

Contrasting Patterns of Nuclear and mtDNA Diversity in Native American Populations

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We report an integrated analysis of nuclear (autosomal, X- and Y-chromosome) short tandem repeat (STR) data and mtDNA D-loop sequences obtained in the same set of 22 Native populations from across the Americas. A north to south gradient of decreasing population diversity was observed, in agreement with a settlement of the Americas from the extreme northwest of the continent. This correlation is stronger with "least cost distances," which consider the coasts as facilitators of migration. Continent-wide estimates of population structure are highest for the Y-chromosome and lowest for the autosomes, consistent with the effective size of the different marker systems

examined. Population differentiation is highest in East South America and lowest in Meso America and the Andean region. Regional analyses suggest a deviation from mutation-drift equilibrium consistent with population expansion in Meso America and the Andes and population contraction in Northwest and East South America. These da