Comparison of camel DNA quantities extracted from blood, saliva, and hair

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1. Introduction

- The single-humped Arabian camel, *Camelus dromedarius*, has always been an important animal to societies in the Arabian gulf.
- This importance mostly stems from its intrinsic qualities, which facilitate its utilization for milk, meat, and wool production, and as a vehicle to transport loads and persons.
- To study the genetic basis of the camel's unique qualities, DNA samples, with associated phenotype, pedigree, and population information, are needed.

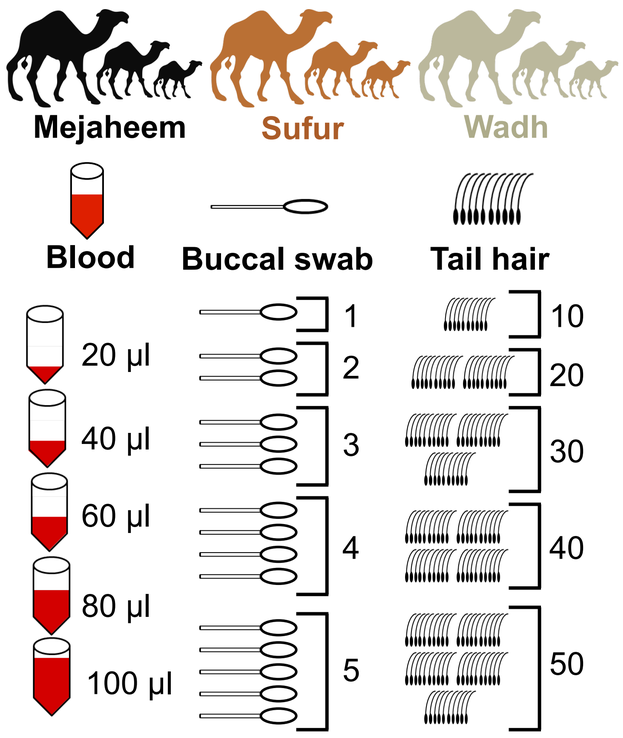
2. Objectives

In this study, we determine if DNA sources from blood, saliva, and hair:

1. provide sufficient DNA quantities for genetic analysis
2. provide consistent DNA quantities across trials
3. provide similar DNA quantities across camel breeds
4. are useful DNA sources to establish a camel biobank

3. Materials and Methods

- Nine unrelated dromedary camels, housed at the Camel Research Center, at the King Faisal University (KSA), were used for this study.
- These camels come from three widely recognized breeds: **Mejaheem** (3F), **Sufur** (3F), and **Wadh** (1M, 2F) .
- For each camel, we collected whole-blood, buccal swabs, and tail-hair follicles.
- For each DNA source, we extracted five different quantities (see figure).
- Three replicated (identical) extractions were performed for each camel, using each of the DNA sources.
- DNA quantity was then measured using Nanodrop spectrophotometry.



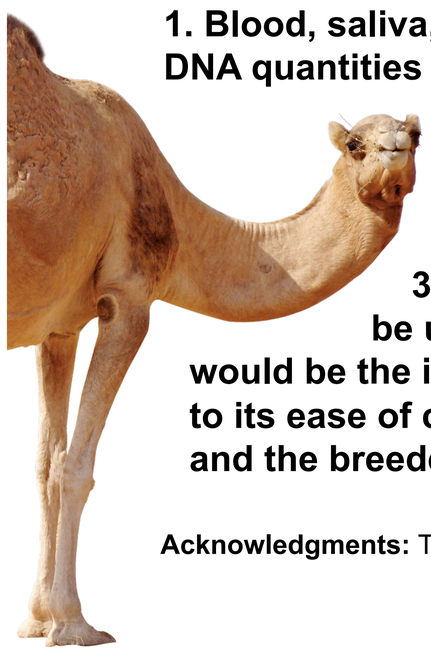
- We then used a Kruskal–Wallis test to determine if there are statistically significant differences in DNA concentrations between compared groups.
- In comparisons of >2 groups, when the Kruskal–Wallis test detects significant differences, a post-hoc Dunn test for multiple comparisons was performed to determine if pairwise differences were significant.
- The p-values for the Dunn test were adjusted to control for familywise error rates and the false discovery rate, using the Benjamini-Hochberg method.
- Finally, a linear regression was conducted to determine the association between input DNA quantity, and output extracted DNA quantity, for each DNA source.

5. Conclusions

1. Blood, saliva, and hair all give sufficient and consistent DNA quantities across replicas.

2. Blood, saliva, and hair all give similar DNA quantities across breeds.

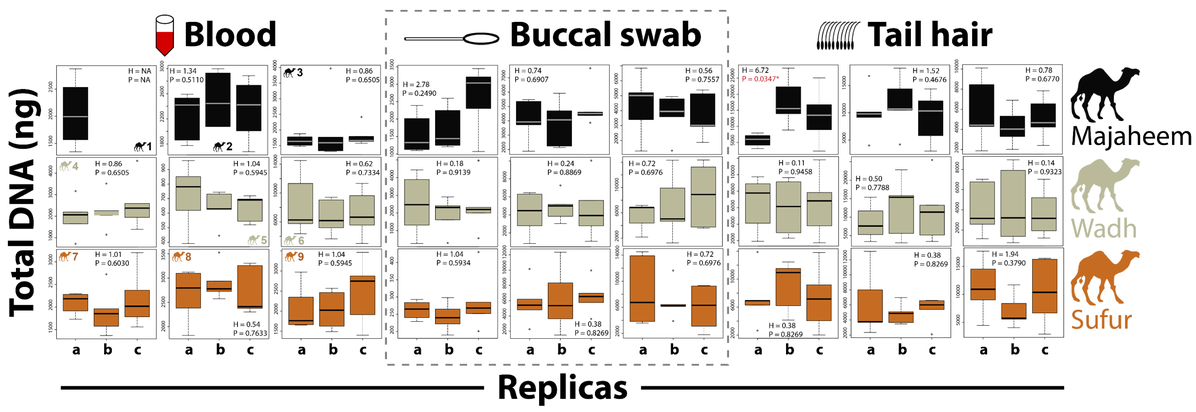
3. While blood, saliva, and hair samples can all be used as camel DNA sources, hair samples would be the ideal choice to establish a camel biobank, due to its ease of collection and storage, being non-pathogenic, and the breeders' willingness to provide it.

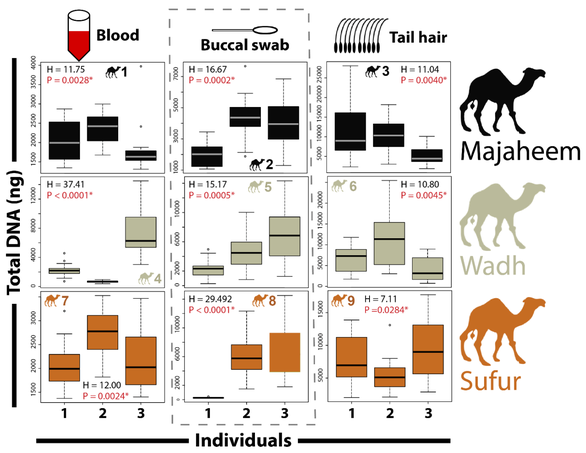


4. Results

1. Are there differences in DNA quantities extracted from each replica?

- We found **no significant differences** in DNA quantities extracted from each replica, within each individual, for all three DNA sources (all P>0.24).



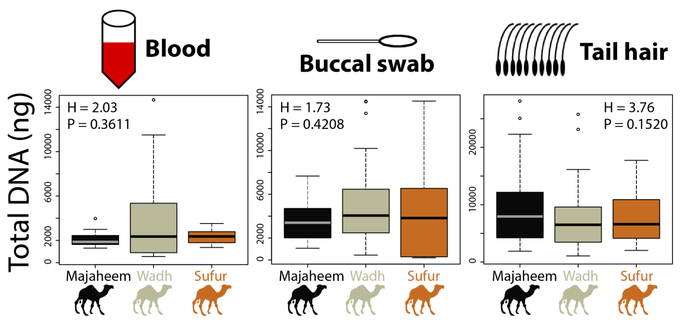


2. Are there differences in DNA quantities extracted from each individual?

- We found **significant differences** in DNA quantities extracted from individuals within each breed, for all three DNA sources (all P<0.0284*).
- Significant differences **remain**, even when breeds are disregarded (all P<0.0001; data not shown).

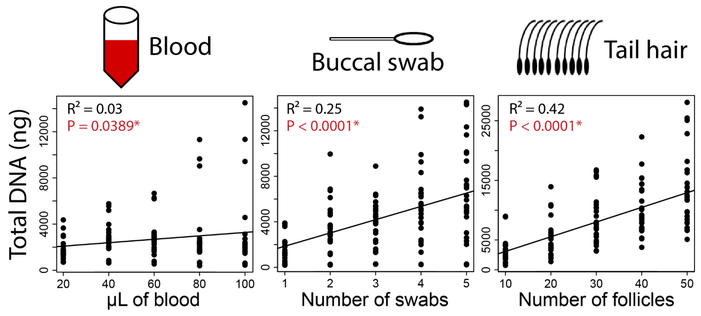
3. Are there significant differences in DNA quantities extracted from each breed?

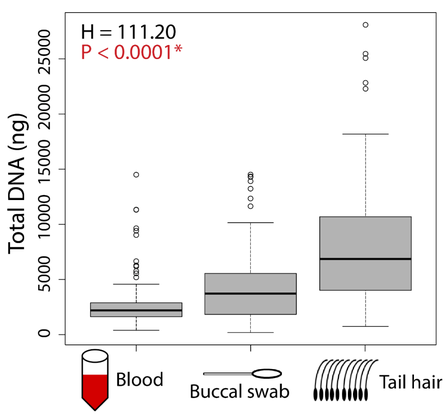
- We found **no significant differences** in DNA quantities extracted from each breed for all three DNA sources (all P>0.1520).



4. Is input DNA quantity correlated with output extracted DNA quantity?

- We found a **significant positive relationship** between input DNA quantity and output extracted DNA quantity for all three DNA sources (all P<0.0389*).
- The strength of the association between these two variables was greatest for hair (R^2 =0.42), followed by saliva (R^2=0.25), and weakest for blood samples (R^2=0.03).





5. Are there significant differences in overall DNA quantities extracted from each DNA source?

- Based on the quantities used in this experiment, we found **significant** differences in DNA qualities extracted from each DNA source (P<0.0001*).
- A post-hoc pairwise comparison indicates that the DNA quantity extracted from hair was **significantly greater** than that extracted from both saliva and blood (P<0.0001*).

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