by Kante (105) and
Adediran (112), who argued that the use of biotechnology to conserve or characterise biodiversity
could not be considered a solution but only a palliative when biodiversity in developing countries was
being destroyed by an economic model based on the economic exploitation of developing countries
and their natural resources.

Nassar (4) suggested that apomixis (i.e. where seeds are produced through asexual processes so
that the genetic make-up of the seeds is identical to that of the mother plant) could contribute to
conservation of certain crop genetic resources and reported that they had produced apomictic
cassava clones in Brazil, confirmed using molecular markers. Vijay (11) agreed and felt that
identification and transfer of apomixis to other cultivated species would have important consequences
for conservation and hybrid seed production.

During the conference, Gupta (23, 87), supported by Vijay (73), also mentioned the new possibilities
of using DNA barcoding, allowing different plant species to be identified and discriminated. Ghamkhar
(118) felt it could help taxonomists to classify, re-classify or identify taxa or new species, when used
together with traditional taxonomy methodologies based on morphological data. Gupta (120) also
pointed out the potential of DNA microarrays for the study of genetic diversity.

### 2.1.2 Forest genetic resources

There were relatively few contributions specifically addressing the use of biotechnology in
characterisation and conservation of forest genetic resources. Oluawsegun (101) reported on the loss
of forest species in Nigeria due to factors like poverty and low education levels among the rural
people, concluding "for any meaningful and lasting conservation programme to be effectively carried
out there must be a conscious effort in involving the local people in maintaining and managing their
environment since the needs of these dwellers must be respected". Muralidharan (67) bemoaned that
there was insufficient effort and funding put into conservation of forest genetic resources compared to
the crop and livestock sectors and wondered whether tropical forest genetic resources could be
successfully conserved in DNA banks as they "are in danger of mass erosion due to degradation of the
habitat". He emphasised, however, that wherever feasible, the more conventional conservation
methods should be used. Ghamkhar (76) shared his concerns and supported the use of ex-situ
conservation methods (seed banks, storing tissues, or DNA banks) as there did not seem to be other
options.

Muchugi (68) too was concerned about conservation of indigenous forest genetic resources, which are
threatened by factors such as increasing population sizes (requiring land for settlement and farming).
Although biotechnology could be of value, through e.g. use of molecular markers to investigate gene
flow or to assist in establishment of ex-situ conservation programmes, she noted that little work had
been carried out on tropical tree species compared to temperate species. She (68, 77) described the advantages, in terms of relative costs and speed, of using RAPD markers and isozymes for molecular characterisation of tropical tree species, but was saddened that renowned molecular genetics journals refused to publish results using these simpler techniques, concluding "this is placing scientists in the developing world with simple labs in a tricky position; we would love to employ the modern state of art sequencers but financial limitations will not allow it. What is the way out then considering the need to study these taxa before we lose them on the earth's surface?". The importance of molecular markers for management of endangered natural forest tree species was also underlined by Dulieu (96).

2.1.3 Animal genetic resources

Aziz (7), supported by Silva (20), noted that livestock production in developing countries is characterised by several major constraints, such as the absence of national recording systems, paucity of breeding programmes, small herd sizes, lack of awareness of the importance of animal genetic resources, national policies to replace local breeds with exotic ones, scarce resources and weak infrastructure. He (82) proposed that, in developing countries, a systematic approach be taken to the documentation, evaluation, conservation and utilisation of their animal genetic resources. Babar (107, 115) emphasised the importance of conserving local breeds in developing countries, especially in ones like Pakistan that are home to several important breeds. He (107) encouraged use of cryopreservation technologies, including embryo and semen storage, and establishment of DNA banks (as they had done in Lahore). Sales (84) said that developing countries had been "swamped" with new livestock breeds and little had been done to conserve their native breeds. All these issues represented obstacles to the application of biotechnology, as communicated by Silva (20) and Tantia (65).

Hassan (61) described the limitations to livestock production in sub-Saharan Africa, which were similar to those previously outlined by Aziz (7). He suggested that although molecular genetics might have a great role to play in revolutionising livestock production in developing countries, "the stage is not yet set" for them to do so and that developing countries should continue the on-going phenotypic characterisation. Maddul (89) mentioned their work on phenotypic characterisation and conservation of pigs and chickens in the northern Luzon highlands of the Philippines, where molecular characterisation had not been carried out due to the lack of a laboratory. Tan (12) described results from molecular characterisation studies of buffaloes in Southeast Asia carried out in the 1990s. Silva (20) reported that in Sri Lanka, applications of biotechnology are limited, involving artificial insemination and, in isolated cases, genetic characterisation of local animals. Osakwe (104) suggested that, although some progress had been reported in plants, there "is no meaningful characterisation and conservation of genetic resources using biotechnology in animals in most developing countries".

Köhler-Rollefson (31) felt that, although scientifically interesting, the relevance of molecular characterisation of livestock breeds for livestock keepers, and for poverty alleviation, had yet to be proven. She also asked whether, when studying livestock domestication and dispersal, molecular data were superior to data from archaeological and ethno-historical investigations, or if they merely confirmed what was already known. Lenstra (35) said that there were several examples where DNA studies had provided additional insights into these issues. For Hanotte (36), molecular characterisation had provided an additional source of information that, together with data from archaeology, linguistics and indigenous knowledge, was making it possible to "complete a puzzle about origin and history of agriculture". P. Jones (59) reported that recent molecular work had substantiated the long-held belief that most of today's donkeys have their origins in northern Africa and that those in southern Africa have different origins, concluding "such a history has implications for management practices and technology transfer, and thus indirectly on poverty alleviation".

Köhler-Rollefson (31) also asked whether genetic uniqueness should be the key criterion for deciding which breeds to prioritise for conservation purposes. Lenstra (35) argued that such a decision should not be made on the basis of marker data alone and that other factors, such as the breeds' relevance to regional tradition, were also important. Tantia (65) thought that molecular characterisation with microsatellites was an excellent tool in this context. Toro (71) argued that the important parameters to consider were phenotypic ones, adaptation to specific environments, possession of economically important traits and cultural/historical value etc. and that "to use molecular markers is not harmful as long as we recognize its subordinate relevance in this context". Hanotte (36) suggested that...
molecular criteria should be considered very important when selecting animals for ex-situ conservation, but caution should be advised for in-situ conservation at the farmer community level. Nimkar (45) argued that areas directly related to poverty alleviation, such as characterising the performance of indigenous breeds (leading to genetic improvement programmes based on simple principles and methods of animal breeding), were being neglected in developing countries like India in favour of biotechnologies, such as molecular characterisation or embryo transfer, blaming this trend on the "glamour" of these biotechnologies. This view was supported by Steane (55), who suggested that one of the problems is that in most countries the funding bodies emphasise research rather than application, concluding "certainly biotech has an important role but it will never be the sole criterion for decisions about conservation and characterisation of breeds". On the general issue of weighting genetic versus non-genetic differences, Rakotonjanahary (92) felt the former should be ranked at a lower level because "socio-economic traits such as culture, market value, degree of endangerment are more related to humankind, which is to be considered the top priority".

Galal (60, 66) suggested it would be useful for conservation purposes to use marker data to verify if phenotypically similar breeds were actually the same or not, although Toro (63, 71) did not see how this could be verified since molecular markers refer to neutral or non-coding genetic variation and genetic distances ignore within breed variation. Lenstra (70), based on results from two recent European Union research projects, suggested that phenotypic distinctness and molecular diversity could both represent valid reasons for conservation, but they were often negatively correlated. Toro (99) argued that genetic distances based on molecular markers were only partially informative, and that there had been too much emphasis on molecular markers, with very few papers published on phylogeny based on phenotypic information compared to "hundreds" on genetic distances using molecular markers. Ghamkhar (100), in response, listed several advantages of molecular markers over morphological data for conservation purposes, including their relative abundance, stability under changing environmental conditions, consistency among laboratories, reduced time requirement and ease of data analysis. Chagunda (113) saw a need for decision support tools to assist in animal genetic resource conservation strategies, where information from different sources (molecular, phenotypic, genotypic, production system, indigenous knowledge, socio-economics etc.) could be combined in a meaningful way to support decisions for conservation strategies.

2.1.4 Fishery genetic resources

R. Jones (14) felt that "fisheries resources are undervalued and underrepresented in discussions on the conservation and sustainable use of germplasm" and that "the application of molecular tools in the relatively unknown world of fisheries and aquatic biodiversity will continue to play roles in determining stock structures of multi-species fisheries (meta-population dynamics) and important taxonomic classification work" (R. Jones, 54). Following the message of Oluawsegun (101), describing the pressures on natural habitats in developing countries, R. Jones (102) urged that those working on conservation of genetic resources in developing countries should think seriously about how to prioritise their efforts. He (64) noted that, because of the high costs involved, most of the molecular work in fisheries was done on commercial or potentially commercial species and wondered how these results might be applied to alleviation of hunger and poverty.

Tan (12) wrote that microsatellites were being used to study three commercial aquatic species in Malaysia - the giant freshwater prawn, the green-lipped mussel and the Asian river catfish. Chinsembu (37) described recent research on the mitochondrial DNA analysis of cichlid fish from five southern African rivers. Results of this work had helped to explain details of the evolution and radiation of the species. Bhassu (62) was enthusiastic about the impacts of biotechnology in stock improvement and characterisation of fish, citing recent work on characterisation of red tilapia stocks with microsatellites; on the phylogeny of freshwater prawns (where mitochondrial DNA analysis confirmed previous findings from morphological and protein data); and on the use of AFLP markers for sex determination in freshwater prawns, noting, however, that little funding was available for such research. Ablan (75) felt that molecular analysis was not as meaningful for cultivated populations as for wild populations, for which they can define spatial distribution of stocks and provide guidance on where to obtain brood stock for restocking programmes. She noted that "we've had cases where molecular genetics provides answers, others where it simply validates observation of the phenotype, local knowledge, value judgements, or even gut feel. And yes, sometimes its usefulness can be forced".

Tan (69) reported that protein and molecular marker analysis had indicated low levels of genetic
diversity in many cultured stocks of prawn and sea bass, which were associated with abnormalities and reduced fertility. He argued that such results had important economic implications, justifying investments in genetic marker studies, and that stock deterioration could therefore be halted based on this knowledge. Toro (71), arguing that the phenomenon of inbreeding depression was already well known, was not convinced that molecular markers would provide useful additional information here. Tan (81), however, noted that aquaculturists in Malaysia usually did not maintain breeding records and paid little heed to inbreeding and so were often surprised when molecular studies revealed that their problem stocks were inbred. Only after seeing the molecular typing results would they begin outcrossing. Kalamujic (110) reported that in Bosnia and Herzegovina, molecular marker characterisation of salmonid species had led to a new freshwater fisheries law, including a provision on obligatory genetic control of material for stocking. R. Jones (14) described how DNA fingerprinting of sturgeon had helped to provide information on stock make-up, potential loss of genetic diversity in Russian brood stocks, the caviar trade and use of ex-situ conservation.

2.2 Priorities and resource constraints in developing countries

Some participants discussed the priority that developing countries give or should give to applying biotechnology for the characterisation and conservation of their genetic resources. For example, Qureshi (3) wrote that conservation of animal genetic resources was neglected in developing countries as the state had failed to support it and it was also not a priority for the farmers. He saw, however, that in this situation, universities could play an important role in applying biotechnology in this area. Huque (52) suggested that policy makers in developing countries did not support animal biotechnology as they preferred to invest in areas promising short-term rather than long-term benefits. Rakotonjanahary (92) said the weak capacity to use biotechnology for characterization/conservation in developing countries was understandable given that, in general, national policy prioritised poverty alleviation, food self sufficiency and increased agricultural productivity over research activities. Komwihangilo (57) argued that farmers in e.g. sub-Saharan Africa were not concerned about characterisation but about their livelihoods and their animals being able to produce. Therefore, molecular characterisation and other new technologies will only be of value to the farmers "if they deliver them from the present trials of life and assure them sustainable futures".

As the majority of the world's poor live in the rural areas of developing countries, Djoulde (16) was sceptical about the merits of using advanced technologies, such as molecular markers or cryopreservation and reproductive technologies, in these areas. De Vicente (27) wondered whether work should therefore cease on solving such problems if the rural people did not care about the solutions and whether effort should be concentrated on ensuring that the research findings reach the rural people. Djoulde (29) supported this latter point and emphasised that the complicated technologies needed to be adapted for easier application in developing countries. Ghamkhar (33) suggested that farmers in rural areas were not expected to employ the new methodologies, but should benefit from the better adapted germplasm resulting from their application. Considering the instability and threats that many genebanks faced in developing countries (due to human or environmental factors, such as war, hurricanes or famine), Murphy (124) questioned the merits of progressing to advanced methods such as molecular markers or tissue culture, concluding "in places where seed banks are being destroyed by looters who are just after the plastic bottles, or where stocks are dying from want of electricity to refrigerate them, we need to question our priorities".

Many participants (e.g. Nkhoma, 1; Krishna, 74) commented on the lack of financial, human and infrastructural resources in developing countries for applications of biotechnology for the characterisation and conservation of genetic resources. As a typical example, Huaman (38) highlighted the difficulties facing researchers in developing countries wishing to use molecular markers, due to lack of laboratory equipment or materials. Aziz (7) and Galal (60) noted that the high costs of biotechnology, along with training, equipment and infrastructure, directed at livestock, represented a constraint. Komwihangilo (57) pointed out that the problem was not biotechnology-specific as there were, in general, low levels of funding for agricultural research. Oluawsegun (101) said economic problems meant that his government was "unable to allocate enough resources for conservation, for research and monitoring of conservation programmes, for the creation of gene banks and education of the public concerning the importance of preserving the biosphere". Urriola (50) reported that despite insufficient funding, human capacity, equipment and infrastructure, researchers in Panama were nevertheless trying to take advantage of the biotechnology resources available. Murphy (124) indicated that there were also serious resource shortages in the flagship
Despite the constraints, some participants urged that developing countries should not be left behind. For example, Vijay (73) considered that, despite the large amount of resources needed, it was important to keep up with the advancing technology: "Developing countries cannot stay aside from the mainstream knowledge as most of the diversity and its end users belong to them". Similarly, Kapoor-Vijay (117) urged that developing countries should not become "technologically excluded" and that "information, knowledge, and expertise associated with biotechnology which is relevant and needed to conserve unique plant, animal and microbial species thriving in diverse and especially extreme environments should be strengthened". For Edema (123), although developing countries did not, on their own, have enough resources to advance in biotechnology, they could not afford to be left behind either. R. Jones (15), on the other hand, warned of the dangers of being seduced by technology in a developing country context, "where the capacities to understand, absorb and if necessary fix and upgrade may be limited or non-existent". He emphasised, however, that no country should be deprived of the knowledge of the technologies available and that it was their choice if or how to apply them.

Not all biotechnologies are, however, equally resource-demanding. Lin (2) commented on the high costs of establishing and operating tissue culture and micropropagation facilities in developing countries, but pointed out that low-cost options had been developed. Thro (106) described one such low-cost initiative for propagating Andean root crops in rural areas. R. Jones (15) commended work being done on development of low-cost, portable cryopreservation technology for fish gametes. Kisha (98), commenting on application of molecular markers, suggested that inexpensive, high throughput technology should be a primary consideration. Muchugi (68, 77) proposed use of cheaper marker systems, such as RAPDs, in preliminary studies to form the basis of conservation strategies. Vijay (79), however, disagreed because of problems of reproducibility of RAPDs, concluding that although funding was the main problem for scientists in developing countries, the "use of outdated technology because of its low cost is not the answer". He (49) emphasised the importance of adoption, moving from "lab to land", to make technology useful for the common good, and that further research could allow the technologies developed to be made user-friendly. Similarly, Prana (58) urged a down-to-earth approach, focusing on appropriate technology adjusted for the real-life resources, local needs and socio-economic factors.

The importance of human capacity was highlighted, with e.g. Prana (56) urging that human resource development be placed highest on the priority list. Uzochukwu (83), supported by Krishna (86) and Osakwe (104), argued that the big funding bodies are interested in providing financial support for biotechnology research but not for training and updating local scientists in the developing countries. Krishna (74), supported by Uzochukwu (83), called for a massive capacity building effort at the national and international level. Caesar (126) 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. Sales (84) identified a need for developing country scientists to be regularly updated on the current trends and innovations relevant in biotechnology. She cited the Asian Maize Biotechnology Network, established to strengthen the biotechnology capacity of national maize research programmes in Asia, as a good model that e.g. livestock scientists might follow. Ghamkhar (85) also pointed out that the CGIAR Generation Challenge Program, previously described by De Vicente (26), provided relevant training programmes. He argued, however, that developing countries could not expect international organisations to cover all their training needs and that the countries should prepare a strategic plan and national training programme to transfer the knowledge accumulated by their already-trained senior scientists to the national research centres and universities.

2.3 Cooperative approaches

A recurring theme throughout the conference was that biotechnology research and application of results to characterisation and conservation of germplasm can benefit from collaborative efforts, particularly at the regional level (e.g. Silva, 20; Ghamkhar, 78). In livestock, Galal (60), noting that the costs of equipment and materials for molecular characterisation were too high for most local institutions, argued that "some regional coordination, possibly with international input, is required to carry out such work". In a similar vein, Muchugi (68), arguing that molecular characterisation of tree species was best approached from an ecological/geographical perspective as their distributions cut across political boundaries, called for "greater collaboration among scientists within the regions in
exchange of plant materials and knowledge gathered". The importance of collaboration between developed and developing country institutions was also highlighted (e.g. Prana, 56; Babar, 107, 115), where Vijay (121) argued that "with the advancement of technology (like use of molecular markers for conservation) there should be a proper collaboration between these two parts of the world". Rakotonjanahary (92) thought that public-private partnerships in developing countries could play an important role, but "only on the condition that characterization and conservation has an evident economic impact, which is not the case for the moment".

Suggestions for increased cooperation were generally made in the interests of pooling scarce resources and reducing costs (e.g. Galal, 60; Muchugi, 94; Chinsembu, 108). De Vicente (25), arguing that it was not realistic for all countries to have facilities to carry out their own work, proposed that institutions consider the possibility of having a hub centre in their region where they could either send their samples for analysis or go there to do the work. Muchugi (94) cited the Biosciences eastern and central Africa (BECA) facilities in Nairobi as a good example to show how pooling of resources could help in the advancement of biotechnology. A universal molecular marker database was suggested by Kisha (6), based on collaboration among germplasm conservation centres and other interested parties. This idea was supported by several participants (e.g. Sales, 19) and Barker (24) emphasised the requirement for "international collaboration and for the data to be maintained in the public domain". The role of international organisations, such as FAO, and of the CGIAR centres in coordinating these collaborative efforts, and in providing funds and contributing to capacity building, was emphasised in several messages (e.g. Ghamkhar, 53, 78; Muchugi, 68; Vijay, 73, 79; Rakotonjanahary, 92; Babar, 107; Caesar, 126).

3. Participation

The conference ran for four weeks, from 6 June to 4 July 2005. There were 645 subscribers to the conference, of whom 64 (10%) submitted at least one message. There were 127 messages in total, of which 61% came from people living in developing countries. Contributions to the conference came from all major regions of the world, with 28% of messages from Asia, 20% from Africa, 17% from Europe, 13% from Latin America and the Caribbean, 13% from North America and 10% from Oceania. Contributors represented 38 countries, the greatest numbers of messages coming from India, Australia, Canada, Brazil, United States, France, Kenya, Malaysia and Nigeria respectively. The majority of messages came from people working in research organisations (45%), including centres of the CGIAR, and universities (43%). The remainder were from independent consultants or from people working for an inter-governmental institute, non-governmental organisation, national development agency or private company.

4. Name and country of participants with referenced messages

Ablan, Menchie. Malaysia
Adediran, Samuel Adeniyi. Gambia
Aziz, Mahmoud Abdel. Egypt
Babar, Masroor Ellahi. Canada
Barker, Guy. United Kingdom
Bhassu, Subha. Malaysia
Buso, Glaucia Salles Cortopassi. Brazil
Caesar, John. Guyana
Chagunda Mizeck. Denmark
Chinsembu, Kazhila Croffat. Namibia
Cummins, Joe. Canada
De Vicente, Carmen. Colombia
Djoulde, Darman Roger. Cameroon
Dulieu, Hubert. France
Edema, Olayinka. Nigeria
Ford-Lloyd, Brian. United Kingdom
Galal, Salah. Egypt
Ghamkhar, Kioumars. Australia
Gupta, P.K. India
Hanotte, Olivier. Kenya
Hassan, W. Akin. Nigeria
Huaman, Zosimo. Peru
5. Acknowledgements

Thanks are extended to all of the Forum members who participated in this conference.

Published by the Food and Agriculture Organization of the United Nations (FAO), 8 November 2005.

Recommended citation for this publication:
FAO. 2005. The role of biotechnology for the characterisation and conservation of crop, forest, animal and fishery genetic resources in developing countries. Summary Document to Conference 13 of the FAO Biotechnology Forum (6 June to 4 July 2005):