**Introduction**

*Ganoderma boninense* is an infamous facultative fungal pathogen that has been the causal agent of basal stem rot (BSR) disease in oil palm (*Elaeis guineensis*). The disease has caused the deaths of palms as young as 12-24 months and has been a serious threat to the oil palm industry in South East Asian countries, especially Malaysia and Indonesia. The acreage of plantation infected with BSR disease in Peninsular Malaysia was recorded to be about 400,000 hectares. Fundamental studies on *G. boninense* are limited, especially on the genes involved in pathogenicity. Therefore, to further understand the fundamental biology of the genes involved in degradation, the mycelial of *G. boninense* was cultivated on two different mediums, fresh potato dextrose agar (PDA) in petri plates as the standard growth media (PER71) and rubber wood blocks (PER71-47) as the comparative.

**Workflow**

- **Genome Construction**
  - **Sequencing**: Sequenced using 454 GS-FLX Titanium (Life Science) NGS platform
  - **Build Reference Transcripts**: Genes in gff3 format was extracted from the PER71 genome with a *Tn* length of 100 bases as to include the UTR region. This is classified as cDNA and will be used as reference transcripts.
  - **Calculate read abundance of the PER71 and PER71-47 RNA-seq data via RNA-Seq by Expectation-Maximization (RSEM)**
  - **Identifying differentially expressed transcripts**: Merge the RSEM estimate abundance values of PER71 and PER71-47 producing the gene matrix expected counts
  - **Using EdgeR Biocomputor Package**: EdgeR (Robinson et al., 2010) on the merged gene matrix counts, a volcano plot of differentially expressed genes was produced

**Results**

- Differential gene expression of the RNA-seq data identified 46 highly expressed genes, where 28 genes had an e-value between 1e-5 to 1e-140. Of these 15 genes were identified from mycelia grown on RWB (PER71-47) and 13 genes were expressed on the PDA plates (PER71).
- Gene functions were identified based on a similarity search against the Pfam database

**Conclusion**

- Results have identified several genes in PER71-47 that appears to be differentially expressed during wood colonization, such as:
  a. Hydrophobin: putatively identified to be involved in pathogenicity (Cho et al, 2008)
  b. Peptidase_M16: Catalytic peptidase of the Metallo group - involved in the physiological and pathological processes
  c. Heat shock protein (HSP70): protect cells from thermal or oxidative stress
  d. PECK-ATP is a key enzyme required for gluconeogenesis, a metabolic pathway that results in the generation of glucose from non-carbohydrate carbon substrates

**References**

4. Robinson et al., (2010), Bioinformatics, 26(1), 139-140.

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