

Summary of the IRRDB Biotechnology Group Meeting

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Introduction

The meeting was chaired by Datuk Dr. Aziz bin SA Kadir, Secretary General of IRRDB. In the opening remarks, the chairman stressed on the following points:

- The theoretical rubber yield potential of rubber tree is 8000 kg/ha/year.
- The rubber industry requires for sustainable production both of rubber and wood. Consequently, research should be geared towards producing fast-growing and high-yielding clones.
- Progress is slow in relation to collaborations in the area of biotechnology, within the IRRDB framework.
- The IRRDB operates on a limited budget, mostly acquired from the nominal fees paid by member organizations, thus unable to undertake the many costly projects in biotechnology; nevertheless the Board aims to pool the available resources to initiate collaborations and to help in the training young researchers from member institutes.

In the past, the following projects have been proposed to the IRRDB Board by the Biotechnology Group:

- Micropropagation of *Hevea*.
- Establishment of a core-collection from the characterized IRRDB 1981 germplasm accessions.
- Sequencing the transcriptome of rubber trees (*Hevea* EST Project).
- Sequencing the *Hevea* genome (*Hevea* Genome Project).

To date however, only a limited numbers of bilateral collaborations have been implemented. Thus the objective of this meeting is to identify new “common” International projects under the IRRDB.

Matters arising

i. Micropropagation

Hevea brasiliensis has been shown to be recalcitrant to tissue culture. Although there has been some progress, somatic embryogenesis and microcutting techniques are not yet available for commercial propagation of *Hevea* clones, which requires conventional grafting of buds on rootstock seedlings (budding). A key factor for progress would be to

combine the good laboratory facilities, good skills and good media compositions set up by some research groups.

Most IRRDB member countries have developed tissue culture techniques and facilities. The shortage of seeds for good rootstock material and the potential of self-rooted plants propagated by somatic embryogenesis obtained in some field trials are some justifications for further developments.

ii. Molecular breeding

Transcripts could serve as molecular markers when polymorphism is detected (SNP markers) in order to have more accurate localization of QTLs for any traits. Based on the experience gathered from the oil palm genomics group (ACGT), genetic linkage mapping is deemed as a more powerful approach for rubber breeding. Thus it was proposed to also explore the use of association mapping in rubber breeding.

iii. Genomics

The IRRDB Biotechnology Group released in October 2009 a technical proposal for the *Hevea* genome sequencing. One difficulty for *Hevea* is its large genome size (> 2000 Mbases), a large number of repeated sequences and its heterozygosity. A reference genome is needed before re-sequencing genomes of clones of agronomic interest. In this proposal, the clone PB 260 was chosen as a model because of the availability of several genetic maps and an efficient track record of genetic transformation on this clone.

So far, the TARRC-MRB is the first institution to have sequenced the *Hevea* genome of RRIM 928, the clone was selected based on its economic potential. The assembly is in progress and no information is yet available on anticipated problems with regards to the large size and the complexity of the genome (repeated sequences and heterozygosity).

Collaboration is fundamental for genome assembly by using notably the transcriptome sequences produced by all countries for gene annotation. For that reason, institutes should co-operate by sharing transcriptome information to help the generation of a *Hevea* genome of reference.

If agreeable by the investors of the TARRC-MRB *Hevea* genome project, a proposal should be put forward to have a central depository, i.e. to have either a public or an IRRDB member restricted access to the database.

According to the oil palm genome sequencing group (ACGT), a high density map is not necessary for the assembly because a linkage map can be identified after assembly if several genotypes could be sequenced.

With regards to the Corynespora leaf fall disease, a proposal was put forward to sequence the genome of *Corynespora*. Further discussions should lead to more specific activities in relation to the proposal.

Conclusions

The participants at the Meeting of the IRRDB Biotechnology Group agreed to propose to the IRRDB Board the following priorities:

- To organize a specific Workshop on *Hevea* micropropagation.
- To have a reference *Hevea* genome available for the scientists of the IRRDB member countries.
- To organize a joint Workshop between the Biotechnology and the Breeding groups on “*Hevea* molecular breeding” with some invited speakers to present examples on other crops, statement on the conventional breeding, course on molecular markers.
- To organize training on Bioinformatics and / or Proteomics based on the needs. This training could be organized in Malaysia (RRIM & UPM), in China (CATAS), in Indonesia (IBRIEC) or in Europe (TARRC & CIRAD) for the duration of one week. Funds from the IRRDB Training Fellowship for 2012 will be allocated for 10 - 15 young scientists to participate in this training program.