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Distribution of *Matricariachamomilla* L. populations surveyed in some districts of Albania

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Abstract

Geographic distribution of 20 chamomiles (*Matricariachamomilla* L.) populations, surveyed and collected in nine districts of Albania, and their comparison with 19 ex situ data of chamomile populations was carried out. The geographic areas, separated into grid cells of 1 x 1 km, and 10 x 10 km was used to assess the geographic distribution, richness and the representativeness of chamomile samples in ex situ collection. Spatial analysis detects areas of high diversity of chamomile population surveyed were Berat and Fieri districts. Comparative analysis of the representativeness indices found that chamomile populations surveyed and collected in other district areas have contributed directly in increasing their representativeness in the ex situ collection of chamomile samples. Highest contribution in increasing the representativeness of chamomile samples in ex situ collection was found in Berat, Fieri and Korca district areas, as in these areas chamomile populations were surveyed and collected far than 10 km from ex situ present points, and mid representativeness contribution was found in Dibra, Lezha and Shkodra districts areas. For the chamomile populations surveyed in Tirana, Durres and Vlora district areas a full representativeness status in ex situ collection of genebank was found. In total there were more than 70% of surveyed point that contributes with chamomile samples collected in new areas, never collected before by any collecting mission.

Key-words: Chamomile samples, geographic distribution, representativeness indices.

1. Introduction

Albania is very rich in biological and landscape diversity, in cultivated crops, in wild plant species. This diversity is attributable to the country's geographic position (geological, hydrological, climatic, and soil and relief factors). Albanian flora represents about 3250 plant species, more than 27% of European Flora [1, 3, 13, 14]. **Collections ofmedicinal and aromatic plants (MAP)** in Albania, compounded by more than 300 species (in the ex situ, in situ and on farm status of conservation) represent about 10% of the Albanian flora. Many of the medicinal and aromatic plants are well-known by the local population, which have a long tradition in collecting them either for individual and family use or for sale. Medicinal and aromatic plants are economically important plants grown over a wide range of ecological habitats in the country [7, 11, 13].

Plant genetic resources (PGR) play a key role in contributing to the sustainable development of agriculture, helping to increase agricultural food productions. Medicinal plant species provide an invaluable source of genes that can be used for the improvement of cultivated species. The information on MAPs biodiversity in Albania is generally lacking especially in terms of species [7]. There are still flora/or taxonomic groups, especially crop wild relatives which are unknown or have not been studied.

Geographic information systems (GIS) provide important information about the geographic distribution and diversity present in specific geographic areas [12] of a target species, and can be used to detect eco-geographical gaps of the representativeness in ex situ collections and subsequently to identify the sites where to prioritize collection efforts. Assessment of the current conservation status, identification of relative gaps, and implementation of more effective collecting strategies, can be improved genetic representativeness [10, 8] in ex situ collections.

The aim of the study was to identify the geographic distribution of chamomile (*Matricaria chamomilla* L.) populations surveyed and observed in nine district of Albania and their contribution on the representativeness of ex situ chamomile collection.

2. Material and methods

Geographic distribution: The study for assessment of the geographic distribution of chamomile (*Matricariachamomilla*L.) populations surveyed in nine district of Albania: Berat (BR), Dibra (DI), Durres (DR), Fieri (FR), Korca (KO), Lezha (LE), Shkoder (SH), Tirana (TR), and Vlora (VL), and the representativeness contribution of surveyed

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chamomile populations on the ex situ chamomile collection, was carried out.

The geographic areas, separated into grid cells of 1 x 1 km radius, and 10 x 10 km radius were used to assess the geographic distribution, richness and the representativeness of chamomile samples in the ex situ collection. The measurement of diversity and geographic distribution were realized: analysing the number of surveyed and collected chamomile populations per district, and the area of occupancy by each chamomile population (= indicator of abundance / rarity of a particular populations) was evaluated.

The relative contribution of surveyed chamomile populations on the genetic representativeness of chamomile samples stored ex situ in genebank was detected creating the circular zones with a 1 and 10 km radius around the ex situ data or ex situ presence points (**Ex situ-PP**), and circular zones with a 1 km radius created around the surveyed presence points (**Surveyed-PP**). When the surveyed presence points intersect the ex situ presence points with a 1 km radius there were non-representativeness contribution (**NRC**) on the ex situ collection of chamomile populations; when surveyed presence points only intersect the ex situ presence points with a 10 km radius, there were mid representativeness contribution (**MRC**) of chamomile populations on ex situ collection; and when the surveyed presence points do not intersect any of the ex situ presence points (those with a 1 km or 10 km radius), there were high representativeness contribution (**HRC**) of chamomile populations on ex situ collection [7].

Diversity indices:Quantitative variables aschamomile population richness (S), Ex situ present points (Ex situ – PP), Surveyed present points (Surveyed – PP), and representativeness indices as: situation of non-representativeness contribution (NRC) on the ex situ collection of chamomile populations; mid representativeness contribution (MRC) of chamomile populations on the ex situ collection; and high representativeness contribution (HRC) of chamomile populations on the ex situ collection were the diversity indices and richness estimators used. A value from 0 to 1 was given to each variable showing respectively 0 no variability and 1 high variability. Diversity indices and richness estimators were calculated and mapped using GIS tools [4]. A cluster analysis method on correlation was used to identify similarity between geo-referenced data using presence/absence of chamomile population. All quantitative variables were calculated using the SAS JPM tools [15].

3. Results and discussion

Collecting and quality of data: Data sampling was realized using information on the total occurrence of chamomile populations gathered from ex situ data or ex situ presence points of chamomile collection stored in Albanian genebank. External data or surveyed presence points, of chamomile populations were collated from EURISCO database[5], published papers [6, 7, 8], and herbarium data [11].

All information collected for 20 surveyed and collected chamomile (*Matricariachamomilla* L.) populations in nine County areas of Albania, and data for other 19 ex situ present point of chamomile populations stored in genebank were checked for data quality [2]including the accuracy and precision of geographic coordinates and for their inconsistencies. Data points without coordinates were removed from chamomile data. Data points with incorrect coordinates on the administrative unit (county and districts) were assigned coordinates where possible while duplicate or doubtful data were removed [16]. The chamomile samples not present physically as genetic material stored in genebank were also removed.

Results about the geographic distribution of 20 chamomile populations surveyed and collected in nine districts of Albania are given on the map as present points distributed in all Albanian territory (Figure 1).

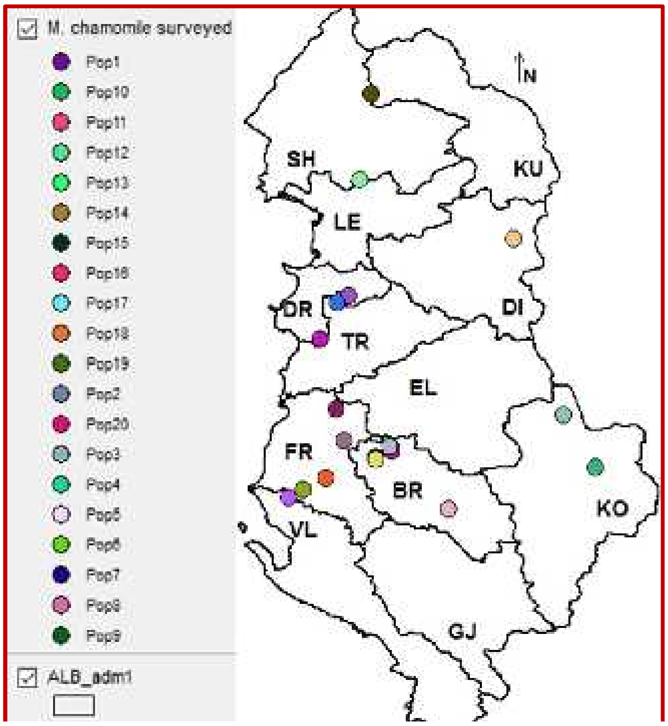

Figure 1. Geographic distribution of 20 chamomile populations collected in nine districts of Albania.

Spatial analysis shows the areas with higher richness (S) of chamomile populations were BR, FR and TRcounty areas. High representativeness of chamomile samples collected and stored ex situ in genebank (Ex situ-PP) were found in the areas of TR, DR, LE, DI and VL Counties. Highsurveyed chamomile populations were also identified in SH, BR, FR and KO county areas (Table 1).

Tale 1. Quantitative variables used to assess the diversity and the representativeness of surveyedchamomile populations on the ex situ data of chamomile collection.

Variables	BR	DI	DR	FR	KO	LE	SH	TR	VL
Richness (S)	7	2	4	7	3	2	1	11	2
Ex situ-PP	0.14	0.50	0.75	0.29	0.33	0.50	0.14	0.82	0.50
Surveyed-PP	0.86	0.50	0.25	0.71	0.67	0.50	0.86	0.18	0.50
NRC	0.14	0.00	0.25	0.00	0.00	0.00	0.00	0.18	0.50
MRC	0.29	0.00	0.00	0.29	0.00	0.00	0.12	0.00	0.00
HRC	0.71	0.50	0.00	0.71	0.67	0.50	0.74	0.00	0.00
Variance (б^2)	7.29	0.54	2.42	7.34	1.27	0.54	0.30	19.40	0.54
St. Dev.	2.70	0.74	1.56	2.71	1.13	0.74	0.55	4.40	0.74

Comparative analysis of the representativeness indices found that chamomile populations surveyed and collected in different county areas (not collected before by any collecting missions) have contributed directly in increasing their representativeness in the ex situ collection of chamomile samples stored in genebank. Highest contribution in increasing the representativeness of chamomile samples in ex situ collection chamomile germplasm was found in SH, BR, FR, KO, DI, and LE county areas. In these areas the surveyed presence points (zones) do not intersect the ex situ presence points (zones) with a 10 km radius, showing "high possible contribution for increasing the representativeness" in ex situ collection of chamomile samples. This means the new camomile populations were surveyed and collected in areas located far than 10 km radius from ex situ chamomile samples (Ex situ-PP) stored in genebank, increasing the representativeness status of chamomile samples stored in genebank. HRC index range respectively from 0.74 (Shkodra areas) to 0.50 (Lezha and Dibra areas) (Table 1, Figure 2).

Mid representativeness contribution of chamomile populations was found in BR, FR and SH conty areas (MRC index range respectively from 0.29 to 0.12). In these areas chamomile populations were surveyed and collected far than 1km from ex situ chamomile samples (Ex situ-PP) stored ex situ ingenebank but not far from the areas of 10 km radius from ex situ chamomile samples (present points) stored in genebank. For the chamomile populations surveyed in TR, DR and VL county areas **non** representativeness contribution of chamomile populations related to chamomile samples stored ex situ in genebank was found. In these areas a full representativeness status of surveyed camomile populations with chamomile samples stored in genebank was found.

This means that chamomile populations were surveyed and collected not far from the areas of 1 km radius from ex situ presence point of chamomile samples stored in genebank (Table 1, Figure 2).

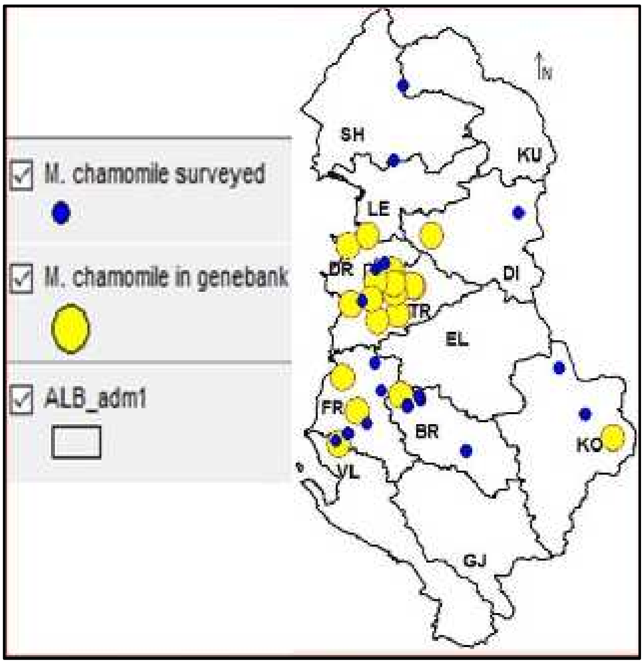

Figure 2. Distribution of chamomile populations collected in comparison with ex situ of chamomile stored in genebank.

In total there were more than 70% of surveyed presence pointsof chamomile populations that were collected collected in new areas, never collected before by any collecting mission, and that contributes really on the representativeness of chamomile samples stored in genebank.

Cluster analysis method on correlation using similarity and correlation matrix data found the presence of similarity among areas where chamomile populations were surveyed and collected (Figure 3). Cluster analysis found highly correlated similarity (coefficient of correlation range from 0.91 to 0.98) among DI and LE county areas (similarity matrix range from 97.5% to 98.9%), and among BR and FR county areas (similarity matrix 97.5% and coefficient of correlation 0.98).

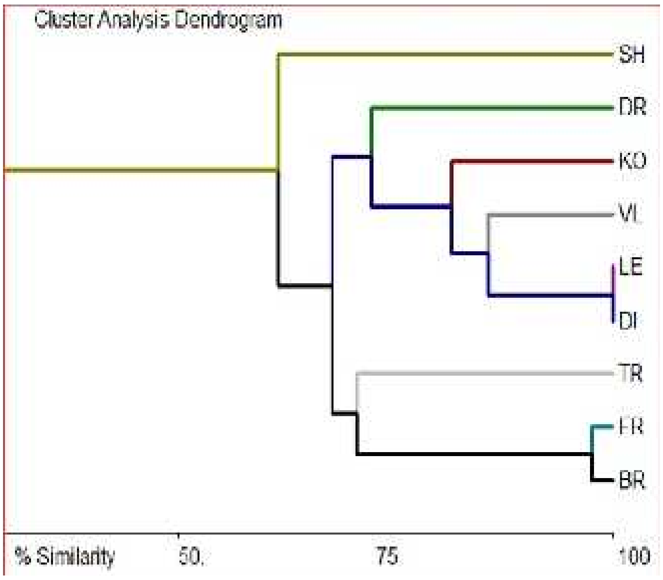

Figure 3. Cluster dendrogram and similarity matrix among chamomile county areas surveyed in Albania.

High similarity was also found among DI and VL and KO county areas where chamomilepopulations were surveyed and collected (similarity matrix range from 81.5% to 85.7% and coefficient of correlation range from 0.91 to 0.97). High grade of similarity between these county areas demonstrate that no any new chamomile populations could be expected to be found in that areas (Table 2).

High distances were found among BR areas and SH, DI, KO, and TR county areas (distance matrix range from 18.48225212 to 38.46154022).Presence of high distances among these areas demonstrate that possible new chamomile populations should be found in that areas.Correlation analysis found strong correlation between BR and DI, DR, FR, KO, LE, TR and VL county areas (coefficient of correlation range from 0.93 to 0.98) (Table 2).

In this study there were SH, BR, LE, KO and FR county areas that contribute more than other areas in increasing the representativeness of chamomile on the ex situ status of chamomile saples stored in genebank.

Table 2. Similarity matrix and correlation among county areas of chamomile populations in Albania

		Similarity Matrix								
		BR	DI	DR	FR	KO	LE	SH	TR	VL
Correlation matrix	BR	*	49.68	62.96	97.57	64.88	49.68	42.34	69.98	43.99
	DI	0.96	*	62.86	52.64	81.52	98.90	61.54	34.18	85.71
	DR	0.97	0.95	*	63.72	72.18	62.86	30.30	58.63	68.57
	FR	0.98	0.96	0.97	*	67.74	52.64	40.33	70.54	44.64
	KO	0.97	0.97	0.95	0.98	*	81.52	61.02	41.66	69.28
	LE	0.96	0.98	0.95	0.96	0.97	*	61.54	34.18	85.71
	SH	0.54	0.62	0.38	0.53	0.65	0.62	*	15.55	46.15
	TR	0.98	0.95	0.97	0.98	0.96	0.95	0.42	*	36.48
	VL	0.93	0.91	0.97	0.93	0.91	0.91	0.37	0.96	*

4. Conclusion

Spatial analysis found significant differences of chamomile diversity between observed areas, in nine districts of Albania.

Comparative analysis related to the representativeness status of chamomile samples in genebank, showed that chamomile populations collected in new areas of Shkodra, Korca, Berat, Fieri and Lezha counties (not collected before) have contributed directly in increasing the representativeness of chamomile in the ex situ status of chamomile collection in genebank.

Highest contribution in increasing the representativeness of chamomile samples in ex situ collection was found in Berat, Fieri and Korca district areas, and mid representativeness contribution was found in Dibra, Lezha and Shkodra districts areas.

Cluster analysis identified diversity and similarity between county areas where chamomile populations were sutveyed /collected, and ranged these areas into three different cluster groups.

Results of the study showed that possible new chamomile population should be found in the areas not collected and situated highly distant geographically (Shkodra, Berat, Korca areas).

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