

Peer Review

Review of: "Microarray Profiling of Arabidopsis thaliana Transcriptome: A Genome-Wide Exploration of High Light Stress Responses"

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The study focuses primarily on bioinformatics analysis of publicly available GEO data to draw insights into high-light mediated responses. Following are some of the key concerns with the manuscript which, if considered, can definitely improve the reliability of the findings.

1. The study primarily uses microarray data for gene expression analysis. While microarrays are a valuable tool, they have inherent limitations compared to more modern techniques like RNA-seq.
2. The current study relies heavily on bioinformatics analysis without wet-lab validation, which is the major limitation of the paper to derive any useful inference.
3. The study appears to analyze whole-plant responses, potentially missing localized adaptations to high-light environments that could be revealed through tissue-specific studies.
4. The study appears to focus on a single time point after high-light exposure. This may miss dynamic changes in gene expression over time.

Declarations

Potential competing interests: No potential competing interests to declare.