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The path from genomic discovery to commercial planting in oil palm

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Statement of the Problem: The objective of oil palm breeding is to produce high-yielding materials. In Southeast Asia, thick-shelled Deli *dura* (D) and shell-less AVROS *pisifera* (P) are maintained separately as maternal and paternal pools, respectively. The reciprocal recurrent selection (RRS) of elite parents is based on the performance of thin-shelled *tenera* progeny derived from DxP crosses. However, large-scale DxP crossing to evaluate every individual of D and P is impossible due to resource constraints. Furthermore, RRS required more than 20 years completing a selection cycle. The snail's-pace breeding will put the oil palm industry at risk, when the planting materials fail to cope with drastic changes in the environment. The paper will cover the experience of developing genetic tools and prediction models for early selective breeding. The challenges of translating the genomic discoveries to commercial deployment also will be discussed.

Methodology & Theoretical Orientation: Sime Darby Plantation sequenced the oil palm genome in 2009. A 200K-SNP array, OP200K was then developed after quality filters. The array was used for genome-wide association study (GWAS) and followed by genomic selection (GS) to further improve prediction accuracy. To facilitate commercial deployment, a high-throughput pipeline was also developed in house.

Findings: About 6 million SNPs were identified throughout the genome, representing important breeding stocks in the industry. Important QTLs for bunch component and oil yield traits were successfully detected. The QTL profile was used as the basics for GS modeling, which achieved >0.5 of prediction accuracy.

Conclusion & Significance: The density-reduced SNP panel with minimal accuracy trade-off is now available for selecting the best yielding seeds in Sime Darby Plantation. The first 100 ha planting of Genome Select seeds with estimated 16% of yield increment were launched in April 2016. The upscaling of Genome Select seed production is currently taking place.

Biography

Chee-Keng Teh holds a position of Chief Molecular Breeder II in Biotechnology and Breeding Department, Sime Darby Plantation R&D Centre. He has his expertise in quantitative genetics, development genetic tools and prediction models to maximize genetic gains in oil palm breeding. He and a team of multidisciplinary scientists in Sime Darby Plantation started genomic discovery programs since 2009, and has successfully realized transition from the discoveries to commercial planting in 2016. Before 8 years of humble service in Sime Darby Plantation, he completed 2-year MSc program in National University of Malaysia based on his research on genetic diversity of oil palm germplasm supported by Malaysia Palm Oil Board (MPOB). Currently, he is pursuing his PhD degree in University of Nottingham.

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