Evolution in a changing environment: the genetic architecture of adaptation outside centers of domestication of *Phaseolus vulgaris* and *P. coccineus*

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WHY BEAN?

Phaseolus vulgaris L.

Family: Leguminosae **- Genus:** *Phaseolus*

Diploid species (2n = 2x = 22)

Annual and predominantly self-pollinating (autogamous) species

- The most important **food and feed legume** for direct consumption
- Crucial **protein, vitamin and mineral source** for farmers in Latin America and Africa
- **Health benefits** and human disease prevention (lower risk of obesity, diabetes, cardiovaskular diseases, and colon, prostate and breast cancer
- Major role in development of **sustainable crop systems**
- Development of genomic tools and genetic resources for **plant breeding**

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Annibale Carracci, *The Bean Eater* , 1584-1585

Vincent Van Gogh - The Potato Eaters 1885

DOMESTICATED BEAN SPECIES

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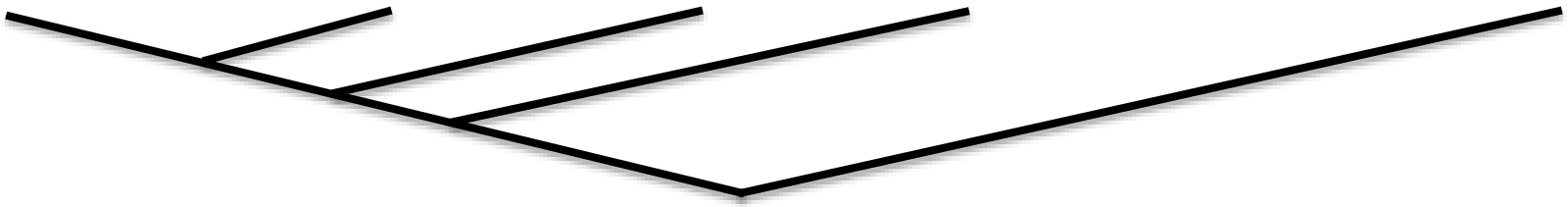
P. vulgaris (common bean)

P. dumosus

P. coccineus (runner bean)

P. acutifolius (tepary bean)

P. Lunatus (lima bean)



P. vulgaris L. in AMERICA

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PNAS

Mesoamerican origin of the common bean (*Phaseolus vulgaris* L.) is revealed by sequence data

Elena Bitocchi[a], Laura Nanni[a], Elisa Bellucci[a], Monica Rossi[a], Alessandro Giardini[a], Pierluigi Spagnoletti Zeuli[b], Giuseppina Logozzo[b], Jens Stougaard[c], Phillip McClean[d], Giovanna Attene[e], and Roberto Papa[a,1]

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New Phytologist
Volume 197, Issue 1, pages 300–313, January 2013
Research

Molecular analysis of the parallel domestication of the common bean (*Phaseolus vulgaris*) in Mesoamerica and the Andes

Elena Bitocchi[1], Elisa Bellucci[1], Alessandro Giardini[1], Domenico Rau[2], Monica Rodriguez[2], Eleonora Biagetti[1], Rodolfo Santilocchi[1], Pierluigi Spagnoletti Zeuli[3], Tania Gioia[3], Giuseppina Logozzo[3], Giovanna Attene[2], Laura Nanni[1] and Roberto Papa[1,4]

Gepts et al. 1986; Gepts & Bliss 1988; Koenig & Gepts 1989; Singh et al. 1991; Rossi et al. 2009; Becerra Velasquez & Gepts 1994; Freyre et al. 1996; Tohme et al. 1996; Papa & Gepts 2003; Blair et al. 2006; Diaz & Blair 2006; Kwak et al. 2009; Kwak & Gepts 2009; Bellucci et al. 2014; Schmutz et al. 2014

BEAN ADAPT

THE PROJECT

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GbS on 11,500 Accessions
Resequencing 560 genotypes
Transcriptomics and Metabolomics
Population genomics
Admixture mapping
GWAS

Genes for adaptation

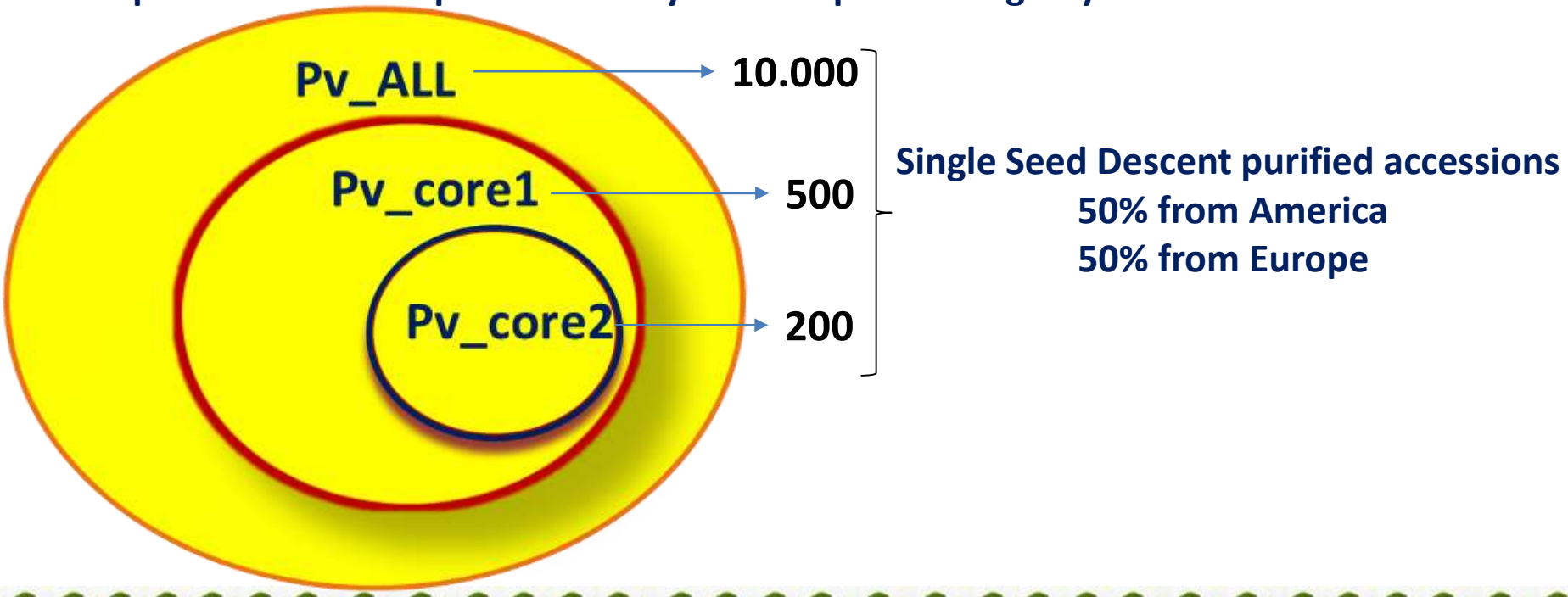
GERMPLASM & DATA

Phaseolus vulgaris

Pv_ALL: GbS

Pv_core1: GbS **WGS, phenotyping (MLFT)**

Pv_core2: GbS WGS, phenotyping (MLFT), **molecular phenotyping: Metabolomics and transcriptomics under tropical short-day vs a temperate long-day environment simulation**



WORKFLOW

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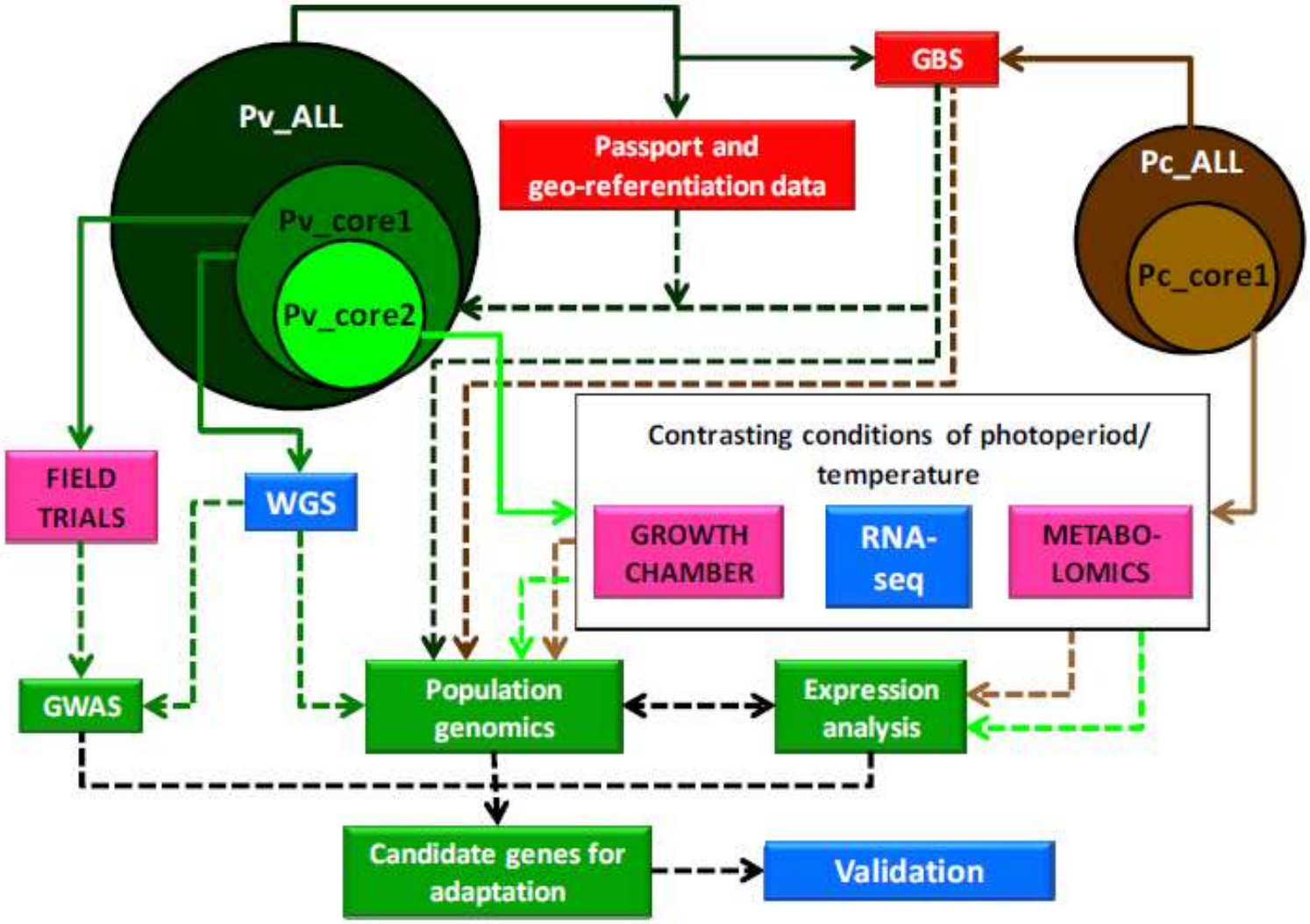

MAIN DELIVERABLES

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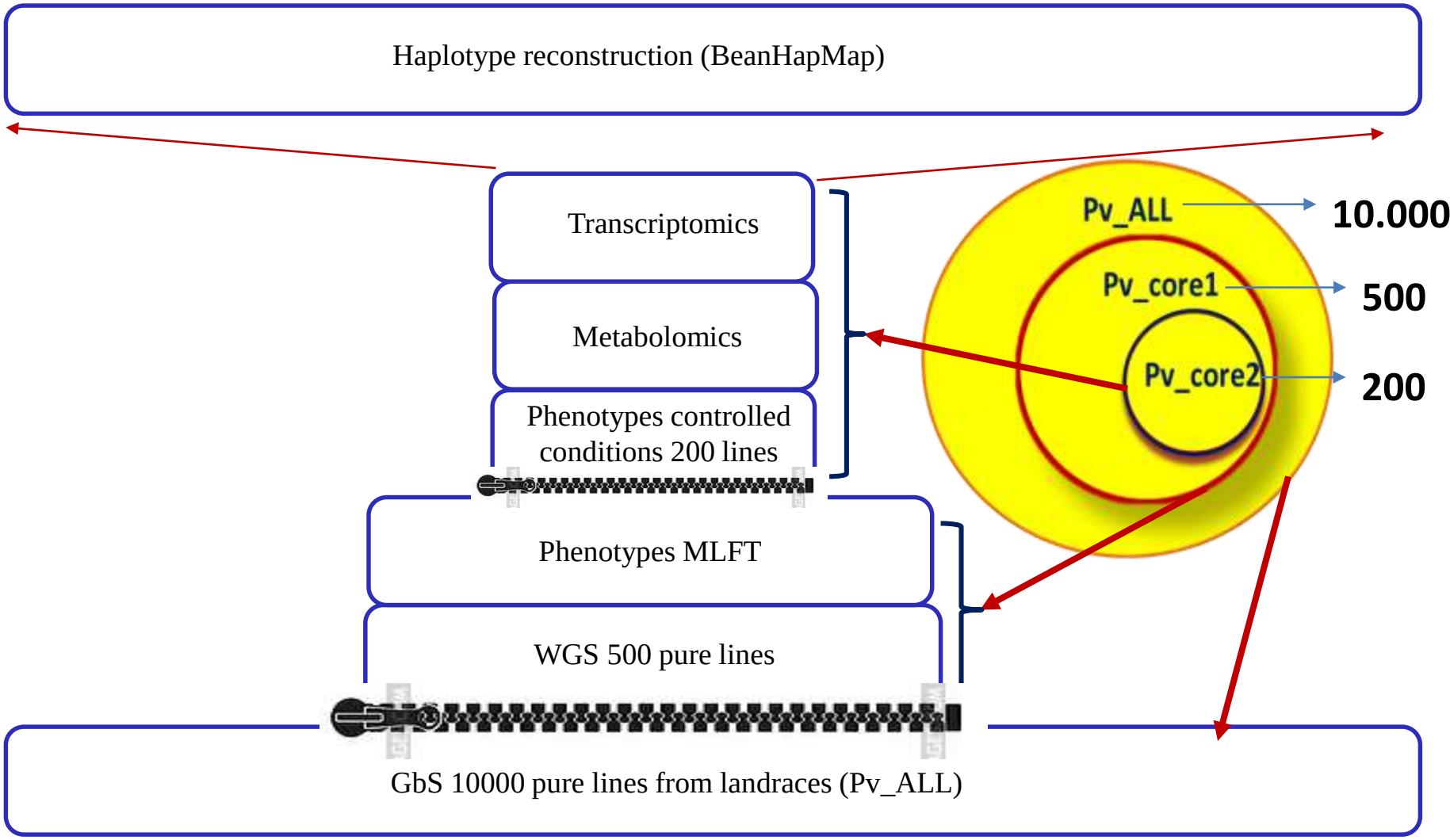
- Computed **haplotypes** from 500 Pv_core1 accessions, and haplotypes for Pv_ALL.
- List of genes and phenotypes showing **signature of selection**.
- List of **loci** significantly associated with **traits and environmental** variables.
- Improved **expression** associated genome **annotation**.
- List of strong candidates for **validation**.
- List of **validated candidates**.

WP5 Data analyses



BEAN_ADAPT Kick-off meeting 11 August 2015, Bonn, Germany

The International Treaty
ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

DivSeek

CROP TRUST

CIAT
Centro Internacional de Agricultura Tropical
Desde 1967 / Ciencia para cultivar el cambio

ESA
Annual Meeting

Expanding the scope and the impact

Associated Partners

- Phenotyping, Filed Trials
- Phenotyping, nutritional value
- Phenotyping, seed traits
- Phenotyping, abiotic stresses and roots
- Genetic resources
- Information (genomic information)
- Molecular data
- Dissemination
- Ex situ Conservation 10,000 lines

JÜLICH
FORSCHUNGSZENTRUM

NS seme

European Cooperative Programme for Plant Genetic Resources
ECP/GR

CNR

University of Saskatchewan

University of Nebraska Lincoln

Agricultural Institute of Slovenia

uniss
Università degli Studi di Sassari

University of Guelph

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WORK PACKAGES

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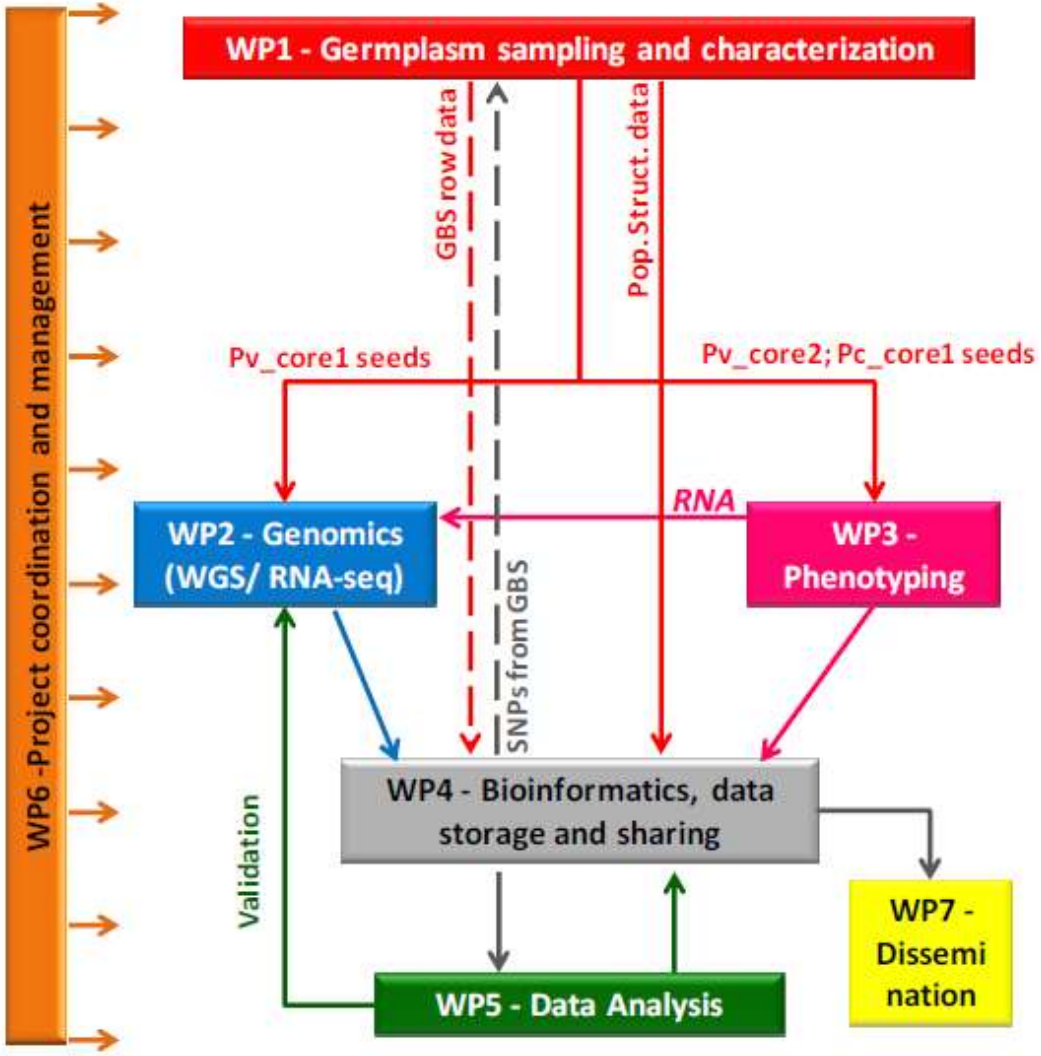

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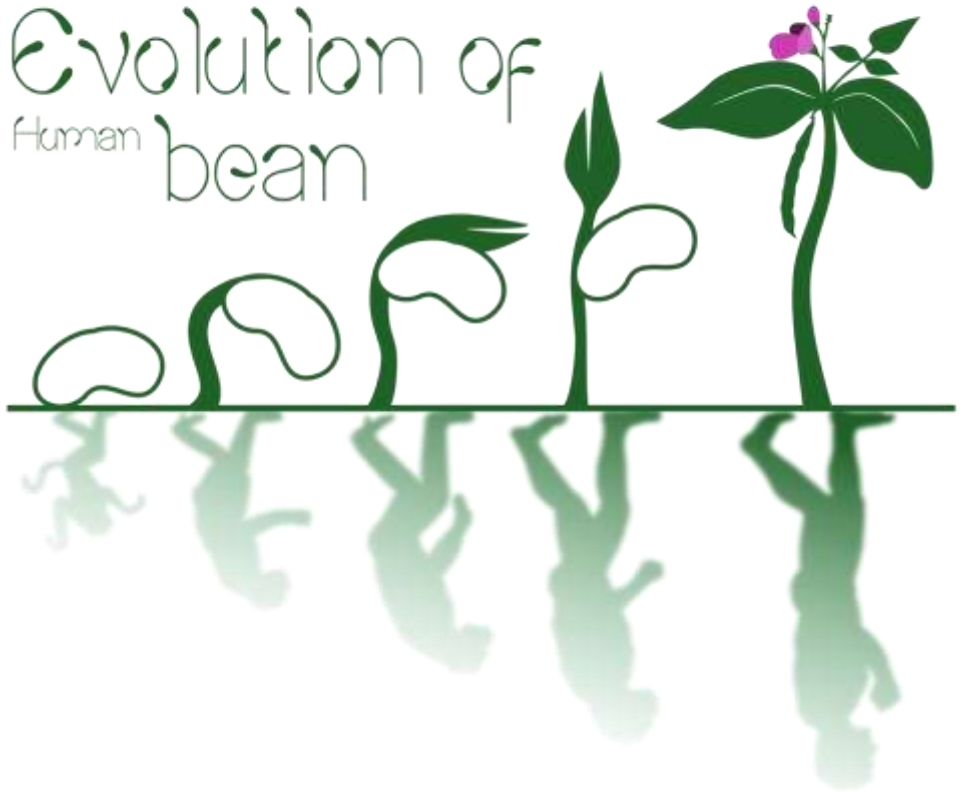
Thanks for your attention