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The Thesis Submitted for the Degree of Master of Science  
(In the field of Plant Breeding)

***In silico* Prediction and Studying of Regulatory Effects of miRNA<sub>s</sub> and  
their Target Genes in *Zingiber officinale* during Biological Processes**

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## **Abstract**

Ginger (*zingiber officinale*) is a native crop in eastern south of Asia which its rhizomes is used as medicinal parts. The miRNAs are important small and regulatory types of RNAs which play some roles during different biological and metabolic processes. In this research, miRNA prediction was performed using a computational pipeline. This pipeline was based on homologous search in order to detect miRNAs in ginger. In this pipeline, it was used the registered miRNAs and EST sequences of ginger in validated database. Then, it was determined the target genes related to these miRNAs. In the next step, molecular functions and biological process related to these target genes were studied using gene ontology enrichment analysis. On the other hands, a novel method was developed to predict such molecules. In this method, firstly, it was constructed the positive and negative database including different vectors; then, classification methods (RF, MLP, NB, SVM and RNN) were used to predict miRNAs and the results were validated by 10-fold cross validation method. Finally, this method can be used to predict such molecules.

**Keywords:** Noncoding RNA, Gene Ontology, Classifier, Machine learning, Bioinformatic