


Estimating the impact of the Mongol expansion upon the gene pool of Tuvans

L.D. Damba^{1,2}, E.V. Balanovskaya^{2,3}, M.K. Zhabagin⁴, Y.M. Yusupov⁵, Y.V. Bogunov^{2,6}, Z.M. Sabitov⁷, A.T. Agdzhojan^{2,6}, N.A. Korotkova^{2,3}, M.B. Lavryashina⁸, B.B. Mongush⁹, U.N. Kavai-ool¹⁰, O.P. Balanovsky^{3,6} 

¹ Research Institute of Medical and Social Problems and Control of the Healthcare Department, Kyzyl, Russia

² Research Centre for Medical Genetics, Moscow, Russia

³ Biobank of Northern Eurasia, Moscow, Russia

⁴ National Center for Biotechnology, Astana, Kazakhstan

⁵ Institute for Strategic Studies of the Republic of Bashkortostan, Ufa, Russia

⁶ Vavilov Institute of General Genetics, RAS, Moscow, Russia

⁷ L.N. Gumilyov Eurasian National University, Astana, Kazakhstan

⁸ Kemerovo State University, Kemerovo, Russia


⁹ Tuvan Institute of Humanitarian and Applied Socio-Economic Studies, Kyzyl, Russia

¹⁰ Tuvan State University, Kyzyl, Russia

With a view to trace the Mongol expansion in Tuvanian gene pool we studied two largest Tuvanian clans – those in which, according to data of humanities, one could expect the highest Central Asian ancestry, connected with the Mongol expansion. Thus, the results of Central Asian ancestry in these two clans component may be used as upper limit of the Mongol influence upon the Tuvanian gene pool in a whole. According to the data of 59 Y-chromosomal SNP markers, the haplogroup spectra in these Tuvanian tribal groups (Mongush, $N = 64$, and Oorzhak, $N = 27$) were similar. On average, two-thirds of their gene pools (63 %) are composed by North Eurasian haplogroups (N*, N1a2, N3a, Q) connected with autochthonous populations of modern area of Tuvans. The Central Asian haplogroups (C2, O2) composed less than fifth part (17 %) of gene pools of the clans studied. The opposite ratio was revealed in Mongols: there were 10 % North Eurasian haplogroups and 75 % Central Asian haplogroups in their gene pool. All the results derived – “genetic portraits”, the matrix of genetic distances, the dendrogram and the multidimensional scaling plot, which mirror the genetic connections between Tuvanian clans and populations of South Siberia and East Asia, demonstrated the prominent similarity of the Tuvanian gene pools with populations from and Khakassia and Altai. It could be therefore assumed that Tuvanian clans *Mongush* and *Oorzhak* originated from autochthonous people (supposedly, from the local Samoyed and Kets substrata). The minor component of Central Asian haplogroups in the gene pool of these clans allowed to suppose that Mongol expansion did not have a significant influence upon the Tuvanian gene pool at a whole.

Key words: Y-chromosome; SNP-polymorphism; haplogroup; ethnogenesis; tribal group; Tuvans.

Оценка вклада монгольской экспансии в генофонд тувинцев

Л.Д. Дамба^{1,2}, Е.В. Балановская^{2,3}, М.К. Жабагин⁴, Ю.М. Юсупов⁵, Ю.В. Богунов^{2,6}, Ж.М. Сабитов⁷, А.Т. Агджоян^{2,6}, Н.А. Короткова^{2,3}, М.Б. Лавряшина⁸, Б.Б. Монгуш⁹, У.Н. Кавай-оол¹⁰, О.П. Балановский^{3,6} 

¹ НИИ медико-социальных проблем и управления Республики Тыва, Кызыл, Россия

² Медико-генетический научный центр, Москва, Россия

³ АНО «Биобанк Северной Евразии», Москва, Россия

⁴ Национальный центр биотехнологии, Астана, Казахстан

⁵ Институт стратегических исследований Республики Башкортостан, Уфа, Россия

⁶ Институт общей генетики им. Н.И. Вавилова Российской академии наук, Москва, Россия

⁷ Евразийский национальный университет им. Л.Н. Гумилева, Астана, Казахстан

⁸ Кемеровский государственный университет, Кемерово, Россия

⁹ Тувинский институт гуманитарных и прикладных социально-экономических исследований, Кызыл, Россия

¹⁰ Тувинский государственный университет, Кызыл, Россия

Для выявления следа монгольской экспансии в генофонде тувинцев впервые изучены генофонды двух самых многочисленных тувинских родов, для которых по данным гуманитарных наук ожидается наибольший вклад центральноазиатского компонента, связываемого с монгольской экспансией. При таком подходе результаты исследования могут служить верхней оценкой «монгольского влияния» на генофонд тувинцев в целом. По данным о 59 SNP-маркерах Y-хромосомы спектры гаплогрупп генофондов этих тувинских родов (монгуш, $N = 64$; ооржак, $N = 27$) оказались сходными. В среднем две трети их генофондов (63 %) составляют «североевразийские» гаплогруппы (N*, N1a2, N3a, Q), связываемые с автохтонным населением современного ареала тувинцев, тогда как «центральноазиатские» гаплогруппы (C2, O2) составляют менее пятой части (17 %) генофонда изученных тувинских родов. Для монголов наблюдается прямо противоположное соотношение: 10 % «североевразийских» и 75 % «центральноазиатских» гаплогрупп. Все полученные результаты – «генетические портреты», матрица генетических расстояний, дендрограмма и график многомерного шкалирования, отражающие генетические связи тувинских родов с популяциями Южной Сибири и Центральной Азии, свидетельствуют о значительном сходстве генофондов тувинских родов с популяциями Хакасии и Алтая и позволяют сделать

вывод о формировании тувинских родов монгуш и ооржак на основе автохтонного населения (предположительно – местного самодийско-кетского субстрата). Малый вклад в генофонд этих родов «центральноазиатских» гаплогрупп позволяет считать, что и на генофонд тувинцев в целом монгольская экспансия не оказала значимого влияния.

Ключевые слова: Y-хромосома; SNP-полиморфизм; гаплогруппа; этногенез; род; тувинцы.

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The Tuvan Republic (Tuva or Tyva) is situated in the very heart of Asia, lying at its geographical center among the mountains and foothills of the Altai-Sayan region. Both ancient and more recent ways of migration passed through Tyva, including the Silk Road that connected the East and the West of Eurasia. That is responsible for sophisticated culture-genesis of indigenous population, as the territory has long been exposed to various tribes mixing and formation, altering of languages (there is one of Turkic languages spoken today) and cultural paradigms (along with buddhism, traditional shamanism is still being practiced). Those processes might have considerably affected the gene pool of the Tuvans. However, one of the most acute problems in revealing the ontogeny is the extent of the Mongol expansion influence.

Tuvanian and Mongoloid tribe groups had long been historically united while being ruled by the Chinese Qing dynasty as a part of Outer Mongolia. After the Mongolian national revolution in 1911 and the events followed, Mongolia declared independence from China, while Tuvans got independent in 1926 to establish the Tuvan People's Republic. In 1944, the Republic became a part of the Soviet Union. The historical destinies interplay of Tuvanian and Mongoloid tribes may have left a considerable mark on the gene pool of modern Tuvans. The most correct way to reveal the impact of the Mongol expansion in the Tuvanian gene pool forming is to study the clans for which this influence is supposed to be most significant.

In 2010, Tuvans numbered 249 thousand people by population census (Results of the All-Russian Census of 2010) and were subdivided into 26 clans (Serdobov, 1971). Unfortunately, the ethnographers from the Tuvan Institute of Humanitarian and Applied Socio-Economic Studies report no integrated historical ethnographic and linguistic research on settling and populations of Tuvanian clans having been conducted since 1970. However, in 7 of 26 clans (namely, Mongush, Oorzhak, Ojun, Kuzhuget, Khertek, Salchak, Donghak), ethnographers suppose the Mongol ancestry to be considerable. Representatives of those seven clans make up to half of all the Tuvanian people, while two of them (Mongush and Oorzhak) comprising about 33 % of the whole population. Thus, to assess the Mongolian influence upon the gene pool of Tuvans, we have studied the gene pools of the two most numerous of those seven clans being presumingly most influenced by the Mongol expansion; it is difficult to make representative samples for the other minor clans. The evaluation obtained is considered as the upper assessment of the Mongolian ancestry; as for the rest of the Tuvans,

ethnographers, historians and linguists conceive the influence to be insignificant.

For Mongush and Oorzhak, West and partially, Central Tyva are the autochthonous territories. However, the Mongush representatives (about 57.5 thousand people) inhabit all the koshuuns of Tyva, and the Oorzhak representatives (about 25 thousand people) live mainly in the western part of Tyva (Barun-Khemchinsky and Dzun-Khemchinsky koshuuns). There has not been consensus either on the scientific etymology of those clans' names, or their ethnogenesis. Two controversial hypotheses (Mongolian and Turkic ones) do interpret different combinations of ethnographic, historical and linguistic data. We have detailed these hypotheses at another paper (Damba et al., 2018), so only brief information is given below.

The “Mongolian” hypothesis. *Mongush.* The most popular is the version of Mongolian origin of the ethnonym directly linking it to the ethnonym “mongol”. Ancient Mongols used to have the form “mongyus”. A famous sinologist N.Ts. Munkuev considered it not only as one of transcriptions, but a special form of the ethnonym “mongol” (Tatarintsev, 1980).

Oorzhak. This ethnonym is referred to medieval mongolisms related to the words “oghurchak” in old written Mongolian (“abandoned”, “left”, “lonely”), and “oortzog” in modern Mongolian (“distinct”, “separate”).

The “Turkic” hypothesis. According to B.I. Tatarintsev (1986), who was a turkologist specializing in Tyva, the ethnonyms “mongush” and “oorzhak” have Turkic origin, so does the ethnonym “tuva”. Most historians agree that this ethnonym was first recorded in Chinese documents of VII century. The tribe “dubo” belonged to Tiele people, along with ancient Uyghurs (Bichurin, 1950). The tribe “tuba” (“tubas”) was also mentioned in the Mongolian document of XIII century “The Secret History of the Mongols” as the one conquered in 1207 (The Secret History, 1941).

Oorzhak. This clan is suggested to get its modern name “Oorzhak”–“Oghurtchak” from the Mongols not later than in XIII–XIV centuries during the Mongol military expansion, as in modern Mongolian language the word “ogurtchak” was changed by “oortzog” (Tatarintsev, 1986). The Oghur tribes are known from the written sources of V–VII centuries. Some of those tribes migrated westward, giving rise to the peoples of Khazar-Bulgarian subgroup of Turkic languages. On the other hand, up to most turkologists, the ethnonym “uyghur” originates from “oghur” as nomadic Uyghurs had been dominating the territories of modern Mongolia and nearby areas for more than a century (745–847 AD). Thus,

the ethnonym “oorzhak” may go back to the Turkic ethnonym “oghur” (Klyashtorny, Savinov, 2005). Later, the Mongols used the word “oghurtchak” to name the tribes migrating from their native lands to escape invaders. It is known that in XVII century, the Oorzhaks were migrating with other clans about Mountain Altai and along the banks of the upper Ob river outside of the present-day Tuva territory (Serdobov, 1971). B.O. Dolgikh (1960) was of the opinion that the Oorzhaks were Mongolian-speaking in XVII–XVIII centuries, nevertheless he cited the document dated to 1652 and referring the Oorzhaks to Turkic-speaking clans.

Mongush. B.I. Tatarintsev gave preference to searching for ethymology of the name “mongush” in South Siberian and Old Turkic languages. In Turkic ethnomy, “mongush” correlates to the Kyrgyz “munghush”, the Bashkir “munash”, the Chuvash “mon”, the Yakut “mun”, and the Old Turkic “mungas” (Old Turkic Dictionary, 1969). B.I. Tatarintsev admitted the presence of Mongolian language component in the Tuvian ethnomy, but he supposed the result to be minimal; thus he did not manage to find its direct reflection on the Tuvian ethnomy and the ethnogenesis of Tuvian clans (Tatarintsev, 1986).

Hence there are two alternative versions of the origin of the both most numerous Tuvian clans. The first one connects their ethnogenesis to Mongols and the entire invasive population from Central Asia, while the other associates their origin with local Turkic-speaking population, the autochthonous people later adopted Turkic.

Purpose of the study: the work targets to analyze the gene pool of most numerous Tuvian clans Mongush and Oorzhak by genotyping of a wide range of the Y-chromosome SNP markers. In those clans a significant impact of Mongolian factor is supposed. The aim is to detect their genetic linkage with peoples of Siberia and Central Asia and establish “the upper assessment of Mongolian influence” upon the entire gene pool of Tuvians.

Materials and methods

As the material for the study, genomic DNA was obtained by phenol-chloroform extraction of venous blood.

The total number of population samples $N = 91$; the samples from the Mongush clan were collected in Chaa-Kholsky koshuun ($N = 64$) and of the Oorzhak clan – in Barun-Khemchiksky koshuun ($N = 27$) of the Tyva Republic (Fig. 1). Blood samples were collected only from male indigenous Tuvan representatives, degree of relatedness between any of them being more than 3, and all the ancestors belonging to the same clan and living at the same territory for more than 3 generations. The informed consent to participate in the investigation controlled by the Commission of Ethics of the Research Centre for Medical Genetics (Moscow) was received from all the individuals under the study.

SNP-markers genotyping was carried out by real-time PCR method at StepOnePlus and 7900HT systems (Applied Biosystems) using Taqman assays (Applied Biosystems). 59 SNP-markers were genotyped: M130, M217, F2613, F2386, F1788, F3918, F3830, M86, F5485, SK1066, F3791, F11899, F5481, F11791, F14768, F3960, P53.1, CTS4021, M407, Z12266, M174, M69, M170, M253, M223, P37, M304, M267, M172, M47, M67, M92, M12, M9, M20,

M231, LLY22g, M178, L708, L666, B211, M2118, VL29, Z236, F4205, P31, M122, M242, M120, M378, M207, M198, M458, M343, M73, M269, M124, M70, and chrY:15310670 T>C. The nomenclature of haplogroups (hg) in the table of hg frequencies (see the Table) is given as defined by ISOGG Y-DNA Haplogroup Tree 2018 (https://isogg.org/tree/ISOGG_YDNATreeTrunk.html), names of new-discovered markers subdividing hg N3 into sub-clades N3a1, N3a2, N3a3, N3a4, and N3a5 being in accordance to proposed by Ilumäe and his colleagues (Ilumäe et al., 2016).

Nei’s genetic distances were calculated by hg frequencies (Nei, 1975). Software Djgenetic (www.genofond.ru) elaborated by Y.A. Seryogin and E.V. Balanovskaya was used for calculations. Multivariate analysis methods were conducted using a STATISTICA 6.0 software package (StatSoft. Inc., 2001) applying Ward’s method. The results were compared with the unpublished data on Y-chromosome hg frequencies in populations of Siberia and Central Asia from “Y-base” database elaborated under the supervision of O.P. Balanovsky (www.genofond.ru).

Results and discussion

“Genetic portraits” of Mongush and Oorzhak clans

In the Mongush clan, there have been revealed 10 haplogroups within the gene pool (see Fig. 1 and Table). Three most frequent hg C2, hg Q, and hg R1a1a comprising more than a half of the entire gene pool were detected with equal frequencies (19%). More than one third of the gene pool (39%) was constituted by sub-clades of hg N. Other haplogroups (total 6%), namely O2, R2a, R1b occurred in single Mongush representatives.

In the gene pool of the Oorzhak clan, there have been detected 9 haplogroups (see Fig. 1 and Table). Hg N3a turned to be the most frequent (30%), while N1a2, N3a5 and R1a1a haplogroups displayed equal frequencies of 15%. Lower frequency was observed for hg Q and hg C2b1a3. Others (total 12%) – C2b1a2a, O2, R1b – were seen in single individuals from the Oorzhak clan.

As a whole, gene pools of the two clans under the study were characterized by similar hg spectra, though their frequencies differed; this can be explained by the fact that one sampling value was twice as large as another. In both clans, two thirds of Y gene pools (in total sample, average 63%) were represented by North Eurasian hg N and hg Q (see Table), while on the contrary, Central Asian hg C2 and hg O had an insignificant place in the gene pools of Tuvian clans, average frequency being about 17%.

Let us consider the hg distribution detected in gene pools of Tuvian clans in detail.

Haplogroup C2 peaks in Central Asia (Wells et al., 2001; Zerial et al., 2003), though its variants are abundant in other peoples of Siberia and Far East. For instance, in one of Buryat clans, namely Ekhirids, hg C2 frequency is 88% (Y-base); in Kazakhs from different regions of Kazakhstan, total occurrence of hg C2 variants averages between 17 and 81% (Abilev et al., 2012; Zhabagin et al., 2013, 2014, 2017), in populations of the Amur River (such as Nanais, Negidals, Nivkhs, Ulchs) – between 40 and 65%, in Evenks – up to 68% (Y-base), in Kyrgyz people of Pamir-Alay – up to 22%, correspondingly; of all Turkic peoples of Altai, relatively

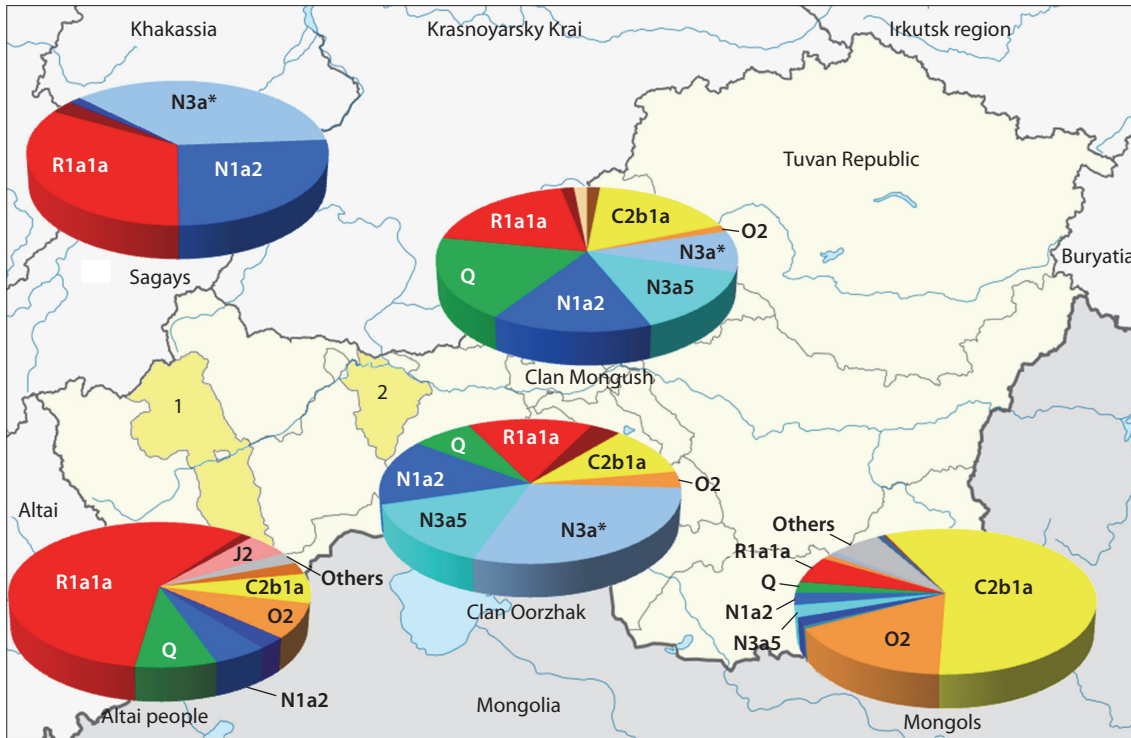


Fig. 1. Y-chromosomal haplogroup spectra in gene pools of Tuvian Oorzhak and Mongush clans and of the neighboring populations of South Siberia and Central Asia.

The sectors of the diagrams display proportions of haplogroups in gene pools. 1 – Barun-Khemchiksky koshuun (site of collecting sample material from Oorzhak representatives); 2 – Chaa-Kholsky koshuun (site of collecting sample material from Mongush representatives).

Y-chromosome frequencies in gene pools of Tuvian clans Oorzhak and Mogush and neighboring populations of South Siberia and Central Asia (%)

Y-chromosomal haplogroup	SNP marker	Clan Oorzhak (N = 27)	Clan Mongush (N = 64)	Mongols (N = 852)	Sagays (N = 69)	Altai people (N = 76)
D	M174	0	0	0.8	0	2.6
C2*	M217	0	1.6	0.4	0	0
C2b1a1	F3918	0	0	4.0	0	0
C2b1a3	F3791	7.4	0	17.5	0	2.6
C2b1a2a	M86	3.7	17.2	26.6	0	3.9
C2c1	F2613	0	0	9.6	0	0
O2	M122	3.7	1.6	16.7	0	7.9
N*	M231	0	0	1.8	1.4	2.6
N3a	L708	29.6	9.4	0	36.2	0
N3a5	F4205	14.8	14.1	2.7	0	0
N1a2	L666	14.8	15.6	2.7	26.1	5.3
Q	M242	7.4	18.8	2.6	0	7.9
R1a1a	M198(xM458)	14.8	18.8	5.9	33.3	57.9
R1b	M343(xM269)	3.7	1.6	1.1	2.9	1.3
R2a	M124	0	1.6	0.9	0	0
J2	M172	0	0	0.7	0	5.3
Others		0	0	6.1	0	2.6
Summary values (%)						
“North Eurasia”	N и Q	67	58	10	64	16
“Central-Asian”	C и O	15	20	75	–	14

Note: Symbol “*” in hg names highlights the ancestral marker presence and absence of mutations of all the daughter haplogroups. “Others” combine the haplogroups with frequency lower than 1 %.

high hg C2 frequency (16 %) is detected only in Telengits (Balanovskaya et al., 2014; Balaganskaya et al., 2011a, 2016). In Tuvinian clans under the study, hg C2 frequency is rather low – 19 % in Mongush and 11 % in Oorzhak, while in Mongols it makes up almost two thirds of the entire gene pool and comprises different genetic lines (subhaplogroups).

Despite being considered as typical for population of Central Asia, **haplogroup O** is rare in Tuvinian clans, that is one carrier of this hg has been detected in each of Mongush and Oorzhak clans, while in Mongols, its frequency is the second and reaches up to 17 % of the entire gene pool (see Fig. 1 and Table).

Hence, in the gene pools of even considered to be the most affected by the Mongol expansion clans, the arbitrarily Central Asian hg C and hg O, which compose three quarters of the Mongolian gene pool (75 %, see Table), are minor. Thus, in the entire Tuvinian gene pool, one can infer that frequency of those haplogroups is considerably lower (judging from the ratio between the populations of clans presumably affected by the Mongol expansion and of clans for which such influence is precluded). Further analysis of distribution throughout Eurasia of hg C and hg O new sub-clades, which can be traced by genome-wide studies of Y-chromosome and mass screening in indigenous peoples of Eurasia by new sub-clades, will permit to clarify the ethnogenetic links between Tuvians and other populations. Yet, the obtained data make us consider the low percentage of “Central Asian” component in gene pools of Tuvinian clans as reflection of a small genetic layer that can probably mark the trace of the Mongol ancestry. However, the other hypotheses need checking. One branch of the Silk Road (an ancient trade route that had connected East Asia and the Mediterranean 15 centuries before the Mongol expansion) crossed Tyva and could bring Central Asian gene pools as well. The territory of present-day Tyva used to be under cultural influence of Hun (Xiongnu or Chanyu) Empire, which could be attended with one of the very first waves of genetic interaction between Central Asian and South Siberian populations.

Haplogroup N is abundant all over North Eurasia from Scandinavia to Far East (Rootsi et al., 2007). The study on whole Y-chromosome sequencing conducted with participation of our group (Ilumäe et al., 2016) subdivided this haplogroup into several branches with their regional distribution. In gene pools of the Tuvians involved, hg N was represented by two sub-clades, namely N1a2 and N3a.

Sub-clade N1a2 peaks in populations of West Siberia (in Nganasans, frequency is 92 %) and South Siberia (in Khakas 34 %, in Tofalars 25 %) (Y-base). In Tuvians, N1a2 occurrence is nearly 16 % in Mongush and 15 % in Oorzhak clans, respectively, while in Mongols, the frequency is three times less (5 %). Hg N1a2 is supposed to display the impact of the Samoyedic component to the gene pool of Tuvinian clans (Kharkov et al., 2013).

Sub-clade N3a is major in the Oorzhak clan comprising almost half of the gene pool (45 %); it is represented by two sub-clades, namely N3a* and N3a5. The same sub-branches are specific to the Mongush clan as well, though with lower frequencies: N3a* – 9 % and N3a5 – 14 % (see Table). In Khori-Buryats from the Transbaikal region, a high frequency is observed – 82 % (Kharkov et al., 2014), while in Mongols, N3a5 occurs rather rarely (6 %). Hg N3a* was

detected in populations of South Siberia only, and was widely spread in Khakas-Sagays and Shors (up to 40 %) (Ilumäe et al., 2016) (Y-base).

Haplogroup Q is most spread in West and South Siberia. It reaches its maximum frequencies (Y-base) in gene pools of Ketic people (84 %), Selkups (66 %), populations of North Altai (more than a half of the gene pool in Chelkans), Koibals and Kyzyl Khakas (44 %) (Balaganskaya et al., 2011b). Hg Q makes up one fifth of the Mongush gene pool, with frequency only 3 % in Mongols. Presence of this haplogroup in Tuvinian clans can reflect the genetic contribution of Samoyedic and Paleosiberian tribes.

Thus, in the gene pools of Oorzhak and Mongush Tuvinian clans, which are speculated to be mostly affected by Mongolian ancestry, two thirds of the entire gene pools are represented by typical “North Eurasian” haplogroups (58 % in Mongush and 67 % in Oorzhak). This proves the hypothesis of significant autochthonous component presence within the gene pools of those clans; moreover, we have not detected hg N3a* anywhere else, but South Siberian populations.

Within the pan-Eurasian **haplogroup R1a1a**, two large genetic lines (sub-haplogroups) are identified: “European” (marker M458) and “Asian” (marker Z93) the latter almost never occurring in Europe (Balanovsky, 2015) but abundant in South Siberia and northern Hindustan. In the Altai-Sayan region, high frequencies of the “Asian” branch are spread in many peoples – Shors, Tubalars, Altai-Kizhi people, Telengits, Sagays, Kyzyl Khakas, Koibals, Teleuts (Y-base) (Kharkov et al., 2009). Hg R1a1a comprises perceptible parts of gene pools of Tuvinian clans (19 % in Mongush, and 15 % in Oorzhak), though its occurrence in Mongols is much lower (6 %). Those results also count in favor of the hypothesis of autochthonous component dominance even in the gene pools of clans potentially most influenced by Mongolian ancestry. If we add R1a1a variants to the “North Eurasian” haplogroups, the “not-Central Asian” component will compose average four fifth of the entire gene pools for Tuvinian clans (in Mongush 77 %, and in Oorzhak 81 %), being only 16 % in Mongols. Such data are definitely contrary to the hypothesis of a crucial influence of the Mongol expansion upon the development of Tuvinian gene pool.

Tuvinian clans position within the genetic space of Siberia and Central Asia

Position of the analyzed Mongush and Oorzhak clans within the genetic space of Siberian and Central Asian peoples by all their haplogroups cumulatively is assessed by the matrix of genetic distances (d) that displays the populations studied by genotyping of the same wide range of the Y chromosomal SNP markers as Tuvians (Fig. 2). The first column presents average genetic distances (\bar{d}) for both clans, then all the populations are ranged by their average genetic affinity to the Tuvinian clans and divided into two classes – of close to the clans’ populations ($\bar{d} < 1$) and of distant ones ($\bar{d} > 1$), highlighted on the grey background, Fig. 2, a).

To begin with, let us note that Khakas-Sagays are almost two times closer genetically to the Oorzhak clan ($d = 0.16$) than both clans to each other ($d = 0.28$), while the other Khakas groups of Koibals and Kyzyl people are the same close to the Mongush clan ($d = 0.26$) as the clans to each other ($d = 0.28$).

a

Populations	\bar{d} genetic distances	Clan Oorzhak	Clan Mongush
Clan Oorzhak	0.28	0	0.28
Clan Mongush	0.28	0.28	0
Sagays	0.31	0.16	0.45
Koibals	0.47	0.68	0.26
Shors	0.53	0.48	0.57
Tubalars	0.69	0.92	0.46
Altai-Kizhi	0.70	0.89	0.51
Chelkans	0.72	1.05	0.40
Kachins	0.79	0.85	0.73
Telengits	0.80	0.95	0.65
Buryats from Transbaikal Region	0.98	0.99	0.97
Mongols	1.01	1.36	0.65
Khamnigans	1.02	1.03	1.01
Kumandins	1.44	1.56	1.32
Kara-Kalpaks	1.49	1.75	1.22
Kirghiz	1.57	1.75	1.39
Kazakh	1.70	1.71	1.70
Buryats from Buryatia	1.86	1.88	1.84
Buryats from Irkutsk Region	3.32	3.37	3.26

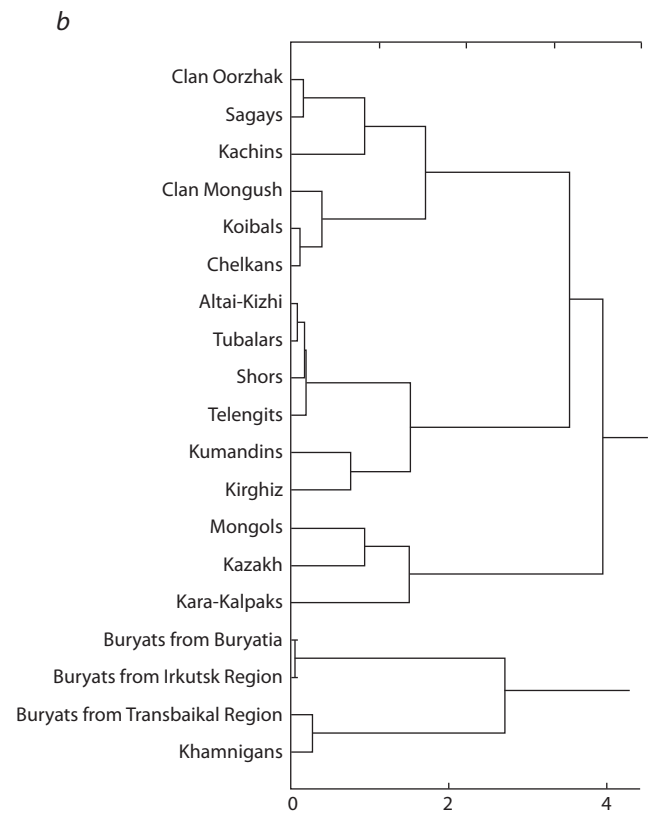


Fig. 2. Matrix of genetical distances from the gene pools of Tuvanian clans Oorzhak and Mongush to the populations of Siberia and Central Asia (a) and dendrogram of their genetic relationship (b).

By and large Khakas, Shors and populations of Northern Altai (but for very peculiar Kumandins; in the dendrogram, they associate with Kyrgyz people) and peoples of Southern Altai. In fact, Buryats of the Transbaikal region are as distant from Tuvans ($\bar{d} = 0.98$) as Mongols are ($\bar{d} = 1.01$). Greater similarity of Transbaikal Buryats to Tuvans, as compared with their geographically neighboring Buryats of Irkutsk region ($d = 3.37$) and of the Buryat Republic ($d = 1.88$), results from a very high frequency of “North Eurasian” hg N3a5 in the Transbaikal region (82 %), which composes about 15 % in Tuvanian clans.

Mongols are the first in the list of populations genetically distant from Tuvanian clans ($\bar{d} > 1$), however the Mongush clan is twice closer to them genetically ($d = 0.65$) than to the Oorzhak clan ($d = 1.36$). The same is observed for the distance to Karakalpaks ($d = 1.22$ from the Mongush clan, and $d = 1.75$ from the Oorzhak one) and to Kyrgyz people ($d = 1.39$ from the Mongush, and $d = 1.75$ from the Oorzhak clans). This fact highlights relatively more significant contribution of the “Central Asian” component to the gene pool of the Mongush clan, being in conformity with ethnography data. Yet, the absolute value of this contribution is less in comparison with the genetic impact of the autochthonous population of the regions, as it is shown in dendrogramme (see Fig. 2, b). The Oorzhak clan is in one cluster with Sagays and Katschins of Khakassia, while the Mongush clan got to the same cluster

with Koibals of Khakassia and Chelkans of Northern Altai. The neighboring cluster comprises Shors and other populations of Altai along with Kyrgyz people. Mongols together with Kazakhs and Karakalpaks are joined to a distant from Tuvans cluster, Buryats and Hamnigans to form an even more genetically remote one. Hence the dendrogram exhibits the conclusion that in Tuvanian gene pool, there prevails the ancestry component from autochthonous population who are genetically similar to their western neighbors (present-day population of Khakassia and Altai), but distant from Mongols and Buryats, who are their neighbors in the west and the south.

Multidimensional scaling plot appears to be more correct and informative, five clusters being presented (Fig. 3). Great variety of Buryat populations is reflected by two well-distinctive clusters of “west Buryats” and “east Buryats”. Southern neighbors Mongols are closer to Tuvans than their eastern neighbors (Buryats of Buryatia and Irkutsk region); but along with other populations of Central Asia (Karakalpaks, Kazakhs and Kyrgyz people), Mongols compose their own “Central Asian” cluster. Within the genetic space of Siberia and Central Asia, a compact cluster of Altai and the Tuvanian-Khakassian one are the closest. In its entirety, the plot does confirm once again the results obtained: both Tuvanian clans have most close relationship to populations of Khakassia and Altai; a weak trace of “Central Asian” component is more distinctive in the Mongush than in the Oorzhak clan.

Conclusion

Gene pools of two largest Tuvian clans appeared to be similar by Y-chromosomal spectra of haplogroups, suggesting the affinity of their origin. Different hg frequencies might mainly result from small samples. However, genetic relation of the Mongush clan to Mongolian populations is slightly closer revealing somewhat stronger influence of their southern neighbors. Though the case in point is rather a weak trace of Central Asian genetic ancestry. It is under the question, whether it can be associated with the late Mongol expansion only (manifested by the ethnonym *mongush*) or to earlier constant migrations from Central Asia. Further detection of noval Y-chromosomal sub-clades and mass screening in population of North, Central and East Asia by SNP markers of those new Y-chromosomal sub-clades might provide the answer.

Nevertheless the source of a weak “Central Asian” genetic ancestry is, the performed study unambiguously indicates that the main part of gene pools of Tuvian clans confidently being associated by ethnographers with the Mongol expansion is inherited from the autochthonous population of the Altai-Sayan highlands. Predominance of “North Eurasian” Q, N1a2 and N3a haplogroups allows to assume that Tuvian gene pool was formed on the basis of Samoyed and Kets tribes having inhabited the territory of present-day Tyva since the Neolithic (6000–3000 BC). The conclusion about rather low proportion of East Eurasian haplogroups within the gene pools of the Mongush and Oorzhak Tuvian clans, referring to a later and less significant genetic layer, correlates well with the anthropological data, which consider the South Siberian component of Tuvian ethnogenesis as an earlier and more relevant in comparison with the South Central Asian one (Aksyanova, 2009). It must be emphasized that genetic and anthropological data betoken only the biological trace of migrations, their demographic intensity and contribution to the gene pool. They say nothing about the intensity of cultural influence, which is the field of ethnographic and historical estimation.

The present study was intentionally concentrated on Y-chromosome paternal (male-specific) lines as they are inherited in the same manner as ethnonyms of clans do. However, gene pools of South Siberian and Central Asian ethnic groups are being analyzed by genotyping of the wide range of the autosomal markers. Hence, the work is just a first step towards reconstruction of interaction between indigenous population of South Siberia and Central Asia. Only integral population-genetic and historical-ethnographic investigations into clan structure of Tuvians, Mongols (as present-day Mongols comprise tribes of various ethnogenesis), and other ethnic groups of Central Asia and Siberia might open some pages of history of the very center of Asia, the largest in both territory and population part of the world.

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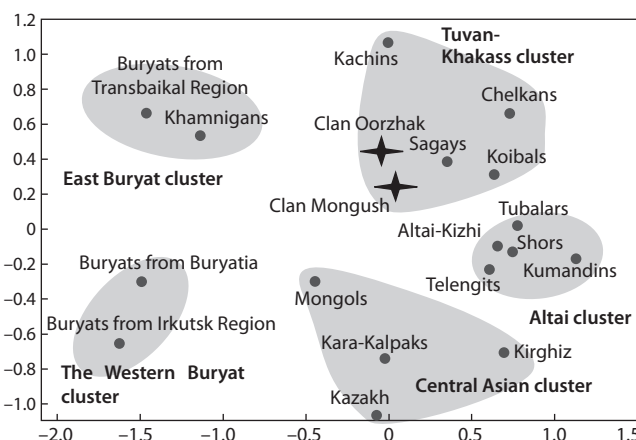


Fig. 3. Gene pools of Tuvian clans Mongush and Oorzhak in the context of the population of South Siberia and Central Asia.

Tuvian populations: Oorzhak clan, Mongush clan; Khakassia ethnic groups: Katschins, Sagays, Koibals; populations of North Altai: Chelkans, Tubalars, Kumandins; populations of South Altai: Altai-Kizhi, Telengits. The multidimensional scaling plot by frequencies of 75 Y-chromosomal haplogroups in 19 populations of South Siberia and Central Asia. Stress value = 0.13; alienation = 0.15.

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Conflict of interest

The authors declare to have no conflict of interest.

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