**Sent:** Saturday, December 8, 2018 2:15 AM  
**To:** Dan Kliebenstein  
**Cc:** [akessler@aspb.org](mailto:akessler@aspb.org); [rinnes@indiana.edu](mailto:rinnes@indiana.edu)  
**Subject:** TPC2018-RA-00857D: Decision Letter

03-Dec-2018   
  
Dear Dr. Daniel Kliebenstein:   
  
We have received reviews of your manuscript entitled "Interactions of tomato and Botrytis genetic diversity: Parsing the contributions of host differentiation, domestication and pathogen variation." On the basis of the advice received, the board of reviewing editors would like to accept your manuscript for publication in The Plant Cell. Reviewer 1 has provided a few minor suggestions for improvement to the manuscript, but I leave it to your discretion as to whether you would like to address these in your final submission. We will not send the manuscript out for review again.   
  
Please use freeze pane options in the supplemental tables.   
  
In future, you should import the figures into a word file with the legend rather than importing text into an image file. This may help with file size.  
  
-Please see the attached file for comments on the figures, which you can correct in the revision. You can download the attachment, open in acrobat and view in comment mode. please apply the comments to all figures in the paper.  
  
Please highlight all changes and include a detailed annotation to changes to the text, with line numbers, and noting your responses to the comments.   
  
To submit your revised manuscript, click:   
  
<https://tpc.msubmit.net/cgi-bin/main.plex?el=A4Is6FkJ6A2BNM1I3A9ftdiHl54VFMtizCfR3D79jiAZ>   
  
Please note the following:   
  
-Supplemental materials should be restricted to large datasets and tables, presentation of replicates, and validation of reagents, methods, or genotypes. Any data that are used to support claims must be in the main manuscript. Supplemental figure legends must indicate what figure in the main manuscript is supported by the supplemental data presented.   
  
-Sampling methods and nature of "biological replicates" should be described precisely (i.e. different plants, parts of plants, pooled tissue, independent pools of tissue, sampled at different times, etc), along with a clear description of and rationale for any statistical analyses conducted. The reader should know exactly what was sampled; what forms the basis of the calculation of any means and statistical parameters reported. This is also necessary to ensure that proper statistical analysis was conducted.   
  
If you have any questions about the revision submission procedures, please contact Annette Kessler at [akessler@aspb.org](mailto:akessler@aspb.org). If you cannot return the revised manuscript within 30 days, please let us know. Otherwise, we will assume that you have elected not to revise the manuscript and withdraw it.   
  
Thank you very much for the privilege of reviewing this work. I look forward to receiving the next version.   
  
On behalf of the editorial board,   
  
Roger Innes, Board of Reviewing Editors   
Roger Innes, Senior Editor   
Sabeeha Merchant, Editor-in-Chief   
  
The Plant Cell   
  
  
Reviewer #1 (Comments for the Author):   
  
Review of Soltis et al. "Interactions of tomato and Botrytis genetic diversity: Parsing the contributions of host differentiation, domestication and pathogen variation"   
  
This is the second time I review this and I find that most of my comments on the previous version has been addressed. I find the analyses well conducted and the results are clearly stated. I only have a few minor comments the authors might want to consider.   
  
One thing you might want to consider is to use the results from the GWAS to calculate your ability to predict pathogen virulence based on genetic data alone. I would be interesting to see how well you can predict pathogen phenotype across different host genotypes. Since you have the ridge regression effect size estimates available, it should not be hard to use those to calculate "polygenic scores" for the pathogen/host combinations. I think it could be a good way to summarize how much of the variation in pathogen virulence you can explain across different hosts from genetic data alone.   
  
In the mixed model analyses, "Experiment" is included as a random factor. As far as I can tell from the text, there were only two independent experiments run, so you are essentially estimating a variance component from two data points. It is generally inadvisable to estimate variance components from less than 5 groups/levels (Gelman A, J. H. 2007. Data Analysis Using Regression and Hierarchical/Multilevel Models. New York: Cambridge University Press). Is this case, you don't even gain any statistical power from including "Experiment" as a random factors since you would anyway only expend one degree of freedom when treating "Experiment" as a fixed effect. It will likely not affect your results, but I would suggest treating "Experiment" as fixed in your analyses.   
  
Figure 6b: What are the numbers in the squares representing? Please state this in the figure legend.   
  
The first sentence in the legend for Figure 7 is rather awkward "..... and using calculated Sensitivity." I would suggest that you reformulate this sentence.   
  
  
  
  
Reviewer #2 (Comments for the Author):   
  
The authors have addressed my previous concerns and suggestions in a very careful and thorough manner.