LiveSeeding

Training in organic breeding

Module 3: Breeding methods fundamentals

Unit 3.3: Calculation and evaluation of key breeding parameters

Authors: Adrian Rodríguez-Burruezo (UPV),
Barbara Pipan (KIS)

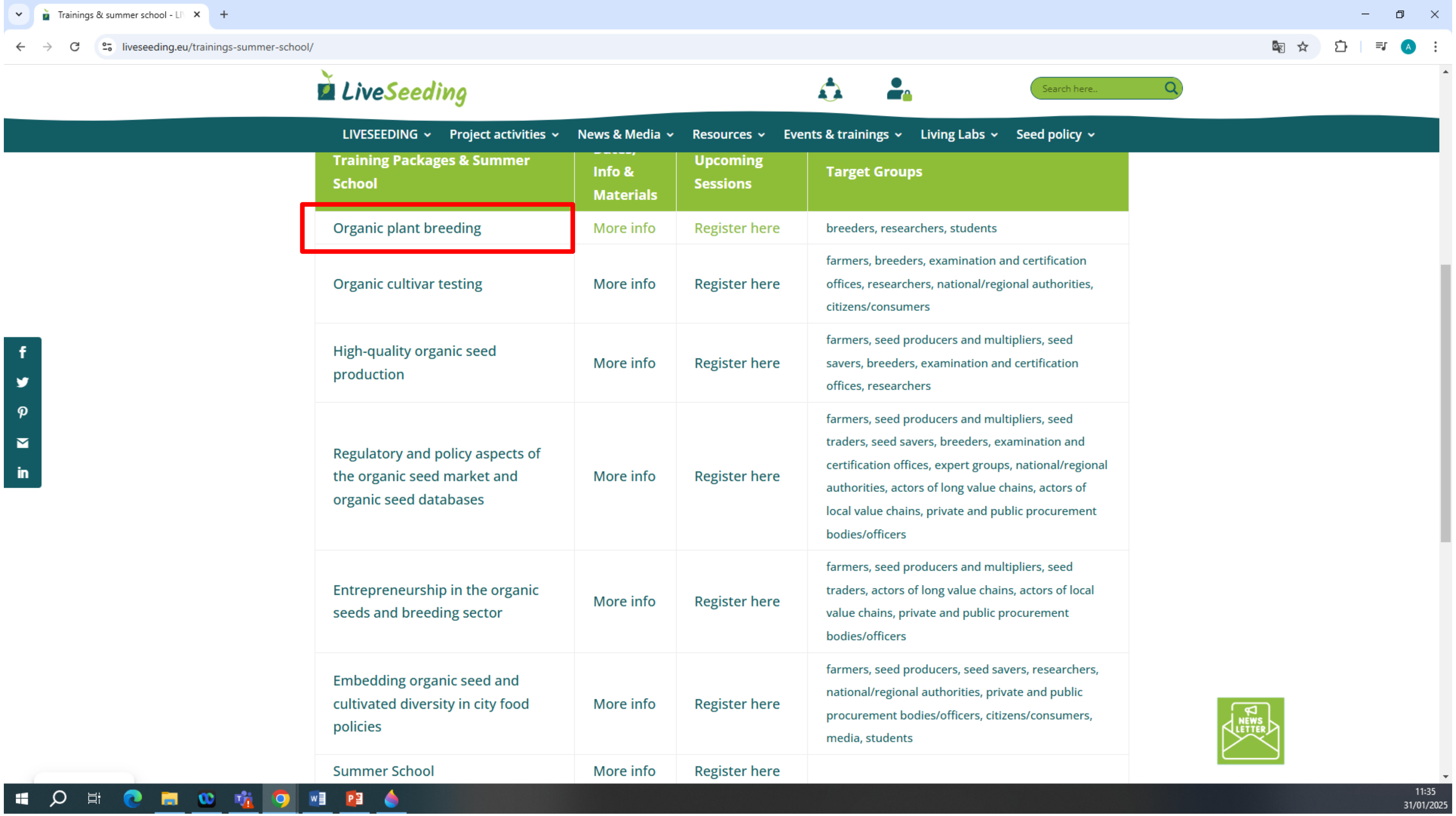
Co-funded by the European Union

Funded by the European Union, the Swiss State Secretariat for Education, Research and Innovation (SERI) and UK Research and Innovation (UKRI).

UK Research and Innovation

CONTEXT: Training in LIVESEEDING project

https://liveseeding.eu/trainings-summer-school/



Training Packages & Summer School	Info & Materials	Upcoming Sessions	Target Groups
Organic plant breeding	More info	Register here	breeders, researchers, students
Organic cultivar testing	More info	Register here	farmers, breeders, examination and certification offices, researchers, national/regional authorities, citizens/consumers
High-quality organic seed production	More info	Register here	farmers, seed producers and multipliers, seed savers, breeders, examination and certification offices, researchers
Regulatory and policy aspects of the organic seed market and organic seed databases	More info	Register here	farmers, seed producers and multipliers, seed traders, seed savers, breeders, examination and certification offices, expert groups, national/regional authorities, actors of long value chains, actors of local value chains, private and public procurement bodies/officers
Entrepreneurship in the organic seeds and breeding sector	More info	Register here	farmers, seed producers and multipliers, seed traders, actors of long value chains, actors of local value chains, private and public procurement bodies/officers
Embedding organic seed and cultivated diversity in city food policies	More info	Register here	farmers, seed producers, seed savers, researchers, national/regional authorities, private and public procurement bodies/officers, citizens/consumers, media, students
Summer School	More info	Register here	

Training in organic breeding organized in 5 Modules

1. **Module 1** - Plant Genetic Resources (PGRs): collection, conservation and exchange to support the increase of agrobiodiversity in farming systems
2. **Module 2 - Phenomics: approaches and tools for genetic resources and breeding material characterisation - FEBRUARY 3rd 2025, 9:00 to 17:30 CET**
3. **Module 3 - Breeding methods fundamentals - FEBRUARY 13th 2025, 9:00 to 18:00 CET**
4. **Module 4** - Development and application of molecular methods in organic breeding - MARCH 4th 2025, 9:00 to 18:00 CET
5. **Module 5** - Organic heterogeneous material (OHM) design and development - MARCH 7th 2025, 9:00 to 18:00 CET

Module 3 – Breeding methods fundamentals

February 13th 2025 - 9:00 to 18:00 CET

Unit 3.1: Generation of new diversity

- 9:00-10:30 - UPV (Adrián Rodríguez-Burruezo, Neus Ortega Albero)

- 10:30-11:00 Break

Unit 3.2: Common methods and strategies in organic breeding

- 11:00-13:00 - IPC (Pedro Mendes Moreira) + UPV (Adrian Rodríguez-Burruezo) + KIS (Barbara Pipan)

- 13:00-14:30 Lunch Break

Unit 3.3: Calculation and evaluation of key breeding parameters

- 14:30-16:00 - UPV (Adrian Rodríguez-Burruezo) + KIS (Barbara Pipan)

- 16:00-16:30 Break

Unit 3.4: Fundamentals in Participatory Plant Breeding

- 16:30-18:00 - IPC (Pedro Mendes Moreira) + INRAe (Véronique Chable)

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M3 – U3 Calculation and evaluation of key breeding parameters

Planned for today

MIXTURE OF:

1. *Presentations about main topics on* ***Kind of traits, ways and parameters to analyse*** *(60 min):*
   - *1.1. Qualitative vs Quantitative – A. Rodríguez-Burruezo (UPV, Spain)*
   - *1.2. Qualitative traits analysis – A. Rodríguez-Burruezo*
   - *1.3. Quantitative traits analysis – A. Rodríguez-Burruezo: Basics, heritability, correlation*
   - *Other parameters & traits of interest during breeding workflow – Barbara Pipan (KIS, Slovenia)*
2. Fast quiz (about 15 min) ***
3. Debate, Wrap up & Proposed homework (about 5-10 min) ***

QUESTIONS: THROUGH THE CHAT (Petra Jelincic will manage)

*** = IMPORTANT for CERTIFICATES (ALL THE UNITS!!!!)

LiveSeeding SEND TO: barbara.pipan@kis.si adrodbur@upv.es petra.jelincic@ips-konzalting.hr

Escola Superior Agrária
Politécnico de Coimbra

M3 – U3 Calculation and evaluation of key breeding parameters

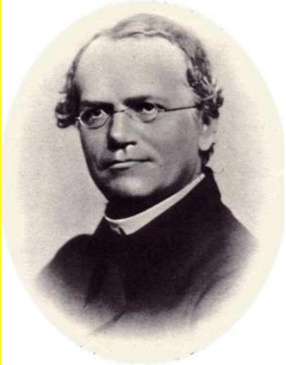
Qualitative vs Quantitative

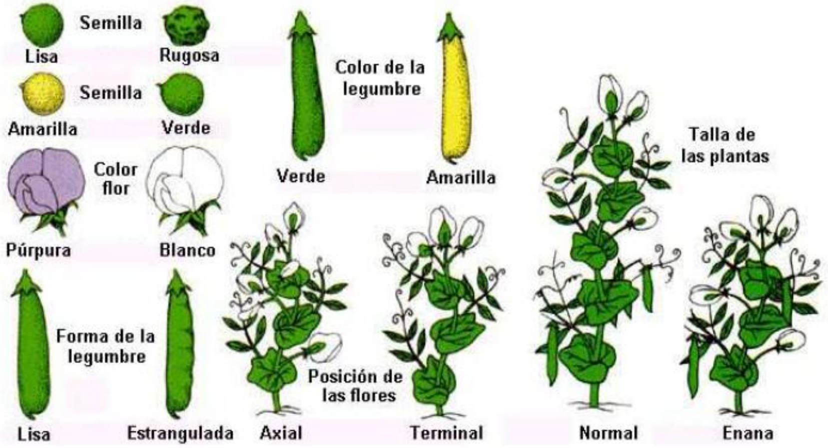
QUALITATIVE

Traits in categories

Individuals distributed in categories

Monogenic or oligogenic traits



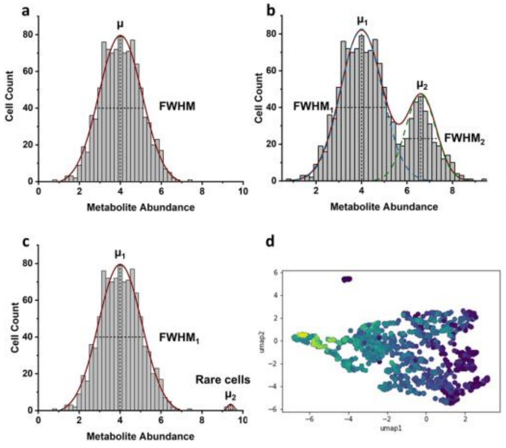


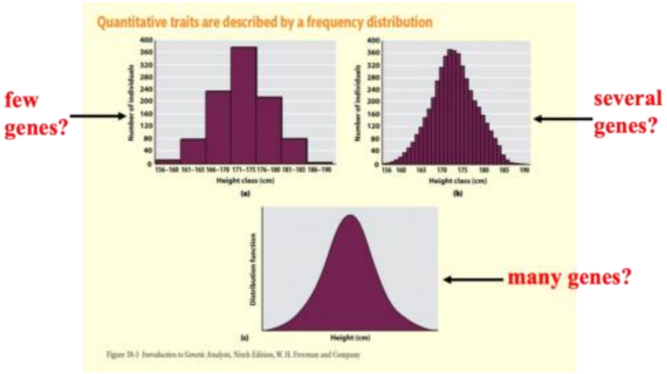
QUANTITATIVE

Traits measured

Individuals continuously distributed

Poligenic traits





few genes?

several genes?

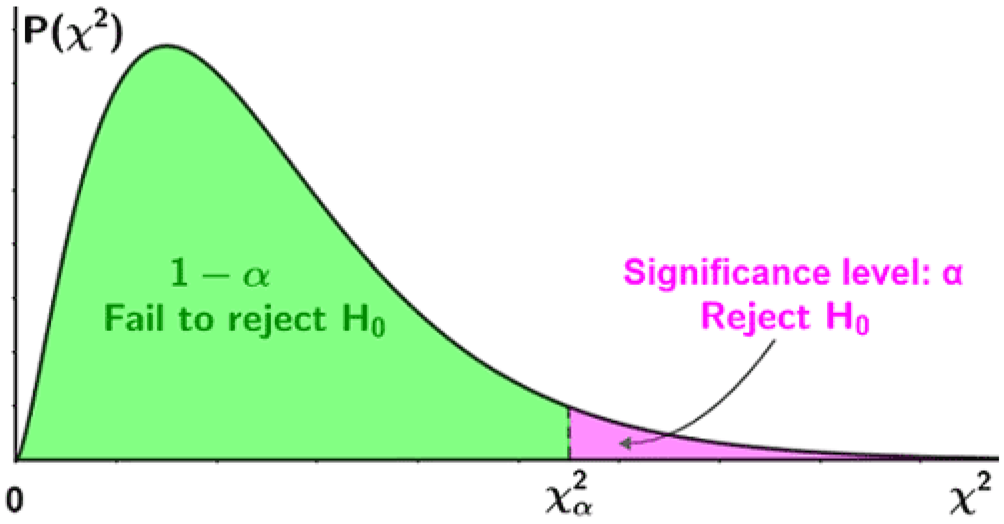
many genes?

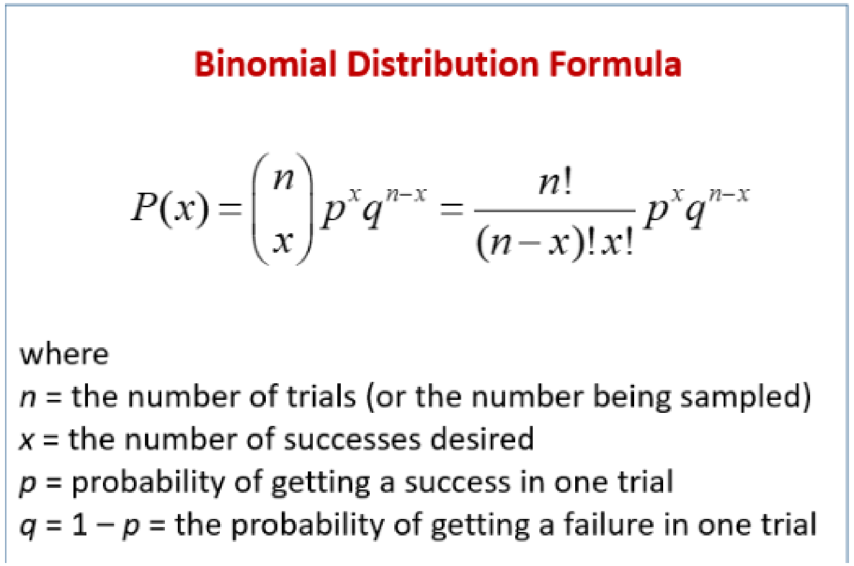
Figure 18-1 Introduction to Genetic Analysis, Ninth Edition, W. H. Freeman and Company

M3 – U3 Calculation and evaluation of key breeding parameters

Qualitative traits analysis

- *Working with number of individuals per category*
- *Check inheritance models statistically with the frequencies of each category*
- *Chi square (X2) and binomial functions*





Binomial Distribution Formula

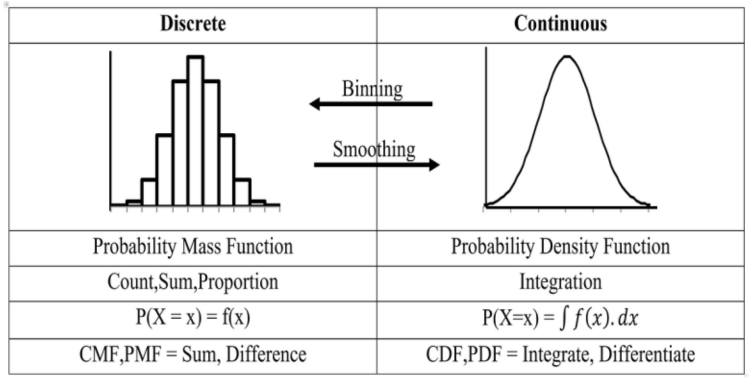
$$P(x) = \binom{n}{x} p^x q^{n-x} = \frac{n!}{(n-x)!\,x!} p^x q^{n-x}$$

where
n = the number of trials (or the number being sampled)
x = the number of successes desired
p = probability of getting a success in one trial
$q = 1 - p$ = the probability of getting a failure in one trial

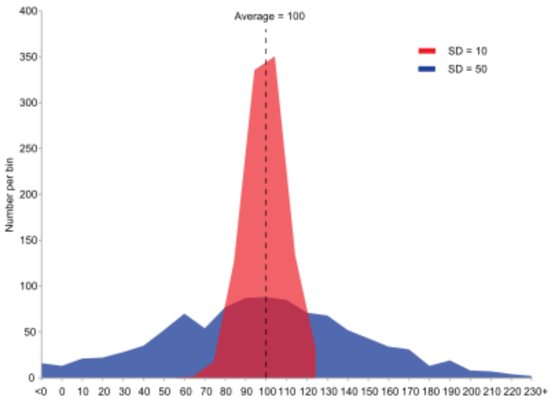
M3 – U3 Calculation and evaluation of key breeding parameters

Quantitative traits analysis

- As traits are measured, no natural categories possible
- Also, as many genes can be involved, environment (E) may modulate the phenotypic expression (P), creating “mirages” and hiding the gene function (G)
- Basic parameters to represent the population: mean (μ) and variance (V or σ^2)
- Manage info for breeders and geneticists with biometrics & quantitative parameters
- Coefficients of variations, covariances, correlations, heritability, GxE interaction



Discrete	Continuous
Probability Mass Function	Probability Density Function
Count,Sum,Proportion	Integration
P(X = x) = f(x)	$P(X=x) = \int f(x).dx$
CMF,PMF = Sum, Difference	CDF,PDF = Integrate, Differentiate



$$CV\ (\%) = \left(\frac{Standard\ deviation}{Mean}\right) \times 100$$

Population Covariance Formula

$$Cov(x,y) = \frac{\Sigma(x_i-\bar{x})(y_i-\bar{y})}{N}$$

Sample Covariance

$$Cov(x,y) = \frac{\Sigma(x_i-\bar{x})(y_i-y)}{N-1}$$

Quantitative traits analysis

Coefficients of variation, covariances, correlations

$$CV\ (\%) = \left(\frac{Standard\ deviation}{Mean}\right) \times 100$$

Population Covariance Formula

$$Cov(x,y) = \frac{\Sigma(x_i\text{-}\bar{x})(y_i\text{-}\bar{y})}{N}$$

Sample Covariance

$$Cov(x,y) = \frac{\Sigma(x_i\text{-}\bar{x})(y_i\text{-}y)}{N\text{-}1}$$

$$r = \frac{\sum(x_i - \bar{x})(y_i - \bar{y}}{\sqrt{\sum(x_i - \bar{x})^2 \sum(y_i -}}$$

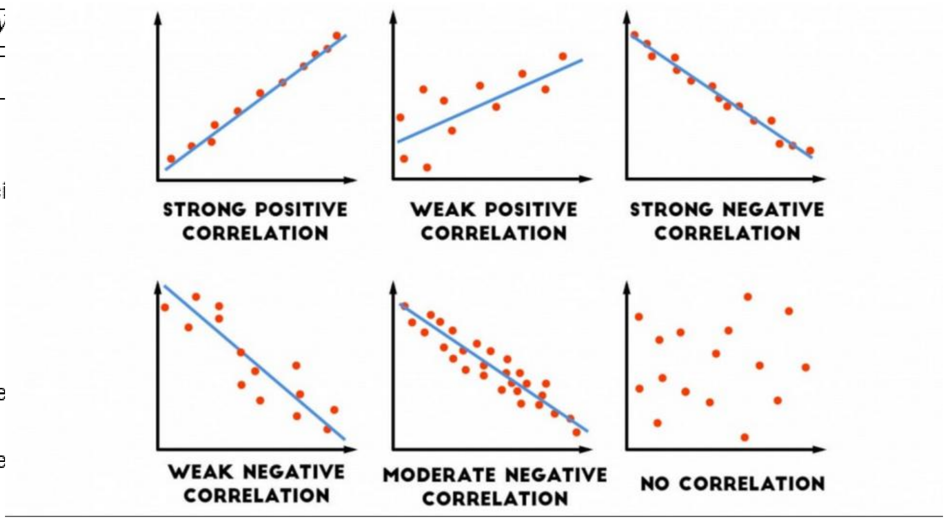
r = Pearson correlation coeffici

x_i = x variable sample

y_i = y variable sample

$\bar{x}$ = mean of values in x variable

$\bar{y}$ = mean of values in y variable



Quantitative traits analysis

HERITABILITY (H^2)

On the whole, it explains to which extent the phenotypic differences you see and record in one population are based in genetic differences…. And will be inherited in next generation

$$P = G + E + (GxE)$$

$$V_P = V_G + V_E + (V_{GxE})$$

- H^2_{bs} Broad sense heritability

$$H_{bs} = V_G/V_P = V_G/[V_G+V_E\ (+V_{GxE})]$$

CONSIDERS: all the genotype pass from one generation to the next

- H^2_{ns} Narrow sense heritability

$$H_{ns} = V_A/V_P = V_A/[V_G+V_E\ (+V_{GxE})] = V_A/[V_A+V_D+ V_E\ (+V_{GxE})]$$

CONSIDERS: only the additive part pass from one generation to the next (dominant and other genetic interactions do not pass)

M3 – U3 Calculation and evaluation of key breeding parameters

Quantitative traits analysis

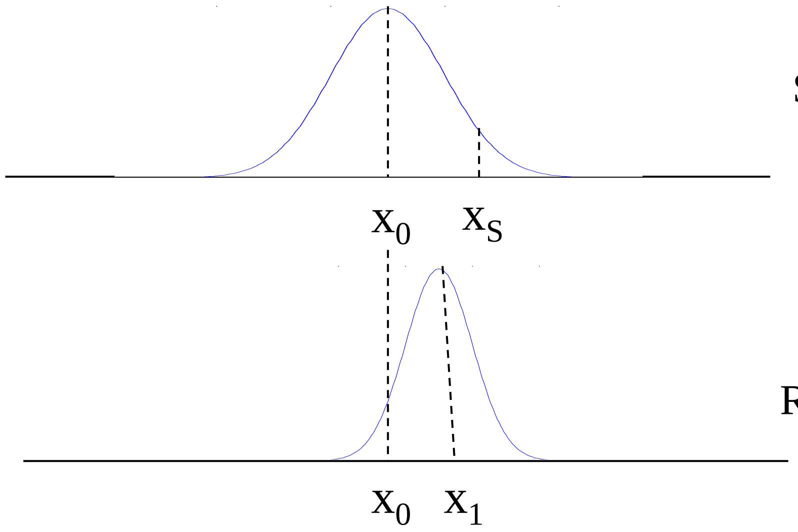
HERITABILITY

H^2_{bs} mainly for clone selection or selection of inbred/autogamous lines

H^2_{ns} mainly for sexually reproduced species, whose populations are allogamous and/or open pollinated

Parents

Offspring



Selection differential (S) = $|x_s - x_o|$

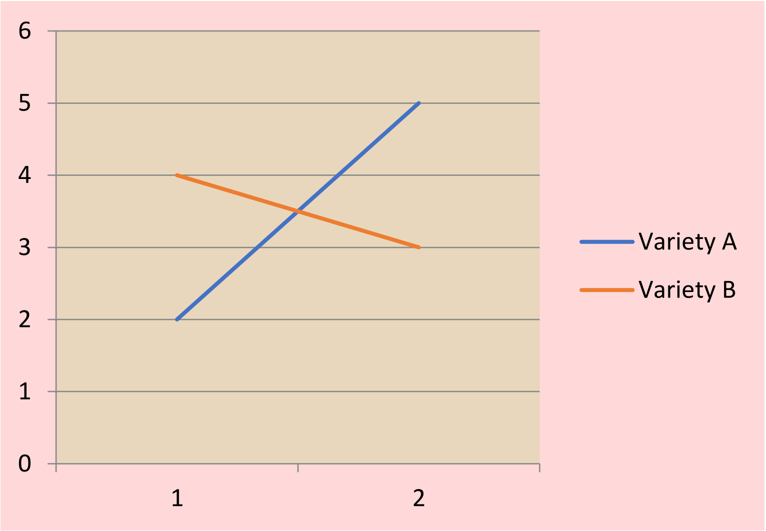
Response to selection (R) = $|x_1 - x_o|$

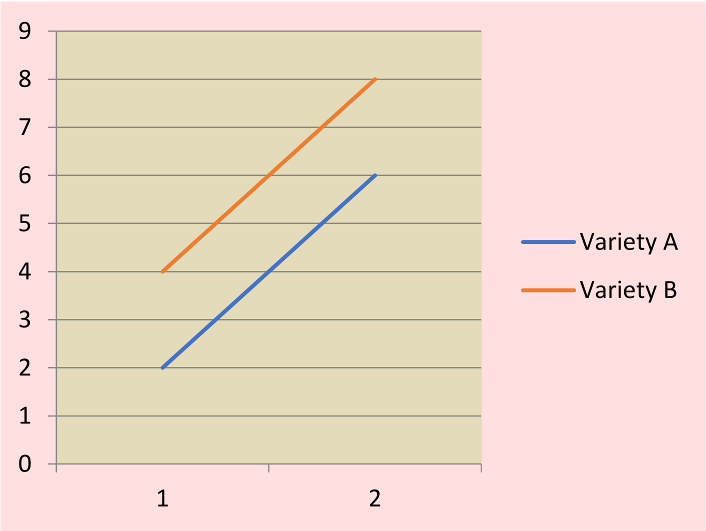
$$\boxed{H^2_{ns} = R / S}$$

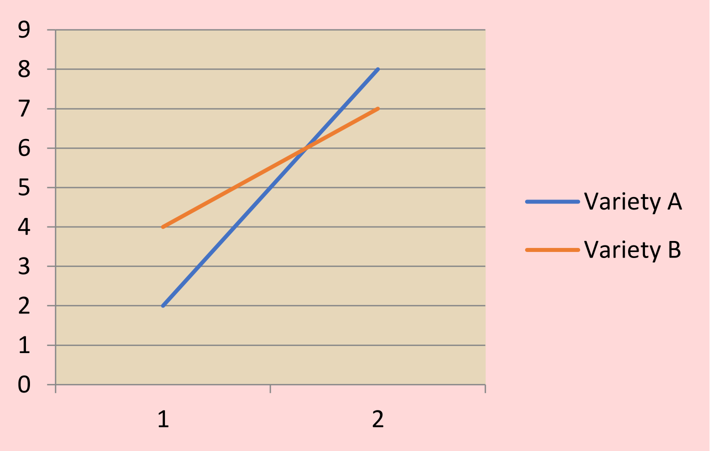
M3 – U3 Calculation and evaluation of key breeding parameters

Quantitative traits analysis

G x E interaction







M3 – U3 Calculation and evaluation of key breeding parameters

Practical: parameters & traits during breeding workflow

Barbara Pipan (Agricultural Institute of Slovenia, KIS)

Agricultural
Institute of
Slovenia

Kmetijski
inštitut
Slovenije

LiveSeeding

Escola Superior
Agrária
Politécnico de Coimbra

Introduction to key breeding parameters

- **Key breeding parameters are essential metrics** and concepts used in plant breeding to **evaluate and improve the (genetic) traits (of interest)**.
- Some key breeding parameters: *Heritability, Genetic Variance, Estimated Breeding Value, Selection Differential, Response to Selection, Genetic Correlation, Inbreeding Coefficient, Best Linear Unbiased Predictio*

- ...but first we need to **observe and record different types of data for our breeding material** in terms of characterisation **at different levels** on **separate filial generations** (*phenotypic, genetic, genomic (other omics data if relevant), biochemical, nutritional, in vitro tests, seed quality parameters,...*)-> from **laboratories, fields, screenhouses,...-> case-by-case** with respect **to plant species -> following the descriptors / specific traits**

- These parameters are crucial for making informed decisions in breeding programs to achieve desired genetic improvements -> **to select the elite breeding lines for registration.**

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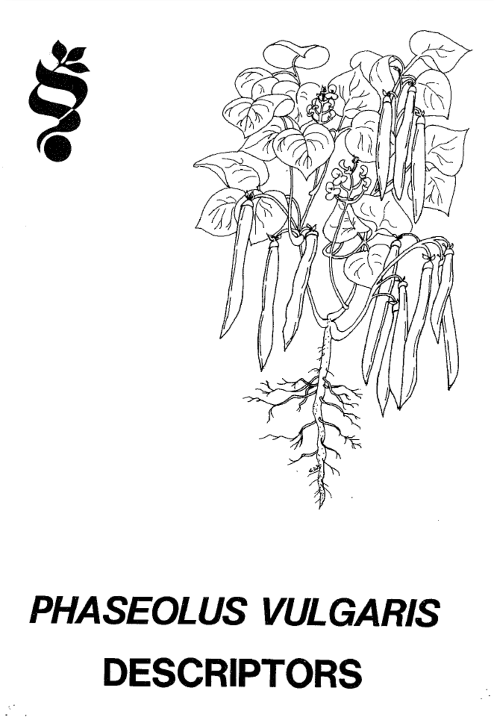
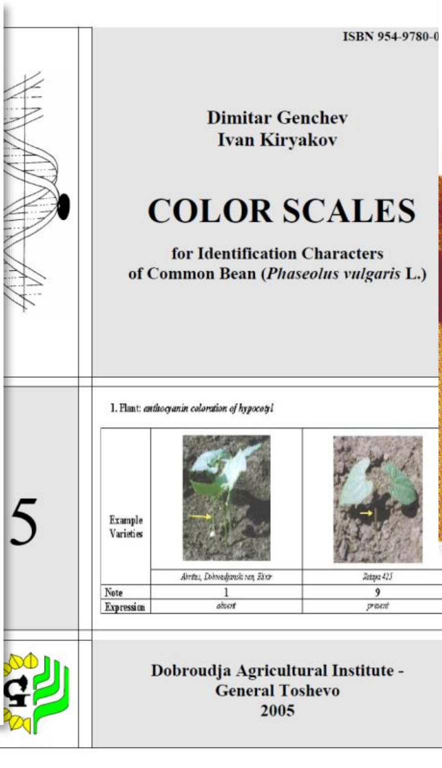
Characterisation of common bean (breeding material)->traits of interest

...when calculating and evaluating key breeding parameters, the traits of interest to be improved by the breeding programme, should be recorded and tracked first...



PHASEOLUS VULGARIS

DESCRIPTORS



ISBN 954-9780-0

Dimitar Genchev
Ivan Kiryakov

COLOR SCALES

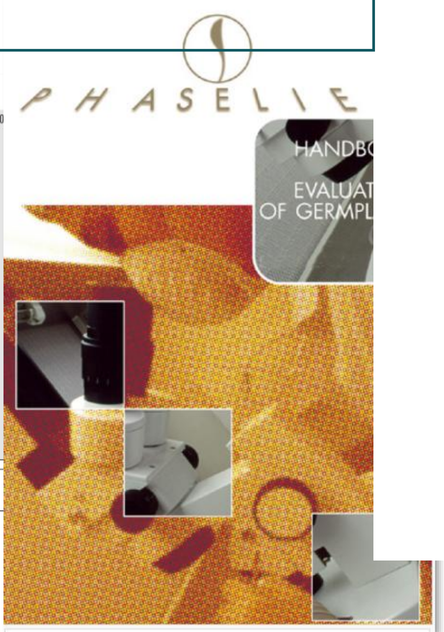
for Identification Characters
of Common Bean (*Phaseolus vulgaris* L.)

5

1. Plant: *anthocyanin coloration of hypocotyl*

Example Varieties	*Abritus, Dobroudjanski ran, Elixir*	*[illegible] 425*
Note	1	9
Expression	*absent*	*present*

Dobroudja Agricultural Institute -
General Toshevo
2005



PHASELIE

HANDBO
EVALUAT
OF GERMPL

Towards the Development, Maintenance, and Standardized Phenotypic Characterization of Single-Seed-Descent Genetic Resources for Common Bean

Gaia Cortinovis,[1] Markus Oppermann,[2] Kerstin Neumann,[2] Andreas Graner,[2] Tania Gioia,[3] Marco Marsella,[4] Saleh Alseekh,[5,6] Alisdair R. Fernie,[5,6] Roberto Papa,[1] Elisa Bellucci,[1,7] and Elena Bitocchi[1,7]

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[2]Research Group Genebank Documentation, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Seeland, Germany
[3]School of Agricultural, Forestry, Food and Environmental Sciences (SAFE), University of Basilicata, Potenza, Italy
[4]International Treaty on Plant Genetic Resources for Food and Agriculture (FAO), Rome, Italy
[5]Department of Molecular Physiology, Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm, Germany
[6]Center for Plant Systems Biology, Plovdiv, Bulgaria
[7]Corresponding authors: *e.bellucci@univpm.it*, *e.bitocchi@univpm.it*

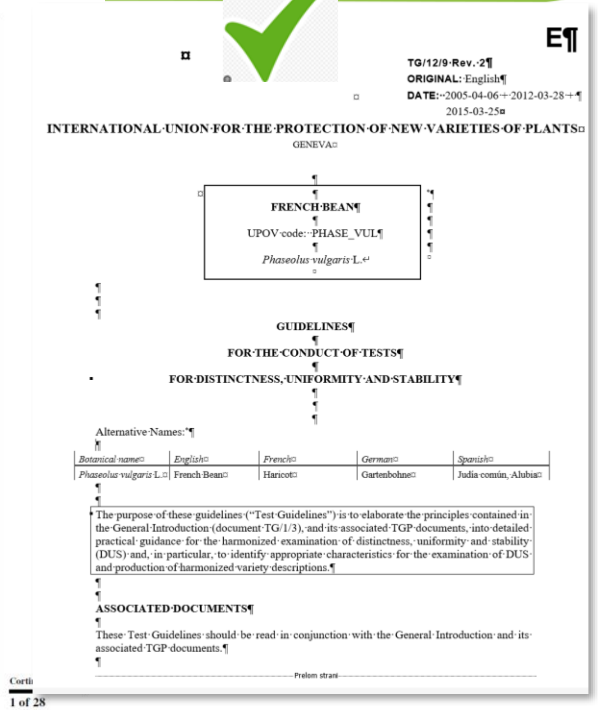
The optimal use of legume genetic resources represents a key prerequisite for coping with current agriculture-related societal challenges, including conservation of agrobiodiversity, agricultural sustainability, food security, and human health. Among legumes, the common bean (*Phaseolus vulgaris*) is the most economically important for human consumption, and its evolutionary trajectories as a species have been crucial to determining the structure and level of its present and available genetic diversity. Genomic advances are considerably enhancing the characterization and assessment of important genetic variants. For this purpose, the development and availability of, and access to, well-described and efficiently managed genetic resource collections that comprise pure lines derived by single-seed-descent cycles will be paramount for the use of the reservoir of common bean variability and for the advanced breeding of legume crops. This is one of the main aims of the new and challenging European project INCREASE, which is the implementation of Intelligent Collections with appropriate standardized protocols that must be characterized, maintained, and made available, along with the related data, to users such as breeders and researchers. © 2021 The Authors. Current Protocols published by Wiley Periodicals LLC.

Basic Protocol 1: Characterizing common bean seeds for seed trait descriptors
Basic Protocol 2: Bean seed imaging
Basic Protocol 3: Characterizing bean lines for plant trait descriptors specific for common bean Primary Seed Increase

Keywords: common bean • genetic diversity • genetic resources • intelligent collections • single-seed-descent line • standardized phenotyping protocols

CURRENT PROTOCOLS

Current Protocols e133, Volume 1
Published in Wiley Online Library (wileyonlinelibrary.com).
doi: 10.1002/cpz1.133



E¶

TG/12/9 Rev. 2¶
ORIGINAL: English¶
DATE: 2005-04-06 + 2012-03-28 +¶
2015-03-25

INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS
GENEVA

FRENCH BEAN¶
UPOV code: PHASE_VUL¶
Phaseolus vulgaris L.

GUIDELINES¶
FOR THE CONDUCT OF TESTS¶
FOR DISTINCTNESS, UNIFORMITY AND STABILITY¶

Alternative Names:*¶

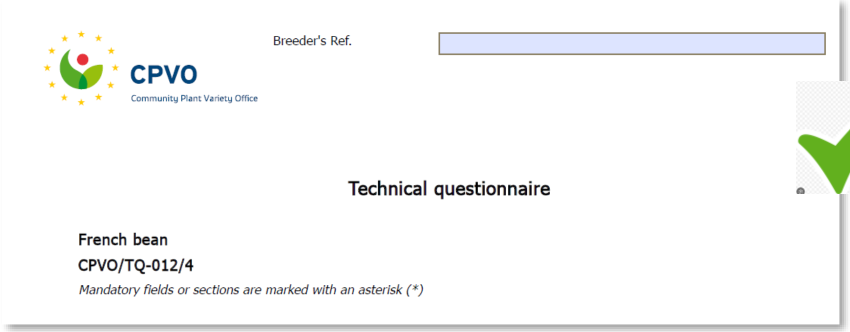
Botanical name	*English*	*French*	*German*	*Spanish*
Phaseolus vulgaris L.	French Bean	Haricot	Gartenbohne	Judía común, Alubia

The purpose of these guidelines ("Test Guidelines") is to elaborate the principles contained in the General Introduction (document TG/1/3), and its associated TGP documents, into detailed practical guidance for the harmonized examination of distinctness, uniformity and stability (DUS) and, in particular, to identify appropriate characteristics for the examination of DUS and production of harmonized variety descriptions.¶

ASSOCIATED DOCUMENTS¶

These Test Guidelines should be read in conjunction with the General Introduction and its associated TGP documents.¶

Prelom strani



Breeder's Ref.

CPVO
Community Plant Variety Office

Technical questionnaire

French bean
CPVO/TQ-012/4
Mandatory fields or sections are marked with an asterisk (*)

Characterisation of common bean breeding material_KIS example - Morfo data+photo material

During different F generations: in a screenhouse, on the field

Obvezno izpolniti za vse lastnosti_please mark the state of expression which best corresponds regarding CPVO Technical Questionare CPVO/TQ-012/4 27/2/2013 (the number in brackets refers to the corresponding characteristic in the CPVO Technical Protocol (PHASE_VUL, adopted 10/4/2023)

05 . 01 . Plant: growth type (2)*	05 . 01.01 . Leaf: intensity of green colour (9) *	05 . 01.02 . Flower: size of bract (15) *	05 . 01.02 . Flower: size of bract (15) * (width x length - mm)	05 . 02 . Flower: colour of standard (16) (G) *	05 . 03 . Dwarf beans only: Pod: length (excluding beak) (18) *	Please indicate length in cm	05 . 04 . Climbing beans only: Pod: length (excluding beak) (19) *	Please indicate length in cm	05 . 04.01 . Pod: width at maximum point (20) *	Please indicate width in mm	05 . 05 . Pod: shape of cross section (through seed) (22) (G) *	05 . 06 . Pod: ground colour (24) (G) *	05 . 06.01 . Pod: intensity of ground colour (25)	05 . 06.02 . Pod: secondary colour (26) *	05 . 07 . Pod: stringiness on ventral suture (29) (G) *	05 . 07.01 . Seed: weight (37) *	Please indicate the 1000 seeds weight	05 . 08 . Seed: number of colours (43) (G) *	05 . 09 . Seed: main colour (largest area) (42) (G) *	05 . 10 . Seed: predominant secondary colour (45) (G) *	05 . 11 . Time of flowering (50% of the plants with at least one flower) (48) *	Please indicate an example variety

Breeder's score

Charactersits regrding Phaselieu and AIS descriptors (minimum descriptor proposed by the PHASELIEU group and the alphanumeric code developed for some of them; p:36-43)

PLANT 1 . First flower days	PLANT 2 . Plant type	LEAF 3 . Shape	FLOWER 4 . Colour of standard	FLOWER 5 . Colour of wings	FLOWER 6 . Veins in the standard	POD 7 . Position in the plant	POD 8 . Fibre hardness	POD 9 . Colour (fresh pod)	POD 10 . Colour (mature pod)	SEED 11. Size: lenght average (mm) of 10 seeds	SEED 11. Size: width average (mm) of 10 seeds	SEED 11. Size: height average (mm) of 10 seeds	SEED 12 . Shape	SEED 13 . 100 seeds weight [g]	Število semen manj kot 100	SEED 14 . Colour (primary and secondary)

General

Sowing date	Harvesting date	Yiled/ harvest [g]	Harvesting date	Yiled/ harvest [g]	No. of plants grown	Total yiled [g]	Yield per plant [g]	Total yiled - cleaned [g]	Yield per plant - cleaned [g]

Additional evaluation

Average leaf area of 10 mature leaves [cm2]	Average leaf length [cm]	Average leaf width [cm]	Average no. of technologically mature pods per plant (from 10 plants)	Weight of one representative technologically mature fresh pod [g]	Yield of fresh pods per plant [g]	Average of technologically mature pod length (10 pods) [cm]	SD from average of technologically mature pod length (10 pods) [cm]	Average of technologically mature pod width (10 pods) [mm]	SD from average of technologically mature pod width (10 pods) [mm]

Visual tolerance to C. lindemuthianum (1-none, 5-complete)	Visual tolerance to BCMV/BCMNV (1-none, 5-complete)	Visual tolerance to bacterial infection (Psevdomonas, Xantomonas,…) (1-none, 5-complete)	Visual tolerance to abiotic stress (high T, water deficit) (1-none, 5-complete)	Earliness for technologicall maturity (1-late, 5-early)	Earliness for physiological maturity (1-late, 5-early)	Presence of bean weevil (*Acanthoscelides obtectus*)

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Characterisation of common bean breeding material_KIS example – genetic background

During F2 generation: in the lab

Lab label	ee	eg	eh	ef	ei	sa	sb	sd	se	sf	sg	sh
Marker	SW13	ROC11	SG6	SBD5	DESU-G1	SW12	SAS13	SZ04	SF10	SN02	SBA16	SW6-800R
Lastnost	BCMV_BCMNV resistance+earliness+yield	BCMV_BCMNV resistance+earliness+yield	BCMV_BCMNV resistance+earliness+yield	BCMV_BCMNV resistance+earliness+yield	bean rust resistance	anthrachnose resistance	anthrachnose resistance	anthrachnose resistance	anthrachnose resistance	ALS resistance	ALS resistance	bean-pod weevil resistance

Lab label	si	
Marker	Phs	
Lastnost	phaseolin + white mold + CBB	
	Andean / hybrid	**Mesoamerican**

	ff	
Marker	BCMV_48289	
Lastnost	BCMV_BCMNV resistance+earliness+yield	

marker x	**makrer y**	**marker w**	**marker c**	**marker f**	**marker d**	**marker aa**	**marker ag**	**marker z**

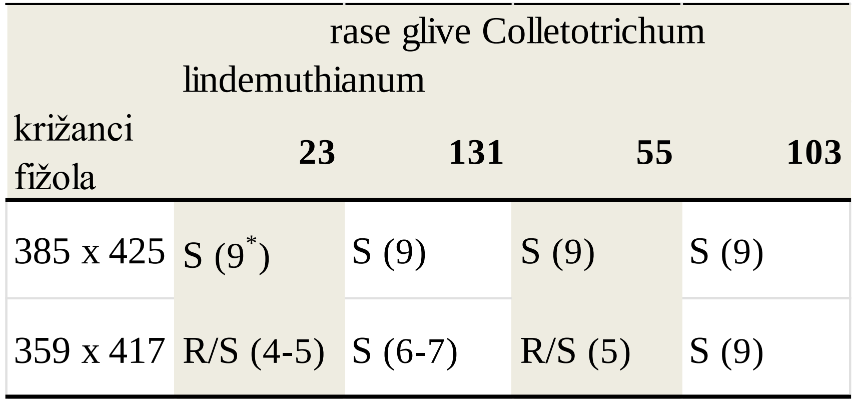
Trait association
gene pool determination
BCMV_BCMNV resistance + earliness+yield
bean rust resistance
Antrachnose resistance
ALS (angular leaf spot)
Bean-pod weevil (bruchid resistance)
Fe+Zn+yield related markers
Low P uptake and favorable root morphology; low P toelrance
drought stress tolerance

LiveSeeding

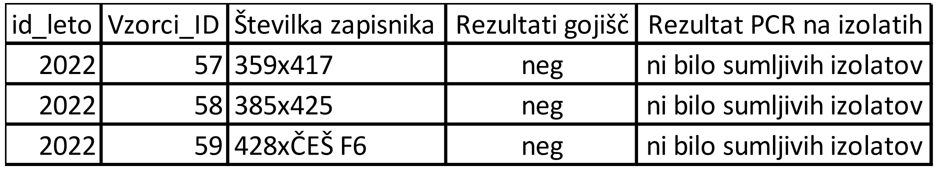
Characterisation of common bean breeding material_KIS example – pathogen resistance

During F5-F7 generation: in the lab (*in-vitro* tests according to CPVO requiremnents)

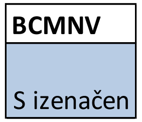
BCMNV, *Colletotrichum lindemuthianum, Pseudomonas phaseoli, Xantomonas pv. phaseoli*



križanci fižola	rase glive Colletotrichum lindemuthianum **23**	**131**	**55**	**103**
385 x 425	S (9*)	S (9)	S (9)	S (9)
359 x 417	R/S (4-5)	S (6-7)	R/S (5)	S (9)



id_leto	Vzorci_ID	Številka zapisnika	Rezultati gojišč	Rezultat PCR na izolatih
2022	57	359x417	neg	ni bilo sumljivih izolatov
2022	58	385x425	neg	ni bilo sumljivih izolatov
2022	59	428xČEŠ F6	neg	ni bilo sumljivih izolatov



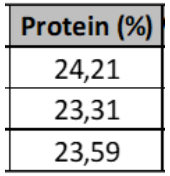
BCMNV
S izenačen

Characterisation of common bean breeding material_KIS example – biochem and organoleptic data

During F5-F7 generation: in the lab

sugar	% inhibition of trypsin	TUI / mg sample

Macroelement (g kg^{-1})					
N	K	P	S	Mg	Ca



Protein (%)
24,21
23,31
23,59

Microelement (mg kg^{-1})							
Fe	Zn	Mn	Na	Cu	Mo	Cr	Co

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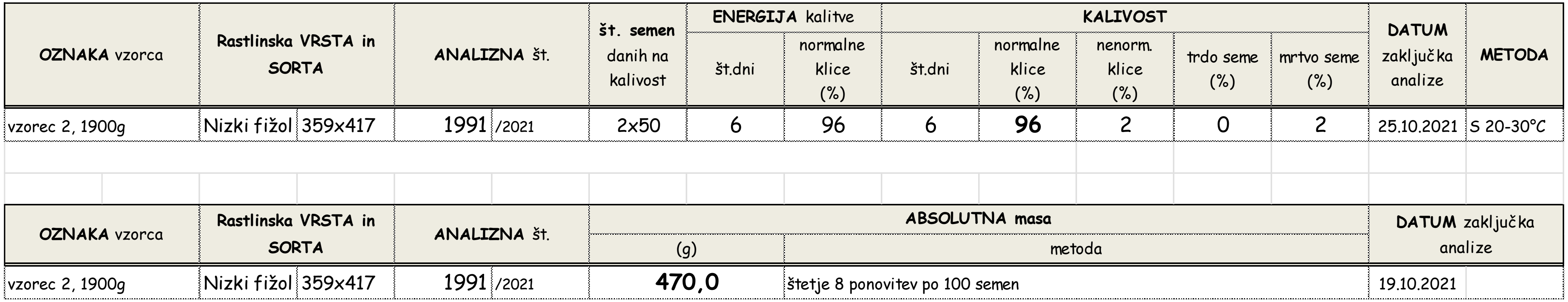
Characterisation of common bean breeding material_KIS example – Seed testing lab results

Germination rate, vigor, ATM



OZNAKA vzorca	Rastlinska VRSTA in SORTA		ANALIZNA št.		št. semen danih na kalivost	ENERGIJA kalitve		KALIVOST					DATUM zaključka analize	METODA
						št.dni	normalne klice (%)	št.dni	normalne klice (%)	nenorm. klice (%)	trdo seme (%)	mrtvo seme (%)		
vzorec 2, 1900g	Nizki fižol	359x417	1991	/2021	2x50	6	96	6	**96**	2	0	2	25.10.2021	S 20-30°C

OZNAKA vzorca	Rastlinska VRSTA in SORTA		ANALIZNA št.		ABSOLUTNA masa		DATUM zaključka analize
					(g)	metoda	
vzorec 2, 1900g	Nizki fižol	359x417	1991	/2021	**470,0**	štetje 8 ponovitev po 100 semen	19.10.2021

Characterisation of common bean breeding material_KIS example – data analysis workflow I.

During different F generations and before registration process -> **select the elite breeding line (s) along with parental lines and /or standard varieties**

- ❑ **To evaluate the variability** within and between the common bean breeding materials, data on **agromorphological-biochemical-molecular traits are analyzed using the R-programming** environment->different packages.
- ❑ Descriptive statistics are used to illustrate variations in both the **quantitative** and **qualitative** traits->including the **coefficient of variation** (CV), **standard error** (Se), **maximum** (Max) and **minimum** (Min) values, and **mean** for quantitative traits.
- ❑ **Population genetics analysis** using the algorithms for **molecular data -> more in Module 4**
- ❑ Determine the **frequency distribution and estimate diversity levels** using the **Shannon-Weaver diversity index (h')** (Shannon &Weaver, 1949) for all traits.
- ❑ To calculate the **Spearman coefficient (ρ)** to assess **pairwise patterns of associations** between traits.
- ❑ To calculate the **Gower distance** (Gower, 1971) to estimate the **similarity between pairwise breeding materials based on all traits analyzed.**

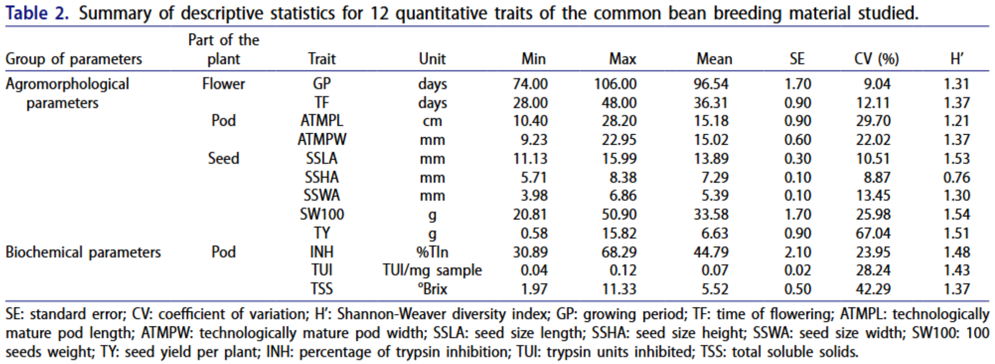


Table 2. Summary of descriptive statistics for 12 quantitative traits of the common bean breeding material studied.

Group of parameters	Part of the plant	Trait	Unit	Min	Max	Mean	SE	CV (%)	H'
Agromorphological parameters	Flower	GP	days	74.00	106.00	96.54	1.70	9.04	1.31
		TF	days	28.00	48.00	36.31	0.90	12.11	1.37
	Pod	ATMPL	cm	10.40	28.20	15.18	0.90	29.70	1.21
		ATMPW	mm	9.23	22.95	15.02	0.60	22.02	1.37
	Seed	SSLA	mm	11.13	15.99	13.89	0.30	10.51	1.53
		SSHA	mm	5.71	8.38	7.29	0.10	8.87	0.76
		SSWA	mm	3.98	6.86	5.39	0.10	13.45	1.30
		SW100	g	20.81	50.90	33.58	1.70	25.98	1.54
		TY	g	0.58	15.82	6.63	0.90	67.04	1.51
Biochemical parameters	Pod	INH	%TIn	30.89	68.29	44.79	2.10	23.95	1.48
		TUI	TUI/mg sample	0.04	0.12	0.07	0.02	28.24	1.43
		TSS	°Brix	1.97	11.33	5.52	0.50	42.29	1.37

SE: standard error; CV: coefficient of variation; H': Shannon-Weaver diversity index; GP: growing period; TF: time of flowering; ATMPL: technologically mature pod length; ATMPW: technologically mature pod width; SSLA: seed size length; SSHA: seed size height; SSWA: seed size width; SW100: 100 seeds weight; TY: seed yield per plant; INH: percentage of trypsin inhibition; TUI: trypsin units inhibited; TSS: total soluble solids.

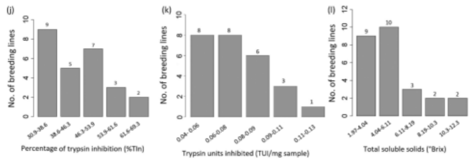


Figure 1. Frequency distribution of 26 common bean breeding materials for 12 quantitative traits related to agromorphological (a–i) and biochemical parameters (j–l).

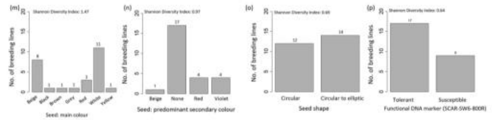


Figure 2. Frequency distribution of 26 common bean breeding materials for 15 quantitative traits related to agromorphological (a–o) and molecular parameters (p).

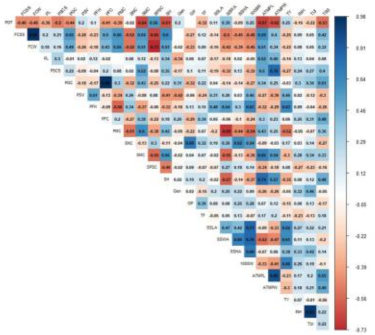


Figure 3. Spearman correlation coefficients for each pairwise comparison are shown in each cell. Positive correlations (from 0 to 1) are displayed in blue, negative correlations in red (from 0 to -1). The color intensity (dark to light) indicates the strength and direction of the relationships between the traits. Empty cells indicate non-significant correlations at $p < 0.01$. The abbreviations are as described in *2.1. Experimental design and data collection.*

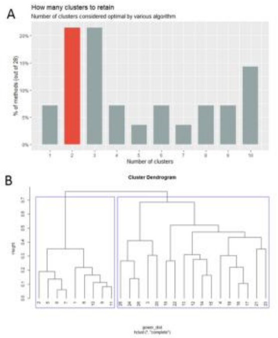


Figure 4. (A) The optimal number of clusters and (B) UPGMA dendrogram based on Gower distance showing the relationship between the studied breeding materials.

Characterisation of common bean breeding material_KIS example – data analysis workflow II

During different F generations and before registration process -> **select the elite breeding line (s) along with parental lines and /or standard varieties**

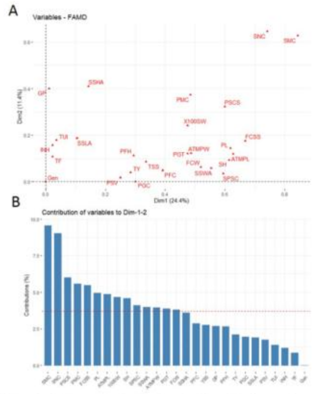


Figure 5. The contribution of qualitative and quantitative traits to the differentiation between the common bean breeding materials studied.

- ❑ **To Factor analysis of mixed data (FAMD) to** investigate the differentiation patterns between breeding materials and to identify the **main factors responsible for this differentiation.**
- ❑ Employed **hierarchical clustering** based on principal components (HCPC),which is commonly used as a **complement to factor analysis**, to further **categorize breeding materials into more specific groups.**
- ❑ Then we are using a comprehensive **multi-criteria decision analysis (MCDA) to evaluate and rank breeding materials based on their suitability for the final selection and registration of new varieties.**

(Our analysis included all qualitative and quantitative traits to ensure a thorough evaluation of the performance of each breeding material. First, we normalized the quantitative traits to a common scale of 0 to 1 using a min-max normalization technique to ensure consistent treatment of all quantitative criteria. In addition, qualitative weights reflecting the relative importance of each categorical trait and quantitative weights representing the importance of numerical measurements were provided. To integrate these weights into the decision-making process, they were normalized to allow fair comparisons between the different criteria. We then calculated the weighted sum of the normalized feature values for each alternative, considering the preference direction for each quantitative feature.)

- ❑ **This resulted in composite scores reflecting the overall performance of each breeding material - Composite performance index; CPI**

$$CPI = \sum_{i=1}^{n}(Wqi \times Qi) + \sum_{j=1}^{m}(Wqj \times Qj \times Dj),$$

where n is the number of qualitative characteristics, m is the number of quantitative characteristics, Wqi and Qi are the normalized weight and normalized value of qualitative trait i, Wqj and Qj are the normalized weight and normalized value to quantitative trait j and Dj is the direction of preference for the quantitative characteristic j, where 1 means that higher values are preferred and 0 means that lower values are preferred.

- ❑ **Finally, the alternatives are ranked based on their CPI, with a score indicating better suitability.**

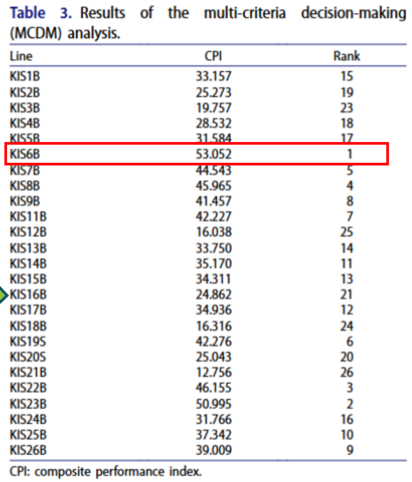


Table 3. Results of the multi-criteria decision-making (MCDM) analysis.

Line	CPI	Rank
KIS1B	33.157	15
KIS2B	25.273	19
KIS3B	19.757	23
KIS4B	28.532	18
KIS5B	31.584	17
KIS6B	53.052	1
KIS7B	44.543	5
KIS8B	45.965	4
KIS9B	41.457	8
KIS11B	42.227	7
KIS12B	16.038	25
KIS13B	33.750	14
KIS14B	35.170	11
KIS15B	34.311	13
KIS16B	24.862	21
KIS17B	34.936	12
KIS18B	16.316	24
KIS19S	42.276	6
KIS20S	25.043	20
KIS21B	12.756	26
KIS22B	46.155	3
KIS23B	50.995	2
KIS24B	31.766	16
KIS25B	37.342	10
KIS26B	39.009	9

CPI: composite performance index.

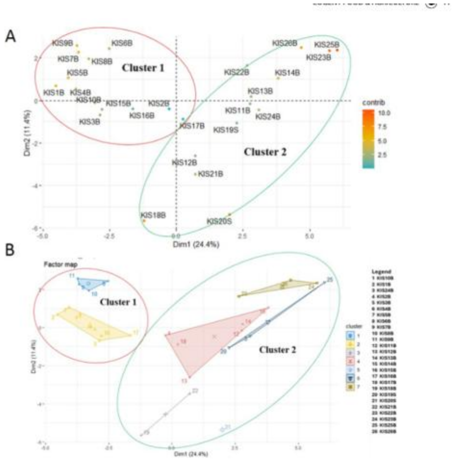


Figure 6. (A) Factor analysis of mixed data (FAMD) biplot and (B) subsequent hierarchical clustering of principal components (HCPC) biplot showing differentiation between common bean breeding materials based on 27 agromorphological-biochemical-molecular traits.

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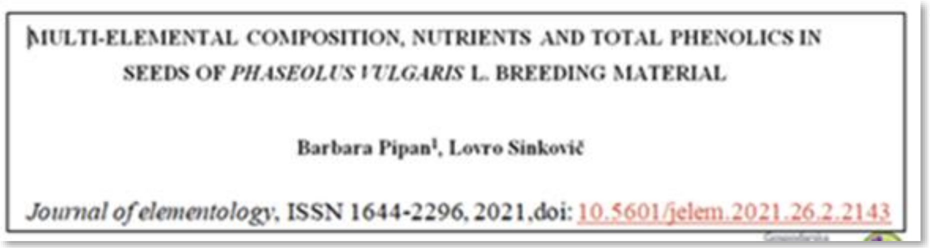
Further reading and available materials



MULTI-ELEMENTAL COMPOSITION, NUTRIENTS AND TOTAL PHENOLICS IN SEEDS OF *PHASEOLUS VULGARIS* L. BREEDING MATERIAL

Barbara Pipan[1], Lovro Sinkovič

Journal of elementology, ISSN 1644-2296, 2021, doi: 10.5601/jelem.2021.26.2.2143

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https://doi.org/10.1080/23311932.2024.2439551

SOIL & CROP SCIENCES | RESEARCH ARTICLE

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Combining multi-criteria decision analysis with agro-morphological-biochemical-molecular traits of interest for use in breeding in promising common bean breeding lines (*Phaseolus vulgaris* L.)

Lovro Sinkovič, Hourieh Tavakoli Hasanaklou, Mohamed Neji, Eva Plestenjak, Peter Dolničar, Vladimir Meglič and Barbara Pipan

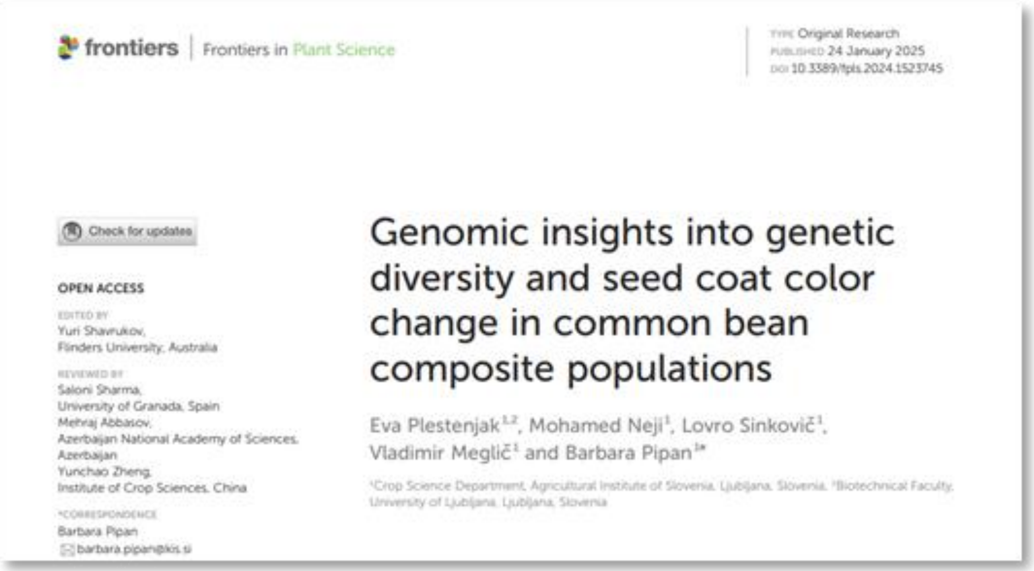
Department of Crop Science, Agricultural Institute of Slovenia, Ljubljana, Slovenia

ACTA AGRICULTURAE SCANDINAVICA, SECTION B — SOIL & PLANT SCIENCE
2024, VOL. 74, NO. 1, 2392507
https://doi.org/10.1080/09064710.2024.2392507

OPEN ACCESS

Nodulation performance and agronomic traits of European common bean (*Phaseolus vulgaris* L.) genetic resources

Eva Plestenjak[a], Vladimir Meglič[a], Lovro Sinkovič[a], Matevž Likar[b], Marjana Regvar[b] and Barbara Pipan[a]



Frontiers in Plant Science

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Genomic insights into genetic diversity and seed coat color change in common bean composite populations

Eva Plestenjak[1,2], Mohamed Neji[1], Lovro Sinkovič[1], Vladimir Meglič[1] and Barbara Pipan[1*]

[1]Crop Science Department, Agricultural Institute of Slovenia, Ljubljana, Slovenia, [2]Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia

M3 – U3 U3 Calculation and evaluation of key breeding parameters

QUIZ

Question 1: Differences between Qualitative and quantitative traits

Question 2: Components of phenotypic variation

Question 3: Why are correlations useful for breeders?

Question 4: Explain the concept of heritability

Question 5: How can G x E interaction exploded by breeders?

Send to :

adrodbur@doctor.upv.es and petra.jelincic@ips-konzalting.hr

In 15 min

LiveSeeding

Wrap up/Main challenges for the future

- To calculate and evaluate **key breeding parameters** is highly complex **covering different types of data and results from different years** within breeding procedure.
- Key breeding parameters are **crucial for final selection** in breeding programms.
- Our main challenge is to make the **breeding process, breeding materials, data and the results digitalised** and to **make key breeding parameters automatically calculated** from the data within breeding workflow-> **platform KISDigi Fižol** is being established.

KISDigi Fižol

CREDIT Vibes

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Root phenotyping and genetic improvement for rotational crops resilient to environmental change

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Javna služba v vrtnarstvu

CORE organic

WRAP UP

- ☐ *What we have learned today?*
- ☐ *Proposed homework: make a search and list at least 5 traits with high heritability and 5 traits with low heritability. Include the literature you are supported for the list*

Send to :

adrodbur@doctor.upv.es and petra.jelincic@ips-konzalting.hr

By next thursday 20th february

Thank you for your attention

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Co-funded by the European Union

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