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Transcriptomic analyses of *Setaria digitata*

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Background: *Setaria digitata* is a common filarial nematode that cause Cerebrospinal Nematodiasis (CSN) in goats, horses and sheeps leading to lumbar paralysis and the eventual death of the animals resulting considerable economic loses on livestock farmers. *S. digitata* also acts as a model organism to study the nematode biology as it poses a greater resemblance in its physical and chemical features with *Wuchcheria bancrofti*, the infective nematode of Lymphatic Filarisis (LF) in humans. Hence, to develop a potential therapeutic measure for both CSN and LF, expanding the knowledge on *S. digitata*'s physiological and biochemical aspects are still at onset.

Objective: Thus, this study is primarily directed towards revealing the whole Transcriptomic data of *S. digitata* by RNA sequencing, mapping and alignment.

Methods & Materials: RNA of *S. digitata* was extracted from a sample of adult three worms of *S. digitata* and they were collected from the peritoneal cavity of cattle (*Bos taurus*) using the RNA Micro kit which was then subjected to Next Generation Sequencing (NGS), in which the Illumina library preparation kit optimized for Whole Transcriptome Sequencing (WGS) was used (TruSeq Stranded Total RNA LT Sample Prep Kit).

Results: In analyses of sequencing, a total of number of 3,285,726,657 bases in 32,791,490 reads were obtained after initial trimming and quality filtering. The draft transcriptome was 3.4 Gbp and the GC percentage was 39.53% while 94.98% of the total reads were above the Q30 score of 94.22. A number of 5,791 of protein sequences were identified and among them, 311 enzymes were associated with 124 pathways.

Conclusion: This study has expanded the knowledge on transcriptome of *S. digitata* and thus, may facilitate the further transcriptomic analysis.