GENOMIC STUDIES ON PLANTATION TREE SPECIES IN SARAWAK

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Abstract

Rapid socio-economic changes in the world are having profound impacts on all sectors, including forestry. 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 cycles (6–8 y). The rationale is that natural forests at the most produce about 3 m^3 ha y^{-1} of commercial timber, whereas plantations can produce annually from 10 m^3 ha y^{-1} of hardwoods to 30 m^3 ha^{-1} 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 the 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, 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 need, we have centred our research on the development of tools via biotechnological innovations for tree breeders. Over the years, we have successfully developed: 1) simple sequence repeat (SSR)