

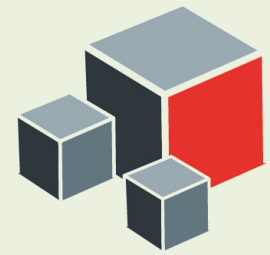
- **Genetic Basis of Bioactive Nutrient Content in Croatian Common Bean Landraces**

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# Project is fully supported by Croatian Science Foundation



## Project team



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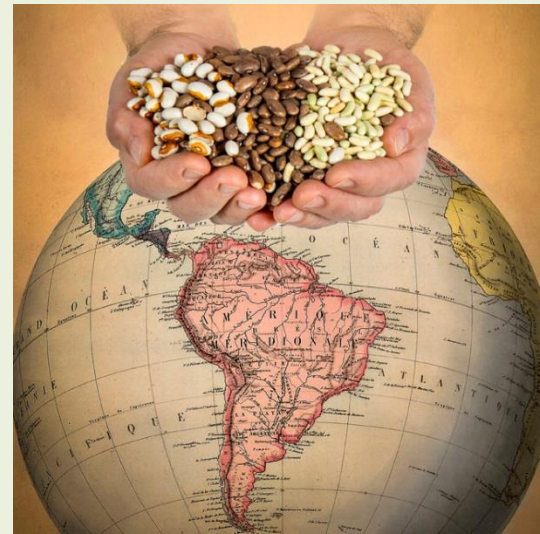
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# Common bean (*Phaseolus vulgaris* L.)

- grown and cultivated worldwide
- domestication occurred independently in Mesoamerica and Andean South America
  - gave rise to two major gene pools
    - both were disseminated all over the world



- the most important grain legume for human consumption in the world
  - valuable source of protein, dietary fibre, vitamins and minerals
  - recently gained great attention as functional food
- in diet it provides macro- and micronutrients such as magnesium, calcium, iron and zinc



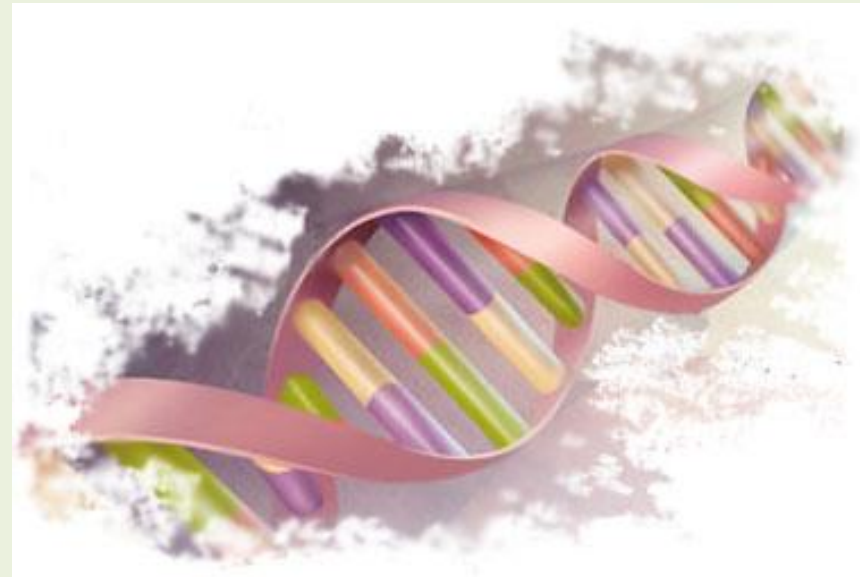
# Common bean in Croatia

- long tradition of cultivation has enabled the evolution of many landraces adapted to restricted areas
- common bean landraces are in danger of genetic erosion caused by complex socio-economic changes in rural communities



# Objectives

- integrated approach will be used by combining bioactive nutrient and PA content analyses with whole genome scan for important marker trait associations to unravel the genetic basis of the mineral content in common bean
- phaseolin seed protein analysis will be used to assess the putative origin of accessions (Andean and Mesoamerican gene pools)
- yield potential will be preliminary assessed
- results will contribute to the improvement of the breeding efforts by providing modern selection tools



# Specific objectives and methods

## 1) Photosynthetic rates measurements

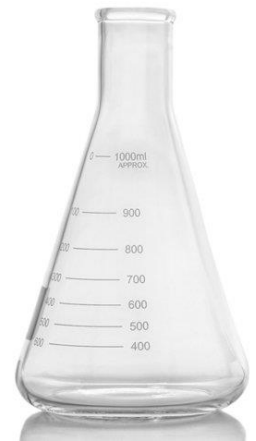
➔ determination of yield potential ( $Y_p$ )

- LCpro portable photosynthesis system
  - photosynthetic rate (A), transpiration rate (E), stomatal conductivity (gs), intercellular CO<sub>2</sub> concentration (ci)



## 2) The assessment of seed mineral diversity (Mg, Ca, Fe, Zn, K, P) and phytic acid content

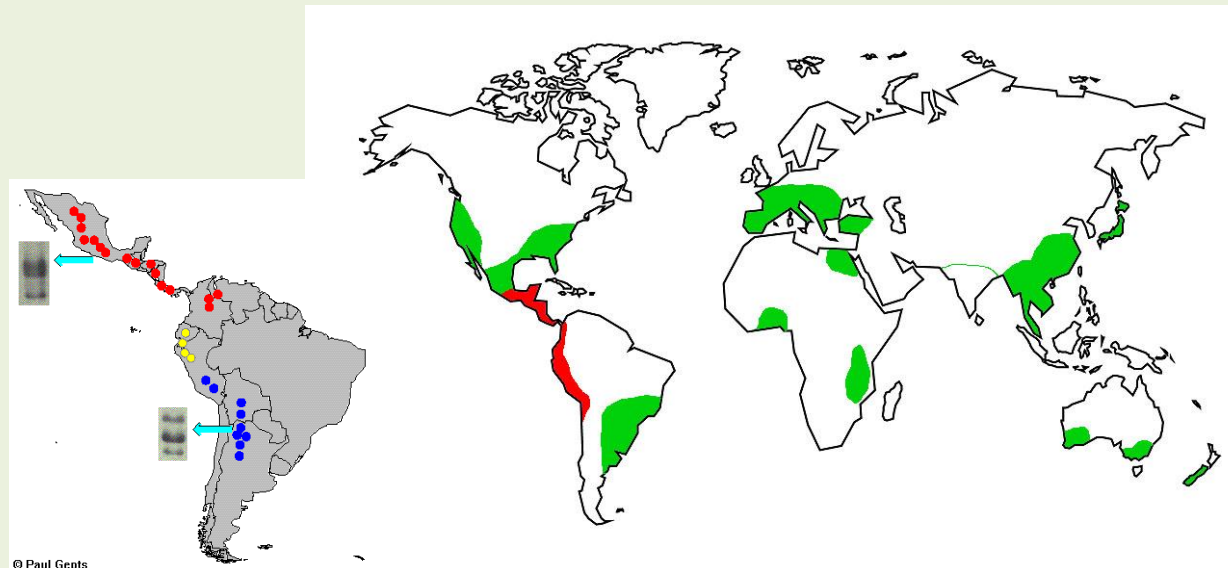
- phosphorus ➡ spectrometer
- potassium ➡ flamephotometer
- calcium, magnesium, iron, and zinc ➡ atomic absorption spectrophotometer
- nitrogen ➡ Kjeldahl method
- phytic acid ➡ spectrophotometer





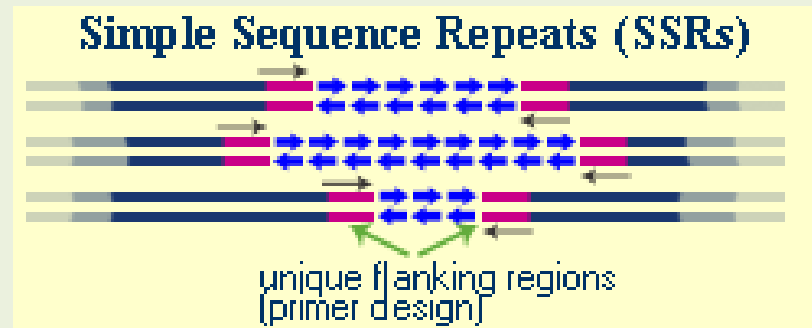
### 3) Phaseolin genotyping

- phaseolin type will be assessed by amplifying the differential region of phaseolin sequence using specific primers described by Kami et al. (1995)



## 4) Microsatellite marker analyses (SSR)

- microsatellites (SSR) → according to the methods described by Radosavljević et al. (2011)
- 50 microsatellites uniformly distributed throughout the genome and selected from the common bean literature



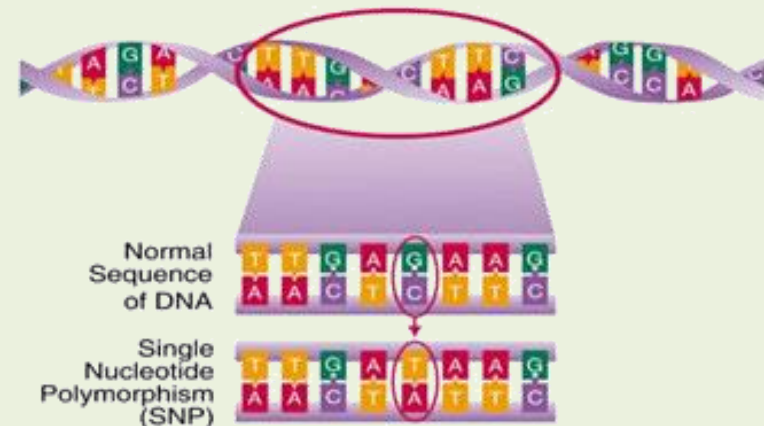
## 5) Construction of the core collection

- core subset of 150 accessions ➡ representing 50% of the entire collection
  - two different algorithms based on M (maximization) strategy will be used
  - to avoid genetically similar accessions and maximize diversity for the association mapping study



## 6) SNP assay design and screening

- up to 1500 SNPs selected from public available source (Hyten et al., 2010)
- design of the GoldenGate assay - out contracted to a European Illumina Certified Service provider (TraitGenetics)



## 7) Association mapping

- objective: to identify genomic regions (SNP markers) associated with bioactive nutrient content in common bean
- model: the mixed-model association mapping approach using kinship coefficients and population structure information
- software: ASReml 3







**Thank you for your attention!**