



# COMPARATIVE STUDY OF THE ISOZYME VARIATION OF GENUS *CENTAUREA* IN SICILY AND SOUTH ITALY

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## Introduction



*Centaurea napifolia*

The genus *Centaurea* is represented in Italy by about 130 taxa (species and subspecies) (Conti & al 2005) and has a very complicated taxonomy. It comprises annual to perennial herbs, rarely dwarf shrubs with undivided to pinnatisect leaves and cylindrical to spheroidal capitula (Dostál 1976). In the Italian flora about 48% of the *Centaurea* taxa have very restricted areal and/or are endemics.

In the current work the data of the isozyme analysis of twenty *Centaurea* taxa from South Italy and Sicily were compared. They belong to *Centaurea parlatoris*, *C. cineraria*, *C. tenorei* and *C. jacea* groups. The first three groups are endemics; the last one shows a large distribution.



*Centaurea sphaerocephala*

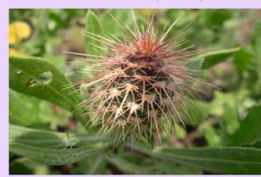
## Material and Methods

The nomenclature of the studied taxa and their localities in Sicily and Southern Italy are shown in Table 1 and Fig. 1. Seventeen are endemics for Sicily or Italy (belonging to *C. parlatoris*, *C. cineraria*, *C. tenorei* groups), whereas three of them have a large distribution (*C. jacea* gr.).

Table 1. List of the Italian *Centaurea* taxa investigated in the study

Taxa	Locality	Distribution
<i>Centaurea tenorei</i> Guss. ex Lacaita f. <i>tenorei</i>	S Italy, Campama, M. S. Angelo	Sarapente Peninsula (Endemic)
<i>C. tenorei</i> var. <i>maritima</i> Lacaita	S Italy, Penisola Sorrentina	Coasts of Amalfi (Endemic)
<i>C. tenorei</i> f. <i>montalensis</i> Lacaita	Southern Italy, M. Avvocata, Maiori village	Coasts of Amalfi (Endemic)
<i>C. saxatilis</i> (Anzalone) Pigo.	C Italy, Abruzzo, Anversa degli Abruzzi village	Abruzzo Region (Endemic)
<i>C. umbrosa</i> Guss.	Abruzzo, Cinquemiglia plane-Roccaraso	Apuane Alps and Appennino Tosco-Emiliano locality (Endemic)
<i>C. parlatoris</i> Heldr. var. <i>siroscrova</i> Guss.	Sicily, M. Occhio, Montelepre village	Sicily, Southern Italy (Endemic)
<i>C. parlatoris</i> Heldr. var. <i>parlatoris</i>	Sicily, Madonie Mts, Vallone Madonie degli Argilli	Sicily (Endemic)
	Sicily, Madonie Mts, Vialact Fagurata	
	Sicily, Madonie Mts, Inello village, in the cliffs	
	Sicily, San Martino delle Scale	
<i>C. sicana</i> Raimondo & Spadaro	Sicily, Monte Cammarata, above the refuge	Sicily (Endemic)
<i>C. giardiniae</i> Raimondo & Spadaro	Sicily, Enna, above Nicolosi village	Sicily (Endemic)
<i>C. cineraria</i> L. subsp. <i>cineraria</i>	Sicily, Enna, Monte Sona	S Italy (Endemic)
	S Italy, Campama, Vietri village	
	S Italy, Campama, Minori village	
<i>C. juncabazensis</i> Guss.	Sicily, Rocca Busambra di Freguzzo	Sicily (Endemic)
<i>C. acrisia</i> Lacaita subsp. <i>acrisia</i>	Sicily, Monte Passo del Lupo	Sicily (Endemic)
	Sicily, Monte Inesi	
	Sicily, Monte Cofano	
<i>C. acrisia</i> subsp. <i>ambrosia</i> (Lacaita) Cella-Ronconi & Viggli	Sicily, Monte Pellegrino	Sicily (Endemic)
<i>C. todari</i> Lacaita	Sicily, near to motorway Palermo-Catania, Bagheria	Sicily (Endemic)
	Sicily, Monte Catirosso, Mongeribato area	
<i>Centaurea erycina</i> Raimondo & Bancheva	Sicily, Castello di Venere - Erice village	Sicily (Endemic)
<i>C. saxatilis</i> Raimondo, Bancheva & Hradil	Sicily, near Scicca village	Sicily (Endemic)
<i>C. solstitialis</i> subsp. <i>schowii</i> (DC.) Dostál	Sicily, near Contessa Entellina, Palermo	Sicily, Calabria, Basilicata Regions (Endemic)
<i>C. sphaerocephala</i> L.	Sicily, Isole di Gela, Calanissetta	SW-Sicily-Mediterranean
<i>C. napifolia</i> L.	Sicily, San Fratello village	SW-Sicily-Mediterranean
<i>C. nicasenoi</i> AB.	Sicily, Piana degli Albanesi	SW-Sicily-Mediterranean

The following parameters of the genetic variability were considered: the total number of the alleles, the mean number of alleles per locus (A), the mean percentage of polymorphic loci (P95), the expected heterozygosity (He) that is a measure of the intra-population diversity (Nei 1973), the Wright's fixation index (F) (1951) and inbreeding coefficient (Fis) that are measures for the deviation from the Hardy-Weinberg equilibrium. Wright's F-statistics (1951) was also employed to analyse genetic structure. The gene flow (Nm) was calculated as  $Nm = (1 - Fst) / 4 Fst$ .



*Centaurea nicaensis*



*Centaurea erycina*

## Results

The total number of the alleles in the different groups ranges from 11 in *C. tenorei* gr. to 23 in *C. parlatoris* gr. The mean number of alleles per locus (A), is comparable in all the studied groups ranging from 1.46 (*C. tenorei* gr.) to 1.75 (*C. cineraria* gr.). The mean proportion of polymorphic loci varies from 41% (*C. cineraria* gr.) to 53.6% (*C. jacea* gr.). In *C. parlatoris* gr. 7 unique alleles and 5 rare ones are determined, while in *C. cineraria* gr. 6 rare alleles and 2 unique ones are registered. In *C. jacea* gr. there are two unique alleles, but no rare alleles are found. The mean values of H range between 0.16 (*C. tenorei* gr.) and 0.28 (*C. jacea* gr.). The high values of the genetic variability are usually associated with a large ecological plasticity. In the majority of *Centaurea* taxa the values of the inbreeding coefficient result negative. The inter-population variability coefficient (Fst) in Italian *Centaurea* taxa ranges from 0.24 (*C. cineraria* gr.) to 0.43 (*C. jacea* gr.) (Tables 2,3). The low values prove a relatively recent differentiation of the taxa. These data are very well supported also by the values of the genetic distances among the studied *Centaurea* groups.

The results of the distribution of the genetic diversity in these groups show that Sicily could be considered as a centre of differentiation of the endemic taxa related to *C. cineraria* and *C. parlatoris*.

Table 2. Comparison among the parameters of genetic diversity in the examined *Centaurea cineraria*, *C. jacea*, *C. parlatoris* and *C. tenorei* groups

	<i>C. cineraria</i>	<i>C. jacea</i>	<i>C. parlatoris</i>	<i>C. tenorei</i>
N° loci	8	7	7	6
N° totale alleli	19	17	20	11
P95	41	53.6	49	49.7
A	1.75	1.68	1.7	1.46
He	0.18	0.28	0.18	0.16
Fis	-0.51	-0.43	-0.51	0.42
Fst	0.24	0.43	0.27	0.34
Dman	0.002	0.244	0	0.079
Dmax	0.158	0.038	0.211	0.318
Dmean	0.077	0.437	0.097	0.197

Table 3. Number of alleles at each locus in the investigated *Centaurea cineraria*, *C. jacea*, and *C. parlatoris* groups

Sistema	Locus	<i>C. cineraria</i>	<i>C. jacea</i>	<i>C. parlatoris</i>
IDH	<i>Idh-1</i>	3	2	3
	<i>Idh-2</i>	-	2	-
	<i>Idh-3</i>	3	3	6
MDH	<i>MDH-1</i>	1	-	1
	<i>MDH-2</i>	2	-	-
6PGD	<i>6Pgd-1</i>	1	-	1
	<i>6Pgd-2</i>	2	-	3
PGI	<i>Pgi-1</i>	3	3	4
	<i>Pgi-2</i>	1	3	1
PGM	<i>Pgm-1</i>	1	3	1
	<i>Pgm-2</i>	3	3	3



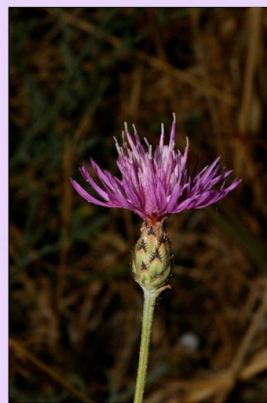
*Centaurea solstitialis* subsp. *schowii*

Fig. 1 – Distribution map of studied Italian *Centaurea* taxa



## References

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*Centaurea sicana*