

## MENDEL'S PEAS SEQUENCED

All pairs of alleles controlling the traits studied by Mendel in *Pisum sativum* have been identified. Recently, Liu et al. (1) sequenced the complete genome of this species, with particular focus on Mendel's genes. Their study included extensive whole-genome association (WGA) analyses to map Mendel's traits, sometimes revealing multiple variants at the same locus. In most cases, their findings aligned with previously identified loci, with one notable exception: the *P* locus (purple-white flower color), which had been mapped to pea chromosome 5. In this study, the authors identified *PsCLE42* on chromosome 1 as an alternative candidate gene for this locus, supported by transcriptome analyses. Since the specific cultivar Mendel used is unknown, this discrepancy cannot be fully resolved.

1. <https://www.nature.com/articles/s41588-024-01867-8>