Characterization and evaluation data of some leguminous plants stored in National Genebank

Mirzaliyeva I.A.¹

Genetic Resources Institute of ANAS

Asadova A.²

Genetic Resources Institute of ANAS

Akparov Z.I.³

Genetic Resources Institute of ANAS

Abstract

Characterization of plant genetic resources is the major description of germplasm for breeding. Their morpho-agronomic, biochemistry and molecular evaluation also plays an important role for creation new valuable varieties. With the support of information technologies, it can be more effective collection, conservation and use of characterization and evaluation data as a database format. So, for this purpose there were created characterization databases on leguminous plants within the structure of Central Databases System. As we mentioned above characterizing of each sample with more traits is very important for the breeding issues. We have tried to achieve it in our research also. For characterization and evaluation data we used international plant descriptors prepared by ICARDA (International Center of Agriculture in Dry Areas), FAO and Bioversity International. It was created the leguminous plants (bean, cow pea, chickpea, horse bean, grass pea) databases by proper database management systems within the structure of Central Database (CDB) on PGR of Azerbaijan based on MS FoxPro. Evaluated samples were taken from the National Genebank collection by proper crop groups.

Keywords: Germplasm, Characterization, Evaluation, Legumineus Plants, Database

¹Genetic Resources Institute of ANAS, International relations, information, coordination.

Correspondence: mirzaliyevai@gmail.com

²Genetic Resources Institute of ANAS, International relations, information, coordination.

³Genetic Resources Institute of ANAS, International relations, information, coordination.

Introduction

The characterization and evaluation of germplasm is essential for the effective conservation of the plant genetic resources. Germplasm characterization is the recording of distinctly identifiable characteristics, which are highly heritable. Germplasm evaluation refers to the agronomic description of the material in Gene Bank, for traits that are generally important to breeders and researches in crop improvement (Training Manual, 2009).

Many morphological, biochemical and various molecular markers are used for the assessment of plant genetic resources based on descriptors provided by Bioversity International (former IPGRI) and FAO. Establishing database summarizing all descriptor data, its maintaining and providing breeders with necessary data are the main steps in Gene Bank management (Akparov et. al., 2007, ISOPlexis Genebank Manual, 2017). Having the database with characterization and evaluation data also shows the value of germplasms stored in Genebank.

The main features of breeding as a science is complex approaching to plants with different and advanced methods. On other side, breeding is not only the evaluation of crops together by physiology, biochemistry, technology, it also plays main role in study of wide scale of species for their submission to law of shaping for valuable physiological and chemical content. Beside the morphological features, tolerance to biotic and a biotic stress factors, including biochemical indicators with comprising different varieties are also important for the breeders (Kobyzova et al., 2013; Vavilov, 1965).

Ecological characterization is composed by identifying with following traits – variety of vegetation period; differences according to the growing phases duration; economic indicators, also the fruits and seeds size and other quantitative dimensions; vegetative symptoms; resistance to stress factors; flowering features (open or close) and etc. (Batygin,1986). It is significant to have such characterization and evaluation data at the Central Database (CDB).

The main priority in legumes breeding are the breeding of medium, medium-fast and early growing varieties with a high yield and quality, and the varieties resistant to different diseases and pests. The shorter vegetation period solves many problems, such as early or late freezing, help to avoid form the drought stress and being infected to the different diseases. Hence, breeding of early growing varieties is one of the important tasks for the expansion of fields for leguminous plants breeding.

The genetic diversity of leguminous plants plays an important role in ensuring food security and sustainability of agriculture. Although, a number of varieties holding valuable traits have been breed up to now, it is impossible to get high productivity in all regions with varying soil and climatic conditions. So, it is necessary to breed new high-yielding varieties adapted to different and specific soil and climate conditions. In this point of view, the comprehensive study of the genetic potential of different accessions by the researchers helps breeder to find the source material for the breeding of new varieties (Omelyanyuk, 2006).

The aim of the study is to collect complex research results and also morphological and physiological data and quality parameters of leguminous plant accessions conserving in National Genbank, in the form of characterization and evaluation data according to the requirements of international descriptors, to create a database for specific plant groups and to ensure its more effective use in plant researches. On the other hands, analyzing collected data was one of the important goals. Therefore, we aim to create a database on leguminous plants within the framework of our Central DataBase. The study results on Genebank collection will appear in the created characterization databases and help plant breeders to identify accessions with some desired properties more effectively (Aliyev, 2002; Mirzaliyeva, 2010; Sosinsky, 2000).

Materials and Methods

The research material consisted of accessions belonging to the genus of *Phaseolus* L., *Vigna savi*, *Vicia* L. and *Lathyrus* L. that seed materials are being conserved at the medium term conservation in National Genebank and have all passport descriptors at Central Database.

First, a proper structure element – tables for adding characterization data from appropriate fields was prepared (Khanna and Neeta, 2017; Stephanie, 2001). Filled tables with data records could transferred to new created characterization database with different program tools. Since the Central Database of exsitu collection in our Genebank is FoxPro based, most of operations have been primarily carried out within the frame of this program. Characterization database for the leguminous plants (bean, cow pea, chickpea, horse bean, grass pea) within the FoxPro based Central database were created using MS FoxPro database management systems, MS Excel, MS Access and other tools and SQL programming language.

We used Plant Characterization and Evaluation Descriptors prepared by ICARDA (International Center of Agriculture in Dry Areas), FAO and Bioversity International for this purpose (Dias et al., 2005; FAO,2001; Mammadov, 2006). Data collected from the laboratory of "Cereals and leguminous plants" of the Genetic Resources Institute (GRI) of ANAS have been standardized and included in the database with appropriate methods. Excel spreadsheet tables for characterization data of each accessions were prepared and all necessary data for proper plant groups were added into appropriate "Characterization" tables of the MS FoxPro database system of the Central Database of PGR (Germier et al. 2001; Karatigin et al. 2000; Konopka et al., 2006).

Results

The size of bean, the seamless garment of beans and the productivity of unripe beans have a particular importance in the breeding of food leguminous. In the present study, we have used characterization data of bean, cow pea, chickpea, horse bean, grass pea conserved in our Genebank and attempted to determine

a frequency of accessions with traits that are preferred by breeders in the breeding programs. One of such preferred characteristics in leguminous plants breeding is the medium height of the plants.

Generally, 50-70 cm height for the determinant form of ordinary bean (*Phaseolus vulgaris L.*), 50-70 cm for cow pea (*Vigna unguiculata L.*), 90-95 cm for horse bean (*Vicia faba L.*) and 80-90 cm for chickpea (*Lathyrus sativus L.*) is considered a positive indicator. As a result of the analysis, it was determined that 8 beans, 3 cow peas, 29 horse beans and 4 chickpea accessions, among all the studied, had the preferred plant height.

Not opening of pods in the maturity phase is one of the constraints that affect yield negatively in legumes. This trait could be less than 10% in order to reduce yield during maturity and mechanical harvesting. In our result, we defined 22 peas, 2 cow peas and 44 chickpeas accessions that show positive results.

Characterization data of 334 accessions out of 443 which is stored in National Genebank, belonging to bean (*Phaseolus L.*), cow pea (*Vigna Savi*), vetch (*Vicia L.*), horse bean (*Vicia faba L.*) and grass pea (*Lathyrus L.*) genus were created and included into proper database. Currently, there are characterization data for 95 beans, 25 cow peas, 60 vetches, 89 horse beans and 67 grass peas accessions out of 110, 33,105, 99 and 96, respectively. Those accessions are conserved at the medium term condition in National Genebank (Figure 1).

All studied species have been evaluated for several important traits. Bean (*Phaseolus vulgaris L.*) accessions were evaluated for 21 traits including days to 50% flowering, flower ground color, days to maturity, height of plant, growth habit, leaf size, number of seeds in bean, length of bean, plant pubescence, color of grain, plant pigmentation, leaf type, number of ground flower, number of ground pods, pod shedding, weight of 100 seeds, protein content, leaf type and etc. Cow pea (*Vigna unguiculata (L.)Walp.*) were evaluated for 19 characterization traits, comprising days to 50% flowering, flower ground color, days to maturity, height of plant, growth habit, leaf size, length of pods, number of seeds in bean, weight of 100 seeds, protein content, leaf type and etc.

Total number of characterization traits for chickpea (*Lathyrus L.*) were 23, including days to 50% flowering, flower ground color, days to maturity, height of plant, growth habit, leaf size, number of bean in plant, number of grains in bean, color of grain, plant pigmentation, number of ground flower, number of ground pods, pod shedding, weight of 100 seeds, protein content, leaf type and some other important traits. Some accessions of vetch species (*Vicia L.*) and also horse bean (*Vicia faba*) accessions were evaluated for 23 traits containing number of days to 50% flowering, flower ground color, days to maturity, height of plant, growth habit, leaf size, number of bean in plant, number of grains in bean, color of grain, plant pigmentation, number of ground flower, number of ground pods, pod shedding, weight of 100 seeds, protein content, leaf type, pod dehiscence and etc.

Totally, 3 species of *Phaseolus* L, 3 species of *Vigna savi.*, 13 species of *Vicia* L. and 6 species of Lathyrus L. genus in the created characterization database were evaluated. Number of leguminous accessions in Gene pool, number of characterized accessions and number of traits evaluated were given in the following table (Table 1.).

Table 1. Classification of legumineus plants for species, characterization data and evaluated traits

Genus	Species	Number of accessions stored in Genebank	Number of evaluated accessions	Number of traits for evaluation
Lathyrus	aphaca chloranthus cyaneus hirsutus sativus setifolius	96	67	23
Phaseolus	aureus lunatus vulgaris	110	93	21
Vicia	cracca ervilia grandiflora hirsuta lathyroides narbonensis sativa tetrasperma truncatula variabilis variegata villosa	105	60	23
Vicia	faba	99	89	23
Vigna	radiata sinensis unguiculata	33	25	21

Characterized leguminous accessions differ from each other by their origin as well. Evaluated 81 bean (*Phaseolus* L.) accessions were originated from Azerbaijan,1 from Iran, 9 from Russia, 1 from Ukraine, and 1 from Uzbekistan. 22 cow pea (*Vigna savi*) accessions among all studeid were native to Azerbaijan, 2 to Russia, 1 to Iran, while 96 out of all evaluated hourse bean (*Vicia faba* L.) accessions were originated from Azerbaijan, 4 from Russia and 1 from Turkey. Regarding to grass pea (*Lathyrus* L.) genotypes, origin of 66 accessions were from Azerbaijan, and only 1 was from Slovak. All of the evaluated vetch (*Vicia* L.) accessions belong to genepool of Azerbaijan.

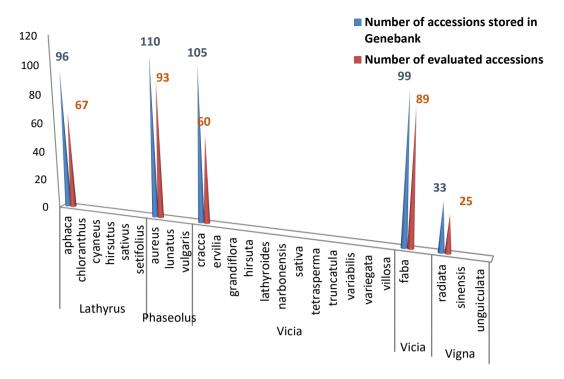


Figure 1. Number of evaluated leguminous accessions

It can be seen from the characterization databases that, 20-56 days were required from sowing until 50% of plant flower, 55-113 days for 90% maturity, depending on the cultivation year and variety of bean accessions (*Phaseolus* L.). Plant height was between 16-155 cm depending on the type of habitat. Leaf type of these plants were complex, 56 accessions had a dense and 37 sparse stem pubescence. Protein content of studied accessions was between 22.00-29.06% according to biochemical characterization data.

Number of days to flowering (50%) and days to maturity (90%) in *Vigna savi* accessions, depending from the cultivation year and variety, were 39-102 days and 69-90 days respectively. Plant height was between 16-155 cm depending on plant growth type. Length of plant 82-193, leaf type was complex, seasonality was spring and yield was 80-260 gr in 1 m². There was no anthocyanin green pigmentation on stem, *V. unguiculata* accessions were hairless, while accessions belonging to *V. radiata* species had a stem pubescence with a different density.

A total of 151 accessions belonging to 13 species and subspecies of *Vicia* L. were characterized for their bio morphological features, where 88 of them were horse bean (*V. faba* L.) accessions, including local and introduced genotypes. The main important traits such as yield (150-585 g), weight of 1000 kernels (778-1215 g) and protein content of kernels (23.98-29.56%) were evaluated.

Vicia sativa L., Vicia villosa Roth. and Vicia panonica Crantz. are the valuable forage crops among the wild species of Vicia L. genus. Since green mass yield are used as a feed, the plant height is considered

one of the main important traits of these species. As a result of evaluation for mentioned trait, the plants heights between the 20-125 cm were observed depending on species.

The number of days to 50% flowering were between 116-161 and days to 90% maturity were between 159-211 for *Lathyrus* L. species. The height of plants and the length of bean were between 25-198 cm and 3.6-42 cm, respectively. The type of leaf were complex in 60 accessions, while simple leaf type were mentioned in other 7 accessions. Seasonality of studied accessions was spring, number of bean in plot were 6-84. Both the hairy and hairless type of stem was observed among studied accessions.

Only the *L. sativus* L. is cultivated as a food and feed purposes among all the studied species and subspecies of *Lathyrus* L. Some wild species of genus, such as *L. aphaca* L., *L. chlorantus* Boiss. and *L. hirsutus* L. are considered very valuable forage species.

Analysis of the characterization data suggests that the evaluation of leguminous plants accessions covers 11 years (Figure 2.). Thus, evaluation of bean accessions has been performed in 2005-2013, cow pea in 2005-2014, horse been in 2006-2015, chickpea in 2006-2015 and grass pea in 2007-2016, respectively (Table 2.)

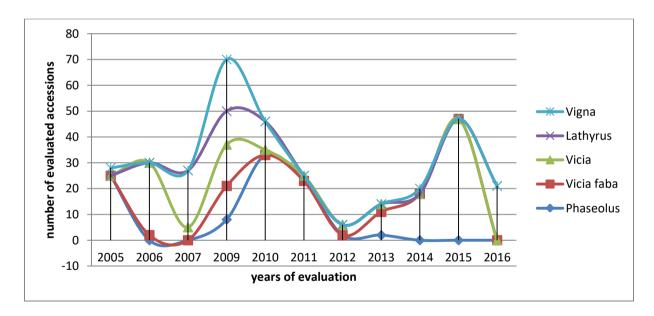
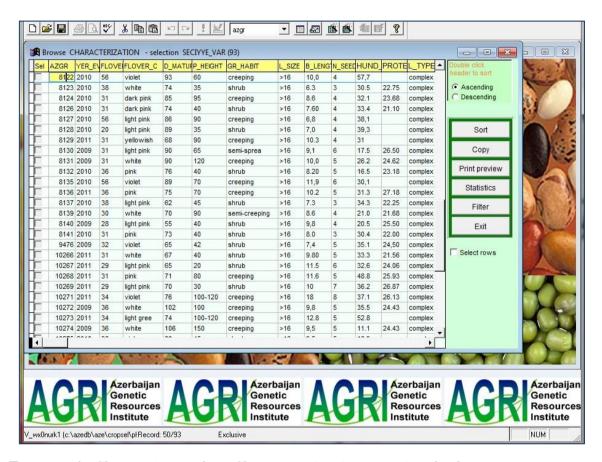


Figure 2. The evaluation level of leguminous plants by years

Table 2. Number of investigated accessions by research years

Genus / years	2005	2006	2007	2009	2010	2011	2012	2013	2014	2015	2016
Phaseolus	25			8	33	23	2	2			
Vicia faba		2		13				9	18	47	
Vicia		28	5	16	2	2	4	3			
Lathyrus			22	13	11						21
Vigna	3			20					2		



Fragment 1. Characterization data of bean accessions in appropriate database

Within the characterized samples there are 7 horse bean accessions and 18 bean accessions are advanced cultivars (varieties). As a research results we can noticed that characterized database was developed with evaluated data of 67 *Lathyrus sativus* L. for 23 traits, 93 *Phaseolus* L. samples for 21 traits, 60 *Vicia* L. samples for 23 traits, 89 *Vicia faba* L. samples for 23 traits and 25 *Vigna L*. samples for 21 traits. Plant breeders can easily access this data and use for their research or selection purposes.

Conclusions

Characterizaton and evaluation data are the records of databases, which were obtained from the Institute breeders and scientists. All these data were only at the notebooks, fieldbooks of breeders, or at their papers, but now they are centralised in one unit Database System. Within the structure of the Central Database System of National Genebank of Azerbaijan there were created characterization and evaluation databases for some legumineus plants by crop. Created database system is an open access for country and Institutional users (breeders, scientists, PhD students, specialists), and in near future will be online like a web-based Information system for all users in the world.

References

- Training Manual. (2009). A Training Module for the International Course on Plant Genetic Resources and Genebank Management, Suwon, Republic of Korea on 7-18 September 2009.
- Akparov Z.İ. and Mammadov A.T. (2007). The information system of Azerbaijan ex situ genetic resources. *ANAS Proceedings of Biological science sessions*, N3-4, Baku: "Elm" p.35-48.
- Akparov Z.İ., and Mammadov A.T. (2007). The major scientific strategies of plant genetic resources. *Azerbaijan Agrarian*, Baku, N1-3, s.120-124. (in Azeri)
- Aliyev J.A., Akparov Z.İ., Plant genetic resources of Azerbaijan. *Proceedings of National Academy of Baku*, 2002, N1-6, p 57-68. (in Azeri)
- Batygin N.F. (1986). Ontogenesis of the higher plants. Agroprodpublish, 100 p. (in Russian)
- Dias, S.R. and S. Gaiji (2005) EURISCO: A window on Europe's plant genetic diversity: Overview of European CWR collections, BI, Rome, Italy.
- FAO/IPGRI Multi-Crop Passport Descriptors list, December 2001.
- Germier Ch.U., Frese L. (2001). A data model for the evaluation and characterization of plant genetic resources. "Broad Variation and Precise Characterization Limitation for the Future". Poznan. Poland, pp.174-177.
- ISOPlexis Genebank Manual. (2017). http://www3.uma.pt/isoplexis/prog_investig_car_rec_fit_eng.html
- Karatigin S., Tikhinov A., Tikhinov L. (2000). Visual FoxPro 6. ZAO «Publishing house BINOM», (in Russian)
- Khanna P.P. and Singh Neeta. (2017). Conservation of Plant Genetic Resources. www.bioversityinternational.org/fileadmin/bioversity/publications/Web_version/174/ch13.htm

- Kobyzova L.N., Tertyshny A.V., Goncharova E.A. (2013). Perspective initial material of leguminous cultures in NTsGRRU for getting new varieties of various groups of ripeness. Leguminous and cereals plants, *Eagle: VNIIZBK*, 2: (6), p. 96-99. (in Russian)
- Konopka J., Mammadov A.T. (2006). The Regional Database of PGR in Central Asia and Caucasus. *I. International Scientific Conference "Genetic Resources of Biodiversity"*, Baku, "Elm", p.257.
- Mammadov A.T., Mirzaliyeva I.A. (2006) The analyses of collecting site data in the Database of National Genbank. *I. International Scientific Conference "Genetic Resources of Biodiversity"*, Baku, "Elm", p.255. (in Azeri)
- Mirzaliyeva I.A., Mammadov A.T, Mammadova S.M. (2010). Characterization database of Genebank collections. *Proc. of Genetic Resources Institute of ANAS*, II vol., Baku, Elm, p. 356.
- Omelyanyuk L.V., Asanov A.M. (2006) Study of pea varieties of VIR world collection in the conditions of the Southern forest-steppe of the Western Siberia / Siberian messenger of agricultural sciences, *Novosibirsk*, №1, p. 17-22. (in Russian)
- Sosinsky B. (2000). Prossessing application in Visual FoxPro 5 sphere. Translation from eng.. Kiev: *«Dialektika»*, p. 448. (in Russian)
- Stephanie L. (2001). Greene. Improving the quality of passport data to enhance germplasm use and management. *PGR Newsletter, FAO-IPGRI*, Published in Issue No.125, , p.1-8.
- Vavilov V.I. (1965). Problems of origin, genetics, selection of plants, crop breeding and agronomics. Select. Vol. 5., M.-L., T.5, p.272-27. (in Russian).