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The manuscript by Feng et al. describes the identification and analysis of *callose synthase* (*CalS*) genes in the 4 cotton genomes. They characterized 27, 28, 16 and 15 CalS from *G. hirsutum*, *G. barbadense*, *G.raimondii* and *G. arboretum*, respectively, by BLAST search the cotton genome. Phylogenetic analysis of these *CalS* genes in combination of those from Arabidopsis revealed 5 clades with distinct gene structures. Selection analysis indicate that these CalS proteins have undergone purify selection during cotton evolution. Further expression analysis and cis element annotation enable the authors to connect the expression CalS genes with hormonal and abiotic stress responses.

The manuscript is generally well-written and contains certain amount of work. The results were clearly described and presented.

I have a few minor points to improve the manuscript:

1. Line 14, “Callose synthase” describe a gene and should be italicised.

2. Line 23 and elsewhere in the MS, change *GHCalSs* into *GhCalSs*.

3. Line 48-50, please be aware the space between the parentheses and the text.

4. Line 59, change “significant” to “important”.

5. Line 59-66, I found myself had a problem in seeing the key question or aim of this study from this paragraph. I would suggest the authors to re-phrase this paragraph.

6. Line 67, “donors” to “genome donors”

7. Line 90, please explain why “incomplete sequences were deleted”

8. Line 110, please define the promote more accurately, “upstream the CalS gene is obscure”.

9. Line 120, in the section of “RNA isolation and qRT-PCR analysis”, please include all the details of how the experiments were conducted, for example, how much RNAs were used as templet for reverse transcription, were the specificity of qRT-PCR primers verified by PCR-Sequencing and Standard Culve, as such, the authors should be aware the transparency of the experiments.

10. Line 177, “chromosomes” to “chromosome”

11. Line 185, “upper and lower ends..” to “upper and lower arms..”

12. Line 207, I appreciated the authors’ efforts in mining the cis-elements in the regulatory regions of all the CalS genes. Nonetheless, a control gene/genes with related function should be set up for comparison.

13. Line 220-221, all these CalS gens at best can be categorized as “abiotic/hormonal responsive” genes based on the presence of corresponding cis-elements in the promoters but rather “abiotic/hormonal signaling”.

14. Line 224, “researches” into “studies”.

15. Line 221-222, the last sentence of this paragraph makes no sense from the data presented, I would suggest to delete it.

16. Line 231, “the above hypothesis”, which hypothesis?

17. Line 242-247, the information of this paragraph is somehow misleading, please re-phrase.

18. Line 255, “materials” into “samples”

19. Line 260, “part” into “role”

20. Line 262-263 and elsewhere in the text and figure legend, latin names should be italicised.

21. Line 280, “distributed” into “identified”

22. Line 286, “short-day induced ABA increased” into “short-day induced ABA biosynthesis/signaling”