

**TRACING THE HUMAN MATERNAL LINEAGES IN THE HIMALAYAS** Tenzin Gayden<sup>1, 2</sup>, Annabel Perez<sup>1, 2</sup>, Patrice J. Persad<sup>1, 2</sup>, Trisha Maloney<sup>1, 2</sup>, Shilpa Chennakrishnaiah<sup>1, 3</sup> and Rene J. Herrera<sup>1, 2</sup> <sup>1</sup>Department of Molecular and Human Genetics, College of Medicine, Florida International University, Miami, Florida, USA 33199 <sup>2</sup>Department of Biological Sciences, Florida International University, Miami, Florida, USA 33199 <sup>3</sup>Department of Chemistry and Biochemistry, Florida International University, Miami, Florida, USA 33199

In the present study, we investigated the maternal sources of three Nepalese populations, namely Kathmandu (77), Newar (66) and Tamang (45), and a general collection from Tibet (156) by sequencing hypervariable regions I and II of mitochondrial DNA. In addition, we performed RFLP analyses of diagnostic SNPs within the coding region to assign the haplogroup for each sample. Our results show that a majority of the samples belong to macrohaplogroup M, with frequencies ranging from 76.9% in Tibet to 63.5% in Newar. Haplogroup M62 (3.2%) is found exclusively among Tibetans, supporting the indigenous origin of the marker on the highland. Macrohaplogroup N, on the other hand, is largely represented by sub-haplogroup U in the Nepalese populations (13-22.2%), while the same mutation is present in limited proportion in the Tibetan collection (1.3%), suggesting that modern humans carrying this subcontinent marker were unsuccessful in crossing the Himalayan massif into the Tibetan plateau.