The Origin of the Khoisan Domestic animals
What do we know

The main domestic species hold by Khoisan are:

The Centers of Origin
Arrival in Africa
Types and Varieties
Genetic Data
Interpretations and Future Directions
Arrival in Africa

Cattle
Types and Varieties
Short - Long Horn - Pooled

The Pastoral period of rock painting spanned between 2-5000 BC.

Tassili-n-Ajjer, southern Algeria where

Wadi Tashwinet, Tadrart Acacus, Libyan Sahara

Egypt - 1-2000 BC
Types of cattle in Today’s Africa

Legend:
- Taurine Trypanotolerant
- Taurine
- Taurine Trypanotolerant & zebu
- Sanga & zebu
- Zebu
- Indian Zebu
Genetic Data

MtDNA

![Genetic Tree Diagram]

- B. taurus
- Near East
- Europe
- B. primigenius (extinct)
- Africa
- B. indicus

![Mutation Network Diagram]

- T1
- T2
- T3
- T4
- 22 mutations
- T1
- 185 057 113
- T2
- 185 057 113
- T3
- 255 302 083 042
- T4
- 084 232 085 141
- I1
- I2a
- I2
Geographic distribution of the zebu lineages

None in Africa
To assess diversity on the male path in cattle populations, six loci were analyzed. The haplogroup explained roughly 80% of the genetic variation. In the model as the only hierarchical factor to be tested, it was found that variation was similar to the proportion of variation explained by haplogroup.

Figure 1 shows Y1-haplotypes and Figure 2 shows Y2-haplotypes. The African-specific haplotypes found in African cattle, including those calculated via correspondence analysis, were important in understanding genetic variation.

The marker BM861, used in Ethiopian cattle by Ginja et al. (2007), and in Portuguese cattle by Li et al. (2009), and three of them previously found in Sub-Saharan cattle, have shown to have erratic behavior with a high rate (55%) of parental incompatibility.

Table 3 presents the haplotypic subfamily, predominant in the cattle breeds sampled in Central Europe, the three European Peninsulas, and Mediterranean Africa. By analyzing the genetic diversity within these areas, the study aimed to differentiate African Y2-haplotypes, confirm phylogenetic importance, and identify parental incompatibility.

The map illustrates the geographical variation of the first principal component, with different colors indicating variation across geographical areas. This differentiation is compatible with the structuring observed.

The results reported by Li et al. (2009) about the introgression into Portuguese cattle based on one allele on the pseudoautosomal region of the Y-chromosome can be differentiated from those of European cattle populations; and this structuring is compatible with a poor overall genetic differentiation except for specific haplotypes for African cattle populations.
Africa, Arabian Peninsula, Indian Subcontinent

15 microsatellite loci
(nearly neutral nuclear markers)

Source: Maghoub et al. 2011
Sheep
Neolithic Rock Jebe Bes Seba, Art Atlas Desert

El Bercheb, Egypt 600 A.C.

Central Arabia Peninsula 1 000 BC

Ndobe Hills, Zimbabwe ???Iron age???
Types and Varieties

sheep in Today's Africa

Fat-Tail
Thin Tail
Both
Revealing the History of Sheep Domestication Using Retrovirus Integrations

Chessa et al.
Lineage C has been observed mostly in fat-tail sheep breeds (Pedrosa et al. 2005; Tapio et al. 2006; Meadows et al. 2007).
Genome Wide Data

Chicken
Source: Miao et al. 2012
is the haplogroup with the largest geographic distribution being observed from Japan to Africa. Haplotype EAA2 for this haplogroup is identical to haplotype A1 from clade A in Muchadeyi et al. (2008). Haplogroup B, represented here with a single haplotype and individual found in Kenya was observed previously in South China and Japan (Liu et al., 2006), Sri Lanka (Silva et al., 2008) and in commercial egg layers (Muchadeyi et al., 2008). Haplogroup C, also represented by a single haplotype in our study, was previously observed in Western China (Liu et al., 2006), Sri Lanka (Silva et al., 2008) and in commercial broilers and populations from Northwest Europe (Muchadeyi et al., 2008). Finally, the last haplogroup in East Africa, haplogroup E, groups together with a set of haplotypes found within the Yunnan province of China (Liu et al., 2006).

4. Discussion

One conspicuous characteristic of village chickens in Africa is their extensive phenotypic variation in colours, feather types; morphology and body size (Msoffe et al., 2001; Halima et al., 2007; Dana et al., 2010a). Microsatellite analysis has also revealed extensive genetic diversity in African village chickens (Wimmers et al., 2000; Muchadeyi et al., 2007). In this study, we analysed partial mtDNA D-loop sequences from 512 village chickens sampled in East Africa to determine their ancestry, origin and dispersal patterns. We reveal the existence of at least five genetically distinct mtDNA D-loop haplogroups, two of which (haplogroups A and D) are shared with other African chicken populations. Specifically, haplogroups D and A have been observed previously in village chickens from the South African region (Muchadeyi et al., 2008; Razafindraibe et al., 2008), haplogroup D in West Africa (Adabambo et al., 2010) while haplogroups B, C and E are reported for the first time for the African continent.

Our results indicate a different origin and history of the two major haplogroups (A and D) in East Africa (Fig. 5 and Table S2). Indeed, they are related to geographically distinct Asian mitochondrial DNA haplogroups, primarily South Asia for haplogroup D and East and South Asia for haplogroup A (Liu et al., 2006). We do observe a distinct geographic distribution of the two haplogroups in East Africa with haplogroup A exclusively found in Kenya and haplogroup D found across all four countries studied. Last but not least AMOVA analyses indicate that the diversity of haplogroup D is found mainly within populations, while 40% of the diversity of haplogroup A is found among populations. It supports an independent and possibly more recent arrival and history of haplogroup A compared to haplogroup D and more particularly a coastal arrival of haplogroup A in Kenya. Mantel test on the other hand reveals...
What we don’t know...

Circa 1880

Multi-species BioProxies: cattle, sheep and chicken
Inclusion of South-West Africa together with Arabian Peninsula and East coast may add missing pieces to the history of Southern Human Populations
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