Генетическая история нивхов
Станислав Дрёмов

Лаборатория молекулярной генетики человека, ИМКБ СО РАН
Генетическая история нивхов

Тысяча лет одиночества
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
<table>
<thead>
<tr>
<th>Гаплогруппы</th>
<th>Северные нивхи</th>
<th>Восточные нивхи</th>
<th>Айны</th>
<th>Айны Эдо</th>
<th>Охотская</th>
<th>Дзёмон Хоккайдо</th>
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<td>55.3</td>
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Частоты митохондриальных гаплогрупп
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 where 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 Ude. The similarity to nearby modern populations and the low levels of additional genetic material in the Ude imply a high level of genetic continuity in this region during the Holocene, a pattern that markedly contrasts with that reported for Europe.

**RESULTS**

**Samples, sequencing, and authenticity.** To fill this gap in our knowledge about the Neolithic in East Asia, we sequenced low-coverage genomes of the early Neolithic burials (DevilGate), 0.059X full cov (DevilGate), 0.032X pod coverage and DevilGate, and DevilGate1, and DevilGate2, respectively) from a single-occupational phase at Devil’s Gate (Chengde) in the Primorye region, Eastern Far East, close to the border with China and North Korea (see the Supplementary Materials). This site dates back to 9.4 to 9.2 ka, with the human remains dated to ~7.7 ka, and it includes some of the world’s earliest evidence of domesticated tordos (10). The people inhabiting Devil’s Gate were hunter-gatherers with no evidence of farming; the fibers of wild plants were the main raw material for textile production (10). We focus on our analysis on the two samples with the highest sequencing coverage. DevilGate1 and DevilGate2, both of which were female. The mitochondrial genome of the individual with higher coverage (DevilGate2) could be assigned to haplogroup O. In this haplogroup is found in present-day populations in East Asia (7) and has also been found in Japanese Ainu in northern Japan (2). For the other individual (DevilGate1), only membership to the M branch (to which O belongs) could be established. Contamination, estimated from the number of discordant calls in the mitochondrial DNA (mtDNA) sequence, was low (0.07% [95% confidence interval (CI), 0.28 to 2.37%] and 0.09% [95% CI, 0.33 to 3.73%]) on nonuniform bases at haplogroup-defining positions for DevilGate1 and DevilGate2, respectively. Using admixture4 (12) on the higher-coverage genome, DevilGate2 also gave low contamination levels (1% [95% CI, 0 to 2%]).

**DISCUSSION**

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

Veronika Siska,1,2,3,4 Eppie Ruth Jones,1,2 Sungwon Jeon,2,3 Youngjune Bhak,2,3 Hak-Min Kim,2 Yun Sung Cho,2 Hyunsoo Kim,2 Ryusang Lee,2 Eizaveta Veselovskaya,4 Tatiana Baluova,5 Marcos Gallego-llerente,6 Michael Hofreiter,7 Daniel G. Bradley,3 Anders Eriksen,3 Ron Pinhasi,3,4 Jong Bhik3,4,11,12 Andrea Manica3,4

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Метод главных компонент
Admixture-анализ предковых компонентов
Admixture History Graph

Восточная Азия

Чукотско-камчатский регион

Восточная Сибирь

Нивхи

Admixture History Graph