“Prerequisites for effective utilization of PGR and Information System”

3rd Part

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1. Assessing the genetic diversity

1.1 Geographic diversity,

1.2 Genetic diversity,

- Representativeness of diversity,
- Gaps analysis,

1.3 Assessment of cultivated crops diversity.

2. Prerequisites for effective utilization of PGR

2.1 Organization of germplasm & documentation

2.2 Utilization of C&E data in practice.

3. Information System

2
Prerequisites for effective utilization of PGR

2.1 Organization of germplasm & documentation.

2.2 Utilization of C&E data in practice

2.1 Organization of germplasm & documentation (methods & criteria)

- **Organization of germplasm:**
  target collections, responsibility of germplasm.
- **Classification of crops diversity:**
  cultivated species, wild species, breeding materials.

❑ Organizing documentation data

- **Passport data** for genetic materials:
  - application of Descriptor Lists
  - application of EURISCO descriptors.
- **Characterization and evaluation data:**
  - application of Multicrops Descriptor Lists
  - application of EURISCO descriptors.
  - application of field trials.

Results: Organizing germplasm data

Germplasm target collections

- **Base collections: 3317** acc., **106** species.
- **Active collections: 270 acc., 19 species.**
- **Pendent** collections (stocks): 594 acc., 50 species.
- **Field collections: 663 acc., 38 species.**
- **Responsibility of germplasm**: researcher, curator, etc
- **Development of NI** database: **4345 acc. 148 species;**

Classification of crops diversity

cultivated species:
- landraces or
- traditional local varieties, **(51%),**

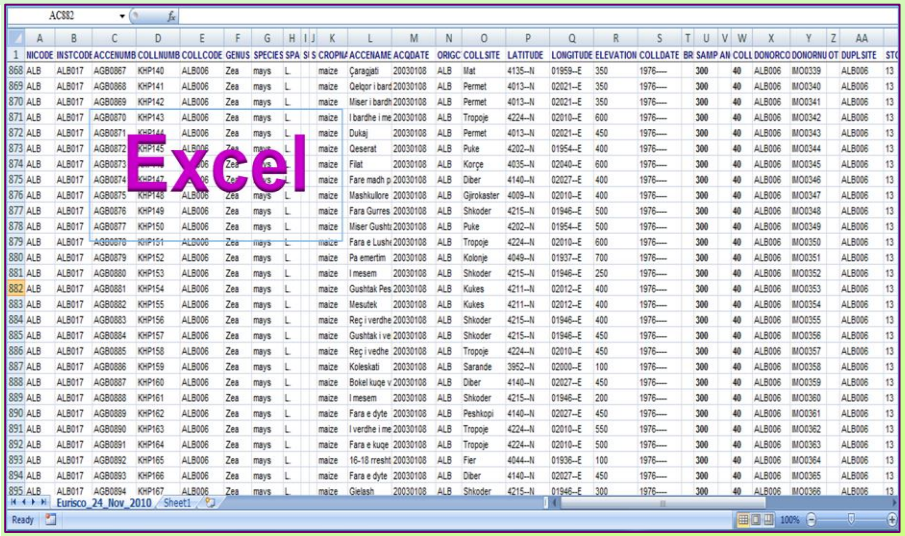
- **wild species:**
  - for direct use,
  - indirect use,
  - potentially utilizable. **(20%),**

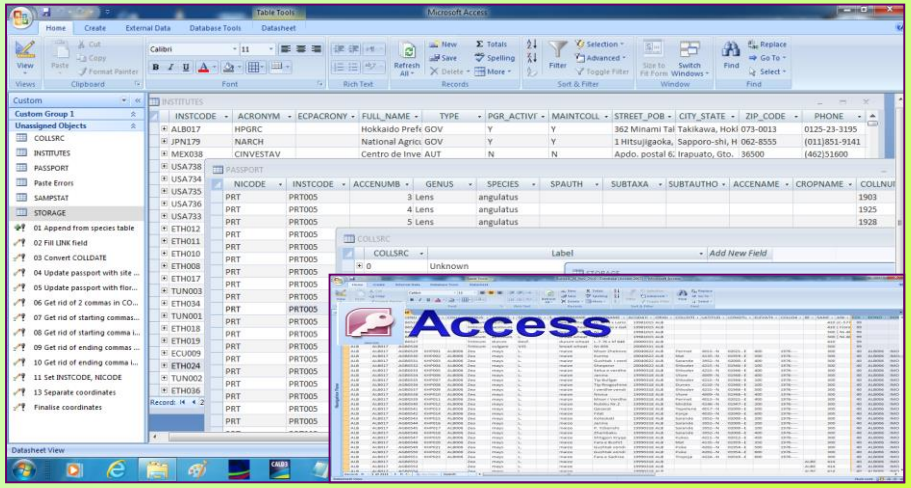
- Breeding lines, advanced cultivars/ **(22%).**
- commercial varieties. **(2%).**

- special **stocks** of cultivated crops.

Organizing documentation = genebank procedures

- 1_Exploring
- 2_Collecting
- 3_Sample Processing
- 4_Registration
- 5_Conservation
- 6_Characterization & Evaluation
- 7_Regeneration
- 8_Documentation & Information
- 9_Distribution
- 10_Management





Results: Passport data

EURISCO Descriptors

0. National Inventory code (NICODE) Example: ALB
1. Institute code (INSTCODE) Example: ALB017
2. Accession number (ACCENUMB) Example: AGB0789
3. Collecting number (COLLNUMB) Example: FE;HS027-11
4. Collecting institute code (COLLCODE) Example: `ALB017`
5. Genus (GENUS) Example: `Allium`
6. Species (SPECIES) Example: `paniculatum`
7. Species authority (SPAUTHOR) Example: `L.`
8. Subtaxa (SUBTAXA) Example: `subsp. fuscum`
9. Subtaxa authority (SUBTAUTHOR) Example: `(Waldst. et Kit.) Arc.`
10. Common crop name (CROPNAME) Example: `malting barley`
11. Accession name (ACCENAME) Example: `Rheinische Vorgebirgstrauben;Emma;Avlon`
12. Acquisition date (ACQDATE) Example: `1968----;` Example: `20020620`
13. Country of origin (ORIGCTY) Example: ALB
14. Location of collecting site (COLLSITE) Ex: `7km south of Curitiba in the state of Parna`
15. Geographical coordinates
16. Elevation of collecting site [masl**] (ELEVATION)** Example: `763`
17. Collecting date of sample [YYYYMMDD] (COLLDATE) Example: `1968----;` Ex: `20020620`
18. Breeding institute code (BREDCODE) FAO Institute Code of the institute that has bred the material.
19. Biological status of accession (SAMPSTAT)
1**00**) Wild; 110) Natural; 120) Semi-natural/wild; **200**) Weedy; **300**) Traditional cultivar/landrace
400) Breeding/research material; 410) Breeder's line; 411) Synthetic population; 412) Hybrid
413) Founder stock/base population; 414) Inbred line (parent of hybrid cultivar); 415) Segregating population;
420) Mutant/genetic stock; 421) Mutant, 423) Other gene stocks **500**) Advanced/improved cultivar; **600**) GMO,
999) Other (Elaborate in REMARKS field)

Results:

Organizing germplasm on target collections & classification of crops diversity
= was found **useful** & **practical** in management of a target collection

Organizing documentation according to genebank procedures using international standards
= was very **practical & effective** in management of germplasm

Using Standard Descriptors for Passport data:

- = **very useful and effective** in:
  - management of plant germplasm
  - identification of germplasm &
  - accessibility information system

2
Prerequisites for effective utilization of PGR

2.1 Organization of germplasm & documentation

2.2 Utilization of C&E data in practice

Characterization & evaluation: criteria

Components of variation: P = G + E + G*E

Characterization, basic criteria

- Description of specific characteristics.
- Characteristics highly inherited (qualitative traits).
- Easy to see and score.
- Expressed consistently in all environments.
- Characters check for the genetic integrity.

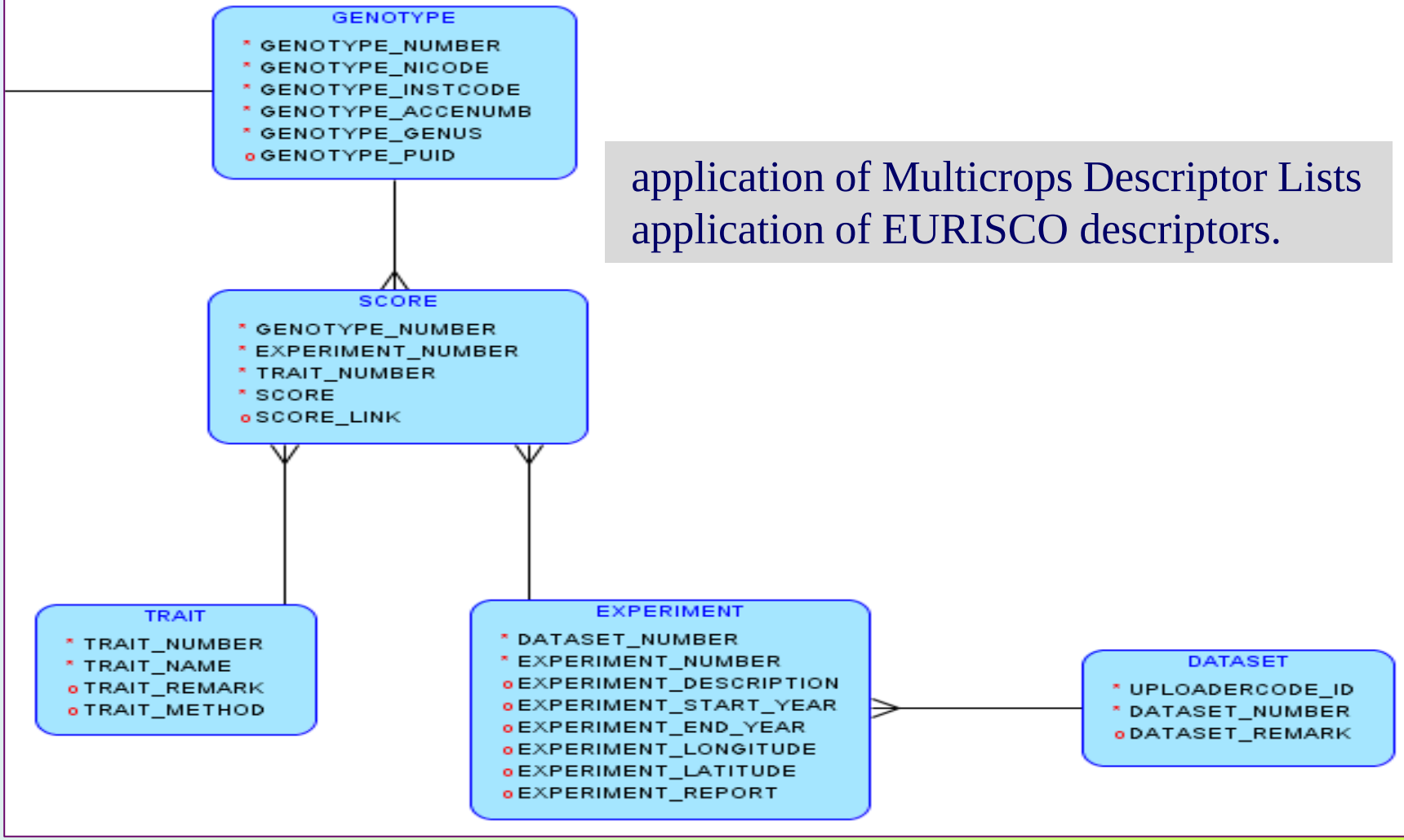
Evaluation, basic criteria

- Carried out in trials with replications.
- Retrieve all possible information on quantitative characteristics.
- Standards, and possibly methods and dataformats
- Photo documentation,
- Products / product documentation

Statistical analysis (C&E data)

- ANOVA, High significance Test, PCo analysis, Genetic Distances, Correlations, PCA.

Results: Characterization & evaluation data



application of Multicrops Descriptor Lists
application of EURISCO descriptors.

Results: Characterization & evaluation data

Results C&E:

1) identified germplasm (genotypes; high inherited traits; useful traits),
2) select germplasm (the best acc., as parents)
3) identified useful traits-= i**mportant for breeding & production.**

Conclusions: organizing germplasm & documentation

- Prerequisites for effective utilization of plant germplasm.
- Passport data facilitate identification & germplasm accessibility.
- Gene reserves for breeding and pre breeding programs.
- Traits useful for plant breeding & production.
- Utilization of collected materials (**landraces and wild species**).
- Designation of Origin (especially): **PDO**- protected designation of origin;
  PGI- protected geographical indication;

= very effective in management of plant germplasm:
(regeneration, characterization, distribution, & in sustainable farmer seeds).

2.2 Utilization of C&E data in practice

Breeding and pre breeding,

- **In genebank breeding has low priority** because:
  - Steps before breeding program,
  - Long term investment,
  - Creation of large population of potential parental lines,
  - Utilization of secondary and tertiary gene pool,
  - In-crossing of unwanted traits,

But:

C&E trials are very **important** because:

- identified **important traits useful for plant breeding & production.**

Results: C&E data in practice

Bio-morphological & molecular data.

- **Pea 28 acc**.** (15 QL traits + 23 QN characters).
- **Pea 28 acc.** (**14 RBIP markers)**

14 retrotransposon-based insertion polymorphism (RBIP)

- **Grass pea 14 acc**.** (10 QL traits + 14 QN characters).
- **Grass pea 14 acc**. **(7 RAPD markers)**.

Random Amplified Polymorphic DNA (RAPD)

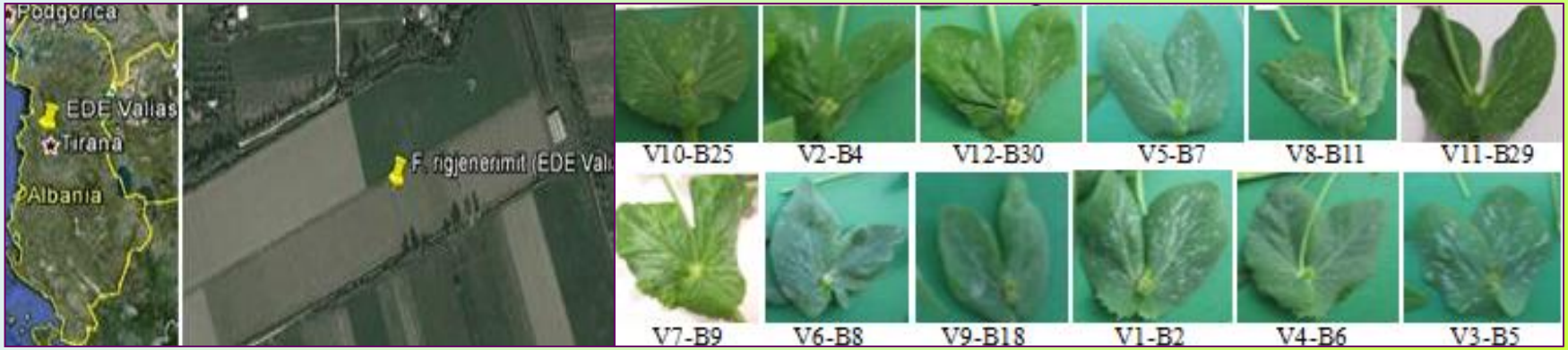
- **Tobacco 24 acc**. (10 QL traits + 14 QN characters).

- **Sorghum 20 acc.** (12 QL traits + 23 QN characters) (2018-19)
- **Sorghum 22 acc.** **DNA analysis in Germany.**

****Pea** & **Grass pea** data in collaboration with co-authors

Results: Pea 28 acc. (15 QL traits + 23 QN characters + 14 RBIP markers)

- **C&E** trials **(**morphological & mol. markers**)** **identified** diversity among pea genotypes.
- **Genetic distances/similarity** by mol. markers showed **higher similarity** in comparison to **conventional** morphological **methods** (UPOV).
- **Mol. markers** r = 0.71 > r = 0.67 (morphological traits) demonstrated the importance of mol. markers in characterization.
- The relationship: **morphological** x **mol. markers** results = **68%.**
- **Results are beneficial to pea germplasm database & to breeding programs in pea.**



Results: Grass pea 14 acc. (10 QL traits + 14 QN characters + 7 RAPD markers)

Conclusion:

The field trials & factorial analysis:

- permitted the **evaluation of genetic variability** of peas landraces group,
- identified the **most important agro-morphological traits** with potential for **sustainable the future peas & grass pea breeding programs**.

- **Factorial analysis** (PCA_{123} =80.5% of var.) found: **agro-morphological traits useful** for **breeding & production:**

- (**agro-morphological** traits **as** DM, DP, DF, PH, LLL (PC_1); LS, NPP, NSP, YG (PC_2), highly correlated (r: 0.72 to 0.93): can be **used successfully as morphological markers.**

- The **amount of genetic variability** found **suggest** the collected landraces **have variability available to the breeders**,

- **Variability** is sufficient for the creation of new favourable gene combinations to sustain field grass pea breeding programs.

Statistical analysis: trials data
(morphological & molecular markers)

Morphological		ANOVA		Eigenvectors		
Quantitative Traits		F Ratio	Prob > F	PC1	PC2	PC3
Days to flowering	DF	1850.328	<.0001*	0.3122	0.2089	0.0612
Days to pods	DP	1685.228	<.0001*	0.3194	0.1986	0.0429
Days to maturity	DM	7834.159	<.0001*	0.3157	0.2048	0.0448
Leaflet length	LLL	61.9905	<.0001*	0.3042	0.2173	0.0607
Leaflet width	LLW	1.3038	0.2491	0.0877	-0.1674	0.5727
Pod-bearing position	PBP	2.1713	0.0291*	0.0218	-0.0120	0.1222
Pod-bearing length	PBL	23.0454	<.0001*	0.3178	-0.1942	-0.0347
No. of pods per plant	NPP	15.9580	<.0001*	-0.2298	0.2806	0.0559
Beak length of pod	BLP	18.6165	0.0508	0.3168	-0.1964	-0.0534
Pod length	PL	9.6813	<.0001*	-0.3578	0.0014	0.0396
Pod width	PW	3.4997	0.0010*	-0.2306	-0.2051	0.1966
No. of seeds per pod	NSP	37.8573	<.0001*	-0.0624	0.3716	0.0122
Seed size (diameter)	SS	3.3226	0.0016*	0.1273	-0.3078	0.1397
1000 seed weight	100SW	13.2197	<.0001*	0.1544	-0.3250	0.1686
Yield per genotype	YG	4.3312	0.0001*	0.0106	0.3298	0.1763

Statistical analysis (C&E data)

- ANOVA, High significance Test, PCo analysis, Genetic Distances, Correlations, PCA.

Statistical analysis: Pea field trials data & molecular markers

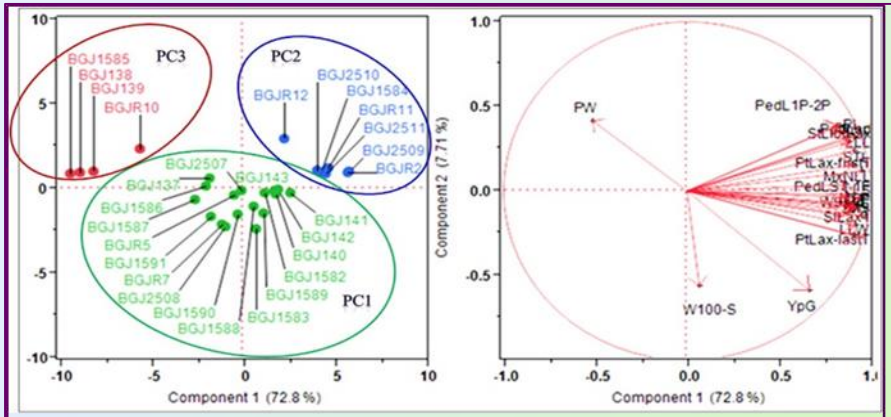


Fig. 1. dimensional relationships among the 28 pea genotypes based on morphological quantitative traits revealed by PCo analyses.

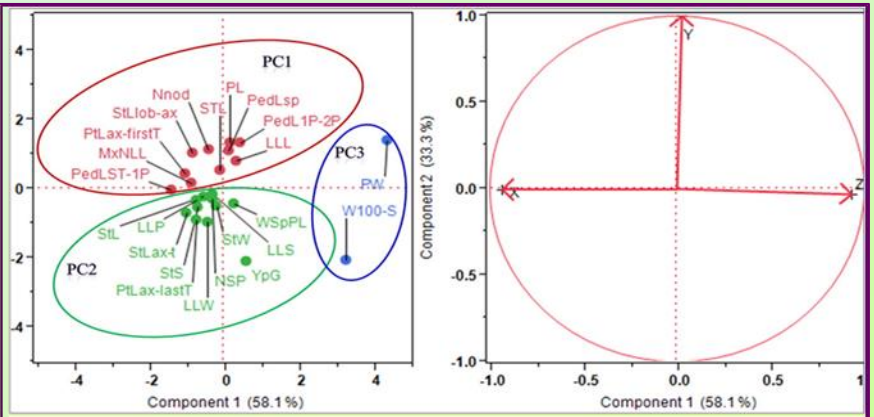


Fig 2. dimensional relationships between the most important pea morphological quantitative traits revealed by PCo analyses.

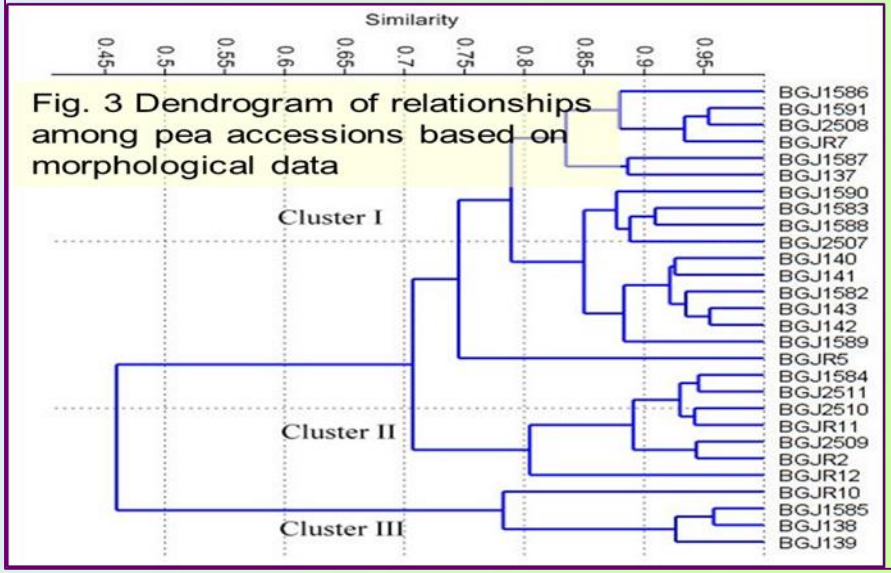
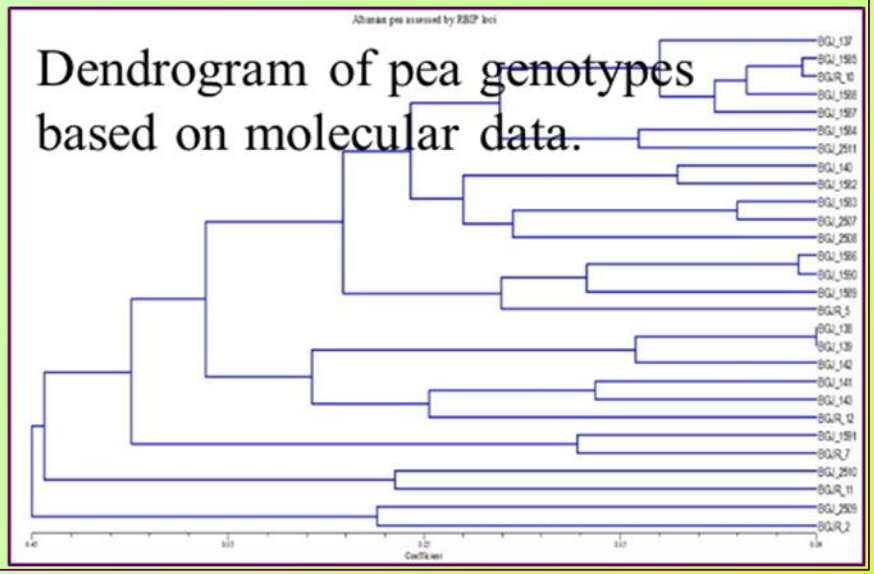


Fig. 3 Dendrogram of relationships among pea accessions based on morphological data



Statistical analysis: Grass pea field trials data & molecular markers

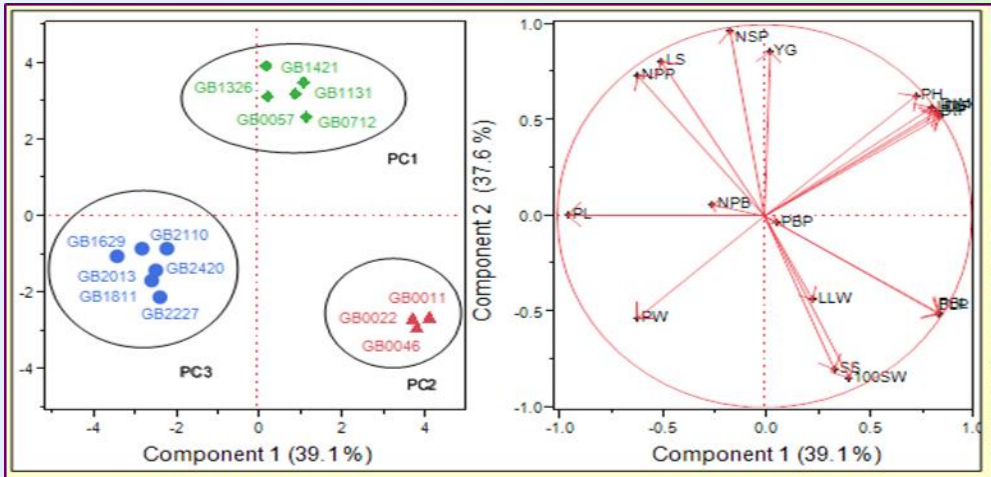


Fig 2. Relationships: grass pea genotypes x morphological quantitative traits (by PCA).

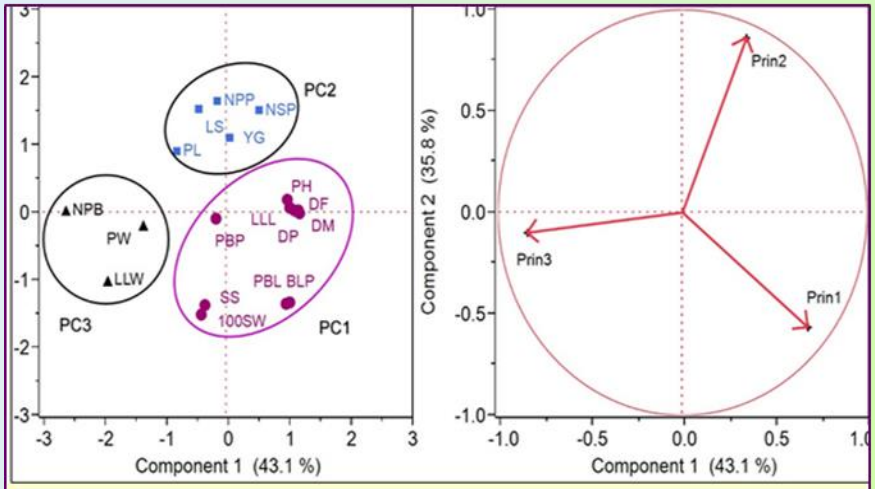


Fig 3. Dimensional relationships among agro-morphological traits (by PCA)

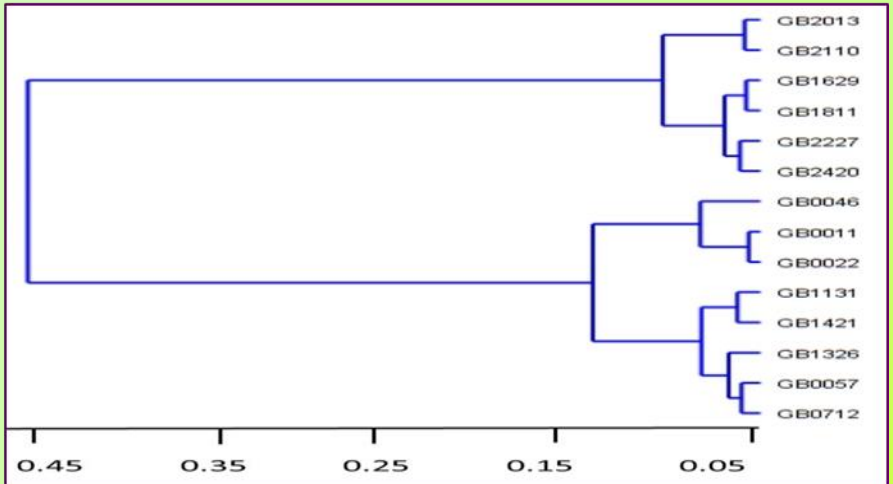


Figure 4. Dendrogram constructed on the basis of RAPD data in 14 genotypes of grass pea

Results: Pea & grass pea genotypes (Photo courtesy: V. Hobdari)

Utilization of C&E data in practice

Characterization of Tobacco 24 acc. (10 QL traits + 14 QN characters).

Genotypes	Flower color	Notes	Corolla Color	Genotypes	Flower color	Notes	Corolla Color
S-99	Medium pink	3		K-21	White-cream	1	
T-30	Medium pink	3		Sh-82	White-cream	1	
R-2	Medium pink	3		Tb-86	White-cream	1	
Rs	Medium pink	3		B-11	Red	5	
R-87	Medium pink	3		B-12	Red	5	
R-S1	Light pink	2		B-21	Red	5	
R4	Light pink	2		C32-B	Red	5	
LR1	Light pink	2		Sh	Dark pink	4	
F-R4	Light pink	2		Sh-11	Dark pink	4	
R12	Light pink	2		C-84	Dark pink	4	
S-94	Light pink	2		P-28	White-cream	1	

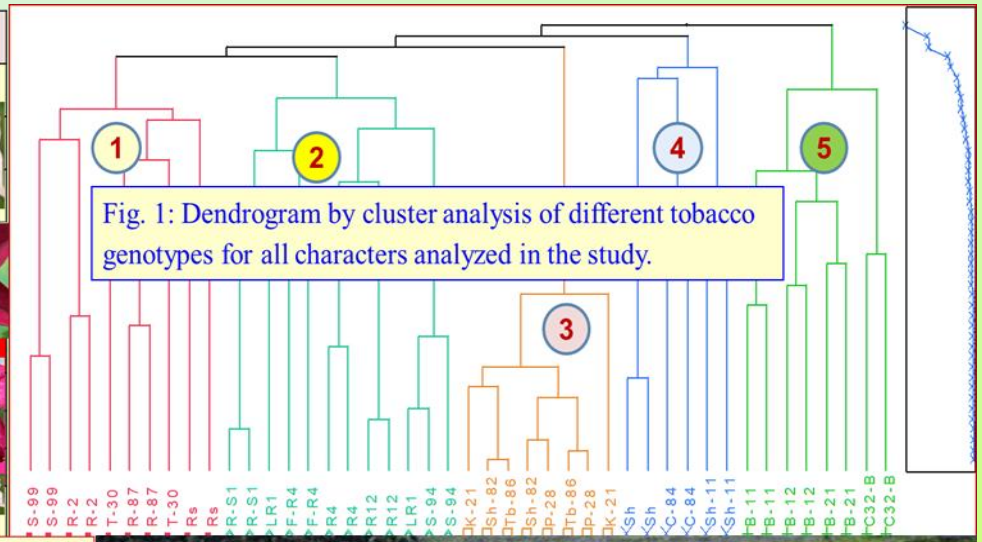
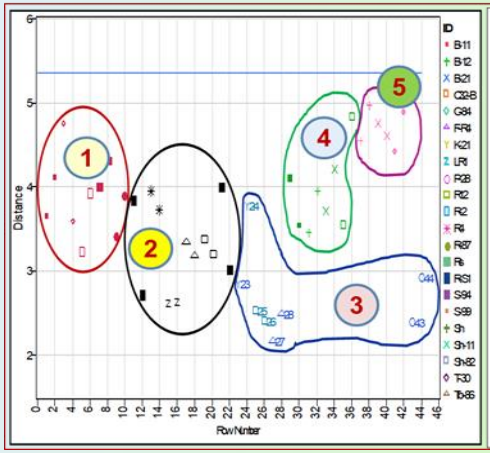
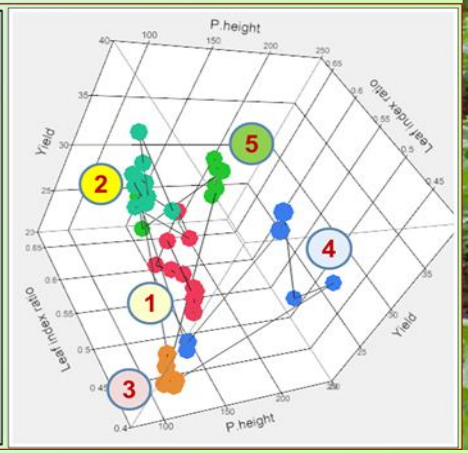


Fig. 1: Dendrogram by cluster analysis of different tobacco genotypes for all characters analyzed in the study.

Tobacco genotypes distances according to outlier analysis of Mahalanobis and their views in Scatterplot 3D





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R-2	Medium pink	3		Tb-86	White-cream	1	
Rs	Medium pink	3		B-11	Red	5	
R-87	Medium pink	3		B-12	Red	5	
R-S1	Light pink	2		B-21	Red	5	
R4	Light pink	2		C32-B	Red	5	
LR1	Light pink	2		Sh	Dark pink	4	
F-R4	Light pink	2		Sh-11	Dark pink	4	
R12	Light pink	2		C-84	Dark pink	4	
S-94	Light pink	2		P-28	White-cream	1	

Tobacco genotypes distances according to outlier analysis of Mahalanobis and their views in Scatterplot 3D

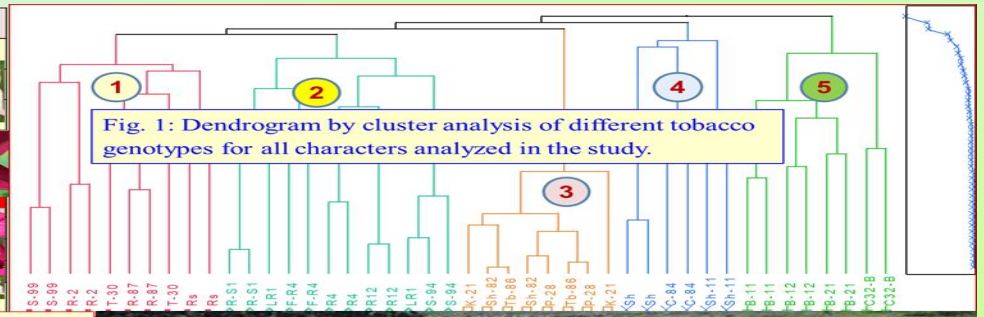
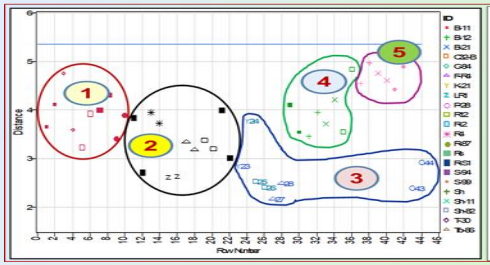
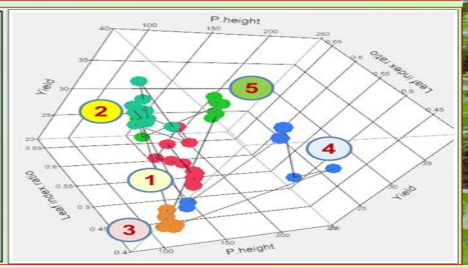


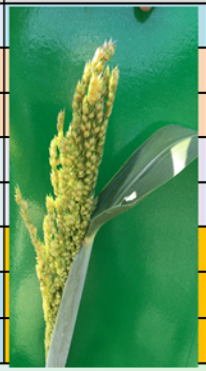
Fig. 1: Dendrogram by cluster analysis of different tobacco genotypes for all characters analyzed in the study.

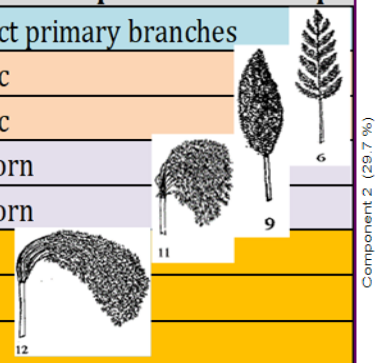




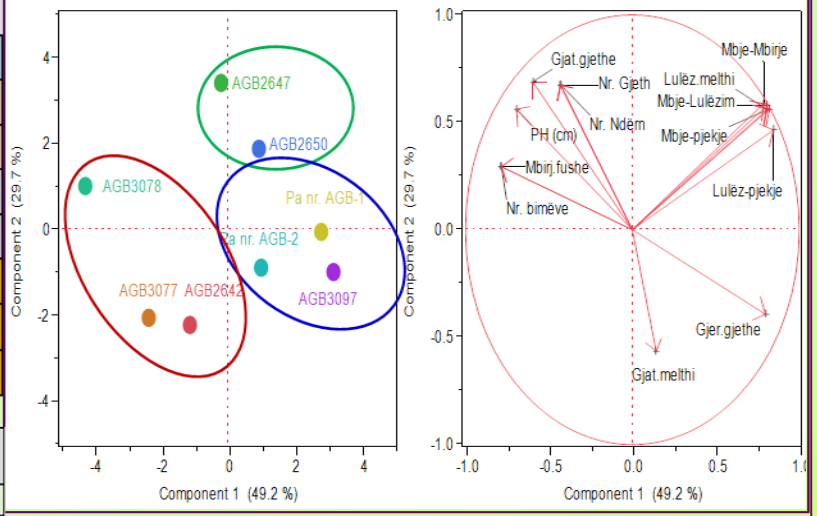
- ✓ Characterization of tobacco germplasm found a very important scientific information on tobacco genetic diversity.
- ✓ Results of the study increase usage value of the tobacco genetic materials conserved in Genebank and they are a concrete contribution for good tobacco information, and an important interest for tobacco germplasm database and for further tobacco breeding programs.

C&E data. Sorghum 8 +12 acc. (12 QL traits + 33 QN characters) + 22 acc. DNA analysis …… in Germany.

Nr	Nr acc.	Forma melthit	4.2.2 Inflorescence compactness and shape
V1	AGB2642		6 Semi-loose erect primary branches
V2	AGB2647		9 Compact elliptic
V3	AGB2650		9 Compact elliptic
V4	AGB3077		11 Half broom corn
V5	AGB3078		11 Half broom corn
V6	AGB3097		12 Broom corn
V7	Pa nr. AGB-1		12 Broom corn
V8	Pa nr. AGB-2		12 Broom corn



NR	Nr acc.	6.2.4 Inflorescence exsertion (4.9)	6.1.1 Seedling vigour (4.3)	6.1.3 Senescence (7.7)
V1	AGB2642	3 Well-exserted	5 Intermediate	3 Slightly senescent
V2	AGB2647	3 Well-exserted	3 Low	3 Slightly senescent
V3	AGB2650	3 Well-exserted	4 Low	3 Slightly senescent
V4	AGB3077	4 Peduncle recurved	5 Intermediate	3 Slightly senescent
V5	AGB3078	4 Peduncle recurved	4 Low	5 Intermediate (about half of leaves dead)
V6	AGB3097	4 Peduncle recurved	4 Low	5 Intermediate (about half of leaves dead)
V7	Pa nr. AGB-1	4 Peduncle recurved	5 Intermediate	5 Intermediate (about half of leaves dead)
V8	Pa nr. AGB-2	4 Peduncle recurved	5 Intermediate	3 Slightly senescent



Number	Eigenvalue	Percent	Cum Percent	ChiSquare	DF	Prob>ChiSq
1	6.4025	**49.2**	**49.2**	319.781	76.698	<.0001*
2	3.8647	**29.7**	**78.9**	233.008	75.169	<.0001*
3	1.8723	14.4	93.381	151.131	69.270	<.0001*
4	0.3998	3.076	96.457	76.809	60.179	0.0729

C& E & molecular data.

- **Sorghum 8 +12 acc.** (12 QL traits + 33 QN characters)
  Sorghum 22 acc. **DNA analysis …… in Germany.**

Conclusion sorghum (1st year):

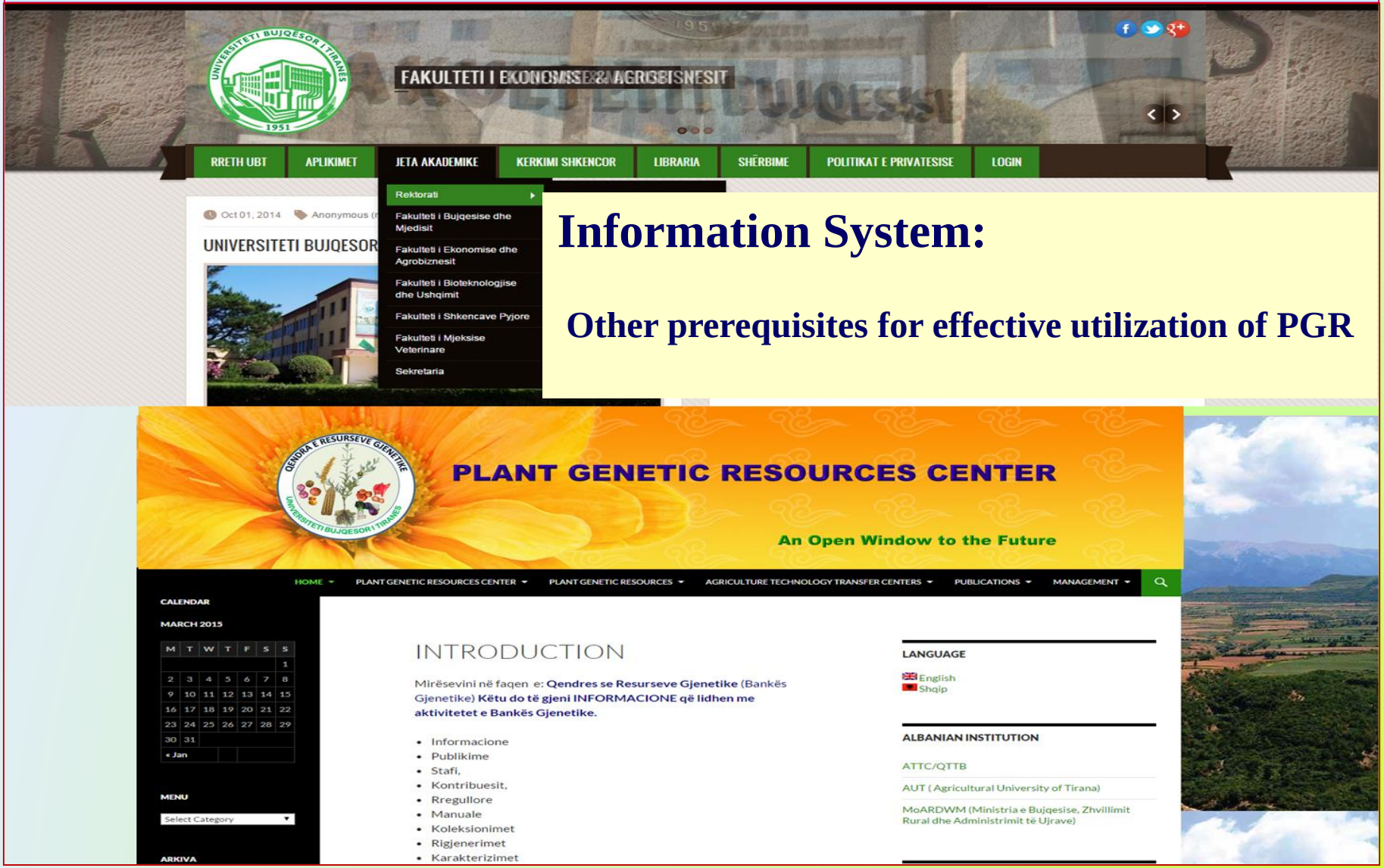
The field trials & statistical analysis:

- assessed **genetic variability** of sorghum germplasm & identified the most important agro-morphological traits with potential for **sustainable the future sorghum breeding programs**.
- **The amount of genetic variability** found suggest that especially **collected** sorghum samples have variability **available to the breeders, sufficient** for the creation of new favourable combinations for an improved variety**.**

3.
Information System

WEB links

3. Information System: WEB links



3. Information System: WEB links

INSTITUTI I RESURSEVE GJENETIKE TË BIMËVE

Institute of Plant Genetic Resources

The Institute of Plant Genetic Resources (IPGR), as a primary unit of Agricultural University of Tirana, is the national institution which coordinates the activities in the field of conservation and management of plant genetic resources (PGR). It is a relatively new institution which had been c

RGJBBU Databazë

Home / RGJBBU Databazë

- **Database i Shqiperise mbi implementimin e Planit të Dytë Global të Veprimit për Resurset Gjenetike Bimore për Bujqësinë dhe Ushqimin** (Për tu lidhur shkruani *Shqiperi* si emer perdoruesi – password – fjalekalim – username)
- **FAO World Information and Early Warning System on PGRFA (WIEWS)**
- **Katalogu EURISCO**
- **Genesys**

Kombëtare.

Qëllimi i përgjithshëm i IRGJB është promovimi i konservimit dhe përdorimit të qëndrueshëm të resurseve gjenetike të bimëve për bujqësinë dhe ushqimin (RGJBBU) në Shqipëri.

Information System: WEB links

IPGR: https://qrgj.org

AUT (Agricultural University of Tirana): http://www.ubt.edu.al,

EURISCO: http://eurisco.ipk-gatersleben.de

Genesys: http://www.genesys-pgr.org

SESTO: http://sesto.nordgen.org

WIEWS: http://www.pgrfa.org/WIEWS/

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