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Dear Dr. Innes and Dr. Merchant,

We have included the edited submission of our manuscript entitled “Interactions of tomato and Botrytis genetic diversity: Parsing the contributions of host differentiation, domestication and pathogen variation” for inclusion into The Plant Cell.

We made minor changes to the figure axes and figure legends as requested by the reviewers and responded to all comments. Please see our detailed annotated changes below and highlighted in the main text and figure document.

Sincerely,

A handwritten signature in cursive script that reads "Dan Kliebenstein".

Daniel J Kliebenstein
Professor of Plant Genomics
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Annotation of changes:

Reviewer 1 asked that we use our GWAS data to calculate our ability to predict virulence from genetic data alone. We agree that this could be an interesting addition but feel that this would extend the complexity of what is already a somewhat circuitous story. We will certainly consider adding this type of analysis to future work related to this research project.

Reviewer 1 asked us to consider using “experiment” as a fixed rather than random effect in our mixed model analysis. We agree with the reviewer’s conclusion that this change would not affect our results. We previously tested model parameters including a fixed effect of “experiment”, and our conclusions as to the significance of terms and partitioning of variance were unchanged. As such, we retain the original model with “experiment” as a random effect.

Figure 1. We corrected “0.0” to “0” throughout the figure y axes.

Figure 3. We corrected “0.0” to “0” on the figure y-axis.

Figure 4. We corrected “0.000” to “0” on the figure a y-axis.

Figure 6. We corrected “0.000” to “0” on the figure a y-axis. We added a sentence to explain the numbers within each square as requested: “The number within each square represents the D’ value for each pairwise comparison if <1.” (Line 821)

Figure 7. We corrected “0e+00” to “0” on the figure a y-axis. We converted the Figure 7a y-axis from cm² to mm² to make easier visual comparison with Figure 6a and Figure 4a. We revised the first sentence of the legend to “Domestication sensitivity of each isolate was estimated as the difference between the average virulence on the wild and domesticated tomato germplasm. This was then utilized for GWA mapping by bigRR.” (Line 825)

Line 949, we updated the citation for Fordyce et al. 2018

Supplemental Table 1. We corrected scientific notation to “n x 10^p” format.

Supplemental Figure 1. We corrected “0e+00” to “0” on the figure a y-axis. We corrected “0.0” to “0” on the figure x-axis. We corrected scientific notation to “n x 10^p” format. We added to the figure legend to indicate that “This is supportive background information on the SNP variation used to calculate Figure 4.”.

Supplemental Figure 2. We removed the figure name from the plot and increased the font size of the “cluster dendrogram” label. The font sizes of the individual isolate names are small, but not intended to be readable; we only intend for the reader to focus on the clustering of these branches.

Supplemental Figure 4. We rescaled the figure to improve visual consistency in font size with previous figures. We corrected “0.0” to “0” on the figure y-axis. In the figure legend, we corrected scientific notation to “n x 10^p” format. We added to the figure legend to indicate that “This supports the mild domestication pattern observed in Figure 3, and the pairwise domestication effect of Table 2.”.