

STATUS OF PLANT GENETIC RESOURCES IN THE ALBANIAN NATIONAL INVENTORY

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ABSTRACT

Biological characteristics of crops, their collecting source, germplasm storage type, acquisition data, donor code and geographic distribution of plant species are here used for the assessment of qualitative and quantitative traits of the Plant Genetic Resources found in the Albanian National Inventory. Modelling distribution of species (interaction species x climatic data) and spatial analysis (geographic, taxonomic, ecological and conservation data) of all 1050 geo-observations helped assess the impact of bioclimatic factors that delimitate the potential distribution of fruit trees species. Comparison analysis showed an increase of quantity of landraces and wild species in ex situ collections of fruit trees, vegetables, and medicinal crops. Representativeness analysis found a high presence of wild and low domesticated genes per species. The reserve of high-quality genes is very important for breeders and field users. Spatial-modelling analysis found fruit tree species sites situated into excellent suitable areas (from 20 to 37%), very high suitable areas (from 10 to 20%), and high suitable areas (from 5 to 10%). Bioclimatic predictors capture information about annual conditions (annual mean temperature, annual precipitation, annual range in temperature and precipitation), as well as seasonal mean climate conditions and intra-year seasonality (temperature of the coldest and warmest months, precipitation of the wettest and driest quarters). So, temperature seasonality, annual precipitation of driest month appears to be the most limiting factors for the distribution of fruit tree species in the northern Albania. The annual mean temperature, and maximum temperature of warmest month for central Albania; and seasonality and maximum temperature of warmest month, precipitation seasonality and precipitation of driest month seems to be the most limiting factors for the southern Albania.

Keywords: bioclimatic factors, genetic resources, tree species distribution

1. INTRODUCTION

Plant Genetic Resources (PGR) refers to germplasm or genetic diversity (GD) of actual or potential value that exists among individuals or group of individuals belonging to a species, and are vital for crop improvement

ensuring food security. They comprise the diversity of genetic material contained in landraces populations and crop wild relatives (LPCWR), modern varieties and other economically important plant species contributing to nutritional, medicinal, energy, shelter, fuel, amenity, and cultural uses. Genetic diversity, providing raw materials for crop improvement (Alina *et al.*, 2017) and abiotic-biotic stresses resistance, adaptation to climate change (Endresen *et al.*, 2011; Khazaei, *et al.*, 2013; Gixhari *et al.*, 2016), allows crops to evolve and adapt, and is a major resource for plant breeders to use and meet the challenges of food security and environmental stability. The full spectrum of PGR consists of diverse type of collections such as those derived from the centres of diversity, centres of domestication, breeding institutions and represent the biological foundation for maintaining and improving crop productivity having played a central role in crop development from antiquity.

In general, geneticists are interested in introducing monogenic or polygenic traits into modern cultivars or in germplasm adapted to specific biotic or abiotic conditions, meanwhile plant breeders seek in genebank for the best genotypes to be used as parents (source of genes) at various stages of crop breeding programme. Production factors such as the reduction of land availability suitable for agriculture, environmental degradation and global climate change make breeders identify the adapted genotypes (AG) that can grow on poor soils or soils with an excess of harmful ions or plants adapted to drought, waterlogging, extreme temperatures or very steep terrain, and other delimited plant growing factors (Witcombe *et al.*, 2008; Gixhari *et al.*, 2012; Butler *et al.*, 2013; Al-maskri *et al.*, 2014; Challinor *et al.*, 2014;).

Plant genetic resources are a means to address the sustainable development of agriculture by helping to increase agricultural food productions. Today, preservation of genetic resources is regarded as an important need for human society. The gene banks are used to store and conserve the GD of plants, and they protect genetic materials, providing the raw material for the improvement of crops. Nowadays the objective and collecting strategies of genebanks for existing germplasm collections aim to fill gaps of the representativeness in genebank shifting the goal for PGR from quantitative perspective to the quality of collections, and to maximize the genetic representativeness (GR) of collection while minimizing the economic cost of collecting missions (Parra-Quijano *et al.*, 2011a; Tyack *et al.*, 2015). Doing this ex-situ collections of genebank are expected to be more representative of the existing genetic variation and the range of environmental adaptation, present in nature or in the field across the distribution of the target taxa or species.

To identify the best adapted genotypes (AG) breeders' need, a high genetic representativeness (GR) in genebank of GD present in nature or in the field, and any information that may help to select parents with the desired traits. The morphological phenotypic characterization and evaluation (C&E) of

PGR, very useful to determine the GR in genebank, have great importance in discovering the genes of interest for a successful breeding crop (Thormann *et al.*, 2016).

Greene and Hart (1999) said that eco-geographical representativeness (ER), (combining climatic, ecological, and geographical data) reflect indirectly the GR, due to the relationships among the environmental components (EC) of a site and the genotypes of the populations occurring at that site through natural selection and local adaptation. Thus, ER, based on the G x E interaction (where g – genotype; e – environment), can be useful in estimating the GR of collections using simple and cost-effective methods.

Albania is mentioned for its rich in plant biodiversity, including wild relatives of cultivated crops. Albanian flora identified about 3 250 species of plants in the country, from 11 000 types of plants that are in Europe (or 29.5%) (Flore de L'Albanie, 1996), but only 162 species (5%) of them is included in the Albanian National Inventory (ANI). Currently, the Albanian National Genebank maintains more than 4500 accessions of 162 plant species. Most of the germplasm, included in the EURISCO (a web-based catalogue that provides information about ex situ plant collections maintained in Europe), is represented by landraces, cultivated and wild plants as wheat, barley, crop wild relatives (CWR), wild vegetable plants (beet, carrot, onion, etc.), leafy vegetables and grain legumes (lentil, vetch, pea, clover, alfalfa, etc.).

Good database on genetic materials conserved in the gene-bank leads to enhanced utilization of germplasm by farmers and ensure that "tomorrow's plant breeders will have today's genetic resources for use in their plant breeding programs". To increase usage value and effective ex situ conservation of plant genetic resources, it is necessary to have all information in a well-organized documentation system (database) and the database must be available for everyone interested (Endresen, 2011; Green *at al.*, 2012).

The present paper aims to: i) evaluate the genetic diversity of plant genetic resources stored in the Albanian National Genebank, and ii) analyse the quality of genes stored in ex situ collections, diversity and amount of data information recorded in the Albanian National Inventory (ANI) database.

2. MATERIALS AND METHODS

Assessment of genetic diversity of Albanian National Inventory (ANI), is carried out via unique accession number, genus and species, common crop name and group of crops (cereals and maize, vegetables, legumes, medicinals, fruit trees, forages and industrials), biological status of accession (wilds, weedy, landraces, breeding materials, advanced cultivars, others); collecting source (wild habitat, farm or cultivated habitat, experimental stations,

research organization or gene-bank); by location of collecting site and geographic coordinates (latitude, longitude and elevation of collecting site), storage status (seed, field, genebank, experimental stations); acquisition data of sample (1996-2000, 2001-2005, 2006-2010, 2011-2015, 2016-2020); collecting institute and donor institute code, total stored accessions and species, using EURISCO Descriptors for uploading passport data to EURISCO (2017); FAO/Biodiversity multi-crop passport descriptors (MCPD), version 2.1, (2015). The statistical data of PGR from the Albanian National Genebank database and EURISCO catalogue database were used, and comparison analysis, synthesis and interpretation of statistical data made.

3. RESULTS AND DISCUSSION

Genetic diversity represented in the National Genebank in 2000

The Albanian National Genebank was set up in 1998, and plant germplasm stored as seeds under long-term storage conditions, until 2000 consisted of 2686 accessions (acc.) of 46 different plant species. Plant germplasm was represented by the most important group of cultivated crops as follow: cereals 28%; maize 26%; legumes 10%; forages 9%; vegetables 7%; industrials 14% and others 6%. Plant germplasm (seeds) was maintained under long-term storage conditions, in cold vertical freezers. Analysis by crops found “no” adequate representativeness of species & cultivated crops in genebank, so only 2 genera (*Triticum*, *Zea*) were more than 50%.

Comparison analysis by source and biological status showed that the 46% of total germplasm (1235 acc.), provided by ex-Research Agricultural Institutes to the genebank, was presented by narrow genetic base materials (breed materials, breeder lines, advanced cultivars). Collected genetic materials, with a potential large genetic base, were only 14% (440 acc.) of the total germplasm stored in genebank, but these materials were without EC information. Kresovich *et al.*, (2006) said that collecting germplasm without ECCS information or geographical data would not be very useful to the breeders. The most useful information on AG and bioclimatic factors that delimitates the distribution of one species, is related to the ECCS, which reveals the most important EC for adaptation and its impact on the heredity process. The results reported that all seed germplasm stored in the National Genebank (1998-2000) was little useful to be used directly by plant breeders and by farmers.

Genetic diversity represented in genebank in 2021: Albanian National Inventory database of PGR was organized in 2008, including for the first time 504 acc., in the NordGen bank database system (SESTO), and at the end of the same year, the ANI database (2111 acc., of 62 species) was included in the EURISCO catalogue database (Gixhari *et al.*, 2013).

Albanian National Inventory by acquisition data: The analysis of ANI by acquisition data of samples; found the most part of plant germplasm (46%) was accepted in the Genebank from 1998-2005 and from 2011-2015 with 23%. Three important collecting activities supported by Agricultural Service Project (ASP) 2003-2005; South Eastern Europe Development Network (SEEDNet) Project (2008-2010) and FAO projects (2014-2015) were carried out during these periods. The most important contributors were SEEDNet Project (630 acc., of 36 species) collecting 17 new species (alleles), and FAO Project (551 acc., of 52 species), collecting 25 new species (alleles) not collected before by other collecting missions.

ANI by donor code: Currently, ANI of PGR in genebank and EURISCO database includes 4570 accessions of 162 plant species. The institutional contributors to the ANI by donor code are as follow: Albanian Genebank (FAO code - ALB026) 40%; Agriculture Technology Transfer Centre of Lushnja (ALB019) 16%; Agriculture Technology Transfer Centre of Shkodra (ALB022) 16%; Agriculture Technology Transfer Centre of Vlora (ALB020) 6%; Agriculture Technology Transfer Centre of Korca (ALB021) 5%; Agriculture Technology Transfer Centre of Fushe-Kruja (ALB023) 5%; Tobacco Station (ALB027) 4%; Repatriated especially from Germany (DEU538) 4%.

ANI by storage type: Conservation of ANI is maintained in two storage forms: as seeds in genebank under long term storage conditions (76%) and under field collection conditions (24%). The principal contributors of plant germplasm conserved as field collections are: Albanian genebank 67%; Agriculture Technology Transfer Centre of Vlora (ALB020) 25%, and Agriculture Technology Transfer Centre of Korca (ALB021) 9%.

Quantitative and qualitative analysis of ANI:

ANI by group of crops: From 2000-2021 composition of ANI is changed in favour of plant species none represented in genebank. There was an increase of legumes and vegetables and especially of fruit trees species not presented before in genebank database. The principal cultivated crops that represent Albanian NI in 2021 were: cereals and maize 32%; vegetables 10%; legumes 7%; Medicinal and aromatic plants 12%; fruit-trees 25%; forages 5% and industrials 9%. Legumes, vegetables and especially the fruit trees species presence which were previously absent in the Genebank database has increased.

ANI by collecting source: Results by collecting source showed the increase of collected materials in wild and farm habitats as follow: genetic materials collected on the wild habitats were 15%; materials collected on the farm habitats were 34% and materials received by experimental stations were only

7%. Wild habitats sites are considered as source of CWR and respective wild genes (highly adapted genotypes), farm habitats are source of primitive and landraces genes (well adapted genotypes), and experimental stations are source of experimental genes (genotypes adapted for the specific areas) where they can be used directly on the farm production. Analysis by collecting source, highly related to the adaptation of genotypes represented in genebank has lead the priority of acquisition in genebank as follow: CWR shaped by the environment and highly adapted to the disfavour environment conditions, primitive and landraces shaped by climate and humans adapted to the disfavour climate conditions and resistance/or tolerance sources especially against parasites, rare and threatened species, modern cultivated crops mostly shaped by humans (plant breeders) adapted to the specific local conditions.

ANI by biological status: Comparison analysis by biological status, highly related to the quality of genotypes (genes) represented in genebank, found that: 16% of all germplasm was composed by CWR and wild food plant species (or wild genes with a very large genetic base); 45% was represented by primitive and landraces (or genes with large genetic base); 18% was represented by breed or experimental materials (or genes with narrow genetic base) and only 2% was represented by advanced cultivars (or genes with very narrow genetic base). The analysis demonstrates the high presence of qualitative genes (wild and landraces) with a very large genetic base and highly adapted to the disfavour environment conditions, which are very useful to fulfil the quality and quantity needs of plant breeders and farmers.

The aim of genebank is to conserve and use PGR providing basic materials to the crop experts to use genetic variability for the development of high yielding cultivars with a broad genetic base. However, the utilization of these genetic resources depends upon their efficient and adequate information related to ecogeographic data, characterization and evaluation data, molecular data (Gixhari *et al.*, 2014), etc., which requires efficient standards and appropriate strategies.

For effective utilization of PGR in practice geographic data of ECCS are very important for the plant breeders. They help the breeders to verify how is the GR in genebank of GD in nature or in the field, and to identify the AG for the specific areas. Witcombe *et al.*, (2008), Mackay, (2011), Bari *et al.*, (2012), Khazaei *et al.*, (2013), Gixhari *et al.*, (2016) stated that germplasm strategy including geographic data of ECCS is highly related to identification of AG that can be grow on delimited growing factors such as poor soils, salt soils, drought, waterlogging, extreme temperatures, etc. as stated in (Fiedler *et al.*, 2016; Cowan *et al.*, 2020). The genetic materials (or GD) of Albanian NI with ECCS information represent 56% of total germplasm stored in genebank.

The environment has empirically been considered as a key factor by farmers and conventional plant breeding (PB) since agriculture began. The phenotype (P) equation $P = G + E + G \times E$ explained the relationship between adaptation and GD and the effect of certain EC in the distribution of species. The most useful information on AG and bioclimatic factors that delimitates the distribution of one species, is related to the ECCS (Hijmans *et al.*, 2005a; Scheldeman *et al.*, 2010; Parra-Quijano *et al.*, 2012 a). The ECCS reveals the most important (EC) for adaptation and its impact on the heredity process. All the data provide accurate information about the EC and bioclimatic factors that either support or delimitate the distribution of one species (Parra-Quijano *et al.*, 2011a; Gixhari 2021).

Application of geographic information systems (GIS), useful to the management of georeferenced data of collecting sites, make the study of the EC under which LPCWR have acquired their adaptive traits possible. The GIS tools were also identified as prerequisites for effective utilization of PGR and as new future tools to improve the conservation and use of PGR (Pacocco *et al.*, 2018). Genebank uses GIS tools to analyse the in-situ status of endangered wild plant species in protected areas (Rodrigues *et al.*, 2004), and to identify the appropriate sites of conservation of CWR (Shehadeh *et al.*, 2013). Analysing the spatial aspect of collecting sites and geographical distances using international genebank descriptors FAO (FAO, 2015; EURISCO, 2017) and distribution of a particular group of species (Gixhari *et al.*, 2012; Parra-Quijano *et al.*, 2015), GIS methodologies improve the GR of ex situ collections, the efficiency of conservation and use of PGR, the field explorations, identification of EC and geographic areas which are likely to contain specific desired traits of interest for breeders (Parra-Quijano *et al.*, 2011b; Rosa *et al.*, 2017; Jostelle *et al.*, 2019).

Using ecogeographical representativeness (ER), and methodology that manage information of ECCS under which LPCWR have acquired their adaptive traits, genebank has identified EC and genetic representativeness (GR) of natural GD presented in NI collections.

An analysis combining trees species occurrence data (genotype) with climatic data (environment), realized by genebank in 10 counties of Albania (Shkodra, Dibra, Kukes and Lezha in the north; Korca, Gjirokastra, Berat and Vlora in the south; Tirana and Elbasan in the centre), to assess the influence of bioclimatic factors that delimitates the potential distribution of each species, was carried out. Interaction analysis of fruits tree species genotypes x 19 bioclimatic factors (G x E) that delimitates the potential distribution of each fruit tree species at the district level demonstrate that: annual precipitations, precipitation of driest month and temperature seasonality, seems to be the most limiting factors for the distribution of fruit tree species in northern part of Albania; and temperature annual range, maximum

temperature of driest month, and annual precipitations for central and central east part of Albania; and precipitation seasonality, temperature seasonality, annual precipitations seems to be the most limiting factors for south and south-western part of Albania (Figure 1).

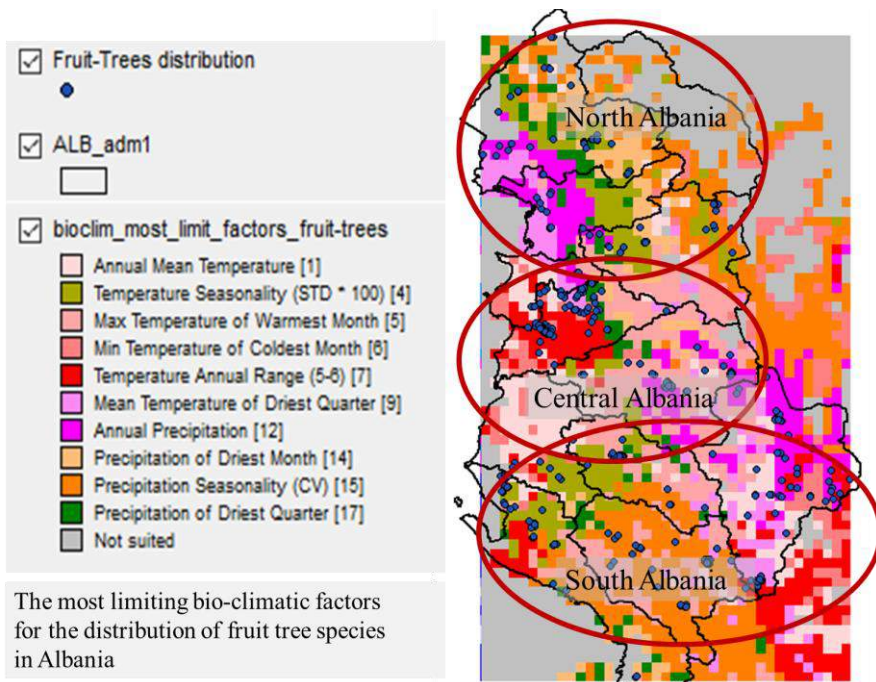


Fig. 1. The most limiting bio-climatic factors for the distribution of fruit tree species in Albania.

4. CONCLUSIONS / PROSPECTS

Ecogeographic studies provide critical information on plant genetic resources (PGR) to assess their current conservation status and prioritize areas for conservation. They have also proven useful for effective genebank management, such as the definition of core collections and identification of collection gaps. Geographic information systems (GIS) are useful tools for mapping ecogeographic distributions of biodiversity. GIS allow complex analyses to be performed, as well as clearly visualizing results in maps, which facilitates decision making and implementation of conservation policies by authorities.

So, the link between genotypes and the environment components, helping plant breeders to select sets of germplasm containing specified interested traits is provided.

Each collecting source can be individually profiled for the most important environment components as precipitation, driest, seasonality, humidity, temperature, agro-climatic zoning, and soil characteristics. Ecogeographic and GIS tools can identify the most suitable sites for conservation and regeneration, as a key factor in reducing genetic erosion.

An increase of ecogeographic and GIS tools in conservation and use of PGR is expected in the present decades, particularly as regards the challenges implied by global climate change for agriculture. Furthermore, studies on adaptation of LPCWR should continue to increase the importance of the environment components in explaining the phenotype, the abiotic-biotic aspect of adaptation, and the influence of farmers on the ecogeographical patterns of cultivated plants.

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