Bean Adapt: The Genomics of Adaptation during Crop Expansion in Bean

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

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, cardiovascular 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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DOMESTICATED BEAN SPECIES

P. vulgaris L. in AMERICA

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

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

P. vulgaris L. in AMERICA

Messomeric gene pool

Independent domestications

Northern Peru and Ecuador

Andean gene pool


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The whole genome and the new era for Phaseolus research

**THE PROJECT**

- GBS on 11,500 Accessions
- Resequencing 500 genotypes
- Transcriptomics and Metabolomics
- Population genomics
- Admixture mapping
- GWAS

**PROJECT AIM**

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.
Most of the PS genes (83%) were fixed in MD, 14.2% presented shared polymorphism and 2.8% fixed in the MW and polymorphic in the MD. DOMESTICATION also increased FUNCTIONAL DIVERSITY.

Results of Mesoamerican wild bean data (SGLMM) Loci that show significant environmental effects, as summarised by PCA3, PCA4 and PCA5, are highlighted as red dots and orange dots.

GERMLASM & 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

GERMLASM & DATA

Phaseolus coccineus

Pv_ALL: GbS
Pv_core1: WGS, standard and molecular phenotyping: Metabolomics and transcriptomics under tropical short-day vs a temperate long-day environment simulation
**Ex-situ resources**

**Phaseolus vulgaris**

- **P. lunatus**: 14,434
- **P. cocineus**: 5,279
- **P. acutifolius**: 1,366
- **P. dumosus**: 956

**Other species (52)**: 1,081

Source: http://www.fao.org/view-

**Largest Genebank collections**

**Phaseolus vulgaris** – total 196 genebanks

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<tr>
<th>Genebank</th>
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<td>COL003</td>
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<td>RWA023</td>
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</tbody>
</table>

Source: http://www.fao.org/view-

**IPK Phaseolus collection**

- **Biostatus**
  - Unknown [8]: 2
  - Wildplant [500]: 75
  - Landrace [500]: 412
  - Genet. Stock [400]: 251
  - Breeding line [410]: 1
  - Hybrid [412]: 10
  - Mutant [412]: 8
  - Cultivar [500]: 25

- **Total**: 440

Source: http://www.fao.org/view-

**WORKFLOW**

**ERA-Net for Coordinating Action in Plant Sciences**

- **Work Package 1**: Data Warehouse
  - **GBIS IPK Genebank information system (Passport, Geo Reference PGR Management), Online ordering**
  - **interfaces**:
    - EURISCO
    - transPLANT
    - de.NBI
    - DivSeek
    - Digital Seed Bank
    - GLIS

**Data generation**

- **storage – analysis – connectivity**
  - **visualisation**
    - Interactive haplotype browser
    - Comparison to existing marker data to guide pre-breeding and collection management
MAIN DELIVERABLES

- An Immortal collection of pure lines in P. vulgaris
- Computed haplotypes from 500 PV_core1 accessions, and haplotypes for PV_ALL
- List of genes and phenotypes showing signature of selection for adaptation
- List of loci significantly associated with traits & environmental variables.
- Improved expression associated genome annotation.
- List of strong candidates for validation.
- List of validated candidates

WP5 Data analyses

Haplotype reconstruction (BeanHapMap)

10.000

500

200

GAS 10000 pure lines from landraces (PV_ALL)

Phenotypes controlled condition 200 lines

WGS 500 pure lines

Transcriptomics

Metabolomics

Phenotypes MLFT

ERA-NET for Coordinating Action in Plant Sciences

Thanks for your attention.