

# Review of: "Regulatory dynamics distinguishing desiccation tolerance strategies within resurrection grasses"

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Using ATACseq and RNAseq, the authors investigated the chromatin architecture and gene expression under desiccation stress in two desiccation-tolerant grasses. The study is very interesting and could facilitate our understanding of the complex regulatory dynamics of desiccation tolerance in plants.

One interesting finding (to me at least) is that the authors found that the desiccated samples had higher FRiP than the controls, while the desiccated samples had fewer open chromatin regions (lines 148-151). The authors provided two possible explanations. One is the chromatin of the desiccated samples is highly condensed and compacted, which has been well documented in desiccated seeds but not in desiccated vegetative tissues. It would be good if the authors could confirm this experimentally by a simple nuclear staining and microscopic observation. The 2nd hypothesis is that the desiccated cells are 'synchronized' for their gene expression. While this makes good sense, a potential problem of this hypothesis is that the 'synchronized' expression could make these genes appeared to be 'up-regulated'. This could mess up the differential expression analysis.

Minor comments:

1. The relative humidity of the growth chamber could be an important factor to desiccation process, or desiccation tolerance response. The authors should provide this information in the M&M section.
2. Legend for Figure 1 - in Line 702, the letter "(b)" should be "(d)".
3. Figure 2. What is the unit for "Avg. Chromatin openness"?
4. What is the difference between "open (chromatin) regions" (line 150) and "accessible chromatin regions" (line 152)?
5. Lines 189-191: "Whereas there were only 424 and 1,307 cases of higher expression in desiccation with more open ACRs in well-watered or vise-versa." I have a hard time understanding this sentence. Please try to rephrase.