IDENTIFICATION AND CHARACTERIZATION OF Y_C LINEAGE ALU ELEMENTS FOR TRACKING POPULATION AFFILIATION

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The identification of "young" Alu subfamilies and their polymorphic insertions has proven useful for both human population genetics and forensic applications. Alu elements are identical by descent and effectively homoplasy-free genetic characters, making them ideally suited genomic "breadcrumbs" for tracking ancestral lineages. Efforts to characterize the AluYc lineage have recently been accomplished. Of the 225 Yc1 and 33 Yc2 elements analyzed, 48 polymorphic Yc1 and 11 polymorphic Yc2 elements have been identified and will contribute to our database of elements utilized to infer an individual's geographic ancestry. One Yc2 and eight Yc1 elements were of particular interest, as their frequency within one of the four populations tested differed by ≥25% from the other three populations tested. These elements are considered population specific polymorphisms. The identification of population specific Yc1 Alus and the relatively high polymorphic rate of the Yc2 subfamily (33%) make them particularly useful for inference of geographic origins. During a criminal investigation the identification of ancestry is a useful tool to narrow the pool of potential suspects.