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RESEARCH ARTICLE

Forensic and population genetic analyses of the GlobalFiler STR loci in the Mongolian population

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Abstract We have analyzed 24 loci including autosomal and Y-chromosomal short tandem repeats (STRs), Y-indel, and sex-determining marker in a sample of 267 unrelated individuals from the Mongolian population using the GlobalFiler™ PCR Amplification Kit to provide an expanded and more reliable forensic database. Khalkh among 15 Mongolian minor-groups accounts for about 80% of the entire Mongolian population. A total of 267 different DNA profiles were found in this work. The highest gene diversity was observed in the *SE33* (0.9376) locus, and the lowest value was found in the *TPOX* (0.6142) locus. Although individual power of discrimination estimates varied at the studied loci, combined probability of match from the 21 STR loci was estimated to be 1.139×10^{-24}, which is highly informative. Based on the results of pairwise F_{ST} genetic distances and multi-dimensional scaling plot showed that Mongolians were clustered into Europeans and Asians, although Mongolia is geographically located in Northeastern Asia. Thus, the present survey of the Mongolian population may help establish a comprehensive reference database for forensic and population genetic analyses.

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Introduction

The analyses of human short tandem repeats (STRs), or microsatellite loci have become a useful tool in forensic genetics due to variation in repeat number, high levels of diversity and stable heredity in the human genome. Their repeat number can also be amplified faithfully using polymerase chain reaction (PCR) (Edwards et al. 1992; Kayser et al. 1997). In general, binary markers such as single nucleotide polymorphisms (SNPs) are best suited for studies of ancient divergences in human evolution, since they tend to have low probabilities of back and parallel mutation, and for which ancestral states can be determined (Hammer and Zegura 1996). In contrast, the genetic features of STR loci may provide more useful information for investigating and reconstructing the phylogeny of the more recently diversified human lineages (Hammer and Zegura 1996; Forster et al. 2000), as well as for forensic and paternity testing (de Knijff et al. 1997).

Applications of STR analysis in forensic casework benefit from large population databases for estimating the probability of identity by chance (Allen et al. 1998; Pfeiffer et al. 2001; Imaizumi et al. 2002). The use of additional STR markers would provide enough forensic parameters for more difficult cases in paternity or maternity analyses, such as deficient cases (i.e., only alleged father and the child are included), missing persons or when mutations are encountered. Many forensic communities proposed the inclusion of additional loci, since the potential false matches with a large number of comparisons being made within and between databases (Weir 2007; Schneider

2009; Hill et al. 2011). Thus, it is important that forensic genetic databases of STR loci continue to be expanded, and become more reliable to provide a better tool for forensic analysis. Although, several databases of STR loci have been published and are used in forensic and population genetics in Mongolia (Varga et al. 2003; Kwak et al. 2005; Zha et al. 2014), the amount of available data for STR loci in the Mongolian population is still limited. Thus, analysis of extended STR loci may potentially be a powerful tool for forensic analyses in the Mongolian population. It leads us to investigate further reliable STR data sets and evaluation their usefulness from the Mongolian population to expand the database for the forensic community.

In this study, thus, we have analyzed 24 loci including autosomal and Y-chromosomal STRs, Y-indel, and sex-determining marker in 267 unrelated individuals from the Mongolian population using the GlobalFiler™ PCR Amplification Kit to provide an expanded and more reliable forensic database.

Materials and methods

Subjects and DNA extraction

In this study, we studied 267 healthy Mongolian DNA samples (Khalkh, n = 216; Bayad, n = 10; Dorwod, n = 9; Kazakh, n = 7; Khotgoid, n = 4; Zakhchin, n = 4; Buriad, n = 3; Torguud, n = 3; Darkhad, n = 2; Uriankhai, n = 2; Uuld, n = 2; Dariganga/Khoton/Myangad/Sartuul/unknown, each n = 1) selected at random (and therefore likely to be unrelated) from Ulaanbaatar in Mongolia. Genomic DNA was extracted from buccal swab using Exgene™ Clinic SV kit (GeneAll, Korea) according to manufacturer's instructions. A separate written informed consent was obtained from all donors before collecting their buccal swab.

PCR and genotyping

PCR amplification of 24 loci (D3S1358, vWA, D16S539, CSF1PO, TPOX, D8S1179, D21S11, D18S51, D2S441, D19S433, TH01, FGA, D22S1045, D5S818, D13S317, D7S820, SE33, D10S1248, D1S1656, D12S391, D2S1338, DYS391, Y-indel, and Amelogenin) was performed using the GlobalFiler™ PCR Amplification Kit (Applied Biosystems, Foster City, CA, USA). PCR reaction was performed on a GeneAmp PCR System 9700 (Applied Biosystems, Foster City, CA, USA) according to the manufacturer's recommendations. PCR products were confirmed by 2% agarose gel electrophoresis. Amplified PCR products were analyzed by capillary electrophoresis using an ABI 3500xl Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) with manufacturer provided allelic ladders, bins, and panels. GeneScan 600 LIZ (Applied Biosystems, Foster City, CA, USA) was used as a size standard for capillary electrophoresis.

Data analysis

The genotype data was analyzed using the GeneMapper ID-X software (Applied Biosystems, Foster City, CA, USA) and Microsoft Excel (Microsoft, Redmond, WA, USA). The exact test was performed for assessing the Hardy–Weinberg equilibrium (HWE) using PowerMarker version 3.25 software (Liu and Muse 2005). Pair-wise genetic distances (F_{ST}) was calculated by Phylip version 3.695 (Felsenstein), F_{ST} values were visualized by multidimensional scaling (MDS) plot using the IBM SPSS Statistics 23 (IBM Korea, Korea). Forensic statistical analysis including allele frequencies, heterozygosities, and polymorphism information content (PIC) was performed with PowerMarker version 3.25 software (Liu and Muse 2005). Forensic paternity testing was calculated using PowerStats version 1.2 (Tereba 1999).

Results and discussion

We assessed statistical parameters of 24 loci including autosomal and Y-chromosomal STRs, Y-indel, and sex-determining marker using the GlobalFiler™ PCR Amplification Kit in a sample of 267 unrelated individuals from the Mongolian population. Khalkh among 15 Mongolian minor-groups accounts for about 80% of the entire Mongolian population. Genetic characteristics of 24 GlobalFiler PCR Amplification kit loci are shown in Table 1. In addition, their allele frequencies and forensic parameters were listed in Table 2. All the loci were found to be highly polymorphic in the population. Exact test demonstrated that no significant deviations from the Hardy–Weinberg equilibrium were observed except CSF1PO and FGA.

The genetic approach to assess the probability used here is to provide valuable information for forensic applications. A total of 267 different DNA profiles were found in this work. The highest gene diversity was observed in the *SE33* (0.9376) locus, and the lowest value was found in the *TPOX* (0.6142) locus. This result indicates that the *SE33* is the most valuable marker from 24 STR loci surveyed here. Although the individual power of discrimination estimates varied at the studied loci, combined probability of a match (PM) from the 21 STR loci was estimated to be 1.139×10^{-24}, which is highly informative.

Although Mongolian forensic DNA laboratories have been generated reliable population data sets using standardized genetic markers (i.e., 13 CODIS STR loci), it is important that forensic genetic databases of STR loci continue to

Table 1 Genetic characteristics of 24 GlobalFiler PCR Amplification kit loci in the present study

Locus	Control 007 allele	Allele spread	Allele size range (bp)	Repeat motif	Chromosomal location
D1S1656	13, 16	9–20.3	154.0–209.5	$[TAGA]_n$	1q42.2
D2S441	14, 15	8–17	75.0–113.5	$[TCWA]_n$	2p14
TPOX	8, 8	5–15	332.5–384.5	$[AATG]_n$	2p23-2per
D2S1338	20, 23	11–28	275.5–355.5	$[TKCC]_n$	2q35
D3S1358	15, 16	9–20	90.5–146.5	$[TCTR]_n$	3p21.31
FGA	24, 26	13–51.2	221.0–380.0	$[YTYY]_n$	4q28
D5S818	11, 11	7–18	133.5–189.5	$[AGAT]_n$	5q21–31
CSF1PO	11, 12	6–15	277.0–325.0	$[AGAT]_n$	5q33.3–34
SE33	17, 25.2	4.2–37	306.0–444.0	$[AAAG]_n$	6q14
D7S820	7, 12	6–15	256.5–304.5	$[GATA]_n$	7q11.21–22
D8S1179	12, 13	5–19	108.5–176.5	$[TCTR]_n$	8q24.13
D10S1248	12, 15	8–19	80.0–132.0	$[GGAA]_n$	10q26.3
TH01	7, 9.3	4–13.3	174.0–219.5	$[TCAT]_n$	11p15.5
D12S391	18, 19	14–27	211.0–270.5	$[AGAY]_n$	12p13.2
vWA	14, 16	11–24	151.0–215.0	$[TCTR]_n$	12p13.31
D13S317	11, 11	5–16	197.0–249.0	$[TATC]_n$	13q22–31
D16S539	9, 10	5–15	221.5–273.5	$[GATA]_n$	16q24.1
D18S51	12, 15	7–27	255.5–347.5	$[AGAA]_n$	18q21.33
D19S433	14, 15	6–19.2	115.5–173.5	$[WAGG]_n$	19q12
D21S11	28, 31	24–38	179.5–246.5	$[TCTR]_n$	21q11.2–q21
D22S1045	11, 16	8–19	83.5–126.5	$[ATT]_n$	22q12.3
DYS391	11	7–13	359.5–395.5	$[TCTA]_n$	Yq11.21
Y indel	2	1, 2	79.5–87.5	–	Yq11.221
Amelogenin	X, Y	X, Y	97.0–107.5	–	X: p22.1–22.3, Y: p11.2

be expanded, and become more reliable to provide a better tool for forensic analysis (Varga et al. 2003; Kwak et al. 2005; Zha et al. 2014). For example, the PowerPlex-16 system has been used as capable of simultaneously amplifying all 13 CODIS STR, amelogenin, and two pentanucleotide STR loci, Penta D and Penta E (Sprecher et al. 2000; Krenke et al. 2002). The 13 CODIS core STR loci are located on 12 different chromosomes, with CSF1PO and D5S818 both residing on chromosome 5, which are separated by approximately 24 centiMorgans (cM) (Bacher et al. 2000). Therefore, it would be expected that the values for paternity index and power of exclusion for the 13 CODIS STR set will be diminished from those expected for completely unlinked loci (Lins et al. 1998) (i.e., ≥50 cM apart). In this study, the combined PM value calculated from the unlinked 17 STR loci (Table 1) is 4.23×10^{-20}, which is also highly informative.

There are known to be about 20 ethnic Mongolian groups, and many people of mixed ethnic origin; the population of Mongolia is known to be homogeneous, with Mongolian-speaking people constituting 95% of the total; the largest subgroup is the Khalkh, accounting for about 80% of the total population. The only substantial non-Mongol groups, representing over 5% of the population, are the Kazakhs, a Turkish-speaking people dwelling in the far West (http://www.un-mongolia.mn). A population comparison based on pairwise F_{ST} genetic distances calculated from allele frequencies of 15 shared STR loci (D2S1338, TPOX, D3S1358, FGA, D5S818, CSF1PO, D7S820, D8S1179, TH01, vWA, D13S317, D16S539, D18S51, D19S433, D21S11) from obtained 25 different Eurasian and African populations is shown in Table 3 (Dobashi et al. 2005; Kraaijenbrink et al. 2007; Toscanini et al. 2015; Yuan et al. 2014; Omran et al. 2009; Sadam et al. 2015; Chaudhari and Dahiya 2014; Tie et al. 2006; Park et al. 2016; Maruyama et al. 2008; Ramos-González et al. 2016; Ota et al. 2007; Smith et al. 2009; Piatek et al. 2008; Almeida et al. 2015; Novković et al. 2010; Tillmar et al. 2009; Babiker et al. 2011; Rerkamnuaychoke et al. 2006; Hill et al. 2013). A multi-dimensional scaling (MDS) plot for 25 Eurasian and African populations by using pairwise F_{ST} genetic distance values was depicted in Fig. 1. The plot showed three distinct clusters (Asians, Europeans/Hispanic, and African). As expected, the Koreans are clustered with Mongolian ethnic groups and East Asian groups including Chinese and Japanese populations (Fig. 1). This result was consistent with a previous report derived from datasets of mitochondrial

Table 2 Allele frequencies and statistical parameters for twenty-one autosomal loci of GlobalFiler PCR Amplification kit in the Mongolian population (n = 267)

	D3S1358		vWA		D16S539		CSF1PO		TPOX		D8S1179		D21S11	
	14	0.0243	13	0.0019	8	0.0187	9	0.0393	8	0.5468	8	0.0019	26	0.0019
	15	0.4026	14	0.118	9	0.2678	10	0.2378	9	0.118	9	0.0019	27	0.0094
	16	0.3258	15	0.0449	10	0.1199	11	0.2865	10	0.0169	10	0.0824	28	0.0524
	17	0.181	16	0.2116	11	0.2079	12	0.3521	11	0.2678	11	0.0637	28.2	0.0281
	18	0.0637	17	0.3052	12	0.221	13	0.0637	12	0.0431	12	0.1404	29	0.2547
	19	0.0019	18	0.2266	13	0.1386	14	0.0187	13	0.0075	13	0.2996	29.2	0.0056
			19	0.0843	14	0.0225	15	0.0019			14	0.1948	30	0.3221
			20	0.0075	15	0.0037					15	0.1479	30.2	0.0075
											16	0.0487	30.3	0.0037
											17	0.015	31	0.0843
											18	0.0019	31.2	0.073
											19	0.0019	32	0.0187
													32.2	0.1067
													33	0.0019
													33.2	0.0281
													34.2	0.0019
H_{obs}		0.6941		0.7876		0.8018		0.7314		0.6142		0.8172		0.8027
H_{exp}		0.6854		0.8090		0.8315		0.7865		0.6404		0.8352		0.7566
x^2-test (P)		0.5760		0.6523		0.6835		0.0410		0.9972		0.8358		0.9330
Exact test (P)[a]		0.4530		0.3336		0.4280		0.0299		0.9846		0.4882		0.2490
PM		0.1460		0.0850		0.0740		0.1340		0.2020		0.0630		0.0630
PD		0.8540		0.9150		0.9260		0.8660		0.7980		0.9370		0.9370
PIC		0.6391		0.7561		0.7725		0.6846		0.5599		0.7943		0.7789
PPE		0.4060		0.6160		0.6590		0.5740		0.3420		0.6660		0.5210
	D18S51		D2S441		D19S433		TH01		FGA		D22S1045		D5S818	
	7	0.0019	9.1	0.0094	11	0.0056	6	0.1348	18	0.0112	10	0.0019	7	0.0281
	11	0.0094	10	0.2191	11.2	0.0019	7	0.3539	19	0.03	11	0.3034	9	0.0562
	12	0.0337	11	0.4401	12	0.0431	8	0.0974	20	0.0187	12	0.0019	10	0.1142
	13	0.1648	11.3	0.0131	13	0.2453	9	0.324	21	0.1311	13	0.0037	11	0.3577
	14	0.2566	12	0.1573	13.2	0.0468	9.3	0.0843	21.2	0.0019	14	0.0187	12	0.2715
	15	0.1423	13	0.0206	14	0.2865	10	0.0056	22	0.1049	15	0.1948	13	0.1592
	16	0.1124	14	0.1311	14.2	0.103			22.2	0.0019	16	0.2772	14	0.0131
	17	0.0787	15	0.0075	15	0.0599			23	0.2266	17	0.1685		
	18	0.0393	16	0.0019	15.2	0.1536			23.2	0.0019	18	0.0262		
	19	0.0543			16	0.0206			24	0.264	19	0.0037		
	20	0.0337			16.2	0.03			24.2	0.0037				
	21	0.0243			17.2	0.0037			25	0.1273				
	22	0.0281							25.2	0.0019				
	23	0.0131							26	0.0599				
	24	0.0056							27	0.0112				
	25	0.0019							28	0.0037				
H_{obs}		0.8595		0.7157		0.8145		0.7350		0.8294		0.7637		0.7558
H_{exp}		0.8914		0.6779		0.8352		0.7378		0.8015		0.7640		0.7753
X^2-test (P)		0.6065		0.9416		0.2225		0.5909		0.0000		0.1888		0.3764
Exact test (P)[a]		0.1915		0.4441		0.1585		0.5077		0.0005		0.0861		0.3871
PM		0.0400		0.1240		0.0660		0.1100		0.0560		0.0990		0.1040
PD		0.9600		0.8760		0.9340		0.8900		0.9440		0.9010		0.8960
PIC		0.8455		0.6755		0.7912		0.6919		0.8085		0.7245		0.7188

Table 2 (continued)

	D18S51		D2S441		D19S433		TH01		FGA		D22S1045		D5S818	
PPE		0.7780		0.3950		0.6660		0.4890		0.6020		0.5340		0.5540
	D13S317		D7S820		SE33		D10S1248		D1S1656		D12S391		D2S1338	
	8	0.2285	7	0.0037	12	0.0019	11	0.0094	11	0.0599	15	0.0056	16	0.0075
	9	0.1236	8	0.2753	13	0.0019	12	0.0843	12	0.0599	16	0.0037	17	0.0712
	10	0.1479	9	0.073	14	0.0056	13	0.3127	13	0.0506	17	0.1292	18	0.0993
	11	0.2135	10	0.1835	15	0.0094	14	0.2584	14	0.0562	17.3	0.0112	19	0.1648
	12	0.2079	10.1	0.0019	16	0.0281	15	0.2154	15	0.2903	18	0.2154	20	0.1199
	13	0.0524	11	0.2959	16.2	0.0019	16	0.0974	15.3	0.0056	18.3	0.0019	21	0.0281
	14	0.0243	12	0.1461	17	0.0487	17	0.0169	16	0.2715	19	0.2228	22	0.0412
	15	0.0019	13	0.0206	18	0.0805	18	0.0056	16.3	0.0094	20	0.2285	23	0.1966
					19	0.1049			17	0.0861	21	0.0712	24	0.1779
					19.2	0.0019			17.3	0.0543	22	0.0543	25	0.0581
					20	0.0824			18	0.0075	23	0.0337	26	0.0206
					20.2	0.0019			18.3	0.0337	24	0.015	27	0.0131
					21	0.088			19	0.0019	25	0.0037	28	0.0019
					22	0.0281			19.3	0.0094	26	0.0037		
					22.2	0.0243			20.3	0.0037				
					23	0.0037								
					23.2	0.0225								
					24.2	0.0412								
					25	0.0019								
					25.2	0.0637								
					26.2	0.0581								
					27	0.0019								
					27.2	0.0581								
					28.2	0.0655								
					29.2	0.0599								
					30.2	0.0506								
					31.2	0.0449								
					32.2	0.0131								
					33.2	0.0037								
					34.2	0.0019								
H_{obs}		0.8185		0.7759		0.9376		0.7720		0.8173		0.8255		0.8667
H_{exp}		0.8202		0.7715		0.9251		0.7978		0.8202		0.8427		0.8539
X^2-test (*P*)		0.7089		0.2442		1.0000		0.0001		0.9700		0.9066		0.2632
Exact test (*P*)[a]		0.5382		0.7250		0.9774		0.1315		0.9005		0.4810		0.1608
PM		0.0610		0.0860		0.0100		0.0940		0.0540		0.0580		0.0360
PD		0.9390		0.9140		0.9900		0.9060		0.9460		0.9420		0.9640
PIC		0.7930		0.7407		0.9341		0.7364		0.7966		0.8027		0.8526
PPE		0.6370		0.5470		0.8470		0.5950		0.6370		0.6810		0.7030

[a]Exact test by Monte Carlo method, H_{obs} observed heterozygosity; H_{exp} expected heterozygosity; *PM* probability of match; *PD* power of discrimination; *PIC* polymorphism information content; *PPE* paternity power of exclusion

DNA and Y-chromosome markers (Jin et al. 2009). MDS plot showed that Mongolians were clustered into Europeans and Asians, although Mongolia is geographically located in Northeastern Asia.

In conclusion, our data can be used to extend the results obtained with other STRs, as well as provide valuable information for forensic and population genetic studies in the Mongolian population.

Table 3 Pair-wise F_{ST} genetic distances of Mongolian and other populations using 15 shared STR loci

		1	2	3	4	5	6	7	8	9	10	11	12	13
1	NEP	–												
2	MAL	0.09674	–											
3	MEX	0.13824	0.08845	–										
4	MON	0.06247	0.04873	0.06482	–									
5	AFA	0.21892	0.13438	0.12662	0.13094	–								
6	CAU	0.14975	0.09180	0.05775	0.08443	0.11120	–							
7	HPU	0.12359	0.07263	0.01658	0.05421	0.09656	0.02617	–						
8	ASU	0.06751	0.05059	0.10123	0.03357	0.16607	0.11317	0.08174	–					
9	BAN	0.08822	0.04892	0.07520	0.04419	0.13050	0.07012	0.05412	0.04943	–				
10	BHU	0.04008	0.04622	0.08953	0.02843	0.15667	0.10601	0.07595	0.03198	0.05244	–			
11	SER	0.14438	0.08258	0.06660	0.07728	0.10613	0.01413	0.03262	0.10417	0.06544	0.09658	–		
12	SOM	0.19664	0.13126	0.10647	0.11798	0.06557	0.10264	0.07680	0.15145	0.10898	0.14330	0.10711	–	
13	SUD	0.17166	0.09521	0.08976	0.08920	0.03685	0.07451	0.05886	0.11766	0.08394	0.11016	0.07253	0.02951	–
14	EST	0.15463	0.09276	0.07604	0.08830	0.10628	0.01417	0.03907	0.10531	0.08411	0.10611	0.01281	0.11670	0.07806
15	EGY	0.11463	0.07077	0.07275	0.06652	0.07755	0.05367	0.04120	0.07667	0.05437	0.07236	0.04464	0.06565	0.03714
16	IND	0.09587	0.06239	0.09794	0.06345	0.14592	0.08520	0.07341	0.06962	0.01888	0.06524	0.07579	0.12582	0.10333
17	INN	0.11343	0.02154	0.11942	0.05989	0.17024	0.12975	0.10288	0.05605	0.07069	0.05728	0.11436	0.16363	0.13148
18	JAP	0.08110	0.05653	0.08436	0.03423	0.15267	0.10537	0.06844	0.01333	0.03910	0.04392	0.09650	0.12959	0.10341
19	CHN	0.08927	0.08044	0.14058	0.07175	0.24081	0.17923	0.13497	0.06711	0.08733	0.07217	0.16509	0.21533	0.19303
20	CHI	0.14290	0.09662	0.01333	0.06909	0.12619	0.04196	0.01432	0.10340	0.07134	0.09320	0.04546	0.10480	0.08687
21	THA	0.08022	0.02010	0.09279	0.03936	0.15851	0.10204	0.07655	0.02772	0.04668	0.03550	0.09528	0.14632	0.11222
22	POR	0.12502	0.07646	0.05259	0.07134	0.09663	0.00956	0.02382	0.09303	0.05914	0.08549	0.01013	0.09686	0.06465
23	POL	0.15124	0.09177	0.07836	0.09337	0.11128	0.01200	0.03831	0.11105	0.07855	0.10441	0.01065	0.11891	0.08281
24	PHI	0.09809	0.02512	0.10649	0.04111	0.14434	0.11587	0.09023	0.03624	0.06136	0.04639	0.10341	0.15115	0.10682
25	KOR	0.05074	0.04835	0.08856	0.02671	0.17450	0.11015	0.07896	0.01297	0.04385	0.02710	0.10210	0.15329	0.12342

		14	15	16	17	18	19	20	21	22	23	24	25
1	NEP												
2	MAL												
3	MEX												
4	MON												
5	AFA												
6	CAU												
7	HPU												
8	ASU												
9	BAN												
10	BHU												
11	SER												
12	SOM												
13	SUD												
14	EST	–											
15	EGY	0.05378	–										
16	IND	0.09905	0.06275	–									
17	INN	0.12629	0.10704	0.09025	–								
18	JAP	0.10050	0.06805	0.05857	0.06420	–							
19	CHN	0.17321	0.13686	0.09401	0.09381	0.06639	–						
20	CHI	0.05402	0.05885	0.08467	0.13018	0.08374	0.14511	–					
21	THA	0.09979	0.07569	0.07177	0.02053	0.03276	0.05840	0.10043	–				
22	POR	0.01336	0.03319	0.06992	0.11150	0.08603	0.15248	0.03469	0.08407	–			
23	POL	0.00694	0.05137	0.08649	0.12879	0.10724	0.16907	0.05441	0.10298	0.01134	–		

Table 3 (continued)

		14	15	16	17	18	19	20	21	22	23	24	25
24	PHI	0.10325	0.08394	0.07175	0.03951	0.04273	0.06822	0.11002	0.02804	0.09344	0.10964	–	
25	KOR	0.10979	0.07584	0.05931	0.05876	0.01213	0.04871	0.09100	0.02609	0.08841	0.11086	0.03543	–

NEP Nepal (Ota et al. 2007), *MAL* Malaysia (Maruyama et al. 2008), *MEX* Mexico (Ramos-González et al. 2016), *MON* Mongolia (present study), *AFA* African American (Hill et al. 2013), *CAU* Caucasian USA (Hill et al. 2013), *HPU* Hispanic USA (Hill et al. 2013), *ASU* Asian USA (Hill et al. 2013), *BAN* Bangladeshi (Dobashi et al. 2005), *BHU* Bhutan (Kraaijenbrink et al. 2007), *SER* Serbia (Novković et al. 2010), *SOM* Somalia (Tillmar et al. 2009), *SUD* Sudan (Babiker et al. 2011), *EST* Estonia (Sadam et al. 2015), *EGY* Egypt (Omran et al. 2009), *IND* India (Chaudhari and Dahiya 2014), *INN* Indonesia (Dobashi et al. 2005), *JAP* Japan (Tie et al. 2006), *CHN* China (Yuan et al. 2014), *CHI* Chile (Toscanini et al. 2015), *THA* Thai (Rerkamnuaychoke et al. 2006), *POR* Portugal (Almeida et al. 2015), *POL* Poland (Piatek et al. 2008), *PHI* Philippines (Smith et al. 2009), *KOR* Korea (Park et al. 2016)

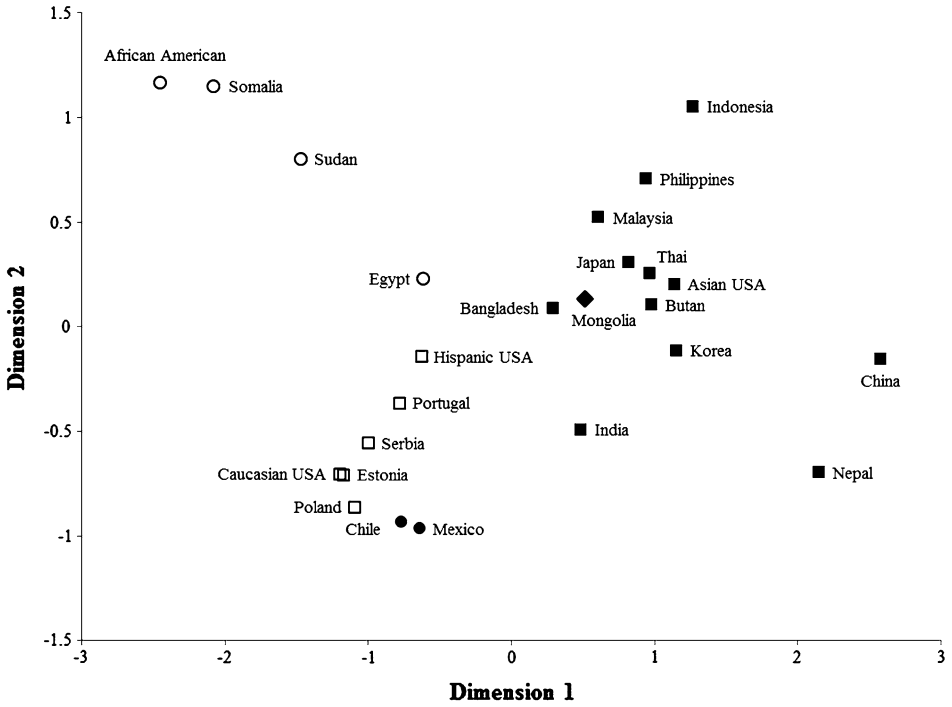

Fig. 1 Multidimensional scaling (MDS) plot based on the result of F_{ST} genetic distances. The Mongolians are represented by a *closed diamond*; Asian by *closed squares*; European origin by *open squares*; American by *closed circles*; and African by *open circles*

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Compliance with Ethical Standards

Conflict of interest All authors declares that they have no conflict of interest.

Ethical approval The study was approved by the Ethics Committee and Institutional Review Board of Dankook University, Republic of Korea.

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