Genochronology: gender differences in the length of generations

[1]F. A. Platonov, [1]G. A. Timofeyev, [2]S. K. Kononova, [1]V. L. Osakovsky, [3]V. B. Ignatyeva
[1]Institute of Health, M. K. Ammosov North-Eastern Federal University,
[2]Yakut Scientific Center of Complex Medical Problems, Siberian Branch of the Russian Academy of Medical Sciences,
[3]Institute of Humanitarian Research and Problems of Indigenous Peoples of the North, Siberian Branch of the Russian Academy of Sciences.

Summary. In the assessment of one of the important fundamentals of genochronology – the length of generations, the authors justify the need for significant amendments in the calculation of ages of mutations depending on the basic types of inheritance in isolated populations. The confirmation of the proposed hypothesis in calculating ages of mutations identified in developmental studies forms a representative basis for the application of new approaches in the method of calculation of reliably dated events in the field of genetic archeology.

Keywords: genochronology, gender, length generation, population, Yakuts.

The gene pool of the Yakut population is characterized by a low level of Y-chromosome diversity (passed from father to son), combined with a wide polymorphism of mitochondrial DNA (passed from mother to children). Moreover, if in mDNA Yakuts are close to other Siberian ethnic groups (in particular, to Tuvins), then in Y-chromosome - they are sharply different from them [1,2,3]. The reported genetic features of Yakuts disagree with the prevailing opinion of their mass migration from the south, and, respectively, suggest different processes in their ethnogenesis [4, 5].

The main dispersal area of the Finno-Ugric peoples include the circumpolar territories of Eurasia, while in the east it is "cut off" on the border with Yakutia, whose male population is genetically related to the Finno-Ugric peoples. Ethnographic literature uses the concept of virilocality of exogamous marriages, whose features include the preservation of fathers' languages in children. In view of the fact that by Yakuts' Y-chromosome relates them to the Finno-Ugric peoples [2], we can assume that: 1) Yakuts (men) changed the language of their ancestors; and 2) peoples who today speak languages, relating to the Finno-Ugric group, at some point in history abandoned their "native" Turkic language. In the latter case, the origin of the Finno-Ugric languages becomes unclear, and thus this assumption does not hold water. In this regard, the most preferred is the assumption of the Turkization of the Yakuts' ancestors' language [4]. By haplogroup 16, the Yakuts are closely related to the Evenkis and the Buryats [3], whose modern languages belong to different language groups, dissimilar to the Turkic or the Finno-Ugric.

Let us consider a manifestation of the "founder effect" on the model of such a geographically isolated population as Yakuts, in which the transfer of SCA1 mutation in generations can be traced over a long historical period. Modern molecular genetics allows us to determine the “lifetime” of the population having a common ancestor. For example, according to these calculations, haplogroup N1c which is widespread among Yakut men came into existence about 6,300 years ago, and the “lifetime” of the Yakut population, measured from the time of their common ancestor is 1400 ± 180 years [6]. One of the main concepts used to form the genochronological structures is “the duration of the interval between the generations", taken to be 25-30 years and which, in our opinion, needs some refinements, depending on the characteristics of the transmission of mDNA and Y-chromosome.

Results of the study of SCA 1 mutation (dominant form of spinocerebellar ataxia) in the Yakut population showed that all of its modern carriers live across the whole territory of Yakutia and have the same chromosome fragment with a haplotype size of 4.3 cM [7]. To determine the time the mutation started in the Yakut population we used the formula proposed by M. Slatkin [8]. The number of generations with the mutation is 36.6. If the duration of the interval between the generations is taken as 25-30 years, the age of the mutation is 915-1098 years. On the historical chronology scale this time corresponds to the 10th or 11th centuries. The main focus of the mutation is the Lena-Aldan interfluve area, which in the end of the first millennium, as well as in our days, was one of the areas densely populated by Yakuts.

Over the past two decades, the Research Institute of Health of the North-Eastern Federal University (previously - NPC “Vilyuisk encephalomyelitis”, Ministry of Health of the Sakha Republic (Yakutia), the Institute of Health Sciences of the Academy of Sciences of the Sakha Republic (Yakutia)) collected 57 genealogies of Yakut families burdened with hereditary spinocerebellar ataxia type 1. On the basis of the available evidence we examined 166 cases of the disease in order to determine the average age of fathers and mothers, in which they started passing the mutation (Fig. 1). The indicators obtained can be regarded as the approximate period of the reproductive function (generation length) of individuals at different stages of historical development of the Yakut society. The patients were born in the period from 1890 to 1976, and during this period the men showed a decline in the average age of the parents at the time of the birth of the first child in a family from 37.4 ± 7.9 years (“more mature” among those born before 1910) to 23.6 ± 2.2 years (born after 1960). A similar pattern is observed in women – a decline in the indicator from 26.3 ± 6.1 to 22.6 ± 2.2 years of age [9]. Thus, in the duration of the interval between the generations, as a result of these gender differences, the historical time of the SCA 1 mutation distribution in the gene pool of the Yakut population may in fact be even more ancient. If on the maternal line, the mutation transmission interval may on an average be 25 years, on the paternal line it can be more than 35 years.

An additional argument in favor of this conclusion are documented data on the expressed difference in the age of the bride and groom, in particular, data from 689 married couples, recorded in parish registers in the period of 1894-1917 of two churches located in Central Yakutia. According to them, in 92.3% of marriages the groom was older than the bride: 44.6% - by 1 to 6 years of age, 25.1% - by 7 to 12 years, 23.8% - by 13 or more [10]. The stability of this phenomenon is evidenced by the observation by V. F. Troshchansky in the 1870s. Thus, summarizing the data of 572 marriages, he found that 44% were cases when the groom was the bride's senior by up to 5 years, 14.2% - up to 10 years, 22.2% - up to 20 years, 3.15% - over 20 years, while in two marriages the groom was 30 years older, in two more cases - 35 years older than the bride [11]. This age structure of the spouses is also an evidence of a pronounced difference in the lengths of generations in the transmission of Y - chromosome and mitochondrial DNA.

Conclusion.

During genochronological studies of isolated populations it is necessary to take into account the fact of pronounced differences in the length of male and female generations. Reaching the age of the male reproductive function is only the lower limit of the length of generation, while the upper limit can reach up to 70 years or more. Average lengths of generations in isolated populations (Yakuts) could have the following indicators: for mDNA the interval is on an average 25-30 years, and Y-chromosome interval - 35 to 55 years or more.

Thus, the historical time of the isolation of Yakuts' ancestors in the Middle Lena should be determined by the age of the Yakut Y-chromosome variant itself with regard to the appropriate length of the male generation, which is significantly higher than that of the female generation. In other words, the predecessors of the Yakut population, in all probability, inhabited Central Yakutia as early as in the first millennium A.D.

References.

1. Klesov A.A. Pervy primer opredeleniya vremeni zhizni obshchego predka po iskopaemym gaplotipam [The first example of determining the lifetime of a common ancestor by fossil haplotypes] Vestnik Possiyskoy Aкademii ДNК-genealogii [Bulletin of the russian Academy of DNAgenealogy V.3, №3, 2010,мart.MichaelTemosh'sStorefront. http://stores.lulu.com/temosh. (in Russian).

2. Osaкovskiy V.L. Shatunov A.Yu. Goldfarb L.G. Platonov F.A. Otsenкa vozrasta mutantnoy khromosomy po genu SCA1 v yakutskoy populyatsii [Estimation of the age of the mutant chromosome SCA1 gene in the Yakut population]// Yakutskiy meditsinskiy zhurnal [Yakut Medical Journal].2004, №2 (6), p.63. (in Russian).

3. Platonov F.A. Nasledstvennaya mozzhechkovaya ataksiya v Yakutii [Hereditary cerebellar ataxia in Yakutia] Dis... dok. med. Nauk [MD thesis]. Moscow, 2003, 158 p. (in Russian).
4. Popov B.N. Sotsialisticheskie preobrazovaniya semeyno-brachnykh otnosheniy u narodov Yakutii: istoriko-sotsiologicheskiy aspekt [Socialist transformations of family relations among the peoples of Yakutia: historical and sociological aspect]. Novosibirsk: Nauka, 1987, P.78. (in Russian).
5. Radloff V.V. Ethnographische Übersicht der Turkstamme Sibiriens und der Mongolei [Ethnographic overview of the Turkic tribes of Siberia and Mongolia]. Leipzig, 1884.
6. Stepanov V.A. Etnogenomika naseleniya Severnoy Evrazii [Ethnogenomics of North Euroasia population] Pechatnaja manufaktura [Print Manufactory]. Tomsk, 2002, 244 p. (in Russian).
7. Tokarev S.A. Ocherk istorii yakutskogo naroda [Essay on the History of the Yakut people]. Moscow, 1940. (in Russian).
8. Troshchanskiy V.F. Лyubov i brak u yakutov [Love and marriage in Yakuts] Zhivaya starina [Living Antiquity]. –1909. –Vyp.1. –P.21. (in Russian).
9. Fedorova S.A. Geneticheskie portrety narodov Respubliki Sakha (Yakutia) [Genetic portraits of the Republic Sakha (Yakutia) people]. –Yakutsk, 2008. –235 pp. (in Russian).
10. Slatkin M. Rannala B. //Estimating allele age.- Annu Rev Genomics Hum Genet. 2000; 1: 225-249.
11. Pakendorf B., Morar B., Tarskaia L.A. et al. Y-chromosomal evidence for a strong reduction in male population size of Yakuts // Hum. Genet. –2002. –Vol.110. –P.198-200.