Genetic Structure of Mongolic-Speaking Kalmyks

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Abstract Genetic polymorphisms of blood groups ABO and RH D, serum proteins HP, TF, and GC, and red cell enzymes ACP1, PGM1, ESD, GLO1, and SOD-A have been reported for three tribes (Torguts, Derbets, and Buzavs) of the Volga's Kalmyk-Oyrats. The Kalmyks exhibit genetic markers that are characteristic of Central Asian populations, namely, high allelic frequencies for *ABO*B, TF*C2, GC*1F*, *ESD*2*, and *GLO1*2,* and the rare incidence of individuals with the RH-negative phenotype. Genetic distance measures reveal that close genetic affinities exist between the Derbets and Buzavs, but both populations differ significantly from the Torguts. Collectively as an ethnic group, the Kalmyks genetically resemble the contemporary Buryats of the Baikal region of southeastern Siberia and the Mongols of Mongolia. The transplantation of the Kalmyk-Oyrats from their homeland near Lake Baikal to their current residence (4500 km) near the Caspian Sea and their subsequent isolation for more than 300 years have not appreciably altered the gene frequencies from the parental populations for frequencies of standard genetic markers.

The Mongolic-speaking Kalmyks currently occupy territories that are located some distance (4500 km) from their original homeland in Central Asia. The contemporary Kalmyks inhabit the steppes to the west of the mouth of the Volga River, which borders the northwestern region of the Caspian Sea coast (see Figure 1). Linguistically, the Kalmyks are closely related to both the Mongols and Buryat, who speak a language that belongs to the Mongolian subdivision of the Altayan linguistic family (Katzner 1986; Ruhlin 1987). The Oyrats (currently known as Kalmyks) began differentiating culturally from the surrounding proto-Mongolian tribes during the middle of the 9th century A.D. (Avliaev 1994; Erdeniev 1985). In the 13th century a new Oyrat confederation of tribes was established consisting of Torguts, Khoshuts, Derbets, and Khoits.

In the 17th century, over a 40-year period, the majority of Torguts, with the approval of the Congress of Oyrat princes (Chuulgn), relocated to their current home in the Volga region (Shilgin Norbo 1999). The primary cause of this trans-

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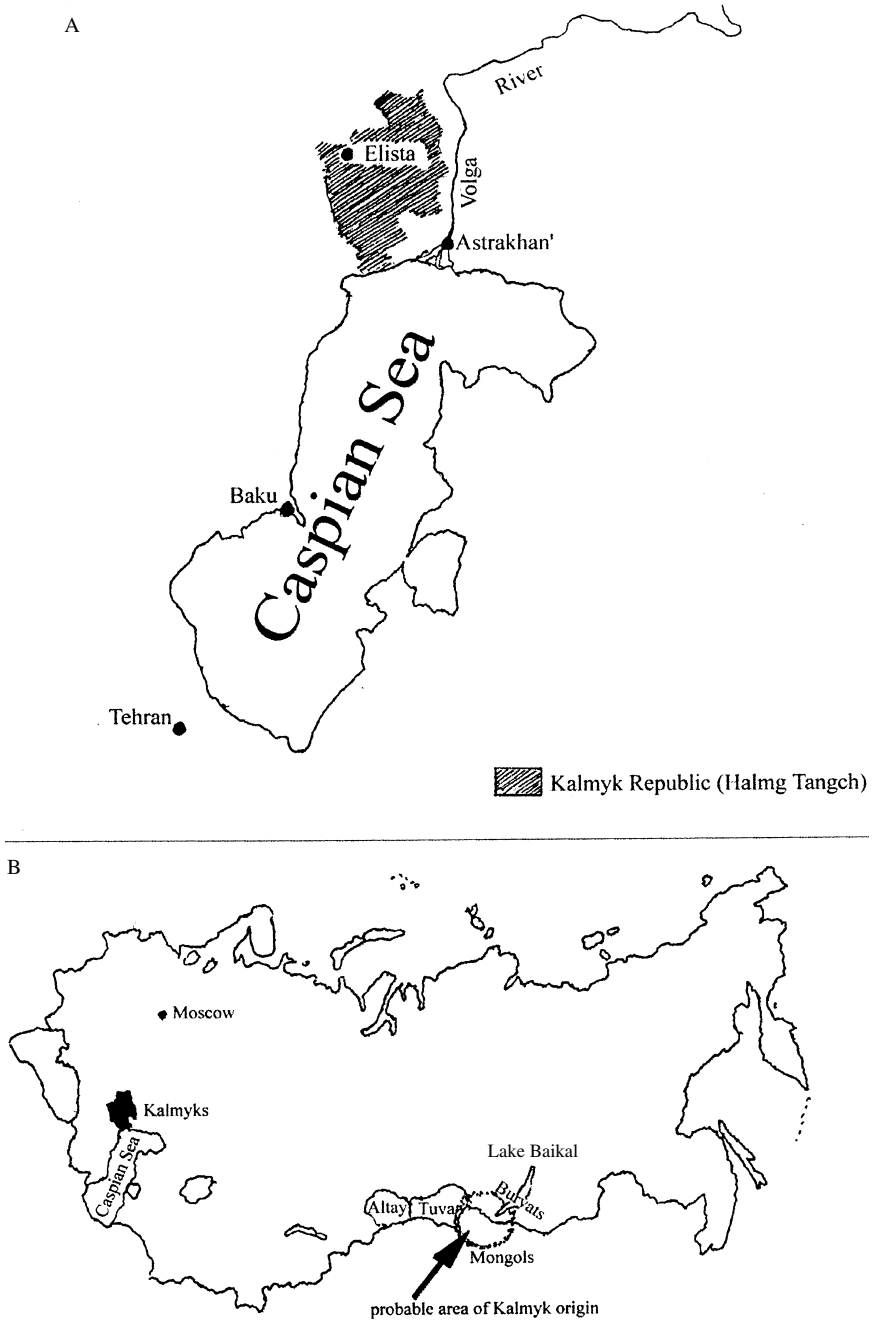


Figure 1. Maps of Russia (**A**) and Eurasia (**B**) provide the location of contemporary Kalmyks near the Caspian Sea and their probable region of origin, proximal to Lake Baikal.

plantation by the Oyrat princes and their subjects was discontent with the centralization of power by competing factions in their homeland (Erdeniev 1985).

The largest number of Oyrats (Torguts) who emigrated to the Volga region were renamed "Kalmyks." They relocated to the left bank of the Volga River and are now found distributed geographically from Astrakhan to Samara. The Derbets were the second largest tribal subdivision of the Oyrats, followed by the Khoshuts. The Zungars, the Khoits, and the Tsaatans were fewer in number. The Kalmyks also occupied lands along the Don, Ural, Kuma, and Terek rivers, and settled in the towns of Chuguev, Beljaev, Stavropolo-na-Volge, and Orenburg.

From the 17th to the 19th centuries, the Kalmyk nomads began to cultivate the land, which led to a gradual change of life-style from pastoral to agricultural subsistence and eventually resulted in the formation of larger settlements. One Kalmyk group differentiated culturally and formed a new ethnic group, termed the Buzavs.

For over 300 years, the Kalmyks of the Volga have lived interspersed among other ethnic groups, who were the original settlers of the region. Currently, the Kalmyk Republic (Halmg Tangch) is part of the Russian Federation (Figure 1).

The contemporary Kalmyks are subdivided into four major tribes or nationalities. In Mongolia these tribes are listed as distinct nationalities, while in Russia all the descendants of the Oyrats are currently classified as Kalmyks—although tribal subdivisions are still acknowledged. The Torguts, located in the eastern and southeastern regions of the Republic, are the numerically dominant subdivision of the Kalmyk population. The Derbets are primarily located in the northern and central regions of the Republic, with traces of this tribe also found in the western region. The Buzavs are a small minority, who after 1957 became dispersed throughout the Republic. The Khoshuts, few in number, are located in only one settlement of the Torgut geographical region.

This research focuses on the Kalmyks of the Volga (descendants of the Oyrats), who inhabit the southeastern region of Europe (Lower Volga and Northern Caucasus) and are the most westerly branch of the Oyrat-Mongols in modern Eurasia. Other descendants of the medieval Oyrats include: the Oyrat-Mongolian groups of Kirghizia (Torguts); the Sintsjan-Uigur of the northwestern province of the Peoples Republic of China (Torguts and Khoshuts); the Kuku-Nor of the Tsynhai provinces; Alashan, Ninsja-Gansu, and others. In the western regions of the Mongolian Republic (Torguts, Derbets, Khoshuts, Mingats, Baits, and others), the Kobdos aimak, the Ubsa-Nur aimak, and the Bulgan aimak are all descended from the original Oyrats (Erdeniev 1985).

In this article we explore the genetic polymorphisms of three tribes of the Kalmykian population residing within the Republic of Kalmykia. The allelic frequencies of these genetic markers are used to reconstruct the genetic structure of separate Kalmykian subpopulations and the Kalmyks collectively. The genetic affinities of the Kalmyks are examined by comparing them with other populations of the Russian Federation and Mongolia.

Materials and Methods

Population Sampling. Blood samples were collected on the bases of ethnicity and membership in subethnic groups from Kalmyk settlements of Elista, the capital of the Republic. Unrelated donors of Kalmykian nationality from Elista and other districts of the Republic were sampled. The donors were interviewed to determine ethnic affiliation (the group termed "total Kalmyks" was compiled from persons who identified themselves as being Kalmyk) and population subdivision (whether they were Torguts, Derbets, or Buzavs).

Based on the ethnicity of the individuals being interviewed, their mother's and father's ethnic identity, and whether both parents belonged to the same population subdivision, they were classified as "unadmixed," i.e., unadmixed Torguts, Derbets, or Buzavs. If ethnic information was based solely on the father's affiliation, the groups were classified within the category "total" (i.e., total Torguts, total Derbets, or total Buzavs). Individuals identified as admixed in the first generation were placed in a separate group (see Table 1). Two individuals were classified within the "other" category because they refused to identify the ethnicity of their fathers.

Laboratory Procedures. The ABO and RH D blood groups were typed using standard serological methods (see Alexseeva et al. 1970). Haptoglobin (HP) genotypes were typed using conventional electrophoresis on vertical polyacrylamide gels with small quantities of hemolysate added to the serum samples (Spitsyn 1985). Transferrin (TF) and group-specific component (GC) were characterized by isoelectric focusing on the same polyacrylamide gel in the presence of Immobilines, after the method of Gorg et al. (1983). GC was typed by isoelectric focusing (IEF) using the method described by Spitsyn and Titenko (1990). In addition, the following erythrocytic enzymes were typed by IEF: acid phosphatase 1 (ACP1) on an agarose gel using the method of Miller et al. (1987); esterase D (ESD) on polyacrylamide gel after the method of Divall (1994). Both phosphoglucomutase-1 (PGM1) and superoxyddismutase-A (SOD-A) were phenotyped using IEF on the same polyacrylamide gels, following the method of Goedde et al. (1981).

Analytical Procedures. The blood gene frequency data were analyzed using several different approaches. Genetic distances were computed using Nei's method (1972) for the Kalmyk populations and comparative groups. Dendro-

Table 1. Total Numbers of Kalmyks Sampled and Population Subdivisions

Population	*Total*	*No Admixture*	*Admixed*	*Others*
Kalmyks	145		4	2
Torguts	61	48		
Derbets	59	44		
Buzavs	19	11		

grams were constructed based on these computed distances. Multidimensional scaling, on the bases of graphic representation, compared Kalmyk populations to several other Eurasian groups (Terehina 1986; Deivison 1988).

Results

Phenotypic and allelic frequencies of serological and biochemical systems in Kalmyk groups are listed in Table 2. Collectively, the Kalmyks can be characterized by a high frequency of the *ABO*B* allele. In the three Kalmykian tribes described in this study, the observed ratio of the frequencies of the three alleles at the ABO blood group system is: O > B > A. This high frequency of the B blood group is characteristic of Mongolian and northern Asian populations. With the exception of one individual, Rhesus-positive blood group antigens occur in all of the Kalmyks tested to date. The high incidence of the *GC*1F* allele observed among the Kalmyks closely resembled the frequencies observed among the Buryats (Novoradovsky et al. 1993). The frequency distribution of *PGM1* alleles in Kalmyks is almost identical to the frequencies observed among the Buryats. This pattern differs markedly from the Evenki, who have significantly higher frequencies of *PGM*1+,* and lower frequencies of *PGM*1–* and *2–* (Crawford et al. 2001). There is considerable variation in the *ESD* allelic frequencies among the various Kalmyk tribes. Although variation exists in the *ESD* allelic frequencies among the Kalmyk tribes, the Kalmyks can be collectively characterized as having a high frequency of *ESD*2* (approximately 20%), an allele common in Asia. The rare *ESD* alleles, *ESD*5* and *ESD*7*, were observed in two of the Kalmyk subdivisions. When compared to European populations, central Asian populations show the highest frequency of the *GLO1*2* allele, 80% to 85%, versus approximately 40% in Europe (Spitsyn et al. 1994). The frequency of the *GLO1*2* allele (83%) in the Kalmyk fits within the observed central Asian pattern. The Kalmyks differ from most Asian populations in the high frequency of superoxyddismutase-A 1 (*SOD-A*1*) allele. The normally rare allele of this enzyme, *SOD-A*2*, was found at polymorphic frequencies (0.017) in the Derbets tribe.

The genetic distances among different tribes of Kalmyks are summarized in Table 3. Table 3 also indicates the genetic affinities among the three tribes of the Kalmyk population, Torguts, Derbets, and Buzavs, sampled in this study.

The relative affinities of the three unadmixed Kalmykian tribes are shown in Figure 2. This dendrogram, based on Nei's (1972) genetic distance measure, was based upon 10 genetic loci (*ABO, RH, ACP1, PGM1, TF, GC, HP, GLO1, ESD, SOD-A*) and indicates that the Derbets and Buzavs are much more similar genetically than either one is to the Torguts. Figure 3 compares the Kalmyks to four populations from northern Asia, and Table 4 provides the genetic distances used in the generation of this dendrogram. Based on historical documentation, it is not surprising that the Kalmyks cluster with the Buryats of Lake Baikal. The Kalmyks differ from the other comparative groups, namely the Sel'kups, Evenks, and Asian Eskimos, to an equivalent degree. The genetic distance between the

Table 2. Phenotypic and Allelic Frequencies of Serological and Biochemical-Genetic Systems in Kalmyk Population

	Phenotypes and Frequencies			
System Alleles	*Torguts*	*Derbets*	*Buzavs*	*Total Kalmyks*
ABO Phenotypes				
ABO O	21	21	4	50
A	14	11	7	34
B	16	25	8	52
AB	12	7	1	20
Alleles				
*ABO*O*	0.480	0.548	0.565	0.529
*ABO*A*	0.249	0.155	0.203	0.198
*ABO*B*	0.271	0.298	0.232	0.273
RH Phenotypes				
RH D+	63	64	20	156
RH D–	0	0	1	1
Allele				
*RH*D*	1.000	1.000	0.782	0.920
HP Phenotypes				
HP 1	6	2	1	10
HP 1, 2	31	24	13	71
HP 2	22	33	5	62
HP 0 (ahaptoglobin)	2	0	0	0
Alleles				
*HP*1*	0.364	0.237	0.395	0.318
*HP*2*	0.636	0.763	0.605	0.682
TF Phenotypes				
TF C1	37	38	10	88
TF C1, C2	12	15	9	37
TF C2	3	3	0	6
TF C1, C3	0	2	0	3
TF C2, C3	0	1	0	1
TF C1, D	8	0	0	8
TF C2, D	2	0	0	2
Alleles				
*HP*1*	0.364	0.237	0.395	0.318
*HP*2*	0.636	0.763	0.605	0.682
TF Phenotypes				
TF C1	37	38	10	88
TF C1, C2	12	15	9	37
TF C2	3	3	0	6
TF C1, C3	0	2	0	4
TF C2, C3	0	1	0	1
TF C1, D	8	0	0	8
TF C2, D	2	0	0	2
Alleles				
*TF*C1*	0.770	0.788	0.763	0.772
*TF*C2*	0.156	0.186	0.237	0.179
*TF*C3*	0.000	0.025	0.000	0.014
*TF*D*	0.074	0.000	0.000	0.035

Table 2. Continued

	Phenotypes and Frequencies			
System Alleles	*Torguts*	*Derbets*	*Buzavs*	*Total Kalmyks*
GC Phenotypes				
GC 1F	18	11	4	35
GC 1S	6	3	5	14
GC 1F, 1S	19	13	0	33
GC 1F, 2	11	17	5	35
GC 1S, 2	5	5	2	12
GC 2	2	10	3	16
Alleles				
*GC*1F*	0.541	0.441	0.342	0.476
*GC*1S*	0.295	0.203	0.316	0.252
*GC*2*	0.164	0.356	0.342	0.272
ACP1 Phenotypes				
ACP1 A	3	3	1	7
ACP1 B	33	28	11	74
ACP1 A, B	24	24	7	59
ACP1 A, C	0	3	0	3
ACP1 B, C	1	1	0	2
Alleles				
*ACP*A*	0.246	0.280	0.237	0.262
*ACP*B*	0.746	0.686	0.763	0.721
*ACP*C*	0.008	0.034	0.000	0.017
PGM1 Phenotypes				
PGM1 1+, 1+	30	25	9	67
PGM1 1+, 2+	14	19	3	38
PGM1 1+, 1–	9	7	3	20
PGM1 1–, 1–	1	0	0	1
PGM1 1+, 2–	2	2	2	6
PGM1 1–, 2+	1	1	0	2
PGM1 1–, 2–	1	1	0	2
PGM1 2+, 2–	1	2	0	3
PGM1 2+, 2+	2	2	2	6
Alleles				
*PGM1*1+*	0.697	0.661	0.684	0.682
*PGM1*1–*	0.107	0.076	0.079	0.090
*PGM1*2+*	0.164	0.220	0.184	0.190
*PGM1*2–*	0.032	0.043	0.053	0.038
ESD Phenotypes				
ESD 1	32	39	15	88
ESD 1, 2	26	16	4	50
ESD 2	2	2	0	4
ESD 1, 5	1	0	0	1
ESD 1, 7	0	2	0	2
Alleles				
*ESD*1*	0.746	0.813	0.895	0.790
*ESD*2*	0.246	0.170	0.105	0.200
*ESD*5*	0.008	0.000	0.000	0.003
*ESD*7*	0.000	0.017	0.000	0.007

Table 2. Continued

	Phenotypes and Frequencies			
System Alleles	*Torguts*	*Derbets*	*Buzavs*	*Total Kalmyks*
GLO1 Phenotypes				
GLO1 1	0	0	0	0
GLO1 1, 2	21	18	7	49
GLO1 2	40	41	12	96
Alleles				
*GLO1*1*	0.172	0.153	0.184	0.169
*GLO1*2*	0.828	0.847	0.816	0.831
SOD-A Phenotypes				
SOD-A 1	61	57	19	143
SOD-A 1, 2	0	2	0	2
Alleles				
*SOD-A*1*	1.000	0.983	1.000	0.993
*SOD-A*2*	0.000	0.017	0.000	0.007

Table 3. Genetic Distances among Three Kalmyk Tribes Measured by the Method of Nei (1972)*

Tribes	*Torguts*	*Derbets*	*Buzavs*
Torguts		0.00213	0.00207
Derbets			0.00030

*Loci used in these computations: *ABO, RH (D), HP, TF, GC, ACP1, PGM1, ESD, GLO1, SOD-A.*

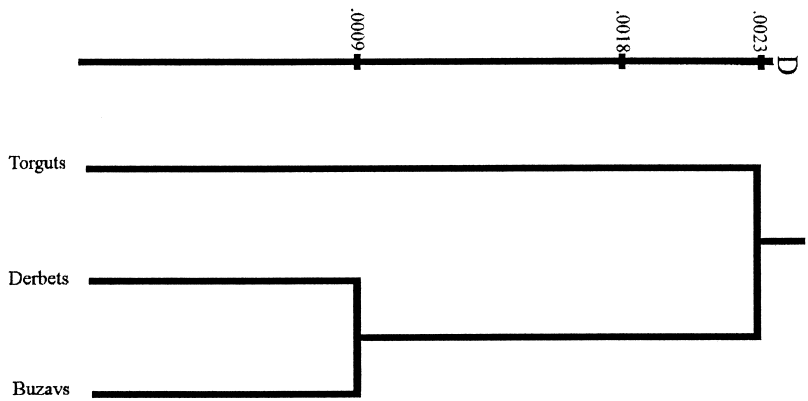


Figure 2. A dendrogram showing genetic affinities of the three Kalmyk tribes. This dendrogram was generated using the genetic distances method as calculated by Nei (1972). The loci used in these calculations are listed in Table 3.

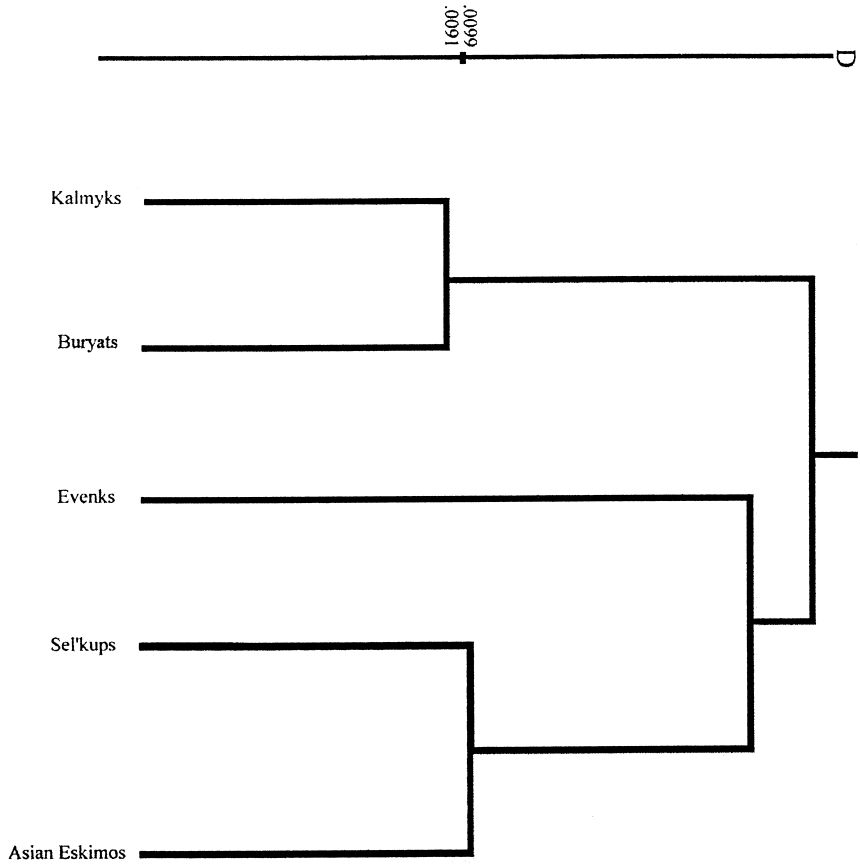


Figure 3. A comparison of the Kalmyks with four populations of Northern Asia. Table 4 provides the genetic distances used in the generation of this dendrogram.

Table 4. Genetic Distances ($\times 10^3$) Computed by the Method of Nei (1972) among the Kalmyks and Other Populations of Northern Asia[a]

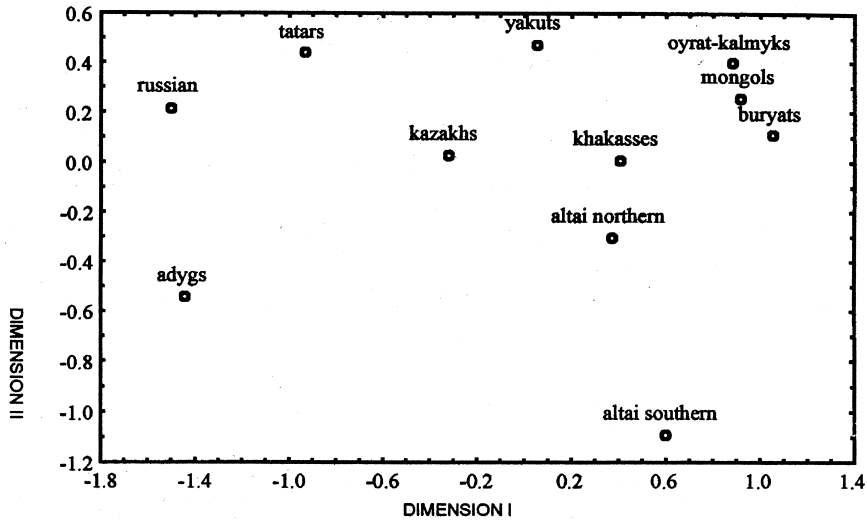
	Kalmyks	*Buryats*	*Evenks*	*Selkups*	*Asian Eskimos*
Kalmyks		0.91	2.07	1.91	2.26
Buryats			2.33	1.73	1.78
Evenks				1.21	2.17
Selkups[b]					0.99

a. Comparative data were extracted from Rychkov et al. (1984), Spitsyn (1985), Sukernik et al. (1981).

b. Unpublished data from the data bank of the Laboratory of Ecogenetics, Research Center for Medical Genetics, Russian Academy of Medical Sciences.

Kalmyks and the Buryats is 2 to 2.5 times smaller than that between the Kalmyks and the other comparative populations of northern Asia.

Lastly, the genetic affinities of the Kalmyks to the different ethnic groups of the Russian Federation were compared on the bases of an unpublished data base from the Ecological Genetics Laboratory of the Research Center for Medical Genetics of the Russian Academy of Medical Sciences. Multidimensional scaling methods developed by Terehina (1986) and Deivison (1988) were employed in this analysis. Multidimensional scaling reveals the most optimal mutual position of the populations in the space of the complex of traits studied. The results of this scaling analysis are presented in Figure 4 and clearly illustrate the close genetic



COORDINATES IN 2 DIMENSIONS

POPULATION	DIMENSION	
	I	II
Oirat-kalmyks	0.88	0.40
Mongols	0.91	0.26
Adygs	-1.45	-0.54
Altai northern	0.37	-0.30
Altai southern	0.59	-1.09
Buryats	1.05	0.11
Kazakhs	-0.33	0.03
Russian	-1.51	0.22
Tatars	-0.94	0.44
Khakasses	0.40	0.01
Yakuts	0.05	0.48

Figure 4. Multidimensional scaling plot comparing the Kalmyks to 10 other Eurasian populations using the methods of Terehina (1986) and Deivison (1988). The gene frequencies used in this comparison are from a data base of the Ecological Genetics Laboratory of the Research Center for Medical Genetics of the Russian Academy of Medical Sciences, Moscow.

affinities between the Kalmyks and Buryats. The plot also reflects a strong geographic gradient (clines of gene frequencies) of populations in an east-west direction along the territory of the Russian Federation.

Discussion

The allelic frequencies displayed in Table 2 clearly indicate that the Kalmyks are an Asian population. The almost complete absence of the RH D–negative phenotype and high frequencies of alleles *ABO*B* (circa 27%), *TF*C2* of transferrin system (18%), *GC*1F* of the vitamin D–binding protein (48%), *ESD*2* of red cell esterase D locus (20%), *GLO1*2* of erythrocytic glyoxalase-1, all combine to demonstrate that the Kalmyks are representatives of central Asia. They have close genetic affinities to the Buryats (Novoradovsky et al. 1993) and Mongols (Batsuur et al. 1991). The Kalmyks differ significantly from European populations in at least six of the loci presented in this study.

The individual Kalmyk tribes have also differentiated genetically from one another. In particular, the Buzavs and Derbets have lower frequencies of *ABO*B, GC*1F,* and *ESD*2*—alleles used to distinguish central Asian populations. European marker alleles, namely, *TF*C3* and AC*P1*C,* were identified at polymorphic frequencies (0.025 and 00.034, respectively) among Derbets. The sole RH-negative individual was found among the Buzavs. Based on morphological traits and a typological approach, Ashilova (1971) and Cheboksarov (1935) have argued that there was a so-called "weakening" of the complex of Asian (Mongoloid) traits among some of the Kalmyks. The more likely explanation for the morphological variation observed among the Kalmyks is that in the last 200 to 300 years these populations have experienced some admixture with surrounding Turkic groups. Yet, the allelic frequencies of the Kalmyks have not diverged significantly from the related Mongolian populations. The morphological traits, being more ecosensitive, may have diverged from the Mongolian ancestral populations during the last few hundred years. These conclusions are supported by the lack of congruence between morphological and genetic affinities among Mennonite populations of common ancestry, but relocated for more than 100 years (Crawford et al. 2000).

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