

PLENARY 2:

**FROM CONSERVATION TO INNOVATION: BUILDING RESEARCH CAPACITY
FOR PLANTED FOREST DEVELOPMENT IN SARAWAK**

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Abstract

The increase in global demand for wood requires increase in forest productivity. The alternative is to farm trees in plantations composed of fast-growing species with short rotation cycle (6-8 years). The rationale is that natural forests at the most produce about 3m³/ha/yr of commercial timber, whereas plantations can produce annually from 10m³/ha of hardwoods to 30m³/ha of softwoods and thus, decrease the effects of human pressure on our ecosystems while increasing the competitiveness of Sarawak's forest industry. This is in line with State Government's aspiration to establish one million hectares of planted forests by year 2020 to meet the increasing demand from both domestic and international markets for raw materials. It is estimated at least 30 million seedlings are required for annual planting or reforestation programmes. In this regard, the forest genomics research will help respond to the need to develop adequate tools that enable us to produce quality planting materials that are of faster growth, high-yield and high wood quality, and also adapted to local conditions, so that we may achieve economic benefits of great significance. Realizing the needs, we have centered our research on the development of tools via biotechnological innovations for tree breeders. We have successfully developed: 1) an array of highly informative and polymorphic DNA markers specific for identifying the genetic makeup of two fast growing indigenous tree species, i.e. Kelampayan and Sawih; 2) the one step 'Touch-incubate-PCR' approach for preparing plant tissues for high throughput genotyping, and 3) a genomic resource database, aka CADAMOMICS (10,368 ESTs) for wood formation in Kelampayan via high-throughput DNA sequencing. These tools will greatly facilitate the selection of quality planting materials for planted forest development in Sarawak as well as long-term tree improvement activities by integrating genomics into our breeding programme via association mapping. The overall benefit of genomics application to tree improvement programme will be in terms of greater certainty in the outcome of results, specifically the