

Development of two multiplex mini-sequencing panels of ancestry informative SNPs for studies in Latin Americans: an application to populations of the State of Minas Gerais (Brazil)

M.C.F. Silva^{1,2*}, L.W. Zuccherato^{2*}, G.B. Soares-Souza^{1,2}, Z.M. Vieira¹,
L. Cabrera³, P. Herrera³, J. Balqui^{3,4}, C. Romero^{3,4}, H. Jahuir^{3,4},
R.H. Gilman^{3,5}, M.L. Martins¹ and E. Tarazona-Santos²

¹Fundação Hemominas, Belo Horizonte, MG, Brasil

²Departamento de Biologia Geral, Instituto de Ciências Biológicas,
Universidade Federal de Minas Gerais, Belo Horizonte, MG, Brasil

³Asociación Benéfica PRISMA, Urbanización Maranga, Lima, Peru

⁴Laboratorio de Investigación en Enfermedades Infecciosas,
Universidad Peruana Cayetano Heredia, San Martín de Porres, Lima, Peru

⁵Department of International Health, Bloomberg School of Public Health,
Johns Hopkins University, Baltimore, MD, USA

*These authors contributed equally to this study.

Corresponding author: E. Tarazona-Santos

E-mail: edutars@icb.ufmg.br

Genet. Mol. Res. 9 (4): 2069-2085 (2010)

Received May 21, 2010

Accepted July 23, 2010

Published October 19, 2010

DOI 10.4238/vol9-4gmr911

ABSTRACT. Admixture occurs when individuals from parental populations that have been isolated for hundreds of generations form a new hybrid population. Currently, interest in measuring biogeographic ancestry has spread from anthropology to forensic sciences, direct-to-consumers personal genomics, and civil rights issues of minorities, and it is critical for genetic epidemiology studies of admixed populations. Markers with highly differentiated frequencies among human populations are informative of ancestry and are called ancestry informative markers (AIMs). For tri-hybrid Latin American populations, ancestry information is required for Africans,

Europeans and Native Americans. We developed two multiplex panels of AIMs (for 14 SNPs) to be genotyped by two mini-sequencing reactions, suitable for investigators of medium-small laboratories to estimate admixture of Latin American populations. We tested the performance of these AIMs by comparing results obtained with our 14 AIMs with those obtained using 108 AIMs genotyped in the same individuals, for which DNA samples is available for other investigators. We emphasize that this type of comparison should be made when new admixture/population structure panels are developed. At the population level, our 14 AIMs were useful to estimate European admixture, though they overestimated African admixture and underestimated Native American admixture. Combined with more AIMs, our panel could be used to infer individual admixture. We used our panel to infer the pattern of admixture in two urban populations (Montes Claros and Manhuaçu) of the State of Minas Gerais (southeastern Brazil), obtaining a snapshot of their genetic structure in the context of their demographic history.

Key words: Admixture; Latin American; Mini-sequencing