Evolution in a changing environment: the genetic architecture of adaptation outside centers of domestication of *Phaseolus vulgaris* and *P. coccineus*
To dissect out the genetic basis and phenotypic consequences of the adaptation to new environments of the common bean and the runner bean, through the study of their introduction, from their respective centers of domestication in the Americas, and expansion through Europe, as a recent and historically well-defined event of rapid adaptation.
PROJECT AIM

GbS on 11,500 Accessions
Resequencing 260 genotypes
Transcriptomics and
Metabolomics
Population genomics
Admixture mapping
GWAS

Genes for adaptation
MAIN DELIVERABLES

• An immortal collection of pure lines in *P. vulgaris*

• Complete molecular and phenotypic characterization and Computed haplotypes for all the collection

• Genes controlling adaptation (signature of selection, traits-environmental variable association, expression analysis, validation of candidates genes)
WORK PACKAGES and WORKFLOW

WP1 - Germplasm sampling and characterization

WP2 - Genomics (WGS/ RNA-seq)

WP3 - Phenotyping

WP4 - Bioinformatics, data storage and sharing

WP5 - Data Analysis

WP6 - Project coordination and management

WP7 - Dissemination
Deep genomic and phenotypic characterization of the whole collection and Haplotype reconstruction (BeanHapMap)

**ACTIVITIES and OUTCOMES**

- Transcriptomics
- Metabolomics
- Phenotypes controlled conditions 200 lines
- Phenotypes MLFT
- WGS 200 pure lines and GbS on 500
- GbS 10,000 pure lines from landraces (Pv_ALL)

single seed purified accessions
50% from America and 50% from Europe

P. vulgaris

10,000

500

200
51° N - IPK Gatersleben
Germany
Average Summer Sunhour
220 hour/month
Daylight hours 16/8
Day temperature 22°C

40° N – UNIBAS Potenza
Italy
Average Summer Sunhour
300 hour/month
Daylight hours 14/10
Day Temperature 23°C
GERMANY Field trial 2016 (seed increase)
Max Planck Golm
Metabolomic – RNA seq experiment
Max Planck
Metabolomic – RNA seq experiment

Harvested third fully expanded true leaf

RNA seq →

LC-MS
GC-MS
Center for Applied Genetic Technologies
GBS activity

- DNA extraction
- Enzyme digestion
- 96 Barcoded Adapter Ligation
- 96 Pool & PCR
- NextSeq 96-plex, SE150

NextSeq 500
DNA extraction
DNA fragmentation
Illumina PCR free library construction
HiSeq2000
→ Germplasm and sample definition

→ Field activities and seed increase (tropical environment condition)
expanding the scope and the impact

ASSOCIATED PARTNERS

Collaborative network
cooperation and association to specific activities

Phenotyping (field trials, seed traits, nutritional value, abiotic and biotic stress, roots)
Genetic resources and germplasm
Genomic information and molecular data
Dissemination
Ex situ conservation of 10,000 pure lines

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Thanks for your attention

Evolution of Human bean