No genomes, no genes:
mtDNA d-loop diversity in Bronze Age alpine cattle

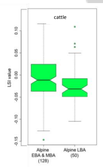
José Granado[1], Marianna Harmath[1], Umberto Tecchiati[3], Miki Bopp-Ito[1], Jörg Schibler[1], Klaus Oeggl[2], Angela Schlumbaum[1]

[1]IPAS University Basel, Spalenring 145, CH 4055 Basel, [2]University Innsbruck Institut für Botanik, Sternwartestrasse 15, A-6020 Innsbruck, [3]Amt für Bodendenkmäler Autonome Provinz Bozen Südtirol, Armando Diaz Straße 8, I-39100 Bozen

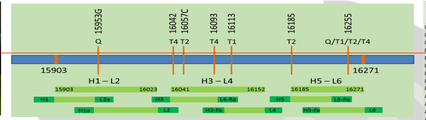
Question:

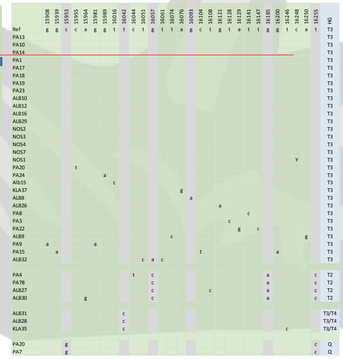
During Bronze Age economic and agricultural changes took place, which is also reflected in different crop plants and domestic animals compared to earlier periods (e.g. millets, spelt, lentil, horse). In the Alps (Italy, Austria, Switzerland), settlements related to **mining activities** were established at high altitudes, their inhabitants in need of food resources. Whether this was accompanied by farming at high altitudes, increased transhumance, adaptation/import of e.g. cattle specialized in grazing on alpine meadows, or transport of meat from the valley, is a matter of debate.

Here we use domestic animals as proxies for human actions and sequenced short fragments of mtDNA d-loop in cattle from metallurgic sites in the Eisack valley, Italy and Savognin-Padnal, Switzerland. Archaeogenetics is part of the interdisciplinary project team of archaeobotanists, archaeozoologists, archaeologists and stable isotope researchers.

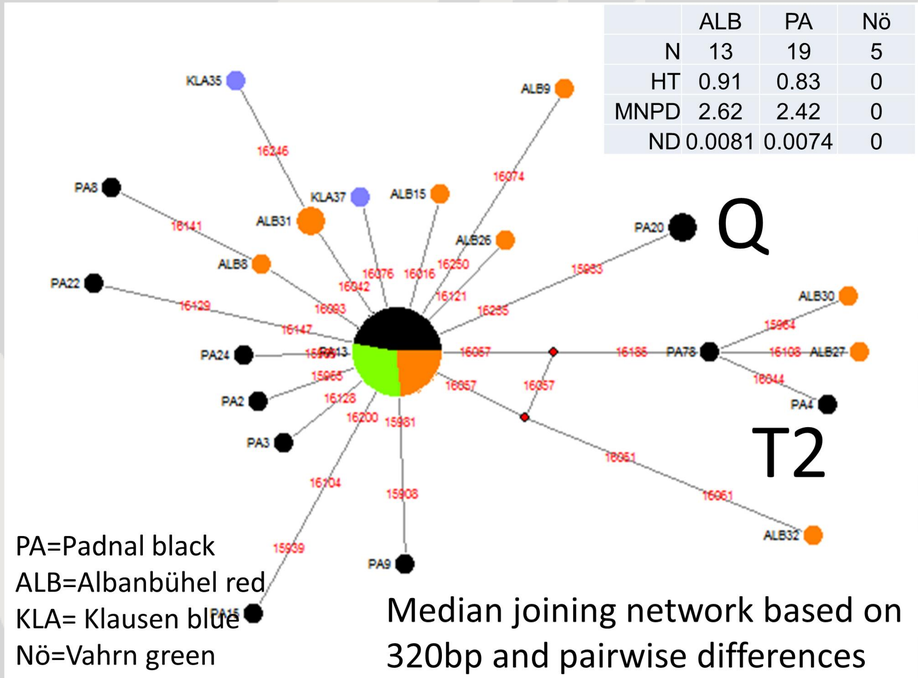


B. Albanbühel (ALB) was a **farming site, Early to Middle BA**; V. Nössingbühel (Nö) was a **military settlement, Early BA**, K. Gufidaun (KLA) was an **ore-processing site**, S. Padnal (PA) was a **farming/pastoralist site with copper mining activities, Early to Late BA**. With Late Bronze Age a decrease in cattle size is observed.

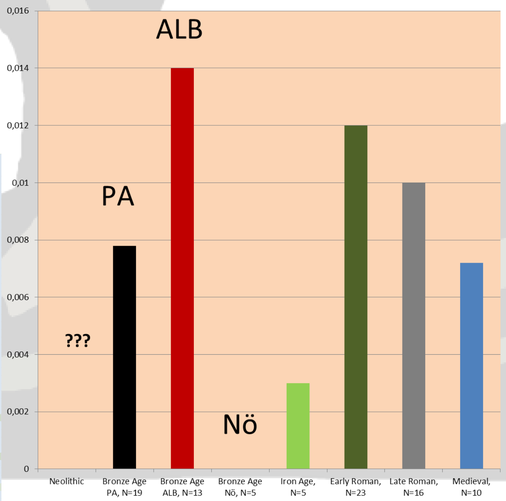


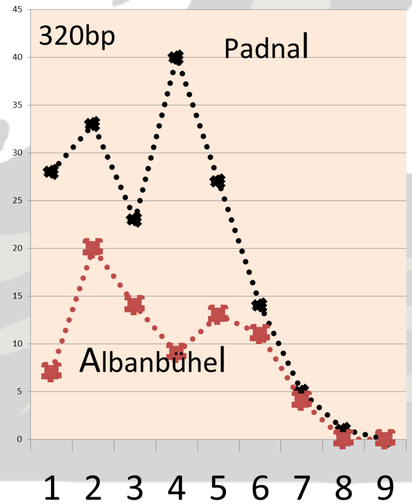


Mitochondrial (mtDNA) d-loop fragments of different sizes were amplified , spanning in total 320bp. Sequences were aligned and mutations recorded. Haplogroup diagnostic SNPs (single nucleotide polymorphisms) are highlighted in grey.



Median joining network based on 320bp and pairwise differences





We found:

- High diversity measures
  the presence of cattle belonging to the main European T3 haplogroup variants
  early presence of T2 and Q haplogroups.
- Diversity measures based on pairwise differences
  differ between ALB, PA and Nö. Nö cattle are strongly bottlenecked.
  - Presence of T2 and Q indicates contact to Eastern Europe.
- Mismatch analysis indicates similar population histories in the two regions including periods of secondary introductions and bottlenecks.
  Tajima's D indicates population expansions after bottleneck.

Our questions are:

Are phenotypic changes related to genetics?
Are there differences between sites and do they relate to setllement type?
Are genetic diversities related to time?
Does genetics indicate import of cattle?
Does genetics give a clue on origins?
How do stable isotopes relate to genetics or cattle size?
Etc etc etc.....

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