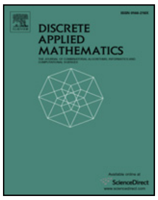
Discrete Applied Mathematics 157 (2009) 2341–2348

Contents lists available at ScienceDirect

Discrete Applied Mathematics

journal homepage: www.elsevier.com/locate/dam



The Asian contribution to the Turkish population with respect to the Balkans: Y-chromosome perspective

Ceren Caner Berkman [*], İnci Togan

Department of Biological Sciences, Middle East Technical University, 06531 Ankara, Turkey

ARTICLE INFO

Article history:
Received 12 January 2007
Received in revised form 28 June 2007
Accepted 11 June 2008
Available online 20 September 2008

Keywords:
Turkish population
Central Asia
Admixture
Y-chromosome
Genetic drift

ABSTRACT

Admixture analysis is one of the methods that can be used to calculate the contribution of migrations. There are several admixture estimation methods. In the present study, Chikhi et al.'s admixture method, which considers the effect of genetic drift, was used to estimate the male genetic contribution of Central Asia to hybrids. It was observed that the male contribution from Central Asia to Turkish population with reference to the Balkans was 13%. Comparison of the admixture estimate for Turkey with those of neighboring populations pointed out that the Central Asian contribution was lowest in Turkey. This observation might be explained by the homogenization between the males of the Balkans and Anatolia.

1. Introduction

Recent developments in molecular genetic techniques resulted in accumulation of molecular data in databases. Likewise, many new computational methods were developed. Some of these in turn allowed scientists to uncover past population processes more deeply. Contribution by migrations to the gene pool of populations can be partitioned by analyzing the current pattern of genetic variation with admixture analysis. For the interpretation of the past population processes from current patterns of genetic variation, interaction of the various evolutionary forces, such as migration, mutation and genetic drift, must be considered. Furthermore, in genetic analysis, populations are represented by a small number of samples in comparison to real population sizes. Therefore, estimation errors that result from sampling should also be considered.

Many statistical methods (for example, of Roberts and Hiorns [27]; of Long [24]; of Chakraborty [8]; of Bertorelle and Excoffier [4]; of Chikhi et al. [10]) have been developed to estimate admixture proportions from genetic data [20]. Methods differ based on the incorporation of the effects of sampling, genetic drift, and mutation. For example, the method of Robert and Hiorns ignores all of these factors [20]. The method of Bertorelle and Excoffier includes the effect of sampling and mutations [4], while Chikhi et al.'s method considers the effects of genetic drift together with the effects of sampling [10].

The Y-chromosome haplogroups are lineages determined by the biallelic markers found on the non-recombining region of the chromosome [16,36]. Admixture estimates based on Y-chromosomal markers show the male contributions. However, due to the low effective population size [20] and higher reproductive variability of males [6,9], the Y-chromosome is more prone to genetic drift then the mtDNA, X-chromosome, and autosomal chromosomes. Therefore, to calculate the admixture estimates for males, methods that consider the effect of genetic drift should be favored.

Anatolia, the Asian part of Turkey, is at the junction between the Balkans, the Near East and the Caucasus. The area has been occupied since lower Paleolithic times [22]. Because of its geographical location, Anatolia has acted as a bridge and reservoir for numerous population movements of modern human beings since very early times. For example, during the

---

[*] Corresponding author. Tel.: +90 312 210 51 67; fax: +90 312 210 79 76.
E-mail addresses: cerenberkman@gmail.com (C. Caner Berkman), togan@metu.edu.tr (İ. Togan).

0166-218X/$ – see front matter © 2008 Elsevier B.V. All rights reserved.
doi:10.1016/j.dam.2008.06.037

Table 1
List of employed populations, their sample sizes and related references

	Region	Population from	N_P	N_R	References
Parental populations	Balkans[a]	Greece	76	127	[30]
		Albania	51		[30]
	Central Asia[a]	Uighur	109	1009	[21,35]
		Kazakhstan	84		[21,35]
		Altai	29		[21]
		Kyrgyzstan	105		[21,35]
		Turkmenistan	47		[21,35]
		Uzbekistan	635		[21,35]
Hybrids	Turkey[a]	Turkey	553	553	[12,30]
	Northern Caucasus[a]	Ingushetia	22	140	[25]
		Kabardino-Balkaria	58		[25]
		Abkhazia	14		[25]
		Chechnya	20		[25]
		Dagestan	26		[25]
	Southern Caucasus	Georgia[a]	207	460	[25,30,35]
		Azerbaijan[a]	105		[25,35]
		Armenia[a]	148		[25,35]
	Near east	Syria[a]	20	293	[30]
		Iraq[a]	139		[2]
		Lebanon[a]	81		[30,35]
		Iran[a]	53		[35]

N_P: sample size of population, N_R: sample size of region.

[a] Populations which were used as parent or hybrid in admixture analysis.

harsh climatic conditions of the Last Glacial Maximum (LGM), together with Iberia, Anatolia became a refuge for modern humans [12]. Again, it was an important reservoir for the farming industry as the farming culture spread through towards Europe. After the shift to sedentary life, Anatolia was populated by various civilizations, such as the Hattians, Hurries, Hittites, Phrygians, Lydians, Urartians, Persians, Meds, Romans, Sassanids, Byzantines, Seljuk Turks, and Ottomans [1]. Therefore, Anatolia continued to be subjected to migrations from different regions throughout time. The last well-known cultural influence of Central Asian migrations occurred around the 11th Century CE (Common Era) with the migrations of Turkic speaking nomadic groups known as the Oghuz Turks into the area. [23,34]. In parallel to these migrations, the language of the region started to be replaced by the Turkic language.

Genetic similarity of the Turkish population to that of Europe and Central Asia was analyzed in several studies. Correspondence analysis based on protein markers [5], phylogenetic analysis of mtDNA [7,14,15] and comparison of Y-chromosome based markers [12,28,35] all indicate the relative genetic proximity of the Anatolian population to that of the European populations. Hence, these results revealed that Central Asian populations had little genetic effect on the current day Turkish gene pool. On the other hand, in the only study that used an admixture analysis method (method which considered the effects of mutation and sampling errors), the Central Asian contribution to the Turkish gene pool with respect to the Balkans was estimated as 30% [3]. It was argued that after the language replacement in the region, Turkey might have become the center of attraction for the Turkic speaking groups. Hence, the genetic contribution is attributed mainly to the migrations of Turkic speaking groups over the last 1,000 years [3].

In the present study, Central Asian contribution to Turkish gene pool in terms of males was quantified by using an admixture method that considers the effects of genetic drift and sampling errors. Furthermore, to obtain a broader perspective about the past population histories of Western Asia, in addition to Turkey, neighboring regions (Northern Caucasus, Azerbaijan, Armenia, Georgia, Syria, Lebanon, Iran, and Iraq) were also analyzed.

2. Materials and methods

2.1. Compiled data

In the present study, data for 2582 individuals from 21 populations was compiled from literature between 2004 and 2005. The sample sizes and related references for the analyzed populations are given in Table 1.

As well as individual populations such as population from Turkey, regional populations specified in Table 1 were considered. Central Asia and the Balkans were accepted as the parental populations. Populations from Kazakhstan, Kyrgyzstan, Uighur, Altai, Uzbekistan, and Turkmenistan form the composite population of Central Asia, whereas the composite population of the Balkans harbor populations from Greece and Albania. Admixed, hybrid populations were compiled from Turkey, the Southern Caucasus (Azerbaijan, Armenia and Georgia), the Northern Caucasus (Ingushetia, Kabardino-Balkaria, Abkhazia, Dagestan and Chechnya) and the Near East (Syria, Iraq, Lebanon and Iran).