ALLOZYMIC AND BIOMETRIC VARIATION IN *DRYOMYS NITEDULA* (PALLAS, 1778)

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ABSTRACT – Biometric and genetic variation were analysed among populations of *D. nitedula* from Italy, Balkan Peninsula, Asia Minor and Israel. The biometric analysis was carried out on 84 specimens using 13 linear skull measurements. Variations in metrical characters among samples were studied by standard and multivariate analyses. The genetic analysis was carried out on 29 specimens by electrophoresis of 40 gene loci. In both analyses the Israeli sample was the most distinct. Skulls of Israeli specimens are characterized by longer mandibular tooth row, higher rhamus mandibulae, longer bullae, and narrower braincase breadth, rostral breadth and interorbital constriction. Electrophoretically the Israeli sample can be discriminated from European populations by four loci *(Ldh-I, G6pdh, Pep-1,* and *Lap-2)* fixed for new alleles. The mean value of Nei's genetic distance between Israeli and European populations was $D = 0.186$, ranging from 0.153 to 0.227. The Israeli population, commonly attributed to the taxon *phrygius,* was different from this by bioinetric analysis. *D. n. phrygius* from the topotype locality in Asia Minor clustered with the European population from Turkish Thrace. In order to clarify the phylogenetic relationships of the Israeli forest dormouse, a comparison with other populations from the Caucasus and Iran and with *Dryomys laniger* from Turkey is suggested.

Key words: *Dryomys nitedula*, Allozyme variation, Biometric variation, Biochemical evolution.

RIASSUNTO – *Variabilita genetica e biometrica in* Dryomys nitedula *(Pallas, 1778)* – Variabilita biometrica e genetica sono state analizzate tra popolazioni di *D. nitetula* provenienti da Italia, Penisola Balcanica, Asia Minore ed Israele. L'analisi biometrica è stata condotta su 84 esemplari mediante 13 misurazioni craniche lineari. La variazione nei caratteri metrici tra i campioni e stata studiata mediante analisi standard e multivariata. L'analisi genetica e stata condotta su 29 esemplari mediante elettroforesi di 40 loci genici. In entrainbe le analisi il campione israeliano e risultato il piu distinto. Il cranio degli esemplari israeliani è caratterizzato da fila molare mandibolare più lunga, rhamus mandibolae piu alto, bullae piu lunghe e da una riduzione nella larghezza della costrizione interorbitale, della scatola cranica e del rostro. Elettroforeticamente il campione israeliano può essere distinto dalle popolazioni europee sulla base di quattro loci fissati per nuovi alleli (*Ldh-1, G6pdh, Pep-I* e *Lap-2).* Il valore medio della distanza genetica di Nei tra le popolazioni europee e quella israeliana e $D = 0.186$, con range compreso tra 0.153 e 0.227. La popolazione israeliana, generalmente attribuita al taxon *phrygius,* si differenzia da questo su base morfologica. *D. n. phrygius* della localita topotipica in Asia Minore risulta affine alla popolazione europea della Tracia turca. Per chiarire i rapporti

filogenetici del driomio israeliano si suggerisce il confronto con altre popolazioni del Caucaso e dell'Iran e con *Dryomys laniger* della Turchia.

Parole chiave: *Dryomys nitedula,* Variabilita genetica, Variabilita biometrica, Evoluzione biochimica.

INTRODUCTION

Among myoxids, *Dryomys* is the only genus characterized by a wide but fragmentary distribution, ranging from eastern Switzerland and Italy *to* Tien Shan Mountains in China. The more widespread species, *Dryomys nitedula,* has isolated populations in the southern part of its area (Honacki et al., 1982). The second species, *Dryonzys laniger,* is endemic to Turkey being known only from the western and central Taurus (Felten & Storch, 1968; Felten et al., 1973).

Due to its infrequent appearance, information about the forest dormouse is scarce and generally based on few specimens. The systematics of *Dryomys nitedula* is complicated by the description of numerous subspecies (in South-Eastern Europe and Central Asia) and phylogenetic relationships among them are still unclear.

According to Roesler & Witte (1968) the taxa *aspromontis* von Lehmann, 1964 (Southern Italy) and *intermedius* (Nehring, 1902) (the Alps, Hungary, Slovenia and Bosnia) represent a western group of subspecies characterized by grey pelage. The taxon *diamesus* von Lehmann, 1959 (Montenegro) can probably be included in this group of subspecies having intermediate characters. **A** second group of subspecies is represented by south-eastern taxa, characterized by brownish-yellow pelage: *wingei* (Nehring, 1902) (central and southern Greece), *ravijojla* Paspaleff, Martino & Pecheff, 1953 (Macedonia) and *phrygius* Thomas, 1907 (Asia Minor, Syria and Israel). More recently *D. n. ravjojla* was considered synonymous with *D. n. wingei* (Storch, 1978) and the East European subspecies *D. n. robustus* Miller, 1910, *D. n carphaticus* Brohmer, 1927 and *D. n. diamesus* von Lehmann 1959 were included in *D. n. nitedula.* According to Kryštufek (1985) in former Yugoslavia two subspecies can be identified: *D. n. intermedius* (the Alps, the Northern Dinaric Alps) and *D. n. ravijojla* (Macedonia). Forest dormice from Herzegovina, Montenegro and Kosovo display signs of transition between these two subspecies.

Even more complicated is the systematics of Central Asiatic populations, grouped by Ognev (1947) in nine subspecies: *D. n. dagestanicus* Ognev & Turov, 1935 (North-eastern Ciscaucasus); *D. n. caucasicus* Ognev & Turov, 1935 (Central-western Ciscaucasus); *D. n. tichonzirovi* Satunin, 1920 (Transcaucasus, Armenia, and Kurdistan); *D. n. ognevi* Heptner & Formosov, 1928 (South Dagestan); *D. n. bilkjewiczi* Ognev & Heptner, 1928 (Kopet Dag); *D. n. angelus* Thomas, 1906 (Uzbekistan, Kirgiz); *D. n. pallidus* Ognev & Turov, 1935 (Turkestan): *D. n. saxatilis* Rosanov, 1935 (Pamir); *D. n. pictus* Blanford, 1875 (Iran). According to Ognev (1947) *D. n. tichonzirovi* is differentiated from other Caucasian dormice (chiefly *D. n. caucasicus* and *D. n. ognevi*) and it is probably related to the Iranian dormouse *D .n. pictus.* Specimens from Cilo Daglari (South eastern Turkey), attributed to the taxon *D. n. pictus,* displayed significantly different features with respect to *D. nitedula* and it was supposed that they could

represent a separate species (Mursaloglu, 1973). According to Kumerloeve (1975) a revision of Turkish populations of *Dryomys* is needed.

In the present study allozymic and biometric variations are analysed among populations of *Dryomys nitedula* from Italy, Balkan Peninsula, Asia Minor and Israel.

MATERIAL AND METHODS

Analysis of morphoinetric variation among populations of *Dryomys nitedula* was carried out on 84 specimens assigned to **6** geographic samples (Fig. 1). Sample areas were kept as small as possible and selected so as to represent an integral geographic area. Sample 1: south-eastern Alps and north-western Dinaric Alps in Slovenia and Croatia (n=11). Sample 2: southern Dinaric Alps in Herzegovina, Montenegro and Kosovo (n=11). Sample 3: Macedonia (n=11). Sample 4: European Turkey (n=22). Sample 5: Murat Dagi, Asia Minor (topotypes of *D. n. phrygius*; n=12). Sample 6: Israel (n=17). For exact localities of samples 1 to *3* see KryStufek (1985).

Twenty-nine specimens were analysed for electrophoretic variations. Their collecting sites, the number of specimens examined for each population, and sample designations were as follows: Piani di Ruggio, Mt.Pollino, Basilicata (Italy): n=4, POL; Tarvisio, Friuli (Italy): n=9, **TAR;** Altipiano di Asiago, Venetia (Italy): n=4, ASI; Idrija, Slovenia: n=1, IDR; Boracko Jezero, Bosnia-Herzegovina: n=1, BOR; Mt. Pelister, Macedonia; n=1, PEL; Edirne, Turkey; n=8, EDI; Hurfesh, Upper Galilee (Israel): n=1, HUR.

Specimens are preserved in the Natural History Museum of Slovenia, in the Department of Biology of Trakya University, and in the Zoological Museum of Tel Aviv University.

Biometric analysis - Thirteen linear measurements were taken on each of the adult skulls and recorded to the nearest 0.1 mm.: condylobasal length (CbL), maxillary tooth row length (MxT), braincase breadth (ZgB), breadth over molars (MoB), breadth of rostrum (RoB), interorbital constriction (IoC), braincase height per bullae (BhB), bullae length (BuL), rostrum height (RoH), mandible length (MdL), height of rhamus mandibulae (RmH), mandibular tooth row length (MdT). See KryStufek (1985) for definitions. Since sexual dimorphism is insignificant in *Dryomys nitedula* (KryStufek, 1985) the sexes were not separated. Only skull measurements of adult animals, i.e. of specimens that had overwintered at least once, were studied. Skulls with missing measurements were also excluded.

Variations in metrical characters among samples were analysed using standard and multivariate analyses. The differences among six samples in single characters were investigated by one-way analysis of variance. Interpopulation comparisons involving the entire character set was done by discriminant function analysis and by clustering (UPGMA on the Average taxonomic distance matrix of z-standardized data; Rohlf, 1989). Analyses were done using raw and transformed data. Measurements were first converted to a logarithmic scale to produce a linear relationship between the two variates. Condylobasal length was taken as a vector that is related to size. The effect of that vector was removed from the data set by

regressing CbL against all other variables. The residuals from this analysis indicated the relative size of each variable (Lemen, 1983).

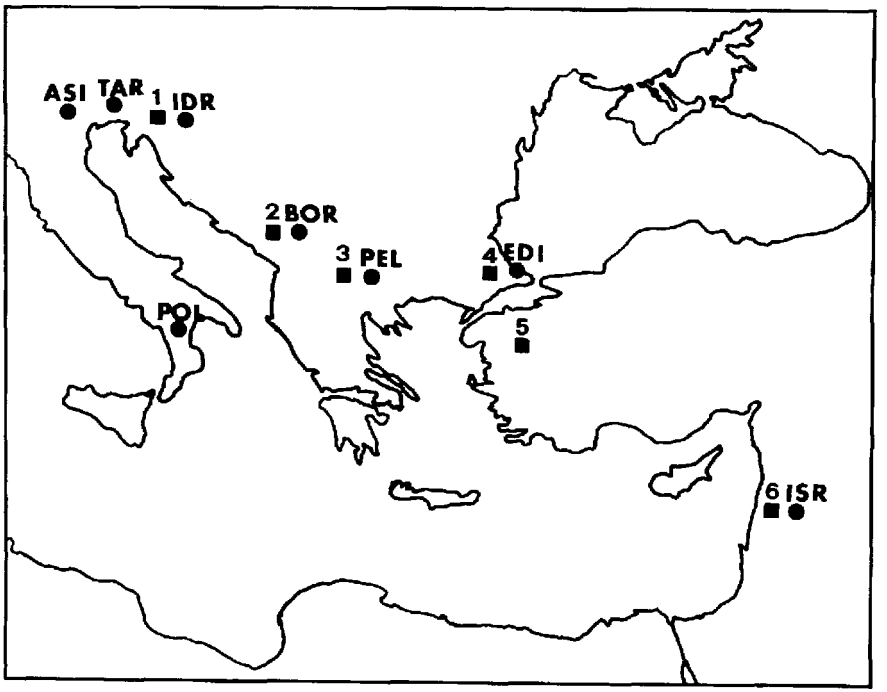

Fig. 1 – Geographic distribution of the samples of *Dryomys nitedula* used in this study. ● = clcctrophoretic analysis; ■ = biometric analysis.

Electrophoretic analysis - Genic variation of structural genes encoding for enzymatic and non-enzymatic proteins was assessed using standard horizontal starch-gel electrophoresis. Tissues of each specimen were preserved in the laboratory at -80° C until required for processing. Homogenates for electrophoresis were obtained from portions of muscle or kidney tissue crushed in distilled water. **All** gels were prepared using an 11% suspension of Connaught hydrolyzed starch.

Forty loci were analysed, encoding for two non enzymatic proteins and for 28 enzymes. Details on the scored loci are given by Filippucci & Kotsakis (1995). The electrophoretic techniques used were those described for *Eliomys* by Filippucci et al. (1988).

Isozymes were numbered in order of decreasing mobility from the most anodal; allozymes were numbered according to their mobility relative to the commonest allele (=100) in the reference population of *Dryomys* from Friuli (TAR). Allozymic data were analysed as genotype frequencies with the BIOSYS-1 program of Swofford and Selander (1981). Intrapopulational genetic variation was estimated by means of: the mean heterozygosity per locus (expected: *He,* and observed: *Ho*), the proportion of polymorphic loci in the population (*P1%* and *P5%*), the average number of alleles per locus ***(A).*** The amount of genetic

divergence between populations was estimated from the indices of standard genetic identity *(I)* and distance *(D)* proposed by Nei (1978). The high number of loci analysed compensates for the small sample size of some populations. Values of heterozygosity and genetic distances are therefore reliable with a reasonable margin of precision (Sarich, 1977; Nei, 1978; Gorman & Renzi, 1979; Sage et al., 1986). A dendrogram of the genetic relationships among populations was obtained using the unweighted pair group cluster analysis UPGMA (Sokal & Sneath, 1963).

RESULTS

Biometric analysis

Ten characters differed significantly ($p<0.005$) among the six geographic samples (Table 1). Condylobasal length of skull, which could be regarded as a single measure best representing size, was not affected by interpopulation variation. Highest values for the F-test were for IoC, MdL, RmH, and MdT. It is evident that variation between samples was best expressed by mandible measurements.

Of the 84 specimens subjected to the discriminant function analysis based on raw data, 67 (i.e. 80 %) were classified correctly and 17 (i.e. 20 %) were missclassified. The Israeli animals were most distinct (Fig. 2), and were all classified into the correct group. They were segregated from the remaining samples by the first canonical variate, which explained 69.6 % of the variance in the original data set. The second variate was responsible for 23.4 % of variance. Characteristic for Israeli specimens were longer mandibular tooth row, higher rhamus mandibulae, longer bullae, and narrower braincase breadth, rostral breadth and interorbital constriction. Dormice from European Turkey and Asia Minor overlapped considerably, suggesting they are phenetically close. Group centroids of the remaining three samples (1 to 3) shared, in the projection on the first two discriminant functions, the pattern of their geographic origin. A clinal nature of the phenon is suggested in *Dryomys* populations along the eastern Adriatic coast. Essentialy identical were results by discrimination on residuals (Fig. 3). Sixty-six specimens (i.e. 79 %) were allocated to the actual group. The first two canonical variates explained 73.0 % and 21.4 % of the variance in the original data set, respectively.

Clustering of the residuals suggested three groups (Fig. 4) and was well in accordance with the geographic origin of the samples as well as with the results of the above discriminant function analyses. The Israeli sample was the most distinct.

Electrophoretic analysis

Genetic pattern - Twenty out of the 40 loci analysed were monomorphic and fixed for the same allele in the populations considered. The allelic frequencies at the polymorphic loci are given in Table 2. The populations from North-Eastern Italy were polymorphic for the following loci: *Ldh-1, Me-2, Idh-2, Got-1, Adk, Est-1, Est-3,* and *Ap-1*. The population of *D. n. aspromontis* from Mt. Pollino was polymorphic for *Me-2, Go/-1, Adk,* and *Lap-2*. The Balkan specimens were polymorphic at the following loci: *αGpdh, Mdh-1, Me-2, G6pdh, Ap-1, Lap-2, Est-1,* and *Est-3*. The Turkish population from Edirne displayed polymorphism at

8 loci: ***Adh,*** *Mdh-1,* ***Np,*** *Aph,* ***Ada, Aldo.*** *Est-I,* and ***Est-3.*** The Israeli specimen showed polymorphism for the following loci: ***Adh,*** *Me-2, Idh-2,* ***6Pgdh,*** and *Hk.*

Genetic variation - Levels of genetic variation within populations are given in Table 2. The observed values of genetic variation were within the range generally reported for other rodents (Selander, 1976; Nevo et al., 1984, 1990). The mean value of observed heterozygosity was $Ho = 0.062$, ranging from 0.019 (POL) to 0.125 (ISR). The values of genetic variation for the Israeli population are only tentative due to the small sample size.

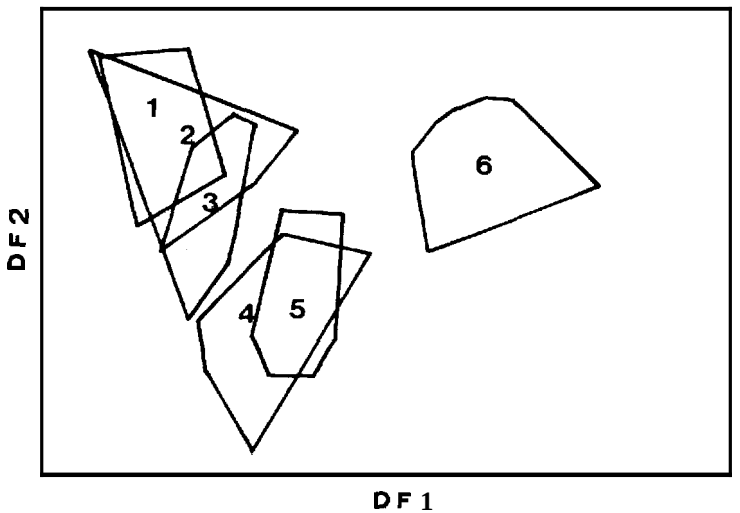

Fig. 2 – Results of discriminant function analysis of raw data. Polygons enclose scores for all individuals within a sample group, and numbers are placed on group centroids. For identifying numbers see Material and Methods.

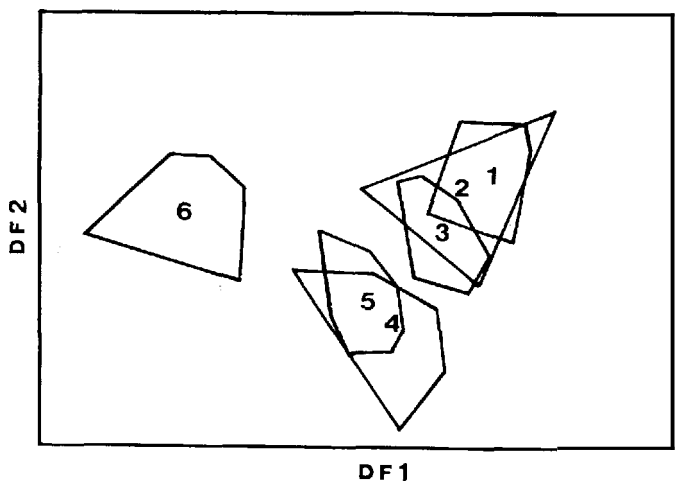

Fig. 3 – Results of discriminant function analysis of residuals. Explanations for Fig. 2.

Tab. 1 – Means and standard deviations of metrical characteristics (in mm) for each of the six geographic samples of *Dryomys nitedula* referenced in Fig. 1. See text for abbreviations. n. s. = not significant.

Sample	N	Cbl	MxT	BoB	ZgB	MoB	RoB	ToC	BhB	BuL	RoH	MdL	RmH	MdT
1	11	24.71 ±0.746	3.87 ±0.135	13.44 ±0.338	15.01 ±0.412	6.22 ±0.178	5.07 ±0.245	4.24 ±0.143	11.05 ±0.420	7.47 ±0.531	4.96 ±0.159	13.92 ±0.490	6.66 ±0.347	3.99 ±0.047
2	11	24.32 ±0.590	3.87 ±0.205	13.21 ±0.416	15.14 ±0.594	6.21 ±0.234	5.07 ±0.276	4.12 ±0.108	11.15 ±0.836	7.18 ±0.218	4.81 ±0.187	13.68 ±0.540	6.75 ±0.375	4.03 ±0.127
3	11	24.15 ±0.550	3.88 ±0.261	13.21 ±0.270	15.21 ±0.268	6.18 ±0.194	4.96 ±0.169	4.09 ±0.152	11.45 ±0.298	7.27 ±0.356	4.68 ±0.182	13.85 ±0.325	6.84 ±0.292	3.97 50.233
4	22	24.46 ±0.654	4.05 ±0.182	13.48 ±0.390	15.61 ±0.416	6.15 20.215	5.07 ±0.152	4.15 ±0.179	11.50 ±0.263	7.53 ±0.306	4.69 ±0.158	13.92 ±0.465	7.22 ±0.338	3.88 ±0.134
5	12	23.69 50.713	3.98 0.160	13.18 ±0.384	15.10 ±0.567	6.03 ±0.201	4.91 ±0.145	3.97 ±0.178	11.22 ±0.406	7.36 ±0.387	4.49 ±0.183	13.32 ±0.612	6.95 ±0.281	3.87 ±0.150
6	17	24.41 20.769	4.00 ±0.078	12.97 ±0.476	15.55 ±0.762	6.14 ±0.214	4.74 ±0.262	3.82 ±0.190	10.99 ±0.403	7.79 ±0.544	4.65 ±0.215	12.90 ±0.500	1.49 ±0.419	4.19 ±0.128
F-test		1.922	3.983	5.485	2.059	1.325	7.737	13.072	5.453	5.023	8.547	13.420	13.789	12.067
P≤		n. s.	.005	.001	n. s.	n. s.	.001	.001	.001	.001	.001	.001	.001	.001

Genetic differentiation - The populations from **ASI,** IDR and ISR are fixed for the allele 100 at the locus *Got-I,* whereas the other populations are characterized by fixation (POL) or predominance of the allele 90. New alleles were found in specimens from Balkan and Thrace at the loci: *Gpdh, Mdh-1,* ***Np,*** *Ap-1, Lap-1. Aph, Ada, Aldo,* and *Est-3.* Four loci (*Ldh-1, G6pdh, Pep-I, Lap-2)* discriminated the Israeli sample from the European populations and other three loci displayed new alleles *(Me-2, 6Pgdh, Hk).*

Genetic distance - Nei's values of genetic identity (*I*) and distance (*D*) were calculated among populations for all pairwise comparisons from the allelic frequencies at 40 loci tested (Table ***3).*** An UPGMA dendrogram summarizing the genetic relationships found among the populations studied is given in Fig. 5. The analysed populations clustered into three distinct groups: 1) Southern and North-Eastern Italy plus Slovenia; *2)* Southern Balkans and Thrace; 3) Israel. The lowest value of genetic distance was observed between the Slovenian specimen and the population from Asiago (*D*=0.007). This specimen displayed relatively higher values of genetic distance in comparison with other Balkan populations: *D*=0.072, ranging from 0.056 with EDI to 0.095 with PEL. The two populations of *D. n. intermedius* from north-eastern Italy showed a low value for genetic distance: D = 0.021. The genetic distance between *D. n. intermedius* and *D. n. aspromontis* was also low: *D* = 0.030. The genetic distance between the Israeli sample and the European populations was much higher: *D* = 0.186, ranging from 0.153 with TAR to *0.227* in comparison with EDI.

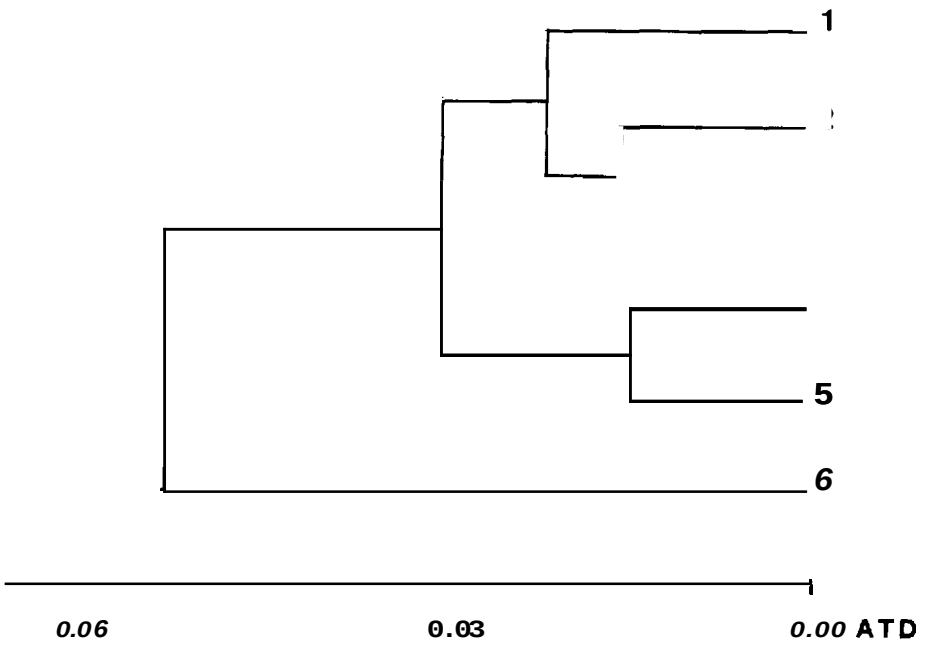

Fig. **4** – UPGMA dendrogram summarizing the Average Taxonomic Distance (ATD) relationships among *Dryomys nitedula* samples. For sample designation see Material and Methods. Cophenetic correlation coefficient r = 0.916.

Tab. 2 – Allelic frequencies observed at 20 of the 40 loci analysed and values for genetic variability observed in populations of *Dryomys nitedula*. For abbreviation of localities see Material and Methods.

Locus (N)		POL 4	ASI 4	TRV 9	IDR 1	BOR 1	PEL 1	EDI 8	ISR 1
Adh	*100*	1.00	1.00	1.00	1.00	1.00	1.00	0.94	0.50
	97	--	--	--	--	--	--	0.06	0.50
αGpdh	*105*	--	--	--	--	--	0.50	--	--
	100	1.00	1.00	1.00	1.00	1.00	0.50	1.00	1.00
Ldh-1	*102*	--	--	--	--	--	--	--	1.00
	100	1.00	1.00	0.56	1.00	1.00	1.00	1.00	--
	85	--	--	0.44	--	--	--	--	--
Mdh-1	*100*	1.00	1.00	1.00	1.00	1.00	0.50	0.94	1.00
	98	--	--	--	--	--	0.50	0.06	--
Me-2	*102*	0.88	0.75	0.33	0.50	--	--	--	0.50
	100	0.12	0.25	0.67	0.50	1.00	1.00	1.00	--
	97	--	--	--	--	--	--	--	0.50
Idh-2	*100*	1.00	1.00	0.50	1.00	1.00	1.00	1.00	0.50
	92	--	--	0.50	--	--	--	--	0.50
6Pgdh	*104*	--	--	--	--	--	--	--	0.50
	100	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50
G6pdh	*104*	--	--	--	--	0.50	--	--	--
	100	1.00	1.00	1.00	1.00	0.50	1.00	1.00	--
	94	--	--	--	--	--	--	--	1.00
Np	*100*	1.00	1.00	1.00	1.00	1.00	1.00	0.25	1.00
	95	--	--	--	--	--	--	0.75	--
Got-1	*100*	0.12	1.00	*0.50*	1.00	--	--	--	1.00
	90	0.88	--	0.50	--	1.00	1.00	1.00	--
Hk	*103*	--	--	--	--	--	--	--	0,50
	100	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.50
Adk	*103*	0.25	--	0.06	--	--	--	--	--
	100	*0.75*	1.00	0.94	1.00	1.00	1.00	1.00	1.00
Ap-1	*103*	--	--	0.06	--	--	--	--	--
	100	1.00	1.00	0.94	1.00	1.00	0.50	1.00	1.00
	95	--	--	--	--	--	0.50	--	--
Pep-1	*100*	1.00	1.00	1.00	1.00	1.00	1.00	1.00	--
	97	--	--	--	--	--	--	--	1.00
Lap-2	*107*	0.12	--	--	--	--	--	--	--
	103	--	--	--	--	--	--	--	1.00
	100	0.88	1.00	1.00	1.00	1.00	*0.50*	1.00	--

Tab. 2 - continued.

Locus (N)		POL 4	ASI 4	TRV 9	IDR 1	BOR 1	PEL 1	EDI 8	ISR 1
Aph	*105*	--	--	--	--	--	--	0.06	--
	100	1.00	1.00	1.00	1.00	1.00	1.00	0.94	1.00
Ada	*100*	1.00	1.00	1.00	1.00	1.00	1.00	0.88	1.00
	95	--	--	--	--	--	--	0.12	--
Aldo	*100*	1.00	1.00	1.00	1.00	1.00	1.00	0.94	1.00
	95	--	--	--	--	--	--	0.06	--
Est-1	*100*	1.00	0.88	1.00	0.50	1.00	1.00	0.75	1.00
	96	--	0.12	--	0.50	--	--	0.25	--
Est-3	*105*	--	--	--	--	0.50	--	0.19	--
	100	1.00	0.25	0.50	--	0.50	1.00	0.31	1.00
	94	--	0.75	0.50	1.00	--	--	0.50	--
	He	0.029	0.028	0.070	0.050	0.050	0.100	0.055	0.125
	Ho	0.019	0.031	0.053	0.050	0.050	0.100	0.047	0.125
	P1%	0.100	0.075	0.175	0.050	0.050	0.100	0.200	0.125
	A	1.100	1.100	1.200	1.050	1.050	1.100	1.225	1.125

The following loci were rnonotnorphic and fixed for the same allele in the populations considered: *Sdh, Ldh-2, Mdh-2, Me-1, Idh-1, Ipo, G3pdh, Got-2, Ck, Pgm, Acph, Ap-2, Pep-2, Pep-3, Lap-I. Fum, Mpi, Pgi, Pt-3,* and *Pt-4.*

DISCUSSION

The mean value for genetic distance observed between the North Italian populations and *D. n. aspromontis* from Basilicata was low (D = 0.030) and corresponded to values generally observed between local populations in small mammals (Zimmerman et al., 1978; Graf, 1982; Filippucci et al., 1991). The southern subspecies, *D. n. aspromontis,* was described by von Lehmann in 1964 and considered a faunistic isolate limited to the Aspromonte area. However, body and cranial measurements correspond to those of *D. n. intermedius,* excluding the colour which is lighter grey and the top of the tail which is clearly white. The population of *D. n. aspromontis* here analysed, was recently found on Mt. Pollino in Basilicata and a more continuous distribution of the forest dormouse along the peninsula was hypothesized (Filippucci et al., 1985; Filippucci, 1986). According to Roesler & Witte (1968) *Dryomys* reached southern Italy only recently, spreading from the Alps to Calabria through the Appennines. The electrophoretic data confirm the recent origin of Southern Italian populations of *Dryomys nitedula.* The mean value of genetic distance between Italian plus Slovenian and South Balkan populations was $D = 0.06$. This value is relatively high and corresponds to those observed among other rodent subspecies (Zimmerman et al., 1978; Graf, 1982; Filippucci et al., 1991). According to Kryštufek (1985) in the area of former

Yugoslavia two subspecies can be identified: *D. n. intermedius* (the Alps, the Northern Dinaric Alps) and *D. n. ravijojla* (Macedonia). Forest dormice from Herzegovina, Montenegro and Kosovo display signs of transition between these two subspecies.

Tab. 3 – Values of Nei's (1978) unbiased genetic distance (below diagonal) and identity (above diagonal), based on 40 gene loci, observed among populations of *Dryomys nitedula.*

	POL	ASI	TAR	IDR	BOR	PEL	EDI	ISR
POL	--	0.967	0.973	0.944	0.967	0.955	0.954	0.847
ASI	0.034	--	0.979	0.995	0.944	0.920	0.946	0.851
TAR	0.027	0.021	--	0.970	0.968	0.948	0.964	0.858
IDR	0.057	0.005	0.030	--	0.936	0.909	0.947	0.830
BOR	0.034	0.058	0.033	0.066	--	0.961	0.973	0.824
PEL	0.046	0.083	0.053	0.095	0.040	--	0.950	0.808
EDI	0.047	0.056	0.037	0.054	0.027	0.052	--	0.797
ISR	0.166	0.161	0.153	0.186	0.194	0.213	0.227	--

In both biometric and electrophoretic analyses the Israeli sample was the most distinct. Skulls of Israeli specimens are characterized by longer mandibular tooth row, higher rhamus mandibulae, longer bullae, and narrower braincase breadth, rostral breadth and interorbital constriction. The isolated Israeli population is commonly attributed to the taxon *phrygius*, but it differs from this by biometric analysis. *D. n. phrygius* from the topotype locality in Asia Minor clustered with the European population from Turkish Thrace. Electrophoretically the Israeli sample could be discriminated from European populations by four loci (*Ldh-1, G6pdh, Pep-1* and *Lup-2)* fixed for new alleles. The mean value of Nei's genetic distance between Israeli and European populations was D=0.186, ranging from 0.153 to 0.227. The above value of genetic distance is generally observed at different stages of evolutionary divergence, usually associated with closely related, sibling species, especially in Vertebrates (Avise & Aquadro, 1982). According to Thorpe (1982) and Nei (1987) if allopatric populations of dubious status have genetic identities (I) below 0.85 and genetic distances (D) higher than 0.16, it is improbable that they are conspecific.

The hypothesis of a specific separation of the Israeli population could be supported by the ecological and biological differences this marginal population displays in comparison with European animals (Nevo & Amir, 1964):

a) in Israel *Dryomys* is confined to the evergreen oak maquis of Galilee (*Quercus calliprinus-Pistacia palestina* plant association); in Europe it is strongly associated with conifer and beech woods, but it is also present in other broad leaf forests;

b) in Israel it displays a full year activity, occasionally interrupted during the

winter by a few short periods of hibernation and partial hibernation that may last for hours, usually during the day. In Europe activity is instead confined to spring, summer, and part of autumn (Kryštufek, 1985; Paolucci et al., 1987);
c) two - three parturitions per year from March to December in Israel versus one (possibly two) from May to August in Europe.

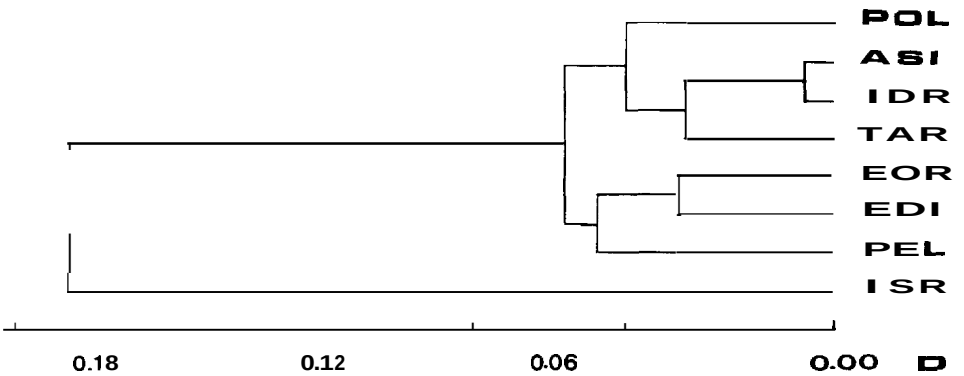

Fig. 5 – UPGMA dendrogram summarizing the genelic relationships among the studied populations of *Dryomys nitedula*. *D*: Nei's (1978) unbiased genetic distance. based on 40 loci. The cophenetic correlation coefficient is 0.960.

In order to clarify the phylogenetic relationships of the Israeli forest dormouse, a comparison with other populations of the taxa *D. n. tichomirovi* and *D. n. pictus* from Transcaucasus, Armenia, South-eastern Turkey and Iran, as well as of *D. laniger* from Turkey, **is** therefore needed.

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