

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

**Report of the BEAN\_ADAPT kick-off meeting  
10-11 August, Bonn, Germany**

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1. **Object of participation:** Participation in BEAN\_ADAPT kick-off meeting organised at the Global Crop Diversity Trust, Bonn (Germany). The participation was performed as Chair of the ECPGR Grain Legumes Working Group, at the invitation of the BEAN\_ADAPT project Consortium.
2. **Location and period:** Bonn, Germany, 10–11 August 2015.
3. **Description of activity:** The meeting was designed for one afternoon (10 August) and one full day of discussions (11 August).
  - **On the first day** of the meeting Prof. Roberto Papa, the coordinator of the project, gave a succinct presentation of the project.

BEAN\_ADAPT is an ERA\_CAPS project, developed by a consortium of five European and American research entities, structured in seven Work Packages (WPs) and funded for a period of three years, starting April 2015.

This project seeks to understand the genetic architecture of adaptation of the common bean (*Phaseolus vulgaris*; *Pv*) and its cross-compatible sister species, the runner bean (*Phaseolus coccineus*; *Pc*), in their centers of origin in the Americas and following their dispersal to Europe, as a model for future major environmental and socio-economic changes, such as increases in temperature, variability in rainfall, and new consumer preferences.

The main aim of this project is to dissect out the genetic basis and phenotypic consequences of the adaptation to new environments of the common bean and its sister species, 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.

Discovering genes and genetic mechanisms that contribute to phenotypic adaptation associated with environmental conditions and their mapping along the reference genome will provide a useful genetic tool for geneticists and breeders for the constitution of novel varieties. This is a crucial aspect towards future major environmental and socio-economic changes, such as increases in temperature, differences in rainfall, and new consumer preferences. These outcomes will also be a step towards complete identification of all the functional elements encoded in the plant genome, which is one of the major scientific targets of plant research.

To reach this goal, the proposal plans to apply the most recent 'omics' technologies using a multidisciplinary approach (genomics, population/quantitative genetics, biochemistry, plant physiology) to highlight the complex relationship between the genotypic and phenotypic diversity in plant populations.

Taking into account the importance of the project, one purpose is to involve other research institutes and researchers in order to raise up the value of project results, and to offer a better overview, using different approaches.

The specific aims of this project include:

- Comparative analysis of the genetic diversity and population structure between the American and European germplasm of *P. vulgaris* (*Pv*) and *P. coccineus* (*Pc*), using genomics, molecular phenotyping (transcriptomics, metabolomics) and field trials at multiple locations. Identification of genes/QTLs that control important agronomic and adaptive traits, particularly phenology.
- Develop a unified information system that will integrate the large amount of data generated by BEAN\_ADAPT, which will also facilitate data sharing, both within the project and externally, by linking up the data to the European Search Catalogue of Plant Genetic Resources (EURISCO).
- Promote the efficient use of *Phaseolus* PGRs by the development of an integrated information system that will be linked with Genebanks management and enhanced by the development and characterisation of 20,000 *Pv* purified lines.
- Dissemination of the results to scientists, genebank curators and breeders.



**Fig. 1. Species investigated in the project – core collection for each species**

**In the next part of the meeting**, representatives of the Global Crop Diversity Trust, Bonn, presented some “lessons” – successes and failures from previous projects, in order to exchange information that can facilitate the development of the project.

The following presentations were given:

- Peter Wenzl (Global Crop Diversity Trust) – ‘DivSeek: Current status & some lessons learned from a large-scale genebank characterization effort’
- Paula Bramel (Global Crop Diversity Trust) – ‘Global conservation strategy for common beans and *Phaseolus* spp.’
- Ulrich Schurr (Jülich Forschungszentrum) – ‘Phenotyping plant genetic resources’

➤ **The second day of the meeting was divided in three sections:**

▪ **In the first part** of the meeting, the coordinator and the leaders of the BEAN\_ADAPT WPs presented each WP and pointed out all objectives, activities and expected deliverables.

- WP1 Germplasm sampling & characterization
- WP2 Genomics
- WP3 Phenotyping
- WP4 Bioinformatics, data storage & sharing
- WP5 Data analysis
- WP6 Coordination and management
- WP7 Dissemination

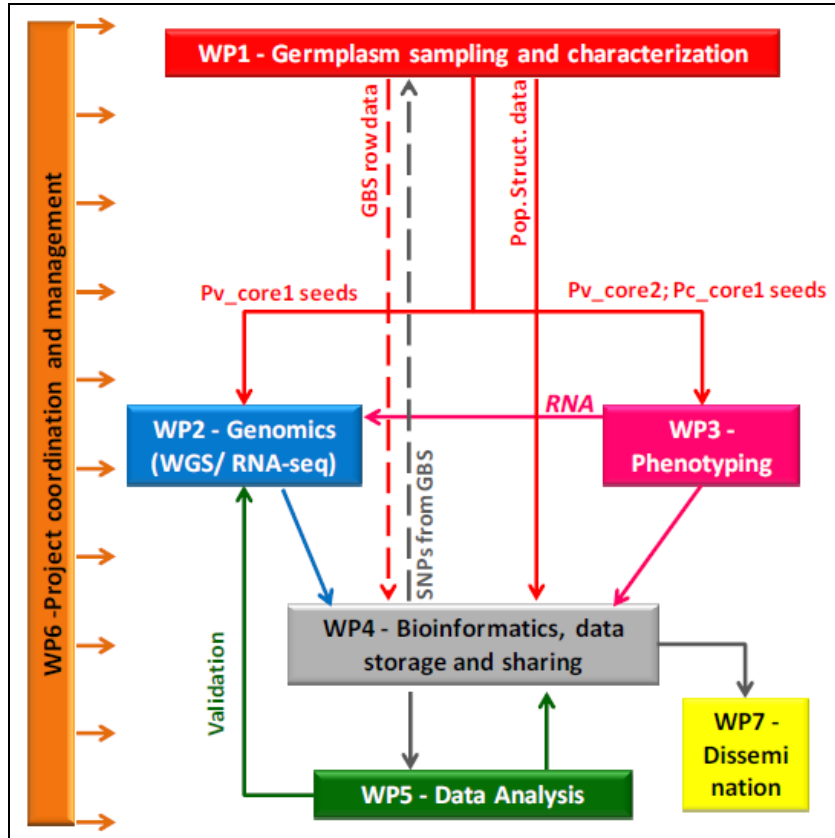


Fig. 2. Work packages of the BEAN\_ADAPT project

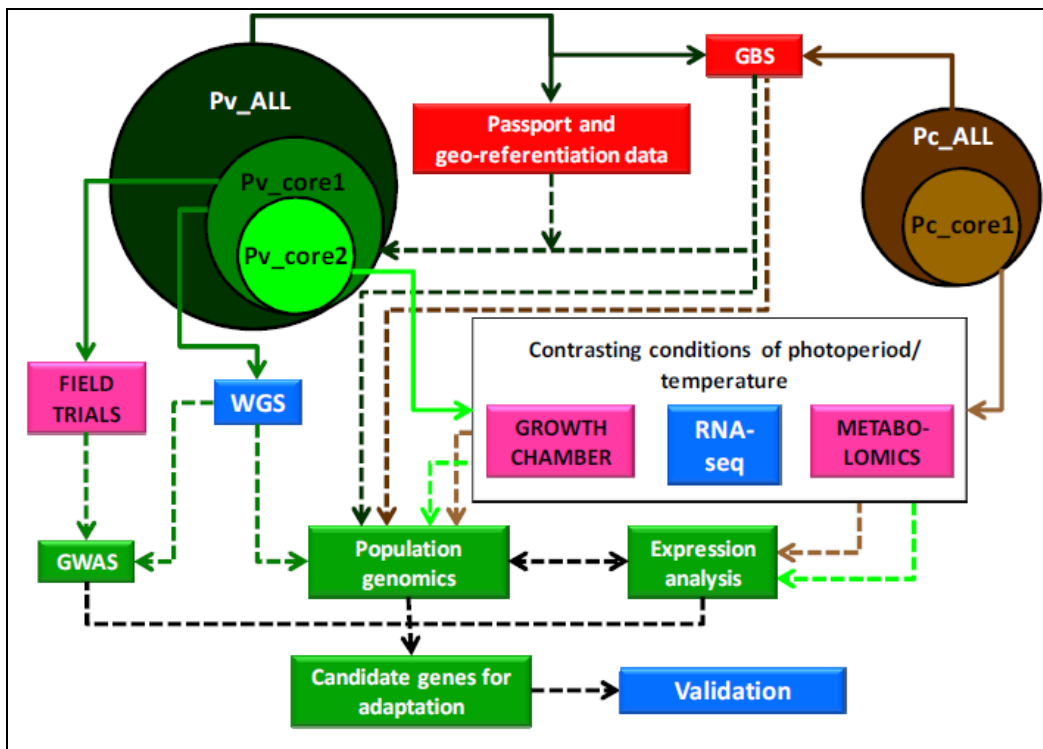


Fig. 3. Work flow of the BEAN\_ADAPT project

## **Objectives of the project structured for each WP:**

### **WP 1 Germplasm sampling & characterization**

#### **Objectives**

- Assembly of a *Phaseolus* germplasm and generation of single-seed-derived DNA stock set comprising 20,000 *Pv* (*Pv\_ALL*) and 1,500 *Pc* (*Pc\_ALL*). For *Pv*, also the generation of single plant progenies.
- Assembly of a core collection and seed increase of 500 *Pv* accessions, *Pv\_core1*, included in *Pv\_ALL*, that will be used for both sequencing and multi-site field trials (common garden experiments).
- Definition of two samples, *Pv\_core2* (200 accessions) and *Pc\_core1* (60 accessions), for phenotyping (RNA-seq, metabolomics, growth chamber).
- GBS characterisation of *Pv\_ALL* and *Pc\_ALL* samples.
- Well-characterised core collections (*Pv\_core1*, *Pv\_core2*, *Pc\_core1*) for other WPs and reference information for 'molecular accession passports' for the management of *ex situ* collections.
- Development of a data warehouse to integrate the sequence data with existing databases for plant genetic resources.

### **WP2 Genomics**

#### **Objectives**

- In-depth genotyping of 500 core *Pv* accessions (*Pv\_core1*).
- RNA sequencing of 200 *Pv* (*Pv\_core2*) and 60 *Pc* (*Pc\_core1*).
- BSA-seq validation of gene-phenotype correlations in segregating populations.
- Validation of expression differences between accessions and populations on a gene-by-gene basis using standard quantitative RT-PCR.

### **WP3 Phenomics**

#### **Objectives**

- Obtain phenotypic data under contrasting conditions in field (*Pv\_core1*) and growth chamber (*Pv\_core2*, *Pc\_core1*).
- Obtain samples for RNA-seq from the growth chamber trial.
- Score metabolic traits in *Pv* and *Pc* from the growth chamber trial.

### **WP 4 Bioinformatics, data storage & sharing**

#### **Objectives**

- SNPs dataset from analysis of raw GBS data of *Pv\_ALL* and *Pc\_ALL*.
- Identification of genes up/down-regulated to light/temperature treatments, transcript variants, and alternative splicing.
- WGS data analysis to provide baseline information on variants and computation of haplotypes for *Pv\_core1*.
- Project (imputation) of haplotypes of *Pv\_ALL* through WGS and GBS data.
- Data integration and sharing: ensure access to raw and processed data, integrate and migrate data to public repositories.

### **WP5 Data analyses**

#### **Objectives**

- Molecular and functional characterisation of the diversity of domesticated *Pv* and *Pc*, and its association to environmental changes.
- Identification of loci and key phenotypes putatively under selection.
- Integration and validation of the main results.
- Development of a large set of accessions based on pure lines (*Pv*) with genomic and phenotypic information.

Among the main outcomes of BEAN\_ADAPT are the development in *Pv* of haplotypes of all 20,000 accessions (HapBean), along with associated information and seed stocks, which will represent a unique tool for plant scientists.

For *Pc*, the project team will also have a well-defined set of information that will constitute the foundation for the development and application of its genomic resources.

▪ **In the second part of the meeting** the invited people from different research institutes/organizations presented their activity as potential participants in the project, highlighting the strengths and the facts that make them important participants in the BEAN\_ADAPT project.

- Bodo Raatz (CIAT, Colombia) – ‘CIAT Genetic Resources Unit: genetic stocks and functions of the germplasm bank’.
- Creola Brezeanu (European Cooperative Programme for Plant Genetic Resources, ECPGR) – ‘ECPGR – a safety network for our crops’.
- Maria Carlota Vaz Patto (ITQB – Instituto de Tecnologia Quimica e Biologica / UNL – Universidade NOVA de Lisboa, Portugal) ‘Portugal at the diverse common bean world’.
- Vladimir Meglič (Dept. of Crop Science, Agricultural Institute of Slovenia, Slovenia) – ‘From Genetic Diversity to proteomic analyses of South East European Beans’
- Domenico Rau (Università di Sassari, Italy) – ‘Research activities on *Phaseolus* spp. at the UNISS’
- Tania Gioia (Università di Sassari, Italy) – ‘The European common bean: research activities at the UNIBAS’.
- Alessia Cogliandro (European Seed Association) – ‘ESA European Seed Association activities and the seed sector in Europe’.
- Peter Pauls (Dept of Plant Agriculture, University of Guelph) – ‘The OAC Rex genome a Meso American bean with *Phaseolus acutifolius* introgressions’.
- Juan Jose Ferreira (Servicio Regional de Investigación y Desarrollo Agroalimentario, Spain) – ‘The plant genetic group of SERIDA working lines and last results’.
- Aleksandra Savić (Institute of Field and Vegetable Crops, Dept. for Vegetable production, Novi Sad, Serbia) – ‘Bean breeding program and research activities at IFVC Novi Sad Serbia’.
- Francesca Sparvoli (IIBBA, CNR, Italy) – ‘Bean seed components and seed nutritional quality’.
- Siegfried Jahnke (Jülich Forschungszentrum, Germany) – ‘Possible cooperation for whole plant and/or seed phenotyping’.

▪ **The third part of the meeting** was dedicated to conclusions. The BEAN\_ADAPT consortium and potential participants tried to design bridges for future cooperations, according to the BEAN\_ADAPT objectives and related with developed research activities of the potential participants in the project.

#### 4. Proposals for future cooperation

The ECPGR proposals for future cooperation were:

- Provision of genebank accessions to the project;
- Offer of evaluation sites in different environments;
- Exchange of information;
- Dissemination of results through ECPGR channels (websites, bulletins).

A letter of expression of interest was signed for the above activities.

The Chair and the other ECPGR Grain Legumes WG members participating in the meeting agreed on the need to explore possibilities for funding in the framework of ECPGR, in order to link the BEAN\_ADAPT project and ECPGR.