Dear Editors,

Thank you for considering this work for publication in *Genetics*. Our manuscript, “Genetic Associations in Four Decades of Multi-Environment Trials Reveal Agronomic Trait Evolution in Common Bean”, is suitable for publication in *Genetics* for three reasons.

First, to our knowledge, our work is the first to take a phenotypic dataset with no planned genetic component and show that genome-wide association (GWAS) using these phenotypes can recover strong genomic associations. In doing this, we circumvent the “phenotypic bottleneck” slowing progress in creating genotype-phenotype maps in a novel way: adding genetic resources to an impressive phenotypic resource created by crop breeders, the Cooperative Dry Bean Nursery dataset (CDBN). These GWAS, conducted on over twenty CDBN phenotypes, uncover both strong, novel genomic associations, and associations that overlap those found in GWAS from balanced field trials of common bean.

Second, our manuscript should be of broad interest to the *Genetics* community because it uses a new method to look for genomic regions that affect multiple phenotypes: mash, or multivariate adaptive shrinkage. Recently published in *Nature Genetics*, mash is an exciting new methodology that, to our knowledge, has yet to be used outside of the context of human genetics. We use mash to look for shared genetic effects on 20 phenotypes from the CDBN. We discover two genomic regions with substantial pleiotropy, or linked effects on multiple phenotypes, that have likely been selected on during breeding for a common bean ideotype over the decades of the CDBN. This result should be of particular interest to any reader who has conducted multiple genome-wide association studies and wished to rigorously compare them.

Finally, our results provide a proof of principle that multi-year, multi-environment crop trials, even those without a planned genetic component, can usefully support genetic analyses. This advance should thus inspire further genetic research using this and other multi-environment phenotypic datasets.

All the best,

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