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Alu Indel Polymorphisms as a Tool for Genomic Diversity Study in Naga Tribes

Magdalene Kiewhuo[1], A. O. Semsadangla[1], Moamenla Singson[2],
Bupesh Giridharan[3] and Nandakumar Rangasamy[1,*]

[1]Department of Zoology, St. Joseph University, Dimapur 797 115, Nagaland, India
[2]Eden Hospital, Dimapur, 797 115, Nagaland, India
[3]Department of Forest Science, Nagaland University, Lumami 797 004, Nagaland, India

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ABSTRACT The current study aims to find out the genomic relationship and affinities within and between the tribes and to compare the genomic of Nagas with that of the other populations. Four Naga tribes namely Angami, Lotha, Tikhir and Chakhesang were studied. Eight autosomal DNA markers of the Aluindel that is, ACE, CD4, PLAT, PV92, TPA25, FXIIIB, APO and D1 are used as a tool to find the diversity. Genotypes were determined for several Alu insertion/deletion loci after DNA was obtained, amplified by PCR, processed on agarose gel electrophoresis, and isolated DNA was amplified.The average heterozygosity is found to be moderated in all the four studied populations. At AluCD4 (GST=24.8%), the four study groups appear to differ the most, while Alu PLAT (GST=0.2%) shows the least variation. The GST value, which may be attributed to population variance, was 7.5 percent when all the markers are taken into account together. The heat map indicates the affinities of the studied population with the Irula tribe of the South India population. According to this study, the Naga population groupings are more genetically related to Southeast Asia than to either Africa or Europe.