

Involvement of genomics in rubber breeding

Pascal Montoro, K. Annamalai Nathan, Thakurdas Saha, Sigit Ismawanto, Chamil Nayanakantha, Thitaporn Phumichai, Roslinda Sajari, Emma Sales, Chaorong Tang, Dinh Minh Tran

1. Objective of the CATAS/IRRDB Workshop on Rubber genomics and molecular genetics

The 5-year strategic plan of IRRDB has highlighted that studies on physiology, molecular biology and biotechnology are involved in a range of research areas dealing with the sustainable rubber production (productivity, adaptation, NR quality, development of new products and environmentally friendly practices), the preservation of natural resources (Hevea genetic resources, biodiversity in rubber plantation), and the reduction of greenhouse gas emissions (carbon sequestration). These researches have been leading to a better understanding of important agronomic traits and to develop new high yielding rubber clones with better tolerance to biotic and abiotic stress in a context of climate change. Molecular mechanisms involved in NR production and plant defence have complex regulations requiring global research approach through omics technologies. Application of these technologies has led to decipher molecular bases of important agronomic traits and to assist breeding programmes.

The main objective of the CATAS-IRRDB workshop on Rubber genomics and molecular genetics was to share knowledge and experiences in genomics, transcriptomics, proteomics, metabolomics, molecular genetics and breeding among researchers and scientists especially from the IRRDB member countries. Updated information on genomics and transcriptomics in rubber and genome-based applications has been delivered by keynote speakers, and a round table discussion was conducted to identify topics for developing international initiatives.

2. Summary of the workshop outputs

The CATAS-IRRDB Workshop on Rubber Genomics and Molecular Genetics was held in Haikou, China from 27 to 29 September 2017. This workshop gathered 81 participants from 7 countries (China, India, Indonesia, Japan, France, Malaysia, and Thailand).

The workshop was organized on three sessions (Session 1: Country reports (China, India, France, Malaysia, Thailand); Session 2: Omics and molecular physiology; Session 3: Rubber molecular genetics and breeding), where 24 papers were presented.

This workshop revealed a change of paradigm in rubber science thanks to the adoption of omics technologies. Four draft genome sequences were published during the last 3 years, and probably two other were developed by private consortia. Numerous transcriptome analyses led to characterize the regulation of major function such as rubber biosynthesis, laticifer differentiation, Tapping Panel Dryness, plant diseases, etc. Some proteomic studies allowed to identify major proteins involved in the response to ethephon or in the rubber biosynthesis. Genome-wide analyses were also carried out at the transcriptional, posttranscriptional and posttranslational levels in response to ethephon or the occurrence of TPD. Several organizations (CATAS, CIRAD, IRRI, RAOT, RRII, RRIV, USM in the Philippines) have implemented modern breeding programmes including the utilization of molecular markers for legitimacy testing, high density mapping using SNPs, QTL mapping on biparental population, GWAS on a large set of genotypes.

New challenges are the improvement of the sequence of rubber genome, and the adoption of the best standard of molecular breeding for successful quick selection of climate-smart rubber clones suitable to smallholders. IRRDB may help such development by initiating multidisciplinary workshops to define the best ideotype for the new generation of rubber plantations, and to draw a way for a quick adoption of this new material.

This workshop revealed that there is an active scientific community that attended this workshop. This successful workshop may conduce to a better attractiveness of IRRDB activities for other important scientific teams from University of Sao Paolo in Brazil, USM in Malaysia, Biotec in Thailand, IRIBB in Indonesia, etc.

3. Summary of the round table discussion

Twenty-six participants from seven countries participated to the round table discussion. The objective was to identify topics for international collaborative research programmes and the IRRDB strategy to facilitate these initiatives.

The following topics was suggested as of common interest:

- Improvement of one of the four draft genome sequences. This will require to select the most suitable clone and to define a strategy for sequencing technology and assembly tools. Discussion outcome: Pr Songnian Hu from BIG (Beijing Institute of Genomics) has suggested a suitable strategy for improving the Reyan7-33-97 rubber genome assembly.
- Creation a Hevea Genome Hub to facilitate access to scientists from rubber community (such as genome browser, integrated transcriptomic and proteomic data, proteomes, SNP detection tool, etc.). Discussion outcome: Pr Songnian Hu from BIG has offered to host the rubber genomic data in the BIG Data Centre. A MoU between BIG and IRRDB might be prepared. This bioinformatical platform may have an integrated database for various sources and type of data. Public and private data might be easily managed through this platform. BIG has suggested to publish Hevea raw data directly in the BIG Data Centre.
- CIRAD has offered facilities to characterize Hevea-specific function in rubber transgenic material.
- Molecular breeding (marker-assisted selection (MAS), genome-wide association studies (GWAS), or genomic selection (GS) must be adopted by breeders. Discussion outcome: it was concluded that there is a need to organize an IRRDB Meeting between plant breeders and molecular geneticists to discuss the latest advances in molecular breeding and to define the specific needs (training, workshop) for a better adoption of these modern breeding technologies. The organizer of this 2-day meeting must be identified. Malaysia is a possible host, however the facilities for such bioinformatics training will only be available when the new research building is ready in 3 years, otherwise, support from a local bioinformatics collaborator will have to be sought.
- Applications of omics technology are to provide the latest clones and recommendation for harvesting.