

Understanding the Complexity of Nematode Genome through Transcriptomics Approach

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ARTICLE ID: 34

Introduction

To overcome the complexity of genome sequences and large data analysis, we go for transcriptomics. It is the study of gene expression of specific organ at specific time. Transcriptomics is the study of transcriptome of a cell, whereas transcriptome is the total mRNA present in cell. Mainly it conclude mRNA only because it actually code for proteins. It include tRNA, rRNA, junk RNA, microRNA and siRNA also. Measuring the expression of an organism's genes in different tissues, conditions, or time points gives information on how genes are regulated and reveals details of an organism's biology.

Methods to analyze transcriptome

RNA sequencing is a high through output sequencing method. Single cell transcriptome is advance approach in modern era. Single cell transcriptomics is the study of transcript of a single cell isolated from any organism. Junk and non-coding region are absent in transcript. By this approach we can study gene expression profiles of specific organ system at specific time interval. Analysis of transcriptomics enable us to study change in gene expression at different stages of organism and large no. of genes analyzed at one time although transcriptomics data assembly and interpretation is a tough task. Through transcriptomics approach differential expression of genes and novel gene expression analysis are possible. RNA sequencing used to characterize transcriptomic differences among different species or different stages of single species and to identify genes associated with host specificity, parasitism and survival.

Single cell Transcriptomics: By extending the spatiotemporal resolution of our investigations to the level of the individual cell, single-cell techniques are rapidly transforming our perspective on biological systems. With the emergence of single-cell transcriptomics, we are

now able to examine the genetic profiles of individual cells at unprecedented scale and depth. Focusing on single cell is what a researcher actually need. It increase the efficiency of assembly and interpretation. It reduces raw data size and time to analyze also. It highlights the importance of novel genes. In field of plant nematology it is new approach and can be useful to study gland cells, reproductive cells separately in comparison of whole nematode transcriptomic study.

Nematode Transcriptome	Reference
<i>Ditylenchus destructor</i>	Ma et al. 2020
<i>Heterodera schachtii</i>	Elashry et al. 2020
<i>Bursaphelenchus xylophilus</i>	Lu et al. 2019
<i>Meloidogyne chitwoodi</i>	Bali et al. 2019
<i>Meloidogyne incognita</i>	Choi et al. 2017
<i>Aphelenchoides ritzemabosi</i>	Xiang et al. 2016
<i>Aphelenchoides besseyi</i>	Wang et al. 2014
<i>Heterodera avenae</i>	Kumar et al. 2014
<i>Heterorhabditis bacteriophora TTO1</i>	Bai et al. 2009

Table: List of the recent studies related to nematode transcriptome

Nematode Transcriptomics: It helps to study molecular interaction of plant and nematode. Even before the introduction of juvenile nematodes into host plants, nematode-induced gene expression alterations might occur. This provide insight into stage-specific development, reproduction, infection, host–parasite interactions, and many aspects of the biology of these and other parasites. It helps to determine the relationship between transcriptome evolution and morphological divergences among nematodes. Since many plant parasitic nematodes are obligate parasites, it is often difficult to efficiently obtain sufficient amounts of nematodes for transcriptomic studies.

Future scope

Transcriptomics has paved the way for a comprehensive understanding of how genes are expressed and interconnected. Survey indicates that model species cannot show the genetic and genomic diversity of even their own phylum, and that continuing, phylogenetically informed genome sequencing is essential for advances in genomics, evolution and infectious disease biology. A detail explanation of the transcriptomes of esophageal glands with the target of identifying nematode effectors is a promising avenue to understanding nematode parasitism and its evolutionary origins as well as to devising nematode control strategies. Analyzing the transcriptome sequences in order to identify the secretome of plant parasitic nematode species is a valuable source to investigate the nature of the biological processes (Pathways) associated with this type of parasitism.

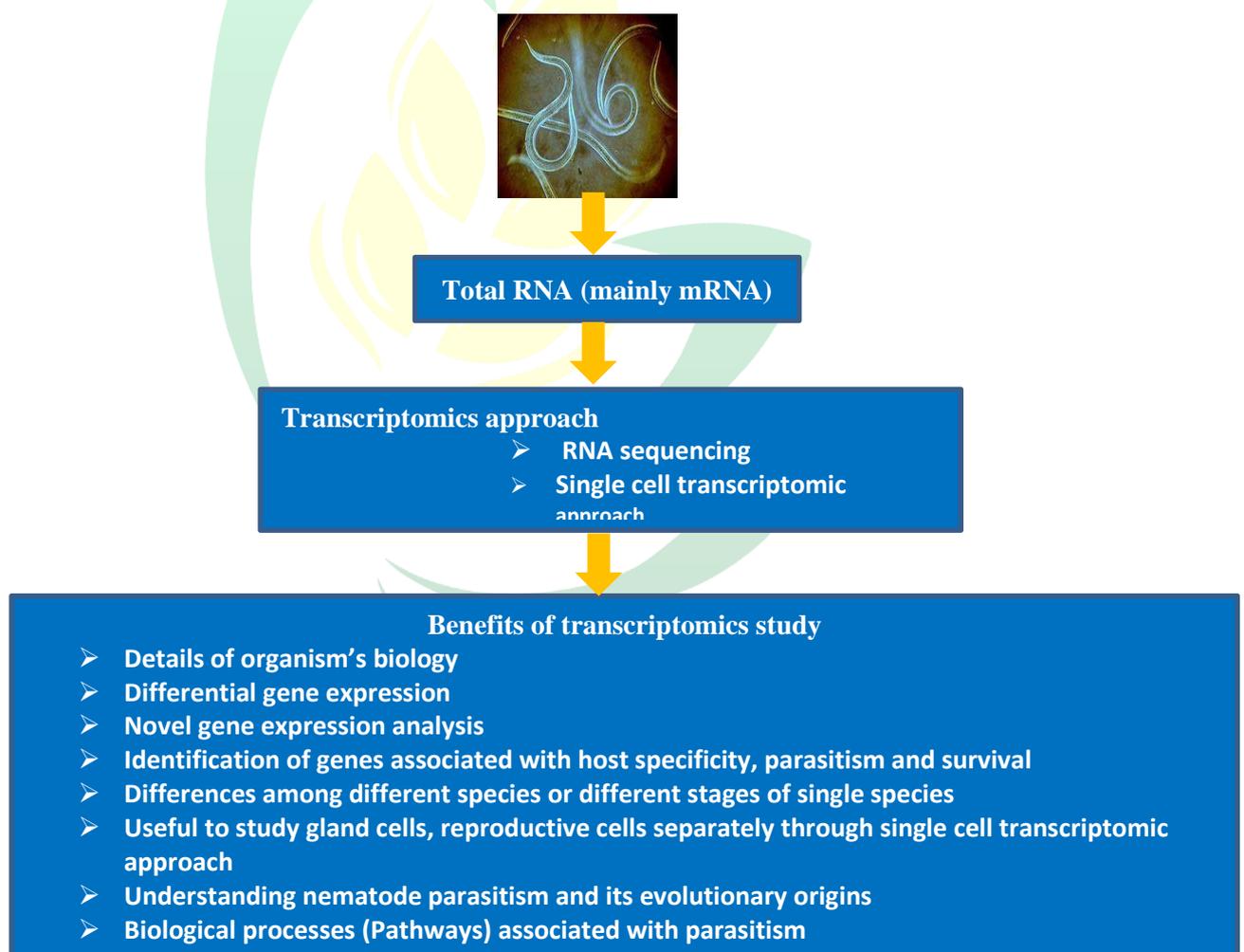


Figure: Study of nematode transcriptomics

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