Review of: "Time-course transcriptome and WGCNA analysis revealed the drought response mechanism of two sunflower inbred lines"

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This research was performed by Inner Mongolia Agricultural University, which reveals to a certain extent the changes of molecular mechanism of sunflower under drought stress environment in relation to the time of stress, which is a good guide for the next search of molecular pathways of drought tolerance response in sunflower.

However, several problems still exist:

1. The similarity of each biological replicate was analyzed using principal component analysis it can be seen that the images show that the sum of PC1 and PC2 does not exceed 90% in Fig 2. This requires a certain amount of explanation.
2. In BP GO term enrichment analysis (Fig. 4), somatic embryogenesis was a common GO term over-presented in both up-regulated DEGs of DS and DT at day 7, however, the GO term does not present in the results of GO enrichment analysis of all identified up-regulated DEGs shown in supplemental figure 2. It is inconsistent with this two parts.

The enrichment of blue4 module in WGCNA analysis revealed a significant correlation between glycerol metabolism and drought stress in sunflower, which has important implications for oil production in sunflower, and this aspect may be the focus of the next research.