Am. J. Hum. Genet. 69:904, 2001

Patterns of Y-Chromosome Variation in South Amerindians

To the Editor:
Tarazona-Santos et al. (2001) compute estimates of within- and among-group genetic variability for South Amerindian Y-chromosome samples that are thought to represent tribal populations living in various major geoecological regions of South America: the Andean highlands, the Brazilian plateau, the Chaco region, the Argentinian pampa, and the Chilean rain forest.

The samples are agglomerated into two groups, one representing populations from the Andean highlands and the other representing populations from Amazonia, the Brazilian plateau, and the Chaco. Variability estimates are computed for both subdivisions and are consequently compared, with the Andean group exhibiting higher values. For apparently unjustified reasons, a sample from the tropical forest of Ecuador that has an Amazonian origin and exhibits the highest within-group variability is excluded from the analysis, unfortunately casting doubt on the reliability of the results.

Various among-group variability estimates and their association with distances among map locations of places where samples were presumably collected are computed next. We are aware of the difficulties in obtaining Amerindian samples, but the extremely small size of some samples used in this study (the central Brazilian plateau is represented by five individuals) precludes the possibility that among-group variability statistics are unbiased estimators of *population* relationships. The lack of association between genetic and geographic distances may be a reflection of this shortcoming.

On the basis of their results, Tarazona-Santos et al. (2001) conclude that two Y-chromosome microevolutionary models that involve differential patterns of genetic drift and gene flow characterize South Amerindians. Andean populations exhibit low rates of genetic drift and high rates of gene flow, whereas populations from Amazonia, the Brazilian plateau, and the Chaco exhibit high rates of drift and low rates of gene flow. It seems to us that this is a rash generalization, if it is based on the variability estimates presented in this study. Furthermore, it presupposes that non-Andean South Amerindian tribes living far apart, in markedly different geoecological areas, can be agglomerated and treated as one homogeneous group sharing the same population structure. We are not convinced that this is a realistic assumption.

FRANCISCO ROTHHAMMER AND MAURICIO MORAGA
Programa de Genética Humana
Instituto de Ciencias Biomédicas
Facultad de Medicina
Universidad de Chile
Santiago, Chile

Reference

Tarazona-Santos E, Carvalho-Silva DR, Pettener D, Luiselli D, De Stefano GF, Martinez Labarga C, Richards O, Tyler-Smith C, Pena SDJ, Santos F (2001) Genetic differentiation in South Amerindians is related to environmental and cultural diversity: evidence from the Y chromosome. Am J Hum Genet 68:1485–1496

Address for correspondence and reprints: Dr. Francisco Rothhammer, Programa de Genética Humana, Instituto de Ciencias Biomédicas, Facultad de Medicina, Universidad de Chile, Av. Independencia 1027, Casilla 700061, Santiago 7, Chile. E-mail: frothham@machi.med.uchile.cl

0002-9297/2001/6904-0026$02.00

Am. J. Hum. Genet. 69:904–906, 2001

Reply to Rothhammer and Moraga

To the Editor:
Rothhammer and Moraga raise objections to the conclusions in our article describing global patterns of Y-chromosome diversity among South Amerindian populations (Tarazona-Santos et al. 2001). We do not think that their criticisms are valid, for the following reasons.

First, Rothhammer and Moraga argue that our conclusions are not well grounded, since they were only based on the Y-chromosome data presented in our article. This is not correct. In the article, we present and discuss the good concordance between our Y-chromosome data and the analyses of classical marker variability