



# Genetic and Genomic Resources of Grain Legume Improvement: 3. Peas

*Petr Smýkal, Clarice Coyne, Robert Redden, Nigel Maxted*

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Pea is an important temperate region pulse, with feed, fodder and vegetable uses. It originated and was domesticated in Middle East and Mediterranean regions, and formed important dietary components of early civilizations. Although *Pisum* is a very small genus with two or three species, it is diverse and structured, reflecting taxonomy, ecogeography and breeding gene pools. This diversity has been preserved in collections totalling about 90,000 accessions. Core collections have been formed, facilitating phenotypic and agronomic evaluations. However, only 3% of ex situ collections are wild *Pisum* sp., with substantially larger diversity. The genomic resources allow initiation of association mapping, linking genetic diversity with trait manifestation. So far, only a small part of wild gene pools have been exploited in breeding for biotic and abiotic stresses. Current genomic knowledge and technologies can facilitate allele mining for novel traits and incorporation from wild *Pisum* sp. into elite domestic genetic backgrounds.

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