Table 6. Isolation model parameter estimates for South American and non South American populations based on variation in nuclear and mitochondrial loci.

Parameter	Nuclear	Mitochondrial
θ_1	2.85 (0.80-5.58)	4.95 (0.18-14.79)
θ_2	14.06	7.21 (0.56-18.03)
θ_A	14.51 (4.64-26.44)	45.38 (22.28-71.26)
t	1.64 (0.08-7.76)	1.39
m_1	4.35	4.03
m_2	14.63 (7.83-19.99)	2.57 (0.01-10.23)

In estimating these parameters the inheritance scalar was set to 1.0 and 0.25 for the nuclear and mitochondrial loci, respectively. In the table, the parameters are as follows: θ_1, θ_2, and θ_A, are the mean population mutation rates for South American (SA), Non South American (NSA) and the ancestral population, respectively; t, is the mean time of divergence of SA and NSA populations from a common ancestor; m_1 is the mean number of migrants into SA; m_2 is the mean number of migrants into NSA. The 90% highest posterior density interval is shown in parentheses for those parameters in which the complete posterior distribution was estimated from the data.