RNA-seq data of Ganoderma boninense at axenic culture condition and under in planta pathogen-oil palm (Elaeis guineensis Jacq.) interaction

ABSTRACT

Objective: Basal stem rot disease causes severe economic losses to oil palm production in South-east Asia and little is known on the pathogenicity of the pathogen, the basidiomyceteous Ganoderma boninense. Our data presented here aims to identify both the house-keeping and pathogenicity genes of G. boninense using Illumina sequencing reads. Description: The hemibiotroph G. boninense establishes via root contact during early stage of colonization and subsequently kills the host tissue as the disease progresses. Information on the pathogenicity factors/genes that causes BSR remain poorly understood. In addition, the molecular expressions corresponding to G. boninense growth and pathogenicity are not reported. Here, six transcriptome datasets of G. boninense from two contrasting conditions (three biological replicates per condition) are presented. The first datasets, collected from a 7day-old axenic condition provide an insight onto genes responsible for sustenance, growth and development of G. boninense while datasets of the infecting G. boninense collected from oil palm-G. boninense pathosystem (in planta condition) at 1 month post-inoculation offer a comprehensive avenue to understand G. boninense pathogenesis and infection especially in regard to molecular mechanisms and pathways. Raw sequences deposited in Sequence Read Archive (SRA) are available at NCBI SRA portal with PRJNA514399, bioproject ID.

Keyword: Ganoderma boninense; Basidiomycete; Transcriptome; Basal stem rot; Pathogenicity factors