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Reply to Tarazona-Santos and Santos

To the Editor:

Tarazona-Santos and Santos (2002 [in this issue]) make two arguments against our proposal that there was a second Y-chromosome migration from the Amur River/Sea of Okhotsk region of eastern Siberia that contributed to northern Native American populations. Their first argument is that the S4Y Y-chromosome lineage found in northern Native Americans may have been derived from central Siberia, rather than from eastern Siberia, as we proposed. There are several reasons why an eastern Siberian origin for S4Y Y chromosomes is much more likely than a central Siberian origin. First, a broad survey of Asian Y chromosomes has indicated that S4Y was brought to Siberia from Southeast Asia, primarily via a coastal migration (Su et al. 2000). Consistent with this assertion, there is very limited S4Y Y-chromosomal variation in central Siberia, which is best explained by recent admixture, rather than an ancient origin. For example, the limited number of S4Y Y chromosomes reported by Karafat et al. (1999) in the Selkups and Kets were most likely derived from the recent expansion of the Evenks from the Lake Baikal region of eastern Siberia into the Lower and Middle Yenisey River region (Tugolukov 1985). Similarly, the Tuvan, which are currently dispersed in the extreme south of Siberia, were most likely derived from the greater Manchuria homeland of Altaic speakers, which includes the Lower Amur River Basin. Indeed, nomadic Altaic speakers had occupied Tuva long after the migration bringing the S4Y chromosome to the Americas took place (Janhunen 1996). Finally, the current average S4Y Y-chromosome frequency in North American is likely to be much lower than the S4Y Y-chromosome frequency in the original second migration, simply because these Y chromosomes would have been diluted by the predominant M3 Y chromosomes already in residence from the first Native American migration. Given these facts, Tarazona-Santos and Santos's Bernstein admixture calculation does not provide a compelling argument against a second migration.

Tarazona-Santos and Santos's second argument is that the M45b Y-chromosome haplotypes that we identified in northern Native Americans are not Siberian in origin, but European. However, this argument would require that the proposed European male input into the Native American populations not only was extensive but also brought only a limited number of Y-chromosome haplotypes—specifically, those with the microsatellite alleles DYS19(11 repeats)-DYS388(11 repeats)-DYS390(11 repeats)-DYS391(10 or 11 repeats). This possibility is contrary to the historical fact that European male admixture into Native American populations has been continuous over the past 500 years and that it has been derived from populations throughout western Europe. By contrast, the M45b Y-chromosome microsatellite markers that we found in northern North Americans are either identical to or closely related to those that we found in eastern Siberia. Hence, we feel that it is much more likely that the M45b Y chromosomes, which are common in northern Native Americans, came from the Siberian Pacific, where the remnants of their exact counterparts are currently located.

Any hypothesis is subject to question and, with compelling data, should be revised. Therefore, we appreciate Tarazona-Santos and Santos's thoughts on this matter. Indeed, we also initially considered a possible European origin for the M45b Y chromosomes in northern Native Americans. However, after careful analysis of the existing data, we concluded that a two-Siberian-migration hypothesis for the origin of Native American Y chromosomes provided the most reasonable explanation for the available observations.

Jeffrey T. Lell,[1] Rem I. Sukernik,[2]
and Douglas C. Wallace[1]
[1]*Center for Molecular Medicine, Emory University School of Medicine, Atlanta; and* [2]*Institute of Cytology and Genetics, Russian Academy of Sciences, Novosibirsk, Russia*

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Address for correspondence and reprints: Dr. Douglas C. Wallace, Center for Molecular Medicine, Emory University School of Medicine, 1462 Clifton Road, Atlanta, GA 30322. E-mail: dwallace@gen.emory.edu

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