





FOREVA ACTIVITIES ASSOCIATED WITH OTHER PROJECTS AT KIS

Barbara Pipan Crop Science Department, Slovenia

ForEVA – Fostering the need of implementation of the ECPGR's European Evaluation Network (EVA) on Grain legumes

10-11 October 2023, Bucharest, Romania



Agricultural Institute of Slovenia/KIS_Short presentation





Leading public research institution in Slovenia

Location: Ljubljana, experimental infrastructure in Jablje

Main activities:

- Crop Science
 Plant Protection/Plant Protection Laboratory
 Animal Production
 Fruit Growing, Viticulture and Oenology
 Agricultural Economics
 Agricultural Engineering and Energetics
 Agricultural Ecology and Natural Resources
 Central Laboratory
 Genetics Laboratory
 Project Management Office
 Technology Transfer Office
 State of art equipment
 Seed Testing Laboratory (ISTA accredited)
 Experimental fields
 Plant Gene Bank

 Staff: 251
 Researchers: 93
 PhD: 59

- PhD: 59
- MSc: 34

Other staff: 158

- professional staff: 146
- technical and administrative staff: 12



Active projects_associated with legumes



































KIS legume collection

Grain legume collection:

- Common bean (Phaseolus vulgaris): 1037 ACC
- Runner bean (Phaseolus coccineus): 62 ACC
- Fababean (Vicia faba): 36 ACC
- Pea (Pisum sativum): 3 ACC
- Cowpea (Vigna unguiculata): 1 ACC
- Grass pea (Lathyrus sativus): 1 ACC
- White lupin (Lupinus albus): 1 ACC
- Meadow vetching (Lathyrus pratensis): 11 ACC

Some other Fabaceae species:

- Common vetch (Vicia sativa): 2 ACC
- Narrow leaved vetch (Vicia angustifolia sin.. Vicia sativa subsp. angustifolia): 1 ACC

pan and Meglič BMC Plant Biology (2019) 19:442 tos://doi.org/10.1186/s12870-019-2051-0

Diversification and genetic structure of the

western-to-eastern progression of European

Morpho-Agronomic Characterisation of Runner Bean

(Phaseolus coccineus L.) from South-Eastern Europe

Phaseolus vulgaris L. germplasm

- Cow vetch (Vicia cracca): 15 ACC
- Large yellow vetch (Vicia grandiflora): 5 ACC
- Vicia sepium: 7 ACC
- Vicia sp.: 11 ACC
- ✓ For all collected genetic resources, 'Multi crop passport descriptors' are available containing basic general data on an individual sample (place and date of collection, description of location, who collected the sample, etc.).
- ✓ For individual genetic resources, we have more detailed data on the characterisation and evaluation based on common descriptors for an individual plant species.

BMC Plant Biology

✓ Seed exchange upon request via SMTA -> for all the ACCs available

Naš fižol







The publication in front of you represents a complex and comprehensive inventory of the bean genetic resources stored at the Slovene Plant Gene Bank of the Agricultural Institute of Slovenia. A 955 common (Phaseolus vulgaris L.) and 47 runner bean (Phaseolus coccineus L.) accessions were evaluated and characterized using numerous Phaseolus spp. seed descriptors (UPOV, CPVO, IBPGR, PHASELIEU) and morphometric parameters. Tenfully developed and undamaged seeds of each accession were measured using six quantitative (numerical) parameters: seed length; seed thickness; seed width; length/width ratio; width/thickness ratio; and 100 or 10 seeds weight for common and runner bean accessions respectively. In addition, seeds were evaluated using seven qualitative (descriptive) parameters: seed colour; number of seed colours; primary seed colour; predominant secondary seed colour; distribution of secondary seed colour; seed veining; and seed shape. For each accession high-resolution photography was recorded. On the basis of six numerical parameters, the geographical origin for the common bean accessions was explained. Of the six numerical parameters used, 10 seeds weight was the most important parameter to distinguish runner bean accessions. Based on seven descriptive parameters, two groups were formed in each of the bean collections. The first group included seeds with a primary and secondary colour, the second group represents seeds with the primary colour of different light or dark colours/shades. On the basis of all trinaist morphometric parameters, two groups could be clearly distinguished in both collections. The first group included accessions from Andean and second from the Mesoamerican origin.

This book is intended to be used by a wide circle of readers, from gardeners, farmers and students to breeders and researchers, who can acquaint themselves with the large collection stored for future generations at the Agricultural Institute of Slovenia. We dedicate this book to all researchers and enthusiasts who have worked or are still active in the field of genetic resources of agricultural plants, collecting genetic material and knowledge and with that contributing to the conservation and preservation of the natural and cultural heritage in Slovenia.

Agricultural Institute of Slovenia

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Genetic diversity of Lathyrus sativus L. collection and

characteristics of seeds produced in Slovenia and Serbia Lovro Sinkovič^{1*}, Barbara Pipan¹, Aleksandra Savić², Mirjana Vasić², Vladimir Meglič¹

Original scientific paper

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 Original scientific paper
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 Journal

Morpho-Agronomic Diversity of *Lathyrus sativus* L. Genetic Resources from Slovenia and Bosnia and Herzegovina

Lovro Sinkovič¹, Barbara Pipan¹, Marina Antić², Vida Todorović² Sonja Rašeta², Vladimir Meglič¹ Volume 2019, Article ID 6376948 https://doi.org/10.1155/2019/6376

Research Artic

Morphological Seed Characterization of Common (*Phaseolus vulgaris* L.) and Runner (*Phaseolus coccineus* L.) Bean Germplasm: A Slovenian Gene Bank Example

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Expectations from EVA legumes

- Knowledge/material transfer associated with different legume species in terms of their characterization and agronomic behaviour under different growing environments/locations -> network with diverse expertise and stakeholders in terms of conservation, breeding, farming.

- Data about GR from different levels (morphologic, genetic, genomic, metabolomic,...) available for implementing into GL/cb breeding programme(s) -> increase efficiency

- Further collaborations on GL within new projects proposals.



Thank you for your attention!







