

Генетическая история нивхов

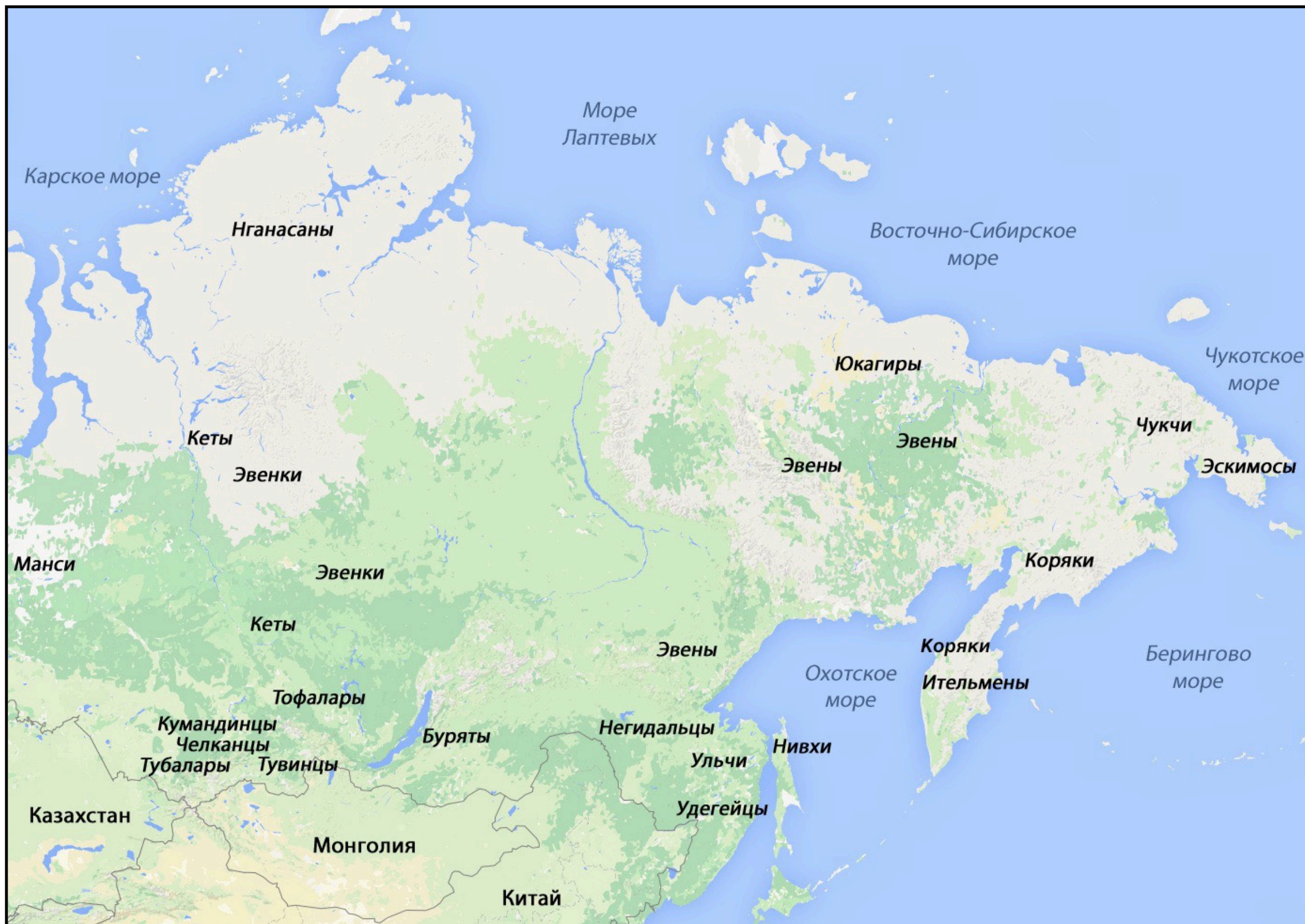
Станислав Дрёмов

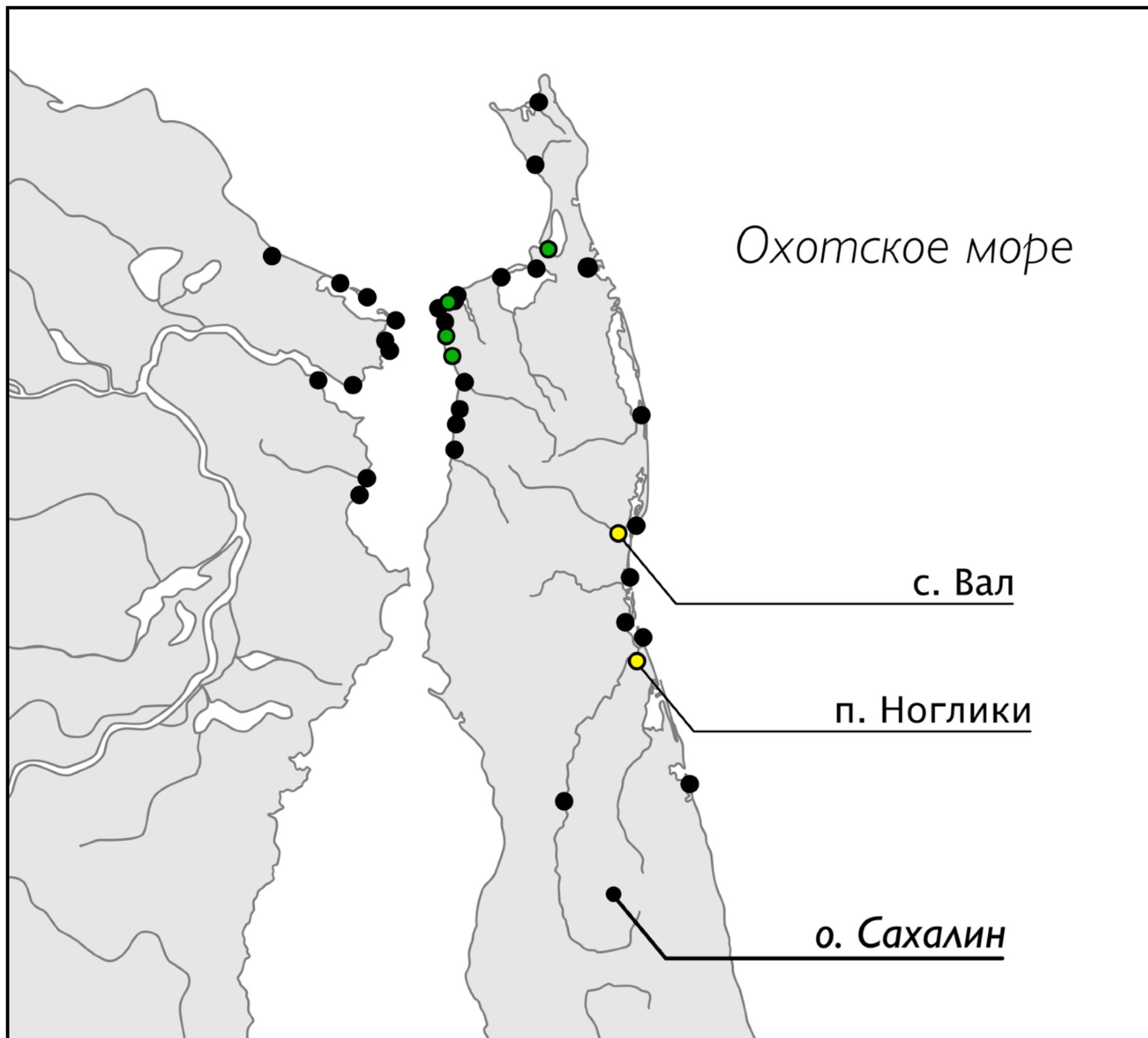
Лаборатория молекулярной генетики человека, ИМКБ СО РАН

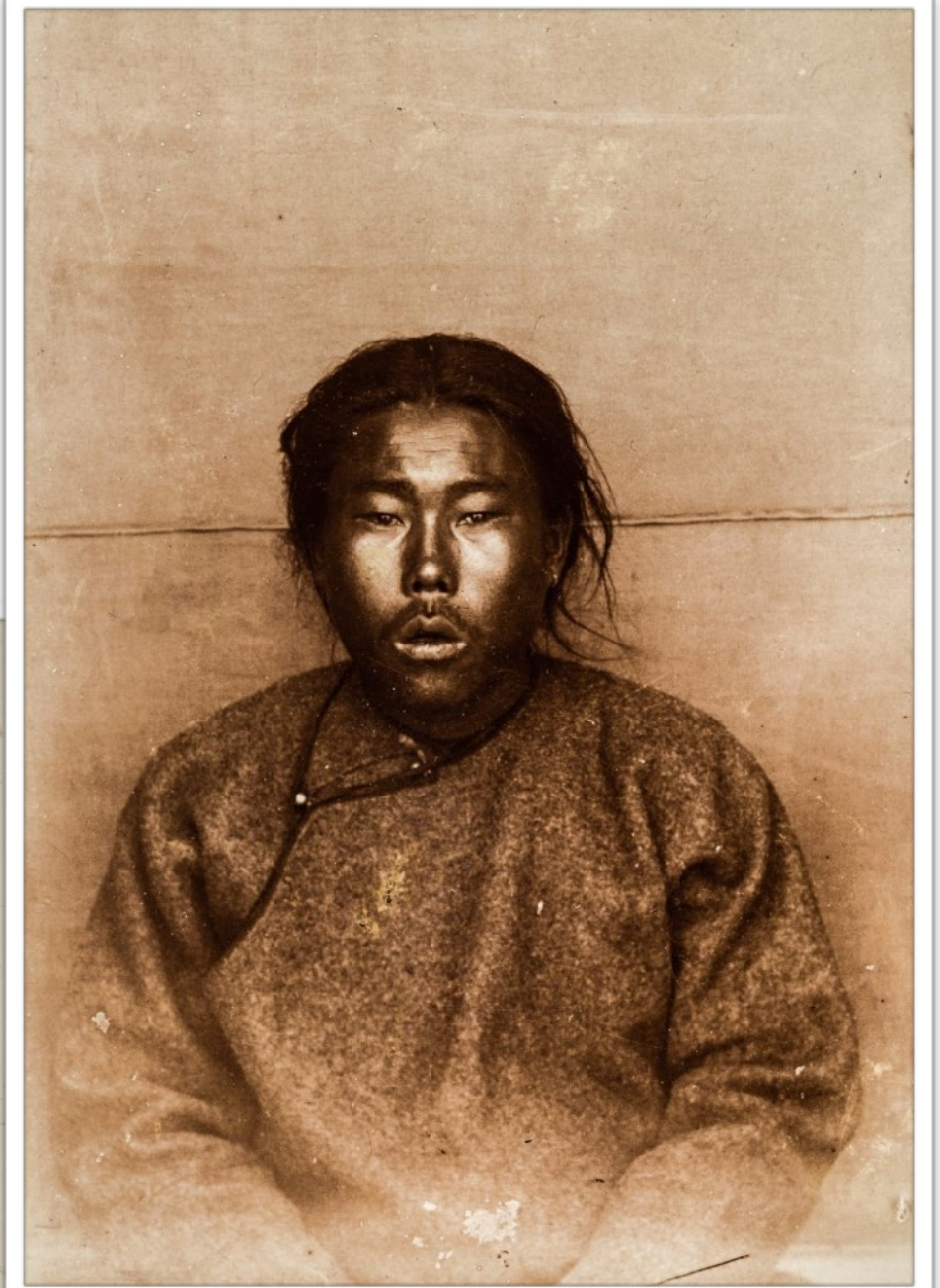


Генетическая история НИВХОВ

Тысяча
лет
одинокчества



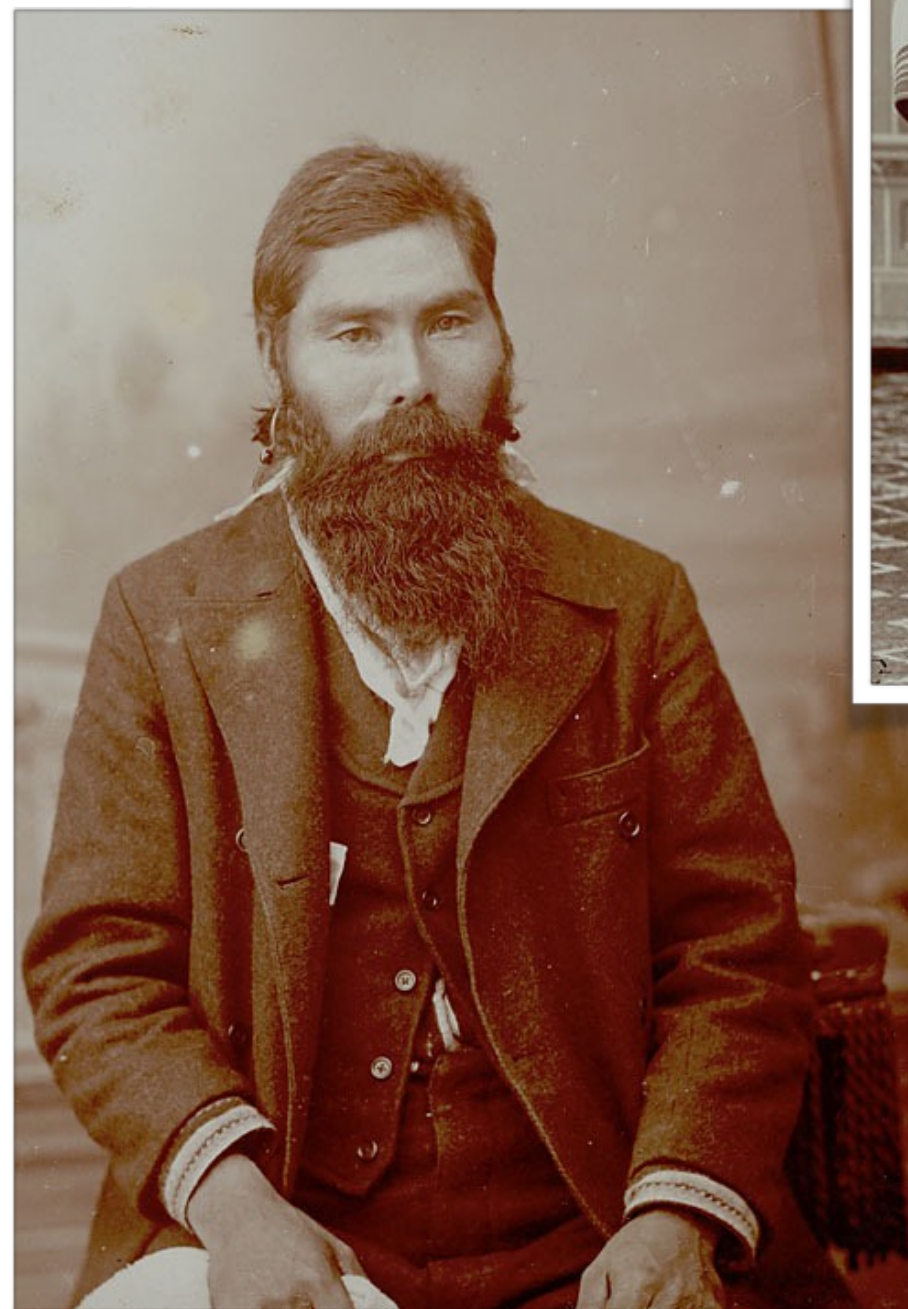




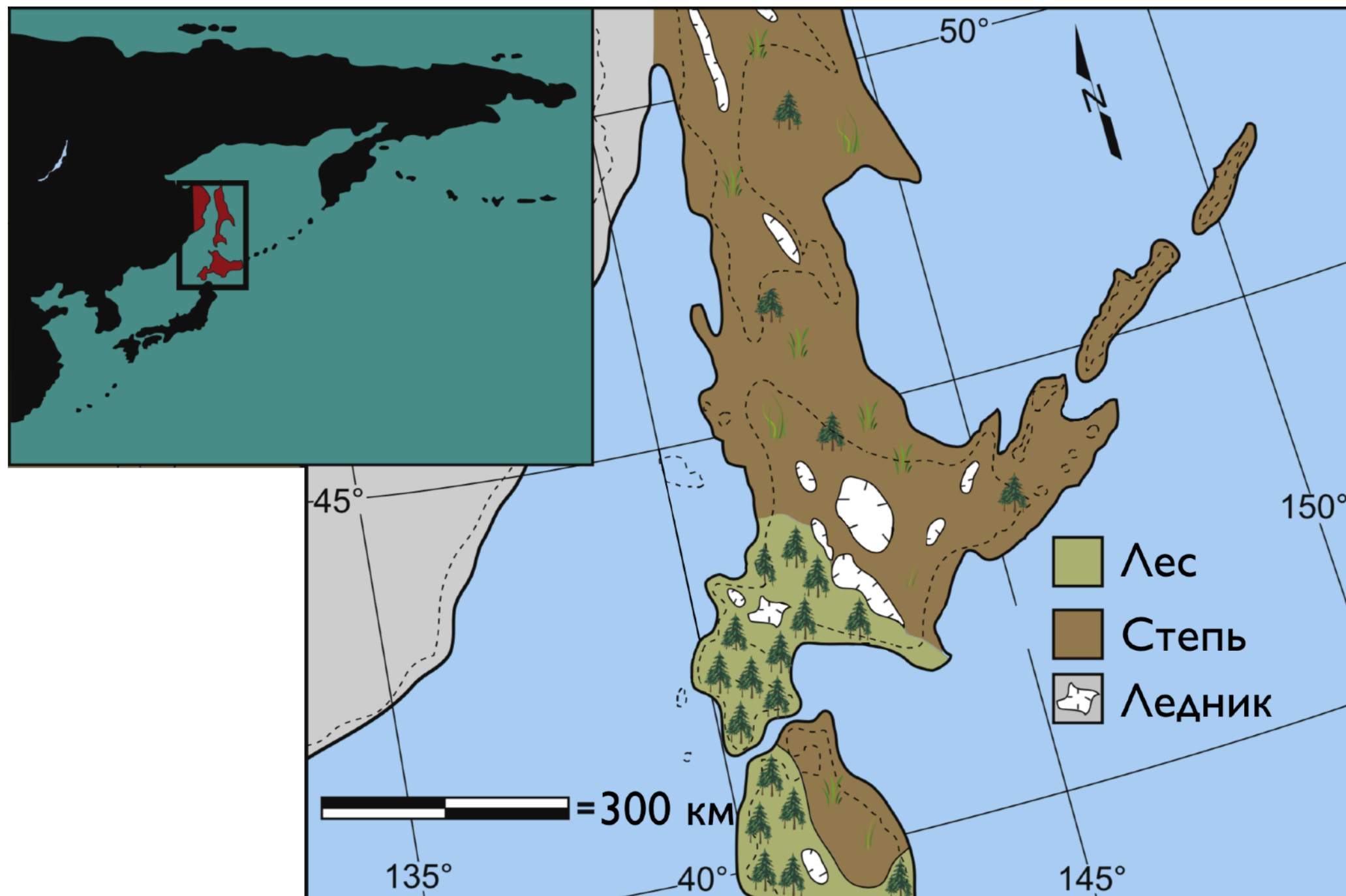
Нивхи





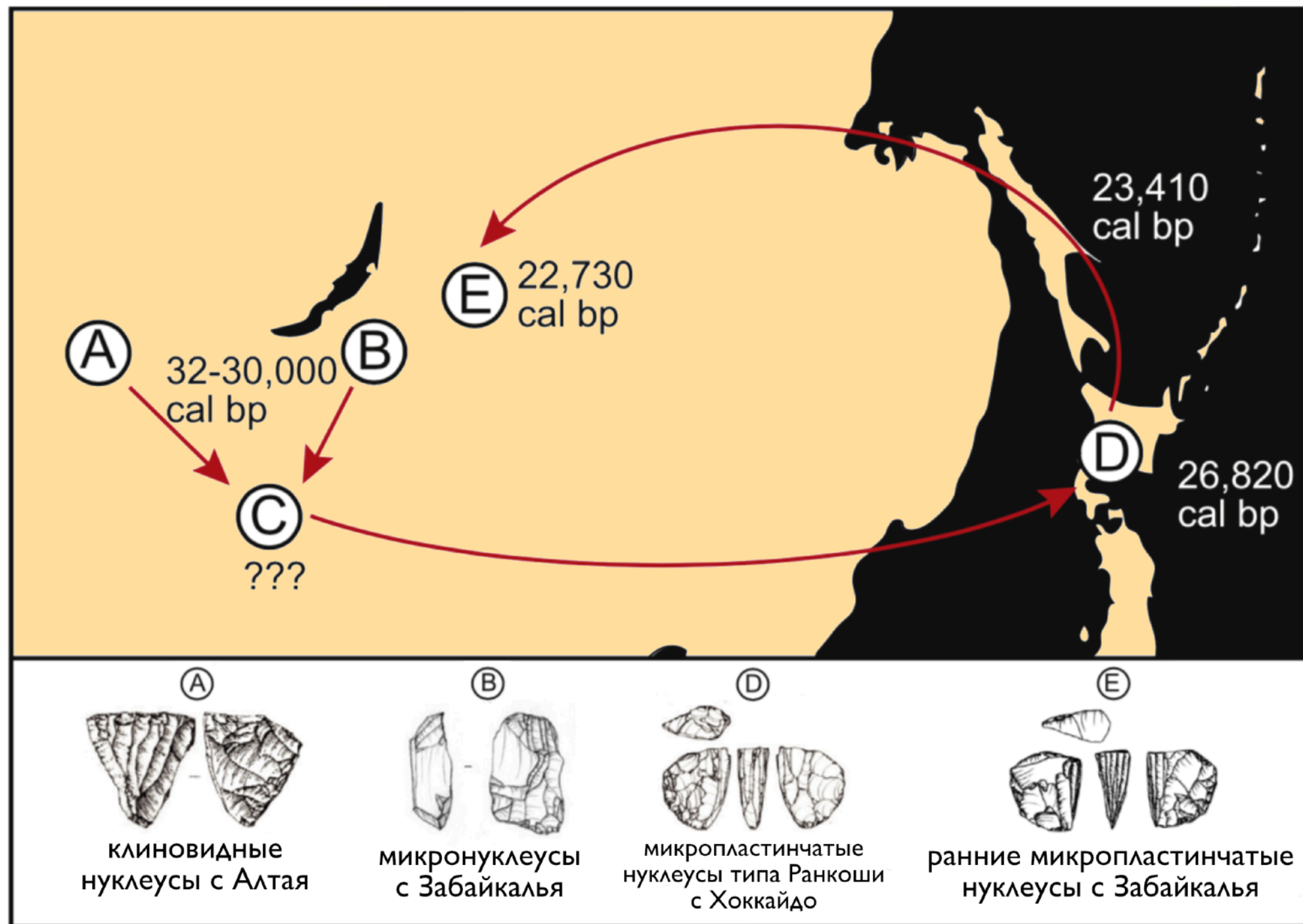


Айны



Ландшафт Сахалина, Хоккайдо и Курил

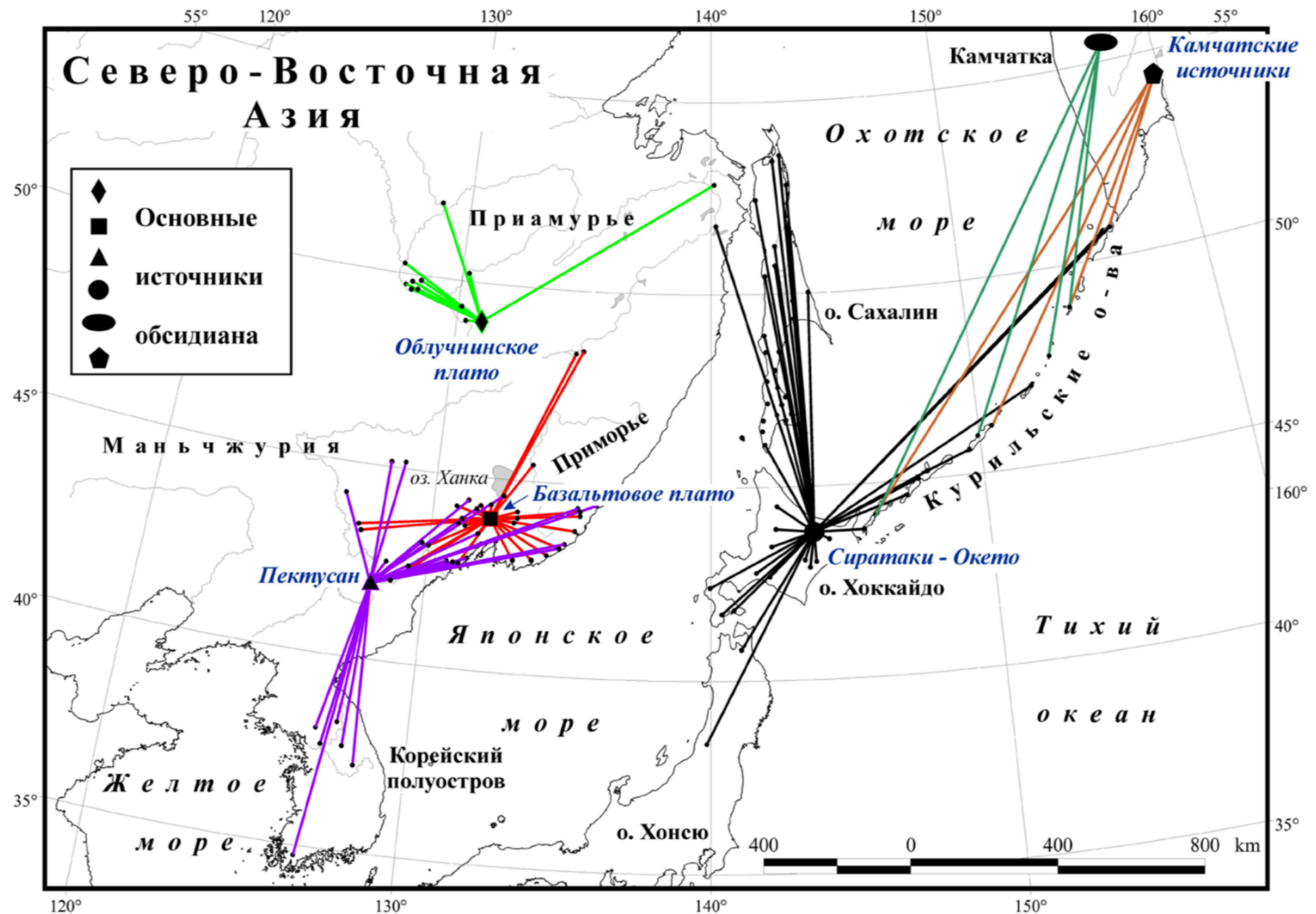
Во времена максимума последнего оледенения



Распространение микропластинчатых нуклеусов

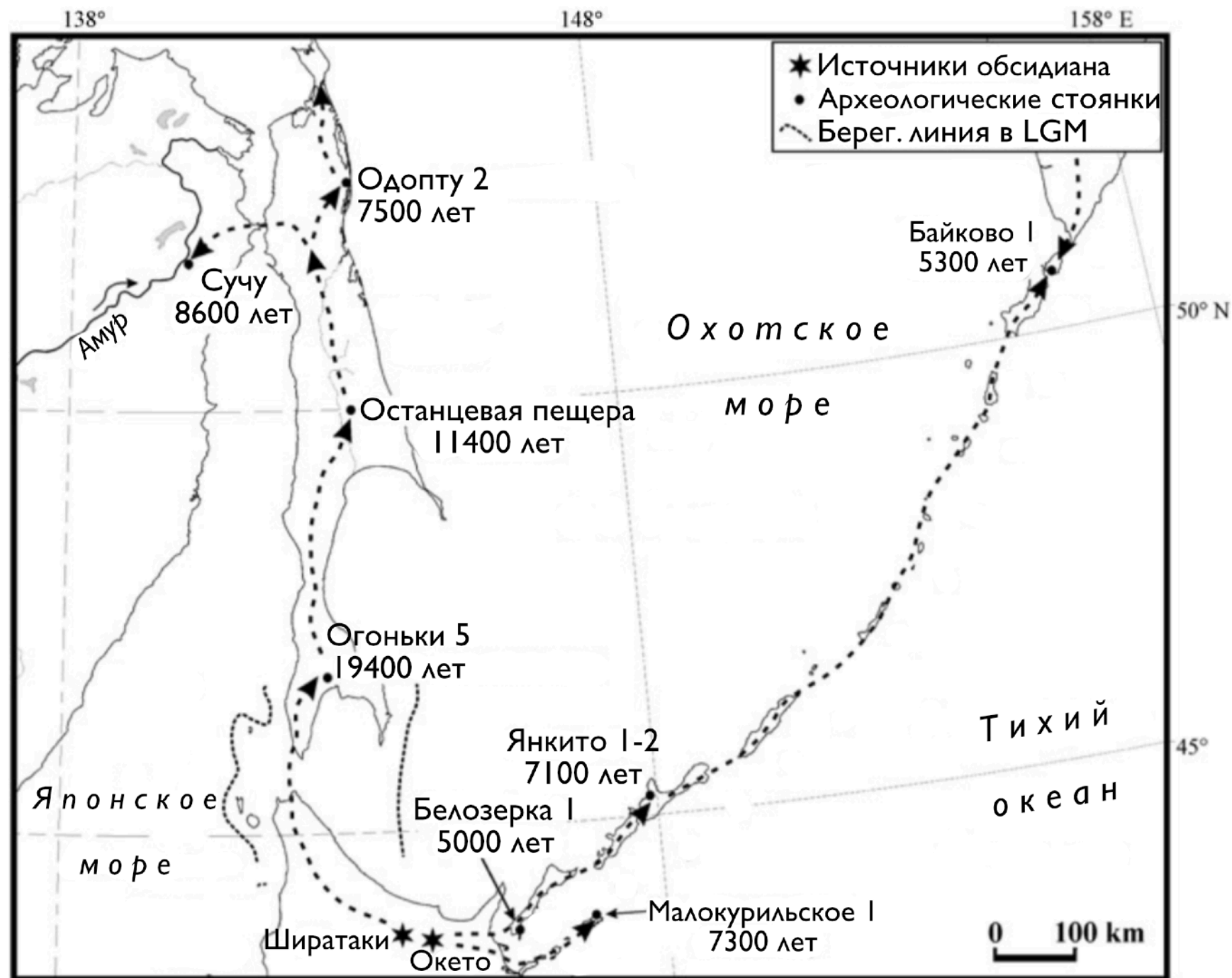
Во времена максимума последнего оледенения





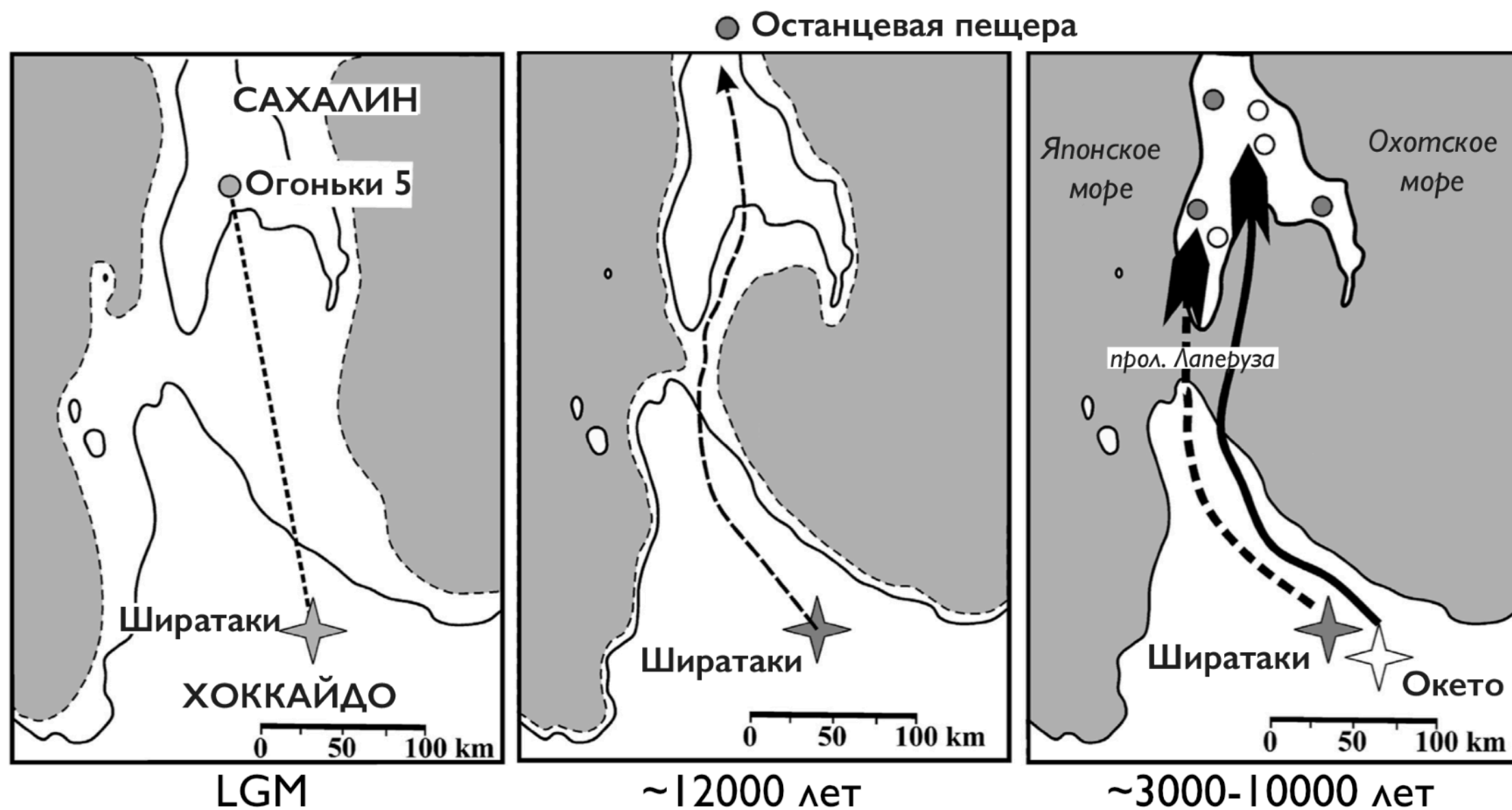
Сети доисторического обмена обсидианом

Распространение и возраст



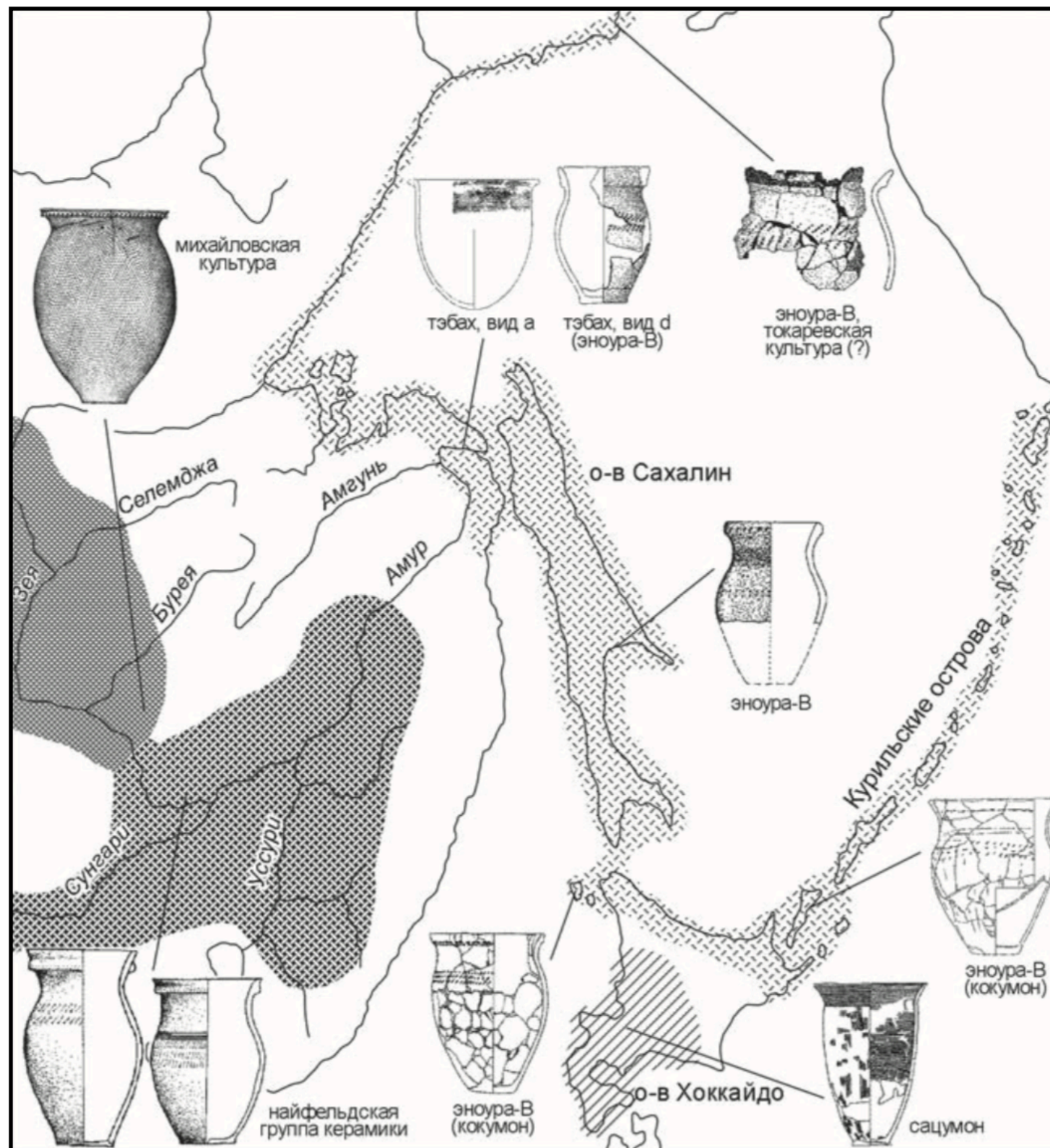
Сети доисторического обмена обсидианом

Расстояние и маршрут

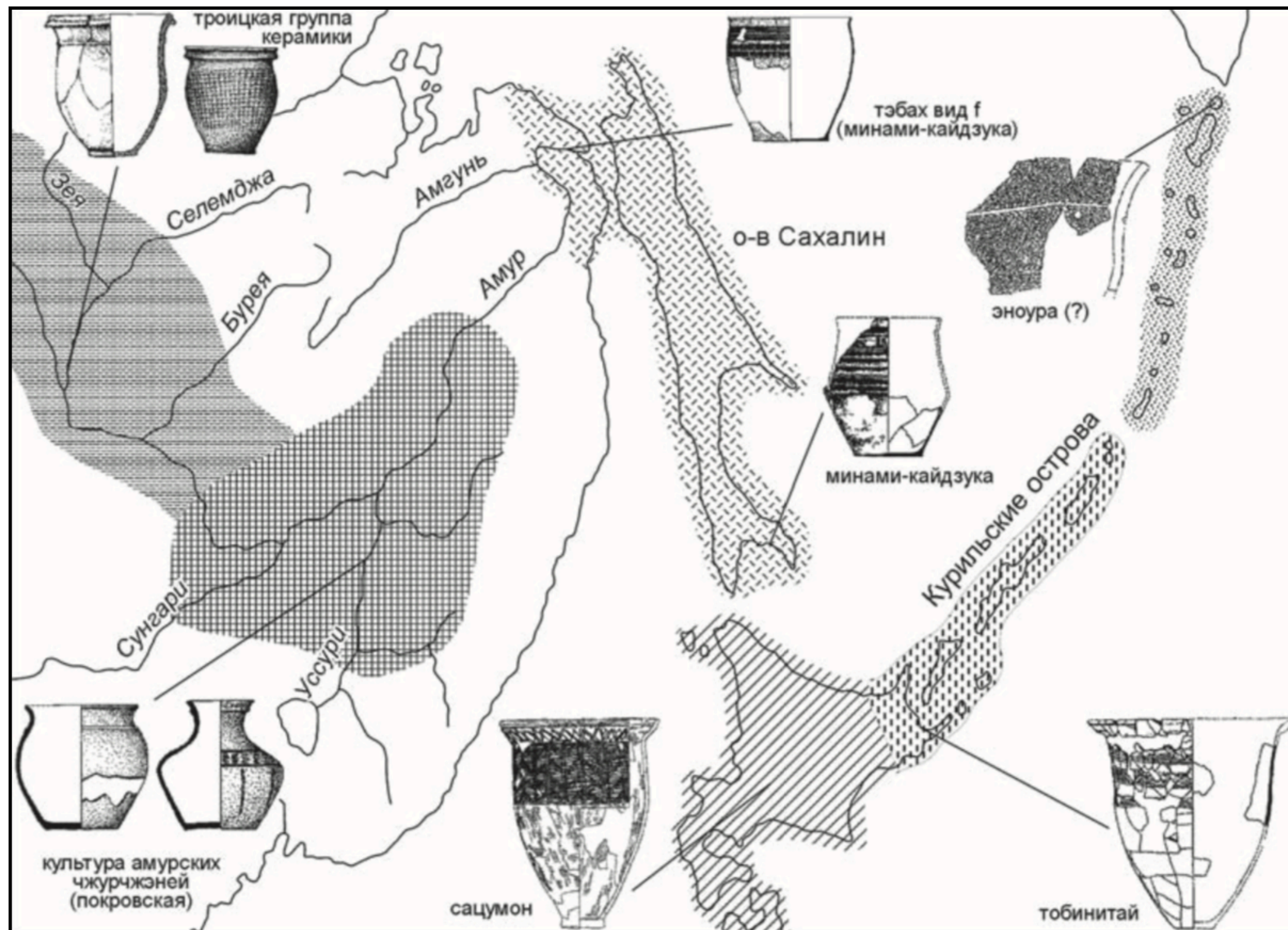


Сети доисторического обмена обсидианом

Препятствия



Основные керамические традиции, VII век

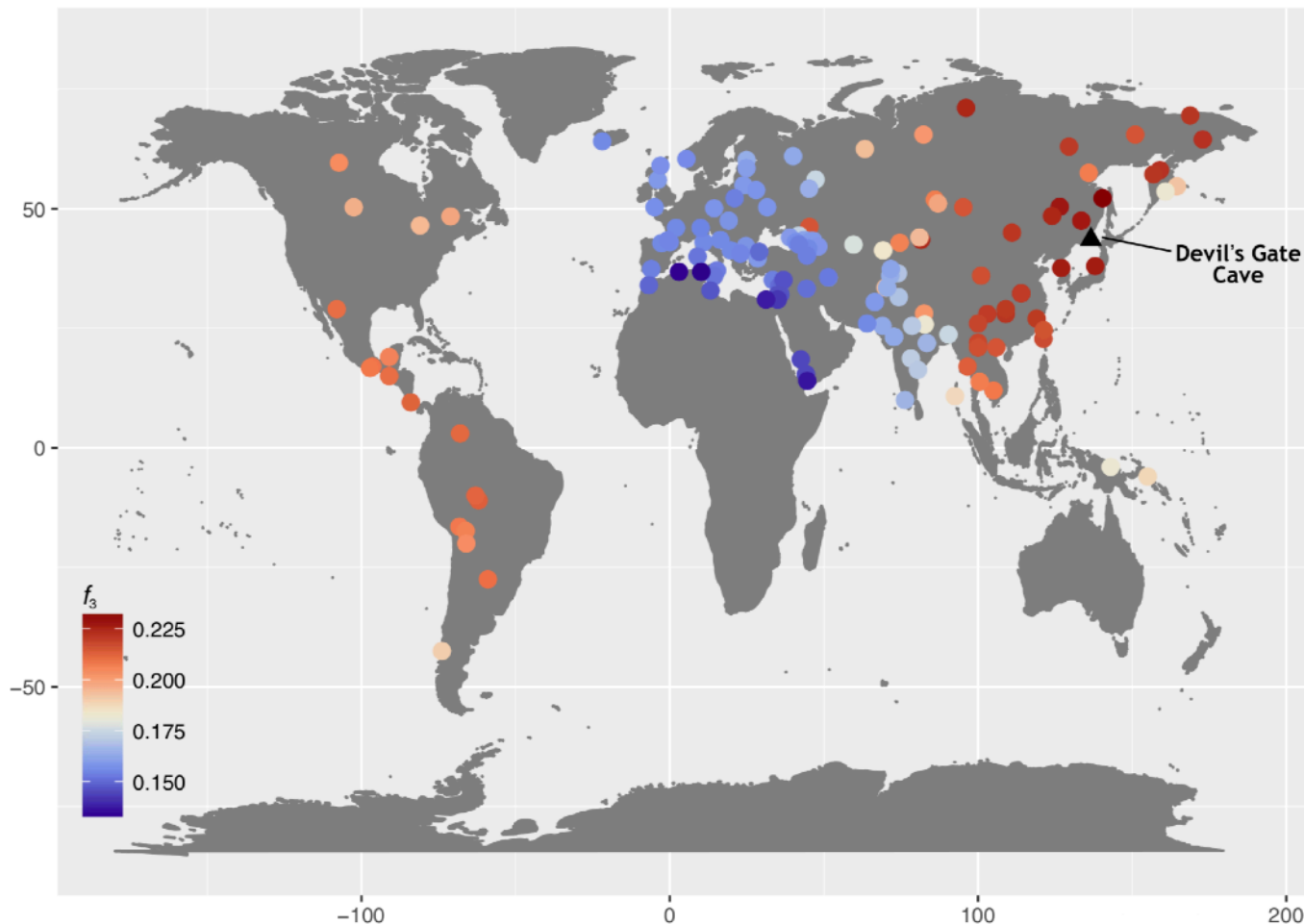


Основные керамические традиции, IX-X век

	Северные нивхи	Восточные нивхи	Айны	Айны Эдо	Охотская	Дзёмон Хоккайдо
YI	63.7	91.2	19.6	31.9	43.2	-
D4m	22.4	-	-	-	-	-
D4o	5.2	-	-	2.1	-	-
G1	8.7	4.4	21.6	9.6	24.3	11.1
G2	-	2.2	3.9	-	-	-
M9a	-	2.2	2.0	1.1	-	-
Прочие	-	-	52.9	55.3	32.5	88.9

Частоты митохондриальных гаплогрупп

$f_3(X, \text{DevilsGate1}; \text{Khomani})$



EVOLUTIONARY GENETICS

Genome-wide data from two early Neolithic East Asian individuals dating to 7700 years ago

Veronika Siska,^{1*} Eppie Ruth Jones,^{1,2} Sungwon Jeon,³ Youngjune Bhak,³ Hak-Min Kim,³ Yun Sung Cho,³ Hyunho Kim,⁴ Kyusang Lee,⁵ Elizaveta Veselovskaya,⁶ Tatiana Balueva,⁶ Marcos Gallego-Llorente,¹ Michael Hofreiter,⁷ Daniel G. Bradley,² Anders Eriksson,¹ Ron Pinhasi,^{8,*†} Jong Bhak,^{3,4,*†‡} Andrea Manica^{1,*†}

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Ancient genomes have revolutionized our understanding of Holocene prehistory and, particularly, the Neolithic transition in western Eurasia. In contrast, East Asia has so far received little attention, despite representing a core region at which the Neolithic transition took place independently ~3 millennia after its onset in the Near East. We report genome-wide data from two hunter-gatherers from Devil's Gate, an early Neolithic cave site (dated to ~7.7 thousand years ago) located in East Asia, on the border between Russia and Korea. Both of these individuals are genetically most similar to geographically close modern populations from the Amur Basin, all speaking Tungusic languages, and, in particular, to the Ulchi. The similarity to nearby modern populations and the low levels of additional genetic material in the Ulchi imply a high level of genetic continuity in this region during the Holocene, a pattern that markedly contrasts with that reported for Europe.

INTRODUCTION

Ancient genomes from western Asia have revealed a degree of genetic continuity between preagricultural hunter-gatherers and early farmers 12 to 8 thousand years ago (ka) (1, 2). In contrast, studies on southeast and central Europe indicate a major population replacement of Mesolithic hunter-gatherers by Neolithic farmers of a Near Eastern origin during the period 8.5 to 7 ka. This is then followed by a progressive "resurgence" of local hunter-gatherer lineages in some regions during the Middle/Late Neolithic and Eneolithic periods and a major contribution from the Asian Steppe later, ~5.5 ka, coinciding with the advent of the Bronze Age (3–5). Compared to western Eurasia, for which hundreds of partial ancient genomes have already been sequenced, East Asia has been largely neglected by ancient DNA studies to date, with the exception of the Siberian Arctic belt, which has received attention in the context of the colonization of the Americas (6, 7). However, East Asia represents an extremely interesting region as the shift to reliance on agriculture appears to have taken a different course from that in western Eurasia. In the latter region, pottery, farming, and animal husbandry were closely associated. In contrast, Early Neolithic societies in the Russian Far East, Japan, and Korea started to manufacture and use pottery and basketry 10.5 to 15 ka, but domesticated crops and livestock arrived several millennia later (8, 9). Because of the current lack of ancient genomes from East Asia, we do not know the extent to which this gradual Neolithic transition, which happened independently from the one taking place in western Eurasia, reflected actual

migrations, as found in Europe, or the cultural diffusion associated with population continuity.

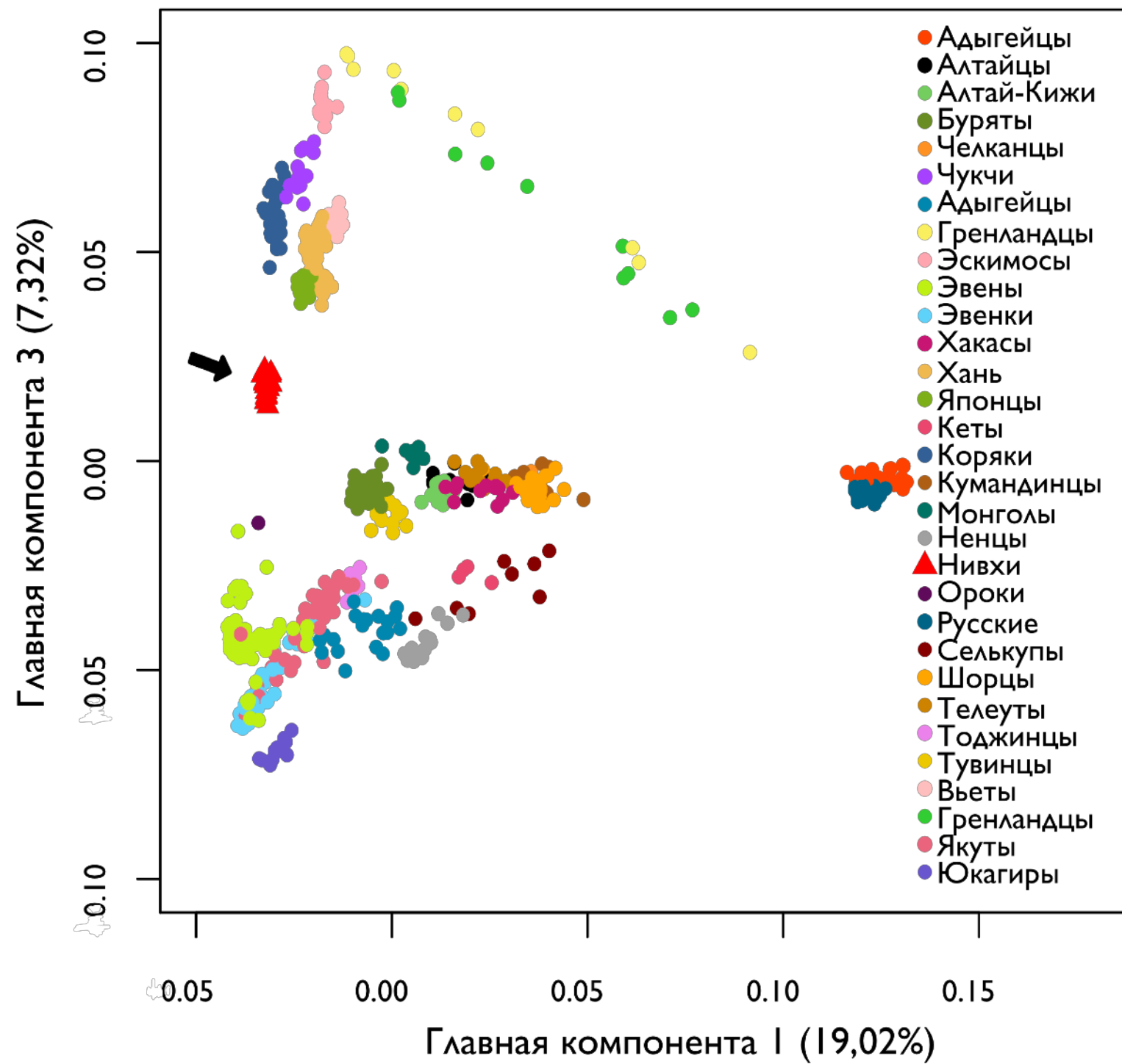
RESULTS

Samples, sequencing, and authenticity

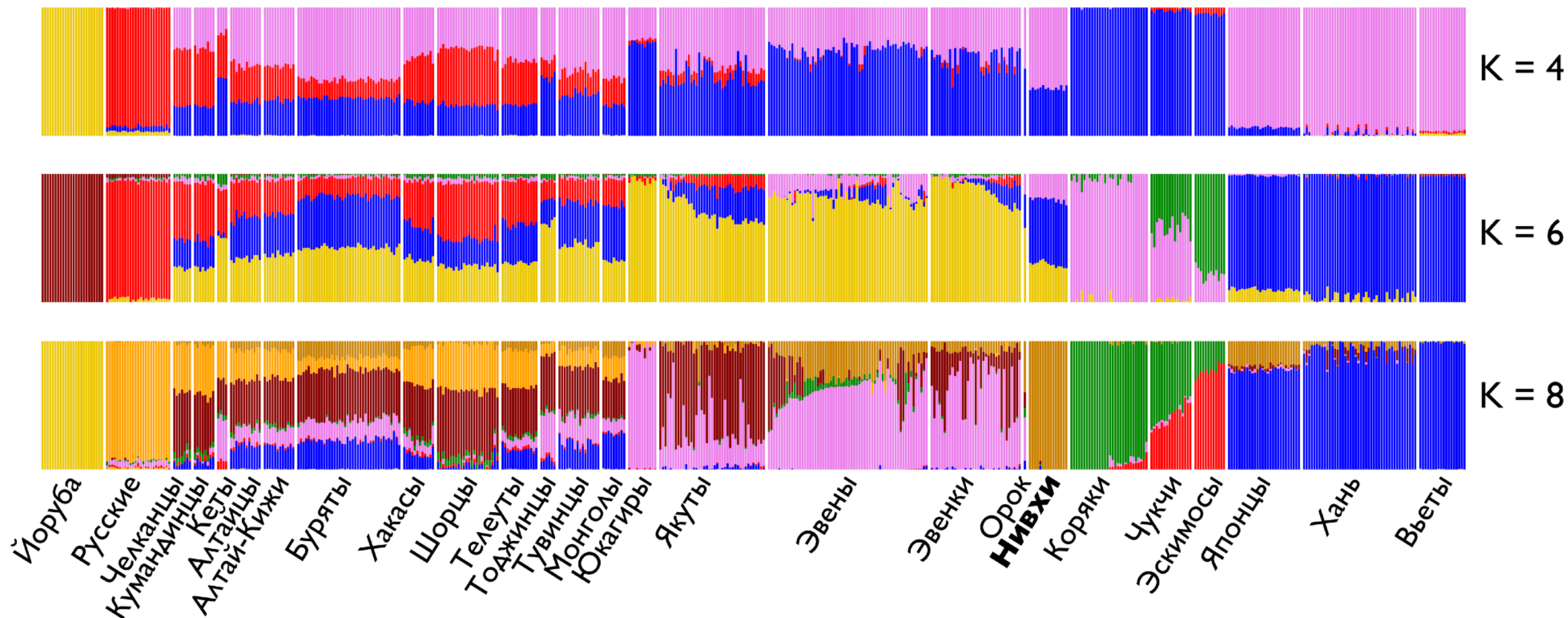
To fill this gap in our knowledge about the Neolithic in East Asia, we sequenced to low coverage the genomes of five early Neolithic burials (DevilsGate1, 0.059-fold coverage; DevilsGate2, 0.023-fold coverage; and DevilsGate3, DevilsGate4, and DevilsGate5, <0.001-fold coverage) from a single occupational phase at Devil's Gate (Chertovyy Vorota) Cave in the Primorye Region, Russian Far East, close to the border with China and North Korea (see the Supplementary Materials). This site dates back to 9.4 to 7.2 ka, with the human remains dating to ~7.7 ka, and it includes some of the world's earliest evidence of ancient textiles (10). The people inhabiting Devil's Gate were hunter-fisher-gatherers with no evidence of farming; the fibers of wild plants were the main raw material for textile production (10). We focus our analysis on the two samples with the highest sequencing coverage, DevilsGate1 and DevilsGate2, both of which were female. The mitochondrial genome of the individual with higher coverage (DevilsGate1) could be assigned to haplogroup D4; this haplogroup is found in present-day populations in East Asia (11) and has also been found in Jomon skeletons in northern Japan (2). For the other individual (DevilsGate2), only membership to the M branch (to which D4 belongs) could be established. Contamination, estimated from the number of discordant calls in the mitochondrial DNA (mtDNA) sequence, was low [0.87% [95% confidence interval (CI), 0.28 to 2.37%] and 0.59% (95% CI, 0.03 to 3.753%)] on nonconsensus bases at haplogroup-defining positions for DevilsGate1 and DevilsGate2, respectively. Using schmutzi (12) on the higher-coverage genome, DevilsGate1 also gives low contamination levels [1% (95% CI, 0 to 2%); see the Supplementary Materials]. As a further check against the possible confounding effect of contamination, we made sure that our most important analyses [outgroup f_3 scores and principal components analysis (PCA)] were qualitatively replicated using only reads showing evidence of postmortem damage (PMD score of at least 3) (13), although these latter results had a high level of noise due to the low coverage (0.005X for DevilsGate1 and 0.001X for DevilsGate2).

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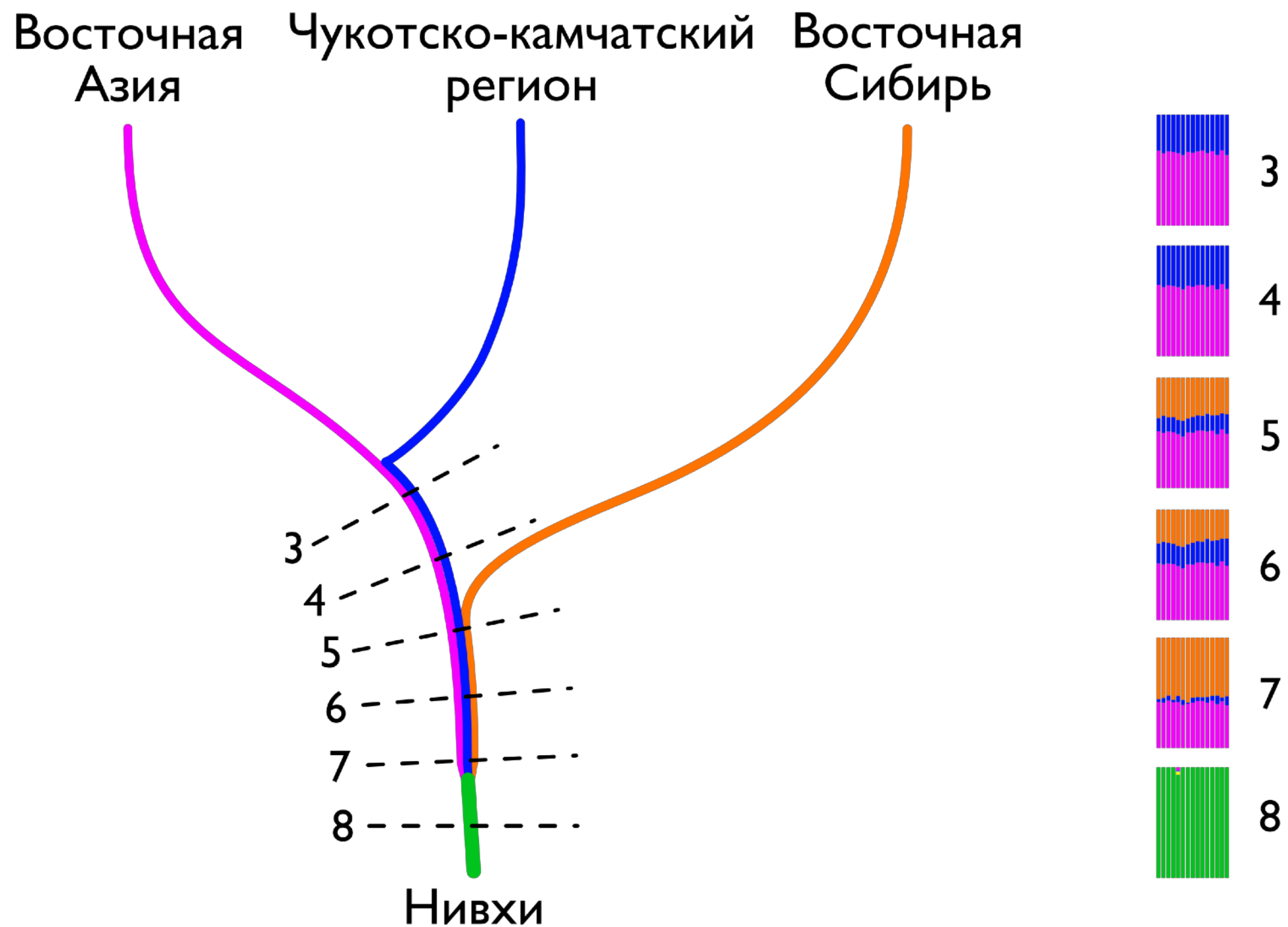
Люди из Чёртовых ворот - носители D4m



Метод главных компонент



Admixture-анализ предковых компонентов



Admixture History Graph