

**Table 1**  
**Estimated  $N_e$  Values for Nuclear Systems**

Genetic System	Published $N_e$ Estimate	95% Range of Estimate	Sources
Human-specific <i>Alu</i> polymorphisms . . . . .	17,500	14,000–35,000	Batzer et al. (1992), Harpending et al. (1998), Sherry (1996)
$\beta$ -globin . . . . .	10,000	10,000–55,000	Harding et al. (1997)
$\psi\eta$ -globin . . . . .	—	9,000–68,000	Bailey et al. (1992)
$\gamma$ -globin . . . . .	—	7,000–57,000	Bailey et al. (1992)
$\delta$ -globin . . . . .	—	18,000–160,000	Maeda, Bliska, and Smithies (1983)
HLA intraallelic data . . . . .	10,000	—	Takahata and Satta (1998)
HLA interallelic data . . . . .	100,000	—	Ayala (1995)
Single-nucleotide polymorphisms . . . . .	10,000–100,000	—	Wang et al. (1998)
ZFY . . . . .	3,000–28,000	0–96,000	Dorit, Akashi and Gilbert (1995)
YAP . . . . .	2,000–26,000	—	Hammer (1995)
ZFX . . . . .	3,000–15,000	1,000–18,000	Huang et al. (1998)

NOTES.—We obtained these ranges using a coalescent simulation approach (Hudson 1990). For polymorphic *Alu* insertions, a simulation technique was developed that was similar to those of other studies (Sherry et al. 1997). Our technique required that we assume a constant population size for the human lineage, an assumption shared by all other means of estimating  $N_e$ , because  $N_e$  is a long-term average over the time period to the most recent common ancestor of a genetic locus. We also assume a date of 5 Myr for the chimpanzee-human species divergence (Takahata, Satta, and Klein 1995), a chimpanzee generation length of 19.6 years (Teleki, Hunt, and Pfiffering 1976), and a human generation length of 23.1 years for the period of coalescence. The long-term human generation length of approximately 23 years is midway between the observed chimpanzee value of 19.6 years and the generation length osteologically estimated for a recent, precontact human hunter-gatherer sample, 26.6 years (from Lovejoy et al. 1977). Finally, we assume a population size of the chimpanzee-human ancestor species of 100,000 (Ayala 1995; Takahata, Satta, and Klein 1995), as assumed in other studies (Sherry 1996; Sherry et al. 1997). For each locus, 1,000 simulations were performed for each of a range of possible population sizes in order to determine a confidence interval for  $N_e$  estimation. The range of population sizes tested began at zero and was increased in increments of 500 until an upper bound on population size was reached. For polymorphic *Alu* elements, the estimated confidence interval includes those values of  $N_e$  that produced numbers of polymorphic sites as extreme as or more extreme than the observed value in at least 5% of the simulations. For haplotype data discussed in the text, we used the same assumptions to simulate the gene genealogies consistent with the loci under study. For these genes, either the average pairwise difference or the maximum pairwise difference was used as the test statistic. Values of population size are included in the confidence interval if at least 5% of simulations produce test statistics as extreme as or more extreme than the observed value. Other assumptions and techniques are the same as those for the *Alu* procedure. In some cases not enough published data were available for these procedures, but either  $N_e$  estimates or coalescence time estimates have been published. In these cases, published estimates of coalescence times have been converted to long-term average  $N_e$  estimates for purposes of comparison.