**Response to Reviewer 2**

**- Please include SNP loci and alleles associated with those important traits in a table.**

Thank you for this suggestion. We added this as supplemental table 1.

**- We have got to a similar situation when analyzing cultivated and wild germplasm panels in our program, substantially reducing SNPs for some wild species. With that, it will be helpful to find filtered sets of SNPs across all three species and see the genetic structure with combined datasets to reveal how the three species will separate/group. If interesting to your group, please add them.**

This is a good suggestion for a future study. We are currently collecting resequencing data and creating a pangenome, which would enable a cross-species comparison, for this purpose and will be glad to report on it in a subsequent publication.

**- Similar low LD decay (few Kb) is also found in spinach, an outcrossing vegetable crop. Some differences in LD among cultivated and wild species were noted using GBS markers recently.**

Interesting, good to know the trends in our data are consistent with trends in other crops with similar types of data.

**- Please revise this info to make it more clear- to emphasize the advantage of genomic selection for traits with low heritability and governed by many minor alleles. "Traits with a more complex architecture are not amenable to GWAS analysis. These traits are better targets for prediction using genome-wide markers".**

Good clarification, we added this at L290.

- **My opinion on L306: Not only biparental but we could proceed with multiparent or mixed populations segregating for the trait locus.**

This is a good point. We added a note on multiparent populations here.

**-L313: This study did not test for genomic selection potential for any of the traits, and I will not escalate the use of these markers on their potential use for GS.**

We did not test genomic selection per se, but we did use genomic markers to measure genomic heritability. The square root of genomic heritability gives a theoretical upper limit of genomic selection prediction accuracy. This is a promising sign that whole-genome models would be better for these traits. More to your point, the fact that these exact makers may not be ideal for any given breeding program is well taken. We added clarification that these markers could serve as **source of markers** to be integrated into marker panels for GS at L313.

**- Figure 1 may not be that important to present in the main text and could be moved to supplementary info.**

We like having Figure 1 in the main text. After re-evaluating our figures we thought Figure 2 was more fitting for supplemental. So we limited our figures by moving Figure 2 to supplemental.

**Lines 27-28: mention the other two Cucurbita species that have been domesticated**

Since this paper only addresses the diversity of *pepo*, *moschata*, and *maxima* we removed the reference to the five species to avoid confusion.

**Line 198: Add “subsp.” pepo?  
Line 234: Add “In C. pepo” the bush/vine phenotype  
Figure 7: Add a dot “.” after panel b.  
Figure 9: Be consistent with the use of dots “.” after panel a and panel b relative to other legends. Also, double check capitalization after panel a/b in legends.**

Thank you, these changes have been made.

**Line 245: Provide a list of the accessions assigned to the core collections as supplemental data.**

Thank you for this suggestion. Please find potential core collections as supplemental now.

**Lines 283-285: Adding data from the other two domesticated Cucurbita species would also enhance the available data to reference across species.**

While there are other domesticated species, we would stop short of considering them cultivated species. We chose to limit the scope to the three most popular species, and we only generated GBS data for these species. It would be interesting to do another study in the other species too.

**Response to Reviewer 4**

**The authors provide data characterizing three USDA collections of Cucurbita species, C. pepo, C. moschata and C. maxima. Results focus on newly generated data from genotype-by-sequencing. The authors go on to identify SNPs and conduct genome-wide associate studies. Valuable information is presented that will help direct future research directions. Overall, the manuscript is well written, however a few minor revisions are requested. Here are my suggestions for edits:  
  
Lines 27-28: mention the other two Cucurbita species that have been domesticated  
Line 198: Add “subsp.” pepo?  
Line 234: Add “In C. pepo” the bush/vine phenotype  
Line 245: Provide a list of the accessions assigned to the core collections as supplemental data.  
Lines 283-285: Adding data from the other two domesticated Cucurbita species would also enhance the available data to reference across species.  
Figure 7: Add a dot “.” after panel b.  
Figure 9: Be consistent with the use of dots “.” after panel a and panel b relative to other legends. Also, double check capitalization after panel a/b in legends.  
  
I have no major concerns.**

Thank you for your review! The changes you have suggested have been made.