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Source: Human Biology, 86(2):113-130. Published By: Wayne State University Press DOI: http://dx.doi.org/10.3378/027.086.0205

URL: http://www.bioone.org/doi/full/10.3378/027.086.0205

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Human Paternal Lineages, Languages, and Environment in the Caucasus

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ABSTRACT

Publications that describe the composition of the human Y-DNA haplogroup in different ethnic or linguistic groups and geographic regions provide no explicit explanation of the distribution of human paternal lineages in relation to specific ecological conditions. Our research attempts to address this topic for the Caucasus, a geographic region that encompasses a relatively small area but harbors high linguistic, ethnic, and Y-DNA haplogroup diversity. We genotyped 224 men that identified themselves as ethnic Georgian for 23 Y-chromosome short tandem-repeat markers and assigned them to their geographic places of origin. The genotyped data were supplemented with published data on haplogroup composition and location of other ethnic groups of the Caucasus. We used multivariate statistical methods to see if linguistics, climate, and landscape accounted for geographical differences in frequencies of the Y-DNA haplogroups G2, Rla, Rlb, Jl, and J2. The analysis showed significant associations of (1) G2 with wellforested mountains, (2) [2 with warm areas or poorly forested mountains, and (3) [1 with poorly forested mountains. Rlb showed no association with environment. Haplogroups Jl and Rla were significantly associated with Daghestanian and Kipchak speakers, respectively, but the other haplogroups showed no such simple associations with languages. Climate and landscape in the context of competition over productive areas among different paternal lineages, arriving in the Caucasus in different times, have played an important role in shaping the present-day spatial distribution of patrilineages in the Caucasus. This spatial pattern had formed before linguistic subdivisions were finally shaped, probably in the Neolithic to Bronze Age. Later historical turmoil had little influence on the patrilineage composition and spatial distribution. Based on our results, the scenario of postglacial expansions of humans and their languages to the Caucasus from the Middle East, western Eurasia, and the East European Plain is plausible.

PDNA haplogroup diversity is most commonly used to analyze ancestry of individual ethnic groups or linguistic families (Kayser et al. 1997; Brisighelli 2012), because Y-DNA haplogroups generally show more distinct ethnogeographic patterns than does matrilineally

inherited mitochondrial DNA (Comas et al. 2000; Nasidze et al. 2003, 2004a), most likely because of higher dispersal rates of women (Seielstad et al. 1998; Oota et al. 2001; Nasidze et al. 2004b), the effects of selective pressures on the mitochondrial genome (Mishmar et al. 2003), and/or sex ratio

KEY WORDS: Y-DNA HAPLOGROUP, PATERNAL LINEAGE, CAUCASUS, GLACIAL REFUGIA, HUMAN ECOLOGY, LANDSCAPE GENETICS, ETHNOGENESIS. LANGUAGE.

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