



INCREASE




Valorizzazione e utilizzazione delle risorse genetiche in agricoltura,



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 Pulses Increase

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nell'80° anniversario dalla sua morte
nel carcere sovietico di Saratov

Nikolaj Vavilov

La storia e l'eredità

13 ottobre 2023

Castello Morando Bolognini
Sant'Angelo Lodigiano

in streaming sul canale YouTube
@SpazioMULSA

09:00 Registrazione

09:30 Apertura e saluti istituzionali

09:40 Introduzione al seminario, F. Salamini (Accademia dei Lincei)

10:00 Lo stalinismo e la scienza, L. Mariani (MULSA e Università di Brescia) e D. Maghradze (Georgian Technical University)

10:20 Nikolaj Vavilov: breve biografia e opera scientifica, O. Falta (MULSA e Università di Milano)

10:40 La domesticazione delle piante: una questione di caratteri, P. Morandini (MULSA e Università di Milano)

11:00 Cooperazione in Europa per la conservazione del germoplasma vegetale, L. Maggioni (European Cooperative Programme for Plant Genetic Resources - ECPGR)

11:20 Valorizzazione e utilizzazione delle risorse genetiche in agricoltura, R. Papa (Università Politecnica delle Marche)

11:40 Sulle orme di Vavilov: la ricerca delle resistenze alle malattie fungine della vite nel Caucaso, S. Tofflatti e G. De Lorenzis (Università di Milano)

12:00 Discussione e considerazioni conclusive

12:30 Inaugurazione del nuovo punto espositivo del MULSA sulla "Domesticazione delle piante" dedicato a Carlo Soave, T. Maggiore (MULSA e Università di Milano) e A. Dalì (MULSA)

Roberto Papa

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UNIVERSITÀ
POLITECNICA
DELLE MARCHE



INCREASE – Intelligent Collections of Food Legumes Genetic Resources for European Agrofood Systems

The INCREASE project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 862862.



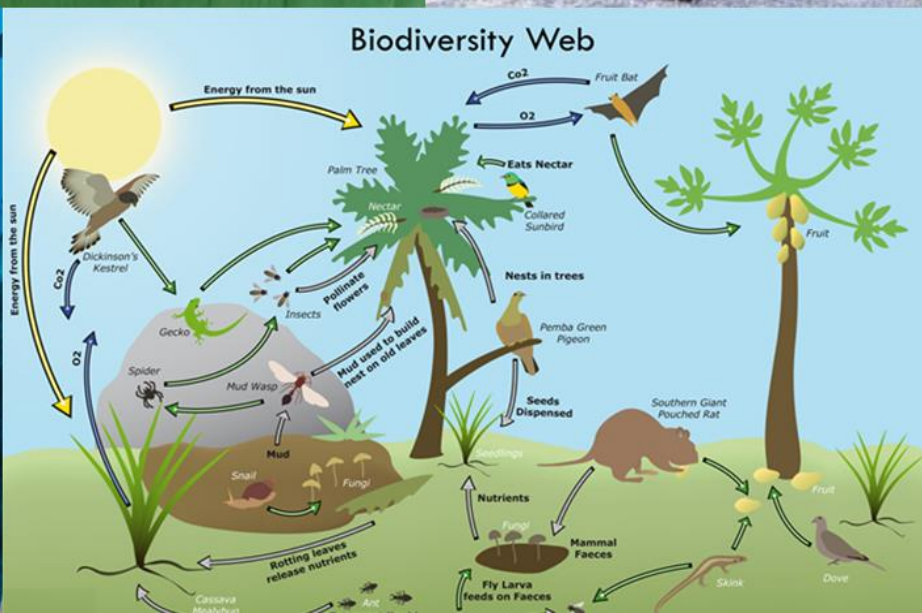
The INCR

ment No 862862.

While agrobiodiversity and agricultural genetic resources are crucial for global food security, their conservation is insufficient.



We should be drawing from the existing genetic wealth preserved in seed banks and putting this diversity to use. That is the goal of the INCREASE project, including an innovative, decentralised approach to seed conservation

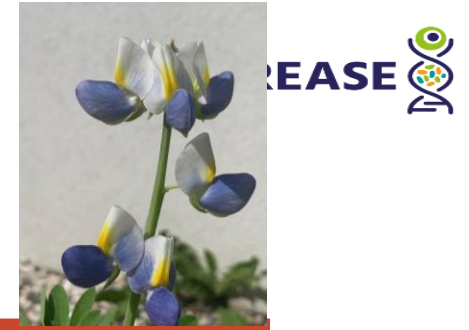


Common bean germplasm trials in Himalayan Kashmir valley India

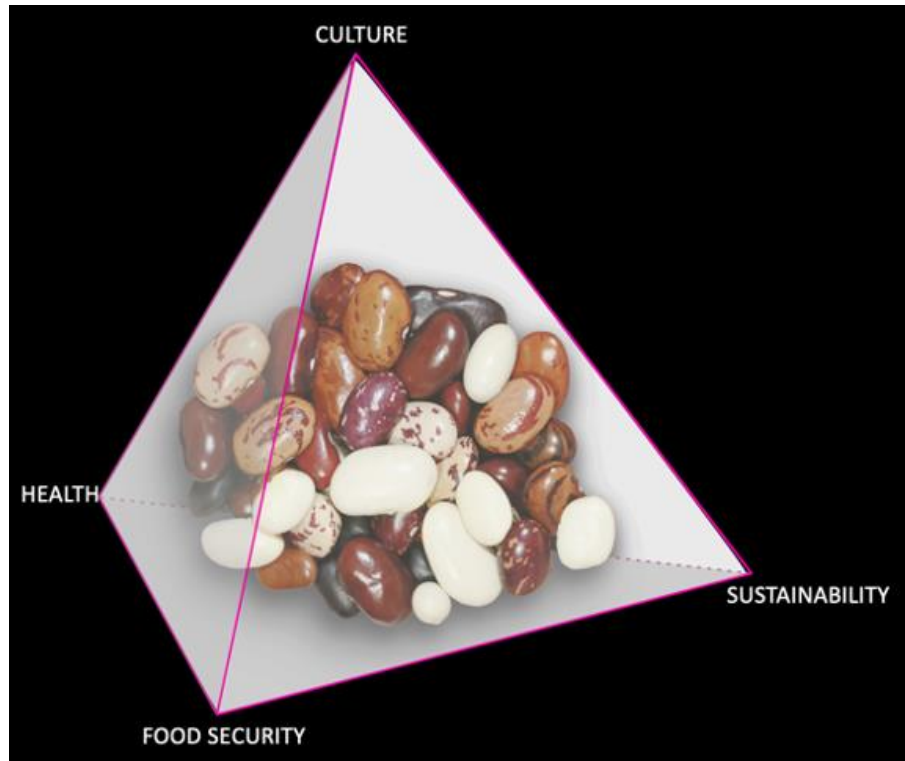


($2n=50$; $\sim 450M$)

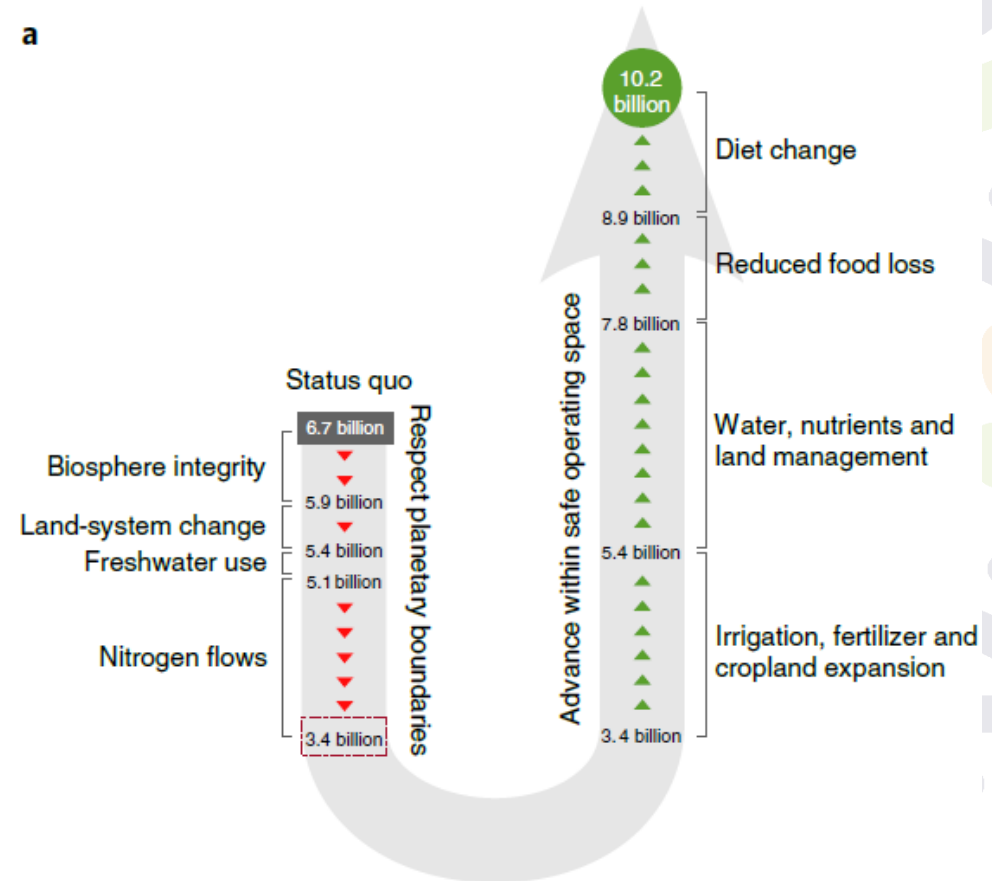
FOOD LEGUMES: Feeding the growing population respecting planetary boundaries



NATURE SUSTAINABILITY



a



Chickpea
Cicer arietinum
 (2n=2x=16; ~740Mbp)

Common bean
Phaseolus vulgaris
 (2n=2x=22; ~520Mbp)



Lentil
Lens culinaris
 (2n = 14, ~4Gb)

White Lupin
Lupinus albus
 (2n=50; ~450Mbp)



L. mutabilis (2n=48; ~930 Mbp)

PERSPECTIVES

The INCREASE project: Intelligent Collections of food-legume genetic resources for European agrofood systems

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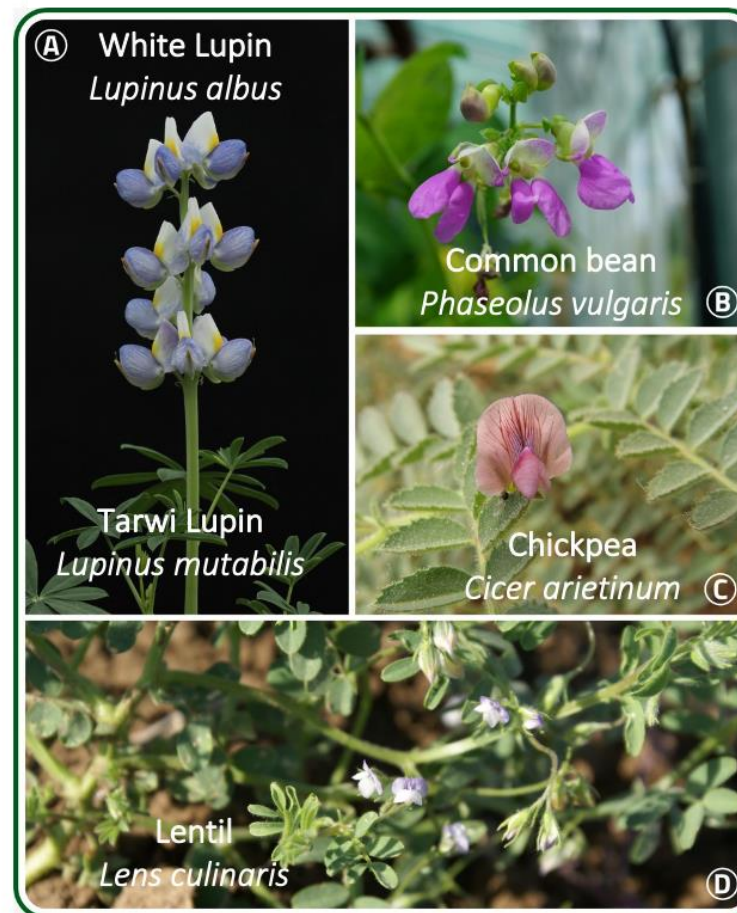
²⁷Center of Excellence in Genomics and Systems Biology (CEGSB), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India,

²⁸State Agricultural Biotechnology Centre, Centre for Crop and Food Innovation, Food Futures Institute, Murdoch University, Murdoch, Western Australia, Australia,








²⁹CBOF - Centro de Biotecnologia e Quimica Fina - Laboratório Associado, Escola Superior de Biotecnologia, Universidade Católica Portuguesa, Rua Diogo Botelho 1327, Porto 4169-005, Portugal,

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-  SSD lines included in the different intelligent collections (sample size)
-  SSD passport data
-  Genotyping (at different depths and coverage, GBS, WGS, PanGenomes)
-  Whole Plant Classical and Molecular Phenotyping
-  MLFT (Multi Location Field Trials)
-  Image Analyses
-  Controlled condition experiments
-  Quality and Nutritional phenotyping

CURRENT PROTOCOLS

PROTOCOL |  Open Access |    

Towards the Development, Maintenance, and Standardized Phenotypic Characterization of Single-Seed-Descent Genetic Resources for Common Bean

<https://www.pulsesincrease.eu/publications/academic-publications>

CURRENT PROTOCOLS

PROTOCOL |  Open Access |    

Towards Development, Maintenance, and Standardized Phenotypic Characterization of Single-Seed-Descent Genetic Resources for Lupins

Magdalena Kroc, Magdalena Tomaszewska, Katarzyna Czepiel, Elena Bitocchi, Markus Oppermann, Kerstin Neumann, Luis Guasch, Elisa Bellucci, Saleh Alseikh, Andreas Graner, Alisdair R. Fernie, Roberto Papa, Karolina Susek ... See fewer authors

CURRENT PROTOCOLS

PROTOCOL |  Open Access |    

Intelligent Characterization of Lentil Genetic Resources: Evolutionary History, Genetic Diversity of Germplasm, and the Need for Well-Represented Collections

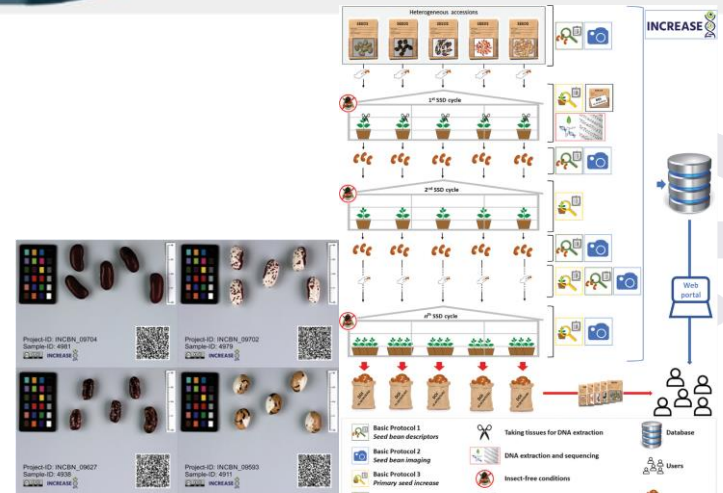
CURRENT PROTOCOLS

PROTOCOL |  Open Access |    

Towards the Development, Maintenance and Standardized Phenotypic Characterization of Single-Seed-Descent Genetic Resources for Chickpea

Lorenzo Rocchetti, Tania Gioia, Giuseppina Logozzo, Creola Brezeanu, Luis Guasch Pereira, Lucia De la Rosa, Stefania Marzario, Alice Pieri, Alisdair R. Fernie, Saleh Alseikh, Karolina Susek, Douglas R. Cook, Rajeev K. Varshney, Shiv Kumar Agrawal, Aladdin Hamwieh, Elena Bitocchi, Roberto Papa ... See fewer authors

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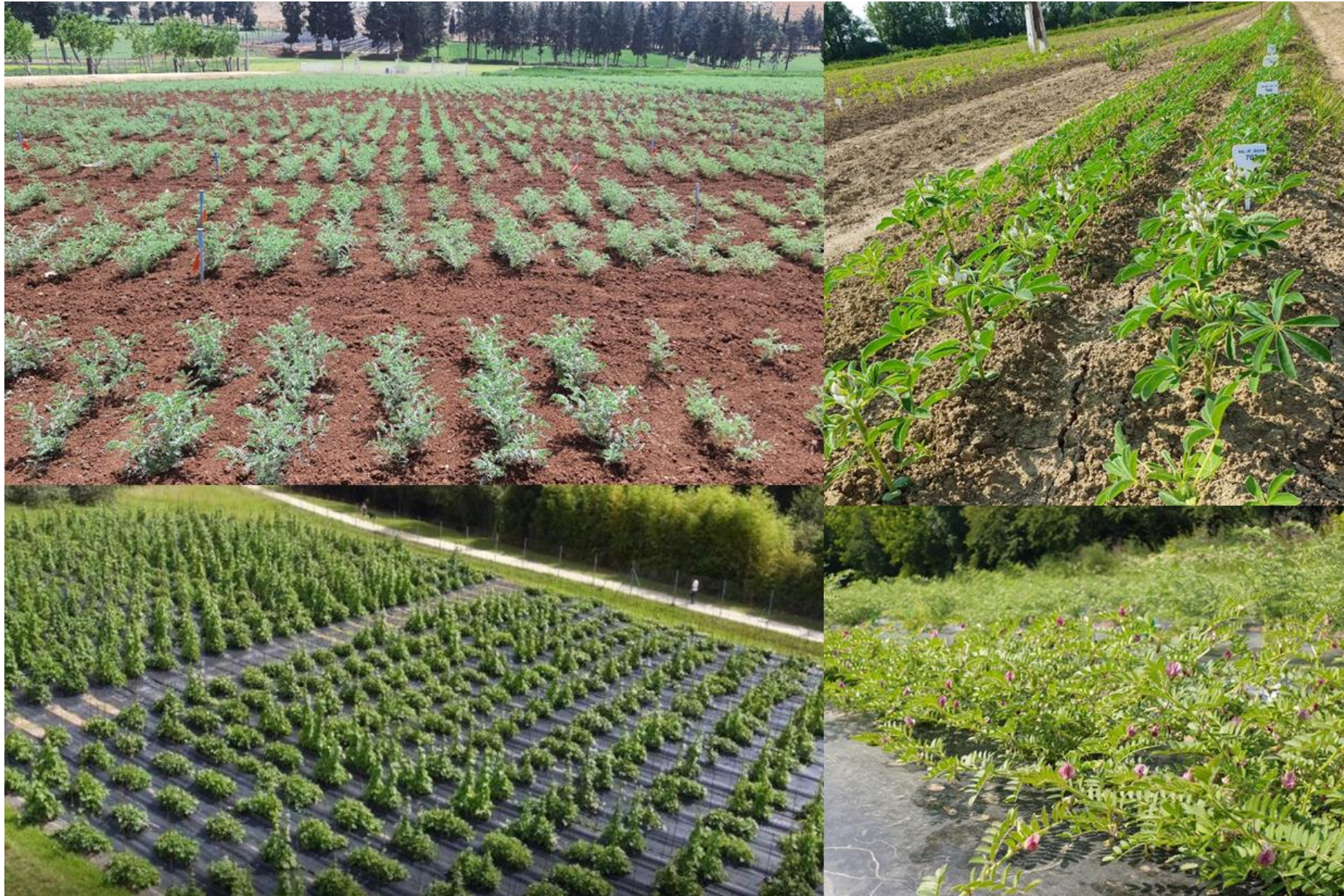


SSD development and seed increase





Multi-location field trials





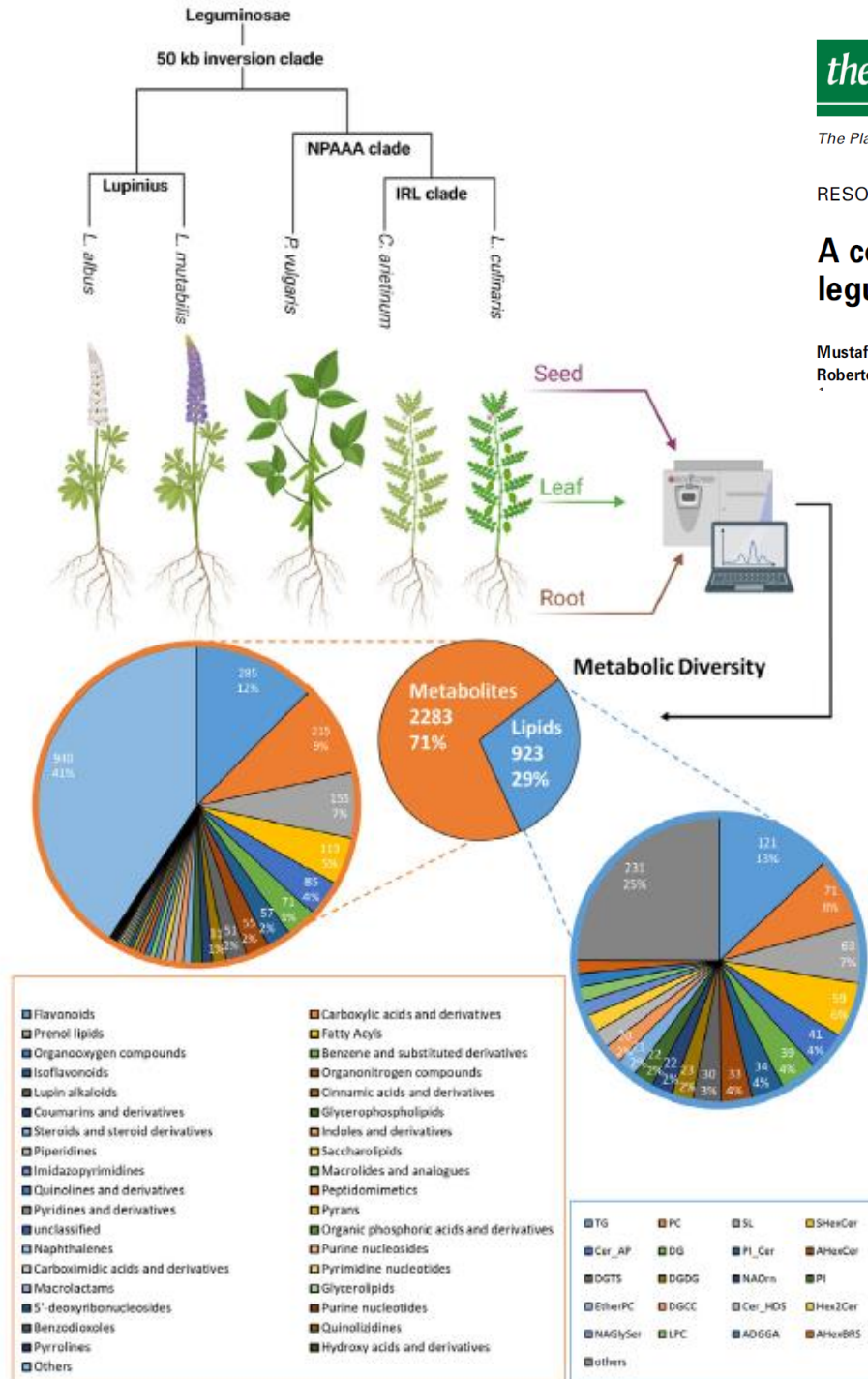
Testing for drought in controlled conditions



RESOURCE

A comprehensive metabolomics and lipidomics atlas for the legumes common bean, chickpea, lentil and lupin

Mustafa Bulut¹, Regina Wendenburg¹, Elena Bitocchi², Elisa Bellucci², Magdalena Kroc³, Tania Gioia⁴, Karolina Susek³, Roberto Papa², Alisdair R. Fernie^{1,5,7} and Saleh Alseekh^{1,5,7}




Metabolomics

Nutritional quality

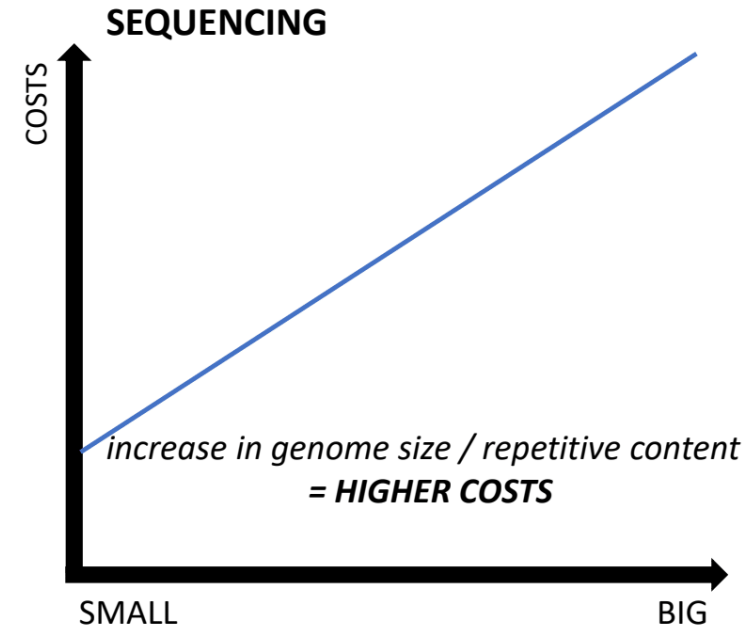
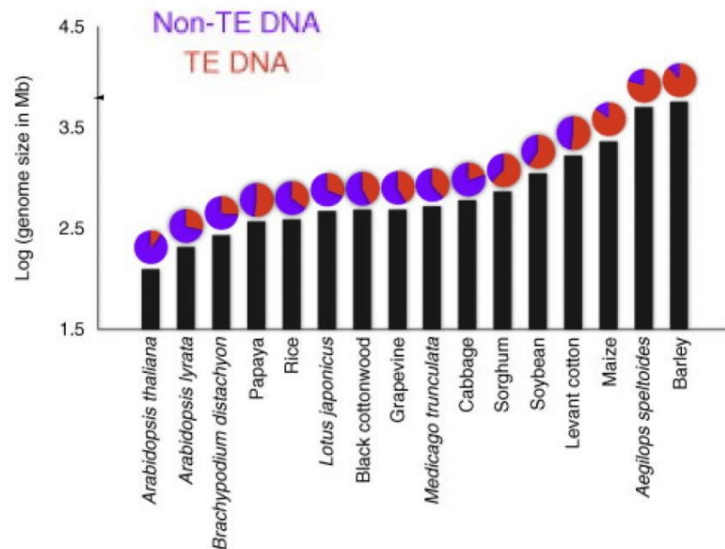
- > Mineral
- > Moisture
- > Nitrogen
- > Crude fibre
- > Amino acid
- > Flavonoids
- > Anthocyanins
- > Tocopherol
- > Phytosterol contents
- > Along with the determination of seed's technological traits



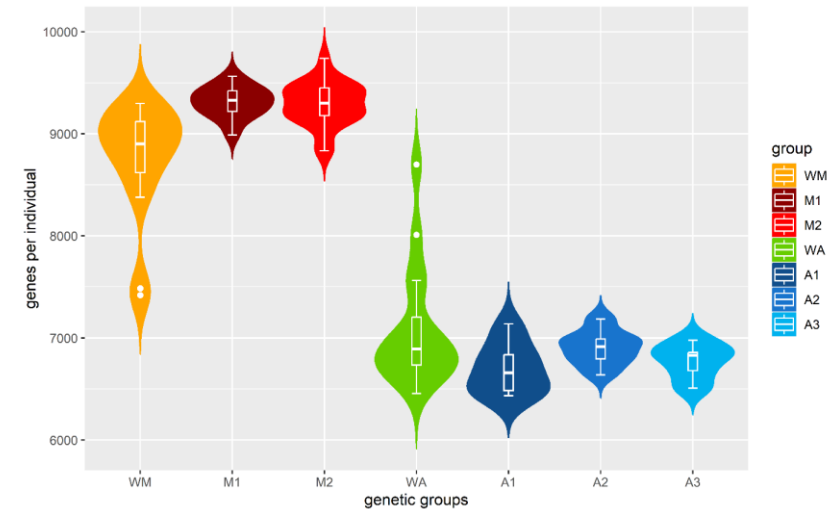
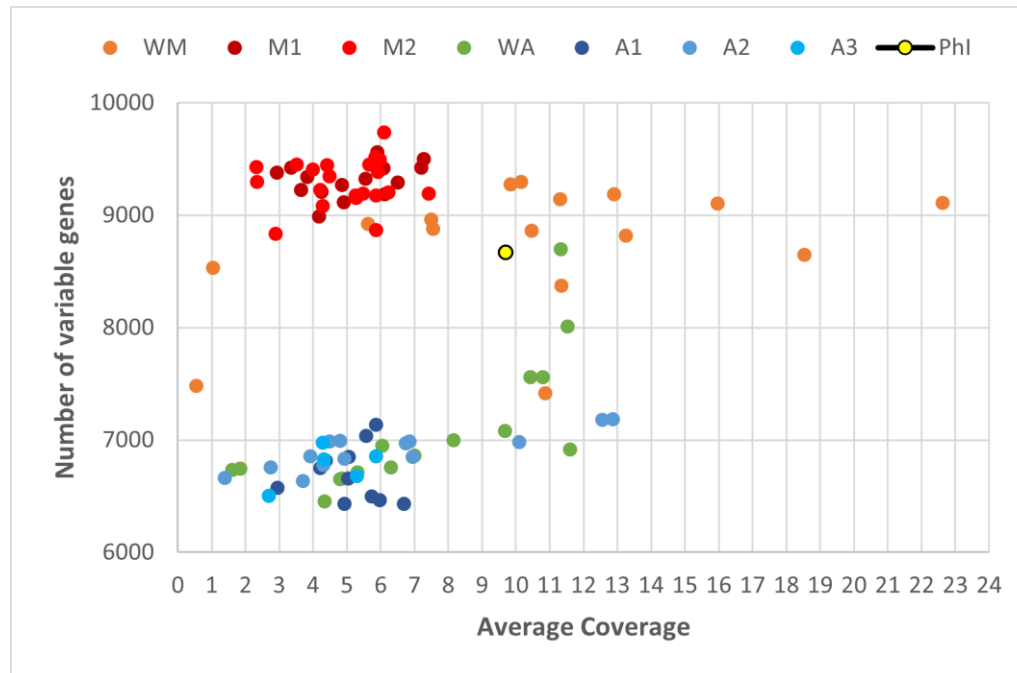
CRISPR/Cas9-based repeat depletion for the high-throughput genotyping of complex plant genomes

 Marzia Rossato, Luca Marcolungo, Luca De Antoni, Giulia Lopatriello, Elisa Bellucci, Gaia Cortinovis, Giulia Frascarelli, Laura Nanni, Elena Bitocchi, Valerio Di Vittori, Leonardo Vincenzi, Filippo Lucchini,
 Kirstin E. Bett, Larissa Ramsay, David James Konkin, Massimo Delledonne, Roberto Papa

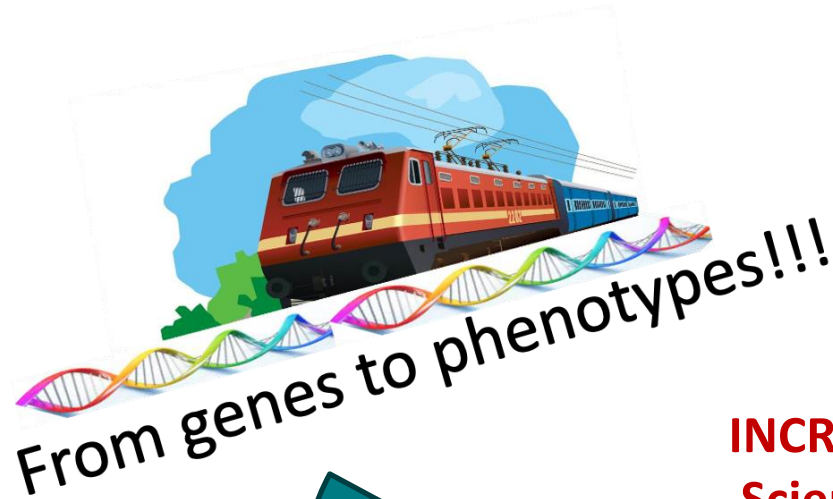
BIG GENOMES HAVE ALSO LARGE FRACTIONS OF REPETITIVE REGIONS – bigger genome, higher repetitive content -



5 high-quality genomes and the whole-genome reads of 339 genotypes. We identified ~242.78Mb sequences containing 7,495 new protein-coding genes absent from the reference and a high proportion of presence-absence variations (PAV 42%)



INCREASE primo pilastro: sviluppo dell'infrastruttura genomica per valorizzare le risorse genetiche dei legumi alimentari



Caratteri e ambienti di interesse, Scienza Partecipativa, Tecnologie innovative e smart



INCREASE: secondo pilastro: Scienza partecipata, coinvolgimento degli stakeholders e scienza dei cittadini

Collezioni basate su line pure, Collezioni ben studiate utilizzando la genomica e la Phenomica: predizione genomica e sistemi di visualizzazione dei dati di facile utilizzazione



RICERCA PARTECIPATA

Sort by countries Sort by main area of interest

Australia
> Professor David Edwards - University of Western Australia

Belgium
> Meise Botanic Garden
> Inagro
> ILVO

Bulgaria
> Roman Rachkov / Bulgarian association for biological plant protection

China
> Fardous Mohammad Safiul /

Colombia
> Universidad de la Amazonia

Czech Republic
> Agricultural Research, Ltd.

France
> ALPAD-Association Landaisi
> Semences de Provence
> CRBA - Centre de Ressource
> Cérience

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> Hof Sprenger / Benedikt Spr
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> Institute for Crop Science ar
> Forschungszentrum Jülich PI
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> Tiny Farms Leiber & Fels GbR
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> COMUNE DI VALDAGNO (per Museo Civico D. Dal Lago e E
> Arca sri Benefit
> Istituto di Istruzione Superiore "Caravaggio"
> Istituto di Istruzione Superiore "Arrigo Serpieri"
> LEGUMI CHE PASSIONE
> L'orto di Mendel
> Raffaella Maria Balestrini
> VIVOSEM Sri
> Orto Botanico di Bergamo "Lorenzo Rota"
> ASD CALICANTO ONLUS
> Valdibella Cooperativa Agricola
> We are here Venice
> Società Agricola Monte Monaco sri
> Francesco d'Assisi Soc. Coop. Soc.
> Federazione delle Associazioni Rurali Italiane (FARI)
> Vallesina Bio
> ECPGR
> Comizio Agrario
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> Fondazione Alessio Tavecchio Onlus
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> Istituto di Istruzione Superiore Bruno Munari - Istituto Professionale per l'Agricoltura e L'ambiente Be
> Istituto di Istruzione Superiore "VERGANI - NAVARRA"
> Pro Loco Appignano A.P.S
> Terre Paduli Azienda Agricola di Gianni Casaluce

> Istituto Tecnico Agrario "Dionisio Anzilotti"
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Lithuania
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Poland
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> Fundacja Alter Eko (FAE)

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> Agrovegetal S.a.
> Instituto de Educación Secundaria Aljarafe
> Colegio Aljarafe SCA

Switzerland
> gzpK

The Netherlands
> Pulsbio

Turkey
> Aysen Yumurtaci

USA
> Eric von Wettberg, University of Vermont

Ukraine
> Institute of Oilseed Crops of the National Academy of Agrarian Sciences
> OIha Vazhenina / Plant Production Institute named after V.Ya. Yuriev of NAAS

United Kingdom
> Legumology Limited
> Andrea Bertocco / Herbalife Nutrition
> Christine Helen Foyer
> The James Hutton Institute
> Royal Botanic Gardens Kew
> University of Nottingham





Special aim: Prebreeding in genetic resources of Common bean



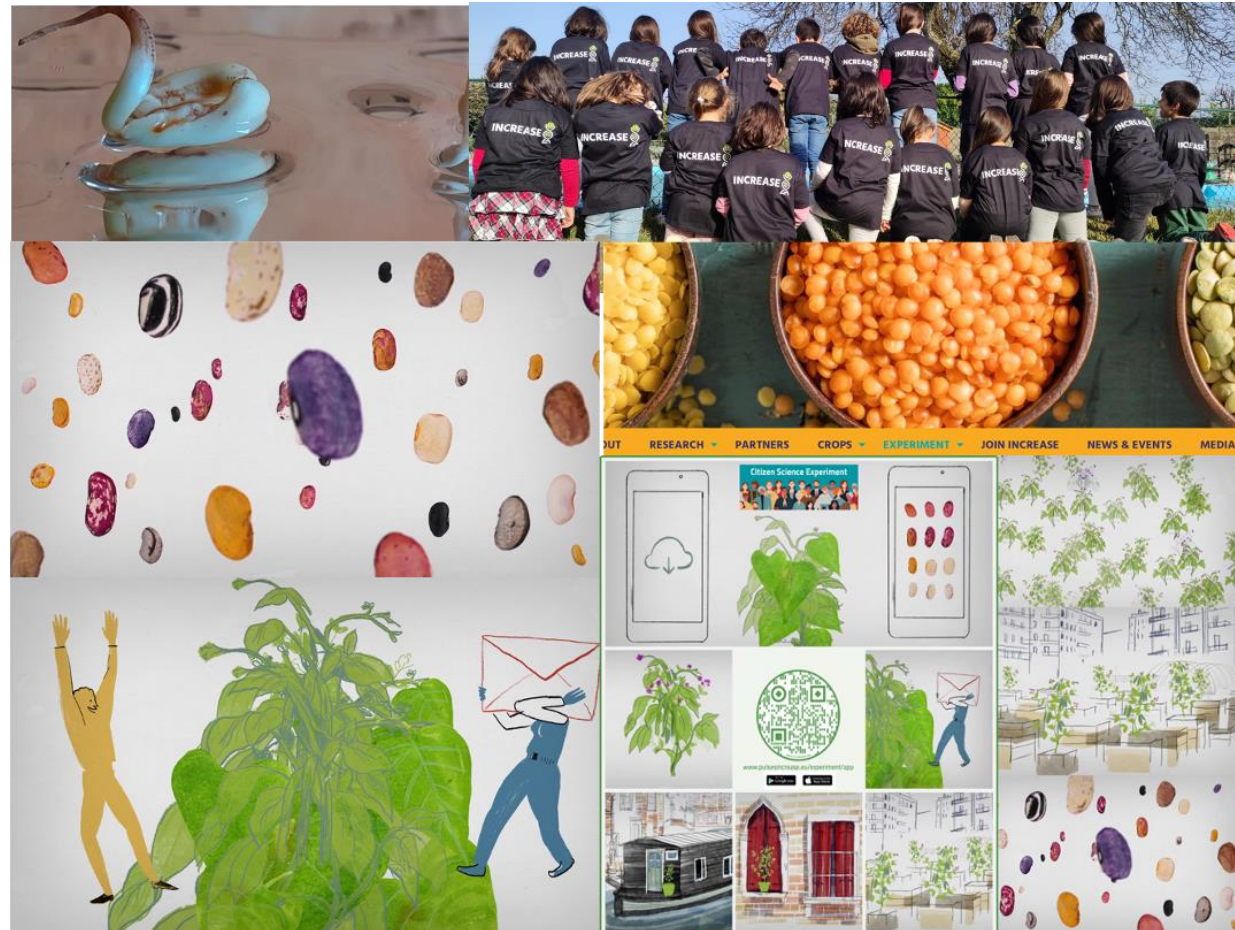
Citizen Science Experiment

Main aims:

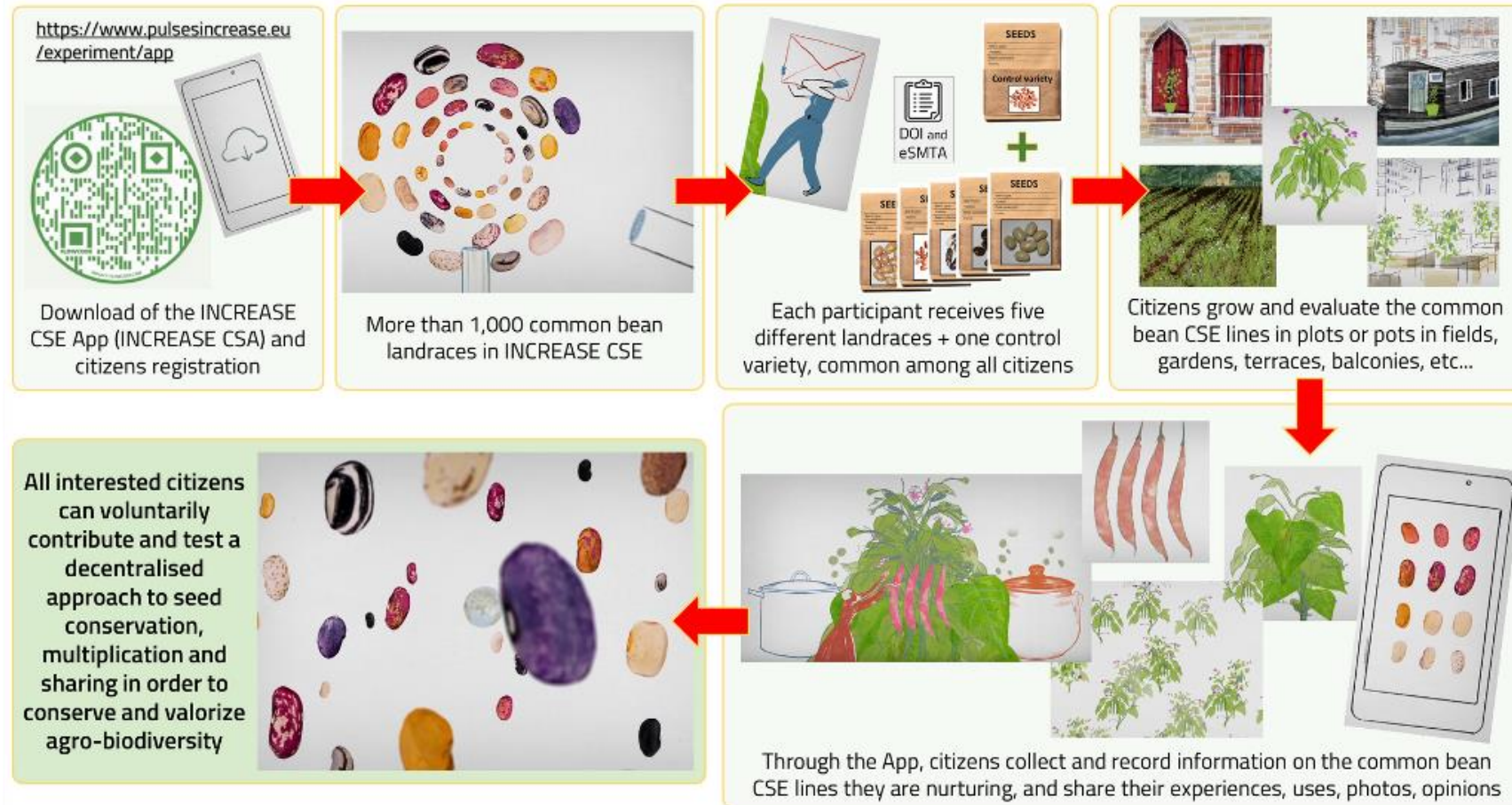
Increase citizen awareness about PGR

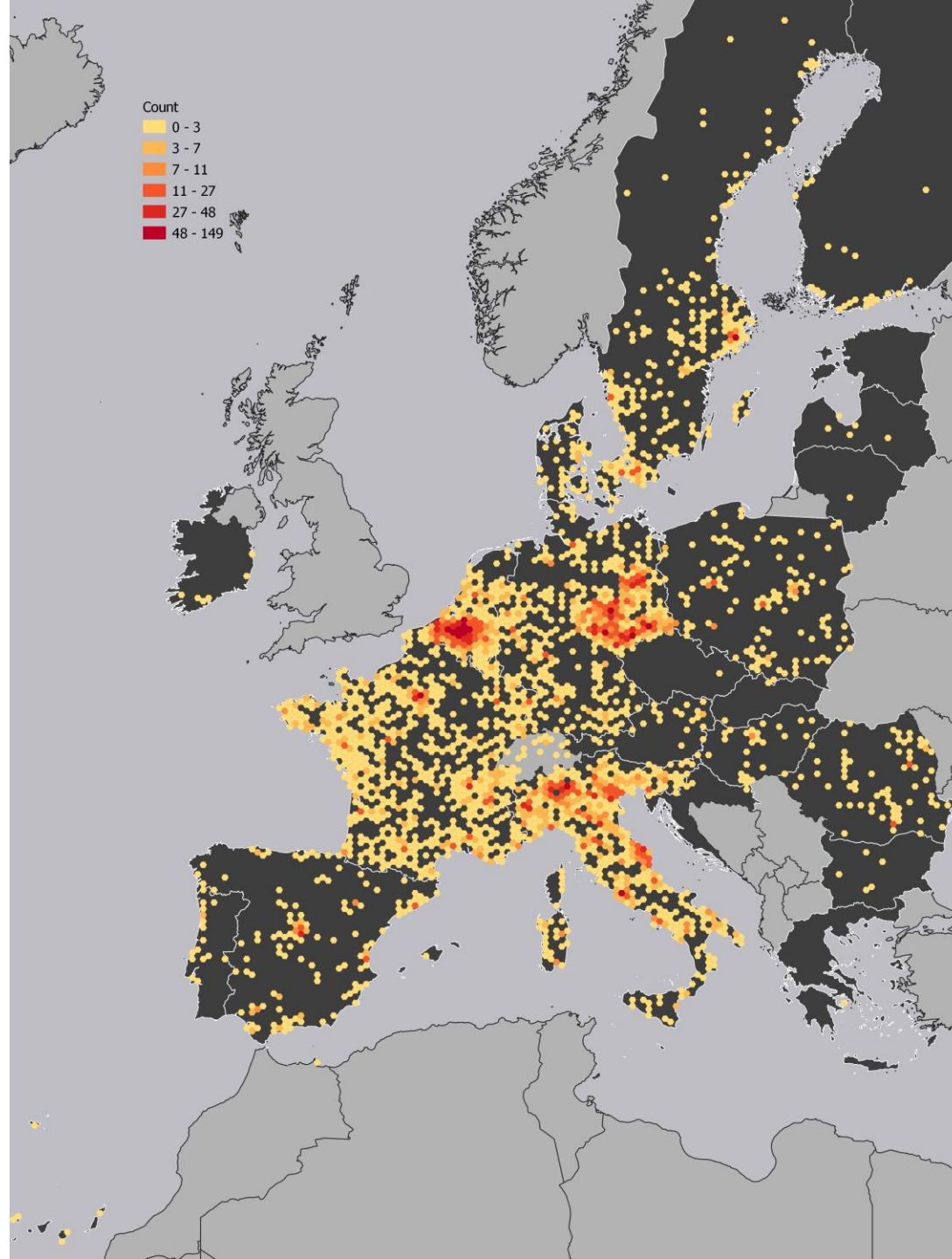
Phenotyping more than 1000 SSD lines of *P. vulgaris* across multiple environments

Test a decentralised conservation approach feasibility and develop a prototype



The CSE in a nutshell



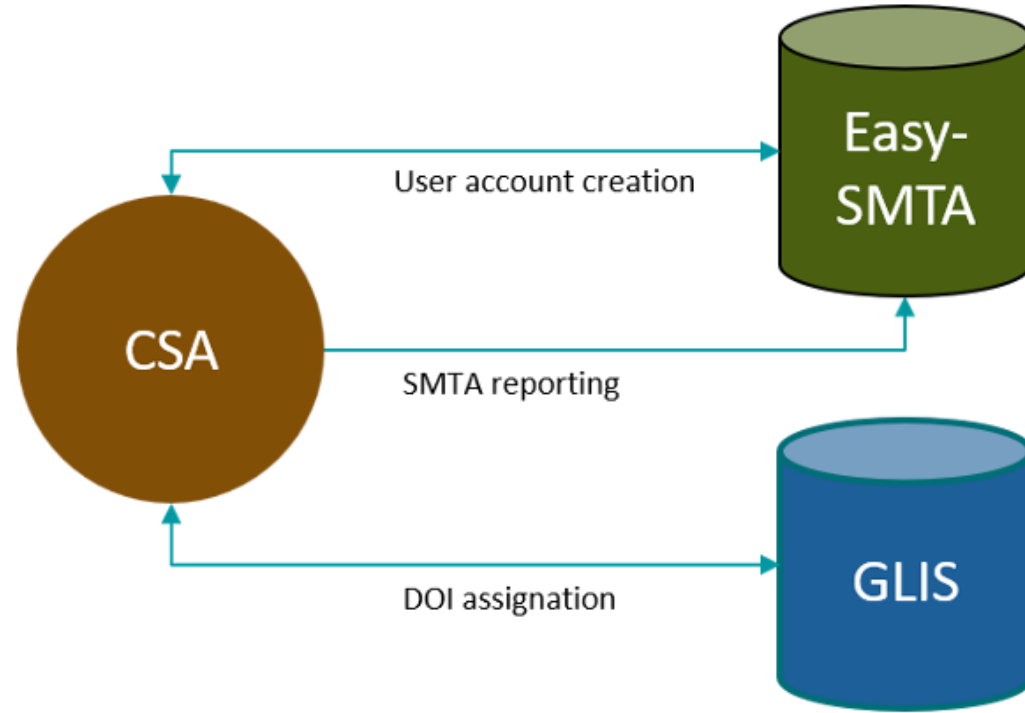


2023:
9293 cittadini
registrati da 29 paesi

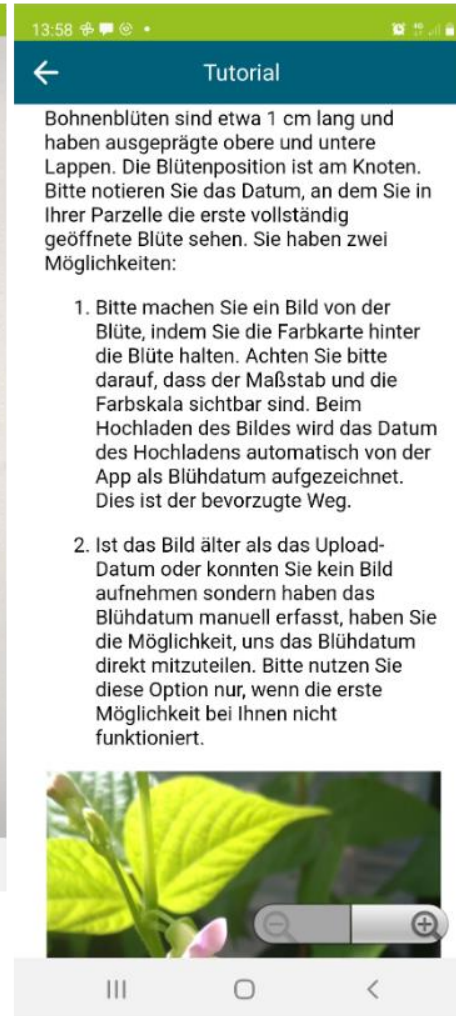
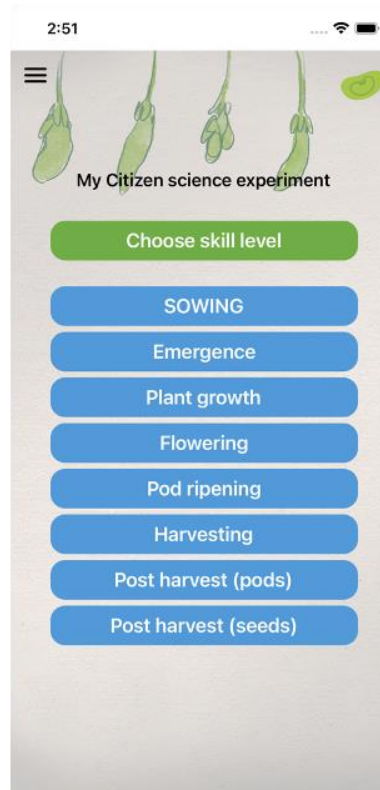
2021-2023
16799 cittadini
+ 270% incremento
rispetto 2021



Tracciabilità e integrazione nel Sistema GLIS gestito dall' ITPGRFA-FAO



Phenotyping beans with help of App INCREASE CSA



Selection and adaptive introgression guided the complex evolutionary history of the European common bean

Received: 1 June 2022

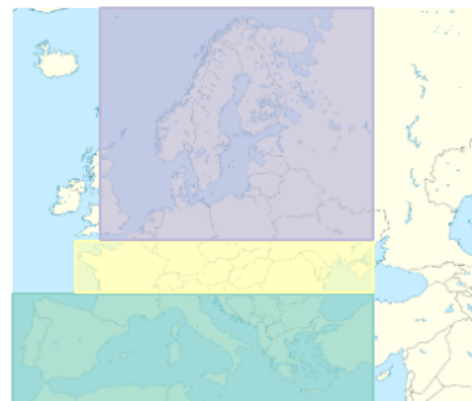
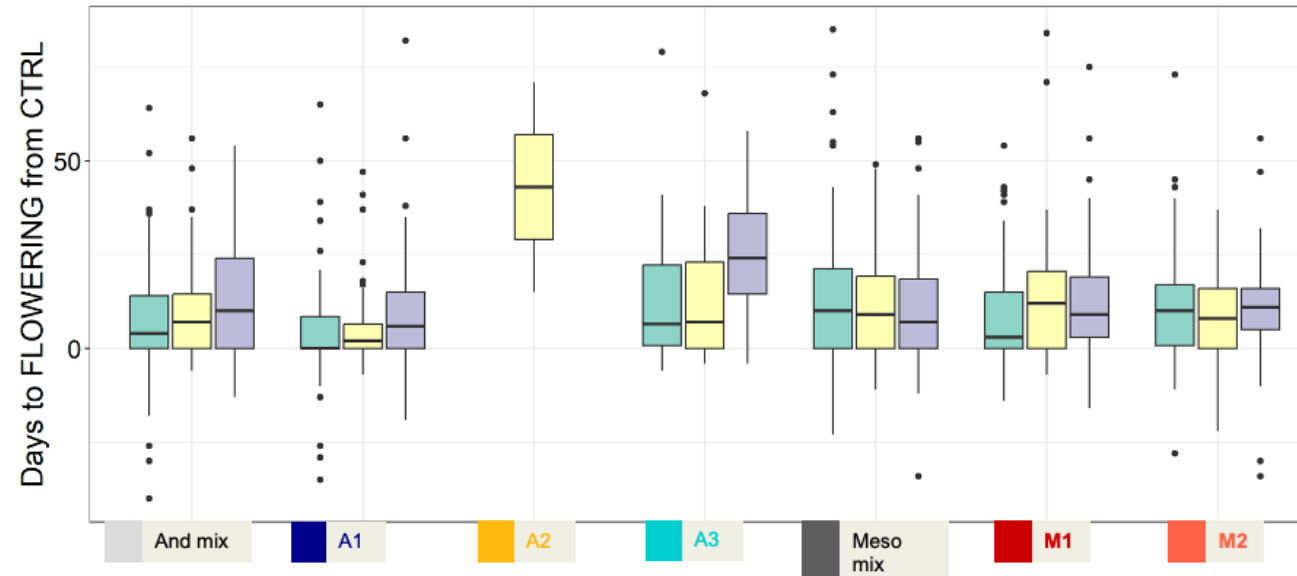
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 Check for updates

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 Alisdair R. Fernie^{6,7,10}, Scott A. Jackson^{3,10} & Roberto Papa^{1,14,10} ✉

Distribution of days to FLOWERING standardized with the CTRL line (DAYS BEFORE/AFTER THE CTRL) of the different Gene pools across European Geographical Areas



South	
A1	- 78
A2	- 0
A3	- 24
And mix	- 73
M1	- 85
M2	- 80
Meso mix	- 84

Center	
A1	- 43
A2	- 2
A3	- 21
And mix	- 59
M1	- 63
M2	- 53
Meso mix	- 76

North	
A1	- 71
A2	- 0
A3	- 23
And mix	- 45
M1	- 67
M2	- 70
Meso mix	- 86



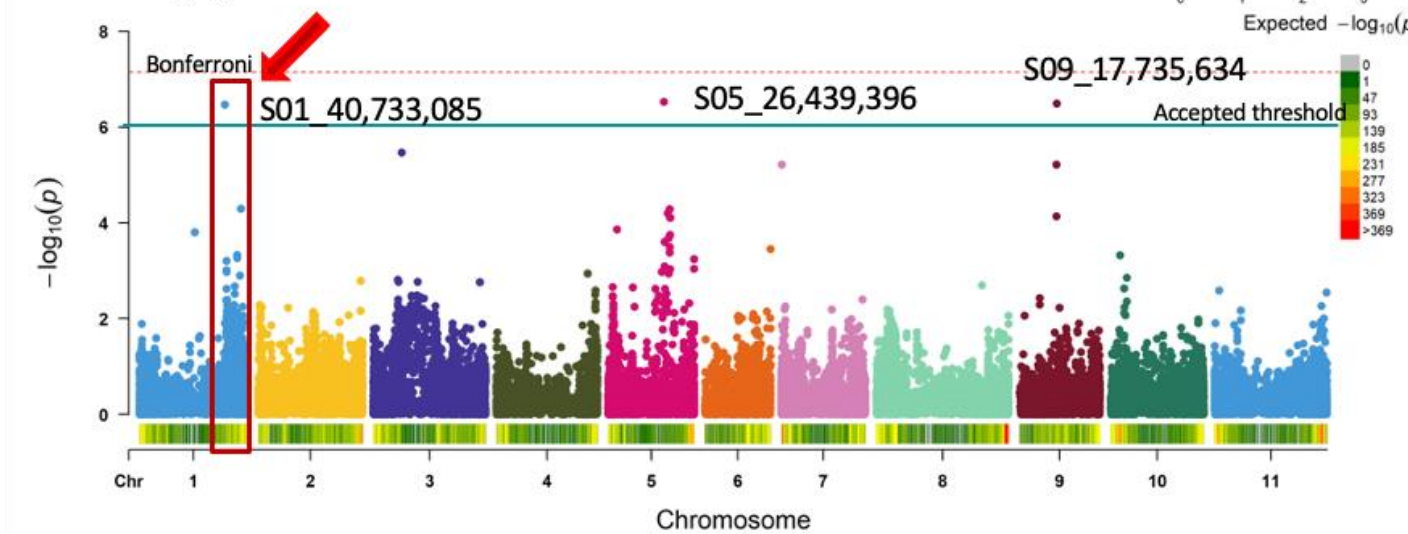
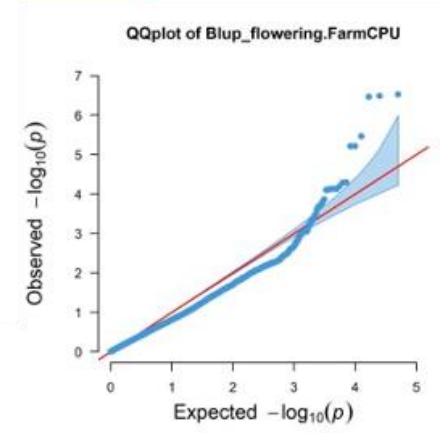
Ongoing...
Flowering GWAS – explorative results

3) **GWAS** model FarmCPU

$$Y = G + Q + K$$

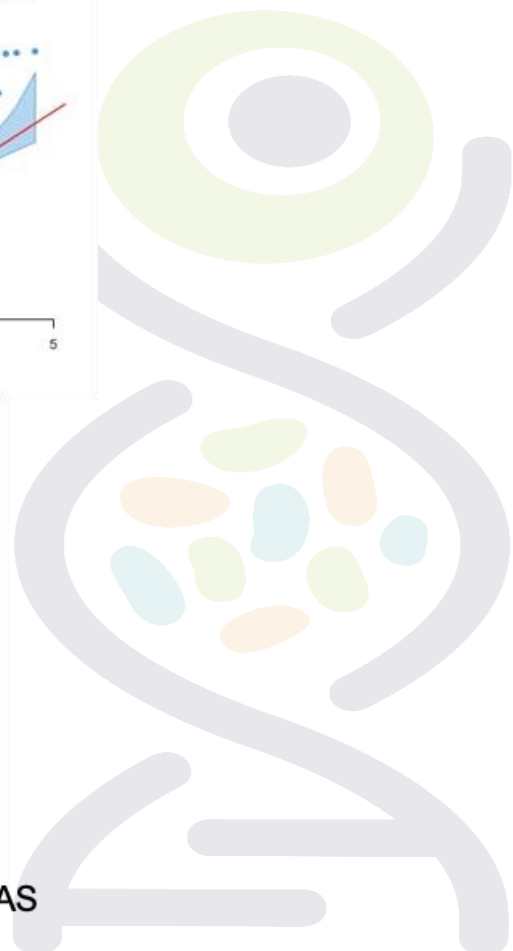
\downarrow BLUP values
 \downarrow Admixtur e Qi values K=2
 \downarrow Kinship matrix IBD

- 669 genotypes
- 50,155 GBS SNPs



On Chr1 hotspot region of genes associated to flowering observed also in BeanAdapt GWAS

- Awaiting daily weather data
- More replicates per genotype (Round 3)
- Additional Sequence data – also WGS





Dalla scienza dei cittadini alla Conservazione decentralizzata delle risorse genetiche agrarie





Grazie!!

