



LEGumes for the
Agriculture of TOvermorrow



"LEGumes for the Agriculture of TOvermorrow, (LEGATO), an FP7 KBBE project (2014-2017)"



SLU, Sweden

AM2 LEGATO, Cordoba, 1-2 December, 2015



LEGumes for the
Agriculture of TOmorrow



Vital Statistics

- 17 academic partners
- 10 industrial (SME or larger) or associations (6 breeding, 2 molecular biology, 2 food processing)
- INRA Transfert for assistance with project management
- IAMZ-CIHEAM for training/outreach

Budget breakdown

- Total budget ca. 6.9M€
- 5M€ EU subsidy, of which:
- 770K€ SME

4-year project, started 1 january 2014

<http://legato-fp7.eu/>

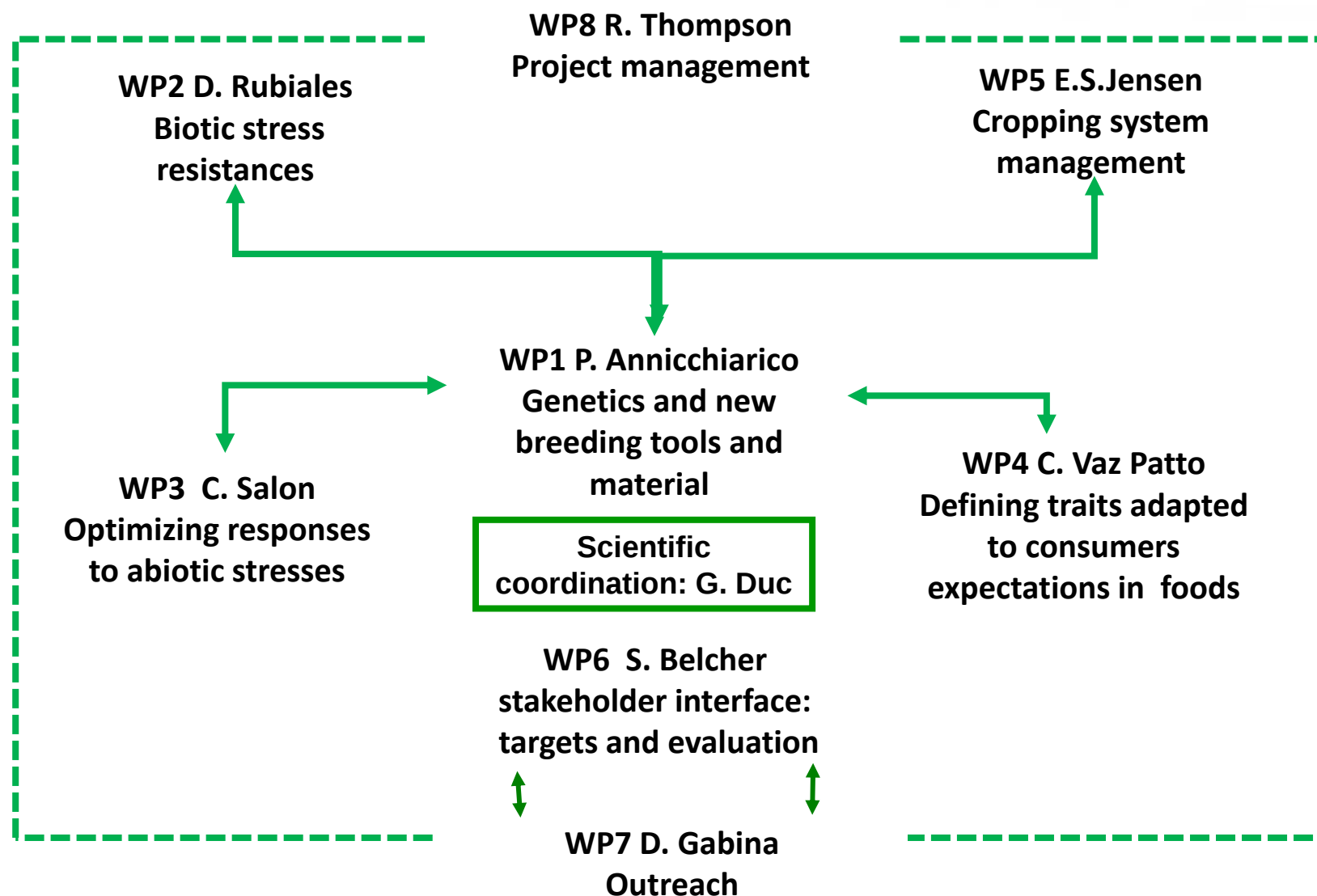


The 29 LEGATO partners

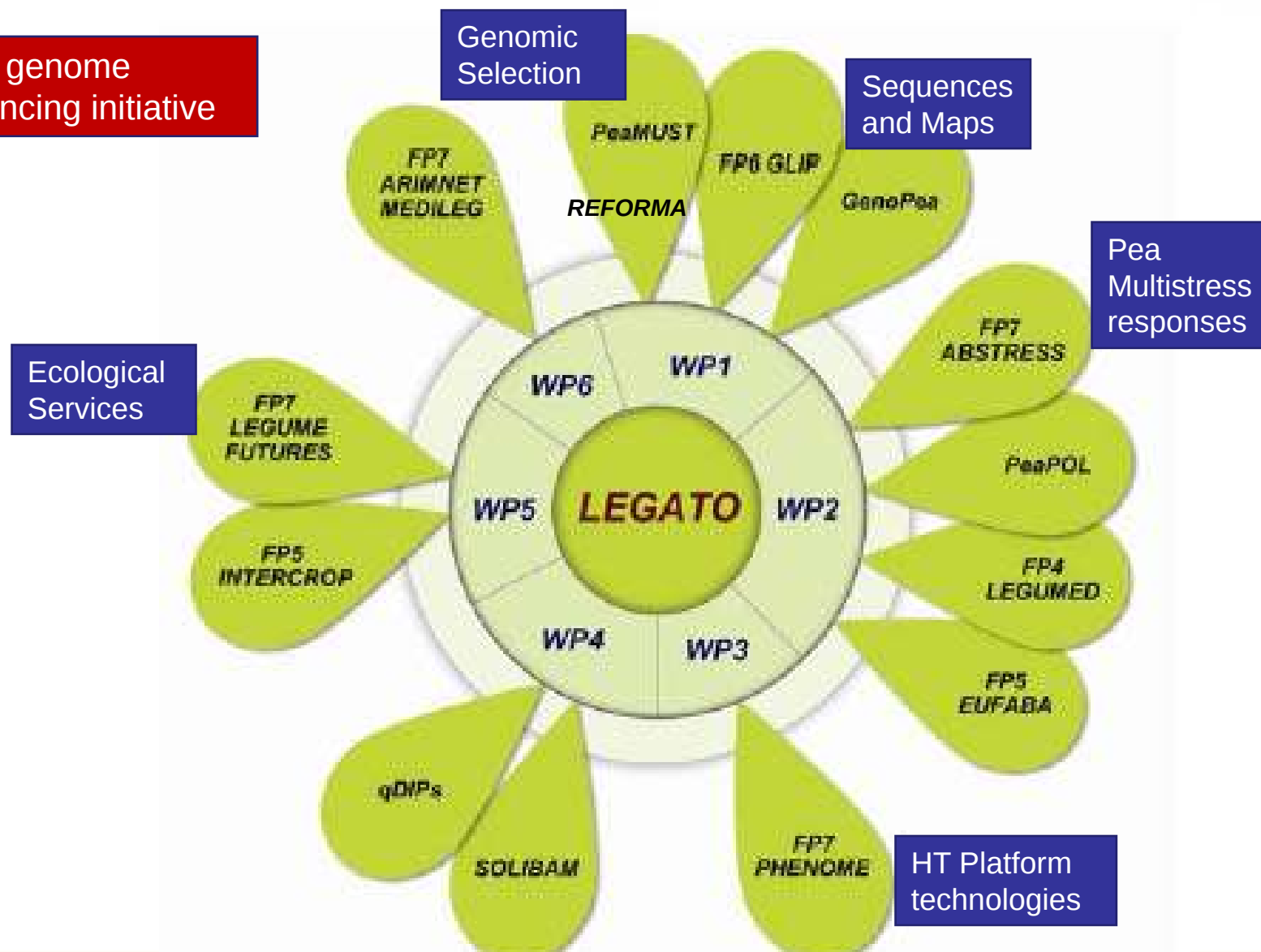


1. INRA
2. AU
3. Agritec
4. Agrovegetal
5. CRA
6. CSIC
7. Juelich
8. GXP
9. IFAPA
10. IFVCNS
11. INIAV
12. IT
13. ITOB
14. IFG
15. JIC
16. IAMZ-CIHEAM
17. Decollogne
18. NPZ
19. Patrimys
20. PGRO
21. SZG
22. SFH
23. SLU
24. UNIP
25. UCO
26. ULE
27. UNINA
28. UPOL
29. UY





+ Pea genome
sequencing initiative



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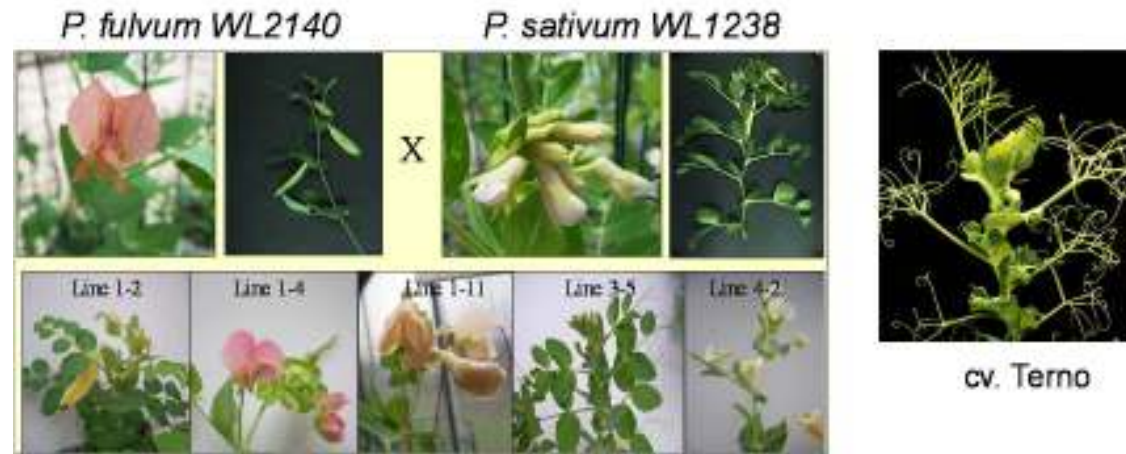


What is **new** in LEGATO?

- Exploit NGS (eg., pea genome sequence data) for marker refinement and test new markers (*mfn*, vicine, autofertility) in breeding programmes (WP1, WP6)
- Focus on previously under-exploited areas (eg., weevil resistance, non-host resistance, gene bank exploitation using new genomic/genetic tools (WP1,2)
- Understand how water stress limits N-fixation in legumes (WP3)
- Explore possibilities for increasing legume uptake in diet including local value chains and considering consumer preferences (WP4)
- Novel GL-based cropping systems including intercropping (WP5)
- Cropping Systems: Relevance for local needs: MASC and Europe-wide trials network (WP5, WP6)

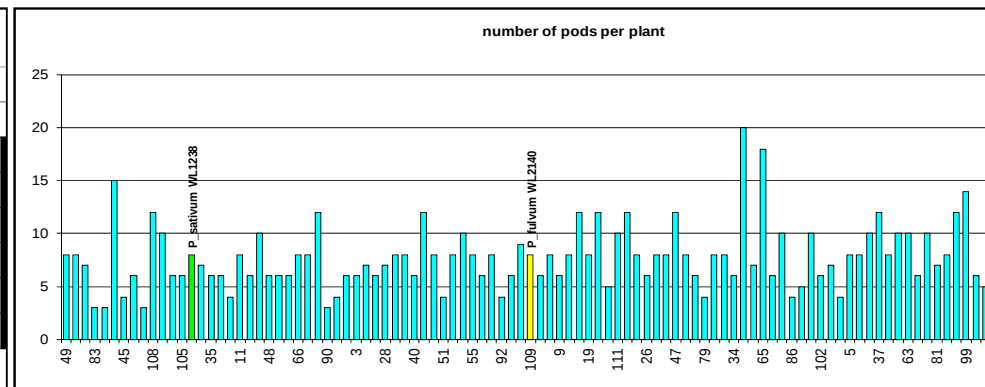
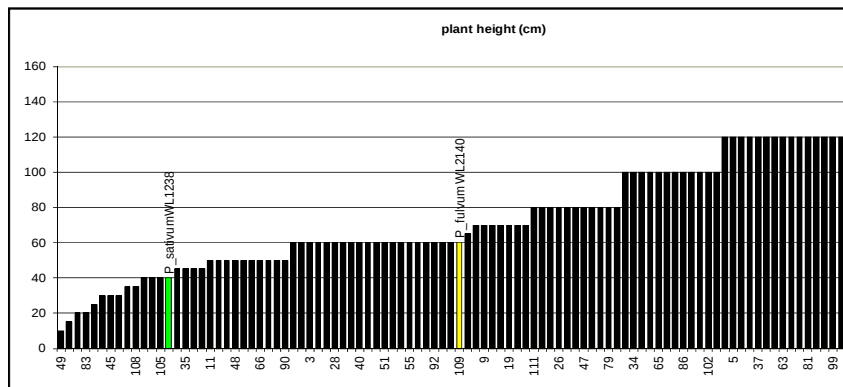
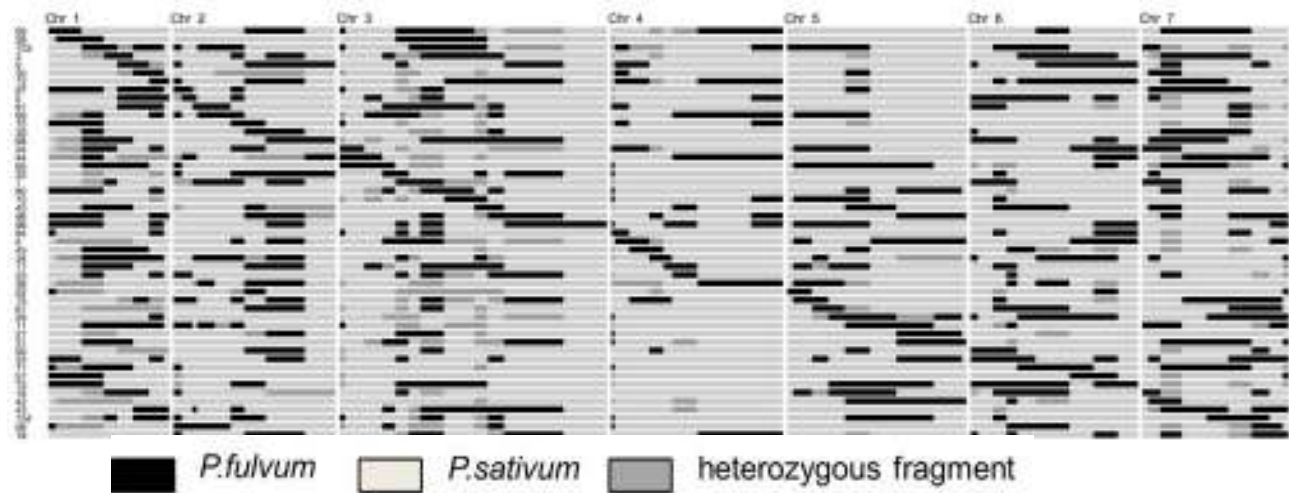
Capturing and evaluating novel genetic diversity (here from a wild pea accession)

Parent and progeny lines



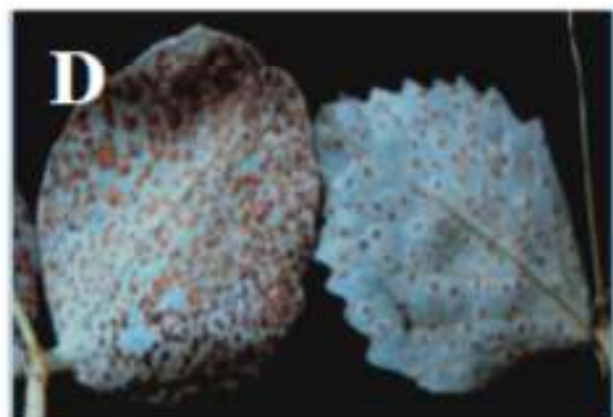
Genotyping revealing homozygous segments of P. fulvum DNA introgressed into recurrent pea parent

Morphophysiological evaluation of introgression lines

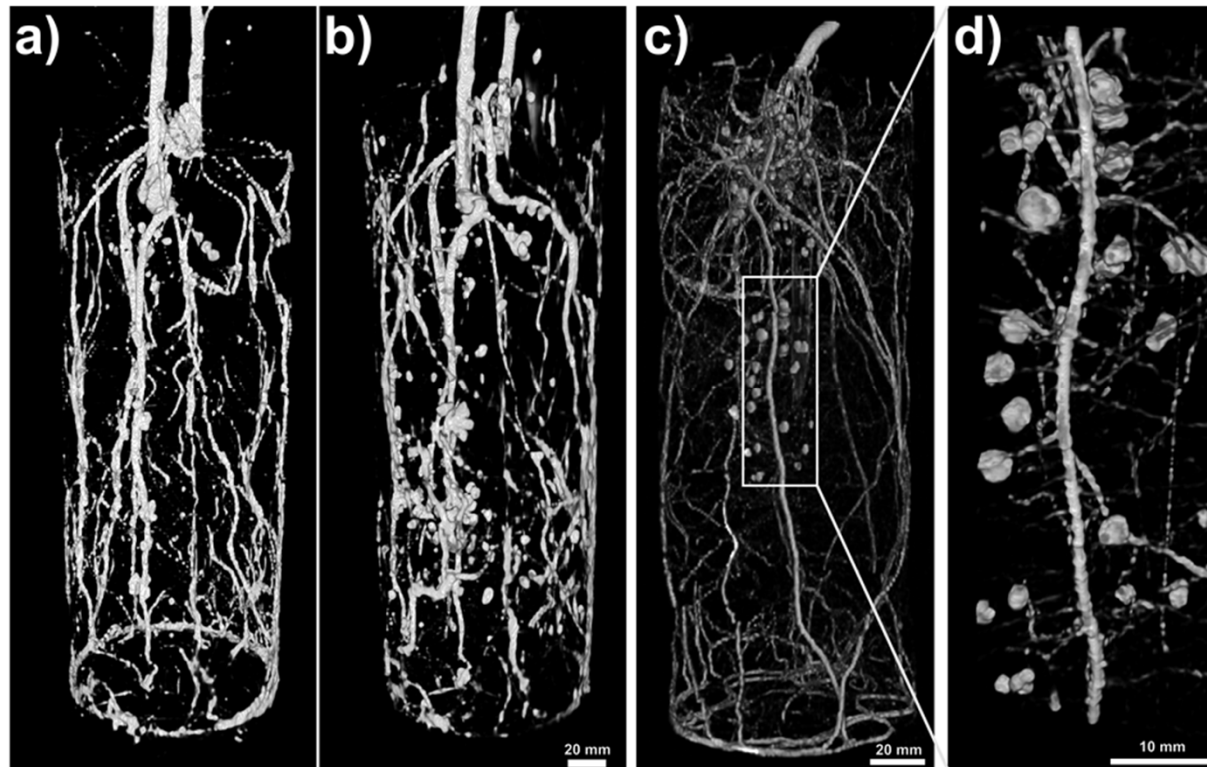


Identifying new sources of pest and disease resistance

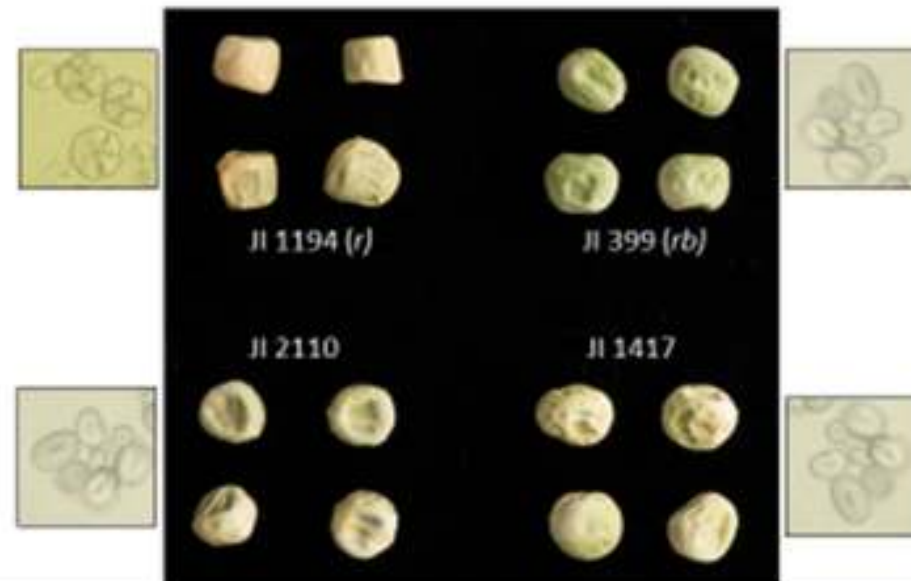
Figure WP2. Symptoms of main pea diseases or pests on susceptible (left) and resistant (right) pea accessions: (A) broomrape; (B) ascochyta blight; (C) powdery mildew; (D) rust; (E) aphid (F) weevil



Visualizing root and nodule structure by Magnetic Resonance Imaging to follow their development under drought conditions



Identifying pea lines with novel seed composition



Identification of novel variants in pea germplasm. Seeds of the four lines shown in the main photograph are wrinkled-seeded. The upper two lines are *r* and *rb* mutants. While both JI 2110 and JI 1417 have simple starch grains like JI 399, they lack a mutation at the *rb* locus. JI 2110 does not complement any of the five known mutations in the starch biosynthetic pathway leading to a wrinkled-seeded phenotype. Compound and simple starch grain morphology is shown in the small images.

Design and testing of legume-based cropping systems



Running a Pan-European GL trials Network

- 3 Climatic Zones across Europe – Mediterranean, Continental & Maritime
- 17 trials locations across climatic zones, with reference varieties and recent leaders
- 15 mainly commercial breeder partners involved: UK, France, Germany, Czech Republic, Serbia, Austria, Estonia, Greece, Italy, Spain, Portugal
- Six winter and spring legume species (mostly peas and faba bean)
Pea, faba bean, chick pea, grass pea, white & yellow lupin
- Detailed phenotypic evaluation over 2 seasons





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**Thank you for your
attention**

<http://legato-fp7.eu/>