

Influence of climatic factors on genetic diversity of midday gerbil (*Meriones meridianus* Pallas, 1773)

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Received: 13 August 2012

Accepted after revision: 13 December 2012

Environmental factors are considered important in shaping the genetic diversity of animal populations. Mitochondrial DNA sequences of cytochrome b gene (Cyt-b) of 264 midday gerbils (*Meriones meridianus* Pallas, 1773) from 21 populations were used to investigate the genetic structure and the relationship between genetic diversity and climatic factors. The results showed that the populations were divided into two clades by the Tian Shan Mountains and significant differentiation was found between most populations. The genetic diversity showed a significant relationship with the variation coefficients for sunshine hours and wind speed. The variation coefficients for annual mean temperature, precipitation, and wind speed were negatively related to nucleotide diversity. We conclude that environmental barriers have limited the gene flow between populations and have played a role on the observed phylogenetic pattern. Sunshine hours and wind speed have important effects on nucleotide diversity in midday gerbils, in terms of energy conservation, search for food in winter, reproduction, and mortality. Thus, unstable environments could lead to a decline in genetic diversity and disappearance of individuals that do not adapt to fluctuating environments.

Key words: *Meriones meridianus*, mtDNA Cyt-b, genetic diversity, climatic fluctuations.

INTRODUCTION

The persistence of a species depends on its vulnerability to environmental changes which is determined by its genetic constitution and physiological tolerance (Lynch & Lande, 1993). The impact of climatic fluctuations on the distribution and divergence of species may vary extensively according to different species habitats (Voje *et al.*, 2009). Populations of species are dynamic units and adapt to their environment both physiologically and genetically. Natural selection that favours adaptation to local environmental conditions could lead to genetic differentiation among local populations (Slatkin, 1987). Genetic markers have been used to assess whether environmental changes influence the pattern of genetic diversity in populations of some species. For instance, one study found that the genetic diversity of chukar partridge (*Alectoris chukar*) decreased with a decrease in latitude, altitude, and variation coefficients of temperature and rainfall

clines, but increased with an increase in longitude, rainfall, and temperature (Huang *et al.*, 2005). Another study found that the genetic diversity of the lizard *Phrynocephalus vlangalii* was lower when temperature decreased and the rainfall increased. However, the genetic diversity of the species increased with a decrease in the variation coefficients of temperature and rainfall (Jin & Liu, 2008). It seems that there is no universal pattern for understanding the relationship between climatic factors and genetic diversity. The environmental impacts on animals may be different and a certain species has its own ecological strategy for life.

Midday gerbils (*Meriones meridianus* Pallas, 1773) are commonly found in sandy areas in Mongolia and northern China and can be found as far west as the Caspian Sea (Luo *et al.*, 2000). These rodents have a strong ability to survive and adapt to environments ranging from areas with heavy rainfall to those having arid conditions. In the same way, there are populations occupying an altitudinal interval range from 150

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m below sea level to 3200 m above sea level. As a widely distributed species, midday gerbils are exposed to a variety of environmental conditions, including adverse conditions such as low temperatures, low oxygen level at high altitudes, and food shortages caused by short frost-free periods.

On the basis of the genetic structure of midday gerbils, we assume that these rodents have adaptations that enable them to inhabit and occupy a variety of habitats. However, environmental factors play a vital role when inhabiting those places. In this study, we investigated the genetic diversity and phylogeography of *M. meridianus* in China. The main objective was to examine the impacts of environmental factors on the genetic diversity in populations of midday gerbils. We also tested the potential geographic barriers that shaped the genetic diversity of different local populations.

MATERIALS AND METHODS

In total 264 midday gerbils, which were trapped from 21 collecting sites, were studied (Fig. 1 and Table 1). All the specimens were preserved in the School of Life Sciences, Lanzhou University. Muscle tissue samples were taken and stored in 95% ethanol immedi-

tely after removal. DNA was extracted from the muscle tissues by using a DNA whole genome kit (Dneasy Tissue Kit, QIAGEN). Partial mitochondrial cytochrome b (Cyt-b) sequences were amplified using two newly designed oligonucleotide primers, H1801a (5'-CTCTACTGGTTGCCCTCC-3') and L1801b (5'-TATTGACCTTCCCCTCC-3'). The PCR mixture (50 μ l) contained the following chemicals: 10 mmol l⁻¹ Tris-HCl (pH 8.3), 50 mmol l⁻¹ KCl, 75 mmol l⁻¹ MgCl₂, 100 mmol l⁻¹ dNTPs, 10 pmol l⁻¹ primers, and 100 ng of template DNA. The PCR conditions were as follows: 94 °C for 2 min; 35 cycles of 94 °C for 1 min, 49 °C for 1 min, 72 °C for 1.5 min; and 72 °C for 5 min.

The PCR products were purified and sequenced in both directions with each of the PCR primers by using an ABI 373 automated sequencer. All haplotypes were deposited in GenBank (Accession nos JQ065512-JQ065613).

Sequences were aligned using ClustalX 1.8 (Thompson *et al.*, 1997) and refined manually. Base compositional information was estimated from the aligned sequences by using MEGA5 (Tamura *et al.*, 2011). Haplotype diversity and nucleotide diversity values were calculated for groups of haplotypes to measure DNA

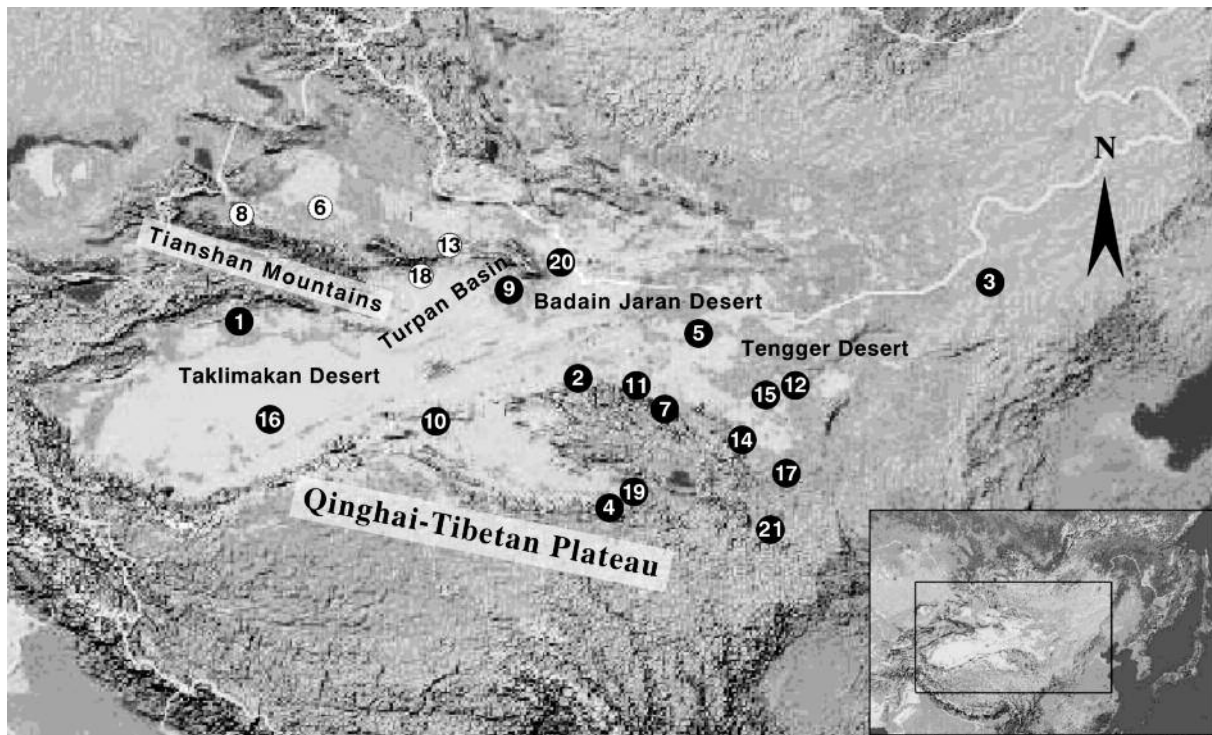


FIG. 1. Sampling locations of *Meriones meridianus* analyzed in this study. Population codes and localities are summarized in Table 1.

TABLE 1. Localities where specimens of midday gerbils (*Meriones meridianus*) were collected as well as haplotype (Hd) and nucleotide (π) diversities of each local population

Code	Locality	Sample size	Hd	π	Longitude	Latitude	Altitude (m)
1	Alar, Xinjiang	13	0.9615	0.0543	81° 48' 09"	40° 37' 19"	985
2	Anxi, Gansu	9	0.8889	0.0028	96° 17' 09"	40° 15' 08"	1365
3	Bayannaoer, Inner Mongolia	11	0.7818	0.0040	114° 29' 08"	43° 07' 02"	1087
4	Caidamo, Qinghai	15	0.7429	0.0047	97° 54'	36° 25'	2800
5	Ejinaqi, Inner Mongolia	10	0.8000	0.0022	101° 04' 47"	41° 58' 55"	920
6	Gurto, Xinjiang	18	0.9673	0.0427	83° 59' 37"	44° 40' 56"	311
7	Gaotai, Gansu	9	0.7500	0.0022	99° 54' 48"	39° 21' 03"	1347
8	Huocheng, Xinjiang	18	0.8497	0.0382	80° 35' 22"	43° 57' 51"	576
9	Hami, Xinjiang	8	0.8929	0.0036	93° 25' 34"	42° 35' 36"	555
10	Huatugou, Qinghai	8	0.7500	0.0026	90° 49' 42"	38° 14' 12"	2898
11	Jinta, Gansu	9	0.8889	0.0012	98° 55'	39° 58'	1300
12	Menggen, Inner Mongolia	11	0.8364	0.0033	103° 52' 08"	40° 00' 58"	1389
13	Mulei, Xinjiang	15	0.8857	0.0043	90° 08' 19"	44° 11' 35"	756
14	Minqin, Gansu	11	0.7635	0.0036	102° 59'	38° 34'	1375
15	Nuoergong, Inner Mongolia	10	0.8667	0.0032	104° 49' 32"	40° 10' 14"	1297
16	Qiemu, Xinjiang	12	0.8333	0.0038	84° 08' 12"	37° 45' 04"	1298
17	Shapotou, Ningxia	13	0.6282	0.0020	104° 48'	37° 25'	1400
18	Turpan, Xinjiang	26	0.5015	0.0016	89° 11' 06"	42° 51' 29"	-103
19	Wulan, Qinghai	9	0.7500	0.0042	98° 28' 51"	36° 57' 24"	3050
20	Yiwu, Xinjiang	15	0.9143	0.0056	94° 53' 29"	43° 47' 03"	422
21	Yuzhong, Gansu	14	0.6044	0.0023	104° 05'	35° 52'	1714

polymorphism by using the DnaSP program ver. 5 (Librado & Rozas, 2009). Based on the haplotypes, we constructed a neighbor joining (NJ) tree in PAUP* 4.0b10 (Swofford, 2003) using 1000 bootstrap replicates. *Tscherskia triton* (GenBank Accession no. EU 584099) and *Rhombomys opimus* (GenBank Accession no. AB381907) were used as outgroups. An analysis of molecular variance (AMOVA) (Excoffier *et al.*, 1992) was performed by using ARLEQUIN 3.1 (Excoffier *et al.*, 2005) to estimate the proportion of genetic variation at different hierarchical levels using information from the geographical distribution of haplotypes and the pairwise distances between them. The Mantel test (Mantel, 1967) was used to test for potential correlation between genetic distance ($F_{ST}/(1 - F_{ST})$) and the geographical distance (in kilometers) among populations using Excel 2003 and XLSTAT 2012 trial version.

For many species, the primary impact of climate change may be mediated through effects on synchrony with the species' food and habitat resources (Parmesan, 2006). As grazers, midday gerbils are directly dependent on primary plant productivity which is influenced by climatic factors. Diversity of soil, vegetation and geomorphologic and altitude difference, an-

nual solar radiant energy, and mean annual rainfall play a dominant role in affecting the distribution of gerbils (Zhou *et al.*, 2001). We collected meteorological data from 1981 to 2010 (30 years) for the sampling localities from the National Climatic Data Center. The data included annual mean temperature, highest annual mean temperature, mean minimum temperature, extreme high temperature, extreme minimum temperature, annual mean relative humidity, annual precipitation, annual mean wind speed, and annual sunshine hours. Latitude, longitude, and altitude are usually used as proxies of environmental factors such as temperature, air pressure, and oxygen concentration. The interactions between populations in different localities should be considered when dealing with climatic data. Coefficients of variation were obtained by calculating the ratio of means and standard deviations of 30 years meteorological data. Factor Analysis (Principal Components Analysis) was used to remove redundant (highly correlated) variables from the environmental data. We paid attention to the most highly correlated factors of the four components in rotated component matrices.

We tested the relationship between genetic diversity and environmental factors using bivariate corre-

lation analysis. We applied linear regression analyses with environmental parameters as independent variables and the genetic diversities as dependent variables to determine which of the involved independent variables would best predict the values of the dependent variables. We ran the stepwise model method, which included the factors reduced by principal components, to investigate the effect of climatic fluctuation on population genetic diversity. The variation coefficients (V) of climatic data over 30 years were compared with the genetic diversity level within each population. Calculations were performed using SPSS 16.0.

RESULTS

Cytochrome b sequence fragments with a length of 755 base pairs were obtained and were found to include 652 invariable (monomorphic) sites and 103 variable (polymorphic) sites. Mean A+T and C+G content was 60.5 and 39.5%, respectively. In 264 individuals we identified 90 haplotypes. The major haplotype was shared by 39 individuals from 10 populations (Fig. 2). Haplotype diversity (Hd) estimates were between 0.5015 and 0.9673 ($Hd \pm s.d. = 0.8028 \pm 0.1178$) and nucleotide diversity (π) ranged from 0.0012 to 0.0543 ($\pi \pm s.d. = 0.0092 \pm 0.0153$) (Table 1). The genetic diversities were significantly different among population groups (Hd: $t = 31.235$, $df = 20$, $p < 0.001$; π : $t = 2.747$, $df = 20$, $p < 0.05$).

A NJ tree of *M. meridianus* haplotypes was constructed in which the haplotypes were divided into two clades (Fig. 2). Clade A included the populations from Huocheng, Gurto, Mulei, and Turpan. Clade B included Alar, Anxi, Bayannaer, Caidamo, Ejinaqi, Gaotai, Hami, Huatugou, Jinta, Menggen, Minqin, Nuoergong, Qiemo, Shapotou, Wulan, Yiwu, and Yuzhong. Haplotypes from Alar individuals were both found in clades A and B.

An AMOVA revealed that most (77.78%) of the observed genetic variation was accounted for by with-

in population diversity whereas among population diversity explained 18.54% of variation. The proportion of variation between group A and group B was only 3.67%, although statistically significant ($p < 0.05$) (Table 2). The pairwise population differentiation (F_{ST}) ranged between 0.003 and 0.528 and most of the estimates (88.1%) were statistically significant. The Alar population, which showed the highest nucleotide diversity ($\pi = 0.0543$), was not significantly differentiated from populations of both clade A (Gurto, Huocheng) and clade B (Qiemo, Yiwu) (Table 3) indicating high levels of gene flow.

The correlation between genetic distance ($F_{ST}/(1 - F_{ST})$) and geographical distance was found to be non-significant ($r = -0.024$, $p = 0.743$) when all populations were tested together. Similar results were found when clade A ($r = -0.001$, $p = 0.989$) and clade B ($r = -0.086$, $p = 0.321$) was tested separately. The genetic differentiation in the studied populations was not positively related to physical distance.

Using a One-Way ANOVA we confirmed that all genetic diversities did not have a significant relationship (Hd: $F = 1.759$, $df = 20$, $p = 0.187$; π : $F = 0.794$, $df = 20$, $p = 0.630$) to sample size.

The significant results of the Kolmogorov-Smirnov test showed that nucleotide diversities (π) did not follow a normal distribution ($Z = 2.059$, $n = 21$, $p < 0.001$). We therefore \log_{10} -transformed them to meet the normality requirements.

Of the variability in the original 12 variables, the first four principal components explained 81.87% (Table 4, Fig. 3) and thus it considerably reduced the complexity of the data set using these components. The results indicated that the components were most highly correlated with altitude (ALT), latitude (LAT), longitude (LON), coefficients of variation of annual mean temperature (VTem), coefficients of variation of annual highest temperature (VHAT), coefficients of variation of annual precipitation (VPre), coefficients of variation of annual average wind days (VWin),

TABLE 2. AMOVA analysis of genetic variation in *Meriones meridianus* populations

Source of variation	df	Sum of squares	Percentage of variation	Fixation indices	p -value
Among groups	1	4.07	3.67	$F_{CT} = 0.0368$	< 0.05
Among populations within groups	19	28.876	18.54	$F_{SC} = 0.1925$	< 0.001
Within populations	243	93.945	77.78	$F_{ST} = 0.2222$	< 0.001
Total	263	126.89			

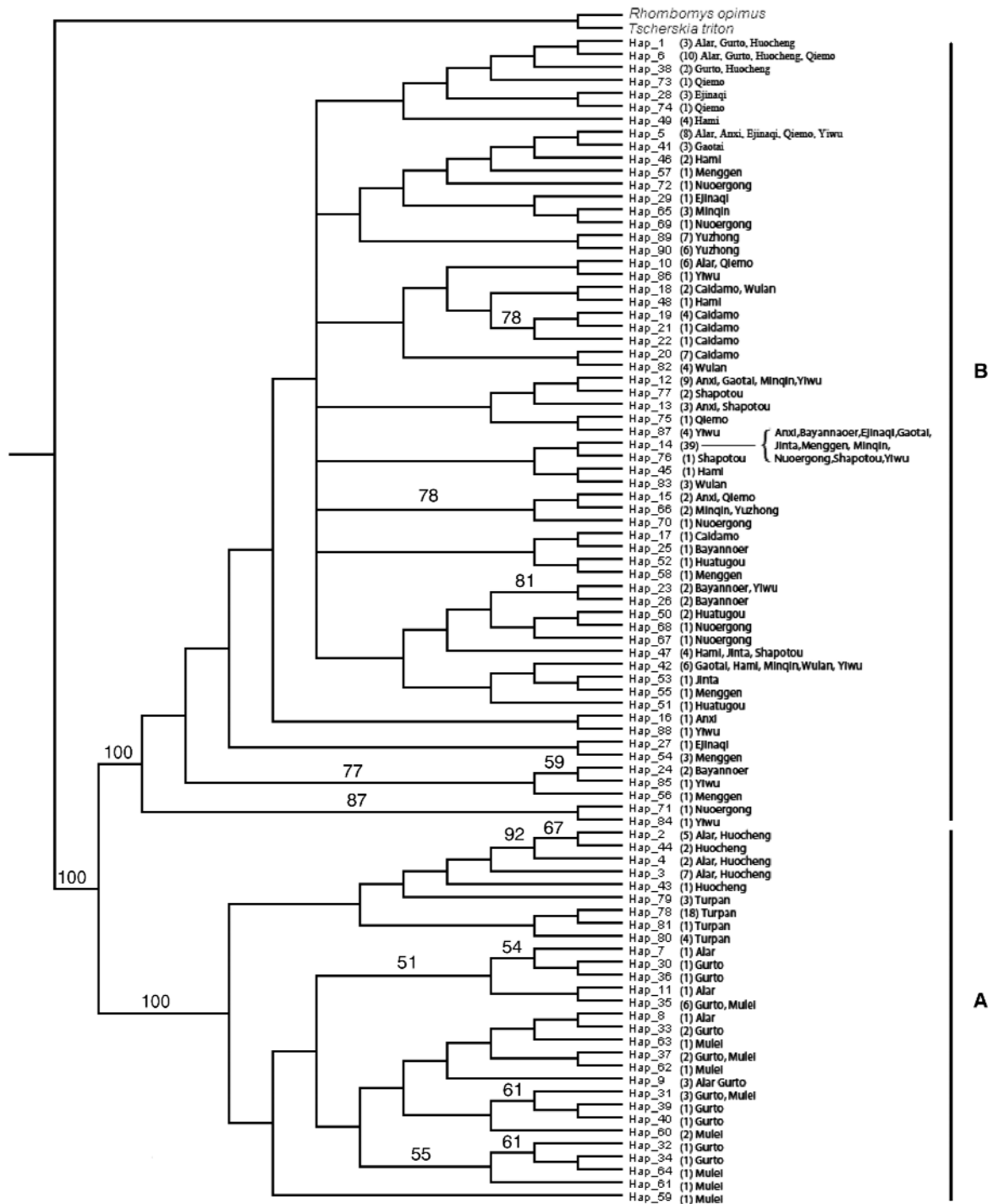


FIG. 2. NJ tree of 90 haplotypes from 264 *Meriones meridianus* specimens based on cytochrome b sequences. The numbers above the branches are bootstrap values (%; only greater than 50% are displayed) from 1000 bootstrap replicates. *Tscherskia triton* and *Rhombomys opimus* were used as outgroups. Shown are the populations to which haplotypes belong as well as the numbers of individuals in parentheses.

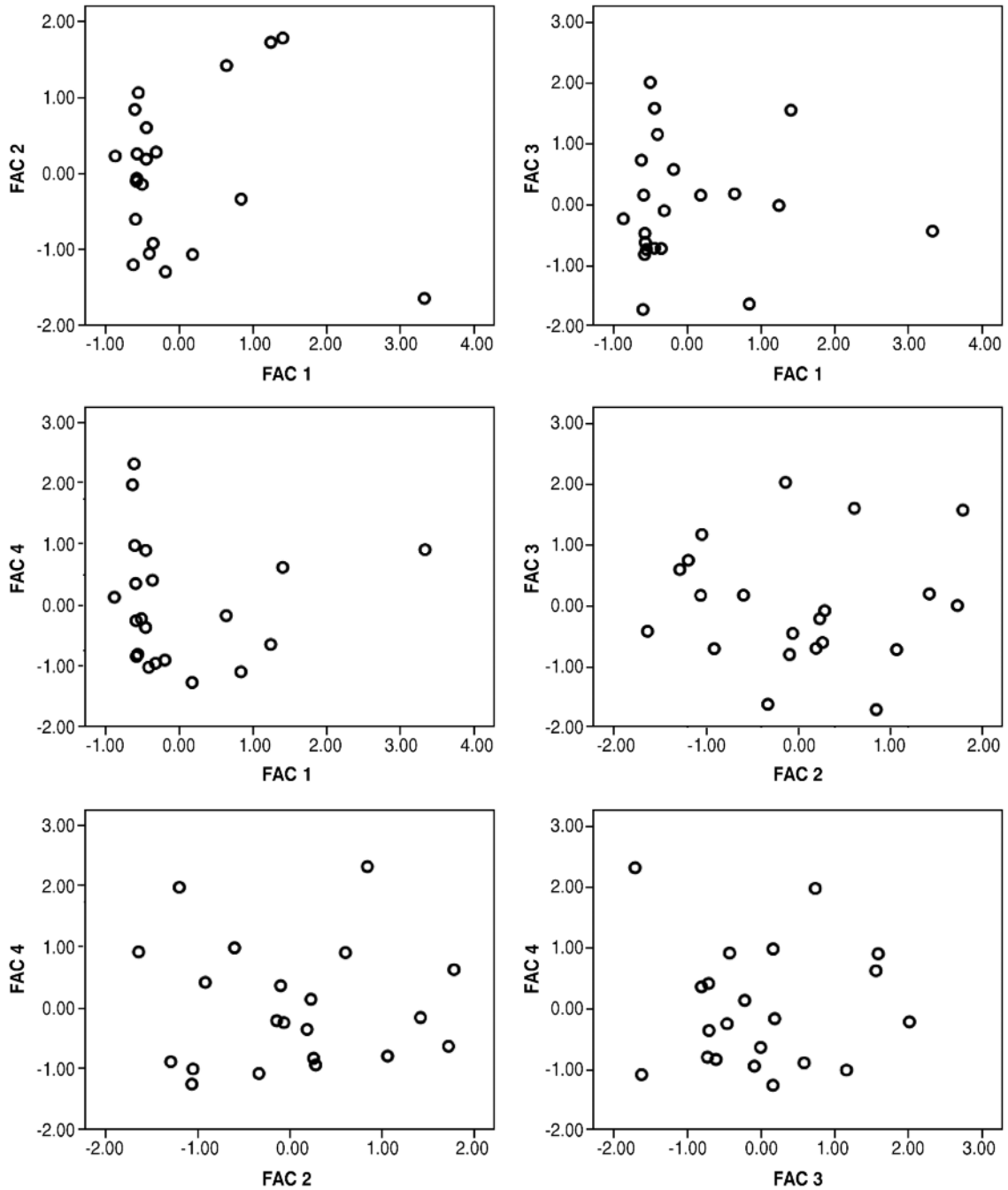


FIG. 3. The scatterplot matrix of the regression factor scores by principal component analysis based on 12 environmental variables in localities of *M. meridianus* populations.

and coefficients of variation of annual sunshine days (VSun). We focused on these environment factors in the further analyses.

Bivariate correlation analysis showed that only VWin was significantly negatively correlated to Hd while π had a negative and significant relationship to longitude and VSun (Table 5). In addition, the nucleotide diversity had a negative trend with altitude, VTem,

VPre, and VWin but none of them was significant.

During linear regression analyses, we got two models to explain the relationship between variation coefficients of environmental factors and genetic diversity. In all of the variation coefficients of environmental factors, VSun and VWin were chosen as the best predictors and they explained 55.9% of all genetic variation (Table 6).

TABLE 3. Population pairwise F_{ST} values (below diagonal) and geographic distance (Km, above diagonal) of *Mertiones meridianus*. The bold numbers are statistically significant ($p < 0.05$). The code numbers of each population are according to Table 1

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1		1228	2712	1480	1620	487	1550	371	990	819	1455	1871	793	1831	1949	379	2020	664	1503	1136	2021
2	0.065		1552	445	448	1120	323	1360	355	525	223	650	673	604	733	1090	804	659	418	411	838
3	0.126	0.122		1599	1108	2447	1292	2728	1720	2075	1348	952	1968	1093	870	2636	1042	2059	1523	1589	1199
4	0.150	0.191	0.239		678	1489	373	1694	785	659	416	659	1088	508	747	1236	635	1037	80	863	562
5	0.088	0.107	0.172	0.231		1416	310	1683	636	969	292	320	921	415	367	1520	598	990	608	600	720
6	0.017	0.069	0.120	0.142	0.110		1447	285	800	916	1335	1720	494	1717	1775	776	1921	468	1495	879	1965
7	0.138	0.024	0.193	0.254	0.216	0.131		1690	656	800	112	345	973	280	434	1392	482	978	437	645	535
8	0.020	0.133	0.182	0.202	0.173	0.069	0.194		1052	1069	1582	1979	771	1966	2049	752	2160	712	1703	1157	2199
9	0.071	0.109	0.166	0.191	0.156	0.066	0.157	0.131		533	544	923	314	922	996	959	1129	349	773	179	1184
10	0.136	0.179	0.233	0.254	0.224	0.129	0.250	0.193	0.179		728	1149	669	1072	1230	593	1233	535	687	708	1206
11	0.288	0.285	0.065	0.398	0.335	0.270	0.361	0.333	0.334	0.423		423	866	384	509	1307	588	877	336	543	643
12	0.100	0.102	0.031	0.213	0.151	0.094	0.172	0.157	0.137	0.204	0.117		1225	176	86	1742	304	1263	580	857	301
13	0.077	0.113	0.164	0.186	0.154	0.045	0.176	0.133	0.111	0.175	0.321	0.138		1244	1298	873	1444	170	1071	384	1507
14	0.135	0.103	0.026	0.247	0.181	0.128	0.158	0.190	0.156	0.243	0.079	0.042	0.172		238	1658	203	1255	436	894	317
15	0.084	0.082	0.007	0.200	0.132	0.080	0.153	0.143	0.121	0.189	0.064	0.004	0.123	0.004		1817	308	1339	661	915	487
16	0.027	0.124	0.192	0.214	0.155	0.071	0.206	0.142	0.139	0.205	0.359	0.165	0.140	0.201	0.151		1824	713	1272	1125	1796
17	0.205	0.180	0.023	0.313	0.244	0.194	0.266	0.254	0.238	0.318	0.025	0.059	0.240	0.035	0.013	0.271		1460	569	1100	184
18	0.299	0.349	0.386	0.393	0.382	0.281	0.406	0.338	0.353	0.409	0.528	0.363	0.328	0.394	0.354	0.361	0.446		1028	477	1503
19	0.138	0.181	0.233	0.248	0.224	0.131	0.241	0.194	0.157	0.250	0.417	0.205	0.176	0.235	0.190	0.206	0.316	0.406		824	515
20	0.058	0.048	0.058	0.171	0.098	0.059	0.109	0.119	0.080	0.159	0.186	0.055	0.100	0.062	0.031	0.120	0.118	0.314	0.155		1183
21	0.219	0.267	0.312	0.325	0.305	0.207	0.331	0.267	0.269	0.333	0.477	0.286	0.253	0.316	0.274	0.285	0.384	0.455	0.331	0.239	

TABLE 4. Results of principal component factor analysis showing the variance explained by the initial eigenvalues

Component	Eigenvalues	Variance (%)
1	4.102	34.18
2	2.301	19.17
3	2.028	16.90
4	1.394	11.62
5	0.712	5.93
6	0.519	4.32
7	0.349	2.91
8	0.309	2.58
9	0.147	1.23
10	0.097	0.81
11	0.027	0.23
12	0.015	0.12
total	12.000	100.00

DISCUSSION

Haplotype (Hd: 0.5015-0.9673) and nucleotide diversity (π : 0.0012-0.0543) of midday gerbils were much less than those of Mongolian gerbils (*M. unguiculatus*) (Hd: 0.25-1.00; π : 0.022-0.999) (Liang et al., 2007), a related species inhabiting semi-deserts and sandy steppes. The phylogenetic analysis showed that the midday gerbil populations were divided into two distinct clades. Clade A included populations Huocheng, Gurto, Mulei, and Turpan located mainly in the north region of Tian Shan Mountains. Clade B was quite widespread, including populations from the western edge of the Taklimakan Desert to the eastern edge of the Badain Jaran Desert. The Tian Shan Mountains have been previously reported as physical barriers for animals with significant effects on their phylo-

genetic patterns (Macey et al., 1999; Mahmut et al., 2002; Pang et al., 2003; Ludt et al., 2004; Zhang et al., 2008). The phylogenetic pattern of midday gerbils has been also affected by the Tian Shan Mountains. Most population pairwise F_{ST} values were significant demonstrating a relatively lower degree of genetic connectivity across this geographic range in China. This result is in contrast to that of Mongolian gerbils, in which no significant genetic subdivision existed between most populations (Liang et al., 2007).

Midday gerbils may have colonized China through Africa, southwest of Asia, and Turan Plain lowland via Alataw Pass (Zhou et al., 2001). This might be a possible reason that Alar population shows the highest nucleotide diversity. The results of Mantel test showed that there was no significant relationship between nucleotide diversity and geographic distance. The natural barriers might have decreased the gene flow between some of the populations. This result is supported by the NJ tree in which populations are divided into clade A and clade B by the Tian Shan Mountains. Turpan population, which is geographically close to Alar, has the lowest haplotypic diversity (Hd = 0.5015) and a very low nucleotide diversity (π = 0.0016). Turpan also lacks efficient gene flow with adjacent populations such as Mulei and Hami. This is because in Turpan basin the gravel gobi, which is an unfavorable habitat for *M. meridianus*, has possibly acted as a barrier between Turpan and other populations.

The genetic diversity of midday gerbils was significantly negatively related to VSun and VWin. A significantly positive relationship was observed between

TABLE 5. Correlation between latitude, longitude, altitude, variation coefficients of climate factors and haplotype (Hd) and nucleotide (π) diversity of *Meriones meridianus*

	Lon	Lat	Alt	VSun	VTem	VAMH	VPre	VWin
Hd	-0.312	0.420	-0.166	0.238	0.002	0.080	-0.065	-0.392*
π	-0.627*	0.296	-0.248	0.586*	-0.054	0.007	-0.082	-0.217

*: $p < 0.05$

TABLE 6. Results of linear regression analyses showing the best predictors of climate factors for genetic diversity in *Meriones meridianus* (VSun stands for coefficient of annual mean sunshine hours and Vwin for annual mean wind speed)

ANOVA				
Regression equation	R^2	df	F	p
$\log \pi = 21.64VSun - 3.284$	0.344	20	9.957	<0.01
$\log \pi = 28.37VSun - 3.106Vwin - 2.805$	0.559	20	11.394	<0.001

the nucleotide diversity and longitude. Geographic measurements, such as latitude, longitude, and altitude are usually used as proxies of other environmental variables (temperature, precipitation, oxygen concentration, etc). As the longitude had a significantly negative relationship to VSun ($r = -0.703$, $p < 0.001$, $n = 21$), its effects on nucleotide diversity can actually be taken as the effects of VSun.

At any given time, the distribution of a species and its diversity are heavily influenced by environmental heterogeneity (Bracheta *et al.*, 1999; Wakeley & Aliacar, 2001; Hanski & Ovaskainen, 2003). There was a significant difference in the nucleotide diversity of local populations of midday gerbils. However, only the variation coefficient of sunshine hours significantly correlated with nucleotide diversity.

Midday gerbils are mainly active at night during the summer and in the daytime during the winter and do not undergo hibernation (Liu *et al.*, 1984; Song & Liu, 1984). Food sources are relatively scarce in the desert, and although midday gerbils have a habit of storing food in autumn, they continue to forage because the stored food is not adequate to meet their nutritional needs during the winter months. They only forage during the day because the temperature in northwest China is very low during the winter.

Furthermore, the additional sunshine hours provide heat for the midday gerbils to warm their bodies and reduce their energy output. Common behavioral strategies include avoiding extremes of hot or cold by remaining in dens and burrows (Du Plessis *et al.*, 1992) and using solar heat by basking (Mzilikazi *et al.*, 2002; Geiser & Drury, 2003; McKechnie & Wolf, 2004). Basking is considered an important heat source in some mammals, especially for those inhabiting arid and food-limited environments (Geiser *et al.*, 2002, 2004; Brown & Downs 2005, 2007; Schwaibold & Pillay, 2006; Pavey & Geiser, 2008; Warnecke *et al.*, 2008). Striped mice use basking as an active behavioral strategy (Schradin *et al.*, 2007; Scantlebury *et al.*, 2010) and reduce their oxygen consumption by absorbing solar radiation. Therefore, basking may be important in minimizing energy expenditure, which is useful at the time of the year when food resources are limited. Midday gerbils might reduce their foraging time by basking, thus reducing the risk of becoming prey.

Moreover, midday gerbils belong to the long sunshine-type rodent group (Liao & Li, 1999). Long sunshine hours have a benefit on the reproduction of midday gerbils: longer periods of light allow the testes

to descend and make copulation more effective. Environmental lighting can also reach rats' fetus at intensities sufficient to influence their development (Jacques *et al.*, 1987).

Wind plays an important role on affecting mammal body temperature and subsequently metabolic rates. High wind speed and low air temperature interact and increase the metabolic rate of animals (Tregear, 1965; Rogowitz & Gessaman, 1990). The increased body temperature with wind during winter appears to be an over-compensation of heat production to the increased convective heat loss and extremely windy winter storms would lead to high mortality (Stoddart, 1985; Rogowitz & Gessaman, 1990). It was reported that wind promoted the carcinogenic effect of chronic ultraviolet radiation in hairless mice (Owens *et al.*, 1977). Increasing mortality will result to a decrease of population genetic diversity.

It should be noted that both VPre and VWin tended to show negative correlations with haplotype diversity and nucleotide diversity. Natural selection will tend to adapt a population to local environmental conditions. Many kinds of genotypes can exist in more stable climatic areas with relaxed environmental pressures, resulting in higher genetic diversity. In unstable climatic areas, however, only the individuals with genotypes adapted to changeable conditions can survive; thus, the population in such areas possesses lower genetic diversity (Owens *et al.*, 1977; Huang *et al.*, 2005, 2007; Jin & Liu, 2008). As a widely distributed species, midday gerbils have an extraordinary ability to adapt to various habitats, from 150 meters below the sea level to 3200 meters above the sea level and from monsoon regions to arid regions. In the case of the midday gerbils, the fluctuations in the climatic factors seemed to have not reached the threshold necessary to significantly influence their genetic diversity.

ACKNOWLEDGEMENTS

This work was supported by the National Natural Science Foundation of China (Nos. 30770301, 30870294) and the National Key Technology R&D Program in 11th Five-Year Plan Period (2008BAC39B04). We thank the National Climatic Data Center for providing the historical climatic data. We are grateful to BAO, X. K., ZHANG, L. X., DONG, Y., WANG, L. C., LI, J. Q., SONG, S. and ZHAO, W. of School of Life Sciences, Lanzhou University who provided help in the process of sampling.

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