Review

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August 13th, 2014

General Comments

Pan *et al.* constructed 12 segregating populations and analyzed the genetic recombination landscape of these populations. The authors present nice data sets that could be used for genetic studies, but I am not convinced by the interpretation of the data, and more work need to be done to either clarify their methods and distinguish their results from those of {X *et al.*}[^c1]. Below I include comments on specific aspects of the paper; I hope they may be useful in revising the manuscript. There are a number of places with typo (e.g. `non-colineraity` on page 9 should be `non-colinearity`) or grammatical error (e.g.), careful revision of the text with this in mind would improve legibility. Please do not hesitate to contact me if you need help to clarify questions or comments.

Background

- Bulleted list of concerns
- Only concerns that are sufficiently important that they should prevent publication of the paper

Results

- The number of recombination bins and the length of genetic maps were calculated using the same set of SNPs to measure recombination events in different ways, it is obvious to me that the two values should be highly correlated. I do not think it is necessary to present this correlation unless you have a point to make.
- I have concerns about the claim that you have improved the reference genome. Because B73 is not a founder line for most of the 12 populations, gaven the large number of genomic variations of maize [^c2], is it possible that the non-colinearity regions you observed are population specific inversions but not reference genome errors? And how did you rule out the possibilities that they were not caused by genotyping errors or mis-placement on the genetic map.To improve the reference genome, more evidences should be provided.

- For a better comparison of recombination events in 12 popualtions, x-axis and band width of the histograms in **Figure S2** should keep the same. And you should backup this statement `As expected, the longer the chomosome is the more recombination events occur` or drop it.
- It may be not statistically legitimate to compare genomic features of hotspot regions with randomly selected genomic regions given SNPs on the SNP50 array may enriched in genic regions. And most of the *P* values lower than 2.2e-16 seem worrisome. Instead of choosing random genomic regions, recombinant coldspot regions of same size and SNP density should be selected for testing as described in {Myers *et al.*}[^c3]. In addition, SNP array suffers from some degree of ascertainment bias, I do not know how much it will affect this analysis, but address this concern here or in discussion seems warranted.

Discussion

Methods

- Bulleted list of concerns
- Even if the authors didn't fix these the papers would be ok, but they might improve the paper.

Tables and Figures

Pick one of:

- Reject
- Major revisions
- Minor revisions
- Accept

Reject if you think that the methods, results, or claims are blatantly false. Reject if you think the paper has major flaws that could not be corrected. Reject if the paper is clearly not an improvement on the current state of the art.

Pick major revisions if you think there are serious problems with the paper but that they can be corrected. If you ask for major revisions your default plan should be that if they can/do correct all of the major issues you pointed out, you would be prepared to accept the paper.

Do not ask for major revisions if you think the paper is uninteresting and you wouldn't accept it even if they did everything you said.

Pick minor revisions if there are only minor issues with the paper that you are pretty sure the authors can correct and you would be prepared to accept if the authors address those issues.

Pick accept if there are only minor issues and those issues are only judgement calls on your part, as opposed to things that need to be fixed to justify the claims or to make methods/results/data clear. It is perfectly acceptable in this case to list the minor issues and to suggest acceptance.