

Population history and contact in northeastern Siberia: molecular anthropological perspectives

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Recent innovations in laboratory methods and computational analyses have revolutionised molecular anthropology, opening up new linguistically relevant insights into human prehistory. In this talk, I will provide a review of the recent literature dealing with northeastern Asia and highlight genetic results that might be of importance for linguists working on language contact in the region. While population changes before and during the Last Glacial Maximum (~26,500-19,000 years ago) are too ancient to be of linguistic interest, a further change in the genetic composition of Siberian populations occurred in the past 5000 years. At this time, peoples from the Amur region and southern Siberia started moving to the north, replacing the original inhabitants over large parts of Siberia. A notable exception, however, are the Chukotko-Kamchatkan peoples, who have been shown to be descendants of the Mesolithic settlers of northeastern Siberia (Sikora et al. 2019, Flegontov et al. 2019). Modern-day Yupik-speaking populations of Chukotka are clearly descended from Iron Age peoples settled in Uelen and Ekven (Sikora et al. 2019, Flegontov et al. 2019), who themselves migrated back from the New World (Pugach et al. 2016, Flegontov et al. 2019). This back migration brought the Yupik into contact with the Chukchi, leading to bidirectional, but unequal admixture (Pugach et al. 2016, Flegontov et al. 2019): whereas the Naukan Yupik carry only about 7% of Chukchi ancestry, the Chukchi carry approximately 40% Naukan ancestry. This points to the possibility of finding linguistic substrate influence from Yupik in Chukchi. Furthermore, eastern Even groups from Berëzovka and especially Central Kamchatka can be shown to have incorporated Koryak or Itelmen ancestry, which might also correlate with contact-induced changes. Finally, the Yukaghirs show high levels of recent and ongoing admixture (Fedorova et al. 2013, Pugach et al. 2016) – so much so that detailed analyses of their genetic history are unfortunately impossible. However, possible sources of individual admixture might be Sakha (Yakuts) and Chukchi.