**Genomic variation in diverse pea accessions uncovers the genetic basis of seed protein content**

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To enhance the understanding of genetic determinants of seed protein concentration in pea, we developed a high-quality, chromosome-level genome assembly of CDC Amarillo using long-read sequencing technology. The assembly spans over 4.1 Gb with contig N50 size exceeding 17 Mbp. We utilized a Genome-wide association study (GWAS) panel of 233 diverse pea accessions to evaluate the phenotypic diversity of seed protein concentration. The panel was initially genotyped using an Axiom® 90K SNP array followed by whole genome resequencing at 5x coverage. Through association mapping based on seed protein concentration data from multi-site, multi-environment field trials, we identified several genetic loci and SNP markers linked to this trait. We will present detailed findings on the genome assembly, and the trait-associated genetic markers, illustrating their implications for molecular breeding for high seed protein concentration.