RESEARCH ARTICLE



Variability of chamomile (*Matricaria chamomilla* L.) populations as a valuable medicinal plant in Albania evaluated by morphological traits

NDRIÇIM ZHURI^{1*}, BELUL GIXHARI², ALBAN IBRALIU¹

Corresponding author e-mail: cimizhuri@yahoo.com

Abstract

Study for the evaluation of variability of 30 chamomile (Matricaria chamomilla L.) samples, representing 10 chamomile populations collected in nine different natural growing areas of Albania (Berat, Fier, Skrapar, Tirana, Lezha, Lushnja, Korca, Kucova and Kruja), using morphological traits was carried out in the Experimental field of Agricultural University of Tirana, during two growing seasons. The 10 chamomile populations, grown in a randomized block with three replications, were assessed by seven quantitative morphological characters (plant height, number of principal branches, length of internodes, leaf length, number of cones produced per plant, fresh cones yield and dry cones yield). ANOVA, PCA on correlation and cluster analysis reveal presence of significant diversity, and the association among different morphological characters. Comparisons of means for each pair using Student test (t = 2.08596 and = 0.05) show the significant differences between chamomile genotypes at the $P_{0.05}$ and $P_{0.01}$ levels of the probability. Relationships between the morphological characters and chamomile genotypes using Principal Component analysis found the morphological traits: plant height, number of cones produced per plant, leaf length and internode length as the most important for the PC1 that account for 36.46% of the total variance, and internode length, fresh and dry yield of cones for the PC2 that account for 31.24% of the total variance. Cluster analysis (Ward's method) divides the whole chamomile populations into three cluster groups. Correlation relationships among morphological quantitative traits range from 0.27 (internode length and dry yield of cones) to 0.76 (number of cones produced per plant and leaf length). The study identifies number of cones produced per plant, leaf length and internode length as characters with agronomic interest which account for evaluation of genetic diversity and breeding programs of chamomile populations.

Keywords: Chamomile(*Matricaria chamomilla*), morphological characters, cluster analysis.

1. Introduction

Chamomile (*Matricaria chamomilla* L.) is one of the important medicinal herb native to southern and eastern Europe. Chamomile is a widely recognized herb in Western culture. Its medicinal usage dates back to an[2]. Chamomile has been used in herbal remedies for thousands of years, known in ancient Egypt, Greece, and Rome[8].

Chamomile (*Matricaria chamomilla* L.) is a well-known medicinal plant species from the Asteraceae family often referred to as the "star among medicinal species." Nowadays it is a highly favored and much used medicinal plant in traditional medicine. It's multitherapeutic, cosmetic, and nutritional values have been established through years of traditional and scientific use and research.

Chamomile is a rich source of natural products, and its chemical constituents of essential oils and plant parts have valuable pharmacological properties. Today chamomile is a common ingredient in herbal teas because of its calming, carminative, and spasmolytic properties. It is also a popular ingredient in topical health and beauty products for its soothing and anti-inflammatory effects on skin. Chamomile is used mainly as an anti-inflammatory and antiseptic, also antispasmodic and mildly sudorific [13]. The chamomile drug is included in the pharmacopoeia of 26 countries[14] because of several pharmacological actions as antibacterial, antifungal, anti-inflammatory, antispasmodic, anti-ulcer, antiviral, and sedative effects. The flowers of *M. chamomilla* contain the blue

¹Agronomic Science Department, Agricultural University of Tirana, Tirana, Albania

²Institute of Plant Genetic Resources, Agricultural University of Tirana, Tirana, Albania

essential oil from 0.2 to 1.9%, [4];[12] which finds a variety of uses.

There are two species of chamomile, generally, used in traditional herbalism, Matricaria chamomilla or Chamomilla recutita(German chamomile chamomile), or Hungarian and Chamaemelumnobile(Roman chamomile). In most formularies and reference books, Matricaria chamomilla L. is regarded as the correct species name. However, according to the International Rules of Botanical Nomenclature, Chamomilla recutita(L.) Rauschert is the legitimate name for this species [17]. Both annual herbs belong the Asteraceae/Compositae family and are similar in physical appearance, chemical properties, and general applications. German chamomile, however, is the more familiar and more commonly used of the two. The two species of Chamomile (Roman and German) have been used for medicinal purposes for more than a thousand years [11]. Both species are among the most widely used medicinal plants in the world.

Chamomile plant is considered indigenous to northern Europe and grows wild in central Europeancountries; it is especially abundant in Eastern Europe including Albania. Chamomile is also found in westernAsia, the Mediterranean region of northern Africa, and the United States of America. It is cultivated in many countries [1]; [21]; [20].

Albania with its geographical position in the Mediterranean region and in the Balkan Peninsula is very rich in medicinal and aromatic plants. Medicinal aromatic plant collections of compounded by more than 300 species (in the ex situ, in situ and on farm status of conservation), and 10% of represent about the Albanian flora[3].Medicinal and aromatic plants are economically important plants grown over a wide range of ecological habitats in the country [15];[18];[7]. Chamomile plants Matricaria chamomilla (L.) are collected and used as raw materials in the pharmaceutical, cosmetic and food industry [15].

Domestic and foreign markets for medicinal plants are growing rapidly and provide important opportunities for the development and diversification of Albanian agriculture. Currently, sage (Salvia officinalis) dominates the medicinal crops of Albania. Smaller surfaces are also cultivated with other medicinal species including chamomile (Matricaria chamomilla). Despite its economic importance, however, chamomile is little known about the extent and nature of the variability of this species. Therefore, the information about extent of uses of various gene pools are extremely valuable for the rational planning of the use of germplasm in breeding programs [22];[7];[6].

The aim of the study was the analysis of variability between chamomile (*Matricaria chamomilla*) populations growing naturally in different areas of Albania, and identification of the most important morphological characters, to be used in breeding programs of chamomile germplasm.

2. Materials and methods

Plant material: The analysis was performed on ten 10 chamomile (Matricaria chamomilla L.) populations, originated from nine collecting areas of Albania (Berat, Fier, Skrapar, Tirana, Lezha, Lushnja, Korca, Kucova and Kruja).

Morphological characters: Plant height (PH) (cm), Number of branches per plant (No.br), length of internodes (L.Int), leaf length (LL), number of cones per plant (No.C), fresh yield of 1000 cones (YF) and dry yield of 1000 cones (YD).

The experimental site and field observations: The study for the assessment of chamomile variability was carried out at the experimental field of Agriculture University of Tirana (latitude: 402405N; longitude: 0194108E; elevation: 40m). Chamomile populations were grown in a randomized block design with three replication and field observations and measurements of morphological traits were realized on 20 plants of each plot.

Statistical Analysis: The differences between chamomile populations for the mean values of

quantitative traits evaluated were carried out using ANOVA analysis. Identification of chamomile populations of relatively similar or different characteristics and identification of the most important morphological characters that influence highly on the total variation, was realized using Principal Components Analysis (PCA) on correlation and cluster analysis methods. All statistics data were calculated employing the [19], and a dendrogram (ward method) and a relationship diagram (chamomile populations x morphological characters) were carried out.

3. Results and Discussions

Analysis of morphological quantitative traits: ANOVA analysis found the presence of differences between chamomile populations for the most number of morphological traits significant at the probability $P_{0.05}$ and $P_{0.01}$. Except leaf length (LL), all other traits were significant at the probability $P_{0.05}$ (Table 1). High degree of variation was observed for No.C, No.br, and YF traits.

Tab.1. Analysis of variance for all chamomile traits analysed

Source of	Sum of Squares	Sum of Squares			Mean		
Variance.	(population)	(Error)	C. Total	Mean Square	Square	F'	
Traits	(df=9)	(df= 20)	(df = 29)	(population)	(Error)	Ratio	Prob>F
PH	103.57575	41.95357	145.52932	11.5084	2.0977	5.4863	0.0008*
No.br	1.0084300	0.059000	1.0674300	0.112048	0.00295	37.9823	<.0001**
L.Int	0.9542133	0.0519333	1.0061467	0.106024	0.002597	40.8307	<.0001**
LL	0.8187867	0.9584000	1.7771867	0.090976	0.047920	1.8985	0.1115
No.C	848.5787	538.5933	1387.1720	94.2865	26.9297	3.5012	0.0094*
YF	3631.4083	359.1667	3990.5750	403.490	17.958	22.4681	<.0001**
YD	124.35867	18.80000	143.15867	13.8176	0.9400	14.6996	<.0001**
F ratio values significant at the $P_{0.05}$ level of the probability (*) and $P_{0.01}$ level of the probability (**).							

Principal Components Analysis: Principal Components Analysis on Correlations identified the variances of the principal components and the proportion of the total variance each factor accounts for (Table 2). Based on the mineigen criterion [10] three principal components that account for 84.5% of the total variation are retained for further analysis. PCA results show that the major sources of variation in the measurements are given by the first two PCs (67.7%).

All quantitative variables contribute to 100% of total variation. The percentages of total variation accounted for by each of the first three PCs are 36.5%; 31.2% and 16.8% respectively (Table 2). The first three PCs explain 84.5% of the original variation, and the variation > 80.0% is acceptable for evaluation of plant populations in general and for characterization of plant collections in a genebank [5]; [9].

Tab. 2. Eigenvalues of principal components (chamomile populations x morphological traits)

Principal Components/factor analysis							
PC	C No.	Eigenvalue	Percent variance	Cumulative Percent	2	df	Prob. > 2
	1	2.5521	36.459	36.459	129.455	19.859	<.0001*
	2	2.1868	31.241	67.699	103.760	17.182	<.0001*
	3	1.1789	16.841	84.540	65.681	14.112	<.0001*
	4	0.5532	7.902	92.443	36.730	9.643	<.0001*

² – Chi Square, df–degree of freedom; Prob.–probability; *significance equal to 0.05 / 0.01 of probability

The maximum information from morphological data was received using ordination methods in combination with cluster analyses [9]. Dimensional scaling of relationships (chamomile populations x morphological traits) that contributes for the larger proportion of the total variance in PC1, PC2 and PC3 revealed by PCA indicate that the contribution of each chamomile populations and of each quantitative morphological traits on the total of variation was found not equal.

PCA and cluster analysis found 10chamomile samples included in PC1 representing the

characteristics of three chamomile populations (Karbunare, Verbas and Dukas), 8 chamomile samples included in PC2 representing especially characteristics of two chamomile populations (Poshnje and Provnik), and twelve chamomile samples in PC3 representing the characteristics of three chamomile populations (Mat, F. Preze and Kozare). Two chamomile populations as Larushk and Sheqeras have presented mix of characteristics like chamomile populations of PC3 and PC1 (Table 3, Figure 1; Figure 2).

Tab. 3. Matrix of vectors of three PC for 10 chamomile populations x 7 morphological traits

No	Morphological quantitative traits	PC1	PC2	PC3	
1	Plant height	PH	0.51859	0.10957	-0.27035
2	Number of branches per plant	No.br	-0.12810	0.14227	0.83706
3	Length of internodes	L.Int	0.31650	0.33258	0.37598
4	Leaf length	LL	0.54347	0.00746	0.17438
5	Number of cones per plant	No.C	0.55962	-0.14228	0.02963
6	Fresh yield of 1000 cones	YF	-0.06664	0.64893	-0.15723
7	Dry yield of 1000 cones	YD	-0.03883	0.64477	-0.16992

In bold all eigenvectors > 0.30

For PC1 (with 36.5% contribute on the total variation) characters as PH, L.Int, LL and No.Cwere the most important source for the variation of PC1.The characters as No.br, YF and YD showed not important negative influence on the PC1 variance (Table 3, Figure 1).

Variation in PC2 (= 31.2% of total variation) was mainly result of differences in L.Int, YF and YD morphological traits. Traits as YF and YD account for nearly the same amount of variance on PC2 (Table 3, Figure 1).

For PC3 (with only 16.8% contribute on the total variation) characters as No.br and L.Intwere the most important source for the variation on the PC3 variance. The characters as PH, YF and YD showed negative influence on the PC3 variance (Table 3, Figure 1).

Cluster analysis: Relationships between 30 chamomile samples that represent 10 chamomile populations assessed by quantitative morphological

traits and genetic similarity/distances coefficients revealed by cluster analyses categorized all chamomile samples (populations) into three clusters (Figure 2).

There were five morphological quantitative traits of PC1 and PC2 that have influenced on the differentiation of three clusters. The first cluster (with ten samples of three chamomile populations) was differentiated by PH, L.Int, LL and No.C traits of PC1.Correlation analysis found moderate and strong positive correlation between these characters (r range from 0.36 to 0.76). Negative correlation was found between PH and No.br (r = -0.33). The second cluster includes eight samples of three chamomile populations and was differentiated by L.Int, YF and YD traits of PC2.Moderate positive correlation between these traits was found (r range from 0.27 to 0.33). The third cluster includes twelve samples of three chamomile populations and was differentiated by No.br and L.Int traits of PC3 (Figure 2).

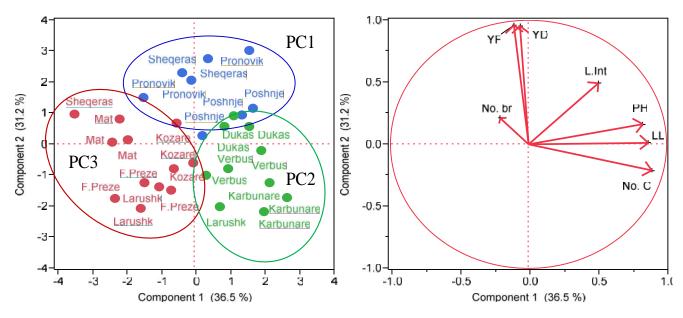


Fig. 1.Relationships among 10 chamomile populations on morphological traits revealed by PCA

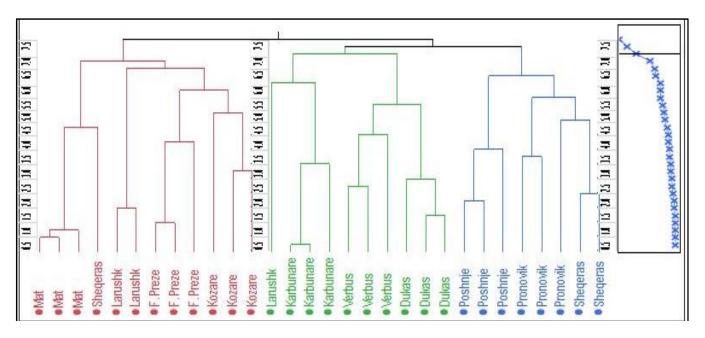


Fig. 2. Dendrogram of relationships among chamomile populations and morphological quantitative traits

PCA and cluster analysis found clear differences among following chamomile populations collected in Karbunare, Verbas, DukasPoshnje, Provnik, Mat, F. Preze and Kozare. Chamomile populations collected in Larushk and Sheqeras sites present a mix of characteristics. So, Larushk chamomile show similar morphological characteristics with chamomile collected in F. Preze and Karbunare. AndSheqeras chamomile show similarity with chamomile collected in Provonik and Mat (Figure 2).

Knowledge of genetic similarity or distances generates a better understanding of germplasm sampling. Separation of chamomile populations into three clusters could be useful with regard to chamomile cultivation and chamomile breeding purposes.

4. Conclusions

The field evaluation test permitted the first evaluation of chamomile populations collected in different areas of Albania and identified the most important morphological traits with high medicinal value.

PCA and cluster analysis identified the morphological traits with more significant weighting on PC1 variance (PH, L.Int, LL, No.C), which can be used successfully as morphological markers for evaluation of the chamomile germplasm.

The amount of genetic variability found in this study is sufficient for selection of desirable traits for creation of new gene combinations to sustain chamomile breeding programs.

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