

Population structure and phenotypic variation of *Sclerotinia sclerotiorum* from dry bean in the United States by Kamvar et al. utilized microsatellite loci to answer number of interesting questions including evaluating phenotypic and genetic diversity of *S. sclerotiorum* in the nurseries (here referred as natural populations since no control was used to limit disease spread) using regional differences and across different time intervals (span of nine years). In addition, the authors investigated correlation between mycelial compatibility groups and multilocus haplotypes among these populations. Introduction is a bit short and I would suggest expanding few sections (please see specific comments below). Materials and methods are precise and well written and I really appreciated data availability, including all sorts of analyses, which was refreshing. I also like the acknowledgment of shortcomings of the analyses (compound microsats example), which can be challenging to work with. Results were explained well with few exceptions that need some clarification. Overall, well written manuscript with interesting and relevant results for nursery producers/growers. As such, I recommend it for publication with minor revisions.

Specific comments:

1. Please add scientific name to dry bean in your title. This is to avoid confusion for non-U.S. scientists.
2. In your abstract, add 11 U.S.A states, instead of 11 states only.

Line 31 – please provide citation(s) to support this statement.

Line 44 – what are the standard protocols? Citation of existing protocol would be helpful.

I would expand introduction a bit to describe the symptoms in greater details, maybe even provide some information regarding economic damage (if available) to nursery production. I was wondering what cultivars previous studies focused on – the authors provided 3 cultivars at the end of introduction. Maybe adding another paragraph on differences among cultivars – they chose 3 with different levels of resistance but how was that selected (assuming some preliminary data)? For someone not familiar with the host, I would like to have more details on both host and pathogen.

Lines 58-67 – since mixed results were shown in other studies using microsats, it would be helpful have a specific question addressed in this study that will untangle this issue (maybe stated at the end of this paragraph).

Line 70 – put states/countries in alphabetical order.

Line 80 – I would eliminate word hope – often times avoided in scientific/grant writing. Use stronger words such as determine, investigate, evaluate and so on.

Line 84 – how many isolates were already published? Please provide the number. This was provided later in line 103 – I would just move it at the beginning so the reader doesn't have to search for this information.

Line 105-112 – If there is an image to provide for SOM, that would be really nice visualize and to demonstrate the lack of compatibility.

Lines 141-142 – I really like this concept of reproducibility and data availability. I applaud authors for putting all the analyses out there for anyone reading this paper to see. I think it is fantastic idea and I really appreciate that.

Lines 178-184 – What exactly was measured as a result of aggressiveness? Please clarify that.

Line 240 – put states/country in alphabetical order. Also, Table S1 in the PDF is not linking to S1 table.

Line 239-243 – Which dataset is being used here – 11 SRRs or 16 (that should be cleared moving forward). This was well explained in M&M section but please reiterate what method is being used in subsequent analyses. After getting to Table 1 that is clear but please specify in the text as well. For table 1, I would prefer to what repeat motif was used instead of di or tri only. However, that is my personal preference and slightly better visual presentation.

Figure 1 A is very hard to read and bars as small - please adjust y axes to reflect that. Any chance of having some colors since this is very hard to differentiate. You've done that for Fig S1 – so similar is suggested here.

Figure 1B – again, it is a bit too small to see, maybe getting a bit larger images would help.

For S1 – dotted nodes are very hard to see. I'd suggest something easier to see (maybe bolding or using different color).

Line 247 – please indicate what figure was that in SOM. Currently, that curve is not included.

Line 249 – I would rephrase we were left with 318 isolates. It is too colloquial. Maybe *after clone correction, a total of 48 individuals were removed from dataset, resulting in 318 isolates that were used in subsequent analyses.*

Line 251 – The fact that genotypic diversity in poppr uses H, G and lambda should be clarified here. It should reflect the results interpretation as well. According to Table 2, MI and NE subpopulations exhibit high genotypic diversity when compared to other subpopulations (3.6, 29 and 0.97 for H, G and lambda, respectively for MI and 3.2, 17.8 and 0.94 for NE). If this was based on evenness, that should be explained as well. It can be confusing stated like this. When you shift focus onto diversity (h), the story changes – so please clarify this section to reflect that.

Line 276 – please correct plot to lower case.

Lines 275 and 278 – correct P values to  $<0.001$ , to keep consistent throughout the manuscript. This was done several times throughout the manuscript, so please correct it accordingly.

Lines 295-6 – place states in alphabetical order (and this goes for any other places further in the document).

Figure 4 – I would correct probability values to reflect what was used throughout the manuscript ( $P<0.001$ , for example). I assume bolding was typo in the figure explanation.

Line 313 – what table/figure you are referring to here – please specify for SOM.

Line 315 – was performed by grouping.

Line 414 – DAPC – This was really neat finding of shared haplotypes and years in which they shifted their population structure. Having said that, what were STRUCTURE results across 11 and 16 microsats and did they agree with DAPC based on years and regions? Just curious.