**Editor's Comments:**

Your manuscript has been reviewed by two experts. Both of the reviewers were supportive on the significance of your findings. However, both of the reviewers also raised several major concerns on your manuscript. Especially, the manuscript has problems of redundancy and lack of describing implication of your findings. I recommend English editing, major revision of your manuscript before resubmit for further round of review processes.

**Author’s response:** Thank you for giving me the opportunity to revise my article entitled “Genome-wide identification and characterization of WRKY gene family in *Salix suchowensis*”. We greatly appreciate the concerns and suggestions provided by the editor and two reviewers, and have tried our best to make our manuscript more clearly by careful correction. Additionally, we have exerted extensive efforts to improve the language, and also asked help from a professional copyeditor to polish the writings. We hope that the language in this revision would be considered as significantly improved and the revised text now is suitable for publication in PeerJ. The detailed replies to each reviewer will be outlined one by one as follows.

**Response to reviewer 1：**

Major concerns

1. The manuscript reads like a list of results, so there needs to be more discussion, and implication of the analysis. Much of discussion has redundancy and it feels like a review of other species WRKY rather than discussion of willow WRKY.

**Author’s response:** Thanks for this comment. According to the reviewer’s suggestions, we have removed lots of redundancies in the ‘Discussion’ section, and added some implications of the WRKY genes in this section, please see lines 534-537, 577-579, 608-611, etc. Additionally, we have added a ‘Conclusion’ section to show the key results in our study, please see lines 681-693.

Minor concerns

1. Page 1, line 12; there are WRKY genes in the lineage of non-plant eukaryotes, as the authors mentioned.

**Author’s response:** We have made the corrections, please see line 15.

2. Page 2, line 21; reference of cotton WRKY is missing (Ref32).

**Author’s response:** We have added the reference in lines 50-52.

3. Page 3, line17-18; references are outdated.

**Author’s response:** Thanks for this comment, and we have updated the references with some new publications, please see lines 83-85.

4. Page 4, line6-11; the order of the sentences should be changed.

**Author’s response:** We have reordered the sentences with a more logical order, please see lines 112-119.

5. Page 9, line3-5; the list of excluded gene is not needed.

**Author’s response:** We have deleted the list of excluded genes, please see lines 281-283.

6. Page 13, line16-19; interesting point should be found in SsWRKY, not OsWRKY in this manuscript.

**Author’s response:** This is a good suggestion,we have made the changes accordingly, please see line 408.

7. Page 15, line8; references are missing.

**Author’s response:** We have added the references in lines 453-454.

8. It might be better if the authors mark the WRKY domain region at figure 8 and table 2.

**Author’s response:** Thanks for this suggestion. We have marked the WRKY domain region at Supplemental Figure S2 and Table S2 (former called figure 8 and table 2).

9. Page 18, line2; “the induced plant TFs” is too assertive.

**Author’s response:** We have made the changes in line 526.

10. The manuscript contains many minor errors in grammar. For example,

A. Page 3, line 1; “cis” should be italic.

**Author’s response:** We have corrected the error in line 60.

B. Page 4, line 25; replace “higher” to “high”

**Author’s response:** The word “higher” has been removed, and we have rewritten this section to describe the importance of willow WRKY genes, please see lines 140-154.

C. Page 7, line4; “e-value < 1e-20” or “e-value cutoff = 1e-20

**Author’s response:** We have corrected the error in line 217.

D. Page 9 line 26; replace “list” to “listed”

**Author’s response:** We have corrected the error in line 305.

E. Page 12, line 1; “IIIb” does not exist.

**Author’s response:** We have corrected the error in line 366.

11. References should be confirmed if they are appropriate at the sentence. For example,

A. Page 3, line 22; Ref3.

**Author’s response:** We have corrected the inappropriate reference, please see line 89.

B. Page 4, line 7; Ref36

**Author’s response:** We have corrected the inappropriate reference, please see line 117.

C. Page 4, line10; Ref37

**Author’s response:** We have corrected the inappropriate reference, please see line 114.

D. Page 4, line 17; Ref38

**Author’s response:** After careful checking, this reference is inappropriate there, so we have removed it, please see line 124.

E. Page 10, line18; Ref58

**Author’s response:** We have corrected the inappropriate reference, please see line 325.

F. Page 14, line 25; Ref30

**Author’s response:** We have corrected the inappropriate reference, please see line 444.

Experimental design

1. The figures have not been organized. There are too many main figures. I think Figure 3 and Figure 4 should be integrated (a phylogenetic tree using WRKY domains from willow, Arabidopsis and poplar). In addition, I suggest use of different colors in different species instead of different groups (like figure 5). Figure 5,6,7,8 and table 2 can be represented as supplementary data.

**Author’s response:** This is also a major concern of another reviewer. We tried to integrate Figure 3 and Figure 4 into a single tree, but gene names were too low to see after integration. Therefore, we moved Figure 4 to Supplemental Figure S1 based on another reviewer’s suggestion. Additionally, we have moved the former called Figure 5, 6, 8 and Table 2 to the Supplementary files. Figure 7 shows the important exon-intron structures of SsWRKY proteins, we think it can be represented as a main figure in our article.

2. Figure 2 has to include information of physical cluster the authors mentioned at the page 10, line 18-27. It might be better if the authors use different colors for different groups. In addition, the author has to address the method for defining a cluster.

**Author’s response:** According to the reviewer’s suggestions, we have added the physical clusters to Figure 2, and used different colors to describe different groups. Additionally, we have addressed the method for defining a cluster in lines 242-244.

3. There is no reason to show Ka/Ks ratio as a figure, not a table. I recommend to make this data into table with the gene names of the pairs and ka/ks ratio. This can be represented as supplementary data.

**Author’s response:** We have removed the figure of Ka/Ks ratio, and made this data into a table named Supplemental Table S1.

4. The authors should address how define TDs SDs at M&M section.

**Author’s response:** We have addressed the definition of TDs and SDs at Materials and Methods, please see lines 245-253.

Comments for the author

The authors have used published genome sequence information from willow to mine for WRKY genes. They performed classification and phylogenetic analysis with other species. It has a lot of information, but some major and minor revisions are needed before the manuscript is finally accepted. Also, I strongly recommend the English editing.

**Author’s response:** After careful checking, we have made these major and minor revisions according to the review’s suggestions. We have exerted extensive efforts to improve the language, and also asked help from a professional copyeditor to polish the writings. Wish the revised text now is suitable for publication in PeerJ.

**Response to reviewer Seon-In Yeom：**

Basic reporting

WRKY proteins as plant specific TF are a large family of transcription factors, participating in diverse physiological and developmental roles as well as defense response against biotic and abiotic stresses. The authors report the genome-based survey of WRKY gene family in *Salix suchowensis*. They identified 85 WRKY genes in the willow genome and showed that the distribution of WRKY genes on chromosomes, phylogenetic analysis, classification of WRKY genes, structural feature, and expression analyses in various tissues. I believe that this manuscript is very useful and important for further analysis of WRKY’s function and application in woody plants. But there are some problems in this manuscript. It is necessary to correct/edit some point and describe more details to clear up. It also need to improve the quality of tables or figures with suggesting that some could move into supplementary section to get rid of redundancy.

**Author’s response:** We tried our best to solve all the problems in our manuscript based on the reviewer’s suggestions, and wish the revision would be considered as significantly improved. The detailed replies will be outlined as follows.

Major point

There are informatics figures and tables, which are no doubt to be useful for audience, but some are a kind of redundancy. How about some tables move to supple or combine some figures? For instance, table 2 and table 3 could move to supplementary section.

**Author’s response:** Thanks for these suggestions,we have moved table 2 and table 3 to supplemental Table S2 and S5, respectively.

Fig 3 and Fig. 4 could be combined (one phylogenetic analysis is enough) or Fig. 4 could move to supplementary section.

**Author’s response:** We tried to integrate Fig.3 and Fig. 4 into a single tree, but gene names were too low to see after integration. Therefore, we moved Fig. 4 to Supplemental Figure S1.

Fig 2 quality should be improved. Their resolution of texts like gene names is too low to see it and it needs to indicate the region of gene clusters, which were explained in text (page 10, third paragraph).

**Author’s response:** This is also a major concern of another reviewer. We have increased the font size of gene names and added the physical clusters to Figure 2. Additionally, we used different colors to describe different groups in order to get higher resolution.

In Fig. 7, SsWRKY73 and SsWRKY79 were indicated as duplication gene pair, but there are different clades in phylogenetic tree and showing different gene feature. Please explain it, just mistake?

**Author’s response:** It is just a mistake, and we have corrected it in Figure4.

Fig. 8 conserved Motifs of SsWRKY and table 2 could be depicted in supplementary section. The style and format of Fig. 8, especially, are not suitable for main figure as current state.

**Author’s response:** According to the reviewer’s suggestions, we have marked the conserved Motifs in Supplemental Figure S3 and Supplemental Table S2.

Page 6 line 7, “http://bio.njfu.edu.cn/willow\_chromosome/BuildGff3\_Chr.pl” was not accessible through the Internet. What happened?

**Author’s response:** Our website might be under maintenance at that time, and now it is accessible.

Page 13 line 25-26 and Fig. 6, in table1 and Fig 5, just I founded small No. of WRKY III genes, I can not fid the value ’21 pairs’ WRKY III genes and need to describe values and all pairs used to estimation of Ka/Ks as supplementary table or sole table.

**Author’s response:** In order to clear describe the Ka/Ks ratio of WRKY III genes, we made this data into a table named Supplemental Table S1 and removed the figure of Ka/Ks ratio.

Page 15 line 11~21, please indicate fig or table for 33 homologus gene pairs, I cannot find the value of gene pairs.

**Author’s response:** According to this suggestion, we have made a table named Supplemental Table S3 in Supplementary section to show the 33 homologus gene pairs.

Minor point

Page 4 line 12, the sentence needs to be changed more clearly

**Author’s response:** We have made the changes in lines 119-122.

Page 4, line 22, need to reference about their ecological and economic value and describe importance and the reason of genome wide screening of WRKY genes

**Author’s response:** Thanks for this great suggestion. We have rewritten the statements of their ecological and economic values of WRKY genes, please see lines 140-154 in ‘Introduction’.

Page 4 line 21, E-value = 1e-3 means their cut-off? need to explain more clearly

**Author’s response:** This is an error, andwe have corrected it, please see line 180.

Page 7, line 5, cut-off value e-value e-20 was selected, is there any reason or reference?

**Author’s response:** We have added two references to support the e-value in line 217.

Page 7 line 9, resistance for what? Disease or variable biotic?

**Author’s response:** The WRKY III genes have a prominent impact on disease and drought resistance.We have made the changes, please see lines 222-223.

Page 8 line 8, Blastp? BLASTP, and when describing cut-off please use the same term through manuscript

**Author’s response:** We have changed all ‘Blastp’ to ‘BLASTP’, please see lines 180, 248 and 279.

Page 8 line 14, RNA-Seq reads were generated in this experiment? or used them from previous study? Please clear up this

**Author’s response:** The RNA-Seq data were generated from a previous study, but the article has not been published, so we cannot cite it. Please see line 267.

Page 9 line 1 Blastp? BLASTP please use the same term through manuscript

**Author’s response:** We have changed all ‘Blastp’ to ‘BLASTP’, please see lines 180, 248 and 279.

Page 11 lines 20-25, after explain about Fig. 4, How about depict these?

**Author’s response:** Thanks for this suggestion. We have depicted them in Figure 3 and Supplemental Figure S1.