

Re: Back-Migrations (was: Siberian Arctic site dated to 27,000 BP)

Source: <http://sci.tech-archive.net/Archive/sci.anthropology.paleo/2005-03/0507.html>

From: G Horvat (g-horvat_at_shaw.ca)

Date: 03/23/05

Date: Wed, 23 Mar 2005 01:59:49 GMT

On Tue, 22 Mar 2005 23:38:36 GMT, G Horvat <g-horvat@shaw.ca> wrote:

[...]

>Do you have any Aleut HLA haplotypes yet? (Seems to me you didn't the
>last time we discussed this issue.)

I see an abstract but the article is in Russian:

Genetika. 2003 Dec;39(12):1710-8.

[Genetic history of Aleuts of the Komandor islands from results of analyzing variability of class II HLA genes]

[Article in Russian]

Volod'ko NV, Derbeneva OA, Uinuk-ool TS, Sukernik RI.

Variability of the HLA class II genes (alleles of the DRB1, DQA1, and DQB1 loci) was investigated in a sample of Aleuts of the Commanders (n = 31), whose ancestors inhabited the Commander Islands for many thousand years. Among 19 haplotypes revealed in Aleuts of the Commanders, at most eight were inherited from the native inhabitants of the Commander Islands. Five of these haplotypes (DRB1*0401-DQA1*0301-DQB1*0301, DRB1*1401-DQA1*0101-DQB1*0503, DRB1*0802-DQA1*0401-DQB1*0402, DRB1*1101-DQA1*0501-DQB1*0301, and DRB1*1201-DQA1*0501-DQB1*0301) were typical of Beringian Mongoloids, i.e., Coastal Chukchi and Koryaks, as well as Siberian and Alaskan Eskimos. Genetic contribution of the immigrants to the genetic pool of proper Aleuts constituted about 52%. Phylogenetic analysis based on Transberingian distribution of the DRB1 allele frequencies favored the hypothesis on the common origin of Paleo-Aleuts, Paleo-Eskimos, and the Indians from the northwestern North America, whose direct ancestors survived in Beringian/southwestern Alaskan coastal refugia during the late Ice Age.

Disregarding the data for a moment, how do the authors *know* that the

direct ancestors of the Aleuts "survived in Beringian/southwestern Alaskan coastal refugia during the last Ice Age"? Because they are living in the north now? The reason I ask is because mtDNA sequences have more than likely usually been interpreted in the same way to explain the similarities on both sides of the Bering Strait. However, Aleut, in particular, mtDNA sequences can be separated into 2 groups (disregard the Inuit & Chukchi haplotypes for a second): 1) the ones which are most frequently found in North America and phylogenetically closest to those of the Nadenes (A) and 2) the ones which must have come directly from Asia (D2) and which are more numerous than the other. I wonder if the same pattern can be observed in the HLA haplotypes.

Aleuts (N=163) (of the Commander Islands)

Haplogroup A – 34.3%

Haplogroup D2– 65.6%

Siberian Eskimo (N=77)

haplogroup A – 76.6%

haplogroup C – 2.6%

haplogroup D2 – 15.6%

Haplogroup D3 – 5.2%

Greenland Eskimo (N=98)

haplogroup A – 99.0%

haplogroup D3 – 1.0%

I reiterate – the D2 & D3 sequences are not the Native American type. The haplogroup A sequences are.

Gisele