Comprehensive Protein-Protein Interaction Network Analysis of *Xylella fastidiosa* in Fruit Tree Crops

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Abstract

Xylella fastidiosa, a notorious bacterium, poses a significant worldwide threat to fruit tree crops by disrupting the sophisticated mechanisms of water and nutrient transport within the xylem, crucial for plant growth and development, and its impact results in devastating symptoms such as leaf scorching, wilting, and the gradual dieback of branches or entire trees, severely compromising agricultural productivity and economic stability. A meta-analysis approach was employed to understand and address the challenges posed by *X. fastidiosa* infections in fruit tree crops [1][2][3] by integrating and comparing multiple RNA-Seq datasets from various studies, providing a comprehensive view of gene expression dynamics across different plant species affected by the bacterium. An appropriate bioinformatics pipeline was applied to identify genes that exhibit differential expression patterns in response to *X. fastidiosa* infection. Gene Ontology analysis was performed on the identified differential gene expression data which uncovered enriched GO terms annotating genes crucial to regulatory functions that coordinate the plant's immune response. Mapping and visualizing gene expression data onto key metabolic pathways provided a clear overview of how gene activity influences metabolic processes, which helped identify pathways significantly affected by changes in gene expression and thereby pinpoint critical biological responses. Protein-protein interaction network analysis was conducted to decipher the pathogenic mechanisms of *X. fastidiosa* in these crops utilizing high-throughput sequencing data, protein interaction databases, and network analysis tools. The identification of hub proteins will aid in targeting the pivotal nodes, which have the potential to interfere with multiple pathways simultaneously offering a promising strategy for controlling the infection.

References

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