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Modeling the influence of human kinship systems on genetic diversity

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Introduction

Human kinship systems are shaped by 3 major rules :

- the descent rule
- the alliance rule
- the post-marital residence rule

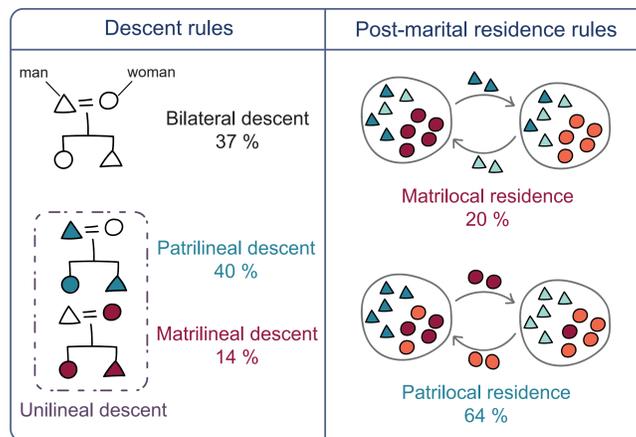
Definitions

descent rules define to which kinship group an individual is affiliated in a population.

unilineal descent is often associated with lineage exogamy, lineage fission and transmission of reproductive success.

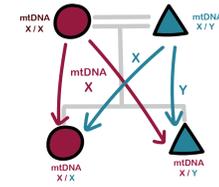
post-marital residence rules determine the place where a couple settles after marriage.

Most modern human populations are patrilocal and patrilineal. But little is known about the history of human kinship systems and in particular, about when patrilocality and patrilineality became overrepresented in human populations.



[7]

Several studies have highlighted that kinship systems can leave genetic signatures on uniparental markers [2, 10] and on X chromosomes [11], that are differentially transmitted according to the sex of individuals :



By modeling human populations displaying different descent and post-marital residence rules, and computing several diversity estimators on different markers (Y, mt, X, autosomes), we will **evaluate to which extent kinship rules impact genetic diversity in human populations, in order to trace back the history of kinship systems using genetic data.**

Methods

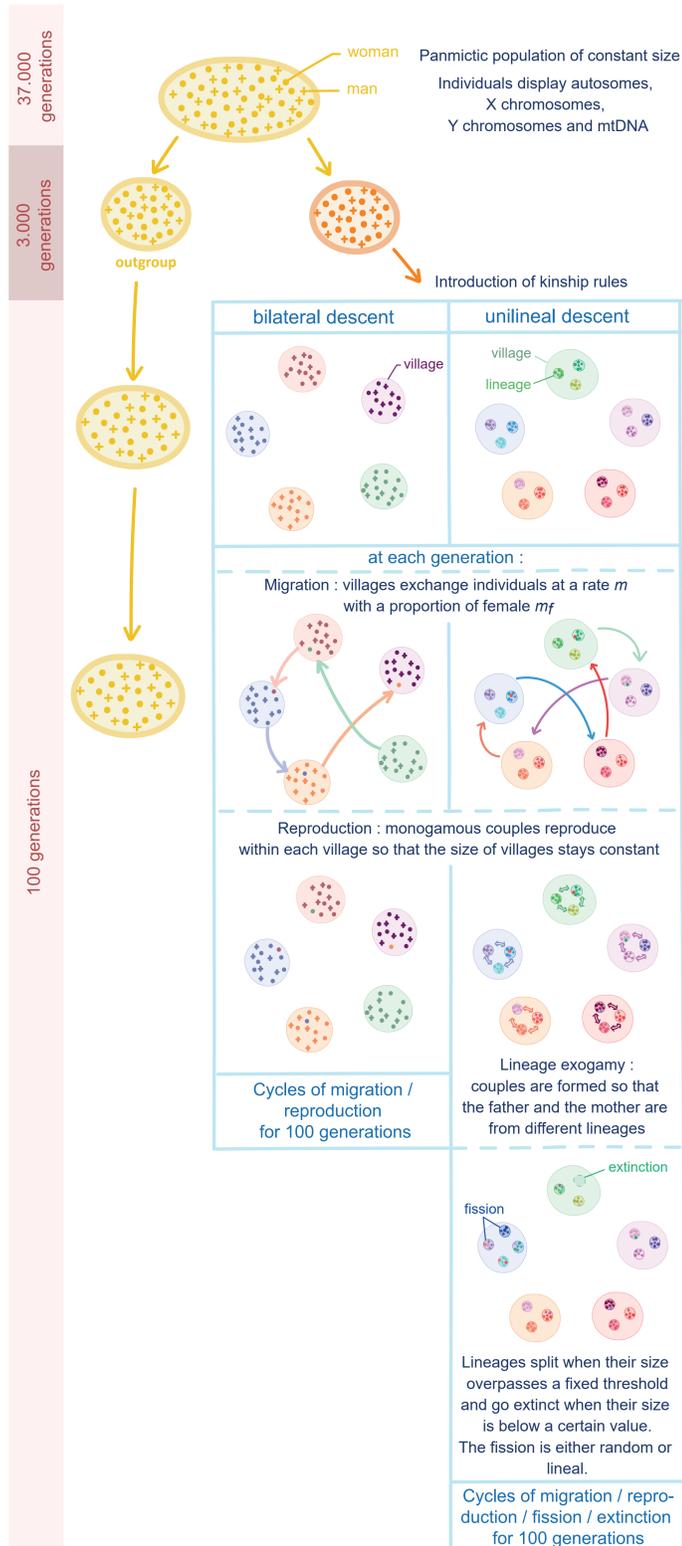
1) Run simulations with SLiM [3]



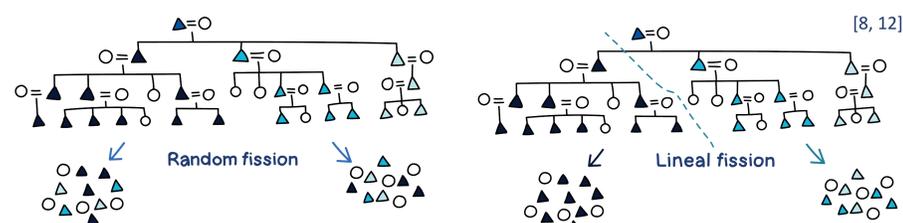
2) Handle tree sequences and generate VCF files with *tskit* [6] and *msprime* [1]



3) Compute diversity estimators



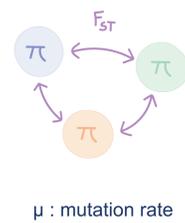
Two different fission types



[8, 12]

Results

Diversity estimators



μ : mutation rate

Nucleotide diversity π
Mean pairwise differences within a village [9]

• X / autosomes diversity ratio :

$$Q_{\pi} = \frac{\pi_X}{\pi_A} \times \frac{\mu_A}{\mu_X} \quad [4]$$

• mt / Y diversity ratio :

$$\pi^{mt/Y} = \frac{\pi_{mt}}{\pi_Y} \times \frac{\mu_Y}{\mu_{mt}}$$

Genetic differentiation F_{ST}
between villages [13]

• X / autosomes diversity ratio :

$$Q_{F_{ST}} = \frac{\ln(1 - 2 F_{ST A})}{\ln(1 - 2 F_{ST X})} \quad [5]$$

• mt / Y diversity ratio :

$$F_{ST}^{Y/mt} = \frac{F_{ST Y}}{F_{ST mt}}$$

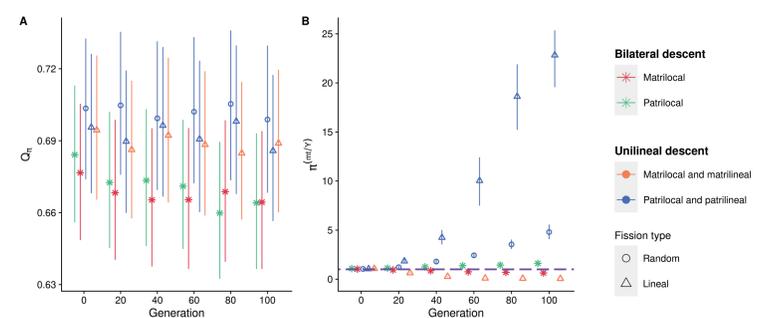


Fig 1 . Ratios of nucleotide diversity across generations from the introduction of kinship rules in villages

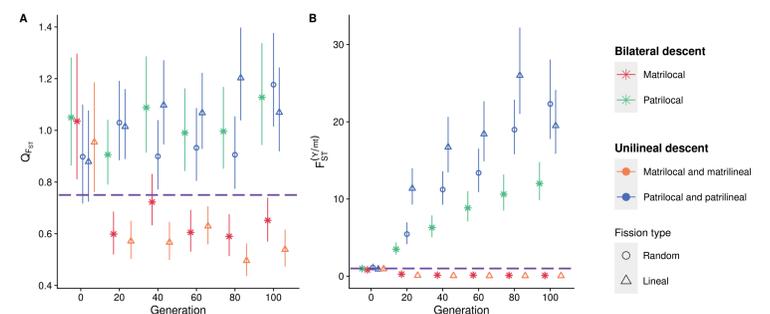


Fig 2 . Ratios of genetic differentiation across generations from the introduction of kinship rules in villages

Discussion

Diversity ratios allow the differentiation between kinship rules (Fig 1, 2). In particular, all ratios, except Q_{π} , enable to discriminate between **patrilocal / patrilineal** and **matrilocal / matrilineal** villages. However, only ratios using uniparental markers are able to make the difference between **patrilocal** villages with **bilateral** descent and **patrilocal** villages with **patrilineal** descent, as well as between **random** and **lineal** fission.

Perspectives :

- 1 - Identify other relevant estimators
- 2 - Test for the robustness of these estimators to low samples size and damaged pseudo-haploid sequences (aDNA)
- 3 - Compute these estimators on ancient DNA data
- 4 - Compare the results with the expected ratios generated under different models
- 5 - Trace back the history of human kinship systems

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