Simulating multiple wave human dispersals out of Africa

Jiaoyang Ruan\textsuperscript{1,2} and Axel Timmermann\textsuperscript{1,2}
\textsuperscript{1}Center for Climate Physics, Institute for Basic Science, Busan, South Korea
\textsuperscript{2}Pusan National University, Busan, South Korea

Human fossil and archeological findings indicate that Anatomically Modern Humans (AMHs) may have migrated from Africa into Eurasia multiple times during the last glacial period. However, mtDNA-based genetic data (haplogroup L3 & its daughters M, N) appear to be more consistent with a single wave dispersal ~ 70-60 ka, coinciding with one of the driest periods in northeastern Africa.

To reconcile this discrepancy and better understand the migration routes and interactions of different groups of AMHs, we developed a new version of the Hominin Dispersal Model (HDM, version 2). The phenomenological reaction diffusion model simulates a realistic human dispersal in a spatio-temporally varying climatic environment. In our configuration, we introduce a group which represents individuals which dispersed into Asia prior to 60 ka and a group which migrated into Eurasia post-60 ka. An ensemble of parameter sensitivity experiments suggests that their interaction caused a characteristic east-west gradient in admixture across Eurasia, which is consistent with latest genetic datasets, which reveal a faint signal of pre-60 ka dispersal waves in Southeast Asians and individuals from Papua New Guinea. Moreover, our simulations provide new insights into possible migration routes of AMHs. Based on this analysis we propose a new hypothesis to explain the increased Neanderthal DNA percentage in present-day Asians relative to Europeans.