

	Description	Latinos mean \pm std	Native Hawaiians mean \pm std
t_1	Time of admixture (gen)	24.8 \pm 9.1	18.9 \pm 2.3
t_2	Time when indigenous Americans or Polynesians split from Asians (gen)	353 \pm 49	411 \pm 42
t_3	Time when Asians split from Europeans (gen)	1018 \pm 172	1040 \pm 87
t_4	Time when Europeans split from Africans (gen)	2094 \pm 326	2004 \pm 58
r_1	African admixture proportion	0.107 \pm 0.068	0.0
r_2	European admixture proportion	0.442 \pm 0.148	0.198 \pm 0.012
r_3	Asian admixture proportion	0.0	0.334 \pm 0.036
N	population size at admixture	41579 \pm 16850	35682 \pm 10656
N_{afr}	African population size	4986 \pm 426	NA
N_{eur}	European population size	13341 \pm 4701	13388 \pm 2388
N_{asia}	Asian population size	NA	25234 \pm 6984
$N_{\text{ia/pol}}$	indigenous Americans or Polynesians population size	73170 \pm 28939	15695 \pm 7392
N_{aa}	Asian population size between t_2 and t_3	3092 \pm 958	2702 \pm 795
N_{ooa}	European population size between t_3 and t_4	2948 \pm 612	2470 \pm 558
N_{anc}	African population size before t_4	2846 \pm 716	2665 \pm 444
gr	Growth rate of admixed population (per gen)	0.132 \pm 0.012	0.078 \pm 0.009

Table S1. Latinos and Native Hawaiians parameters estimates and uncertainties.

Estimated quantities corresponding to the results in **Figure 6**. Uncertainty was calculated as the standard deviation cross 20 independent threads, each thread containing 10 distant and selectively neutral trees (see **Methods**). Population size estimates marked as NA are not estimable, because the admixture proportion from such population was estimated to be zero.

	Sequencing data gLike mean \pm std	Array data gLike mean \pm std	Relative difference
t_1	40.7 \pm 6.9	32.4 \pm 2.4	-20.3%
t_2	71.3 \pm 9.3	55.5 \pm 12.3	-22.2%
t_3	8474 \pm 483	7321 \pm 391	-13.6%
r_1	0.418 \pm 0.056	0.425 \pm 0.039	1.6%
r_2	0.680 \pm 0.079	0.693 \pm 0.065	1.9%
N	3946 \pm 194	3212 \pm 48	-18.6%
N_A	20078 \pm 3364	16434 \pm 1820	-18.1%
N_B	3398 \pm 1006	2932 \pm 1417	-13.7%
N_C	29484 \pm 3163	21871 \pm 3069	-25.8%
N_D	10328 \pm 1866	7879 \pm 1376	-23.7%
N_E	13534 \pm 4654	10892 \pm 2404	-19.5%

Table S2. Bias in inferred parameters from gLike using tdate-inferred trees from simulated array vs. sequencing data. The same three-way admixture demography as **Figure 2A** was simulated. Genotypes were subsampled from simulated sequencing data to match the empirical MAF distribution in the Latinos genotyping data (**Methods**). tdate was used to infer the ARG based on either the simulated genotype data or the sequencing data. Genealogical trees from each ARG were sampled and analyzed by gLike to compare the bias in parameter estimates due to using only a subset of variations typically found on an array.