Dear Editors,

Thank you for considering this work for publication in *New Phytologist*. Our research results elucidate the genomic regions associated with trait variation in common bean, an important source of plant protein. Our manuscript should be of broad interest to the plant community, because it succeeds in making use of a phenotypic resource available for many species, a multi-environment breeding trial. We are submitting the research paper entitled “Genetic Associations in Four Decades of Multi-Environment Trials Reveal Agronomic Trait Evolution in Common Bean”. Additionally, our answers to the three covering letter questions are as follows:

**What hypotheses or questions does this work address?**

The phenotypic bottleneck slows exploration of the genotype-phenotype map in many species. Could adding genetic resources to the impressive phenotypic resource of a multi-environment breeding trial circumvent this bottleneck? If so, can we recover strong genomic associations, and do we recapture the known genetics of trait variation in the species?

**How does this work advance our current understanding of plant science?**

We use this new phenotypic and genotypic resource to uncover four genomic regions with pleiotropy or linked associations for multiple agronomic traits, to identify specific genomic regions intentionally and unintentionally introduced during 30 years of breeding, and to discover a novel candidate gene that may improve seed yield by 9-16%.

**Why is this work important and timely?**

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 improves the genotype-phenotype map in common bean, an important crop species, and should inspire further genetic research using this and other multi-environment phenotypic datasets.

All the best,

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