

## Omics approach in the study of natural hybridization in *Nepenthes* species

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The *Nepenthes* genus consists of carnivorous plants that have evolved intricate pitcher formation at the tip of their leaves for nutrient acquisition from insect trapping. Previous studies reported several proteins present in the pitcher fluid, including aspartic proteases (nepenthesin I and II) and pathogenesis related proteins ( $\beta$ -1, 3-glucanase, class IV chitinase and thaumatin like protein) which are enzymatically stable albeit exposed to external environment. We are interested in understanding the effect of natural hybridization on the expression of enzymes in the pitcher fluids of *Nepenthes*. *N. ampullaria*, *N. rafflesiana* and their natural hybrid, *Nepenthes x hookeriana* were chosen as the model due to the distinct feeding habits of *N. ampullaria* as a detritivore which feeds on leaf litter, while *N. rafflesiana* and *Nepenthes x hookeriana* remain carnivorous. To identify novel proteins in the pitcher fluids will require transcript information for the inference of peptide sequences through proteomics informed by transcriptomics (PIT) approach. PacBio isoform sequencing (Iso-Seq) provides unprecedented full length transcriptome profiles of all three species as reference databases for protein identification. Comparative transcriptomic analysis was performed through orthologous clustering of predicted peptide sequences. The hybrid, *Nepenthes x hookeriana* has the highest number of predicted proteins, whereby more proteins were shared with *N. rafflesiana* than *N. ampullaria*. This is consistent with previous genetic study and morphological observation. We are currently investigating allele specific gene expression and whether novel transcripts are generated as a consequence of hybridization.

## Biography

Hoe-Han Goh was graduated from the University of Sheffield, UK. He has started his first academic position at the Institute of Systems Biology, Universiti Kebangsaan (National University) Malaysia in Nov 2011. He has trained himself on the applications of NGS by attending courses and workshops on NGS data analysis held at BGI-Shenzhen and TGAC UK. Since then, he has established a plant functional genomics research group with a focus on crop improvement and molecular exploration of tropical plant species using NGS and functional genomics approaches. In Jun 2014, he was appointed as Head of Plant Biotechnology Centre.

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