Advanced Course

Genotyping and phenotyping in legumes: Tools, data and decisions for legume breeding

Córdoba (Spain) • 12-16 April 2027

BELIS Breeding European Legumes — Funded by the European Union — CIHEAM ZARAGOZA — CSIC — Instituto de Agricultura Sostenible IAS



Objectives

Legume breeding is being reshaped by two sets of technologies that have matured at very different speeds. On the genotyping side, the fall in sequencing costs, the consolidation of genotyping-by-sequencing, targeted genotyping and SNP arrays, and the recent availability of reference genomes and pangenomes for the main legume species have turned marker information into something a breeding programme can generate routinely rather than exceptionally. On the phenotyping side, remote sensing, UAV imagery, spectroscopy and image analysis have begun to clear the measurement bottleneck that has historically limited the number of genotypes a programme can evaluate, and machine learning is changing how both kinds of data are analysed. Between the two sets of technologies sit prediction models—marker-assisted, genomic and phenomic selection —which have moved from proof of concept to formal integration with phenotypic selection in both grain and forage legumes. Policy frameworks such as the European Green Deal, the Farm to Fork strategy and the European push for protein autonomy have simultaneously raised the demand for improved legume varieties, and with it the demand for professionals able to combine these tools in a coherent breeding strategy.

These opportunities reach legumes under conditions that differ markedly from those of the major cereals. Legume breeding applies to a heterogeneous group of species —chickpea, faba bean, pea and lentil among the grain legumes, lucerne and clovers among the forages— that span inbred and outbred reproductive systems, annual and perennial cycles, and very different levels of genomic resources and community size. Breeding programmes are usually small and work with limited budgets, with support from a range of funding sources, including public funds. In this context, the choice between a cheap marker panel and a dense genotyping platform, or between manual measurement and an image-derived trait, has real consequences for costs and accuracy rather than being merely a technical detail. Environmental changing conditions add their own constraints: from cold in autumn-sown crops to drought and heat, impact on crop cycles, soil-borne pathogens, foliar diseases and pests, and quality traits such as protein content and antinutritional compounds that determine the end use of the harvest. Expertise on these questions is fragmented across institutions, disciplines and countries, and methods developed for other crops or other climates cannot simply be transferred. There is therefore a clear need for an advanced, integrated course that brings genotyping, phenotyping and the analytical tools that connect them into a single framework, applied to legume species and to Mediterranean and European breeding contexts.

By the end of the course participants will:

- Acquire a comprehensive understanding of the genotyping and sequencing technologies currently available for forage and grain legumes, and of their significance for breeding programmes of different size, species and budget.
- Select an appropriate genotyping platform for a given breeding objective and follow the steps that lead from raw sequence data to a quality-controlled marker dataset.
- Move from QTL and GWAS results to validated, breeder-ready diagnostic markers, and apply marker-assisted selection in practice on grain and forage legume material.
- Understand how genomic and phenomic prediction models are built, trained and validated, what prediction accuracy means, and how it translates into genetic gain per unit of time and cost within perennial and annual legume breeding schemes.
- Design a phenotyping protocol for a target trait, choosing scoring scales, experimental designs and levels of precision appropriate to the trait, the species and the resources available.
- Set up and interpret evaluation assays for biotic stresses, abiotic stresses and seed quality traits in grain and forage legumes.
- Plan and interpret image-based phenotyping, from flight planning, ground control points and image acquisition to plot segmentation, extraction of vegetation indices and the export of a phenotypic table ready for analysis.
- Integrate genotypic and phenotypic information, and adapt it to design sound, context-specific genotyping and phenotyping strategies.

Organisation

The course is organised by CIHEAM Zaragoza within the framework of the EU-funded project BELIS (Breeding European Legumes for Increased Sustainability) with the support of IAS-CSIC and in collaboration with INRAE. Legume Generation. UCO, IFAPA, CREA, ILVO, and ICARDA.

The course will be held face-to-face for one week, in morning and afternoon sessions at IAS-CSIC Córdoba (Spain). Qualified lecturers from research centres, universities, or private companies will deliver the programme. The course requires personal work and interaction among participants and with lecturers. The international characteristics of the course favour the exchange of experiences and points of view.

The programme has an applied approach. lectures are complemented by guided debates, case studies, hands-on sessions, a technical visit and group work.

Programme

1. Official opening. Course presentation, objectives, participants & working approach (1 h)

2. Genotyping and sequencing technologies (4 h)

2.1. Overview of genotyping and sequencing technologies in forage and grain legume breeding: from SSR to GBS, DArT, targeted genotyping, SNP arrays and low-coverage whole-genome sequencing; reference genomes and pangenomes available for the main legume species.

2.2. From raw sequence data to usable marker data: quality control, variant calling, filtering, imputation and management of genotyping datasets in a breeding programme.

2.3. Guided debate & case study: Which genotyping platform for which breeding objective? Cost, throughput and sample logistics criteria.

3. From markers to selection decisions (7 h)

3.1. KASP markers linked to key agronomic traits for chickpea breeding: from QTL and GWAS results to validated, breeder-ready diagnostic markers; marker-assisted selection in practice.

3.2. Practical session: designing and validating a diagnostic marker on a real chickpea, faba & red clover bean dataset.

3.3. Including genomic selection in perennial and grain legume breeding schemes: recap of major breeding schemes for outbred and inbred crops and the position and roles of genomic selection within them; choice of reference population(s) and target environments; application and validation strategies; proof-of-concept studies and formal comparisons of genomic vs. phenotypic selection.

3.4. Genomic selection in forage and grain legume breeding: statistical models, design and size of training populations, prediction accuracy and its translation into genetic gain per unit of time and cost.

3.5. Phenomic selection in pea: NIRS-based prediction as a low-cost complement or alternative to genotyping.

3.6. Is artificial intelligence revolutionising bioinformatics analyses? What machine learning and large models do and do not change in the analysis of genomic data.

4. Phenotyping: designing the measurement (6 h)

4.1. Introduction to phenotyping in legume breeding: trait definition and scoring scales, experimental design, precision and repeatability, heritability, genotype × environment interaction and the cost of a phenotype.

4.2. Case study, biotic #1: How to set up disease tolerance assays in legume breeding: Soil pathogens.

4.3. Case study, biotic #2: How to set up disease tolerance assays in legume breeding: Pest inoculation - Aphids and weevils.

4.4. Case study, biotic #3: How to set up disease tolerance assays in legume breeding: inoculum production, controlled and field assays, scoring, and interpretation of resistance vs. tolerance. (Red clover: Powdery mildew, anthracnose, etc.).

4.5. Abiotic stress.

4.6. Case study, abiotic #1: Drought.

4.7. Case study, abiotic #2: Cold.

4.8. Use of spectroscopy for quality-related-trait evaluation in legumes.

4.9. Case study, quality. NIRS and vicine/convicine, tannins and protein in faba bean.

5. From images to phenotypes (4 h)

5.1. Remote sensing in grain and forage legume breeding: sensors, platforms and indices; what can be measured, at what scale and how accurately, in a breeding nursery.

5.2. Spectral, spatial and AI concepts in (UAV) imagery: spectral bands and vegetation indices, spatial resolution and plot segmentation, flight planning, ground control points and common sources of error.

5.3. Case study: Pixels to phenotypes: Lucerne. A complete pipeline from raw images to trait values usable in a selection index.

5.4. Case study: Counting flowers using drone images to non-destructively predict seed yield of red clover accessions.

5.5. Practical session: from images to trait values — plot segmentation, extraction of vegetation indices, quality control and export of a phenotypic table ready for analysis.

6. Technical visit and field demo (2 h)

7. Wrap-up and close (4 h)

7.1. Group work and final debate: designing a combined genotyping and phenotyping strategy for a given breeding objective and budget. Presentations, final synthesis and course evaluation.

7.2. Closing session

Lecturers

Annicchiarico, Paolo – CREA, Italy
Barilli, Eleonora – IAS-CSIC, Spain
Castro, Patricia – UCO, Spain
González, Mario – IAS-CSIC, Spain
Gutiérrez, Natalia – IFAPA, Spain
Julier, Bernadette – INRAE, France
Kasprzak, Arno – ILVO, Belgium
Lootens, Peter – ILVO, Belgium
Mahmood, Anser – Legume Generation, Czech Republic
Muylle, Hilde – ILVO, Belgium
Pégard, Marie – INRAE, France
Rojas, José Manuel – IFAPA, Spain
Rubiales, Diego – IAS-CSIC, Spain
Visioni, Andrea – ICARDA, Morrocco

Admission

The course is designed for 25 participants with a university degree and aimed at plant breeders from public institutions and from seed and breeding companies, researchers, PhD candidates, technicians of breeding and evaluation programmes, agricultural extension agents, advisors and practitioners from Mediterranean and European countries involved in legume breeding, plant genetics, plant pathology, agronomy, crop phenotyping and variety evaluation. A basic background in quantitative genetics is assumed, and participants are asked to bring a laptop for the practical sessions.

Registration

Candidates may apply online at the following address:
https://admission.iamz.ciheam.org/en/

Applications must include the curriculum vitae and a copy of the support documents most related to the subject of the course. The deadline for the submission of applications is **13 December 2026.**

Applications from candidates requiring authorisation to attend the course may be accepted provisionally.

There are no registration fees for this course, but participants must cover their own travel and accommodation costs.

Financial support

Candidates from CIHEAM member countries, the European Union, and neighbouring countries may receive financial support for travel and accommodation costs. The deadline to apply for financial support is **13 December 2026.**

Preference will be given to low- and medium-income countries. If you wish to request financial support, please complete the relevant section when you apply online to participate in the course.

Candidates from other countries who require financial support should apply directly to national or international institutions.

All applications are subject to a selection process based on the profiles submitted.

Insurance

It is compulsory for participants to have medical insurance valid for Spain. Proof of insurance cover must be given at the beginning of the course. Those who so wish may participate in a collective insurance policy taken out by the Organisation, upon payment of the stipulated sum.

In collaboration with:

INRAE · Legume Generation · Universidad de Córdoba · crea · Instituto Andaluz de Investigación y Formación Agraria, Pesquera, Alimentaria y de la Producción Ecológica, Consejería de Agricultura, Pesca, Agua y Desarrollo Rural · ICARDA · CGIAR · ILVO

Contact:
Balduque, Joaquín
Academic coordinator
iamz@zaragoza.ciheam.org