INFERENCE OF HUMAN GEOGRAPHIC ORIGINS USING *ALU* INSERTION POLYMORPHISMS

David A. Ray[a§], Jerilyn A.Walker[a§], Ashley Hall[b], Barbara Llewellyn[c],
Jack Ballantyne[b], Allen T. Christian[d], Kenneth Turteltaub[d], and Mark A. Batzer[a]

[a] Department of Biological Sciences, Biological Computation and Visualization Center,
Louisiana State University, 202 Life Sciences Building, Baton Rouge, LA 70803, USA

[b] National Center for Forensic Science, University of Central Florida Post Office Box
162367, Orlando, FL 32816-2367, USA

[c] Illinois State Police, Forensic Science Center at Chicago, 1941 W. Roosevelt Road,
Chicago, IL 60608, USA

[d] Lawrence Livermore National Laboratory, Biology and Biotechnology Research
Program, PO Box 808, L-452 Livermore, CA 94551, USA

[§] These authors contributed equally to this work.

The inference of an individual's geographic ancestry or origin can be critical in narrowing the field of potential suspects in a criminal investigation. Most current technologies rely on single nucleotide polymorphism (SNP) genotypes to accomplish this task. However, SNPs can introduce homoplasy into an analysis since they are often only identical-by-state. In addition, genotyping large numbers of SNPs has the potential to be very costly and requires specialized equipment. Insertion polymorphisms based on short interspersed elements (SINEs) can overcome these limitations. SINE polymorphisms are identical-by-descent, essentially homoplasy-free, and inexpensive to genotype using a variety of detection systems. Herein, we present results of a blinded study using 100 *Alu* insertion polymorphisms to infer the geographic ancestry of 18 unknown individuals from a variety of geographic locations. Using a Structure analysis of the *Alu* insertion polymorphism based genotypes, we were able to correctly infer the geographic affiliation of all 18 unknown individuals with high levels of confidence.