**Reference genome sequence and population genomic analysis of peas provide insights into the genetic basis of Mendelian traits and beyond**

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Peas are important sources of starch, protein, dietary fiber, and other nutrients for humans. As the genetic model used to discover Mendel’s laws of inheritance, the study of agronomic traits in peas served as the foundation of modern genetics. In this study, we reported a de novo assembly of the chromosome-level genome for the elite vegetable pea cultivar 'Zhewan No.1' and used 314 accessions encompassing wild relatives, landraces, and cultivars resequencing data to resolve the genetic variation map of pea. We uncovered 235 candidate loci associated with fifty-seven important agronomic traits using genome-wide association studies (GWAS). In particular, we anchored the causal gene haplotypes of *PsGA3ox1*, *PsbHLH*, *PsSGR*, and *PsSBE1* associated with four Mendel’s traits of stem length (*Le*/*le*), flower color (*A*/*a*), cotyledon color (*I*/*i*), and seed shape (*R*/*r*), respectively. Furthermore, *PsCLE42* and *PsPPO1* encoding a CLAVATA/ESR (CLE)-related protein and a polyphenol oxidase were mapped as causative genes controlling the resultant traits of pod form (Mendelian *P*/*p*) and hilum color by integrating GWAS and bulked segregant analysis (BSA) approaches. In addition, we constructed a spatio-temporal gene expression atlas via transcriptome analysis across twenty-two tissues and highlighted the gene modules involving in pod and seed development. These findings provide valuable pea genomic information and will facilitate the future genome-informed improvement of pea crops.