



POPULATION HISTORY AT THE MICROSCALE: CRANIOMETRICS OF THE CAYO SANTIAGO MACAQUES

Darice R. Westphal¹, Gregory E. Blomquist¹

¹ Department of Anthropology



Introduction

General Theory

- Quantitative traits are influenced by both genetic and environmental variation
- The influence of environmental variation was thought to limit the application of quantitative traits, however, when environmental variables are restricted and heritability known, polygenic traits contain the same information which is informative for population structure as single-locus markers (Rodgers and Harpending, 1983)
- Genetic distances derived from quantitative data can be used to understand the relationships between populations; therefore, the larger the genetic distance between any two populations, the more dissimilar they are genetically
- These ideas can be applied to understanding the relationships between social groups within a single population and change over time

Background (Lineage Effects)

- Groups fission periodically in response to resource pressures
- Fission of social groups could be a major cause of genetic differences between groups
- Example:
 - Several lineages make up a single group
 - Group splits to create new daughter groups
 - Daughter groups more genetically similar because both groups are derived from the same ancestral group

Background (Temporal Sequence)

- Use of linear distances on cranial and post-cranial features to infer genetic distance between social groups
- Differences between groups over time should be distinguishable
 - Groups that are separated by more time should be more genetically different
- Konigsberg's (1990) use of temporal sequencing to distinguish mound building societies
 - Use of linear measurements on skeletonized remains
 - Sites separated spatially and temporally → environmental factors skew temporal sequence results
- Cayo Santiago macaque data removes environmental skew as all individuals are under same environmental pressures

Importance

- Refine ability to tease out population history from skeletonized remains
- Quantitative traits are sometimes the only source of information for historic populations
- Relates to larger questions of socioecology, such as male migration, preferential male mating, and female choice
- Applicable to analyzing population structure of human societies



Figure 1. Grouping of Cayo Santiago macaques on the island.



Figure 2. An aerial view of Cayo Santiago in December 1999. The white scale bar in the bottom left corner is 500 meters.

Materials and Methods

Cayo Santiago macaques (*Macaca mulatta*):

- Skeletonized remains of individuals who die naturally or are removed
- Macaques have free range on island with provisioning
- Males leave natal group between 3-4 years of age and join another social group to mate
- Females remain in natal group and form hierarchical matriline

Materials and Methods Continued

- Linear measurements collected by Blomquist (2009) for 90 female macaques
 - Cranial measurements: mesial canine to distal M² distance, orbital height, glenoid tubercle to endomolare, basion to external auditory meatus, lateralmost infraorbital foramen to external auditory meatus, bizygomatic width, cranial length (alveolare to most posterior point)
 - Post cranial measurements: humerus length, humeral anterior to posterior diameter at midshaft, radius length, 3rd metacarpal length, femur length, femoral anterior to posterior diameter at midshaft, tibia length, 3rd metatarsal length, clavicle length, pelvis length, scapular width, scapular spine length
- Demographic information: group membership, age at death, cohort membership, how death occurred, genealogical information
- Analyzed with Rmet (Relethford, 2004) with heritability assumed to be 1 and population size estimated using arithmetic mean of annual social group census

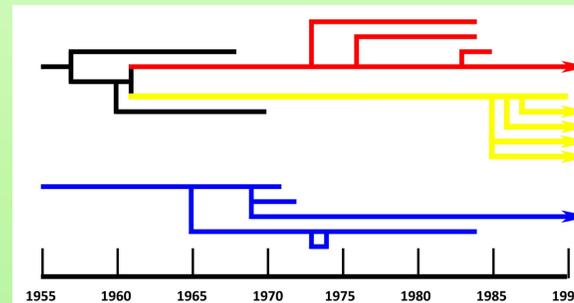
Time period	Lineage AJNKL	Lineage FM	Lineage IQRS	Sum
Pre 1965	12	3	4	19
1965-1969	2	6	1	9
1970-1974	5	7	5	17
1975-1979	1	6	1	8
Post 1980	1	8	8	17
Sum	21	30	19	70

Table 1. Temporal sequencing (5 time periods). Social groups lumped together and then divided into 5 time periods. Sample sizes included within each cell.

Lineage	n
AJNKL	28
FM	37
IQRS	25
Sum	90

Table 2. Sample sizes for amalgamated lineages formed from separate social groups (A, J, N, K, L, F, M, I, Q, R, S)

Figure 3. Schematic of social group fissions and fusions from 1955 to 1990. Red coloring corresponds to FM lineage amalgamation, blue to AJNKL, and yellow to IQRS.



Predictions

- Lineage effects (3 groups): Lineages FM and IQRS are more closely related to each other than either is to AJNKL because they resulted from the fission of a single parent group
- Temporal sequencing (5 time periods): The youngest time period should be most similar to the time period that directly precedes it, with increasing dissimilarity compared to earlier time periods

Results

Lineage Effects (3 groups)

Lineage	AJNKL	FM	IQRS
AJNKL	0.000	0.033	0.023
FM	-0.011	0.012	0.027
IQRS	-0.008	-0.001	0.013

Table 3. Mahalanobis distances (D²) for three lineages with h²=1 on top half of matrix with corresponding R values on bottom half of matrix. R(ii) values are displayed along the diagonal.

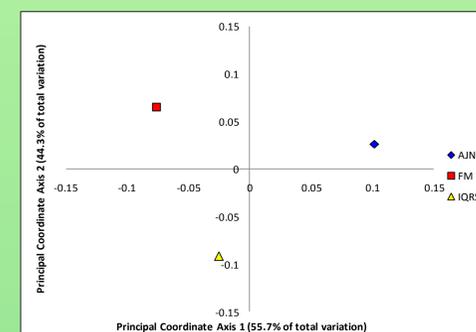


Figure 4. Plot of scaled Eigenvectors from postcranial and cranial distances for three lineages with h²=1

Results Continued

Temporal Sequencing (5 time periods)

Temporal Groups	Pre 1965	1965-1970	1970-1975	1975-1980	Post 1980
Pre 1965	0.045	0.014	0.071	0.164	0.177
1965-1970	0.022	0.013	0.042	0.101	0.152
1970-1975	-0.007	-0.008	0.013	0.054	0.117
1975-1980	-0.047	-0.032	-0.008	0.026	0.09
Post 1980	-0.036	-0.02	-0.022	-0.002	0.061

Table 4. Mahalanobis distance (D²) for all lineages combined divided into 5 time periods with h²=1 on top half of matrix. The blue shading represents the stepwise jumps in dissimilarity between the temporal groups. The corresponding R values are displayed on the bottom half of the matrix. R(ii) values are displayed along the diagonal.

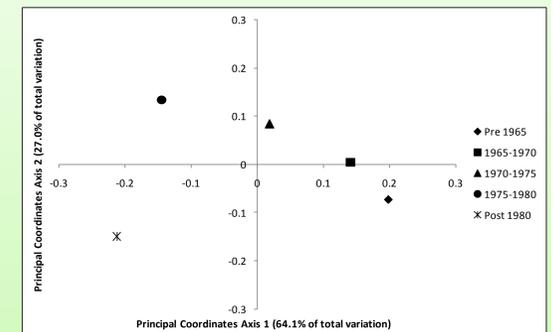


Figure 5. Plot of scaled Eigenvectors from postcranial and cranial distances for all lineages divided into 5 time periods with h²=1

Discussion

Lineage effects (3 groups)

- Social groups can be distinguished from one another based on linear measurements
- Prediction that two most similar groups (FM and IQRS) are derived from same social group that split was supported, however it does not account for all variation
- Dissimilarities are small as a result of the complex nature of relatedness between groups or simply because of the small spatial and temporal scale used in this analysis
- Further analysis including both males and females and data accumulated since collection could allow social groups to be represented instead of amalgamated lineages used in this analysis and provide clarification on what models may be at work

Temporal sequencing (5 time periods)

- All temporal periods are derived from same founder population, therefore all differences between periods over time are due to genetic drift
- Temporal sequence analysis supported the hypothesis that genetic drift increases the genetic differences through time
- Further definition of temporal sequence could be achieved by including males and extending the time period

Conclusions

- Quantitative traits can be used infer patterns of population structure
- Patterns relating to socioecology such as male migration, differential male mating, and female choice could also be analyzed with larger sample size and inclusion of male data
- Temporal sequencing analysis can be utilized understand the temporal relationship between closely related populations that occupy the same spatial area

Selected Bibliography

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