

The phylogeography and regionalization of human Y-chromosomes

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Abstract:

Human history has experienced numerous episodes of population size fluctuations, fissions/fusions and migrations that create considerable complexity in the contemporary gene pool. One approach is to disentangle the sequestered genetic memory to help understand migrations, population origins, substructure and histories. Non-recombining haploid systems like the Y-chromosome provide an accessible way forward. Pronounced non-random correlations between Y-chromosome varieties and geography often manifest as clines in frequency and/or accumulated diversity. These phylogeographic patterns of genetic diversification provide a molecular perspective to migratory routes, genetic barriers and polarity of net gene flow. Such data concerning chromosome differentiation offers stimulating clues concerning the origins of contemporary population affinities and substructure and provides an independent perspective to investigate ambiguities concerning resemblances and origins of populations based upon material culture, linguistic and other genetic knowledge. Illustrative examples will be presented.