General Comments from Authors:
The authors thank both the reviewers and the editor. Reviewers had analyzed our manuscript very deeply and had provided important and crucial points that helped in making this paper improved and statistically correct. Such in-depth review would have taken a reasonable amount of time and thus we are highly grateful to the reviewers for helping us improve our paper.

Response to Reviewer 1 Comments

Point 1: Line 17. “GA” suddenly appears. Please explain this acronym there as “GA (gibberellin acid)”.
Response 1: In the abstract section, line 17, ‘GA 3β-hydroxylase’ has been replaced by ‘gibberellin 3β-hydroxylase (GA 3β-hydroxylase)’

Point 2: Line 166. “...biosynthetic pathway that activated by...” Please delete “that”.
Response 2: The word ‘that’ has been deleted

Point 3: Line 167. Please cite one or more references after “...in a cal-1 and ap1-1 background”.
Response 3: In line, “…in a cal-1 and ap1-1 background” has been supported by the following references (Gomez-Mena et al., 2005; Wellmer et al., 2006).

NB: the sentence “……gibberellic acid biosynthetic pathway activated by AGAMOUS in a cal-1 and ap1-1 background” was the blast result from TAIR https://www.arabidopsis.org/servlets/TairObject?id=136522 &type =locus not from previous works.
Point 4: Line 174 and Materials and Methods section. There is no explanation and references on “UniProt” and “SMART”. Authors should add them.

Response 4: To describe Uniprot and SMART in line 174, we added a new subheading 4.5 entitled ‘Protein Domain, Phylogenetic Analysis and Verification of the Short Internode using an InDel Marker’ in materials and methods section. Therefore, we added the following sentence (line 409-412):

The protein sequence alignment was performed using Uniprot (https://www.uniprot.org/) and SMART (https://blast.ncbi.nlm.nih.gov/smartblast/ databases to illustrate the domain structure. Phylogenetic analysis was performed using MEGA 7 software with a bootstrap method and 1000 replications (Kumar et al., 2016).


Point 5: Line 176. Candidate gene, Cla015407, contains 208bp deletion. Does this deletion lose a hydroxylase domain? Illustration of domain structure of this gene may aid in understanding this mutation.

Response 5: Our candidate gene (Cla015407) encodes GA 3β-hydroxylase enzyme contains 13bp deletion; however, the candidate gene (Cla015407) shared 57.10% sequence similarity with Arabidopsis AT1G15550 and the AT1G15550 gene contains 208bp deletion. Therefore, the 208bp deletion is in the homologous gene not in our candidate Cla015407 gene. The protein domain analysis result has been added under the Results section, subheading ‘Protein Domain, Phylogenetic Analysis and Verification of the Short Internode using an InDel Marker’. Therefore, the following domain structure analysis result has been added in lines 179-184:

Furthermore, we generate the protein domain structure for Cla015407 using the online Pfam database (http://pfam.xfam.org/). The sequence alignment using UniProt and SMART indicated that Cla015407 shared 57.10% sequence identity with AT1G15550 in Arabidopsis thaliana, which contains two domains:
DIOX_N and 2OG-Fell_Oxy (Williams et al., 1998). The deletion in the CDS region of short internode watermelon caused a premature stop codon, producing a truncated protein with only 173 amino acid residues, losing the 2OG-Fell_Oxy domain.

Moreover, the title for Figure 4 `Phylogenetic tree for the Cla015407. The tree was constructed using MEGA 7 with Bootstrap values calculated from 1000 replicates. The Cla015407 is circled in red` has been modified as: `Figure 4. The phylogenetic analysis and conserved domains of the candidate gene. (A) Phylogenetic tree for the Cla015407. The tree was constructed using MEGA 7 with Bootstrap values calculated from 1000 replicates. The Cla015407 is circled in red. (B) The conserved domain of Cla015407 gene, which was analyzed by online Pfam database.`

173 amino acid residues


Point 6: Line 237. There is no description on analysis using InDel marker in Materials and Methods section. Authors should add it.

Response 6: Under the newly added subheading 4.5 entitled `Protein Domain, Phylogenetic Analysis and Verification of the Short Internode using an InDel Marker`, line 412-414, the sentence `Moreover, to validate the causal mutation, an InDel marker was developed conferring to the 13bp sequence of Cla015407 and 135 F2 population including the recombinant individuals were selected to check the polymorphism of the marker has been added`.

Point 7: Line 258. Please rephrase “have” with “has”.

Response 7: The word 'have' has been replaced with 'has'

Point 8: Line 276. Please show “Li et al. 2011” by numbering.

Response 8: Since Li et al. 2011 does not change to [ ] method of citation using endnote we have been deleted it and replaced with [63, 64]

Point 9: Throughout the text, “many” reference numbers may be unsuitable. Please carefully check and correct references. For example, No. 55 cited in line 275 is a paper regarding wheat but not watermelon.
Response 9:
Extensive reference citation numbers and references checking has been made. Since we include additional references the order of all the references in the whole manuscript and references has been rearranged.

References