

CGIAR Genomics Task Force

# **Enhancing the delivery of genomics research outcomes**

Genomics Research in the CGIAR:  
Effective means of establishing joint platforms  
and cooperative systems for enhanced genetic research

**October 2006**

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## Executive Summary

The CGIAR conducts genetics and genomics<sup>1</sup> research to assist the conservation, characterization, and enhancement of species important for food, feed and livelihoods in developing countries. In this document we use the term “genomics” in a broad sense and include application of molecular biology techniques in food crops, trees, livestock and fish.

There is currently a great variety of means through which Centers access required technology. However, the technology is changing rapidly and new opportunities for technology application are continuously arising. Therefore, Centers should consider how the technologies are going to develop, and whether this will entail adaptations by the CGIAR System. The Science Council has commissioned this Report to consider if there are opportunities to develop more unified approaches or generic platforms to streamline genomics research in a cost effective manner and thereby maximize impacts from investments. The Report is based on an evaluation of current best practice in public and private sector research and breeding to best assess the needs at the Centers. The Report and a Recommended Strategy have been developed with input from all the biotechnology focal points in the CGIAR Centers and Challenge Programs who in turn have consulted colleagues in their respective institutions.

It is proposed that a CGIAR Genomics Taskforce (GTF) be convened comprising one representative from each plant (crop and tree), livestock and fish Center across the System. The remit of the GTF will be, with a ten year horizon, to identify opportunities for synergy, added value and increased impact through coordination of genomics activities within the System. In particular, the GTF will seek to identify where genomics may be applied to achieve maximum impact on management and utilization of genetic resources, and on the scope and pace of breeding gains at the Centers, whilst also providing the most appropriate assistance to national agricultural research program partners, thereby optimizing returns on genomics research and capital investments.

The GTF should be a science advocacy group for the CGIAR acting as the focal point for the Centers in interactions with public and private sector, national and international, funding, research, bioscience and breeding organizations and networks who are interested in the application of genomics. Its principle role will be to identify the optimal deployment of CGIAR resources for molecular biology-based activities such as genomics, genetic transformation, marker-assisted breeding, molecular diagnostics, proteomics, metabolomics, vaccine development, genetic diversity, population structure and strain variation, and various allied informatics applications, through the development of a ‘Strategy for the delivery of genomics-based technologies by the CGIAR Centers over the next ten years’. The GTF will also consider opportunities for maximizing leverage from pan-System purchases and contracts, and thus facilitate rational and strategic investments across the System. In addition, the GTF will contribute to the work of Centers by:

- **Priority targets and flagship projects:** working with scientists in CGIAR, NARS and SME (small to medium-sized enterprise) breeding programs to identify high priority traits for incorporation in CGIAR commodities using genomics-assisted approaches, and support these as high profile flagship projects at the system level;

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<sup>1</sup> For the purposes of this document the use of the term 'genomics' implies structural, functional, comparative, associative and statistical genomics including integration with essential allied disciplines such as informatics, biometrics and computational biology. In addition, in this document when we use this term we also include the use of molecular biology techniques for (i) vaccine development, (ii) diagnostics for plant and animal pathogens, and soil microbes, and (iii) gene identification, isolation and validation for genetic transformation.

- **Breeders networks and information resources** : working with breeders and scientists from CGIAR and NARS, to establish or enhance an international network of breeders and develop a set of priority traits for marker-assisted selection and optimal molecular breeding strategies, and to promote best practices in genomics-based research and application.
- **Integration and cooperation:** working with ARIs (advanced research institutions), MNC (multinational corporations), CGIAR, NARS and SMEs to enhance integration among the institutes, to streamline the flow of genomics knowledge and its application to genetic improvement, and to provide access to genomics tools and harmonize research activities, where ever potential synergies of collective action may exist.
- **Regional training and technology hubs:** working with CGIAR and NARS to identify optimal locations for regional training and technology ‘Hubs’ and promote the development of training materials on the application of biotechnology tools and products;
- **Out-sourcing and brokering:** working with Centers, national programs, and ARIs, develop ways in which research collaboration can be undertaken whilst maximizing the comparative advantage of each party, while negotiating favorable terms on behalf of the Centers when certain services require outsourcing to private sectors.
- **Phenotyping and biometrics capacity:** working with CGIAR, NARS and SME (small to medium-sized enterprise) breeders to ensure that the most accurate phenotypic data can be provided for genomics studies and that all breeding programs have access to biometrics best practices and general modernization of phenotyping and statistical tools;
- **Bioinformatics capacity:** working with Center bioinformaticists and their non-CGIAR collaborators (e.g. within the Generation Challenge Programme (GCP) and beyond) to develop common platforms (or tools to link existing platforms) for storage, management and analysis of data from genomics and allied activities, and deploy them System-wide;
- **Population genomics:** working with scientists in CGIAR, NARS and national programs to exploit the potential of population genomics for sustainable development and security of future generations through conservation and utilization of biodiversity;

Finally, the GTF will strive to facilitate and catalyze the natural transition of the CGIAR from a focus on biotechnology data generation to an emphasis on experimental design and coordination together with data integration and interpretation linking bioscience research and genetic resource management and utilization with breeding gains and impacts.

### **Composition of the CGIAR Genomics Task Force (GTF)**

Chair:	Jonathan Crouch (CIMMYT)
Executive Committee members:	David Hoisington (ICRISAT), Etienne de Villiers (ILRI)
Members:	
Africa Rice Center (WARDA)	Marie-Noelle Ndjiondjop
CIAT	Joe Tohme
CIP	Meredith Bonierbale
ICARDA	Michael Baum
IITA	Morag Ferguson
Bioversity International (IPGRI)	Carmen de Vicente
IRRI	Hei Leung
World Agroforestry Center (ICRAF)	Ramni Jamnadass
WorldFish (ICLARM)	Malcolm Beveridge
Generation Challenge Program (GCP)	Jean-Marcel Ribaut

# 1. Background

The use of genomics technologies is central to modern bioscience research and new technology-assisted applications in agricultural development in support of the CGIAR mission “To achieve sustainable food security and reduce poverty in developing countries through scientific research and research-related activities in the fields of agriculture, forestry, fisheries, policy, and environment.” Moreover, in a world where 75 percent of poor people depend on agriculture to survive, poverty cannot be reduced without investment in agriculture. Many of the countries with the strongest agricultural sectors have a record of sustained investment in agricultural science and technology. The evidence is clear: research for development generates agricultural growth and reduces poverty. Furthermore, investments in genomics are an increasingly important component of agricultural research. Thus, genomics is a critical component of the CGIAR's research-for-development activities that bring the benefits of modern science to poor farmers all over the world. Similarly, transgenics, conservation genetics, and population genomics<sup>2</sup> could offer important options for meeting food demand and environmental challenges; many scientists dedicated to reducing hunger and creating wealth among poor farmers consider such new technologies to be one part of the tool box of possible solutions.

The CGIAR has placed its germplasm collections under the auspices of the FAO within the International Network of Ex Situ Collections. The terms of the agreements signed between the FAO and CGIAR Centers stipulate that the germplasm within the in-trust collections will be made available without restriction to researchers around the world, on the understanding that no intellectual property protection is to be applied to the material. Samples of the in-trust germplasm are thus made available by the individual Centers under a new standard Material Transfer Agreement (SMTA).<sup>3</sup> In this respect the CGIAR's research in genomics provides an excellent opportunity for creating pro-poor international public goods through genetically embedding technological advances into seed. CGIAR centers are also making tremendous efforts to place as much of their data as possible in the public domain through initiatives such as the Systemwide Information Network for Genetic Resources (SINGER)<sup>4</sup>, International Crop Information System (ICIS)<sup>5</sup>, Crop Research Informatics Lab (CRIL)<sup>6</sup>, Domestic Animal Genetic Resources Information System (DAGRIS)<sup>7</sup>, FishBase<sup>8</sup> and ReefBase<sup>9</sup>.

Evaluating the development of the CGIAR's genomics capacity and associated future requirements has been on the agenda since 2001, when the first CGIAR Task Force for Genomics was established to “consider the System-wide accountability and organization needed for flexible, efficient, sustainable, cost effective genomics for the mandate crops”<sup>10</sup>. In light of the rapid pace of change in biotechnologies which can support CGIAR research, the CGIAR's Science Council's Standing Panel on Priorities and Strategies (SPPS) considered in

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<sup>2</sup> Population genomics is an emerging discipline that combines genome-wide sampling with traditional population genetic approaches deciphering allelic effects on phenotypes and identifying patterns of adaptive variation at the landscape level – it is a useful tool to design conservation strategies for trees in landscapes .

<sup>3</sup> The current SMTA can be found at <http://www.cgiar.org/impact/genebanksdatabases.html>. The new SMTA, reflecting the recent outcome of the International Treaty on Plant Genetic Resources for Food and Agriculture, is expected to be introduced in the near future.

<sup>4</sup> <http://singer.grinfo.net/>

<sup>5</sup> <http://www.icis.cgiar.org:8080/>

<sup>6</sup> CRIL is a unified unit combining the biometrics, crop informatics, computational biology, simulation and modelling capacity of IRRI and CIMMYT under the IRRI-CIMMYT Alliance.

<sup>7</sup> <http://dagris.ilri.cgiar.org/>

<sup>8</sup> <http://www.fishbase.org/home.htm>

<sup>9</sup> <http://www.reefbase.org/>

<sup>10</sup> Interim Science Council discussion document “Applications of Molecular Biology and Genomics to Genetic Enhancement of Crop Tolerance to Abiotic Stress” (<http://www.sciencecouncil.cgiar.org/publications/pdf/genomicsgc.pdf>)

2004 that there was again a need to engage in a System-wide discussion on the current state of the CGIAR's genomics capacity and associated future requirements.

There are six key areas of delivery for the outcomes of genomics from CGIAR research:

1. Improved conservation and utilization of crops, trees, livestock and fish (and their associated wild relatives) through the application of genomic tools;
2. Crop, tree, livestock and fish improvement through the application of molecular markers to improve the sophistication, speed and flexibility of selection and breeding;
3. Genetic modification or engineering of CGIAR target organisms;
4. Livestock improvement through the development of vaccines;
5. Diagnostics for plant and animal pathogens, parasites and soil microbes; and
6. Application of computational systems to improve breeding efficiency (including bioinformatics, modeling, biometrics and data integration/ management).

In addition to product development, genomics research will also help us understand the characteristics, behavior and expression of the genome and is becoming increasingly valuable in understanding the nature of genetic variation and support the analysis, conservation and utilization of crop, livestock and fish genetic resources.

However, while biotechnology now permeates most areas of biological research, it has been slow to demonstrate real outcomes for primary producers and consumers. The limited uptake of foodstuffs derived from biotech crops and animals has clearly hindered technology delivery. It is also noteworthy that despite large gene discovery programs in both the public and private sector, GM (genetically modified) cropping areas are still dominated by just two groups of genes - insect resistance (predominantly through *Bt*), and herbicide resistance (mainly glyphosate tolerance). Other genes, including virus resistance and modified quality traits have also been important but only released on a small scale. Adoption of other biotechnologies, notably molecular markers in breeding programs, has also been slower and less extensively adopted than anticipated although an increasing number of varieties and advanced lines selected with markers have now been released.

In contrast, we have seen rapid adoption of biotechnology in the medical and veterinary areas with the majority of protein-based pharmaceuticals now derived from gene technology. Also DNA-based methods are now widely used in medical, forensic and veterinary diagnostics. The high level of funding available for research, high value of returns and ready consumer acceptance have all been important in this rapid adoption.

The rate of adoption of biotechnology in the agricultural sector has been slower than advocated by some researchers and some funding agencies, and this has placed added pressure on the large research investment in genomics. The growth in funding for genomics seen over the past decade may not continue and in many countries public and private investment in genomics is already declining. However, when compared to the adoption of other technologies in agriculture, has biotechnology really been slow?

Breeding new strains of food crops, trees, livestock and fish is not a rapid process. For example, for annual crops it is not unusual for a period of 10 to 20 years to elapse between the first cross and release of a new variety. Thus, it is within this product development time frame that we need to consider whether application of molecular technologies has been delayed or constrained. In addition, it should be remembered that the first reports of useful marker-trait associations in the major staples appeared in the literature only about 10 to 15 years ago, and

these were based on marker systems, such as RFLP, that were technically difficult, expensive, time consuming and, by today's standards, very slow throughput technologies.

Over the past decade the focus of genomics research has been on technology development, establishment of key genomics resources, such as sequence databases and gene expression platforms, and creating a better understanding of gene and genome structure and regulation. There have been only a few serious efforts to examine the processes, paths and mechanisms for delivery of genomics outcomes to the end-users namely, breeders, farmers and consumers. An important task will be to convert the information generated into efficient tools and novel strategies that can be readily implemented to increase rates of genetic gain for target species in target environments.

The objective of this first initiative of the CGIAR GTF has been to:

1. Develop a view of where the technology may be in five to ten year's time regarding research and applications in crop plants, trees, livestock and fish;
2. Examine the capabilities, processes and mechanisms that will be required if the application of genomics becomes a routine and suitable component of genetic resources conservation, characterization, and breeding;
3. Identify factors that may limit or inhibit the use of genomics by the CGIAR and its partners;
4. Recommend the ideal level of adoption and engagement of genomics technologies in the Centers and national partner breeding programs; and
5. Devise an action plan that will help to maximize impact of genomics technologies developed and deployed by the CGIAR System and national partners on the livelihoods of poor farmers as well as on the environment, including in the timely delivery of genomics-based products.

The GTF has been provided with a technology driven framework but this has been complemented by detailed interactions by GTF members with a range of allied disciplines in their respective centers – feedback from this holistic dialogue has been incorporated into this document. Moreover the GTF is committed to rapidly moving away from advocacy to a focus on demonstrated cost-benefit and impact assessment of intermediate products from genomics research in IARC, NARS and SME breeding programs.

### **CGIAR Genomics and the Generation Challenge Program**

The goals of the GTF and GCP are very much aligned but also highly complementary: the GCP aspires to bridge research in advanced research institutions to impacts in NARS breeding programs and farmers fields with a particular reference to harnessing the power of genomics to drive rapid progress in drought tolerance breeding of major crop staples. The GTF has a broader scope encompassing all appropriate economic traits across all relevant organisms (crop plants, trees, livestock and fish) but is likely to initially focus on low hanging fruit for proof-of-concept flagship applications as opposed to the grand challenge of complex traits such as drought tolerance. Similarly the GCP focuses on operational funds for research projects whilst providing only small investments in infrastructure at CGIAR centers (primarily for bioinformatics) and at NARS (in phenotyping and marker application facilities). In contrast, the GTF aspires to raise funds to foster facilities that will optimize operational logistics for genomics research and application across the CGIAR – these facilities may be in advanced research organizations, CGIAR centers or regional centers of excellence. In many cases, linkages and coordination across commodities and between organisms will have a substantial

impact on the pace and scope of innovation. Clearly, the GCP and the GTF should strive to be intensely collaborative, mutually reinforcing and highly synergistic.

### **CGIAR Genomics and the HarvestPlus Challenge Program**

HarvestPlus genomics and biotechnology activities are well integrated with the breeding programs of the different CGIAR centers and NARS institutions. HarvestPlus conducts breeding programs for six staple foods<sup>11</sup> and feasibility studies for 10 additional staples<sup>12</sup>, undertaking nutritional genomics research to identify and understand the underlying molecular and biochemical mechanisms of specific genes and loci affecting micronutrients. In particular, the nutritional genomics teams from the CGIAR, NARS and ARI are focusing on (i) the use of MAS for specific genes related to iron and zinc, (ii) the identification of new biosynthetic and regulatory genes controlling provitamin A levels; (iii) testing the potential of identified genes for altering micronutrient levels; (iv) identifying and cloning genes affecting seed micronutrient levels; (v) identifying promoters and providing tested constructs to HarvestPlus molecular biologists in the CGIAR; (vi) the development of transgenic lines for seven crops that either do not have the desired traits or do not have the targeted level. A strong partnership and collaboration between HarvestPlus and GTF would therefore also be beneficial for all involved.

## **2. Process followed in developing this document**

In 2004 the SPPS, under the Chairmanship of Dr Mike Gale, commissioned a study of the issues related to “*Genomics Research in the CGIAR: effective means of establishing platforms for genetic research*” by convening a second CGIAR Genomics Task Force. The first draft plan was developed based on a workshop held in Rome on 3-4 October 2005, following the GCP annual review meeting. The Task Force meeting and the subsequent development of the first draft of this document was facilitated by Dr. Peter Langridge (ACPF, Australia) with input from all members. At the workshop Dr. Langridge reported on the status and strategy of marker applications based on recent visits to various leading public and private sector genomics facilities. A preliminary report and action plan for the CGIAR was developed during the workshop. The draft report and action plan was then refined by a sub-group of GTF members at a second discussion held in San Diego on 17 January 2006. All members then provided further input by e-mail which Drs. Langridge and Gale used in drafting the Report that was presented at the fifth meeting of the Science Council (SC5). A one day meeting was held in Sao Paulo on 17 September 2006, following the GCP annual review meeting. At this meeting, the general contents of the Report were finalized and a GTF Chair and Executive elected. Finally, all members provided one last round of inputs by e-mail that was used in developing the final version of the document presented here.

## **3. Visions of the development of genomics over the next 10 years**

Attempts to estimate demands for particular technologies ten years into the future is fraught with difficulties and many factors may influence the ultimate extent of application. Perhaps the easiest way to make realistic estimates is to look at the current scales in breeding programs where the technology is well integrated and assume that the overall scale of the breeding

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<sup>11</sup> They are: rice, wheat, maize, cassava, sweet potatoes, and common beans.

<sup>12</sup> Bananas/plantains, barley, cowpeas, groundnuts, lentils, millet, pigeon peas, potatoes, sorghum, and yams.



programs will remain constant but the technology costs will reduce significantly. Models for the path genomics technologies are following can be seen in human research, in large scale private maize and soybean breeding programs, and also in population, evolutionary and ecological genomic studies.

Genomics is primarily about understanding the function of an organism. This allows several avenues for exploitation including: marker-assisted gene transfer, introgression and pyramiding, improved means of identifying appropriate genotypes based on improved understanding of genetic factors and genotype-by-environment interaction, development of transgenic organisms and the development of new vaccines arising from improved understanding of basic biology. Computational systems are playing an increasingly important role in integrating large and complex datasets in a usable form for routine applications in breeding and other product development pipelines. Genomics also plays an important role in environmental management of genetic resources for improved targeting of agricultural biodiversity conservation and utilization.

It is also important to remember that one of the key areas of genomics research has been a detailed understanding of the control of key traits and developmental processes. The outcomes derived from this new knowledge can be delivered through conventional or transgenic crops, livestock and fish improvement programs (including diagnostics and vaccine development) and in the development of strategies for conservation and management of genetic resources.

### **3.1 Molecular markers**

Large reductions in costs per data point are expected to continue, given the trend over the past few years and the new technologies for high throughput marker screening that are in the pipeline. However, the unit cost reductions for marker screening overall are likely to be closely related to throughput. Nevertheless, as the cost per data point will decline, the numbers of markers screened will rise, although the costs of the high throughput genotyping equipment required will almost certainly remain high or even increase, but this will lead to improvements in the pace, efficiency, selection response and scope of breeding programs.

Whole genome screening, albeit at a generally low marker density, is already attainable for some species and it is probable that assay systems that simultaneously determine genotypes at 10,000 loci or even more will soon become available. This is already feasible for human and mouse genetic studies as well as several species of livestock (notably cow, chicken, and pig) and in the private sector, for maize and soybean. Preliminary public sector projects in crops are also underway towards routine screening of 500-10,000 loci. Meanwhile, it is envisaged that even genotyping platforms that allow simultaneous low cost screening of 100 loci will offer dramatic advances in molecular breeding applications and are an ideal focal point for driving initial success stories.

Future very high throughput assay systems are likely to be based on genetic polymorphism detection techniques using SNP (Single Nucleotide Polymorphism) markers that require large genomics resource bases. This may appear to limit access to these new systems to the major species of study but large reductions in sequencing costs are also expected over the next few years so it is reasonable to assume that it will be possible to generate large EST (Expressed Sequence Tag) or genomic sequencing databases at increasingly lower cost and faster speeds. However, as the development of marker technologies can be species specific and related to the level of available resources, it is also probable that a series of "transition phase" technologies, probably SSR (Simple Sequence Repeat) or STS (Sequence Tagged Sites)-based, will still be required to carry less developed species through the early stages of marker implementation. Array-based systems such as Diversity Arrays Technology (DArT) may also be efficient

platforms for relatively high throughput, genome-wide genotyping, that require minimal genomics information (but careful optimization) in a given species.

Rapid advances in DNA sequencing technology will lead to many more whole genome sequences becoming available. Indeed, it is possible that genome sequences will be available for most major crop, livestock and fish species within the next 10 years. This will underpin the development of broad scale screening capabilities and increase options for whole genome analysis. It is possible that sequencing costs will even drop low enough to allow many lines or varieties within a species to be completely or partially sequenced and we may move to a position where full sequences are available for most key breeders' lines. For less well-studied crops these developments should make it possible to move directly to creating large-scale SNP-based screening platforms. Comparative genomics is already playing an important role in identifying targets for development of vaccines and diagnostics in livestock and fish and will increase in the future as more genomes are sequenced.

The reduction in marker screening costs and the availability of whole genome precision screening capabilities will allow large numbers of lines to be assessed. This will drive a change in breeding strategies from analysis of specific loci to an assessment of the entire genome and a consideration of background genome effects. Therefore, a consequence of the high marker density will be the possibility for breeders to screen for recombination events in any specific chromosome regions, to select for complex haplotypes across large numbers of loci, and to target specific epistatic and heterotic effects in the breeding process. These changes may necessitate an increase in the sizes and nature of populations being developed in breeding programs, although in some cases they may also allow a smaller number of targeted individuals to be phenotyped rather than the entire population. In any event breeding protocols and optimum population sizes at different generations will change dramatically with the incorporation of MAS at any level. Modeling or simulation of molecular breeding strategies will provide a critical link in this process. However, access to appropriately trained and skilled staff will remain a crucial bottleneck. With respect to natural resource management, molecular markers will also play an important role in the selection of populations for establishing *in situ* and *ex situ* genetic reserves which will be facilitated by new-generation conservation strategies based on population genomics.

Finally, the continuing development of platforms for gene expression profiling at the mRNA, protein and metabolite levels can be expected to open the option of screening based on expression information. Integration of genomic markers with comparative mapping and gene expression analysis is already giving insights into mechanisms of disease resistance in many species. Links and collaborative projects with ARI's are likely to be critical in accessing and applying current and future technologies.

### **3.2 Transgenics**

The ability to insert and/or modify specific genes in an organism via genetic engineering provides unique opportunities to develop not only improved products for farmers but also valuable materials for genomics research. Genetic engineered materials often are the best isolines for studying the effects of single genes on a phenotype or expression pattern. Such materials usually remain in the laboratory or contained greenhouse, and thus are generally not controversial and are considered a valuable research tool.

Much of the polarized debate on genetic engineering focuses on the development and deployment of actual products for farmers, although the technology has been the most rapidly growing area of agriculture over the past several years (particularly in the private sector). Many believe that the general acceptance of transgenics will increase in the future, although it

remains a major impediment to the release of many products at the moment. Products have been released and are being grown by many farmers globally, even in many developing countries. Given the interest by most national programs, and the belief by the CGIAR Centers that the products of genetic engineering are important components of sustainable agricultural systems in developing countries, it is critical that the Centers are able to develop transgenics varieties in an effective and efficient manner.

The adoption of transgenic crops is not expected to continue to increase over the next ten years, although it is unclear when general acceptance will occur. For several CGIAR Centers it is seen as important to retain a capacity in the development of transgenic germplasm and in brokering access to the necessary genes and technologies. This is especially true to be able to develop materials for more basic genomics research studies.

However, it is expected that the current dominance of the commercial sector in transgenic products for the major crops will remain and several donors are beginning to actively support this by a pro-public-private sector partnership approach. Nevertheless, there has also been an increase in transgenic activities in public research institutes in developing countries which may offer ideal opportunities for building linkages with CGIAR Centers. Transgenic activities in the Centers are expected to focus on crops or traits not covered by the private sector. The high regulatory costs and costs associated with food safety testing may prove a major impediment to the timely delivery of transgenic crops and animals. It is important to remember that the level of investment by the commercial sector in specific species, specific products, and specific traits is very large compared to the public sector where not only are many species being tackled but also a large diversity of traits. It is possible that some requirements in developing countries will never be covered by private sectors because of the small or low-profit market targets. Links to the private sector will be valuable in accessing suitable technologies, genes and supporting some of the regulatory costs and procedures. However, we should also not underestimate the collective scale of research being carried out in the public sector. Where effective coordination has occurred, significant advances have been achieved.

### **3.3 Vaccines and Diagnostics**

Most of the vaccines currently in use for the control of animal diseases have been developed through conventional approaches. However, genomics offers new opportunities through gene sequencing and a range of other new techniques. These will allow the identification of the genes in pathogenic agents that are responsible for causing ill effects or stimulating an immune response. This will not only enable the development of potential vaccine strains in which the genes causing the disease have been disabled or removed, while preserving the immunogenicity inducing potency of the strain, but will also provide new diagnostic candidates. Another alternative is to formulate the identified vaccine candidate genes by themselves into appropriate vaccine delivery systems.

More effective delivery systems for vaccines are required to replace the present cumbersome and invasive techniques. Novel vaccines produced in plants or insect cells are under development, which could lead to new delivery systems in the form of edible and vector borne products. Plant-based vaccines have potential as a locally sustainable production system and can benefit from research on marker-assisted breeding and/or transgenic crops.

Progress in genome sequencing of livestock species is opening new ways for the identification and improved understanding of economically important traits and genes. These developments are catalyzing the emergence of new tools, e.g., bioinformatics and microarrays, the application of which represents new opportunities with significant potential for gene discovery research. These are common platforms/technologies for both vaccine research (i.e. antigen identification)

and genetic improvement.

Disease resistance is important for both animal and fish health and welfare. Genomics will accelerate the understanding of the genetic basis of disease resistance and will help in breeding resistant animals and fish and in designing new drugs. Understanding the genes that govern the immune response will enable researchers to design better vaccines and tailor specific vaccines to different breeds or species.

### **3.4 Other applications**

While molecular markers and transgenics are the most widely advocated directions of application for genomics tools, it is important to remember that these technologies have the potential to enhance our understanding of a wide range of features of an organism's behaviour, both in isolation and within a population. Genomics can address some fundamental and difficult environmental and ecological questions such as “how do ecosystems function”; “what is biodiversity and how might it have been changing”; and “how do organisms really behave in natural environments”? Genomics can also be applied to help monitor, treat or prevent environmental pollution. We can therefore expect to see increasing implications of genomics technologies for environmental management and in characterising and conserving biodiversity.

## **4. Infrastructure required to meet predicted needs**

### **4.1 Molecular markers**

If the rate of technology development and application continues to differ between species, it is likely that the high throughput equipment requirements will also vary. However, if universal platforms do become available this commonality will drive substantial advances for lesser-studied species. It is certain that the preferred technologies for marker detection will continue to change rapidly and costs will continue to plummet. Consequently there is a very real danger of the Centers being trapped with outdated and obsolete equipment. It is also important to note that the new developments in equipment for marker detection have focused on high throughput and low cost per data point. Most Centers have already moved from flat-bed gel detection methods through to the use of multi-channel capillary systems in recent years. Platforms based on microarrays, fluorescent particle sorters and mass spectrometry are now gaining momentum and are likely to dominate marker screening within a few years.

The high equipment costs and the need for constant usage at high throughput to justify these costs and to keep operating costs low will drive centralization of marker screening facilities that are shared by CGIAR centers, NARS and others or a general move towards outsourcing. However, it is still expected that Centers will require access to internal and/or low and mid-throughput molecular laboratories for marker development and validation and continued research on marker-trait associations. The centralized facilities are then likely to provide the high throughput screening needed by the breeding or genetic resources programs especially in crops with a large commercial market. For those crops with a smaller base of breeding programs, high throughput screening may require more time to develop and more support from CGIAR genomics research programs. An addition complication, for immediate applications, is that the genotyping service market has yet to mature. Thus, many currently available service providers struggle to provide high quality low cost high throughput genotyping within typical breeders' decision window. It is expected that as more commercial service providers expand into this area, that market forces will drive improvements in timeliness, quality and cost. Ultimately, service providers are expected to represent the most efficient method for ensuring

widespread access to marker screening and to keep costs low by supporting many high throughput requirements, but questions regarding movement of seed, tissues, or DNA across international borders must be resolved for this solution to be truly viable, as not every country will have an appropriate commercial genotyping service. Commercial service providers will be particularly important for providing DNA sequencing capabilities and for offering a variety of SNP detection platforms. Service providers could even develop as "spin-offs" from Center programs providing routine services to Centers, NARS and others. These could have access to new developments coming out of the Centers' research programs. They could also interact with Centers in delivery of training programs. Finally, it is possible for a universal SNP genotyping platform to eventually become available and acceptable for all species.

An advantage of commercial service providers is that they would provide a large-scale commercial focus to activities and help ensure efficient, competitive service provision and accountability. The use of service providers should also help address problems of trouble shooting, maintenance and repairs to equipment that can be expensive and difficult to access at some sites. It is envisaged that the GTF would work with leading service providers to address the issues of ensuring timely delivery of high quality low cost results to remote facilities across the System and to help optimize processes for the transfer of biological material between sites. There is, of course, the danger that commercial service providers would focus activities on species and breeding programs where there was high turnover and greater opportunities for profit than those presented by species for which there was only a small breeding or genomics community. This will need to be closely monitored but demand across multiple species from Centers, their partners and collaborators should help ensure sufficient business to maintain efficient service provision to all CGIAR species. The service providers could offer a wide range of assays and the breeders would then identify which assays were required at a predetermined annual throughput for analysis. Mixed models will also be evaluated, for example where service providers build alliances with medium throughput facilities near to or coupled with breeding programs. This type of arrangement may be particularly important for improving the sampling to selection time for MAS-based decisions in certain annual crop breeding programs.

In addition and in partnership with service providers a set of service Hubs could be developed that would not necessarily have "state-of-the-art" equipment but would have capabilities to act as learning centers for teaching and would have procedures in place to ensure access to "state-of-the-art" equipment. For commercial service providers it may be necessary to pay for access to suitable training courses. These Hubs could be located within Centers to provide regional support and act as a source for intellectual input into breeding programs and other biotechnology applications both within the Centers themselves and also within NARS. Alternatively, the Hubs could also provide centralized marker screening services for their respective regions.

An example of such a Hub is the *Biosciences eastern and central Africa* (BecA) genomics and bioinformatics platform that is being established at ILRI, Nairobi. This platform will serve as a hub for eastern and central Africa, including CGIAR Centers in the region and national research institutes and universities. South Africa is also developing a similar platform to serve the southern African region, which will probably have a great emphasis on bioinformatics. Both these platforms were developed in Africa, and they could serve system wide needs in Africa, and partner with other players not yet involved.

Another potential Hub is the Crop Research Informatics Laboratory (CRIL) of the IRRI-CIMMYT alliance which is a unified critical mass of expertise in biometrics, crop informatics, computational biology, simulation and modeling for applications in genetic resources, genomics and crop improvement of rice, maize and wheat. Looking towards having an

effective service provision network and a series of regional Hubs, the Centers should prepare to focus more of their activities on (i) experimental design and coordinated implementation, (ii) development of decision-support tools including those required for data management, coordination, integration and interpretation, and (iii) development and validation of new molecular breeding strategies. Thus, CRIL aspires to provide a facilitating environment for this transition and expects to build strategic alliances with ARIs, advanced NARS and key CGIAR centers in order to foster this transition.

Increasingly, it will not be necessary for the CGIAR to have direct involvement in the technology or in actual data generation at every level but it is expected that the CGIAR will play an increasing role in coordinating overall systems in close collaboration with NARS and SME partners whilst building effective linkages with ARI and MNC technology providers. In this scenario, NARS and CGIAR scientists would still need access to well-established molecular laboratories to allow them to conduct preliminary analyses, undertake preparation of samples that are sent for out-sourced analysis, and for interpretation and utilization of the data, in order to obtain maximum benefits from data generation of service providers and training and advice provided by the Hubs. It is envisaged that the GCP's new 'Genotyping Support Service' would provide an important source of support in this area, perhaps even developing into a virtual Hub for coordinated and facilitated genotyping services support.

## **4.2 Transgenics**

It is considered important that Centers develop and retain capacity to generate and evaluate transgenic organisms. However, this may also become a sphere of activity for service providers as has already happened for some species. A change in community acceptance of GM crops and animals will necessitate a rapid response from Centers even though there may appear to be limited scope for exploiting GM organisms at present. CGIAR breeding programs must prepare themselves for breeding with transgenic materials from a variety of sources. One option may be to establish a transgenic facility, particularly for field testing, in a country or region with a long history of field evaluation of GM. Such an option will require serious consideration of issues such as intellectual property rights and international transport constraints associated with GM materials.

However, the regulatory issues surrounding transgenic crops and animals will require attention. The Science Council's biosafety study of 2004 made a series of useful recommendations including the proposal that the CGIAR Centers should pay attention to regulatory issues and costs early in the research process.

Centers may also need to maintain research capabilities in the development of transformation protocols for orphan species and for the discovery of genes controlling traits and development of breeding products that may be of major importance to pro-poor communities but unlikely to attract the attention of ARIs.

Centers should also ensure that they have access to a capacity for rapid phenotyping and genotyping of transgenic organisms, again possibly through access to field resources in a country with a long history of field evaluation of GM organisms. Should GM technology and its products become widely used, it is highly probable that careful checking and monitoring of transgenes, for example using molecular markers, will be a high priority. The phenotypic evaluation of transgenic organisms should include a capacity for transcript, protein and metabolite profiling. This activity could well be provided by external groups of service labs.

### **4.3 Vaccines and diagnostics**

Vaccine research is labor-intensive, requires a multi-disciplinary approach and is of unpredictable duration. The success rate in producing candidate antigens for a vaccine, for example can be low with less than 10% of projects reaching a successful conclusion. Costs are steep as a result of the technologies involved and the containment facilities needed to protect both human and animal health.

In order to exploit the results of vaccine and diagnostic research and to deliver new products, a number of important stages in the R&D chain need to be successfully completed. These involve an integrated approach to product development, production, good manufacturing practice, initial clinical trials and finally large-scale field trials in order to reduce the time-to-market and cost of product development. To achieve this, engagement of strategic partners in both public and private sector are crucial in the process from discovery to delivery. Given the nature of this research, it is especially important to work closely with commercial companies to move innovations to actual products, but at the same time to also have a range of partners to undertake fundamental strategic research to identify better vaccines and tests.

Research carried out in the countries of origin of livestock and fish diseases will be essential to provide insight into the epidemiology of the problem. It not only allows for the testing of control approaches including vaccines and diagnostics but many epizootic pathogens cannot legally be introduced into Europe or the USA for research purposes. In this aspect the Centers have a competitive advantage and could be a strategic partner for initiatives such as the “European Technology Platform for Global Animal Health”.

Establishing a common platform for vaccine and diagnostic development in conjunction with a genomics platform at a Center or hub such as BecA, will enable such a Center not only to play a major role in vaccine research, but will put it in a strong position to be a strategic partner for vaccine and diagnostic development projects in Europe and/or the USA. The availability of suitable containment and small animal facilities at such a Center will be of strategic importance. Finally, the experience that CGIAR livestock scientists have in building public-private partnerships will be of substantial general value to the rest of the System.

## **5. Mechanisms for ensuring access to genomics infrastructure**

Four strategies are proposed to help accelerate the development of effective methods for accessing the facilities, capabilities and information needed to ensure outcomes from genomics research and applications and in turn impacts in farmers’ fields.

1. Options and potential roles for service providers are described above. In practical terms a group will need to take responsibility for helping to foster the success or establishment of the most appropriate service providers and to negotiate with these groups or organizations to develop and deliver the most appropriate services at the best price. This is probably best achieved by arranging sub-groups with similar genomic resources, breeding systems or taxonomic relatedness in order to facilitate the most effective negotiation with possible service providers.
2. Access to information and data on marker systems, genes and technologies requires the enhancement of informatics capabilities. Access to expertise in biometrics, informatics, computational biology, simulation and modeling will be as important in the future as access to genomics data generation facilities. A critical mass of facilities and expertise should be established to improve our use of data and help facilitate the evolutionary shift of emphasis from data generation to data utilization.

3. Training programs in genomics technologies, particularly marker training programs, should shift their focus to the incorporation of technology into ongoing programs rather than on the technology itself. This will require careful revision of current courses and strategic maintenance of key facilities to retain a high level of training for scientists who will work in-house in the CGIAR and its partners, even in the face of increasing out-sourcing of genomics data generation.
4. It is important to identify high priority targets and use these to demonstrate effective out-sourcing strategies. Centers should lead by example through demonstrating effective out-sourcing of certain capabilities. This will require carefully designed incentive systems for research and application scientists within Centers and our partners.

## **6. Delivery of genomics outcomes**

There is a great need to establish a clear path and set of mechanisms for delivering the products of genomics research and applications to farmers. In many cases, the key delivery path is likely to be from Centers to NARS and SMEs to farmers. However, the nature and timing of the interaction in relation to the overall value chain is changing. The path(s) will need to consider issues of germplasm supply and distribution and where necessary, intervention may be needed to ensure effective flow. The importance of careful and strategic management of intellectual property will become increasingly critical for genomics-assisted product development and delivery. It is also important to allow for the wide differences that already exist in the capabilities and resources of NARS and private sector breeding programs. The role of the Hubs in technology delivery will require tailoring to the needs of individual NARS and SMEs and their client farmers; some NARS will need very little external assistance, in some cases taking over the traditional role of CGIAR in their respective regions and thereby maximizing the gain from south-south collaboration.

It is expected that there will be shifts in the relationship between the groups involved in the delivery over time. Initially, the Centers are likely to play a lead role in not only the technology development but also in the delivery. The concept of technology development here is largely directed to adapting technologies that have been established in model or well studied species and often by ARIs, to less-well studied and more challenging species of importance to Centers. It is unlikely that Centers will be directly involved in adapting and translating the base technologies which are now largely carried out in highly specialized laboratories. Over time, this role of the Centers will move more to germplasm enhancement (pre-breeding) and intermediate bioscience products, with the NARS and SME focused on adaptive breeding, and, development and finished varieties and final products. As the technology becomes widely adopted and forms an integral component of the NARS breeding programs, the Centers will be able to move more into technology validation and refinement, focus on using the molecular information to devise new breeding strategies, identify new marker-trait associations not of interest to ARIs, investigate key issues of genome behavior and help solve complex genetic problems that can help increase the speed and sophistication of the germplasm development work in the Centers and the varietal development in the NARS. As quickly as possible each NARS and SME needs to become involved in the development and validation of new breeding strategies with the Centers helping to catalyze this process, providing new refinements and working on the next generation of tools and methodologies. Again the speed and nature of these role shifts will vary depending on the technology status, the species and the capabilities of individual NARS and SMEs. In several cases (for example in India, China, South Africa,



and Brazil) the NARS and SMEs already have strong capacity in both technology development and deployment.

## **7. Addressing current limitations to the use of genomics**

A major limitation for the effective application of genomics in research and breeding is the ability to properly phenotype traits of interest. Many agronomically important traits, such as drought tolerance, have a complex genetic basis and are influenced by a multitude of factors that affect the accuracy and precision with which the phenotype can be measured. Even with much simpler traits, it is often difficult to determine an accurate response, or to measure the relative response of a specific genotype. Such difficulties are compounded when the number of individuals is large as is the case in many mapping studies and when the phenotyping has to be done under specific environment conditions that need special facilities. This is the same problem that breeders have been facing in plant improvement for the past century. Fortunately the CGIAR and their NARS partners have developed considerable expertise in precision phenotyping of many traits that are important to resource-poor farmers. However, while some institutes have invested in improving the capacity to measure specific traits, such investments have remained lower priority in today's poor economic climate for agricultural research in many countries, leading to lack of facilities and/or capacity in many national programs. This is clearly a case where shared facilities and/or cooperative systems can have dramatic effects.

Another key limitation to an effective use strategy will be the strength of breeding, product development and deployment capabilities in NARS. For some species and NARS, neither the infrastructure nor intellectual capacity is in place to allow effective use of genomics technologies. Consequently in many cases, the bottleneck for use may, in many cases, be the capacity and speed of NARS breeding programs. Therefore, Centers must retain their traditional emphasis on training in modern plant breeding skills and foster integrated breeding strategies through systemic collaboration with NARS breeding programs. This problem can be partially addressed through new training programs, development of networks and collaborative groups to share knowledge and expertise. However, the availability of tailored and iterative technical backstopping is critical for trouble shooting and problem solving. The GTF should also play a major role in the careful design and provision of incentives for technology adoption both within Centers and our partners. The Hubs and existing partnerships will play a key role in this aspect and should favor the development of efficient delivery plans. However, regional coordination across crops, institutions and sectors will be a critical element for success of the model. The GCP is giving this area particular emphasis which the GTF should align with in order to fill gaps in the broader agenda.

Strengthening the breeding and delivery capacity in NARS will also help address several other problems that have tended to hamper biotechnology-based product development and delivery in the past. Of particular importance is ensuring that the technology is delivered to farmers in well adapted and market accepted lines. Conversely, information on the best lines to use for marker-assisted backcrossing of specific traits is most likely to be provided by NARS scientists, small to medium-size companies and farmers. Bottlenecks to the efficient delivery of improved varieties, such as weak extension or seed systems, must also be anticipated; this is something the CGIAR is already working intensively upon for the improved delivery of its more traditionally developed improved materials. And the CGIAR, in its emerging role of coordinating value chains in which it is working, should ensure that appropriate players are engaged to properly resolve these issues and their linkage in the overall delivery pathway.

Close involvement of NARS scientists in the Hubs and networks that encompass delivery strategies including seed and regulatory systems would engage these scientists in the

biotechnology programs and help allay some concerns that may exist on the nature and value of the technology. Strong linkages between the technology developers and breeders, through the Hubs would also provide stimulating scientific discussion and raise awareness about advances in breeding methodologies. This would help stimulate interest in the use of biotechnology in plant and animal breeding as a challenging scientific endeavor and help address the decline in the number of young scientists moving into breeding. The association between Centers and NARS scientists through the Hubs will also help provide feedback on key targets for gene discovery and marker development. This will help ensure that work is targeted to major problems.

For many species it is predicted that the applications of marker-aided selection will shift from single gene traits to more complex genetic systems and then to whole genome analysis. This shift will be particularly challenging for scientists who have not had the opportunity for close involvement in the development of the technology. The Centers with their crop expertise and the Hubs with their technology focus will be crucial in helping to drive this integration of disciplines and transition in roles.

Finally, in organizing and managing the Hubs it will be important to consider any rivalries or competitions that may exist between NARS or other groups.

The following three key issues need to be addressed.

1. *Ensuring access to training, service provision, information, tools and data analysis capabilities:* Information access will be crucial in addressing current limitations to technology delivery. An information management system will be needed that is usable across Centers and NARS through the Internet. Although many databases and data analyses tools currently exist, many are not particularly easy to use nor easily linked together. The key criteria will be provision of a system that provides simple and user friendly data entry, retrieval and analysis tools. Ideally the system should comprise both a database integrating all types of data and a series of data interpretation and decision-support tools. This is the driving focus of the IRRI-CIMMYT Crop Research Informatics Lab which has consolidated all data-based activities for rice, maize and wheat.
2. *Developing strong linkages to end-users via germplasm distribution entities:* With an effective service provision network and a series of regional Hubs, the Centers would focus their activities on the interpretation and integration of genomics data, plus, developing and validating new molecular breeding strategies. Increasingly they will not necessarily be directly involved in the technology or in actual data generation at every level but will play an increasing role in coordinating the overall system. Interactions with SMEs and other groups when necessary (for example, non-profit groups or the NARS themselves) for germplasm delivery will often be through NARS but also through direct links with Centers. These SMEs should also have access to Hubs albeit on an appropriate cost recovery basis. In many cases it will be critically important to help build or stimulate development and capabilities of the SMEs. This is not inconsistent with the CGIAR's pro poor mandate, as often it is only these SMEs who have ready access for delivering new germplasm to resource-poor farmers. This could be done by giving priority during the development of varieties to gene and trait targets likely to help build market niches and thereby provide technologies that will support a strong SME industry for seed distribution. In return the SMEs should be required to provide feedback to the NARS and Center programs, via the Hubs to ensure that germplasm well accepted by the end-users is used to deliver products. They should

contribute as full community members regarding information flow in both directions and their role in validation and optimization should not be underestimated.

3. *Generating ownership of genomics technologies for Center and NARS breeders:* There is a need to increase involvement of breeding programs in genomics programs. Breeders from Centers, Hubs, NARS and SMEs should be involved in early decision making for genomics programs to help ensure genomics groups are addressing real issues identified by end-users and likely to generate tools and methodologies tailored to improve efficiency of the end product. The Centers and Hubs can also work with NARS and SME programs to develop succession planning strategies and stimulate broader interest in breeding. This would involve development or re-vitalization of breeder networks as a core component of the effort. The objective will be to develop dynamic and innovative breeder and biotech communities, e.g., molecular breeding communities of practice (such as AMBIONET, AMMANET and those being initiated by the GCP). With an effective service provision network and a series of regional Hubs, the Centers would focus their activities on the interpretation and integration of genomics data, plus developing and validating new molecular breeding strategies. A component of the process would be the development of incentive systems for breeders to reward those who show innovation in technology adoption and large-scale application. However, it will be important to differentiate the diverse infrastructural requirements of research, training and application activities when considering the potential role of large-scale regionally centralized service facilities. This not only has implications on the location of genotype data generation but also the necessary facilitating platform. Nevertheless, biotechnology staff should be strongly encouraged to accept responsibility for the delivery of the outputs of their work and should take leadership in championing the passage of those technologies through the product development and delivery pathway, helping to demonstrating the positive role of the technology.

## **8. Accessing new genomics technologies**

### **8.1 Role of Centers**

The cutting edge of technology development for marker screening currently lies in the medical area and this is likely to remain at the forefront; for example the use of mass spectrometric methods for SNP detection. However, cutting edge science can occur at several levels along the product development and delivery pathway and it is considered important that Centers focus on activities where they will have the greatest impact and where breaks or weaknesses exist along the value chain. Similarly it is important that Centers have access to the latest developments and are not relegated to using outdated and inefficient technologies. The out-sourcing, up-scaling and alliance model will help prevent this relegation from happening.

Genomics technologies are evolving rapidly. Techniques and equipment bought today might be out of date in two to five years. In well researched and resourced species, Centers will be able to conduct research more in the application areas than in the development of technologies; while in poorly researched species, Centers will need to lead the path of technology development and application. This leadership is likely to involve a major advocacy role to encourage ARIs to work on these species. Certain targets, such as some nutritional traits, will require research or strong advocacy from Centers. The recent substantial funding of biofortification projects of staple crops by the Gates Foundation involve complex collaborations between ARIs, CGIAR and NARS and shows that there are ARI partners who are interested in addressing pro-poor targets.

As elsewhere, the role of the Centers in biotechnology will need to be carefully and continually reviewed to ensure Centers are not competing with NARS and ARIs but developing approaches that promote partnerships, synergies and joint impacts. In particular, Centers should be positioned to act as "technology champions". This will involve providing up-to-date training and remaining skilled in the application of the latest technological developments.

A formal group, such as the CGIAR GTF, will provide a good vehicle for providing this oversight, coordinating collective efforts and leverage community synergies.

## **8.2 Gaining access to the latest developments**

Access to some technologies can be achieved directly through service providers where they have sufficient scale and scope of activities. However some technologies may be proprietary, particularly in the area of transgenic technologies. Negotiations with the private sector and ARIs can be complex and time consuming. It will be necessary to develop and strengthen negotiation capabilities and establish processes for broad technology access. Some mechanisms already exist with the CGIAR System and related programs to develop such linkages, such as in the Challenge Programs. However the capacity could be expanded by ensuring information on capabilities, requirements and opportunities, flows from the Hubs and the GTF to the negotiation groups about the types of technologies required and the ways in which they could be deployed.

A centralized database providing details of what technologies are available, information on restrictions or conditions of use, information on unsuitable or poor technologies, and key contacts would be valuable. The compilation of such a list has already been initiated by CAS-IP. However, the confidentiality of such information will need to be carefully managed.

Links with multinational corporations will be highly beneficial in this process not only to access new technologies but also to obtain information on technologies or approaches that have failed. Such information is highly valuable in avoiding investment in failed approaches.

Mechanisms need to be established that provide broad access to technologies and it will be important to avoid creating exclusive groups that may restrict access. This can be an issue when collaborations are established between Centers and private sector or ARIs. Wherever possible the negotiators should seek to gain access for all Centers and freedom to circulate information on the technology and its application throughout the System and to partner NARS. Similarly, collaborations with publicly funded groups in developed countries should be considered as a strategic approach to obtain access to rapidly changing and expensive genomics technologies.

A more comprehensive treatment of access to third party IP by CGIAR scientists will be available from the joint SC-GRPC commissioned studies to be published later this year.

## **8.3 Role of Centers in accessing technology**

In negotiating access to technologies and developing collaborations with organizations involved in technology and resource development, Centers need to be clear on what they have to offer in exchange and the real value to those who it is being offered to. Six capabilities of Centers were identified that could be used to leverage access to technologies:

1. Germplasm in the broad sense. Accessions of landraces, wild relatives, breeders' lines and cultivars. This should also include mutant populations and a wide range of

specialized genetic and cytogenetic stocks. This germplasm is also associated with an increasingly vast amount of valuable phenotype and genotype data.

2. Knowledge and capability for working in many countries under a wide range of cultural and regulatory regimes.
3. Broad experience of commodities and target regions to act as unbiased brokers of collaborations among NARS, with ARIs and commercial groups.
4. Leadership in specific research areas and aspects of technology development and deployment. For example, through coordination of germplasm resources, mutant and tagged populations, working with minor crops species and wild relatives, and international standards for crop information systems (e.g. Generation Challenge Programme, International Crop Information System, SINGER, and Descriptors), etc.
5. Phenotyping capabilities. It was noted that this is declining in some Centers. This could be addressed by renewing commitment to this activity by the CGIAR as a whole (as a cooperative activity), and by developing communities or networks focused on specific problems. Strong phenotyping will also allow Centers to help identify and define important biological problems for research in ARIs.
6. International breeding programs. This goes beyond only phenotyping to include developing and distributing early segregating populations to stronger NARS (as a collaborative shuttle breeding initiative) while continuing to provide near-finished material where the national breeding programs are less developed.

#### **8.4 Attracting and retaining highly skilled genomics staff**

Any strategy for technology delivery will be dependent upon the skills, capacity and motivation of staff. It is recognized that high quality staff with training in genomics and practical plant and animal improvement are in rare supply. This applies at all levels; research leadership, scientific and technical staff. Mechanisms must be implemented that attract and retain the best possible staff. The issues of staff retention can be particularly significant in some countries hosting Centers where there are few options for long-term alternative employment. Under these circumstances staff frequently seek more secure positions in other countries. Conversely, in other countries the opposite problem is becoming a problem, where there are so many well paid alternative jobs, the Centers begin to lose competitiveness as the best employer in the field.

However, Centers do offer scientists the advantages listed above and these aspects should be publicized during recruitment. These advantages can be enhanced by involving staff in broad programs with diverse expertise and wide ranging opportunities for research. The utilization of Hubs and retention of clear focus will help to build critical mass for particular activities. The possibility of allowing staff to work across several Centers is also worth considering.

In addition to the Hubs, technology and delivery networks should be established to help integrate staff in broad research groups. The concept would be to build technology and delivery communities. A range of additional options should be explored to improve incentives for key staff. These should include:

1. Use of linkages to ARIs through targeted funding regimes, such as the USAID linkage program and support for post-docs.
2. Longer term contracts for key staff and improve staff training options.

3. Competitive salary for the biotech and bioinformatics staff compared to the international markets, and for breeding staff who understand and use genomics information in their programs.
4. Commercial linkages to engage scientists in industry research and vice versa, as is being promoted through the SKEP initiative.
5. Develop recognition systems that reflect CGIAR objectives and targets and use this to raise the international profile of staff, such as providing opportunities and encouragement for staff to present work on delivery successes at international meetings.
6. Overall there is a perceived need to raise the profile of CGIAR Centers through improvements and modernization of publicity material, particularly web pages.

## **9. Risks associated with implementation of the strategy**

The success of this strategy is dependent on establishing centralized service facilities and securing the buy-in of NARS and SMEs (the CGIARs clients). At present, particularly in Africa, some NARS have put scarce resources into building, equipping and staffing biotechnology laboratories. Under the proposed strategy, in some instances, activities in the NARS laboratories may be reduced to DNA extraction and some equipment may have to be decommissioned or assigned for training purposes. The GTF will ensure that the strategy proposed is thoroughly discussed with our clients, and that their buy-in is obtained. The GTF will be responsible for developing an appropriate strategy for this dialogue to take place. It is envisaged that some NARS will not be supportive of this shift in emphasis to out-sourcing genomics data generation and thus the careful design and implementation of incentive schemes will be critical.

The success of this strategy is also dependent upon the buy-in of individual Centers. Membership of the GTF will take time away from Centre staff representatives and clearly must be seen to be compensated by the value of outputs to each center from GTF activities. Again, the ability of the GTF to raise funds to create incentive schemes for those who engage in the process will be enormously helpful during the start-up phase of this strategy.

Finally, the success of this strategy is dependent on genomics service providers being able to rise to the challenge of providing Centers with the right services at the right place. Here again the GTF proposes to be proactive in this area in order to minimize this risk. Thus, the GTF will champion the establishment of service facilities or foster the development and refinement of pre-existing providers to help ensure the availability of a tailored service at the right price.

## **10. Roles and responsibilities**

Different genomics technologies will follow differing paths for delivery to breeding programs and other technology users. Several technologies, such as genotyping, sequencing, proteomics and metabolomics will be most appropriately delivered through service providers. Several options exist for ensuring the effective and timely development of such providers where they do not already exist. Centers should collaborate in the establishment of such service providers, or foster pre-existing providers who have the potential to provide tailored services at the right price. This will help set an example to NARS and related organizations regarding the good intentions, feasibility of deployment and benefits of out-sourcing. The "CGIAR Genomics Taskforce" has been re-established and a Chair and Executive Committee have been elected. The roles and responsibilities of the GTF are outlined below.

1. **A Consensus Long-range Strategy:** The first objective of the GTF is to articulate the broad strategy for the delivery of genomics technologies by the CGIAR Centers over the next ten years. To this end the GTF will work closely with CGIAR and NARS genomics researchers, breeders and genetic resources researchers. The GTF will initiate this process by developing an inventory of genomics-based activities at the Centers by collating the genomics (transgenics and bioinformatics) MTPs of each center and compiling brief 10-year genomics strategies from each center. The final strategy document will establish a series of key objectives that demonstrate the value of molecular technologies for addressing simple/complex traits, germplasm characterization and conservation, diagnostics and vaccine development. These would be GTF facilitated flagship activities and developed as models of cross species collaboration and technology delivery. They could be, for example, a set of key traits for a small number of well studied crop and animal species, or whole genome scans for parental selection in orphan crops and trees that could be developed as technology application "Flagship" objectives. The GTF will also take every opportunity to identify opportunities to assist orphan crops to undergo technological leap-frogging through forming function linkages with better studied relatives. In this way, the GTF could foster the development of genomics-based pipelines with champion germplasm specialists or breeders and thereby facilitate flagship application successes. Of course, there are already a few notable success stories, which the GTF should fully analyze, cross-compare, learn lessons from and intensively publicize the positive impacts achieved. The GTF will carry out many of its activities in close collaboration with the GCP.
2. **Genomics Advocacy:** The GTF will use all forms of communication to provide an unbiased, factual account of the benefits that modern bioscience technologies can bring to agricultural development and in turn improved livelihoods of resource-poor farmers. This will also provide the GTF with the opportunity to showcase why the CGIAR is the preferred partner in linking ARI technology providers with national technology-embedded product users. The CGIAR should consider the GTF as a powerful single voice to the outside world on the power of biosciences to enhance agricultural development. This will also provide the GTF with the opportunity to articulate the new value-chain framework that the CGIAR is striving to move towards and that is a founding pillar of the GTF- to identify critical missing elements or poor linkages that are confounding the uptake and impact of genomics-based outputs. Through this advocacy role the GTF will also take every opportunity to capture fund raising opportunities for agreed flagship applications and other GTF activities listed below.
3. **Breeders' Networks:** The involvement of breeders and other scientists from the Centers and NARS should be consolidated through the re-establishment or enhancement of breeders' networks where necessary. During the initial phases, it would be useful to define a set of priority traits for marker-assisted selection or GM technologies that could be integrated through pre-breeding programs and delivered to NARS as well defined packages. This is likely to focus on just a few traits where there are clear champions for low hanging fruit with molecular breeding goals. Clearly, one advantage of moving to a partial or wholly out-sourced genotyping model is that molecular biologists will have much more time to work directly with the breeders in designing new breeding systems that make best use of molecular genotype data. There is no doubt that until the two disciplines work intimately alongside each other, there is only limited opportunity for mutual respect and synergy to emerge. However, in the long-term this will hopefully be resolved by the emergence of interdisciplinary scientists and breeders who are equally comfortable and competent in both areas.

However, until that time, this will remain a time consuming and expensive process, which the GTF should target for intensive fund raising and technical backstopping. The GTF will showcase to breeders' networks major genomics success stories, particularly where the impact has been especially dramatic following the adaptation of breeding systems to make best use of genomics tools and information – thus emphasizing the importance of a holistic approach to molecular breeding as opposed to single point MAS interventions. Similarly, the GTF will foster flagship applications where genomics helps crop improvement specialists quickly focus on the most valuable material. Where possible the GTF will provide leadership in the design and development of optimal genomics-based breeding strategies. The GTF and key breeder representatives will then be able to devise and collectively advocate a detailed model and operating plan for the delivery of genomics technologies in crop improvement programs. It is envisaged that similar networks and activities could be initiated for trees, livestock and fish.

4. **Population Genomics:** The GTF will, through the involvement of conservation biologists from the Centers, NARS, and ARIs, as well as from their natural resource managers, build strength in population genomics, which is an emerging field for the development of conservation strategies.
5. **Genomics Out-sourcing:** The GTF will identify and collaborate with potential service providers to explore options for outsourcing specific technologies. It may be possible to embed Center or NARS staff within a service provider to access critical mass and capabilities. It could be a role of the Hubs to form a close association with specific service providers and provide regular reviews and assessment of breeders needs to the service providers and regular reports on the effectiveness and capacity of the providers to breeders. The Hubs could also investigate and help organize transfer of materials to ensure timely delivery of results – for molecular breeding applications the required turnaround time from sampling to selection decision is sometimes just too short for many service providers. Nevertheless, a guaranteed high throughput demand through a coordinated CGIAR contract should allow a degree of tailoring to our needs. The GTF should develop a database summarizing resources and service providers that will act as a corporate memory as experience is gathered. An example of the type of information that could be included is shown in the table below. The GTF would help lead and coordinate development and maintenance of the information in an easily accessible format. However, one of the most challenging issues for most public and private sector genomics application facilities is to create sustainability by ensuring a consistent optimum throughput demand. It is likely that in the first instance this will require carefully tailored incentive schemes at the institutional level which the GTF could assist in formulating and implementing. However, most critically, the GTF will provide a single point of negotiation for cooperative discounts from genomics service providers and regional hub administrators.

Service	Provider	Cost	Capacity	Comments
DNA sequencing	Company X	\$2 per run	Unlimited	Provide good quality sequence of around 500 bases
Chickpea transformation	Lab Y, University Y	No charge if part of a collaboration	3 gene per year	Can be slow.
Genotyping	Company Z	Depends on species and assay	Unlimited	SSR primers available for cattle SNP platforms for wheat
Whole genome SNP haplotyping	Company A	\$50 per genotype	Unlimited	Turnaround time for big projects may not be quick enough for breeders decision window



6. **Training Hubs:** The GTF should design and articulate training needs and the role of training hubs for breeders and biotechnology staff - these should be equipped to carry out experimental design, diagnostics and marker validation and reflect what would be available in NARS laboratories, but they would not need state-of-the-art high throughput facilities. They should also focus training on experimental design, breeding strategies and data interpretation with an emphasis of applications rather than the technology or the data generation itself. The training should also help teach how to use large datasets that may be generated and integrate high throughput data generation with decision making in the breeding programs. The Hubs should help build intellectual capital, evaluate service providers and negotiate access and could be "virtual". The Centers and Hubs would probably work regionally to provide information, help with problem solving, develop and maintain networks of breeders and researchers and help broker linkages and collaborations. The Hubs should be at the "cutting edge" of technology application in breeding programs and other product development areas but not necessarily at the "cutting edge" of technology development. In close collaboration with the GCP, the GTF will help foster the development and/or collation of appropriate training manuals and standard operating procedures for optimum applications of genomics technologies. Where possible the GTF will make use of pre-existing resources and training programs available in public and private sectors across the developed and developing worlds.
7. **Open-source Software Development:** A further role of the GTF should be to champion the development of software that will find application throughout the System and partner NARS. The GTF should leverage key existing initiatives such as the informatics subprogramme (SP4) of the GCP, which is developing a comprehensive crop information system based on shared data standards, and the IRRI-CIMMYT CRIL which is developing a range of ICIS-based tools and resources. It is recognized that several programs have been established to enhance data capture and utilization for many target species. However, there is scope for improving the utility of databases and data management tools to support and encourage the use of genomics data by breeders, by adapting pre-existing software into a more user-friendly packages. This needs to reinforce the shift to data analysis rather than data generation and could link to the comprehensive crop information system. The bioinformatics systems will need to cover both molecular, breeding, environmental and genebank data. There will need to be a "top-down" policy to develop and use the platforms based around common (broad compatibility) and inter-linked systems.
8. **Maximizing Brokering:** GTF members should seek out and enhance "brokering" capabilities across the Centers to develop collaborative research activities between Centers, national programs and public or private sector ARIs. Several possible structures exist as models for such a system including the Challenge Programs. The GTF should act as an advocate for the capabilities in the Centers and negotiate involvement of Centers in international and national research funding schemes.
9. **Links with International Networks:** The GTF in collaboration with Centers should play a leading role in the establishment of international collaborations and networks in developing and accessing key genomics resources, such as mutant populations, large-scale sequencing, and development of expression databases. The capabilities that Centers have to contribute leadership and access to germplasm and phenotyping capabilities should be exploited. This will require a clear definition of these capabilities.

10. **Phenotyping Hubs:** The Centers should also explore options for strengthening existing phenotyping capacity, including high-throughput phenotyping systems with the capacity for whole plant profiling, sample tracking and data capture, through establishment of phenotyping or technology communities across Centers. The phenotyping capabilities of Centers offer a significant attraction for ARIs to establish joint projects. Experts in the Centers can provide strong biological focus to research activities in many ARIs, and they could also help broker linkages to phenotyping capacities in NARS. In developing this role Centers must remain aware and where possible integrate into the many non-CGIAR initiatives and networks in both mandated and other species. Although Centers do not need to join all such networks they should explore opportunities for sharing data and experiences and help develop global groups to ensure coordination and interaction. To facilitate this process, development of standardized phenotyping protocols and cross-species ontologies is required. This is already being done, for example, by the GCP for drought tolerance.
11. **Environments associated with genomics-based products:** Breeding products will be delivered to specific environments that vary significantly across species and target region. Genotype-by-environment analysis should help develop the best adaptive genotypes for specific environments and identify the best environments for the breeding products for those environments. The GTF will help collate the characterization and classification of worldwide agricultural environments using all environment data associated with multi-species target products.
12. **Information Resources:** The GTF should launch a webspace with a number of information resources for the community, including surveys of genomics service providers and high throughput precision phenotyping facilities plus databases of national import/export regulations for bacterial, fungal, parasite, plant, animal, fish and livestock DNA, or links to pre-existing web pages on these topics. The GTF will also collate case studies on how different institutions have successfully bridged the gap between molecular biologists and breeders, and thereby analyze the common problems and solutions associated with acceptance and uptake of genomics technologies. Finally, the GTF will establish a maintain databases on all available markers available in GCIAR organisms, with associated information on their validation and application. The GTF will also collate details of cost-benefit analyses and impact assessments of a wide range of genomics technology applications.

The above is simply a preliminary list of justifiable options. However, the scope of the GTF could become overwhelmingly broad, and considerable efforts must be made to initially emphasize the 2 or 3 most important issues and then focus on making a difference in these areas before diversifying into other challenges. Thus, in the first instance the GTF needs to establish its credibility in facilitating efficiency improvements through creating coordinated and integrated information resources plus providing tailoring assistance to a range of flagship applications across species, organisms and types of technologies. This will build ownership of the GTF amongst individuals and institutions and in turn empower the group to move onto the next challenge of fostering hyper-efficient hubs for high throughput genomics data generation, precision phenotyping, data management and analysis, and training.

## **Annex I      Explanation of the roles of operational components**

### **A1.1      "Genomics Taskforce (GTF)"**

The key role of the GTF will be as an advocacy and strategic coordination group operating both within the CGIAR system and with external organizations and funders in the area of plant, animal and fish genomics. In consultation with breeders, biotechnologists and other specialists, the GTF will also:

- Devise and advocate a detailed model and operating plan for the delivery of genomics technologies and results to plant, animal and fish improvement programs;
- Act as an advisory committee for the strategic coordination of genomics-based product development and delivery, including monitoring the implementation, carrying out cost-benefit analysis or new tools and methodologies, and coordinating impact assessment of intermediate genomics-based products;
- Facilitate genomics-related research and application activities across the CGIAR system and with key NARS and ARIs;
- Conduct and maintain a detailed analysis and inventory of genomics related work within Centers and associated programs and lead negotiations for effective and efficient service provision to address these requirements; and
- Provide leadership in the design and development of optimal genomics-based breeding strategies.

*GTF composition:* Executive committee will be composed of three members with representation from Africa, Asia and Latin America (one of whom acts as chair) including representation of both crops, and trees, livestock and fish. One member will come from each CGIAR Center with genomics bench activities plus the GCP Director.

*GTF operations:* The activities of the GTF will be consistent with the rules and processes of the CGIAR system. At various times the GTF will invite non-members to act as facilitators and/or advisors. In designating a staff member to join the GTF, Centers should acknowledge that the GTF will have a large, complex and potentially time-consuming role in ensuring effective delivery of genomics technologies that will equate to not less than 5% of the staff members workplan.

### **A1.2      "Hubs"**

The key role of the "Hubs" will be to ensure regional access to technologies and expertise in the area of genomics, informatics, phenotyping, training and other genomics-related breeding strategies. Within defined geographic regions the Hubs will:

- Devise and deliver training programs;
- Provide access to high throughput precision phenotyping (including for transgenic lines)
- Facilitate genomics-based technology access and/or services;
- Raise awareness and improve utilization of genomics information, technologies and applications; and
- Provide transitional support for NARS and other groups to help them develop and use new technologies.

The Hubs may also negotiate technology access and service provision within their target region. In this role they will liaise closely with the GTF to provide information on regional needs and impediments to technology delivery.

### **A1.3 "Networks"**

The key role of "Networks" will be to ensure the latest relevant information on genomics research, molecular breeding and other genomics-based product developments for particular commodities and different organisms are accurately relayed to relevant end-users of the technology, and in-turn that end-user perspectives are relayed back to technology providers.

In addition "Networks" will:

- Organize specialist workshops and training sessions in collaboration with the Hubs; and
- Bring together groups to tackle specific problems or issues that can best be resolved through cooperative action.

The "Networks" will be commodity or organism focused with a global role or regionally focused around Hubs. They could build upon existing activities within Centers but would bring in expertise and strategies on genomics-assisted breeding methodologies and genomics-based product development, and focus on outcomes of technology application.

## Annex II List of Acronyms

ACPFG	The Australian Centre for Plant Functional Genomics
ARI	Advanced Research Institutes
BecA	Biosciences Eastern and Central Africa
<i>Bt</i>	<i>Bacillus thuringiensis</i>
CAS-IP	Central Advisory Service on Intellectual Property
CGIAR	Consultative Group on International Agricultural Research
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)
CIP	Centro Internacional de la Papa (International Potato Center)
CIMMYT	Centro Internacional de Mejoramiento de Maiz y Trigo (International Center Maize and Wheat Improvement Center)
DNA	Deoxyribonucleic acid
EST	Expressed Sequence Tag
FAO	Food and Agriculture Organization of the United Nations
GRPC	Genetic Resource Policy Committee
GCP	Generation Challenge Program (of the CGIAR)
GM	Genetic Modification
GTF	Genomics Task Force
IARC	International Agricultural Research Center
ICARDA	International Center for Agricultural Research in the Dry Areas
ICRAF	World Agroforestry Centre
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
IP	Intellectual Property
IPG	International Public Goods
IPGRI	International Plant Genetic Resources Institute
IRRI	International Rice Research Institute
MAS	Marker-Assisted Selection
mRNA	messenger ribonucleic acid
NARS	National Agricultural Research System
RFLP	Restriction Fragment Length Polymorphism
SC	Science Council
SC5	Fifth meeting of the Science Council
SKEP	Scientific and Know-How Exchange Program
SME	Small to Medium-sized Enterprise
SNP	Single Nucleotide Polymorphism
SPPS	Standing Panel of Priorities and Strategies (of the CGIAR)
SSR	Simple Sequence Repeat
STS	Sequence Tagged Sites
USAID	United States Agency for International Development
WARDA	Africa Rice Center (WARDA)