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Allozyme Variation in Wild Rats *Rattus norvegicus* (Berkenhout 1769) (Mammalia: Rodentia) from Turkey

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Abstract: The genetic diversity of 22 allozyme loci was investigated in 33 wild rat (*Rattus norvegicus*) specimens from 4 sub-populations. Eight of the 22 loci (*Pgm, Hk, Me-M, Ldh, α-Gpdh-1, α-Gpdh-2, Fum, Xdh*) were polymorphic. The level of genetic variation was measured by mean number of alleles per locus (A = 1.18), percentage of polymorphic loci (P = 18.2), mean heterozygosity per locus observed (*Ho* = 0.007), and mean heterozygosity expected under Hardy -Weinberg equilibrium (*He* = 0.057).
Mean F_{ST} value was 0.34, indicating 34% genetic variation and suggesting high-level differentiation between sub-populations of the Turkish wild rat. The number of migrants (Nm) was 0.48 and showed that gene flow was relatively low between sub-populations. Even though a high level of genetic variation was observed, the low Nm value and *Ho* could be evidence of the Wahlund effect or a genetic bottleneck for the sub-populations. It is also suspected that there might be some factors preventing gene flow from the sub-populations, which constitute their own genetic potential for new taxonomic units.

Key words: *Rattus norvegicus*, Allozyme, Turkey

Introduction

The wild rat *Rattus norvegicus* (Berkenhout 1769) is distributed worldwide, is a well-known laboratory rodent, and has been extensively used in experimental research (Musser, Carleton 2005; Kumar *et al.*, 2007). Watts, Baverstock (1995) suggested that murine rodents arose 20 million years ago (MYA) in southern Asia, extensively expanded their range by about 8 MYA, and much more recently spread to continental Asia, reaching Europe early in the 18th century (Innes 1990). Ingrid *et al.* (1997) reported that the overall degree of genetic variability in wild rat remains unclear. Schlick *et al.* (2006) reported that the entire mitochondrial genome available for the genus *Rattus* was from 13 specimens of *R. norvegicus*, and of these only 3 were from wild specimens, the remainder coming from highly inbred laboratory strains. More recently, phylogenetic and dating analyses suggested that the oldest divergence within the genus *Rattus* occurred ~ 3.5 MYA, and that *R. norvegicus* diverged ~ 2.5 MYA within the Asian Island/Southern Asian clade (Robins et al., 2008). Although the wild rat remains very popular as a laboratory animal, they are genetically less known in the wild. Genetic diversity in the wild rat based on allozymic markers was reported by Serov (1972), Erikkson *et al.* (1976), Pasteur *et al.* (1982), Bender

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et al. (1985), CRAMER *et al.* (1988), and YAMADA *et al.* (1993). Most of these studies included a small number of wild rats in confined areas.

Few studies have been conducted on wild specimens of *R. norvegicus* in the Middle East and have focused primarily on distributional records and karyotype (HARRISON, BATES 1991; YIĞIT *et al.* 1998). In addition to these studies, nonspecific esterase patterns and blood serum proteins were studied using starch gel and SDS-PAGE electrophoresis, respectively, and were reported to be taxonomically unimportant (YIĞIT *et al.* 2000, 2001). The present study, the first allozymic study on wild specimens of *R. norvegicus* in the Middle East, aimed to describe genetic variations using allozyme markers and to contribute to the phylogenetic relationship within this genus.

Materials and Methods

In all, 33 specimens of *Rattus norvegicus* were collected from 8 localities in Turkey between the year of 1997 and 2002 (Fig. 1) and the sub-populations were primarily established according to geographic proximity (Table 1). Specimens were caught with Sherman live traps, transferred to the laboratory, and then sacrificed under anesthesia. Identification was performed according to cranial and karyological criteria in YIĞIT *et al.* (1998). Voucher specimens and tissues were deposited at Prof. Dr. N. Yiğit and Prof. Dr. E. Çolak's collection (Ankara University, Faculty of Science, Department of Biology).

Electrophoretic procedures were carried out as described by SHAW, PRASAD (1970) and HARRIS, HOPKINSON (1976); the gel percentage was 12% and samples were run at 120 V for a period of 4-6 hours. Different buffer systems were used in accordance with the enzyme systems used during different parts of the procedure (gel preparation, sample running, and staining). Genetic variation was assessed using conventional horizontal starch gel electrophoresis and 16 enzymes coded for 22 presumptive loci were analyzed.

Homogenates obtained from muscle were processed for the following enzymatic proteins: a-glycerophosphate dehydrogenase (E.C. 1.1.1.8; α-GPDH-1 and α-GPDH-2), sorbitol dehydrogenase (E.C.1.1.1.14; SD), lactate dehydrogenase (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-M and ME-S), isocitrate dehydrogenase (E.C. 1.1.1.42; IDH-1 and IDH-2), glyceraldehyde-phosphate dehydrogenase (E.C. 1.2.1.12; GPD), superoxide dismutase (E.C. 1.15.1.1; SOD-1 and SOD-2), xanthine dehydrogenase (E.C. 1.2.1.37; XDH), hexokinase (E.C. 2.7.1.1; HK), adenylate kinase (E.C. 2.7.4.3; AK-1 and AK-2); phosphoglucomutase (E.C. 2.7.5.1; PGM), aldolase (E.C. 4.1.2.13; ALD), fumarase (E.C. 4.2.1.2, FUM), mannose phosphate isomerase (E.C. 5.3.1.8; MPI), and glucose phosphate isomerase (E.C. 5.3.1.9; GPI).

Allozymic data were analyzed as allele frequencies with Biosys-2 (BLACK 1997; the original version Biosys-1 v.1.7 program of SWOFFORD, SELANDER 1981, and modifications to HDYWBG, FSTAT BY WILLIAM C. Black IV). Genetic variation between intra-specific sub-populations was estimated as mean heterozygosity per locus (*Ho* = observed and *He* = expected and frequencies of heterozygotes under Hardy-Weinberg equilibrium NEI, 1978), proportion of polymorphic loci in the population (a locus was considered polymorphic if the frequency of the common allele was ≤ 0.95), and mean number of alleles per locus. The Fstat program was used to calculate overall and population-specific Wright's F-statistics estimators, including 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. According to the NEI, CHESSER (1983) correction, negative values were considered zero. Estimates of overall gene flow between populations (Nm) were derived from the approximation $F_{ST} = 1/(1 + 4Nm)$, as recommended by SLATKIN, BARTON (1989). The amount of genetic divergence between sub-populations was estimated with the indices of standard genetic identity (I) and distance (D, Nei unbiased distance) proposed by NEI (1978). A dendrogram of the genetic similarity between the sub-populations was constructed using the unweighted pair group method with arithmetic mean UPGMA (SNEATH, SOKAL 1973, ROHLF 2000).

Table 1. Sampling sites, number of specimens (N) and abbreviations for geographic localities (sub-populations) of *Rattus norvegicus* studied. See Fig. 1 for the distribution of localities; RN: *Rattus norvegicus*.

Sub-populations	N	Locations
RN1	14	Ankara
RN2	7	Black Sea (Zonguldak, Samsun)
RN3	8	Turkish Thrace
RN4	4	Iğdır

Results

Habitat and Fur Colour

The wild rat is distributed throughout Turkey, but its abundance is dependent upon habitat requirements, which vary widely. Fieldwork for the present study was performed throughout Turkey. The specimens were captured mostly in the Black Sea coastal region and in city centers in Central Anatolia (Fig. 1). The sub-populations in Turkish Thrace and the costal zone of the Black Sea region prefer moist ground under thistle bushes, whereas in Central Anatolia they primarily occupy city centers. Despite intensive fieldwork in the Mediterranean region, no wild rat specimens were captured. The dorsal fur of the examined specimens varied from dark brownish to ochre. The ventral fur was white or grayish white, and the line of demarcation along the flanks was fairly distinct.

Allozymic Patterns

According to the allozymic patterns, 8 of the 22 loci were polymorphic in the 4 sub-populations of *R. norvegicus*; others were monomorphic and fixed for the same allele. The frequencies of polymorphic loci (*Pgm, Hk, Me-M, Ldh,* α-*Gpdh-1,* α-*Gpdh-2, Fum,* and *Xdh*) are summarized in Table 2. *Pgm* was polymorphic in the RN1, RN2, and RN3 sub-populations, *Hk* was polymorphic in RN1, RN2, and RN4, *Me-M* in RN4, *Ldh* in RN1, α-*Gpdh-1* and , α-*Gpdh-2* in RN1 and RN4, Fum in RN1 and RN3, *and Xdh* in RN2 and RN3. Allozymic patterns did not appear to be location-specific or related to the geographic proximity of the groups, and the polymorphic loci were mostly spread throughout all sub-populations, except for *Ldh* and *Me-M*. (Table 2). A general trend seems to characterize these populations of *R. norvegicus*, which are polymorphic to different degrees. In particular, the RN2 and RN3 populations are less polymorphic than RN1 and RN4. This is supported by all three statistics: A (average number of alleles per locus), P (proportion of polymorphic loci) and H (average number of heterozygous individuals).

Genetic Variation

Mean heterozygosity per locus and mean heterozygosity expected under Hardy-Weinberg equilibrium were *Ho* = 0.007 and *He* = 0.058, respectively,

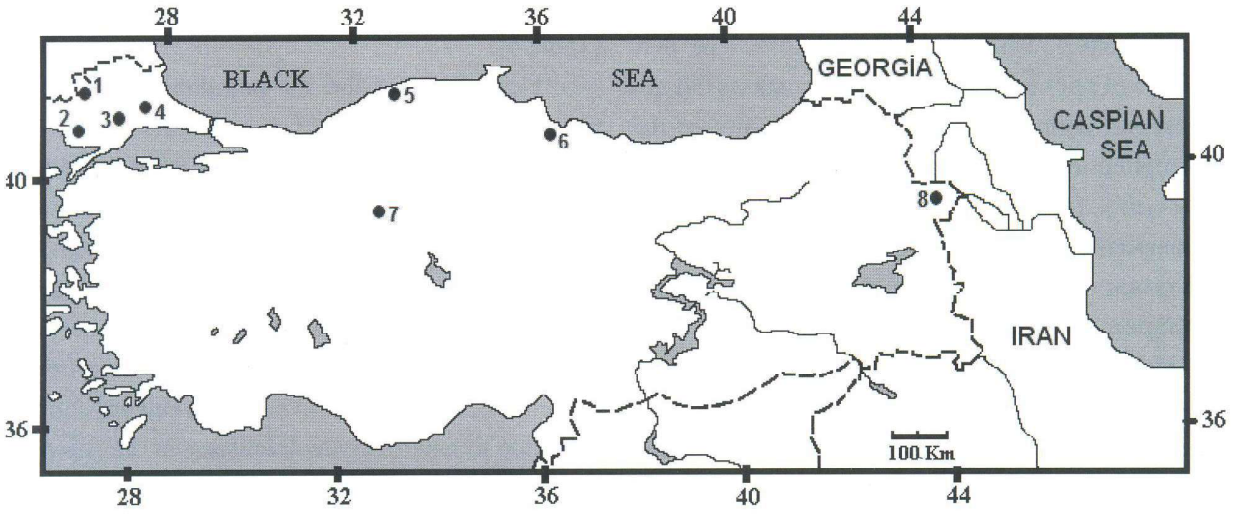

Fig 1. *Rattus norvegicus* collection sites in Turkey. 1-4: Thrace (1: Edirne; 2: İpsala; 3: Tekirdağ; 4: Saray); 5-6: Black Sea (5: Zonguldak; 6: Samsun); 7: Ankara; 8: Iğdır.

Table 2. Allele frequencies of eight polymorphic loci analyzed in *Rattus norvegicus* sub-populations in Turkey.

Lokus	RN1	RN2	RN3	RN4
Pgm1				
A	0.857	0.929	0.938	1.000
B	0.143	0.071	0.063	0.000
Hk				
A	0.607	0.786	1.000	0.250
B	0.393	0.214	0.000	0.750
Me-M				
A	1.000	1.000	1.000	0.750
B	0.000	0.000	0.000	0.250
Ldh				
A	0.929	1.000	1.000	1.000
B	0.071	0.000	0.000	0.000
α-Gpdh-1				
A	0.786	1.000	1.000	0.750
B	0.214	0.000	0.000	0.250
α-Gpdh-2				
A	0.214	0.000	0.000	0.250
B	0.786	1.000	1.000	0.750
Fum				
A	0.857	0.000	0.875	1.000
B	0.143	1.000	0.125	0.000
Xdh				
A	0.000	0.143	0.000	1.000
B	1.000	0.857	0.750	0.000
C	0.000	0.000	0.250	0.000

ranging from 0.034 to 0.084 in the sub-populations studied (Table 3). Overall mean percentage of polymorphic loci for all sub-populations was 18.2 and ranged from 13.6 to 27.3. The highest value was for RN1 (Ankara) and the lowest was for RN2 (Black Sea) and RN3 (Thrace) sub-populations. The percentages of polymorphic loci at the locations did not correspond with the geographical proximity of the sub-populations. Overall mean number of alleles per locus was 1.18, ranging from 1.1 to 1.3 among the sub-populations (Table 3). The sub-populations of wild rat significantly deviated from Hardy-Weinberg equilibrium for *Hk*, *Fum*, α-*Gpdh*-1-2, *Xdh, Ldh, and Me-M* loci, and also showed a significant deficit of heterozygotes. The loci that deviated from Hardy-Weinberg expectations were as follows: *Hk* deviated in RN1 and RN4; *Fum* in RN1 and RN3; *α-Gpdh*-1-2 in RN1 and RN4; *Xdh* in RN2 and RN3; *Ldh* in RN1; *MeM* in RN4. Contingency chi-square analysis of all polymorphic loci indicated that there was substantial differentiation between the sub-populations. The polymorphic loci, except for *Pgm* in all sub-populations and *Hk* in RN2 and RN3 were significantly different between the sub-populations (Table 4).

F-statistics for the sub-populations were used to examine the amount of genetic variation within the sub-populations and are summarized in Table 5. Mean value for the individual inbreeding coefficient was $F_{IS} = 0.86$, which reflects the somewhat high level of deviation of the total population from the genotype frequency via non-random breeding between sub-populations of wild rat. This value also provides evidence of deviation from Hardy-Weinberg equilibrium due to heterozygote deficiency in the sub-populations. Mean value of the overall individual coefficient was $F_{IT} = 0.91$; this value also corresponds to low-level gene flow between sub-populations and

Table 3. Genetic variability at 22 loci in analysed geographic samplings of *Rattus norvegicus* in Turkey. Mean sample size per locus, mean number of alleles, locus, percentage of polymorphic loci, and observed (*Ho*) and expected (*He*) heterozygosities based on NEI (1978).

Sub-populations	N	Mean number of alleles per locus	Percentage of polymorphic loci*	Mean heterozygosity (*Ho*)	Mean heterozygosity (*He*)**
RN1	14	1.3 (0.1)	27.3	0.010 (0.007)	0.084 (0.035)
RN2	7	1.1 (0.1)	13.6	0.013 (0.009)	0.035 (0.021)
RN3	8	1.1 (0.1)	13.6	0.006 (0.006)	0.034 (0.021)
RN4	4	1.2 (0.1)	18.2	0.000 (0.000)	0.078 (0.036)

Standard errors in parentheses. * A locus is considered polymorphic if the frequency of the most common allele does not exceed 0.95; ** Unbiased estimate (NEI 1978).

indicates reduced heterozygosity due to non-random mating in the sub-populations.

Mean value of the fixation index (F_{ST}) for 8 variable loci was 0.34, which indicates 34% of the genetic variation due to the differentiation between the sub-populations and reflects considerable genetic differentiation. Apart from *F*-statistics, WRIGHT (1943) produced a formula (F_{ST} = 1/(4Nm + 1) that is used to estimate gene flow between sub-populations (where Nm = number of migrants). According to this formula, gene flow was determined to range from 0.15 (*Fum*) to 8.28 (*Pgm*) among the sub-populations, with a mean of 0.49. This value suggests that gene flow between sub-populations was low and that the some isolation mechanisms are likely preventing the flow of genes between the sub-populations of *R. norvegicus*.

Genetic Distance

NEI'S (1978) unbiased genetic identity (I) and distance (D) values were computed among the sub-populations of wild rat for all pair-wise comparisons from the allele frequencies of the 22 loci. D values were relatively low among the sub-populations of Turkish wild rat. This result offers reliable evidence of very low gene flow between the Turkish wild rat sub-populations and is consistent with the F_{ST} value.

The value of genetic distance among the *R. norvegicus* sub-populations were the highest (D = 0.105) between RN2 and RN4, the lowest (D= 0.012) between RN3 and RN1. D values were not related to the geographic proximity of the sub-populations (Table 6). The UPGMA dendrogram summarizes the genetic relationships between the sub-populations (Figure 2). The sub-populations of *R. norvegicus* in Turkish Thrace and Ankara (Anatolia) established the first sub-cluster and were close to each other (D = 0.012). Black Sea sub-population (RN2) was connected to RN1 and RN3, with genetic distances of D = 0.041 and 0.039, respectively. The Iğdır sub-population (RN4) gradually connected to this cluster. According to the UPGMA cluster, RN4 appeared to be the most divergent sub-population of Turkish wild rat.

Discussion

Turkish wild rats have no marked colour variation in either their dorsal or ventral fur, and our morphological descriptions are mostly consistent with those of MILLER (1912), ONDRIAS (1966), and HARRISON, BATES (1991). In contrast to the high allelic polymor-

Table 4. Chi-square test for deviation from Hardy-Weinberg equilibrium and significance test using exact probabilities. *A locus shows deviation from Hardy-Weinberg equilibrium.

Groups	Locus	Allel	*Ho*	*He*	χ2	DF	P	Exact test P
Ankara RN1	*Hk*	AA	8	5.037	11.123*	1	0.001	0.002
		AB	1	6.926				
		BB	5	2.037				
	Ldh	AA	13	12.037	27.040*	1	0.000	0.037
		AB	0	1.926				
		BB	1	0.037				
	Gpdh-1	AA	11	8.556	16.343*	1	0.000	0.001
		AB	0	4.889				
		BB	3	0.556				
	Gpdh-2	AA	3	0.556	16.343*	1	0.000	0.001
		AB	0	4.889				
		BB	11	8.556				
	Fum	AA	12	10.222	18.087*	1	0.000	0.004
		AB	0	3.556				
		BB	2	0.222				
Blacksea RN2	*Xdh*	AA	1	0.077	13.091*	1	0.000	0.077
		AB	0	1.846				
		BB	6	5.077				
Thrace RN3	*Fum*	AA	7	6.067	15.077*	1	0.000	0.067
		AB	0	1.867				
		BB	1	0.067				
	Xdh	AA	6	4.400	10.182*	1	0.001	0.015
		AB	0	3.200				
		BB	2	0.400				
Iğdır RN4	*Hk*	AA	1	0.143	7.200*	1	0.007	0.143
		AB	0	1.714				
		BB	3	2.143				
	Me-M	AA	3	2.143	7.200*	1	0.007	0.143
		AB	0	1.714				
		BB	1	0.143				
	Gpdh-1	AA	3	2.143	7.200*	1	0.007	0.143
		AB	0	1.714				
		BB	1	0.143				
	Gpdh-2	AA	1	0.143	7.200*	1	0.007	0.143
		AB	0	1.714				
		BB	3	2.143				

phism in the sub-populations, fur colour was uniform in the specimens examined. This might have been due to similar habitat requirements among the sub-populations. There are relatively few reports with which to elucidate the genetic diversity of the natural wild rat, which also provides controversy concerning genetic variation. Serov (1972) reported that there is no evidence of polymorphism at 20 loci in the Siberian wild rat, but some other researchers reported various degrees of polymorphism in different sub-populations (Erikkson *et al.* 1976, Pasteur *et al.* 1982, Yamada *et al.* 1993). The allozyme differences appeared in the previous reports might be due to differences in the numbers of loci studied. Apart from natural sub-populations, the degree of genetic polymorphism was also reported in inbred strains and mostly on esterase variations (Van Zutphen *et al.* 1981, Bender *et al.* 1994).

Table 5. F-statistics of variable loci in the sub-populations of *R. norvegicus* calculated using the method of WRIGHT (1965).

Loci	F_{IS}	F_{IT}	F_{ST}	Nm
Pgm1	0.2445	0.2667	0.0293	8,2824
Hk	0.8102	0.8565	0.2442	0,7738
Me-M	1.0000	1.0000	0.2266	0,8533
Ldh	1.000	1.000	0.0424	5,6462
α-Gpd-1	1.0000	1.0000	0.1161	1,9033
α-Gpd-2	1.0000	1.0000	0.1161	1,9033
Fum	1.0000	1.0000	0.6285	0,1478
Xdh	1.0000	1.0000	0.5949	0,1702
Mean	0.86	0.91	0.34	0,49

Table 6. Values of NEI's (1978) unbiased genetic distance (D: below the diagonal) and identity (I: above the diagonal) between the *R. norvegicus* sub-populations (Based on NTSYS).

Sub-populations	RN1	RN2	RN3	RN4
RN1	*****	0.959	0.988	0.944
RN2	0.041	*****	0.961	0.895
RN3	0.012	0.039	*****	0.928
RN4	0.056	0.105	0.072	*****

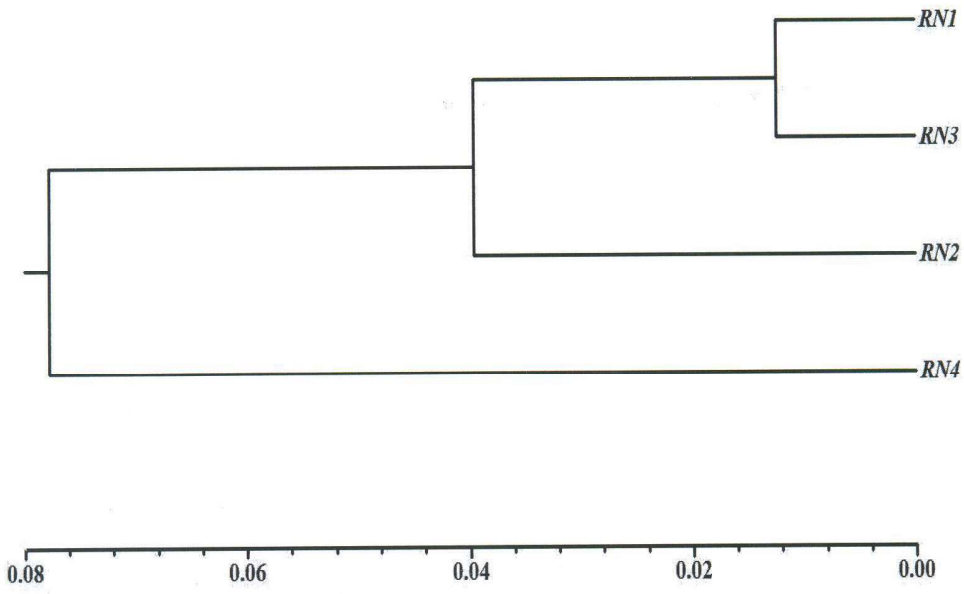

Fig 2. UPGMA dendrogram summarizing the genetic relationships between the *R. norvecigus* sub-populations studied. D = Nei's (1978) unbiased genetic distance, based on 22 enzyme loci. The coefficient of cophenetic correlation is 1.00.

In the present study total genetic variation in the sub-populations of Turkish wild rat was measured according to mean number of alleles per locus (A = 1.18), level of genetic polymorphism (P = 18.2), and mean heterozygosity per locus observed (*Ho*) (range: 0.0 for RN4 to 0.010 for RN1). Genetic polymorphism was greatest in the sub-population of Turkish Thrace (P = 27.3). Erikkson *et al.* (1976) studied enzyme polymorphism in 2 feral sub-populations, and 3 outbred, and 3 inbred strains in Finland. They observed polymorphism in *Es-1*, *Es*-2, *Es*-3, *Fum*, *G-3-pdh*, α-*Gpdh*, 6-*Pghd*, and *Xdh* loci and reported a mean heterozygosity of 0.056 and 0.074 in Helsinki and Janakkala sub-populations, respectively. In Turkish sub-populations, *Fum*, α-*Gpdh*, and *Xdh* loci similarly appeared to be polymorphic, but mean heterozygosity was markedly lower than previously reported. In the Montpellier sub-population (France), wild rat was reported to be polymorphic at 5 loci (*Got-1*, *Hpd*, *Mdh*-2, *Mpi*, and *6-Pgd*) (Pasteur et al., 1982). In contrast to these loci, *Mdh*-2 and *Mpi* were monomorphic in the Turkish sub-populations and were fixed to the same alleles. According to Yamada *et al.* (1993), 6 loci (*Acon-1*, *Es-1*, *Es-2*, *Es-4*, *Lap-1*, and *Pep-3*) in wild rats were polymorphic by two alleles, with 6 heterogeneous loci in Oita city (Japan). They also observed an interesting polymorphism of the *Es*-4 locus with high frequency, which is very rare in laboratory wild rats. The high level of polymorphism in the loci was similar to that in the sub-populations of the Turkish wild rat.

When compared to reported values for other rodents the mean value of polymorphic loci in the wild rat sub-populations (P = 18.2) is higher than those measured in the genus *Sylvaemus* in western Anatolia (Filipucci *et al.* 1996) and *Mesocricetus auratus* (P = 5.9) (Yiğit et al., 2007), *Rattus rattus* (P = 15.1) (Yiğit et al., 2008), but lower than in *Mus musculus domesticus* (P = 25) (Britton-Davidian, 1990) and *Mesocricetus brandti* (P = 29.4) (Yiğit *et al.* 2007). Nevo (1978) estimated the mean heterozygosity for 44 small rodents to be 0.038, with values ranging from 0 to 0.106. This value for the Turkish wild rat was in the range of small rodents but markedly lower than the mean value reported. Cramer *et al.* (1988) reported that the degree of gene diversity for non-alloantigenic loci scattered throughout the rat genome was 0.215. They also reported large and consistent levels of diversity for individuals within each sub-population, suggesting that significant deviation due to random mating occurred within each group. The low mean heterozygosity in the Turkish sub-populations might have been due to a relatively small or unequal number of specimens in each group studied; however, deviation from Hardy-Weinberg predictions indicates a deficit of heterozygotes due to several factors, including natural selection, non-random breeding, the Wahlund effect, and null alleles.

Estimates of *F*-statistics for the Turkish sub-populations also indicate deviation of genotype frequency via non-random breeding between sub-populations (F_{IS}), the level of non-random mating within the sub-populations (F_{IT}), and genetic differentiation via genetic drift between the sub-populations (F_{ST}). Wright (1978) used the following groupings to evaluate F_{ST} values: the range 0-0.05 indicates little genetic differentiation, 0.05-0.15 indicates moderate differentiation, 0.15-0.25 indicates high genetic differentiation, and values greater than 0.25 indicate very high genetic differentiation. According to these criteria, the F_{ST} value (0.34) we observed between the sub-populations of the Turkish wild rat is indicative of very high genetic differentiation. F_{ST} and Nm values also indicate very low gene flow between the sub-populations. The genetic distances (Nei 1978) between the subpopulations of the Turkish wild rat were relatively low. The highest genetic distance was between RN2 and RN4. The genetic distance did not appear to correspond to geographical proximity. Allozyme results also show that local differences in the wild rat sub-populations were due to genetic variation. Based on these results, determining the genetic diversity and bottleneck, especially between the Thrace (RN1) and Anatolian (RN2, RN3 and RN4) sub-populations, will require further research that focuses on the use of genetic markers such as mitochondrial DNA or microsatellite loci.

Conclusion

The present study's findings contribute to our knowledge of the genetic diversity of the Turkish wild rat, which has high percentages of polymorphic loci in the sub-populations, but relatively low Nm values. The lack of gene flow between the sub-populations of the Turkish wild rat, based on Hardy-Weinberg predictions, may be due to the existence of high genetic variation in the local sub-populations, known as the Wahlund effect; therefore, the Wahlund effect may be considered a genetic bottleneck for the Turkish wild rat and the high percentages of polymorphic loci in the sub-populations might also represent the potential for local sub-populations to give rise to a new taxonomic unit.

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References

Bender K., P. Balogii, M.F. Bertrand, M. Den Bieman, O. Von Deimling, S. Eghtessadi, G. A. Gutman, H. J. Hedrich, S. V. Hunt, R. Kluge, K. Matsumoto, D. H. Moralejo, M. Nagel, A. Portal, C. M. Prokop, R.T. Seibert and L. F. M. Van Zutphen 1994. Genetic characterization of inbred strains of the rat (*Rattus norvegicus*). – *Journal of Experimental Animal Science*, **36:** 151–165.

Bender K., S. Bissbort and R. Brdicka 1985. Studies on some selected protein polymorphisms in inbred and wild rats. – *Transplantation Proceedings*, **17:** 1872-1874.

Black W. C. 1997. A computer program for the analysis of allelic variation in genetics. Modification of original version (Biosys-1) by D. L. Swofford & R. B. Selander. Available at: wcb4@lamar.colostate.edu.

Britton-Davidian J. 1990. Genetic differentiation in M. m. domesticus populations from Europe, the Middle East and North Africa: geographic patterns and colonization events. – *Biological Journal of the Linnean Society*, **41:** 27-45.

Cramer D. V., A. Chakravarti, O. Arenas, J. Humprieres. and P. A. Mowery 1988. Genetic diversity within and between natural populations of *Rattus norvegicus*. – *Journal of Heredity*, **79:** 319-324.

Eriksson K., O. Halkka, J. Lokki, and A. Saura 1976. Enzyme polymorphism in feral, outbred and inbred rats (*Rattus norvegicus*). – *Heredity*, **37** (3): 341–349.

Filipucci M. G., G. Storch and M. Macholan 1996. Taxonomy of genus *Sylvaemus* in western Anatolia morphological and electrophoretic evidence (Mammalia: Rodentia, Muridae). – *Senckenbergiana Biologica*, **75:** 1–14.

Harris H., D. A. Hopkinson 1976. Handbook of enzyme electrophoresis in human genetics. American Elsevier Publishing Company, Inc.

Harrison D. L., P. J. J. Bates 1991. The mammals of Arabia. Harrison Zoological Museum Publication, Sevenoaks (Kent). 354 p.

Ingrid K., V. Birger and K. Peter 1997. Comparison of genetic variability at microsatellite loci in wild rats and inbred rat strains. – *Mammalian Genome*, **8:** 589-591.

Innes J. G. 1990. Ship rat. In: King, C.M. (Ed.), The handbook of New Zealand Mammals. Oxford University press, Auckland, Melbourne, Oxford, New York. 206-225.

Kumar B. K., N. V. Bhanu, M. V. Rao and G. Nappanveettil 2007. DNA Fingerprinting and Phylogenetic Analysis of WNIN Rat Strain and Its Obese Mutant Using Microsatellite Markers. – *Biochemical Genetics*, **45:** 77-91.

Miller G. S. 1912. Catalogue of the Mammals of Western Europe. Printed by British Museum, London. 848 -863.

Musser G. G., M.D. Carleton 2005. Family Muridae. – In: Wilson DE, Reeder DM, (Eds.): Mammal Species of the World: A Taxonomic and Geographic Reference. The Johns Hopkins University Press, Baltimore, 894-1531.

Nei M., R. K. Chesser 1983. Estimation of fixation indices and gene diversities. – *The Annals of Human Genetics*, **47:** 253–259.

Nei M. 1978. Estimation of average heterozygosity and genetic distance from a small number of individuals. – *Genetics*, **89:** 583-590.

Nevo E. 1978. Genetic variation in natural populations: patterns and theory. – *Theoretical Population Biology*, **13:** 121–177.

Ondrias J. C. 1966. The taxonomy and geographical distribution of the rodents of Greece. – *Säugetierkundliche Mitteilungen*, **14:** 1-136.

Pasteur N., J. Worms, M. Tohari and D. Iskandar 1982. Genetic differentiation in Indonesian and French rats of the subgenus *Rattus*. – *Biochemical Systematics and Ecology*, **10:** 191-196.

Robins J. H., P. A. Mclenachan, M. J. Phillips, L. Craig, H. A. Ross, E. Matisoo-Smith 2008. Dating of divergences within the *Rattus* genus phylogency using whole mitochondrial genomes. – *Molecular Phylogenetics and Evolution*, **49:** 460-466.

Rohlf F. J. 2000. NTSYS – pc, version 2.1. Numerical Taxonomy and Multivariate Analysis System. Exeter Publishing, Ltd.

Schlick N. E., M. I. Jensen-Seaman, K. Orlebeke, A. E. Kwitek, H. J. Jacob and J. Lazar 2006. Squences analysis of the complete mitochondrial DNA in 10 commonly used inbred rat strains. – *American Journal Physiology Cell Physiology*, **291:** C1183-C1192.

Serov O. L. 1972. Monomorphic state of some structural genes in populations of wild and laboratory rats (*Rattus norvegicus*). – *Dokl. Akad. Nauk.* SSSR, **204:** 978-979.

Shaw C. R.., R. Prasad 1970. Starch gel electrophoresis of enzymes – A compilation of recipes. – *Biochemical Genetics*, **4:** 297-320.

Slatkin M., N. Barton. 1989. A comparison of three indirect methods for estimating average level of gene flow. – *Evolution*, **43:** 1349-1368.

Sneath, P. H. A., R. R. Sokal 1973. Numerical Taxonomy. W. H. Freeman, San Francisco.

Swofford D. L., R.B. Selander 1981. Biosys-1: A Fortran program for the comprehensive analysis of electrophoretic data in population genetics and systematics. – *Journal of Heredity*, **72:** 281-283.

Watts C., P. R. Baverstock 1995. Evolution in the Murinae (Rodentia) assessed by microcomplement fixation of albumin. – *Australian Journal Zoology*, **43:** 105-118.

Wright S. 1943. Isolation by distance. – *Genetics*, **28:** 114-138.

Wright S. 1951. The genetical structure of populations. – *Annual Eugenics*, **15:** 323-354.

Wright S. 1965. The interpretation of population structure by F-statistics with special regard to systems of mating. – *Evolution*, **19:** 395-420.

Wright S. 1978. Evolution and the genetics of populations. Vol. 4. Variability within and among natural populations. Chicago, University of Chicago.

Yamada T., D. Moralejo, K. Tsuchiya, T. Agui and K. Matsumoto 1993. Biochemical Polymorphisms in wild rats (*Rattus norvegicus*) captured in Oita City, Japan. – *Journal Veterinary Medicine Science*, **55** (4): 673-675.

Yiğit N., E. Çolak, M. Sözen and Ş. Özkurt 1998. The taxonomy and karyology of *Rattus norvegicus* (Berkenhout, 1769) and *Rattus rattus* (Linnaeus, 1758) (Rodentia: Muridae) in Turkey. – *Turkish Journal of Zoology*, **22:** 203-212.

Yiğit N., E. Çolak, M. Sözen, Ş. Özkurt and R. Verimli 2000. The distribution morphology,and karyology of the genus *Mesocricetus* (Mammalia: Rodentia) in Turkey. – *Folia Zoolgica*, **49** (3): 167-174.

Yiğit N., R. Verimli, E. Çolak, M. Sözen and Ş. Özkurt 2001. Blood-serum proteins of *Rattus rattus* and *Rattus norvegicus* (Mammalia: Rodentia) in Turkey. – *Turkish Journal of Biology*, **25:** 83–88.

Yiğit N., T. Kankiliç, R. Çolak, E. Çolak, R. Gatterman, K. Neumann, Ş. Özkurt and M.G. Moradi 2007. Allozyme variations and genetic differentiation in *Mesocricetus brandti* Nehring, 1898 and *Mesocricetus auratus* (Waterhouse, 1839) (Mammalia: Rodentia).– *Turkish Journal of Zoology*, **31:** 219-228.

Yiğit N., E. Çolak, I. Kandemir, T. Kankiliç, R. Çolak, Ş. Bulut, P. Çam, F. Saygili, M. Sözen and Ş. Özkurt 2008. Allozyme variation in *Rattus rattus* (Rodentia: Muridae) in Turkey, with particular emphasis on the taxonomy. – *Zoology in the Middle East*, **45:** 19-28.

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Алозимна вариация при диви плъхове *Rattus norvegicus* (Berkenhout, 1769) (Mammalia: Rodentia) от Турция

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(Резюме)

Изследвано е генетичното разнообразие на 22 локуса на 33 плъха *Rattus norvegicus* от 4 субпопулации. Осем от тези 22 локуса (*Pgm, Hk, Me-S, Ldh, α-Gpdh-1, α-Gpdh-2, Fum, Xdh*) бяха полиморфни. Нивото на генетичното вариране беше измерено чрез средния брой алели за локус (A = 1.18), процента на полиморфните локуси (P = 18.2), наблюдаваната средна хетерозиготност за локус (*Ho* = 0.007) и очакваната средна хетерозиготност по Харди-Вайнберг (*He* = 0.057).

Средната стойност за F_{ST} беше 0.34, показвайки 34% генетично вариране и предполагайки висока диференциация между субпопулациите на *Rattus norvegicus*. Броят на мигрантите (Nm) беше 0.48 и показва, че генният поток между субпопулациите е сравнително слаб. Въпреки това беше наблюдавано високо ниво на генетично вариране, ниска стойност на Nm и *Ho* , което може да бъде доказателство за ефект Wahlund или генетично ограничение за субпопулациите. Предполага се също така, че може да има фактори, които да предпазват от изтичане на гени от субпопулациите, което да съставлява техният собствен генетичен потенциал за нови таксономични единици.

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