Recent advances in pea breeding

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CSIC
World average annual yield gain in dry pea in the last 50 years was moderate: Just 15.3 kg/ha/year compared to 39.3 in wheat, 25.3 in soybean or 28.3 in green pea.

lower investment compared to other crops
The greater expansion of dry pea that has occurred in Canada has led to it today being the leading dry pea producer in the world. This is accompanied by a large investment in breeding resulting in 2% yield gain per year.
EUROPE:

- Remarkable increase of soybean

- dry pea is still the major temperate grain legume, far from faba bean, lupin, lentils, chickpea (FAO data)
Limited investment in breeding

Breeding priorities:

- Increased yield, yield stability, Addressing markets demands

• Grower satisfaction: making pea cost effective and attractive for growers
  Good yield, disease resistance, standing ability, adaptation, winter hardiness

• Consumer satisfaction
  Quality requirements varies with pea types (green vs dry pea),
  All pea types require resistance to the same biotic and abiotic stresses and all
developed biomarkers are equally useful for all types

- Pandey et al., 2021. Omic resources and omics-enabled approaches.... TAG 134:755–776
Consumer satisfaction

Quality requirements varies with pea types

- Vegetable peas:
  - edible **seeds** (color, flavor, texture)
  - edible **pods** (parchment)
  - edible leaves

- Dry peas:
  - animal feed
  - human food (protein, starch)

Forage pea biomass, mixcropping
Consumer satisfaction

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  - animal feed
  - human food (protein, starch)

Forage pea biomass, mixcropping

Genetic variation identified to most quality traits, ready for use in breeding

- **Protein content** (Solberg et al. 2017)
- **Folate content** (Jha et al. 2015)
- **Carotenoids** (Ashokkumar et al. 2015)
- **Aroma and flavour** (Malcolmson et al. 2014)
- **Low phytate raising iron bioavailability** (Warkentin et al. 2020)
- **Monogenic**
- **Macro and micronutrients** (Ma et al. 2017)
- **QTLs identified**
- **Iron and Zinc** (Diapari et al 2015)
- **GWAS: SNPs identified**
- **Starch structure and amylose content** (Carpenter et al. 2017)
- **SNPs**
- **Protease inhibitors** (Clemente et al. 2015)
- **Mutants**
- **Sweetness** (Rayner et al. 2017)
Yield stability and adaptation to new growing condition: Priorities change with the pedoclimatic conditions and the cropping system
remarkable progress identifying resistance to stresses

Genetic resources: circa 100K accessions (1% wild); core collections Insufficiently characterized. But:

Primary gene pool:
Cold tolerance (Vann et al. 2018; Liu et al. 2017; Beji et al. 2020) QTLs, SNPs
Salinity tolerance (Leonforte et al. 2013) SNPs discovered
Drought tolerance (Iglesias et al. 2015) QTLs
Variation identified to most biotic stresses and to most quality traits

Secondary gene pool
Ascochyta blight: *P. fulvum* (Jha et al. 2016) QTLs
*Erysiphe pisi* *P. fulvum* (Fondevilla et al. 2007), *Er3* gene, resistant cvs developed
*Uromyces pisi* *P. fulvum* (Barilli et al. 2018) QTLs, SNPs
Bruchus weevil: *P. fulvum* (Aryamanesh et al. 2014)
Pea aphid: *P. fulvum* (Barilli et al. 2019) QTLs
Drought: *P. fulvum* (Naim-Feil et al. 2017)
*Orobanche crenata*: *P. fulvum* (Rubiales et al. 2021) resistant cvs developed

Successful, but slow…
Resistance to most biotic stresses identified
Resistance to most biotic stresses identified and resistant cultivars breed, even derived from wide crosses with *P. fulvum*.
Modern genetics started with pea

Mendel’s laws 1865

After some decades of lagging behind other crops, pea genetics progressed impressively with plenty of resources available today

DNA markers (… SNPs, KASP facilitating MAS)

TILLING populations (http://urgv.evry.inra.fr/UTILLdb)

Reference GENOME (Kreplak et al. 2019)
Marker Assisted Selection already successful for monogenic traits

**Fusarium wilt** (*Fw* gene) (Kwon et al. 2013)

**Powdery mildew** (*er1, er2, Er3*)
Fondevilla et al. 2008
Ghafoor & McGee 2011
Sun et al. 2016

**Pea enation mosaic virus** (*En*; Jain et al. 2013)

**Pea seed borne mosaic virus** (*sbm-1* and *sbm-2*) (Smykal et al. 2010, Grim & Porter, 2020)
For quantitative traits

Several consensus genetic maps, many QTLs identified for many traits, some being introduced by MABC

- Lodging (Zhang et al. 2006) markers for MAS
- Protein content and yield (Klein et al. 2020)
- Multiple traits (Gali et al. 2018)
- Many many others

MABC to combine QTLs for Aphanomyces resistance (Lavaud et al. 2015)

Genome-wide association studies (GWAS) widely used in pea

i.e.
- Aphanomyces resistance (Desgroux et al. 2016)
- Seed quality traits (Gali et al. 2019)
- Micronutrients (Dissanayaka et al. 2020)
- Frost tolerance (Beji et al. 2020)
- Heat stress (Tafesse et al. 2020)

Many others underway
**Genomic Selection** for complex traits already used in pea

first genotypic and phenotypic data from a training population are fitted to a model. The model can then be used as a tool to **predict phenotypes in a testing population which has been genotyped but not phenotyped**

Ascochyta blight resistance (Carpenter et al. 2018) prediction accuracy 0.56

Agronomic traits (Tayeh et al. 2015) PA 0.44 for TSW, 0.59 for DtF

Yield (Annicchiarico et al. 2017, 2019) PA>0.5

Drought (Annicchiarico et al. 2020) GS 18% more efficient than MAS
Still major bottleneck: PHENOTYPING

reliable but fast and cheap methods to screen any trait in large segregating populations…
Portable Imaging systems:
- Biomass, performance (Roth et al. 2018; Quiros et al. 2019)
- Vegetation indexes (Sadras et al. 2013)
- Early vigour (Nguyen et al. 2016)
- Resistance to fusarium (Rispail et al. 2015)

Automated phenotyping platforms already used in pea:
- early vigor (Nguyen et al. 2018)
- Cold tolerance (Humplik et al. 2015)
- Root phenotyping (Zhao et al. 2017; C. Salon)
Speed breeding in pea
to accelerate breeding programs

(Cazzola et al. 2021)

(Mobini & Warkentin 2016)
Thanks