An Improved Molecular Clock to Estimate Reliable Demographic Parameters in Population Genetics

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The molecular clock is fundamental in evolutionary biology as it assumes molecular rate constancy among lineages and provides a time frame for evolution. However, increasing evidence shows a time-dependency of the rates with inflated values obtained over recent calibration time. As calibrations using recent dates ($< 50,000$ years) are virtually non-existent in most species, dating of demographic processes is likely overestimated because of the use of old phylogenetic calibration points (> 1 Myr). To obtain more reliable molecular rates for population studies, I have developed the CDT method (Calibration of Demographic Transition) using the timing of climatic changes over the LGM-Holocene transition ($10,000 - 20,000$ years ago) to calibrate demographic changes in temperate species. This paper describes the evaluation, validation and outcomes of the method using simulated and experimental data. The method was applied to various simulated and experimental data, which confirmed its broad applicability. The time-dependency of the rates and heterogeneity among taxa is confirmed. The estimated expansion dates combined with ecological and demographic evidence confirm the inaccuracy of the phylogenetic rates at population levels. The new calibration is compared to others to investigate the colonisation history of Western Europe by Human (haplogroup H). This new calibration method provides a robust clock for population genetics which opens new possibilities particularly in the evaluation of anthropogenic effects on natural populations.