

Peer Review

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

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In this work, the authors described 143 genes that were differentially expressed in the Control vs Light comparison, and 217 significant genes in the Dark vs Light comparison. Here are my comments:

1- The introduction needs to elaborate on the functional research of light-responsive genes in plant stress resistance.

2- The final paragraph of the Introduction is overly brief and does not clearly define the research gap, the key research objectives, or the significance and potential implications of the findings.

3- The current study is based essentially on bioinformatics analysis without lab experiments, which limits the importance of the work. Here, the authors used microarray data for gene expression analysis, which is an old technique. I would suggest using more recent techniques to identify high light-responsive genes. In addition, the image quality is suboptimal, and the figure styles are inconsistent. Consolidating these results into clear figures would improve clarity and readability.

4- Given that the study found that high light stress upregulates antioxidant genes such as CAT and APX, why were ROS levels in the control and treated samples not measured?

5- The Discussion is somewhat redundant with the results, and it should be more detailed.

6- The manuscript contains several English language errors that require correction. Careful editing is necessary to improve the overall readability and ensure clear, precise communication of the research.

7- Please indicate the exact experimental conditions for treated and non-treated plants.

Declarations

Potential competing interests: No potential competing interests to declare.