Exploring the genetic architecture and improving genomic prediction accuracy for yield, mineral concentration, and canning quality traits in common bean (*Phaseolus vulgaris* L.)

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Common bean (*Phaseolus vulgaris* L.) is the most important legume for human consumption worldwide, and is an important source of protein, vitamins, and micro-nutrients in the human diet. Beans are produced on more than 20 million hectares of land worldwide with seed production around 12 million metric tons per year, with the human population growth, it is very important to increase bean seed production, especially in developing countries where the common bean is an affordable source of high-quality nutrition. This study is focused on identifying the genomic regions associated with seed yield, canning quality, and seed mineral concentration through a combination of meta-QTL analysis (MQTL) and genome-wide association analysis (GWA). For the GWA analysis, a Yellow Diversity Panel (YBC), and a pool of families of black beans (BBL) were used, and for MQTL analysis the data of previous studies that have been reported associations with seed yield, canning quality, and seed mineral concentration were used to identify MQTL regions related with these phenotypes in common bean. The YBC and BBL were genotyped using the genotyping-by-sequencing (GBS) methodology. The regions identified through the meta-analysis and GWA will use as fixed variables in several genomic selection (GS) models to increase the accuracy of them. The GS models and fixed variables with the highest accuracies in the phenotype prediction will be selected to be used in the common bean breeding program.