

## Peer Review Report

# Review Report on Variability of plant transcriptomic responses under stress acclimation: A review from high throughput studies

Review, Acta Biochim. Pol.

Reviewer: Małgorzata Ryngajło

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### EVALUATION

#### Q 1 Please summarize the main theme of the review.

The review by M. Rurek and M. Smolibowski covers the literature on plant transcriptomic responses to a selection of abiotic and biotic stress conditions across plant species (model, crop, medicinal) gauged by the high-throughput RNA sequencing (RNA-seq) technique. The general transcriptomic response of plants to the stressors is discussed as well as the detailed effect on particular gene families. Common and distinct trends, displayed by plant transcriptomes under stress acclimation, are described. The review distinguishes the literature covering different species, tissues, and the quality and the dosage of a stressor.

#### Q 2 Please highlight the limitations and strengths.

Limitations:

- Poor introduction, not describing the advantages of RNA-seq technology well
- Poor quality of the Figures (especially Fig. 1 and Fig. 2)

Strengths:

- Vast and up-to-date literature covered (114 papers cited (several from 2023 and 2024), 2 book chapters).
- Broad scope of plant species and stressors covered
- A good list of published reviews related to the topic discussed in the introduction
- A good quality of the Supplementary Material (Especially, the extensive Supplementary Table 1).

#### Q 3 Does the review include a balanced, comprehensive and critical view of the research area?

Yes.

### Check List

#### Q 4 Is the English language of sufficient quality?

Yes.

#### Q 5 Is the quality of the figure(s) and/or table(s) satisfactory?

No.

#### Q 6 Does this manuscript refer only to published data? (unpublished or original data is not allowed for this article type)

Yes.

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**Q 7** Does the manuscript cover the topic in an objective and analytical manner

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Yes.

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**Q 8** Does the reference list cover the relevant literature adequately and in an unbiased manner?

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Yes.

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**Q 9** Does the manuscript include recent developments?

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Yes.

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**Q 10** Does the review add new insights to the scholarly literature with respect to previously published reviews?

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Yes.

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**Q 11** Please provide your detailed review report to the editor and authors (including any comments on the Check List)

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The review by M. Rurek and M. Smolibowski covers the literature on plant transcriptomic responses to a selection of abiotic and biotic stress conditions across plant species (model, crop, medicinal) gauged by the high-throughput RNA sequencing (RNA-seq) method.

The coverage of the published literature is vast and includes studies on different plant tissues, and stressors quality and dosage. The cited literature includes 114 papers, of which many are recent (< 5 years from publication date) and several were published in 2023 and 2024.

The manuscript describes first the studies related to abiotic stress, such as: UV radiation and chemical treatments, water deficiency (drought), elevated temperature (heat stress), low temperature (cold, freeze). Next, the following biotic stressors are discussed: fungal infections, bacterial infections, viral and viroid infections. The studies related to each stressor are described in separate paragraphs. Particular focus is given to the functions of differentially expressed genes (DEGs) discovered in each study. Additionally, TFs which appeared in the list of DEGs, are highlighted. Every paragraph ends with a summary of the general trends found in the literature covering a particular stressor.

The final paragraph constitutes of a Discussion which summarizes the entire content, highlights the common trends and gives future perspectives for the field.

This manuscript gives a comprehensive review of the current knowledge of the transcriptomic responses of plants to a variety of stressors. Nevertheless, I find this manuscript very tedious and tiresome to read due to long listings of functional categories overrepresented in each study discussed and the insufficient effort put in finding common trends in the results presented. The Figures included are of a rather poor quality and do not draw the attention of the reader.

Main concerns:

- The introduction: What are the benefits of focusing on the transcriptome? Why not other omes? Please elaborate on this.

- Line 88–91, p. 2 – obvious facts about RNA-seq. Why is it such a good approach to study transcriptomes (strengths/limitations)? Which sequencing platform is the most popular? This has to be discussed in the introduction.
- Line 566, p. 12: “...were detected, including new ones ..” - new with respect to what? This is not clear, please clarify.
- Figure 1 - the quality should be improved (e.g., the image of DNA, mitochondrion)
- Figures 3 and 4 are of poor quality and are, in fact, neither figures nor tables. The content covers a boring list of overrepresented GO functional terms. More effort should be put to improve the attractiveness of these Figures. Eg., the GO terms which repeat in more than one stressor could be highlighted to ease the finding of common trends among the DEGs related to different stressors. The lists could also be sorted in alphabetical order. A venn diagram representing common and distinctive terms could also be considered to be included. Additionally “Onthology” should be replaced with “ontology” in the Figures 3&4 caption.
- Figure 5 is boring and should be replaced with The Supplementary Figure 1.

#### QUALITY ASSESSMENT

<b>Q 12</b>	Quality of generalization and summary	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<b>Q 13</b>	Significance to the field	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<b>Q 14</b>	Interest to a general audience	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<b>Q 15</b>	Quality of writing	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>