

# ORAL ABSTRACTS - 30A0

## DE NOVO TRANSCRIPTOME DATASET OF GENE EXPRESSION IN *Durio zibethinus* DURING THE INFECTION OF *Phytophthora palmivora*

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**Abstract:** *Phytophthora palmivora* is a notorious oomycete that causes fatal diseases in tropical perennial crops. Over time, extensive literatures have been published on the destructive diseases caused by *P. palmivora* in *Durio zibethinus* (durian). The sequencing and analyzing of virulence-related genes that are involved during the infection of *P. palmivora* in durian will give a comprehensive understanding about the gene expression and infection mechanism. Healthy durian leave samples were inoculated with *P. palmivora* zoospores and harvested at 3 days-post-inoculation. The process involved transcriptome sequencing using Illumina RNA-seq technology and *de novo* assembly of the transcripts. The transcriptomic analysis managed to annotate 75,945 unigenes and 95,158 unigenes for control and infected sample respectively. The total length, N50 and GC content of Unigenes for control sample are 52,649,717, 1087 and 41.91% while for infected samples are 58,582,609, 911 and 43.24% respectively. 9 necrosis-inducing-Phytophthora-protein 1 (NPP1) genes, 17 elicitors and 45 RxLR proteins are the virulence-related genes acquired through data mining. This transcriptome data will be used to create novel control strategies for *P. palmivora* diseases in durian using molecular technology, resulting in increased durian production in durian-producing countries. The potential new control measures can also be a great benefit for farmers to minimize their exposure to hazardous fungicides.

**Keywords:** *De novo* assembly, RNA-Seq, *Phytophthora palmivora*, durian, gene discovery