

## Correction

### Melanesian origin of Polynesian Y-chromosomes

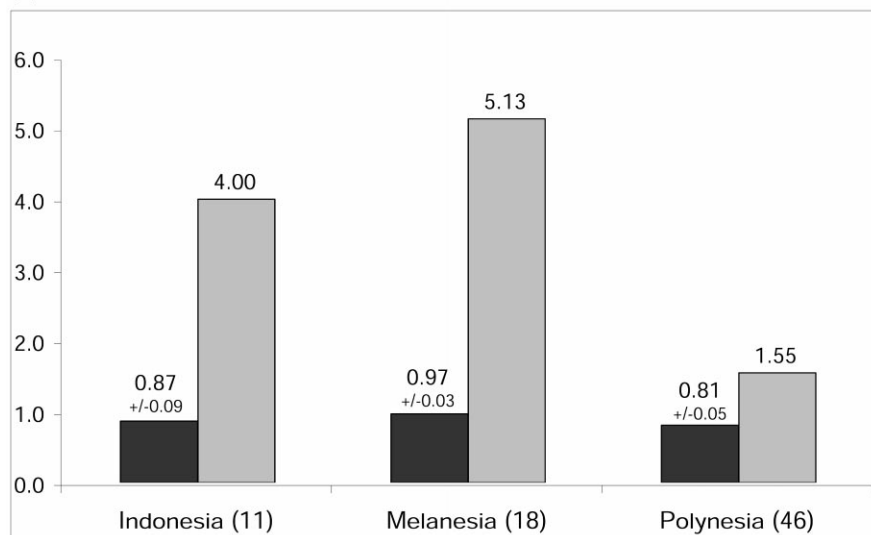
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In our recent Research Paper on the Melanesian origin of Polynesian Y-chromosomes, which appeared in the 19 October 2000 issue of *Current Biology*, we included published data on Y-chromosome haplotypes from the Cook Islands and coastal Papua New Guinea (Hurles et al., *Am J Hum Genet* 1998, **63**:1793-1806). We have since been informed that the allelic designations for DYS19 in this paper are incorrect (Hurles et al., *Am J Hum Genet*, 2001, **68**:298). We corrected and reanalyzed our data, with the

result that three Polynesian Y-STR haplotypes from Hurles et al. (1998), all on the DYS390.3del/RPS4Y711T haplotype, are now identical to haplotypes observed in our sample of Polynesians. The number of DYS390.3del/RPS4Y711T Y-STR haplotypes is thus reduced from 39 to 36, and the demographic inferences (with associated 95% equal-tailed intervals) concerning this haplotype that were presented in Table 2 of the original paper should be as follows: initial effective population size in 1000

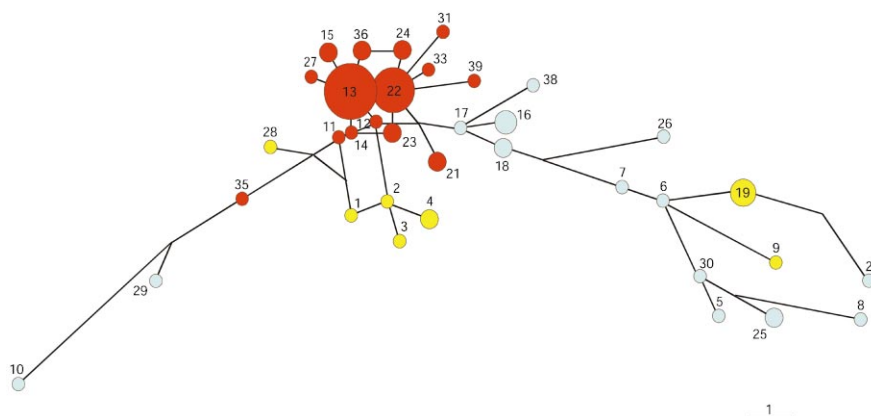
**Figure 3a**

(a)



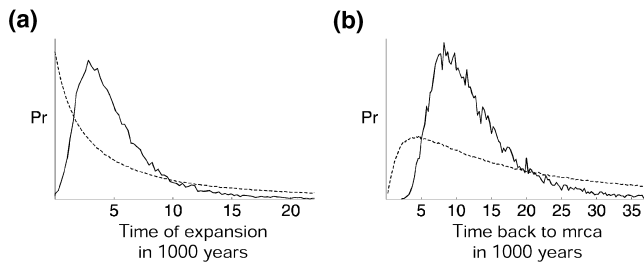
Haplotype diversity (dark gray bars), their standard deviation, and the mean number of pairwise differences (light gray bars) of Y-STR haplotypes of (a) the DYS390.3del/RPS4Y711T haplotype where Indonesia includes 5 Mol, 5 Ten, and 1 Bor; Melanesia includes 1 PNH, 8 PNC, 2 PNG Port Morseby, 5 Tro, and 2 TNB; and Polynesia includes 39 Coo and 7 Western Samoans. The units on the vertical axis are the mean number of pairwise differences (light gray bars) and the haplotype diversity (dark gray bars).

**Figure 4**



Median-joining network of 36 Y-STR haplotypes from 75 individuals belonging to the DYS390.3del/RPS4Y711T haplotype. Circles, Y-STR haplotypes with the area proportional to the number of individuals; lines, mutation steps; parallel lines, identical mutations. Red haplotypes are from Polynesia, blue, from Melanesia, and yellow, from Indonesia. The scale bar indicates one mutation.

Figure 5



Bayesian-based demographic data inferred from Y-STR variation associated with the DYS390.3del/RPS4Y711T haplotype ( $n = 75$ ). Each panel shows the prior (dashed lines) and posterior (continuous lines) probability distribution of **(a)** the time of population expansion and **(b)** the time back to the mrca. Pr indicates probability.

individuals, 0.31 (0.1; 0.97); population growth rate per generation  $\times 10^{-3}$ , 7.4 (1.0, 25.5); time of expansion in 1000 years, 4.25 (0.9; 15.6); time back to mrca in 1,000 years, 10.9 (4.7; 30.9). All references in the text to these particular demographic parameters should also be corrected. New versions of Figures 3a, 4, 5a, and 5b are shown above. All other figures, tables, and analyses are not affected by this error, and none of our conclusions are altered.