



cousin

Crop Cousins, promise for the future

Characterisation and use of wild relatives in pea breeding

Introduction

*Pea (*Pisum sativum*) is a cool season legume crop domesticated from wild and primitive *Pisum* species in the Fertile Crescent some 10,000 years ago. It is today produced worldwide, mainly in temperate regions. Depending on its uses, field peas, vegetable peas, and forage peas, are distinguished, each one with different uses differing therefore in quality requirements. Pea yield can be constrained by a number of biotic and abiotic stresses to which there is insufficient genetic resistance available. Wild relatives, including subspecies of *P. sativum*, or the most distant *P. fulvum* offers a reservoir of sources of resistance and other valuable traits that can be exploited in pea breeding.*



Objectives

COUSIN aims to explore valuable traits in wild pea relatives with the final aim of their exploitation in cultivated peas. The strategy begins by identifying priority traits absent in cultivated forms and searching for them through germplasm screening. This is followed by wide hybridization and breeding at several levels: from classical selection in target environments – at research stations and with participatory farmers – to advanced molecular tools such as QTL mapping and genome-enabled prediction of key traits.

Result

IAS-CSIC is running a long-term pea pre-breeding program which started with a major focus on developing cultivars adapted to Mediterranean rain fed farming conditions. Their first priority was broomrape (*Orobanche crenata*). Since pea germplasm have little resistance to this wild relatives were used to identify potential sources of resistance. After huge efforts in crossing and selection the first cultivars with resistance to broomrape derived from *Pisum fulvum* were registered by CSIC.



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Similarly, we registered the first cultivars carrying the novel powdery resistance gene (Er3) also derived from *P. fulvum*. These pre-existing CWR derived cultivars, together with a large number of segregating populations derived from crosses with other *Pisum* species were made available to COUSIN academic partners for scientific studies and to breeders for testing and selection under their conditions. Additionally, a large *Pisum* spp. germplasm collection is being phenotyped for resistance to a range of diseases (broomrape, rust, powdery mildew, ascochyta blight, fusarium wilt, aphanomyces root rot) and pests (aphid and bruchus weevil) under field conditions (inoculated plots) or/and controlled conditions (seedlings inoculated in growth chambers). New crosses have been made this season with selected resistant accessions. This will continue all along the project.

Recommendations

CWR pea cultivars and near cultivars with valuable traits missing in cultivated pea (i.e. Orobanche resistance) are being made available to farmers. Similarly, missing sources of resistance to other key stresses are being identified and introduced by sexual crossing into segregating populations made available to breeders.

Further readings

- Rubiales et al. 2019. CH20 - Advances in breeding of peas. In: Hochmuth G (Ed), Achieving sustainable cultivation of vegetables, Burleigh Dodds Science Publishing Limited, Cambridge, UK, ISBN-13:9781786762368
- Rubiales et al. 2021. Development of pea breeding lines with resistance to *Orobanche crenata* derived from pea landraces and wild *Pisum* spp. *Agronomy* 11(1): 36, <https://dx.doi.org/10.3390/agronomy11010036>
- Osuna-Caballero et al. 2022. Identification and characterization of novel sources of resistance to rust (*Uromyces pisi*) in *Pisum* spp. *Plants* 11: 2268, <https://doi.org/10.3390/plants11172268>
- Rodriguez-Mena et al. 2024. Identification of Sources of Resistance to *Aphanomyces* Root Rot in *Pisum*. *Plants* 13: 2454. <https://doi.org/10.3390/plants13172454>

