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Biometric and Allozymic Variations in the Genus *Dryomys* (Rodentia: Gliridae) in Turkey

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Abstract: Biometric and allozymic variations were analysed in three populations of *Dryomys nitedula* one population of *Dryomys laniger* from Turkey. Multivariate analysis of 32 external and cranial measurements was performed on 44 specimens. Of the morphometric variables, twenty-six characters were found to be significantly different between both species (Tukey HSD, $p < 0.05$), and the total variance was explained by seven principle components (80.1%). The Black Sea population of *D. nitedula* and that of *D. laniger* were markedly separate on the first two canonical functions. The genetic analysis was carried out on 17 enzyme systems of 36 specimens. Nine out of twenty loci were found to be polymorphic in *D. nitedula* populations and five were polymorphic in *D. laniger. Ldh* and *Gpi* loci were fixed for different alleles between *D. nitedula* and *D. laniger*. The mean value of the fixation index (F_{ST} = 0.13) indicated moderate to high genetic differences between the populations of *D. nitedula*. Nei's measure of genetic distance (D) varied from 0.006 to 0.030 among the populations of *D. nitedula*, whereas the highest genetic distance appeared between the Black Sea population of *D. nitedula* and *D. laniger* (*D*= 0.187).

Key words*:* *Dryomys nitedula*, *Dryomys laniger,* multivariate analysis, allozyme, Turkey.

Introduction

The genus *Dryomys* in Turkey is represented by two species, *Dryomys nitedula* and *Dryomys laniger* (Yiğit *et al.* 2003). *D. nitedula* (Pallas 1779) occurs widely in Turkey, whereas *D. laniger,* first described by Felten and Storch (1968) from Çığlıkara - Elmalı (Antalya), ranges throughout Taurus Mountains (Krystufek, Vorhalik 2005).

A number of studies have dealt with the karyological, morphological, blood serum protein and allozymic variation in Turkish populations of the genus *Dryomys*. The diploid chromosome numbers were reported to be distinct between the two species; *D. nitedula* with $2n = 48$ and *D. laniger* with $2n = 46$ (Doğramacı and Kefelioğlu 1990, Civitelli *et al.* 1995, Kivanç *et al.* 1997). The slight colour variations over the distribution range of *D. nitedula* in Turkey and adjacent countries led to assignation of a number of subspecies, e.g.: *D. n. pictus* (Blanford 1875) from Hakkari province (Eastern Turkey), which has also been considered as a separate species by Mursaloğlu (1973), *D. n. wingei* (Nehring 1902) from Greece, *D. n. phrygius* (Thomas 1907) from Uşak province (Western Turkey), *D. n. robustus* (Miller 1910) from Bulgaria and *D. n. tichormirovi* (Satunin 1920) from Armenia. A similar colour variation was reported between the sub-populations of *D. nitedula* by Yiğit *et al.* (2003) but no substantial cranial variation was found. Apart from this, Yiğit *et al.* (2003) compared *D. nitedula* and *D.*

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laniger, noting that the shape of the braincase, tympanic bullae and mandible morphologically distinguished them. The blood serum proteins were examined using the SDS-PAGE technique and were reported to have no taxonomic importance for these taxa (Yiğit *et al.* 2003). Allozymic and biometric comparisons between sub-populations of *D. nitedula* were also performed by Filipucci *et al.* (1994). According to their results, the Israeli samples were found to be distinguished from European sub-populations by four loci (*Ldh-I, G6pdh, Pep-I* and *Lap-2*). They also reported that seven loci were polymorphic in the sub-population of Edirne (Turkish Thrace); the proportion of polymorphic loci was 20%, the mean heterozygosity observed (*Ho*) was 0. 047, the average number of alleles per locus was 1.2.

However there are no data available, with regard to the allozymic variation between both *Dryomys* species. Such allozymic patterns of *D. laniger*, as well as the biometric differences of *D. laniger* and *D. nitedula*, using discriminant analysis, are given for first time in this study, in an effort to reveal new, discriminatory characters between the two species and further study the interpopulational variation within *D. nitedula*.

Sampling Area and Specimens

Specimens of *Dryomys* were collected from different localities in Turkey between 2005 and 2007. DL1 is represent to Southern Turkey (Elmalı N=2; Bolkar Mountains N=10; Aladağlar N=3, Gökbel Plateau N=1); DN1 is represent to Eastern Black Sea Region (Çamlıhemşin N=4; Çat N=3; Karanlıkmeşe N=1; Şavşat N=1; Çakallı N=1; Cankurtaran N=1; Kaptanpaşa N=1); DN2 is represent to Western Anatolia (Elmalı N=2; Çay N=1; Pınarbaşı N=1; Bolkar Mountains N=2, Bozüyük N=2; Çorum N=1; Kemalpaşa N=1); DN3 is represent to Turkish Thrace (Edirne N=13). The collection details are given in Fig. 1.

Materials and Methods

Morphological study (Statistic evaluations; DL= 14, DN1; 7, DN2; 10, DN3; 13 specimens).

For the morphological comparison, 4 external and 27 skull characteristics were measured in a total of 44 adult specimens, using watch-faced calipers with a sensitivity of 0.01 mm. Measurements of characteristics were analyzed by MANOVA (two-way multivariate analysis of variance). Pair wise comparisons of these species by each variable were performed using the *post hoc* Tukey's HSD test with unequal sample. For ordination analysis, Principal Component Analysis (PCA) was performed with the means of the characteristics measured. Discriminant Function Analysis (DFA) was carried out by SPSS 13. Phenotypic relationships among groups were obtained by UPGMA cluster analysis (Sneath and Sokal 1973, Rohlf 2000; NTSYS-pc version 2.1).

Abbreviations used for characteristic measured: TBL (Total body length), TL (Tail length), HFL (Hind foot length), EL (Ear length), ZB (Zygomatic breadth), IC (Interorbital constriction), CBL (Condylobasal length), CNL (Condylonasal length), ONL (Occipitonasal length), BL (Basal length), NL (Nasal length), NW (Nasal width), FL (Frontal length), PRL (Parietal length), LFR (Length of facial region), LBC (Length of braincase), MAB (Mastoid breadth), BCWB (Braincase height with bullae), BCW (Braincase height without bullae), OW (Occipital width), BW (Braincase width), DL (Diestama length), PL (Palatal length), FI (Foramen incisiva), HTB (Height of tympanic bullae), LTB (Length of tympanic bullae), WTB (Width of tympanic bullae), MAL (Mandible length), MAH (Mandible height), UML (Upper premolar length), LML (Lower premolar length).

Allozymic study (Specimens studied; DL= 12, DN1; 11, DN2; 6, DN3; 7).

The electrophoretic procedures were carried out, following Shaw and Prasad (1970) and Harris and Hopkinson (1976); the percentage of starch gel was 12% and the running of samples was performed during 4 – 6 h at 120 V. The different buffers for running and dying were used in accordance with the enzyme systems Genetic variation was assessed using standard horizontal gel electrophoresis and 17 enzymes coding for 20 presumptive loci were analyzed on 36 specimens (DL: n=12, DN1: n= 11, DN2: n= 6, DN3: n= 7). Homogenates obtained from muscle were run in horizontal starch gel electrophoresis for the following enzymatic proteins: α-glycerophosphate dehydrogenase (E.C. 1.1.1.8; α-Gpdh), lactate de-

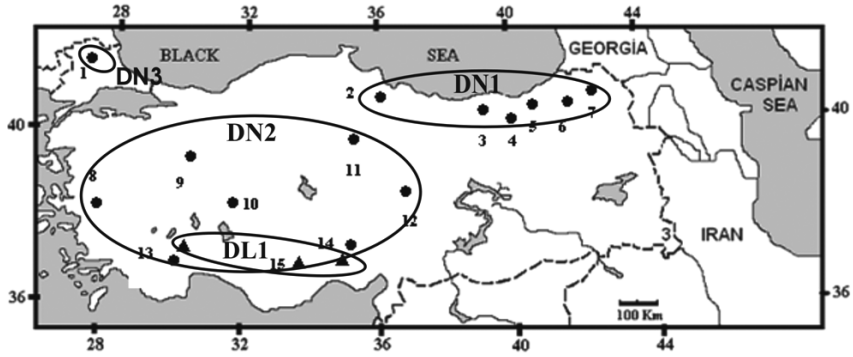

Fig. 1. The collecting cites of specimens in Turkey. 1: Turkish Thrace (Edirne): 2-7: Eastern Black Sea Region (2: Kaptanpaşa, 3: Çamlıhemşin, 4: Çat, 5: Cankurtaran, 6: Karanlıkmeşe, 7: Şavşat) 8-14: Western Anatolia (8: Kemalpaşa, 9: Bozüyük 10: Çay, 11: Çorum, 12: Pınarbaşı, 13: Elmalı, 14: Bolkar Mountains, 15: Aladağlar).
(• *Dryomys nitedula*; ▲ *Dryomys laniger).*

hydrogenase (E.C. 1.1.1.27; Ldh), malate dehydrogenase (E.C. 1.1.1.37, Mdh-1 and Mdh-2), malic enzyme (E.C. 1.1.1.40; Me), isocitrate dehydrogenase (E.C. 1.1.1.42; Idh-1 and Idh-2), phosphogluconate dehydrogenase (E.C. 1.1.1.44; Pgd), glucose-6-phosphate dehydrogenase (E.C. 1.1.1.49; G6pdh), glyceraldehyde-3-phosphate dehydrogenase (E.C. 1.2.1.12; G3pdh), superoxide dismutase (E.C. 1.15.1.1; Sod), phosphoglucomutase (E.C. 2.5.7.1; Pgm), hexokinase (E.C. 2.7.1.1; Hk), aldolase (E.C. 4.1.2.13; Ald), carbonic anhydrase (E.C. 4.2.1.1; Ca-1 and Ca-2), fumarase (E.C. 4.2.1.2; Fum), aconitate hydratase (E.C. 4.2.1.3; Acon), mannose phosphate isomerase (E.C. 5.3.1.8; Mpi), and glucose phosphate isomerase (E.C. 5.3.1.9; Gpi).

The observed electrophoretic band patterns were analysed following the method of Harris and Hopkinson (1976). Presumptive alleles were designated alphabetically by their relative mobility, with the allele variant migrating farthest towards the anode denoted as 'A'. Allozymic data were analysed as allele frequencies with BIOSYS-2 (Black 1997; original version: BIOSYS-1 Release 1.7 program of Swofford and Selander 1989, and modifications to HDYWBG and FSTAT by William C. Black IV). The genetic variation between intra-specific populations was estimated as the mean heterozygosity per locus of observed (*H*o) and expected (H_E) frequencies of heterozygotes under the Hardy-Weinberg equilibrium, the proportion of polymorphic loci in the population, and the mean number of alleles per locus. The BIOSYS-1 Release 1.7 program was used to calculate overall and population-specific Wright's F-statistics estimators of F_{ST}, F_{IT} and F_{IS}. Fixation indices (F-statistics; Wright, 1951, 1965) were used to summarize the distribution of genetic variation within and between populations. Estimates of overall gene flow between populations (N*m*) were derived from the approximation F_{ST} =1 / (1 + 4Nm) as recommended by Slatkin and Barton (1989). The amount of genetic divergence between species was estimated with the indices of standard genetic identity (*I*) and distance (*D*, Nei unbiased distance) proposed by Nei (1978). A Neighbour joining dendrogram of the genetic relationships among the species was constructed by using the allele frequencies obtained from BIOSYS-1 Release 1.7 program.

Results

Biometric Analysis

In multivariate analysis of variance (MANOVA), the pair-wise comparisons performed with Tukey's HSD test, using 31 variables showed significant differences in 26 variables between the three sub-populations of *D. nitedula* and the *D. laniger* population. Of these characteristics, 22 were found to be different between *D. nitedula* and *D. laniger*, and 13 among the three sub-populations of *D. nitedula*. HFL, ZB, NW, BCW, MAL and MAH distinguished *D. laniger* from *D. nitedula* ($p < 0.01$). With regard to *D. nitedula*, DN1 differed from DN2 and DN3, based on MAB, BW, HTB, LTB, UML and LML, and was proven to be the most distinct sub-population.

In PCA, Kaiser-Meyer-Olkin Measure of Sampling Adequacy also showed a moderate level of Sampling Adequacy with the value of 0.642. Principal Component Analyses (PCA) extracted seven PCs that explained 79.9% of the total variance (Table 1). The initial eigenvalues of the components which explain the total variance were poor in discriminating between groups of two species. The first component explained 36.1% total variance and the second 15.7%. The highest contribution to PC1 was found in the characteristics such as CBL, ZB, CNL, ONL, BL, LFR, NW, BCWB, BL, MAL, MAH with the values above of 0.700, and four characteristics (HTB, LTB, BW, WTB) to PC2.

DFA showed that of the 44 specimens from both species, 31 (93.2%) were classified correctly. Total variation was clarified by three components in DFA. The characteristics with Wilks' lambda values assume that the characteristics with low values are more discriminative between the sub-populations and populations. Wilks' lambda values which explain the tests of equality of group means were found significant for most characteristics (P< 0.01). Canonical discriminant function based on three components of 1 through 3 yielded a highly significant Wilks' Lambda of 0.003 (χ^2= 214.455, DF= 30, P< 0.005). The first canonical variate which explained 89.2% of the variance clearly divided *D. laniger* samples from the sub-populations of *D. nitedula*, and also the second component which explained 9.4% of total variability distinguished the Black Sea sub-population from the other sub-populations of *D. nitedula* and *D. laniger* (Fig 2). When considering sub-populations of *D. nitedula*, the first canonical variate markedly separated the DN1 sub-population from DN2 and DN3. However, the second canonical variate distinguished DN2 from DN3. Thus DN2, DN3 and DN1 were somehow separated from each other. The best classified population in *D. nitedula* was DN2, with the value of 100%, followed by DN2 with 90% and by DN1 with 84.6%. According to the results obtained from DFA, *D. laniger* is significantly differentiated from *D. nitedula.* In the populations of *D. nitedula*, the statistical result proved that DN1 had a very distinct group, suggesting that they are phenetically different from other sub-populations (Fig. 3).

Analysis of allozymic variations

Eight of the twenty loci coded by seventeen enzyme

Table 1. Total Variance Explained (First seven principal component explains 79.9 % of total variance).

Component	Initial Eigenvalues		
	Total	% of Variance	Cumulative %
1	11.183	36.076	36.076
2	4.861	15.679	51.755
3	3.143	10.140	61.895
4	1.864	6.013	67.908
5	1.477	4.764	72.672
6	1.233	3.976	76.647
7	1.023	3.301	79.948

Extraction Method: Principal Component Analysis

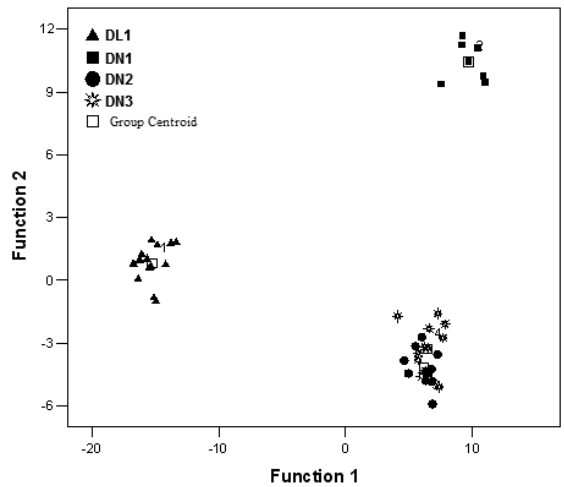

Fig. 2. The result of discriminant function analysis of morphological characters of all populations of *Dryomys* (1=*D. laniger* 'DL1'), (*D. nitedula*; 2=Black Sea region 'DN1'; 3=Central Anatolia 'DN2'; 4=Turkish Thrace 'DN3').

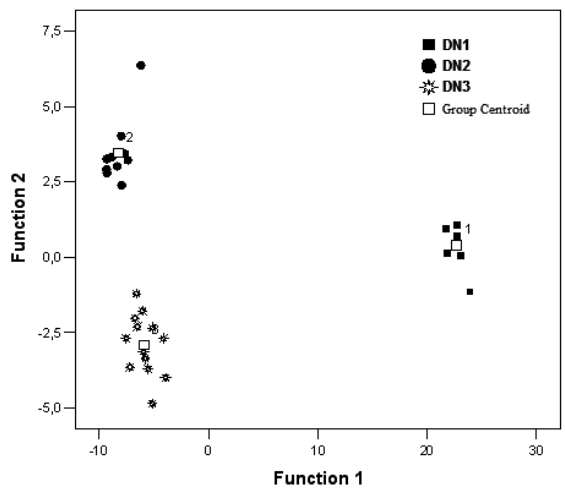

Fig. 3. The result of discriminant function analysis of morphological characters of populations of *Dryomys nitedula* (1=Black Sea region 'DN1'; 2=Central Anatolia 'DN2'; 3=Turkish Thrace 'DN3').

systems analyzed were monomorphic and fixed for the same allele in all populations: *Mdh-1, Mdh-2, Idh-2, G$_3$pdh, Ald, Ca-1, Pgd and Hk.* Of the 20 loci, nine were polymorphic in the sub- populations of *D. nitedula* and five in *D. laniger* (Table 2). The loci *Idh*-1, *Sod*, *Mpi*, *Pgm* were found to be polymorphic in the both species. The loci *Ldh* and *Gpi* clearly distinguished *D. nitedula* from *D. laniger* in the analyzed specimens.

The genetic variation levels within populations are summarized in Table 3. Considering both taxa, it can be said that the genus *Dryomys* has moderate genetic diversity. The expected heterozygosity (H_E) was ranging from 0.073 (DL1) to 0.128 (DN1) in *D.*

Table 2. Allele frequencies of 12 polymorphic loci in populations of *Dryomys* spp.

Locus	***D. nitedula* (DN1) (Black Sea region)**	***D. nitedula* (DN2) (Central Anatolia)**	***D. nitedula* (DN3) (Turkish Thrace)**	***D. laniger* (DL1)**
α-*Gpdh*				
A	0.545	0.583	0.643	1.000
B	0.455	0.417	0.357	0.000
Ldh				
A	1.000	1.000	1.000	0.000
B	0.000	0.000	0.000	1.000
Malic				
A	0.909	0.583	1.000	1.000
B	0.091	0.417	0.000	0.000
Idh-1				
A	0.773	0.750	0.929	0.833
B	0.227	0.250	0.071	0.167
G$_3$pdh				
A	0.909	1.000	1.000	1.000
B	0.091	0.000	0.000	0.000
Sod				
A	0.818	1.000	1.000	0.958
B	0.182	0.000	0.000	0.042
Ca-2				
A	0.045	0.667	0.071	1.000
B	0.955	0.333	0.929	0.000
Gpi				
A	0.000	0.000	0.000	1.000
B	1.000	1.000	1.000	0.000
Acon				
A	0.818	1.000	1.000	1.000
B	0.182	0.000	0.000	0.000
Mpi				
A	0.773	1.000	0.929	0.792
B	0.227	0.000	0.071	0.208
Fumaraz				
A	1.000	1.000	1.000	0.958
B	0.000	0.000	0.000	0.042
Pgm				
A	0.864	0.917	0.571	0.833
B	0.136	0.083	0.429	0.167

Table 3. Levels of genetic variation based on 20 loci in all populations.

Populations	N	Mean number of alleles per locus	Percentage of polymorphic loci*	Mean heterozygosity Direct count (Ho)	Mean heterozygosity Hardy-Weinberg Expected (HE)**
D. nitedula **(DN1)**	11	1.5 (0.1)	40.0	0.064 (0.029)	0.128 (0.038)
D. nitedula **(DN2)**	6	1.3 (0.1)	25.0	0.050 (0.027)	0.106 (0.045)
D. nitedula **(DN3)**	7	1.3 (0.1)	25.0	0.100 (0.054)	0.073 (0.035)
D. laniger **(DL1)**	12	1.3 (0.1)	15.0	0.054 (0.027)	0.055 (0.025)

* A locus is considered polymorphic if the frequency of the most common allele does not exceed 0.95. ** Unbiased estimate (see Nei 1978)

nitedula and was 0.055 in *D. laniger*. However, the observed heterozygosity (H_O) was found to vary from 0.050 to 0.100 in *D. nitedula*, and was 0.054 in *D. laniger*. The mean percentage of polymorphic loci was 30%, ranging from 25% to 40% in *D. nitedula* and 15% in *D. laniger*. The highest percentage of polymorphic loci was found in the population of Black Sea region (DN1) (40%) with the mean number of alleles per locus equal to 1.5. The lowest percentage of polymorphic loci was in the *D. laniger* population. In *D. nitedula*, six loci (α-*Gpdh, Pgm, Me, G6pdh, Acon, Mpi*) violated the Hardy-Weinberg equilibrium in DN1 and one locus (*Ca-2*) in DN2. *Ca-2* was also found to deviate from the Hardy-Weinberg equilibrium in *D. laniger* ($P < 0.05$).

Population structure and distance

Estimates of F-statistics for polymorphic loci of *D. nitedula* were calculated with Biosys-2 (Table 4). *D. laniger* population was excluded from this analysis because it was evaluated as a single group. The mean value of the fixation index $F_{ST} = 0.13$ indicates that 13% genetic variation in *D. nitedula* populations reflect moderate or slightly high genetic differentiation. The loci *Ca-2, Me, Sod, Acon* and *Pgm* significantly contribute to the differentiation between the studied sub-populations (Table 4). The values of F_{IS}, indicating the effect of inbreeding on an individual within samples, were also moderately high (mean 0.2917) and negative for two of nine loci, although negative F_{IS} values were not excessive. The values of F_{IS} were found to be in the range of -0.1534 – 1 in nine loci. Of these loci, *G6pdh and Acon* showed the highest value of F_{IS} indicating the inbreeding effect. The values of F_{IT} with the mean value of 0.3851 indicating the inbreeding effect of an individual on the total population, reflected the similar genetic differentiation of F_{ST} and F_{IS}. The value of N*m* (number of migrants) between sub-populations of *D. nitedula* which was calculated from the approximation $F_{ST} = 1 / (1 + 4Nm)$ indicates the overall gene flow, and there is a negative correlation between the values F_{ST} and Nm. The N*m* was calculated as 0.165, indicating a relatively low level of gene flow between the sub-populations.

The values of Nei's (1978) unbiased genetic identity (*I*) and distance (*D*) were calculated from pairwise comparisons of populations (Table 5). The neighbour

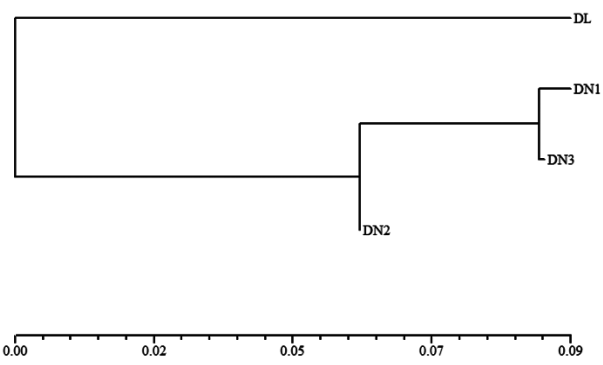

Fig. 4. Neighbour joining dendrogram summarising the genetic relationships among the *Dryomys* populations studied (*D*=Nei's (1978) unbiased genetic distance, based on 20 enzyme loci). (DL: *D. laniger*, DN1: *D. nitedula*1, DN2: *D. nitedula*2, DN3: *D. nitedula*3).

Table 4. *F-statistics* of variable loci in the populations of *D. nitedula* calculated using the method of Wright (1965).

Loci	F_{IS}	F_{IT}	F_{ST}
α-Gpdh	0.1369	0.1429	0.0070
Malic	0.7888	0.8328	0.2081
Idh-1	0.0060	0.0427	0.0370
G_6pdh	1.0000	1.0000	0.0514
Sod	-0.2222	-0.0909	0.1074
Ca-2	0.5604	0.7474	0.4253
Acon	1.0000	1.0000	0.1074
Mpi	0.5827	0.6190	0.0872
Pgm	-0.1534	-0.105	0.1239
Mean	0.2917	0.3851	0.1318

Table 5. Values of Nei's (1978) unbiased distance (*D*; above the diagonal) and genetic identity (*I*; below the diagonal) between *Dryomys* populations

Population	1	2	3	4
1 *D. laniger*	*****	0.187	0.140	0.175
2 *D. nitedula*1	0.829	*****	0.027	0.006
3 *D. nitedula*2	0.869	0.973	*****	0.030
4 *D. nitedula*3	0.839	0.994	0.970	*****

joining dendrogram summarizing the genetic relationships between the populations is given in Fig. 4. The highest genetic distance was found as *D*= 0.187 between *D. nitedula*1 and *D. laniger*. These values varied from *D*= 0.006 to *D*= 0.030 in the sub-population of *D. nitedula*. The highest distance value in the sub-population of *D. nitedula* was calculated as *D*= 0.030 between *D. nitedula2* and *D. nitedula*3. These values indicated that the Black Sea sub-population is genetically close to the sub-population of Turkish Thrace. The specimens from Western Anatolia were connected to this group with a distance of *D*= 0.030.

Discussion

Biometric and allozymic comparisons between sub-populations of *D. nitedula* were performed by Filipucci *et al.* (1994). More recently Yiğit *et al.* (2003) compared two species of the genus *Dryomys* and noted that the shape of the braincase, tympanic bullae and mandible morphologically distinguished *D. nitedula* from *D. laniger*.

In biometrical analyses, Filipucci *et al.* (1994) reported that ten characteristics were significantly different among the six sub-populations of *D. nitedula*. The highest values for the *F*-test were for interorbital constriction, mandible length, height of ramus mandibulae, mandibular tooth row length. They also noted that Israeli specimens were most distinct and that dormice from Turkish Thrace and Western Anatolia overlapped considerably, suggesting they are phenetically close. However Yiğit *et al.* (2003) revealed that nine characteristics including weight and the ratio of the tail length to body length were statistically different between the specimens from Turkish Thrace and Western Anatolia using the *t*-test. In this study, using pair-wise comparisons in Tukey's HSD test, the sub-population from the Black Sea (DN1) was found to be the most distinct sub-population among three sub-populations. Only one characteristic (BL) differed significantly between Turkish Thrace and Western populations. This finding is consistent with that of Filipucci *et al.* (1994). The six sub-populations subjected to discriminant function analyses showed that the Israeli sub-population of *D. nitedula* was also the most distinct population; this sub-population was segregated from the other five sub-populations by two canonical variates which explained 90% of the variance (Filipucci *et al.* 1994). In this study, the total variance was explained by three components and *D. nitedula* and *D. laniger* were clearly separated from each other. In *D. nitedula* sub-populations in Turkey, Black Sea sub-population was found to be the most distinct.

In allozymic comparisons, Filipucci *et al.* (1994) stated that electrophoretically Israeli sample was found to be discriminated from European sub-populations by four loci (*Ldh-I, G6pdh, Pep-I* and *Lap-2*). They also reported that seven loci were found to be polymorphic in the sub-population of Edirne (Turkish Thrace); the proportion of polymorphic loci was 20%, the mean heterozygosity observed (*Ho*) was 0. 047, the average number of alleles per locus was 1.2. According the 20 loci analyzed, a discriminative locus was not found in the specimens from Black Sea (DN1), Western Anatolia (DN2) or Turkish Thrace (DN3). The mean heterozygosity observed and the mean percentages of polymorphic loci were found to be slightly higher than that given for the specimens from Turkish Thrace. However the value of mean heterozygosity of the three sub-populations studied are in the range of the values given for European and Israeli sub-populations. The

genetic distance based on allozymic variations was also reported for the specimens ranging from Italy to Israel (Filipucci *et al.* 1994). The mean value of Nei's genetic distance observed between the two Italian subspecies was lower (D= 0.03), corresponding to values generally observed between local sub-populations, but the Israeli sub-population has four discriminate loci and the mean value of Nei's genetic distance was D= 0.186 for Israeli and European sub-populations. Avise and Aquado (1982) suggested that such a value for genetic distances is generally associated with closely related sibling species. A high value varying from D= 0.140 to D= 0.187 was found between *D. nitedula* and *D. laniger* in Turkey. The highest value (D= 0.030) is similar to the value given for the Italian subspecies of *D. nitedula* by Filipucci *et al.* (1994). They also suggested that the Israeli sub-population of *D. nitedula* could be a separate species. Supporting this suggestion, Thrope (1982) and Nei (1978) stated that allopatric populations of dubious status that have a genetic distance (D) higher than 0.160 are probably not conspecific. Apart from these, the genus *Dryomys* is considered the most recent genus in the family Myoxidae (Storch 1978, Caline and MEIN 1979, Daams 1981). The oldest fossil records known for this species are from Middle Pleistocene age in Central Europe and Chios Island (Greece) (Janossy 1962, Storch 1975, Horacek 1987), but this species was also found to be from Early Pliocene in Poland by Nadachowski (1990). Spitzenberger (1976) noted that *Dryomys* can not be considered as recent due to the sympatric occurrence in Taurus Mountains of *D. nitedula* and *D. laniger*. According to Filipucci *et al.* (1994), the electrophoretic data supports Spitzenberger's hypothesis that the genus *Dryomys* is highly differentiated across a fragmented and large distribution area. The F_{ST} value which shows moderate or slightly high genetic differentiation also supports this hypothesis. In order to establish phylogenetic and paleontological relationships, further research, especially using molecular techniques, and with Caucasian and Iranian specimens included in the evaluation, is necessary for both species.

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