Dear Editor,

Enclosed you will find our manuscript, “Recent demography drives changes in linked selection across the maize genome”. It has been long-established that a population’s demographic characteristics, especially population size, influence the efficacy of natural selection and its impact on diversity at linked sites. To account for this, researchers typically estimate a long-term effective population size (N_e) that collapses dynamic fluctuations into a single value. But a single number such as N_e fails to encapsulate all of a population’s demographic history. We used resequencing data from domesticated maize and its wild ancestor teosinte to investigate the impacts of dynamic population size changes on patterns of linked selection. By comparing diversity in allelic classes of different ages, we show that the impact of purifying selection on linked diversity in maize and teosinte dramatically shifts as a result of the rapid expansion of maize post-domestication. This observation has broad implications across the tree of life: many organisms, from humans to domesticated crops to models such as Arabidopsis and Drosophila, have undergone significant demographic change in their recent past. Our work shows that a detailed understanding of the role of linked selection and the fate of new mutations depends critically on these recent demographic shifts and is not captured well using only estimates of long-term N_e.

We hope that our observations regarding the impact of population size changes on patterns of selection and genome-wide diversity appeal to the broad readership of Nature Genetics, including researchers who work on any species across the genetics and genomics spectrum.

Thank you,

Tim Beissinger & Jeffrey Ross-Ibarra