

Tenaillon et al. used transcriptomics on inbred maize lines under divergent selection regimes to compare the response to selection in terms of gene expression. They chose two inbred lines to undergo 13 generations of selection for early and late flowering time. Transcriptomics data was taken from shoot apical meristems at multiple time points defined by developmental stage. They performed 27 contrasts to identify genes that were differentially expressed under these conditions. They found differential expression by time point, genotype, and selection. The most interesting of these are the genes that are differentially expressed across multiple contrasts. Specifically, there are a subset of the genes that were differentially expressed across the selection contrast in both inbreds pointing to a convergent response to selection. This subset included many genes already known to play a role in flowering time in maize.

Overall this is an interesting study and worthy of recommendation. My comments are mostly confined to things that could be done to improve clarity. Many of the conclusions seem to be dependent on a PCA analysis described in table 3. Table 3 is a little confusing, and I think it might be beneficial to have a figure of the PCA. You mention in the first paragraph of the discussion that you demonstrated that the timing of floral transition is linked to flowering time, but you also mention that floral transition drives flowering time in the introduction as part of the explanation for your work. So I think you need to highlight the specific part of this that's a new discovery. I thought the most exciting part of this study was the discussion section "genetic convergence between inbred lines is detected". But I also felt like the first time it was brought up was on page 21. I think these findings could be more clearly highlighted in the results section.

Some of the results of table 2 are discussed in detail, but I was most surprised by the ones with very low numbers of differentially expressed genes, which seems to be an unexpected result. I think it would be helpful if the authors mentioned what drives particularly low numbers of differentially expressed genes. Is it at these time points turned out not to be meaningful?

Finally, I have a copy editing comment: on page 2 paragraph 2 the phrase "we obtained" is repeated. Also, as someone who is not directly involved in this field, the sheer number of different acronyms made this paper very hard to follow. I recognize that if I had worked on maize or flowering time more recently these would probably be clearer. For example, in table 1 there are 3 meristem statuses V, T, and R and you do define them very early in the paper but I lost track of what they were by the time I got to the table. It would be helpful if you re-defined your acronyms in figure and table legends.