

## **Development of genomic resources: Current status and future prospects – Summary report of the ABDC-10 parallel session<sup>1</sup>**

**Facilitator:** Rajeev K Varshney, India

**Panel Members:** Roberto Tuberosa, Italy; Jasper Rees, South Africa; Jerry Taylor, USA

**Rapporteur:** Michael Baum, Syria

**Participants:** approximately 50 from different institutes from a number of countries

The three Panel Members provided background information on the availability of genomics resources in cereal, legumes, trees and animals. From the presentations, It was clear that access to low cost, next generation sequencing technology will be/is available for many cereal, legume, tree and animal species. To properly utilize this technology, major investments in the bioinformatics and data management will be required. For the main cereal crops (wheat, rice, maize and barley), there is good availability of genomic resources and genomic platforms to identify genes/QTLs for target traits. New strategies such as association mapping have increasingly been deployed. Comparative genomics will play an increasing role for identification and validation of candidate genes following the availability of the sequences of important species such as rice, maize and sorghum, and many more species given the rapid increase in sequencing technology. In legumes, due to coordinated efforts at national and international level, significant amount of genomic resources such as molecular markers, genetic maps, physical maps, genome sequence, and trait-linked markers have been developed in several of important species. Tree breeding is challenging given the long breeding cycle, heterozygous germplasm, and self-incompatibility. Currently, genetic maps for some fruit tree species such as apple are available and contain the location of various types of molecular markers and quantitative trait loci (QTLs) for important traits. Published genome sequences are available for grape and in advanced stage for apple and peach. For cattle/animal breeding, high throughput genotyping using the latest advances in genome sequencing is available and genome re-sequencing, de novo assembly, and mutation discovery is almost routine.

During the discussion, it was made apparent that developing countries should strongly consider investing in strategic partnerships with advanced research institutes to be in the best position to take advantage of the latest technology. If the technology exists for a species, gaining access to it and using in research and breeding is feasible, either with investments in-house, or through partnerships or out-sourcing. It was also clear that there is a strong requirement for investment in capacity building – training and retaining human resources, especially in the area of informatics and data analysis/management. The correlation of genomic and sequencing data with phenotypic information is very challenging, but critical for the effective use of modern genomic tools. Data analysis, data management and data accessibility are most important when the “tsunamis” of genotyping data as well as phenotypic data become available. Finally, modern genomic information needs to be complemented with proper phenotyping, and this information needs to be converted into useful information (e.g., breeding values) so that breeders in developing countries can use this in their breeding programs.

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<sup>1</sup> This is the summary report of the parallel session organized by the Consultative Group on International Agricultural Research (CGIAR) on the second day of the FAO international technical conference on Agricultural Biotechnologies in Developing Countries (ABDC-10) that took place in Guadalajara, Mexico on 1-4 March 2010 (<http://www.fao.org/biotech/abdc/parallel/en>).