



Webinar 5: Pushing the boundaries in legume breeding

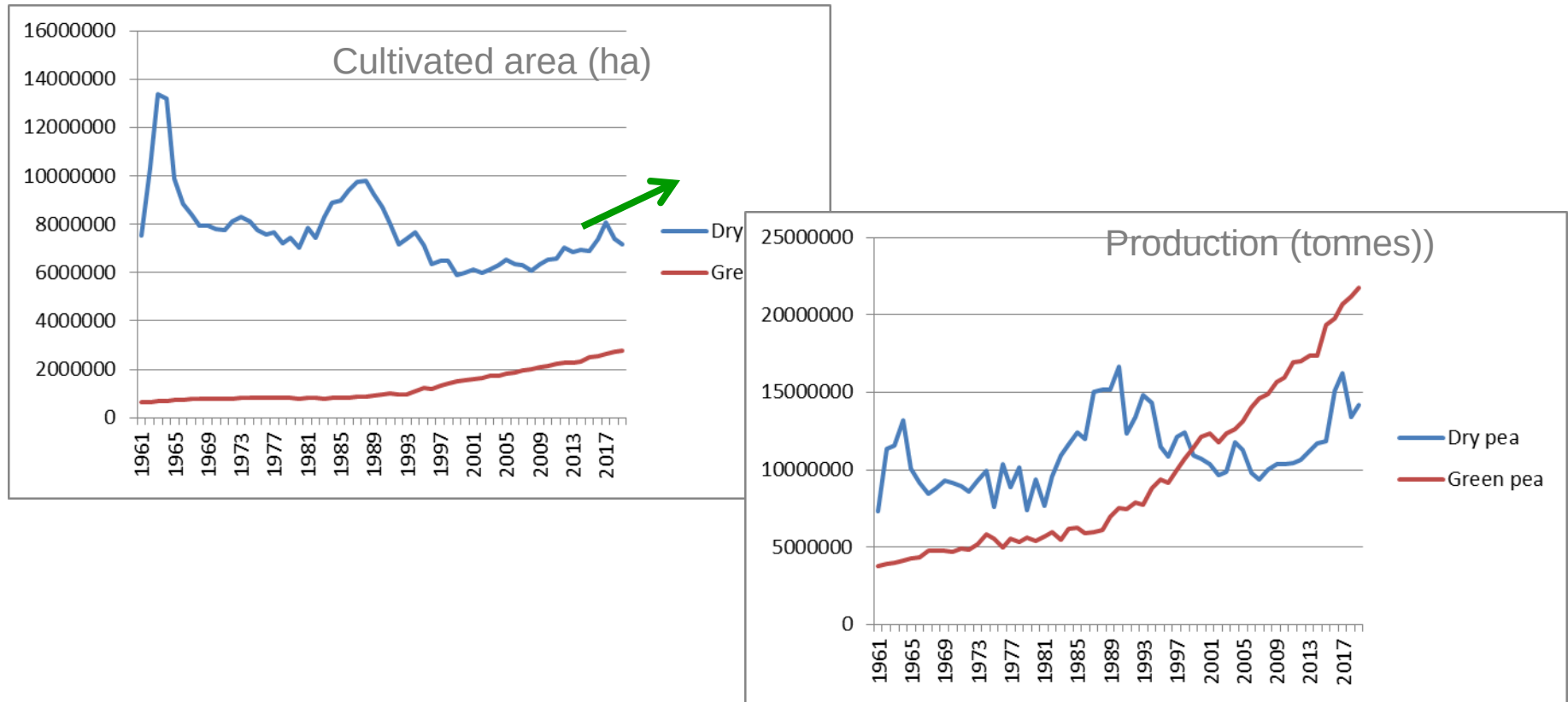
29th April 2021

Recent advances in pea breeding

Diego Rubiales



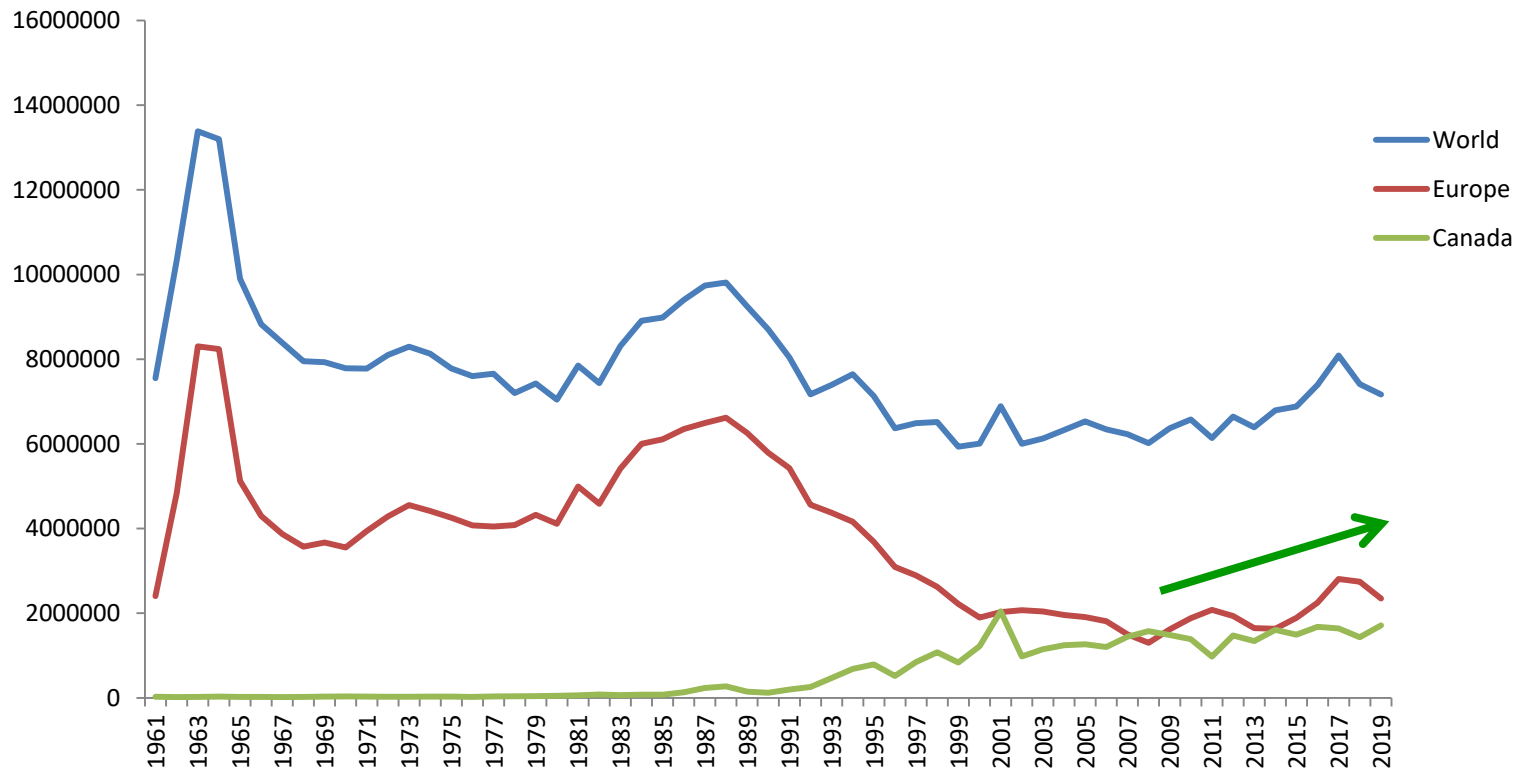
PEA: Global trend (FAO data)



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

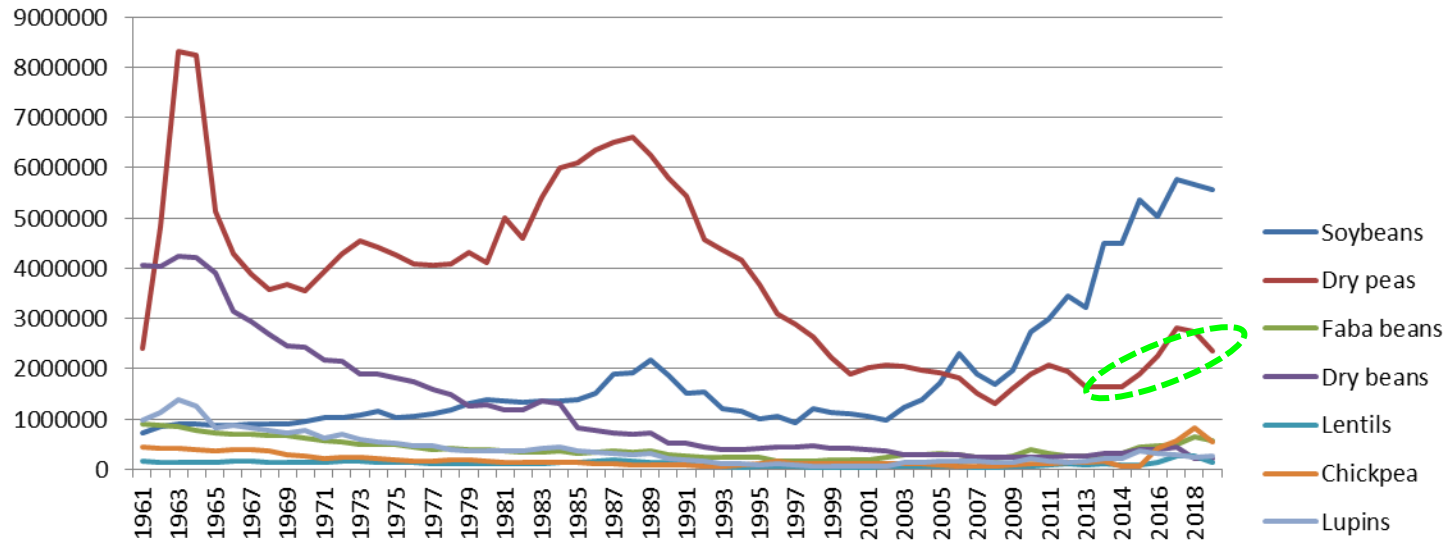
Global trend in dry pea cultivation (FAO data)



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

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

Quality requirements varies with pea types

- Vegeta

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

protein content (Solberg et al. 2017)

folate content (Jha et al. 2015)

- Dr

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) mutants



Forage pea biomass, mixcropping



Yield stability and adaptation to new growing condition: Priorities change with the pedoclimatic conditions and the cropping system



Bacterial blight



Powdery mildew



Fusarium wilt



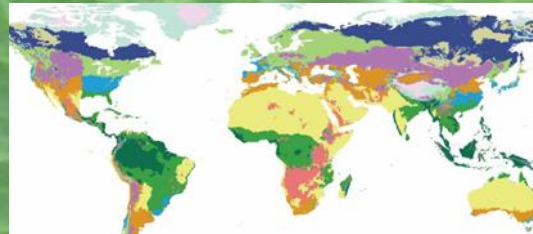
Aphanomyces root rot



Frost damage



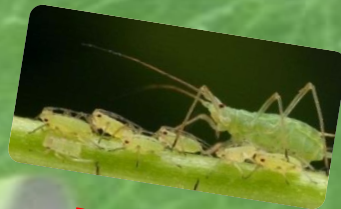
U. pisi



M. pinodes



O. crenata



Pea aphid



Pea weevil



Drought

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)

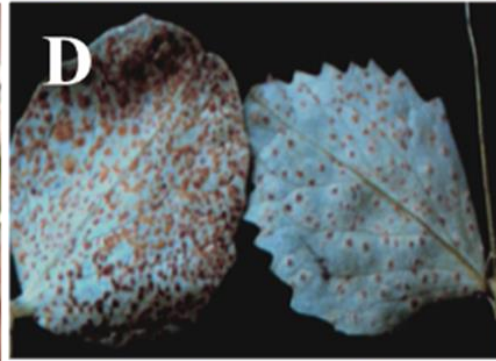
Orobanche crenata: *P. fulvum* (Rubiales et al. 2021) resistant cvs developed

Pseudomonas syringae. *P. abyssinicum* (Elvira-Recuenco et al. 2003)



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*

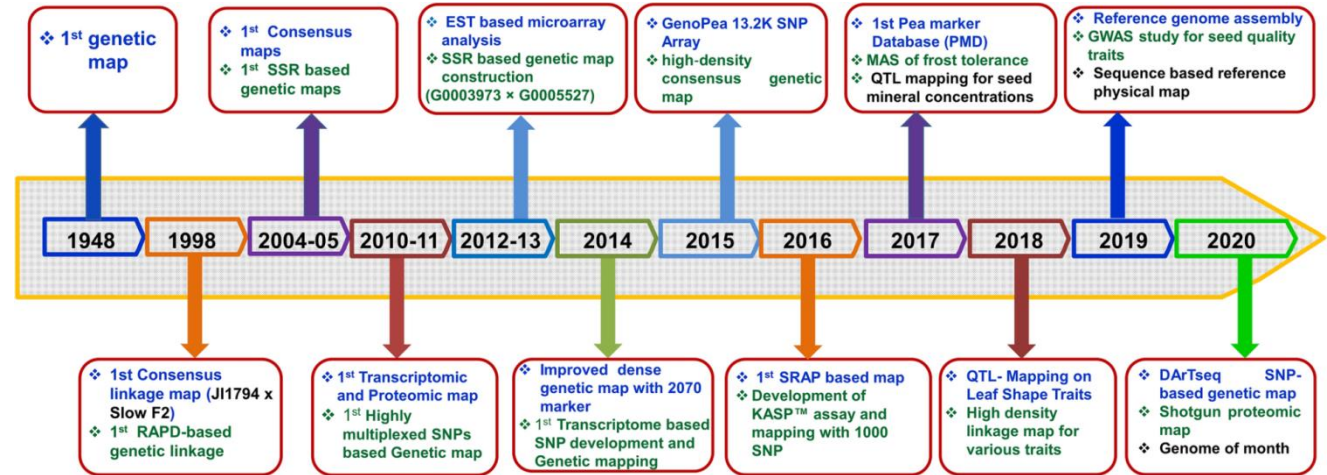


Modern genetics started with pea

	Height	Seed Shape	Seed Color	Seed Coat Color	Pod Shape	Pod Color	Flower Position
Dominant	Tall	Round	Yellow	Green	Inflated (full)	Green	Axial
Recessive Trait	Short	Wrinkled	Green	White	Constricted (flat)	Yellow	Terminal



Mendel's laws 1865



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

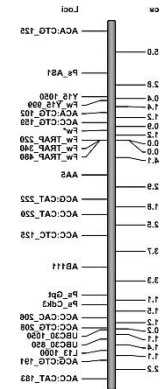
DNA markers (... SNPs, KASP **facilitating MAS**)

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

Reference **GENOME** (Kreplak et al. 2019)

Marker Assisted Selection already sucessfull for monogenic traits

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

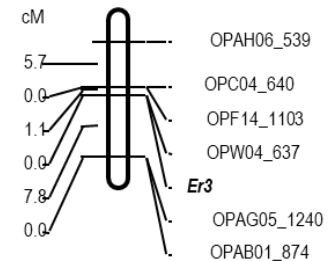
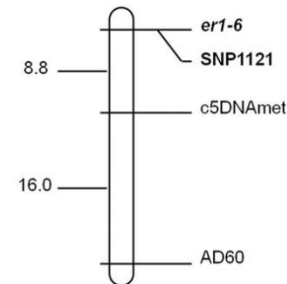


Powdery mildew (*er1*, *er2*, *Er3*)

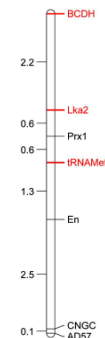
Fondevilla et al. 2008

Ghafoor & McGee 2011

Sun et al. 2016



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



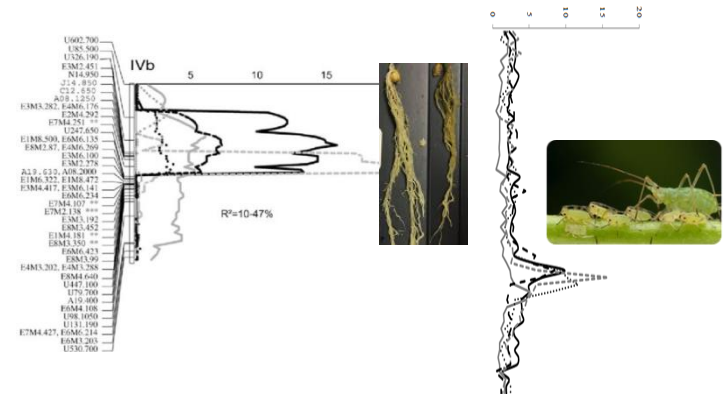
Pea seed borne mosaic virus (*sbm-1* and *sbm-2*) (Smykal et al. 2010, Grim & Porter, 2020)

For quatitative traits

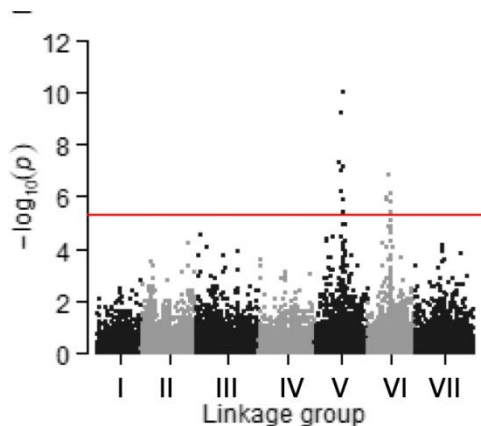
Several consensus genetic **maps**,
many **QTLs** identified for many traits, some being introduced by MABC

- 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

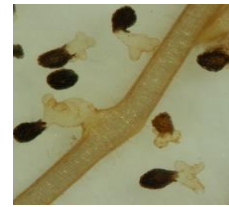
Agronomic traits (Tayeh et al. 2015) PA 0.44 for TSW, 0.59 for DtF

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...



Phenotyping



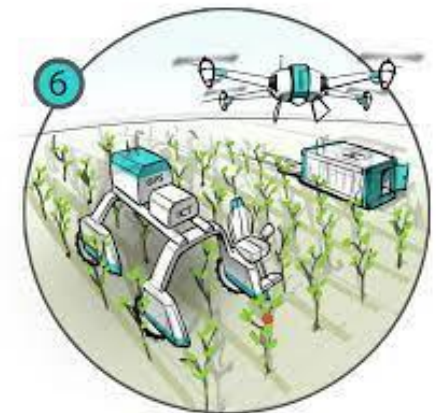
Automated phenotyping platforms already used in pea:

- early vigor (Nguyen et al. 2018)
- Cold tolerance (Humpalik et al. 2015)
- Root phenotyping (Zhao et al. 2017; C. Salon)



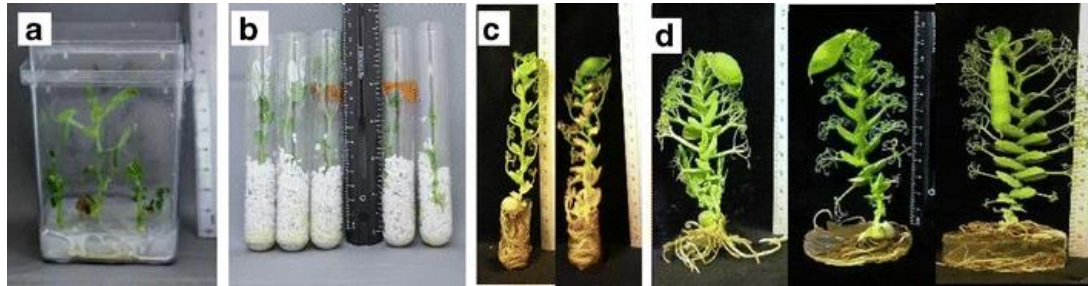
Portable Imaging systems:

- 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 (Rispaill et al. 2015)

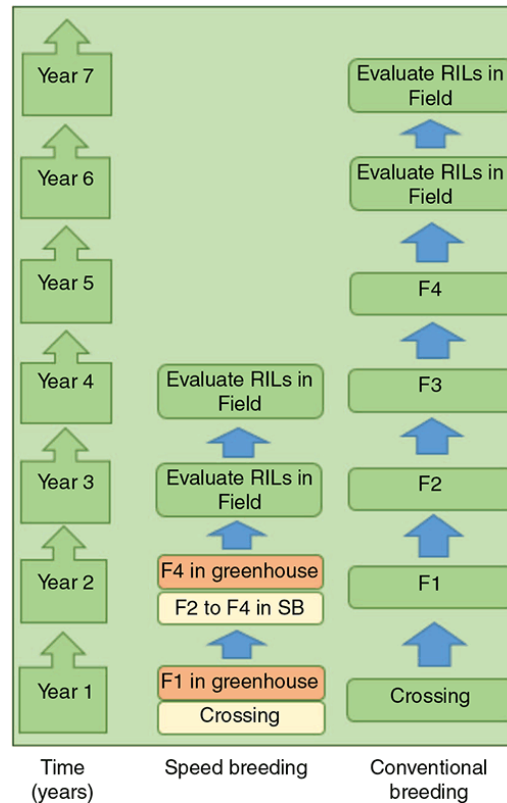


Speed breeding in pea

to accelerate breeding programs



(Mobini & Warkentin 2016)



(Cazzola et al. 2021)

Thanks

