BELIS Course
GENOTYPING AND PHENOTYPING IN LEGUMES:
TOOLS, DATA AND DECISIONS FOR LEGUME BREEDING
Córdoba (Spain), 12-16 April 2027

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. (1,5 h)
   - 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. (1,5 h)
   - 2.3. Guided debate & case study: which genotyping platform for which breeding objective? Cost, throughput and sample logistics criteria. (1 h)

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. (1 h)
   - 3.2. Practical session: designing and validating a diagnostic marker on a real chickpea, faba & red clover bean dataset. (1 h)
   - 3.3. Including genomic selection into 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. (1 h)
   - 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. (2 h)
   - 3.5. Phenomic selection in pea: NIRS-based prediction as a low-cost complement or alternative to genotyping. (1 h)
   - 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. (1 h)

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. (1 h)
    4.2. Case study, biotic #1: How to set up disease tolerance assays in legume breeding: Soil pathogens. (0,5 h)
    4.3. Case study, biotic #2: How to set up disease tolerance assays in legume breeding: Pest inoculation - Aphids & weevils. (0,5 h)
    4.4. Case study, biotic #3 (THEORICAL): 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.). (0,5 h)
    4.5. Abiotic stress. (1 h)
    4.6. Case study, abiotic #1: Drought. (0,5 h)
    4.7. Case study, abiotic #2: Cold. (0,5 h)
    4.8. Use of spectroscopy for quality related traits evaluation on legumes. (1 h)
    4.9. Case study, quality. NIRS & Vicine/convicine, tannins and protein in faba bean. (0,5 h)

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 which scale and with which accuracy, in a breeding nursery. (1 h)
    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. (1 h)
    5.3. Case study: Pixels to phenotypes: the lucerne case. A complete pipeline from raw images to trait values usable in a selection index. (0,5 h)
    5.4. Case study: Counting flowers using drone images to non-destructively predict seed yield of red clover accessions. (0,5 h)
    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. (1 h)

6. **Wrap -up and closure (4 h)**
    6.1. Group work and final debate: designing a combined genotyping and phenotyping strategy for a given breeding objective and budget. Presentations, final synthesis, evaluation and course closure. (3 h)
    6.2. Closing session (1 h)

WEDNESDAY 14 APRIL, AFTERNOON – TECHNICAL VISIT / FIELD DEMO (2 h)

Faba bean in different levels of resistance, lentils, chickpea, peas,