課題名（タイトル）：

De novo assembly of rubber transcriptome

利用者氏名：Minami Matsui*, Ng Kiaw Kiaw*, Ong Wen Dee*, Nyok Lau Sean**
所属：*環境資源科学研究センターバイオマス工学連携部門
**** University of Science Malaysia · Centre for Chemical Biology**

１． 本課題の研究の背景、目的、関係するプロジェクトとの関係

Natural rubber (cis-1.4-polyisoprene) is an essential raw material for many industrial applications, such as heavy duty tires and medical devices. The family Euphorbiaceae is a large family consists of rubber - producing crops, with about 280 genera and 80000 species (Verheye, 2005). Among 2000 rubber producing species, Hevea brasiliensis (Willd, IexI A. Juss.) Mull. Arg. is the only species that gives commercially viable quantities of high quality rubber. The unique qualities of natural rubber such as longer chain length, resilience, elasticity, impact and abrasion resistance, efficient heat dispersion and malleability could not be replaced by any other synthetic rubber (Li et al., 2012).

Global demand for natural rubber is increasing at an alarming rate and is predicted to be 12 million tons in 2020 (Smit and Burger, 1994) . Despite the rapid increase in global demand of rubber, the production of rubber is relatively low. The target yielding potential of rubber tree is 10000 kg/per ha/ year. However, the yield potential of current rubber clones is 3000 kg per ha per year which is far below than the target potential. Thus, it is crucial to increase the rubber production in order to meet rising natural rubber demands, or else, the prices for the rubber related products will have a steep escalation. Now, the general metabolic pathway of rubber biosynthesis is clear and genes involved have been identified. However, molecular regulation of rubber biosynthesis and the functional genomics studies are still in infancy. With the detailed understanding of the molecular mechanism and the identification of key genes involved, we could improve rubber clones via genetic engineering and breeding technologies.

Research Goals:

・ To evaluate the gene expression profiling between control rubber clone (RRIM 600), high-latex yielding clone (PB350) and non-latex producing clone.

・ To identify the key genes that regulate rubber biosynthesis.

・Re-sequence the rubber genome

２． 具体的な利用内容、計算方法

<u>Rubber genome resequencing</u>

A PacBio library with 10 Kb insert size were sequenced with 100 SMRT cells using P5-C3 chemistry. 45.25 Gb of sequences from 6,603,402 reads with a typical average read length of 6,852 bp was generated. The reads have accuracy of ~82% and were corrected with PacBioToCA version 8.2. The latest version of the software included a new probalistic overlapper for self-correction of sequences named MinHash Alignment Process (MHAP) to improve overlapping efficiency and reduce runtime.

３． 結果

The error correction of PacBio reads yielded 14Gb of sequences. The error-corrected PacBio reads coverage is not sufficient for *de novo*

assembly. The PacBio reads will be used for scaffolding of Illumina assembly. The assembly of Illumina paired-end and mate-paired reads with different sizes is currently in progress.

４． まとめ

The upgrading of the rubber genome assembly will serve as a reference for other downstream analysis e.g. agronomic traits analysis.