A more adequate understanding of New World settlements and biologic history is accessible within the context of selected population studies. Examination of regional populations will more completely address the nature of New World settlement within the framework provided by broader studies. Selected regional studies can yield a more refined assessment of settlement scenarios that include intra-continental migration because of the different development histories of each group. The current study examines the population structure of Andean Altiplano populations from the Lake Titicaca Basin within the context of Peruvian populations. We report the mtDNA haplogroup distributions of 454 samples from island and mainland populations of the Lake Titicaca region and identify control region sequence polymorphisms of 58 individuals. A selectively dispersed mtDNA control region motif is also presented as a diagnostic marker for tracing gene flow and founding events within the Lake Titicaca region and surrounding areas.

Populations

Transacted by the border of Peru and Bolivia, the Lake Titicaca Basin in the Andean Altiplano, sustains the densest rural population in the two countries (Fig. 1). Lake Titicaca is over 161 by 64 kilometers, and is located at 3830 meters above sea level. The modern indigenous residents of the Peruvian Altiplano represent a population that has remained in relative isolation until recent times, providing evidence of original Paleo-Indian founding populations. Eight Peruvian Altiplano localities were selected for this study; mainland settlements: Taraco (n=38), Juliaca (n=108), Puno (n=47), Desaguadero (n=21), and islands: Amantani (n=81), Isla Soto (n=29), Taquile (n=39), and the Uru (n=93). Samples were approximately equally divided between mainland (47%) and island (33%) locations.

Haplogroup Distribution

All four major Native American haplogroups were observed in the Peruvian Lake Titicaca Basin samples. Haplogroup B was predominant, with a frequency of 0.782, followed by the less frequent haplogroups C, A, and D (Table 1). The majority of total samples were further classified (i.e. A+/A-) based on the HaeIII site at nt 16519. This polymorphic position can discriminate between closely related lineages and revealed significant substructuring within populations, particularly the exclusivity of haplotype A-(17/17) and D+(10/10) within the Uru sample. This finding is significant to understanding the isolated placement of the Uru within the Lake Titicaca Basin as a historically marginalized group.

mtDNA Diversity of the Peruvian Andean Altiplano

Natalie M. Myres(1), Joel E. Myres(1,2), Mike Malan(2), Jeff Fuller(2), Matt McNairy(2), Mark J. Rowe(2), Ray T. Matheny(2), Heather A. McCammon(1), Robert Hughes(1), Scott R. Woodward(1,2).

mtDNA diversity studies have provided an informative tool for understanding the population structure of Andean Altiplano populations from the Lake Titicaca Basin within the context of Peruvian populations. We report the mtDNA haplogroup distributions of 454 samples from island and mainland populations of the Lake Titicaca region and identify control region sequence polymorphisms of 58 individuals. A selectively dispersed mtDNA control region motif is also presented as a diagnostic marker for tracing gene flow and founding events within the Lake Titicaca region and surrounding areas.

Population

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