

## OP 21

### **Transcriptomic functional analyses of *Setaria digitata* to identify the presence of enzymes that encode for heme, riboflavin and nucleotide biosynthesis**

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**Background:** *Setaria digitata* is a *Wolbachia* free filarial nematode that infects animals such as goats and sheep, causing cerebrospinal nematodiasis in them. Most importantly, *S. digitata* poses a greater similarity in its features with *Wuchereria bancrofti*, which is the major causative nematode of lymphatic filariasis in humans. Thus, *S. digitata* acts as a model organism for deducing the biochemical features of *W. bancrofti*.

**Objective:** To develop a novel therapeutic agent for both disease conditions, it is essential to have an in depth understanding on the biochemical aspects of *S. digitata*. Hence, in this study the transcriptome of *S. digitata* is functionally annotated to identify the enzymes associated with the metabolic pathways of nucleotide, heme, and riboflavin synthesis.

**Methods & Materials:** The draft transcriptome of *S. digitata* was assembled into contigs by the tool “Trinity” and converted to respective protein sequences by “TransDecoder”, which was then functionally annotated using “Blast2GO”.

**Results:** A number of 5,791 of protein sequences were acquired and from the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis, and 311 enzymes associated with 124 pathways were identified. Among them, 26 and 17 enzymes were identified in the purine and pyrimidine metabolism pathways respectively. In the riboflavin metabolism, three enzymes and in the porphyrin and chlorophyll metabolism, five enzymes were identified.

**Conclusion:** As the complete set of enzymes for the *de novo* synthesis of each interested metabolite was absent, it can be concluded that *S. digitata* might be taking intermediate metabolites dihydroorotate, inosine triphosphate, and proto-porphyrin-IX from its host for the synthesis of pyrimidine, purine and heme respectively. It can be also concluded that riboflavin might be taken from outside and converted to Flavin Mononucleotide (FMN). Hence, genes that encode for above identified enzymes might have laterally transferred from *Wolbachia* to ancestral *S. digitata* prior the *Wolbachia* loss.