Correction


Range-wide mtDNA phylogeography yields insights into the origins of Asian elephants

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In Vidya et al. [1], the last paragraph on page 896 (continuing to page 897; Results section) provided the rate of sequence divergence incorrectly as the mutation rate, which was used for the calculation of mean times of expansion and effective population sizes. We provide the correct values in the two paragraphs below. However, these changes do not make any difference to the inferences drawn or to the conclusions of the paper.

The last paragraph on page 896 should read as follows:

Analysis of mismatch distributions showed that observed data were explained by the fitted models, with the combined data of the two clades indicating demographic stability, and the α and β clades indicating population expansion (see electronic supplementary material, S8). The HKY-corrected distance between clades was 0.025 and the rate of sequence divergence in the mtDNA segment was estimated to be 1.6 and 1.2 per cent per Myr based on the mean divergence times, between the Asian and African elephants, of 6.6 and 8.8 Myr ago, respectively. This was considerably lower than the rate (3.5%) calculated by Fleischer et al. [2], partly owing to the different time estimate used and partly owing to the smaller HKY-corrected distance between clades in our larger sample. Based on the values of \( t = \frac{1}{2} \mu \) generations; \( \mu \) is the mutation rate over the entire sequence analysed and \( t \) is the time to expansion of a population with initial effective number of females \( N_0 \) to a final size \( N_f \) from the mismatch distributions, a generation time of 27 years estimated (as the average age of reproducing females) from field data in southern India (C. Arivazhagan, T. N. C. Vidya, R. Sukumar 2001–2003, unpublished data), and rates of sequence divergence of 1.6 per cent (divergence time between clades of 1.6 Myr) and 1.2 per cent (divergence time between clades of 2.1 Myr) per Myr, respectively, the mean times of expansion of the α clade were approximately 255 700 and 340 900 yr ago and mean times of expansion of the β clade were 766 100 and 1 021 400 yr ago. \( N_0 \) was very low in both clades but confidence limits were large and upper limits of \( N_0 \) were 4380 in the α clade and 9615 in the β clade based on a 1.6 Myr divergence between clades and 5841 in the α clade and 12 820 in the β clade based on a 2.1 Myr divergence. \( N_0 \) and \( N_1 \) (= \( \theta_1/2 \mu \); estimation of mutation parameter \( \theta_1 \) thought to be biased upwards [3]) were both approximately 47 000 (based on a 1.6 Myr divergence) or 63 000 (based on a 2.1 Myr divergence) based on the combined data of both clades, although the two clades seemed too different demographically to be combined.

The last but one paragraph on page 900 (Discussion) should read as follows:

An alternative hypothesis to allopatric fragmentation of Elephas hysudricus populations giving rise to the two mtDNA clades is that of lineage retention within a single population. We find that the historical effective population size during the last population bottleneck of less than 50 females in each clade with upper limits of a few to several thousand females in each clade is smaller than the 17 500 females for the α clade or 30 700 females for the β clade that would be required at a minimum for lineage retention based on applying the formula of Georgiadis et al. [4], using coalescence times (from the Bayesian tree) of 0.86 and 1.58 Myr for the α and β clades, respectively. The plausibility of several such bottlenecks in the past make lineage retention an unlikely explanation for the coexistence of the α and β clades.

REFERENCES