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## East Asian and Melanesian Ancestry in Polynesians

*To the Editor:* Kayser et al.<sup>1</sup> estimated the ancestry of Polynesians by using 377 autosomal microsatellite loci and concluded that 0.79 of the ancestry was from East Asians (95% CI, 0.76–0.84) and 0.21 from Melanesians. In contrast, maternally inherited mtDNA ancestry was previously estimated to be 0.94 East Asian and 0.06 Melanesian and paternally inherited Y chromosome ancestry was estimated to be 0.28 East Asian and 0.66 Melanesian.<sup>2</sup> One might guess that the East Asian autosomal ancestry would be approximately the arithmetic average of the mtDNA and Y ancestry, 0.61, but the estimated autosomal ancestry of 0.79 is substantially higher. To account for this difference and the different estimates in ancestry from different chromosomes, strong sex differences in gene flow, occurring in a particular chronological order, are necessary. Here I present a simple two-phase scenario to explain the different observed ancestries for autosomal, mtDNA, and Y markers and then discuss how this scenario could be modified and still result in the observed patterns.

First, assume that a population of East Asian ancestry, which eventually became the Polynesians, settled in Melanesia and that subsequently there was male gene flow from Melanesians into this population. This pattern is consistent with both matrilocality and matrilinearity in this population.<sup>1</sup> The effect of this male gene flow at a rate of  $m_m$  per generation over  $t$  generations on Y ancestry can be given<sup>3</sup> as

$$q_t = (1 - m_m)^t q_0 + [1 - (1 - m_m)^t] q_{Mel}$$

where  $q_0$  and  $q_t$  are the initial and  $t$  generation East Asian ancestry in the population and  $q_{Mel}$  is the East Asian ances-

try in the Melanesian migrants. Assuming that  $q_{Mel} = 0$ ,  $q_0 = 1$ , and  $q_t = 0.28$ , then

$$0.28 = (1 - m_m)^t \text{ or } m_m = 1 - e^{\ln(0.280)/t}.$$

For example, if  $t = 50$ , then  $m_m = 0.0251$ .

For autosomal loci in this population, the East Asian ancestry is

$$q_t = \left[1 - \frac{1}{2}(m_f + m_m)\right]^t q_0 + \left\{1 - \left[1 - \frac{1}{2}(m_f + m_m)\right]^t\right\} q_{Mel}$$

where  $m_f$  is the per-generation rate of female gene flow. Again, assume that  $q_{Mel} = 0$ ,  $q_0 = 1$ ,  $m_f = 0$ , and with the estimated  $m_m$  of 0.0251 used,  $q_t = (0.987)^t$ . For example, if  $t = 50$ , then  $q_t = 0.532$ .

Second, assume that subsequently there was female gene flow from the East Asians into this population for  $x$  generations so that the autosomal East Asian ancestry can be expressed as

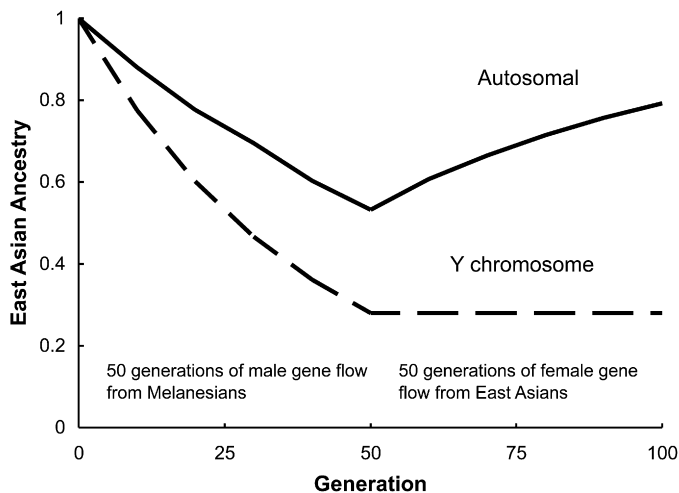
$$q_{t+x} = \left[1 - \frac{1}{2}(m_f + m_m)\right]^x q_t + \left\{1 - \left[1 - \frac{1}{2}(m_f + m_m)\right]^x\right\} q_{EA}$$

where  $q_{EA}$  is the East Asian ancestry in the East Asian female migrants. Assuming that  $q_{EA} = 1$ ,  $q_t = 0.532$ ,  $q_{t+x} = 0.79$ , and  $m_m = 0$ ,

$$0.79 = 1 - 0.468 \left(1 - \frac{1}{2}m_f\right)^x \text{ or } m_f = 2(1 - e^{\ln(0.449)/x}).$$

For example, if  $x = 50$ , then  $m_f = 0.0318$ .

This two-phase scenario is presented in **Figure 1**, which shows a decline in Y and autosomal East Asian



**Figure 1. Change in East Asian Ancestry**

The change in East Asian ancestry in Polynesians for autosomal and Y chromosome loci for 50 generations of male gene flow from Melanesians followed by 50 generations of female gene flow from East Asians.

ancestry over the first 50 generations and then an increase in autosomal East Asian ancestry and no change in Y ancestry over the second 50 generations. Note that the mtDNA East Asian ancestry is 1.0 throughout the whole scenario (essentially the same as the estimated 0.94).

Several models of gene flow can be excluded as possible explanations for the observed pattern of ancestry. First, if gene flow is not sex-specific, then it cannot result in the observed pattern. Second, male gene flow must start before female gene flow (female gene flow from East Asians can influence the East Asian autosomal population ancestry only after it has some Melanesian ancestry). If the female gene flow and the male gene flow start at the same time, then the total amount of female gene flow must be even larger than that given in the above example.

In a more realistic model, the patterns of gene flow may differ somewhat from the above scenario and could vary over generations and still provide similar results. For example, gene flow from the two sexes from the different source populations could overlap; that is, the female gene flow from East Asians could start while male gene flow continues from Melanesians. Also, female gene flow from East Asians may not actually be from outside females with high East Asian ancestry but could occur because females of high East Asian ancestry had higher reproductive success in the population for some social or cultural reasons. Finally, it is possible that the Y ancestry in the

Polynesians has been reduced by genetic drift, making arithmetic average of mtDNA and Y ancestry before genetic drift higher and, therefore, the difference between this average and the estimated autosomal ancestry of 0.79 smaller. Overall, though, it appears that an estimated male Melanesian gene flow of 0.0251 per generation for 50 generations and a subsequent estimated female East Asian gene flow of 0.0318 per generation for 50 generations, or the equivalent, are necessary to result in the observed pattern of ancestry over the autosomal, mtDNA, and Y chromosome markers.

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## Reply to Hedrick

*To the Editor:* Hedrick<sup>1</sup> proposed an interesting model to explain our previous observation that most of the Polynesian autosomal and mitochondrial gene pool is of East Asian origin whereas most of the Polynesian Y chromosomes originate from Melanesia.<sup>2,3</sup> We and others have previously interpreted the discrepancy between the geo-

graphic origins of Polynesian Y chromosomes and mitochondrial DNA by an episode of genetic admixture between Austronesian migrants from East Asia arriving in Melanesia and local non-Austronesians from Melanesia, according to the Slow Boat from East Asia hypothesis.<sup>4</sup> This admixture most likely occurred in a sex-biased way mainly between East Asian women and Melanesian men.<sup>2,3,5</sup> Hedrick's model also postulates sex-biased admixture between East Asians and Melanesians, but in two