

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: Agnieszka Zmienko

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EVALUATION

Q 1 Please summarize the main theme of the review.

In this paper authors attempt to present a wide view of transcriptomic changes in plants in response to various types of stresses (biotic and abiotic), by subsequent description of a substantial number of gene expression studies (mostly RNA-Seq, but also e.g. microarray-based). They took an approach of subsequent presenting a handful of studies related to a given stress, with a short summary for each group.

Q 2 Please highlight the limitations and strengths.

In my opinion, a wide range of the papers and stresses addressed in this review is the biggest strength of this paper. However, it is also a limitation. The similarities and differences among different stresses or different studies addressing a given type of stress are not clearly stated. Some more focus on comparing the studies and generalizing the picture for each stress would be good in this case.

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

The reference section is very rich but the presentation of the studies is rather descriptive not analytic.

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 (unpublished or original data is not allowed for this article type)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.

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

No answer given.

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

Yes.

Q 9 Does the manuscript include recent developments?

No.

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

No.

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

The aim of the authors is very ambitious – to provide an overview of the transcriptomic responses to a wide range of stressors. My impression is that this range is a bit too wide to cover each stress thoroughly and get some new insight. This type of overview calls for an extensive meta-analysis of the transcriptomic data, however, there is no place for such in a review paper.

Here, each type of stress is presented separately from the other ones and there are no links or comparisons between them. Authors managed very well to demonstrate that there is dynamics and variability of the stress responses at the gene expression level. The nature of this dynamics, its causes and consequences are however not clear to me after reading the paper.

For each type of stress, the authors selected and described a handful of studies, including both original experiments and some meta-analyses. In my opinion, the sections devoted to specific stresses are quite descriptive. Authors chose to present the studies one by one and only provide some brief summary at the end of each section. I think that it would be much more helpful to order each section by focusing on specific metabolic pathways (e.g. hormone signalling) induced or repressed in a given stress, to get the generalized view of the transcriptomic responses for a given stress, independent of the plant species or the study details. However, I do not expect nor request that the authors meet my point of view, since it would require rewriting the sections. In its current form the paper may certainly serve as a comprehensive guide of relevant studies regarding a given stress and this is its main strength. However, I would recommend careful reviewing or maybe extending the Supplementary Table listing the studies mentioned in the paper. For example, University of Idaho (line 27) is hardly a informative description of the sequencing platform. Also some more details about the treatments in this table (e.g. times, exact temperature etc) might be a good addition.

I also got an impression that the impact of the technical side of the experiments has been somehow neglected. I would advice some more critical elaboration on the possibilities and the limitations of the current study in drawing the generalized picture based on such a diversity of plants and studies, without any meta- analysis.

Also it seems very unusual to me to finalize the review paper with the discussion section. I would rather recommend restructuring it and renaming into 1-2 thematic sections, e.g. summarizing the differences and similarities of the stress effects on signalling, photosynthesis, transcription factors (are they identical, different, do they target some common pathways and why it may be so?) and an outlook section.

I would recommend deleting Fig. 2. It does not include any relevant information. The authors generally assume that the methodology of the gene expression studies is known. The figure also refers only to RNA-Seq studies, while the review presents various types of studies, eg. microarrays, too.

Fig. 3 is important but to me it is not very useful in its current form. Actually, it is more like a table right now. Again, it would be more informative if it stressed similarities and/or uniqueness among different types of stresses, in any form. Reducing the amount of text in this Fig. would be very welcome.

Finally, I feel that in the introductory section, authors are very critical to previous reviews on the subject (for example for being too fragmentary, Line 101–102). I would recommend some more balanced opinion.

Obviously, there are different approaches and ideas to present this topic. I believe there is no single review, including the paper I am reviewing, that can comprehensively and entirely cover it. It is simply too broad.

Minor:

I did not find the extension of DEG shortcut in the first mentioning in the main text

Line 87. Is it proper to say that plants ADAPT to stress at the transcription level? I would rather say they RESPOND/REACT to it at different levels, including transcriptomic. Adaptation may be quite rapid but it is a process not a direct response to stressing factor.

QUALITY ASSESSMENT

Q 12	Quality of generalization and summary	<div><div></div><div></div><div></div><div></div><div></div></div>
Q 13	Significance to the field	<div><div></div><div></div><div></div><div></div><div></div></div>
Q 14	Interest to a general audience	<div><div></div><div></div><div></div><div></div><div></div></div>
Q 15	Quality of writing	<div><div></div><div></div><div></div><div></div><div></div></div>