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.

Methods

1) Run simulations with SLiM [3]
2) Handle tree sequences and generate VCF files with nix [6] and maprim [1]
3) Compute diversity estimators

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

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Results

Diversity estimators

Nucleotide diversity \( \kappa \) mean pairwise diversity within a village [9]

- X / autosomes diversity ratio : \( Q_{X/A} = \frac{\mu_A}{\mu_X} \)
- mt / Y diversity ratio : \( Q_{MT/Y} = \frac{\mu_Y}{\mu_M} \)

Genetic differentiation \( F_{ST} \) between villages [13]

- X / autosomes diversity ratio : \( F_{X/A} = \frac{1}{1 - 2 F_{ST \times X/A}} \)
- mt / Y diversity ratio : \( F_{MT/Y} = \frac{1}{1 - 2 F_{ST \times MT/Y}} \)

Discussion

Diversity ratios allow the differentiation between kinship rules (Fig 1, 2). In particular, all ratios, except \( Q_{MT/Y} \), 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 small 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

References