## Molecular Breeding of Tropical Acacia

## Shiro SUZUKI<sup>1</sup>, Md. Mahabubur RAHMAN<sup>2</sup>, Takefumi HATTORI<sup>2</sup>, and Toshiaki UMEZAWA<sup>1,2</sup>

<sup>1</sup>Institute of Sustainability Science, Kyoto University <sup>2</sup>Research Institute for Sustainable Humanosphere, Kyoto University

Forest biomass or lignocellulosic biomass, which is the most abundantly accumulated biomass, may be utilized as an alternative carbon resource to fossil resources. Therefore the tree breeding which enables the sustainable production and utilization of forest biomass is critically important.

Molecular breeding based on the genetic information and transformation technology has been expected in the field of the tree improvement, because molecular breeding can confer the superior traits to the trees in a short period, which is very efficient for the breeding of trees with a long lifecycle.

Generally, in order to proceed the tree biotechnology, it is necessary for us to have the efficient genetic transformation/regeneration system, the database of the genome or transcript (expressed gene) sequences, and the characterized genes in model plant species in hand. Although tropical *Acacia* is one of the most important tropical plantation trees in Southeast Asian countries, its biotechnology is still at a primitive stage.

In this context, first, we are attempting to establish protocols of genetic transformation/regeneration of *Acacia mangium* and *A. crassicarpa*. Second, we are constructing a database of transcript sequences of *A. mangium*. Third, we are characterizing the genes involved in the lignification and production of antifungal heartwood extractives in model species to improve *Acacia*. We will outline the on-going research in the poster session.