Mend The Gap



ORIGIN OF CROATIAN COMMON BEAN (Phaseolus vulgaris L.)

Klaudija Carović-Stanko

University of Zagreb, Faculty of Agriculture, Zagreb, Croatia Centre of Excellence for Biodiversity and Molecular Plant Breeding (CoE CroP-BioDiv), Zagreb, Croatia

E-mail: kcarovic@agr.hr



Europska unija Zajedno do fondova EU

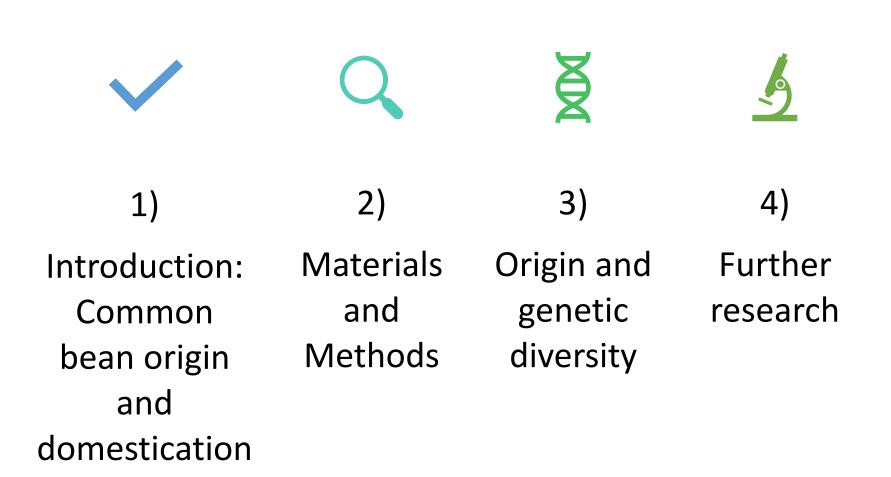


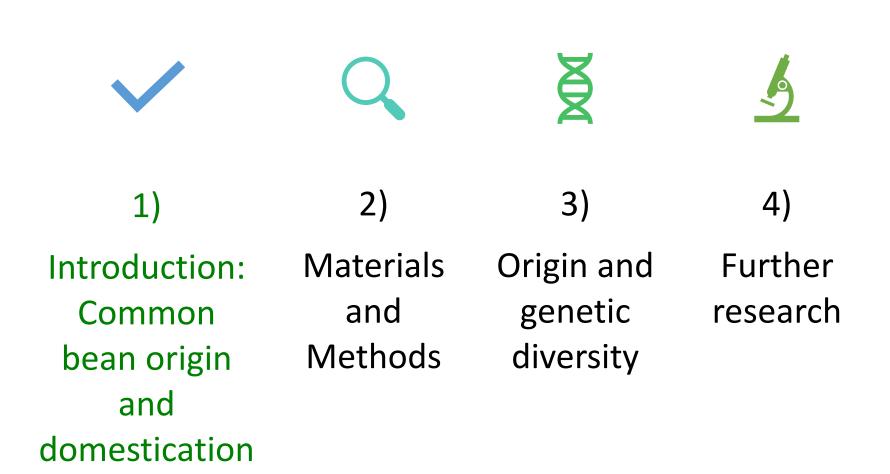




Cambridge, 2018

Republika Hrvatska







(100 – 700 AD)



Phaseolus lunatus L. Lima bean



Bird Runners and Moche Beans



Señor de Sipán



Moche pottery with ceremonial Bean Runners

ORIGIN / DIVERGENCE



Origin of wild common bean:
 Mesoamerica

 Divergence: Andean wild bean diverged from Mesoamerican prior to domestication

DOMESTICATION



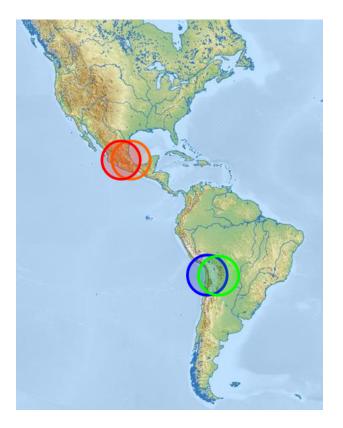
Domestication: Independently domesticated in Mesoamerica and the Andes

 Mesoamerican centre: indeterminate (maize-bean-squash multicrop system)
 Andean centre: determinate types (no suitable crop: root crops, quinoa)





DIVERSIFICATION



Domestication:

- Mesoamerican centre:
 - indeterminate
- Andean centre: determinate

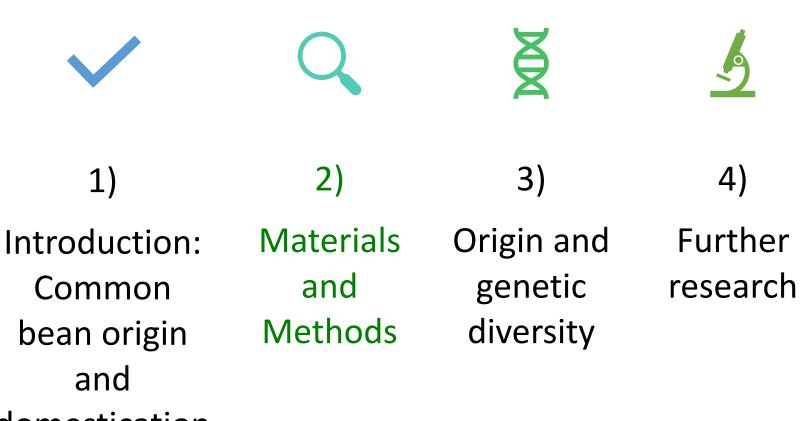
Diversification: Adaptation to new environments and local preferences
Andean centre: indeterminate (after maize introduction)
Mesoamerican centre: determinate (determinacy has been selected independently in both centres)

INTRODUCTION TO EUROPE



Our neighborhood:

- Introduction to Europe: 16th century Portugal and Spain several introductions
 - Origin (phaseoline type):
 Mesoamerican 33%
 Andean 67%
 Hybrids:
 up to 33%
- (A) The proportion of landraces of the Mesoamerican origin tends to increase in eastern and south-eastern Europe (Albania, Bulgaria, Macedonia, Greece)
- (B) The proportions found in accessions from Bosnia and Herzegovina, Croatia, Serbia and Slovenia were very similar to those found in the Iberian Peninsula and Italy indicating that common bean was introduced mainly from the Mediterranean Basin



domestication

MATERIALS: LANDRACES IN CROATIA

- the majority of the common bean production is based on local landraces
- grown by small-scale farmers in low input production systems
- no plant breeding programme
- landraces

known by their traditional names different seed coat patterns and colours also found in neighbouring countries (central Europe, western Balkans) 174 accessions >> 10 morphotypes

- aim: origin and genetic diversity
- goal: association mapping study



'Kukuruzar'

'Tetovac'

1

'Biser'

'Trešnjevac'

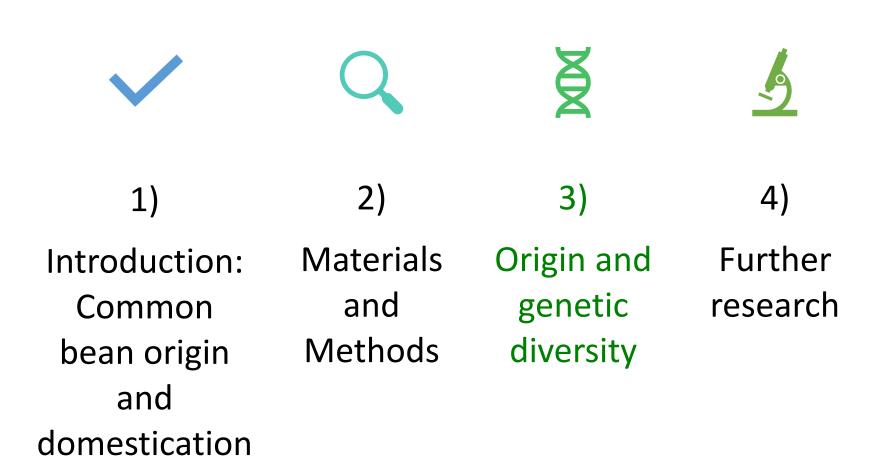
'Puter'

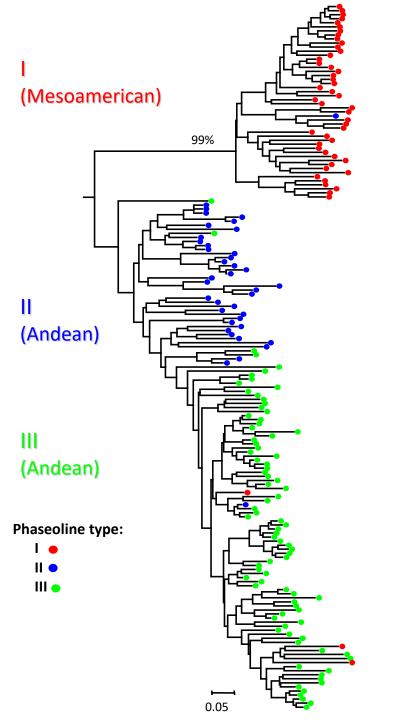
'Dan i noć'

'Zelenčec'

METHODS: MOLECULAR ANALYSES

- (1) Phaseoline type analysis
 - a DNA marker for phaseolin-type diversity
- (2) Microsatellite markers (SSRs)
 - 26 markers / 135 alleles
- (3) DArTseq SNP genotyping (SNPs)
 - 6,599 polymorphic SNP markers





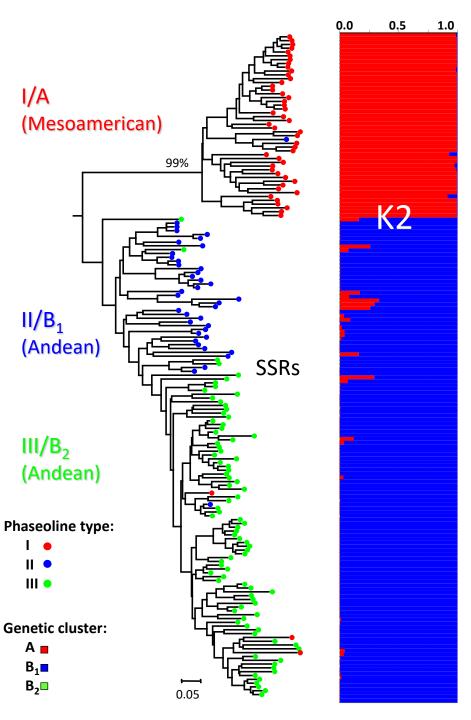
PHASEOLIN TYPE ANALYSIS

(1) Phaseoline type analysis

- three types:

- 1. type I Mesoamerican ('S')
- 2. type II Andean ('H' or 'C')
- 3. type III Andean ('T')
- (2) Microsatellite markers (SSRs)
- genetic distance: D_{psa}
- tree: Neighbor-joining method
- two well-supported clades (Mesoamerican vs Andean)
- subclade

(Andean type III)



SSRs

0.0

0.5

K3

1.0

(3) Microsatellites - Bayesian modelbased clustering method for inferring population structure - proportions of membership (Q) of each accession in each genetic cluster assuming two (K2) or three clusters (K3) - clusters / phaseoline: A - type l Mesoamerican B₁ - type II Andean B₂ - type III Andean

SNPs

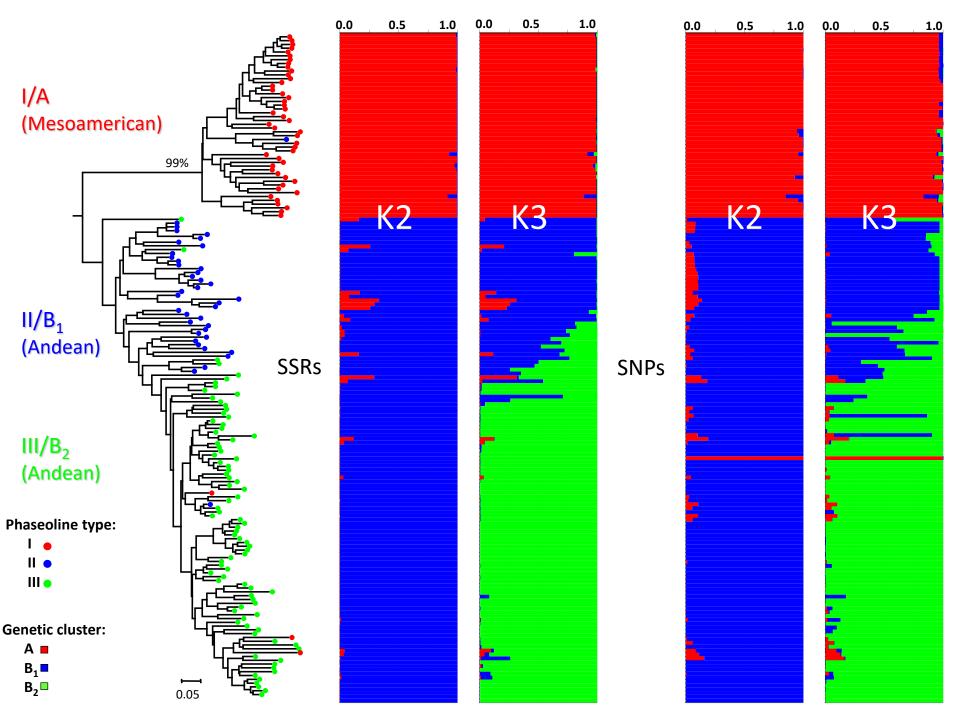


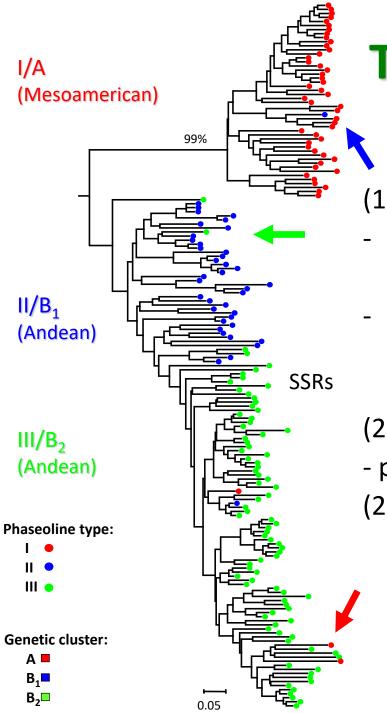
Diversity Arrays Technology (DArT)
 based on genome complexity reduction and SNP
 detection through hybridization of PCR fragments

Schmutz et al. (2014) >> a reference genome for common bean Valdisser et al. (2017) >> characterization of common bean core collection

	Valdisser et al. (2017)	This study
No. of accessions	188*	174
No. of polymorphic markers	5,961	6,599
SNP/Mbp	11.58	12.85
Observed heterozygosity (H _o)	0.037	0.009
Expected heterozygosity (H _E)	0.443	0.373

*91 landraces + 97 cultivars from all over the world





TRUE-TYPES vs OFFTYPES I

(1) True-types

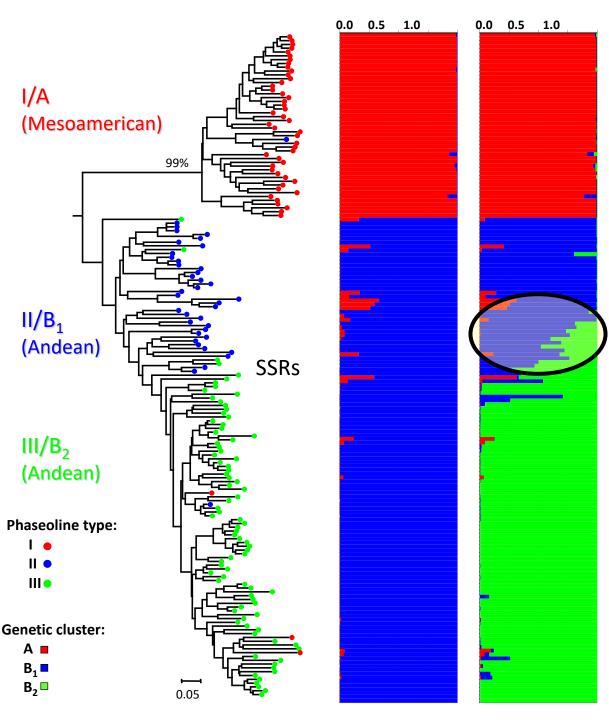
- phaseolin type matches the cluster membership (SSRs and SNPs)
- percentage of cluster membership (Q) higher than 75%

(2) Offtypes

- putative hybrids

(2.1) Non-corresponding

no correspondence between phaseolin types and clusters



OFFTYPES II

(2.2) Mixed origin
percentage of
cluster membership
(Q) lower than 75%
based on SSRs or
SNPs

MORPHO-GENETIC GROUPS

- from 10 morphotypes to 16 morpho-genetic groups

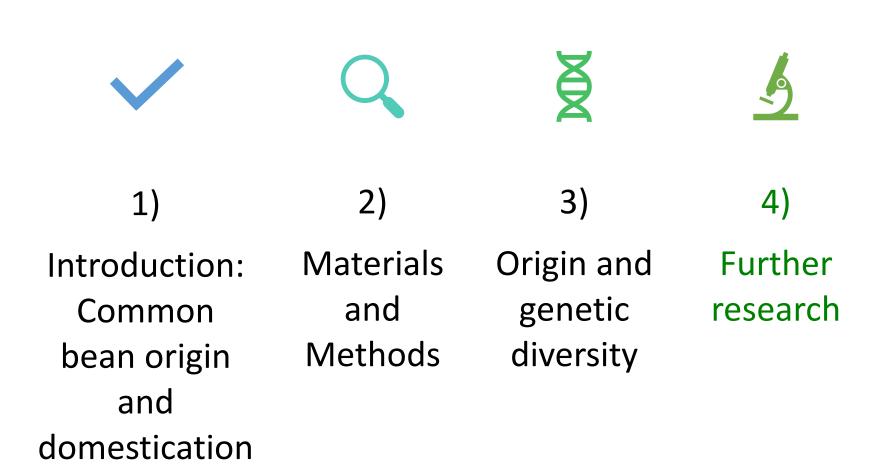
I/A (Mesoamerican)		II/B1 (Andean)		III/B2 (Andean)	
	'Trešnjevac' INDETERMINATE		'Trešnjevac' INDETERMINATE		'Trešnjevac' DETERMINATE
	'Kukuruzar' INDETERMINATE		'Puter'		'Puter' DETERMINATE
	'Tetovac' INDETERMINATE		'Dan i noć' INDETERMINATE		'Dan i noć' DETERMINATE
	'Biser' DETERMINATE		'Sivi' Indeterminate		'Zelenčec' DETERMINATE

MORPHO-GENETIC GROUPS

I/A (Mesoamerican)		II/B1 (Andean)		III/B2 (Andean)	
	'Trešnjevac' INDETERMINATE		'Trešnjevac' INDETERMINATE		'Trešnjevac' DETERMINATE
	'Kukuruzar' INDETERMINATE		'Puter' INDETERMINATE		'Puter' DETERMINATE
	'Tetovac' INDETERMINATE		'Dan i noć' INDETERMINATE		'Dan i noć' DETERMINATE
	'Biser' DETERMINATE		'Sivi' indeterminate		'Zelenčec' DETERMINATE

MORPHO-GENETIC GROUPS

I/A (Mesoamerican)		II/B1 (Andean)		III/B2 (Andean)	
	'Trešnjevac' INDETERMINATE		'Trešnjevac' INDETERMINATE		'Trešnjevac' DETERMINATE
	'Kukuruzar' INDETERMINATE		'Puter' INDETERMINATE		'Puter' DETERMINATE
	'Tetovac' INDETERMINATE		'Dan i noć' INDETERMINATE		'Dan i noć' Determinate
	'Biser' Determinate		'Sivi' indeterminate		'Zelenčec' DETERMINATE



ASSOCIATION MAPPING

- goal: Identification of SNP markers linked to the quantitative trait loci (QTL) related to bioactive nutrient contents in common bean
- 1. PGR: Croatian common bean landraces
- 2. Phenotyping: The assessment of seed mineral diversity

(Mg, Ca, Fe, Zn, K, P) and phytic acid content

3. Genotyping:

- SSRs genetic diversity and structure
- SNPs DArTseq high-density SNP genotyping
- 3. Bioinformatics:

Genome-Wide Association Study (GWAS)

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http://biodiv.iptpo.hr

