

ERRATUM

In the abstract to the paper "Genetic and Evolutionary Relationships Among Asian Macaques" by Don J. Melnick and Kenneth K. Kidd (*International Journal of Primatology*, Volume 6, Number 2, April 1985, pp. 123-160), lines 12 and 13 should have been omitted. The abstract should read in full as follows.

Published gene frequency data, checked for consistency of allele definitions across laboratories and for comparability of geographically identical samples, were pooled into a data set containing frequencies at nine loci for each of 20 populations that encompassed 10 macaque species. Genetic distances were calculated by the methods of Kidd and Cavalli-Sforza (1974). These distances were used to construct phylogenetic trees and to evaluate the relationships between divergence times and effective population sizes. Inter- and intraspecific genetic distances and the groupings defined by phenetic tree analyses support Fooden's (1976) classification of the genus Macaca into four species groups. A paleozoogeographical model of Asia including the known times of major sea-level changes allows us to explain qualitatively the inferred evolutionary relationships among macaque species. Many assumptions are required in order to estimate the variables necessary in the quantitative prediction of genetic differences for a comparison between any two populations. Examination of those assumptions demonstrates the need for more accurate genetic as well as paleozoogeographic information.