

Small RNA sequencing

Introduction

Small RNAs are a group of non-protein-coding RNA molecules that are 18-40 nucleotides in length and play a role in gene-silencing and post-transcriptional regulation of gene expression [1]. They play important roles in gene expression regulation in organisms especially during development, cell proliferation and differentiation, apoptosis and are part of host defense pathways against foreign nucleic acids. Small RNA population varies significantly within tissue types and species [2].

Small RNA sequencing is a Next-Generation Sequencing (NGS) technique that involves isolation and sequencing of small RNA species to explore their abundance in various tissues or under varying conditions where they play important functional roles [3]. It helps to decipher their abundance, function and helps to construct regulatory networks of miRNAs and their target genes [4]. NGS can query thousands of small RNAs and lead to discovery of novel small RNAs their roles in tolerance and defense mechanisms [5].

Small RNA Sequencing at AgriGenome

AgriGenome offers comprehensive small RNA sequencing and bioinformatics analysis for miRNA profiling with the Illumina platform and widely accepted analysis software. Small RNA Sequencing data generation at AgriGenome involves the following steps (Figure 1 & 2).

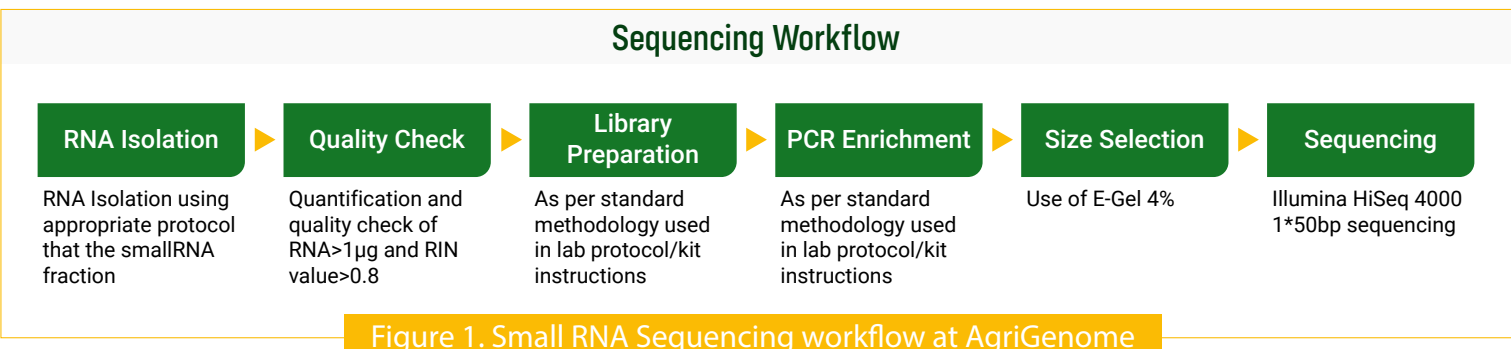


Figure 1. Small RNA Sequencing workflow at AgriGenome

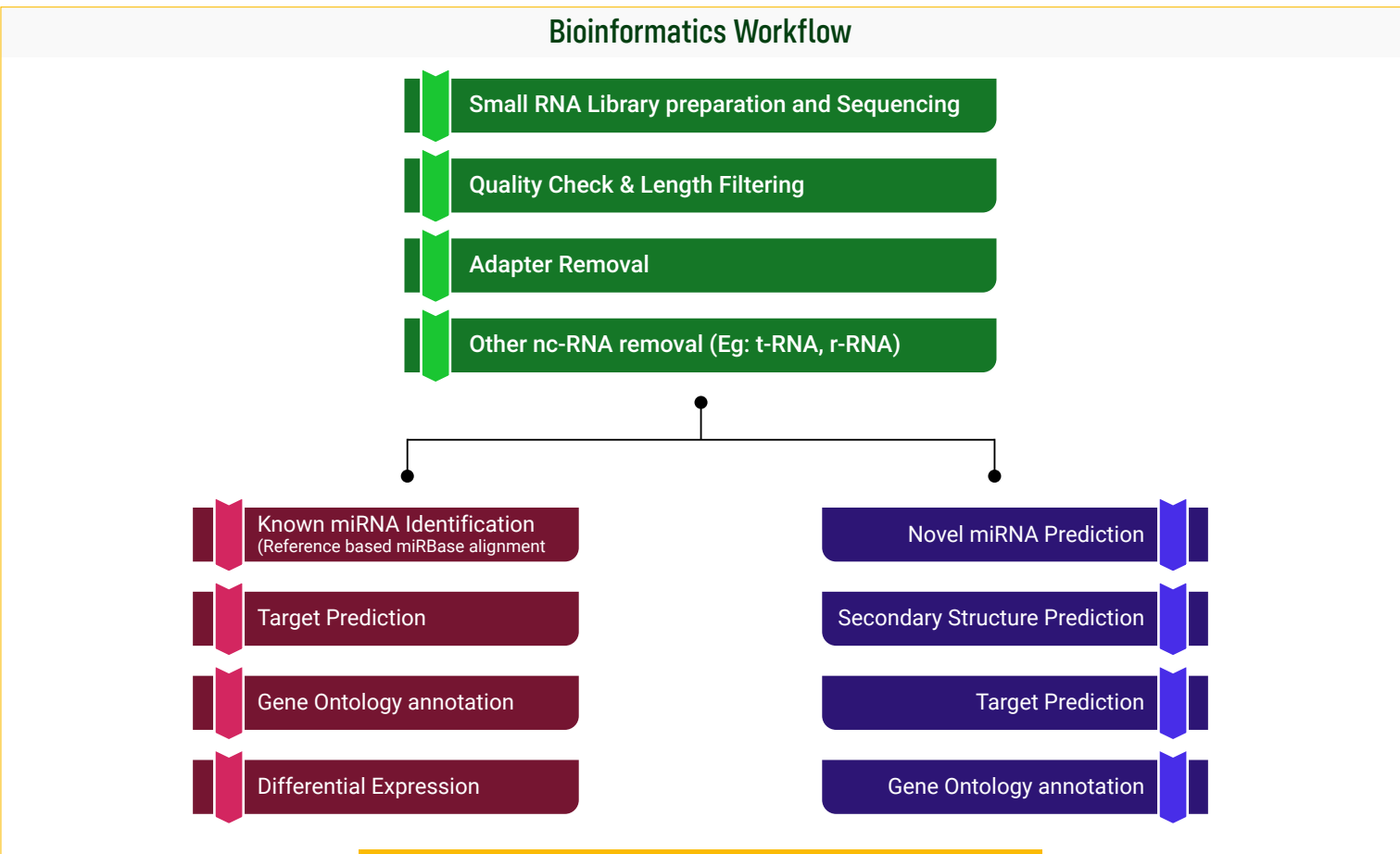


Figure 2. Small RNA analysis pipeline at AgriGenome

Deliverables

We provide the following bioinformatics deliverables after analysis:

- Raw data quality control and length filter
- Reference-based mapping
- Small RNA classification and quantification
- Target gene prediction and annotation
- Identification of novel small RNAs
- Differential expression analysis of small RNAs (GO enrichment and KEGG enrichment)
- Identification of target molecules of novel miRNAs

Application

- Delivers comprehensive view of the small RNA profile in samples
- Understanding how post-transcriptional regulation contributes to the phenotype
- Identifying conserved and novel small RNA
- Capture the small RNA targets and their annotation
- Understanding host-pathogen interactions and disease progression
- Designing antisense-RNA for functionally important gene targets

References

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3. Morozova O, Marra M A. Applications of next-generation sequencing technologies in functional genomics. *Genomics.* 2008, 92(5): 255-64.
4. Broderick J A and Zamore P D. MicroRNA therapeutics. *Gene Therapy.* 2011, 18: 1104–1110.
5. Croce CM, Calin GA. miRNAs, cancer, and stem cell division. *Cell* 2005;122:6-7.

Recent publications from projects executed at AgriGenome

Bhardwaj, V., & Mandal, A. (2019). Next-Generation Sequencing Reveals the Role of Epigallocatechin-3-Gallate in Regulating Putative Novel and Known microRNAs Which Target the MAPK Pathway in Non-Small-Cell Lung Cancer A549 Cells. *Molecules*, 24(2), 368. doi:10.3390/molecules24020368

Sabana, A. A., Rajesh, M. K., & Antony, G. (2020). Dynamic changes in the expression pattern of miRNAs and associated target genes during coconut somatic embryogenesis. *Planta*, 251(4). <https://doi.org/10.1007/s00425-020-03368-4>

Mohanty, J. N., Chand, S. K., & Joshi, R. K. (2019). Multiple microRNAs Regulate the Floral Development and Sex Differentiation in the Dioecious Cucurbit *Coccinia grandis* (L.) Voigt. *Plant Molecular Biology Reporter*. <https://doi.org/10.1007/s11105-019-01143-8>

Singh, P., Golla, N., Singh, P., Baddela, V. S., Chand, S., Baithalu, R. K., et al (2017). Salivary miR-16, miR-191 and miR-223: intuitive indicators of dominant ovarian follicles in buffaloes. *Molecular Genetics and Genomics*, 292(5), 935–953. <https://doi.org/10.1007/s00438-017-1323-3>

Kajal, M., Singh, K. Small RNA profiling for identification of miRNAs involved in regulation of saponins biosynthesis in *Chlorophytum borivillanum*. *BMC Plant Biol* 17, 265 (2017). <https://doi.org/10.1186/s12870-017-1214-0>

Sheeja, T.E., Deepa, K., Santhi, R. et al. Comparative Transcriptome Analysis of Two Species of *Curcuma* Contrasting in a High-Value Compound Curcumin: Insights into Genetic Basis and Regulation of Biosynthesis. *Plant Mol Biol Rep* 33, 1825–1836 (2015). <https://doi.org/10.1007/s11105-015-0878-6>

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