

The genetic interplay in *Impatiens* downy mildew: A transcriptome-based approach to enhancing disease resistance

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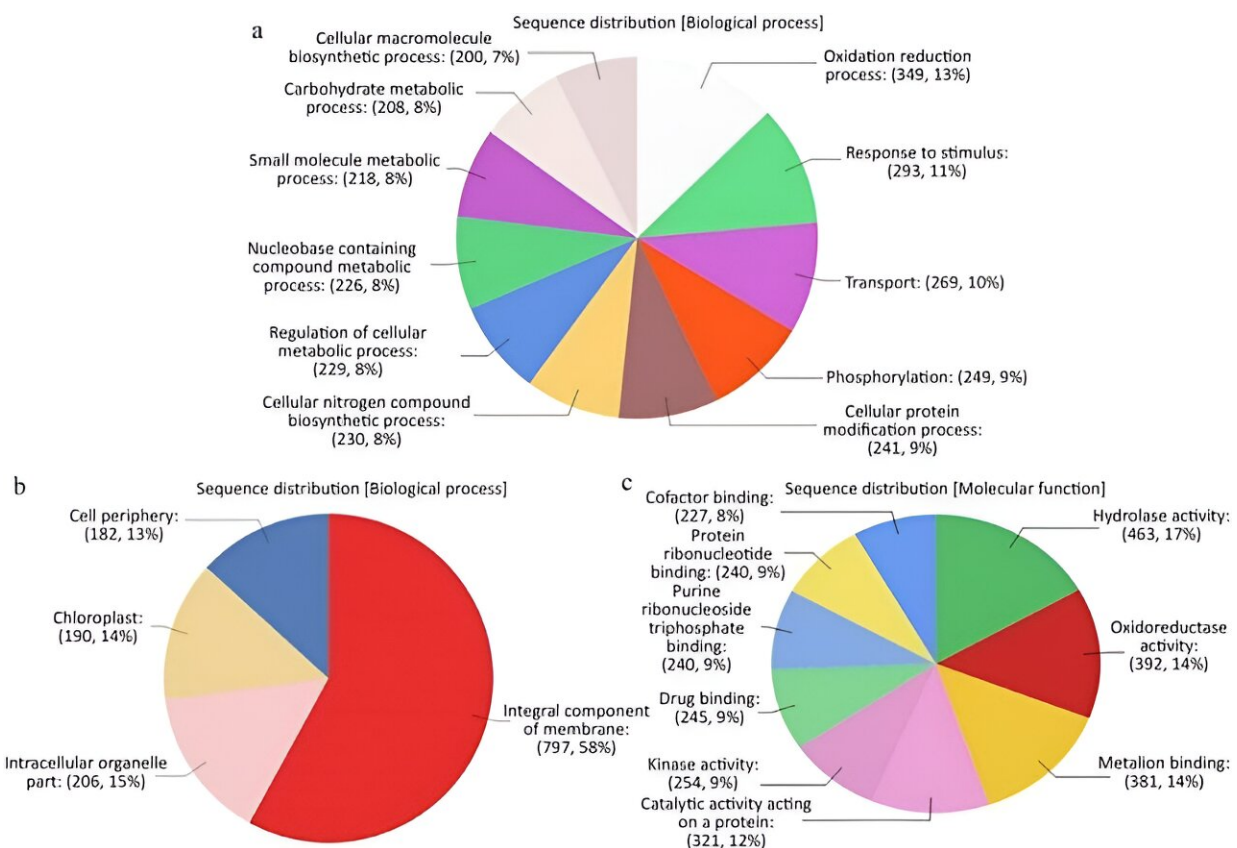


Fig.1 (a) Sequence distribution of DETs among Biological Processes (BP) GO terms. (b) Sequence distribution of DETs among Cellular Components (CC) GO terms. (c) Sequence distribution of DETs among Molecular Functions(MF) GO terms. Credit: *Ornamental Plant Research* (2024). DOI: 10.48130/opr-0024-0006

A research team has meticulously analyzed the transcriptional response of *Impatiens walleriana* to *Plasmopara obducens* infection, revealing between 3,000 and 4,500 differentially expressed transcripts at various stages of the disease.

Through this study, they have constructed a de novo transcriptome assembly that identified key [genes](#) involved in the plant susceptibility, including several stress response genes, receptor-like kinases (RLKs), and resistance genes. This investigation not only enhances our understanding of the molecular interactions between *I. walleriana* and its pathogen, but also provides a fundamental resource for future efforts to engineer disease resistance in this economically significant ornamental crop.

Downy mildews, including *Impatiens* [downy mildew](#) (IDM), pose severe threats to both agronomic and ornamental crops, significantly impacting industries like floriculture. The pathogen, *Plasmopara obducens*, is a recent emergence and has had a major economic impact since it was first detected in cultivated *Impatiens walleriana* in the United States in 2004.

Current research has begun to unravel the genomic basis of the host and pathogen, yet gaps remain in understanding the complete host-pathogen interactions and developing IDM-resistant cultivars.

The study [published in *Ornamental Plant Research*](#) on 27 March 2024, dives into the transcriptome analysis of *I. walleriana* during its infection by *P. obducens*, aiming to pinpoint candidate genes linked to susceptibility. This research is pivotal in guiding future breeding efforts to enhance [resistance](#) against IDM, responding to strong consumer demand for robust *I. walleriana* cultivars.

More information: Stephanie Suarez et al, Transcriptional profiling of *Impatiens walleriana* genes through different stages of downy mildew infection reveals novel genes involved in disease susceptibility, *Ornamental Plant Research* (2024). [DOI: 10.48130/opr-0024-0006](https://doi.org/10.48130/opr-0024-0006)

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