

Mediaeval cattle from Bern (Switzerland): An archaeozoological, genetic and historical approach

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Summary

This study deals with genetic analyses of an assemblage of mediaeval (13th century) cattle metapodials from Bern that had previously been osteometrically examined regarding sex, shape and wither height. The results from the genetic sexing of these small (height 100 to 120 cm) cattle correlate well with the osteometric interpretations. Some few exceptions we interpreted as cows used as draft animals with stouter bones and thus osteometrically determined as males. Two morphologically different groups of cow metatarsals however, we took as proof of the historical fact that Bern relied on livestock from different geographical origins: the town's vicinity and the alpine pastures with their favourable grazing conditions. It was not possible to distinguish them genetically. An analysis of one single nucleotide polymorphism (SNP) in the melanocortin receptor 1 (*MC1R*) showed that predominant coat colour most likely was red-brown. Furthermore, an analysis of the SNP in the Y-chromosomal intron *UTY19* that divide modern taurine cattle in two major haplogroups (Y1 and Y2) showed that the mediaeval cattle belonged to the haplogroup Y2 with one single exception of a Y1.

Keywords: cattle, archaeozoology, metapodials, genetic analysis, history

Rinder im mittelalterlichen Bern (Schweiz): archäozoologische, genetische und historische Untersuchung

In der vorliegenden Arbeit wird über die Genom-Analyse einer Sammlung von Metapodien mittelalterlicher Hausrinder des 13. Jahrhunderts aus Bern berichtet. Geschlecht wie auch Widerristhöhe der zugrundeliegenden Tiere sind zuvor nach osteometrischen und morphologischen Kriterien bestimmt worden. Der genetische Befund der Geschlechtsbestimmung dieser mit einer Widerristhöhe von 100 bis 120 cm als klein befundenen Tieren korreliert gut mit demjenigen der Osteometrie. Davon ausgenommen sind einzelne Metacarpen, die morphologisch als männlich, genetisch jedoch als weiblich bestimmt wurden. Diese zählen wir wegen ihrer kräftigen Morphologie zu den als Zugtiere verwendeten Kühen. Das Vorhandensein von zwei morphologisch unterschiedlichen Gruppen von Kuh-Metatarsen erachten wir als Beleg dafür, dass Bern mit Schlachtvieh verschiedener geografischer Herkunft beliefert wurde: einerseits aus der Umgebung der Stadt und andererseits aus den Alpen, wo günstigere Futterbedingung herrschten. Es war nicht möglich, die beiden Gruppen genetisch zu unterscheiden. Die Untersuchung des Einzelnukleotid-Polymorphismus (SNP) im Melanocortinrezeptor 1 (*MC1R*) ergab für die Fellfarbe vorwiegend rot-braun. Weiter zeigte die Untersuchung des Y-chromosomalen SNPs im Intron des *UTY19*-Gens, nach welchem heutige taurine Rinder in die Haplogruppen Y1 und Y2 eingeteilt werden, dass die untersuchten mittelalterlichen Rinder mit einer Ausnahme (Y1) zur Haplogruppe Y2 gehören.

Schlüsselwörter: Rind, Archäozoologie, Metapodien, Genom-Analyse, Geschichte

18 Originalarbeiten/Original contributions

Introduction

Although historical sources show us a lot about mediaeval society and culture, those codes and chronicles along with contemporary iconographic sources tend to focus mainly on the higher social classes, clergy and aristocracy, their achievements, social life, architecture and artworks, politics, treaties, wars and other heroic exploits and laudable deeds. Details on the lives and struggle of ordinary men, labourers, artisans, shopkeepers, farmers and peasants, their everyday stories and other seemingly less important facts and details are therefore much scarcer and hence hard to find. Moreover, until the 20th century historiography had only scarce interest in the social history of the lower classes. Luckily, this has changed as more and more research on the mediaeval socio-economy is being done using non-traditional sources like e.g. contemporary legal sources, wills, contracts and similar. Nevertheless, mediaeval archaeology and all its related disciplines like e.g. anthropology, archaeobotany and archaeozoology are still necessary in order for us to gain a better understanding of mediaeval life in all its facets and across all segments of society. Since the late 1980s, genetics have joined those ranks inasmuch as it has been made possible to extract, amplify and sequence DNA from ancient human and animal bones. In this paper, we would like to present a study that originated as a standard archaeozoology report about an urban animal bone assemblage, then evolved into a multivariate analysis using osteometric methods to be thereafter handed to the geneticists and finally to a veterinary historian. Our objective was to find out if and to what extent this interdisciplinary approach would contribute to help resolve some questions regarding cattle in late 13th century Bern.

Archaeozoological Background

The present study deals with cattle bones recovered from the historical old town of Bern when the cobble stone pavement of Kram- and Gerechtigkeitsgasse had to be repaired in 2004/05. Subsequently several hundred kilograms of animal bones, mostly from domestic animals, were excavated by the Archaeological Service of the Canton of Bern. Those bones were mainly gathered from layers of the late 13th century, when apparently only a few decades after Bern had been founded in 1191 a first levelling in the main street was considered necessary. An in-depth study (Nussbaumer and Rehazek, submitted for publication) showed their origin to be from contemporary local waste dumps. As in many such mediaeval archaeological sites from towns and cities, nearly all of these animal bones are remains from slaughtering and butchering, either at the butchers or in the kitchen while preparing meals. Remains from game are usually less than 1 %; hunting did not play any role in this context. Besides examining and assessing all archaeozoological remains, another of our focuses was on complete unbroken metapodials from adult cattle. Metapodials are among

the important limb long bones in ungulates. In the thoracic limb, they form the major supporting element; in the pelvic limb, they assume largely locomotive function. Due to their robustness, they often resist destruction or corrosion after their disposal. In Bern, we were lucky to find over one hundred such complete bones. Their morphology and their usefulness for anatomical studies regarding size, growth shape and sex are well documented and have been put to good usage in quite a number of scientific studies (e.g. Grigson, 1982; Bartosiewicz, 1987; Thomas, 1988; Albarella, 1997). In a paper we published recently (Rehazek and Nussbaumer, 2012) we pointed out the reasons why correctly interpreting such bones may lead to an understanding of husbandry, breeding and economic use of cattle in the Middle Ages. If the main aim of breeding either was dairy, beef or draught cattle or a mix thereof, this – if all goes well – also shows in the composition of

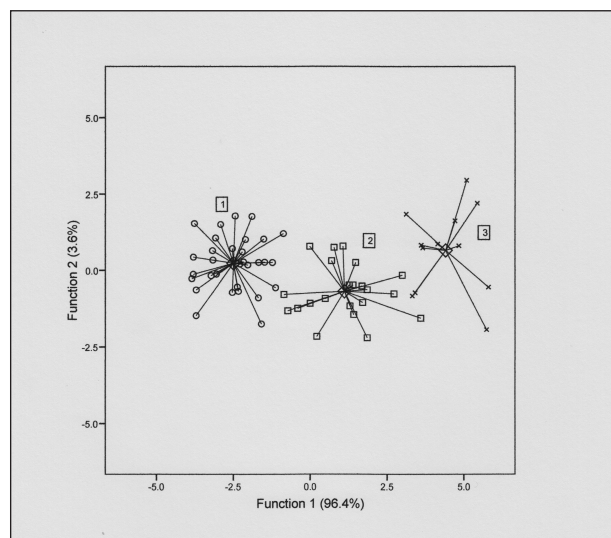


Figure 1: Metacarpals: Scatter plot of both canonical discriminant functions. The percentage in brackets gives the proportion of the total variance for the particular function. (Rehazek and Nussbaumer, 2012).



Figure 2: Three metacarpals from clusters one (left) to three (right). Bones were chosen for closeness to the centroid of their respective cluster and same body side (here, right). (Rehazek and Nussbaumer, 2012).

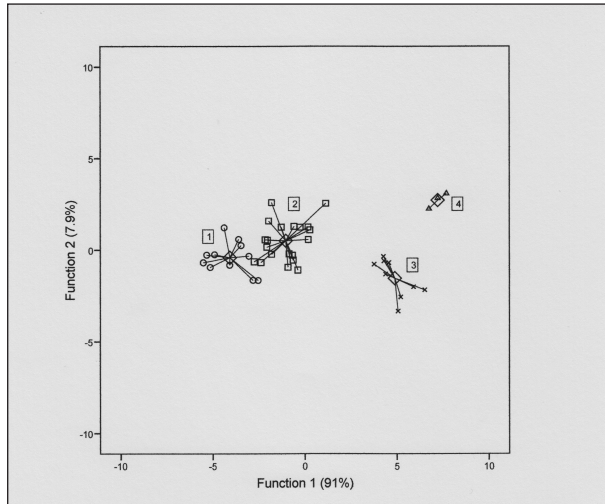


Figure 3: Metatarsals: Scatter plot of both canonical discriminant functions. The percentage in brackets gives the proportion of the total variance for the particular function. (Rehazek and Nussbaumer, 2012).



Figure 4: Four metatarsals from the clusters one (left) to four (right). Bones were chosen for the closeness to the centroid of their respective cluster and same body side (here, left). (Rehazek and Nussbaumer, 2012).

their bony remains. We were thus able to assess body size (height: 100 cm to 115 to 120 cm) and accordingly their weight (75 kg to 150 kg). However, as we found out in our survey using multivariate statistics on seven standard lengths, widths and depths, dimorphism in the metapodials, an important trait to distinguish genders, and thus understand probable breeding purpose, is rather low. No straightforward explanation for the clustering showed up and hence our morphometric approach did not lead to an ideal result of unambiguously identifiable cows, bulls and some oxen as would be anticipated. We actually did find three groups within the metacarpals (Fig. 1 and 2); within the metatarsals, however, we obtained four morphologically distinct clusters (Fig. 3 and 4). Even given some oxen four distinct groups were cause for some concern as that would leave open the possibility for different breeds or at

least strains in the cattle population. Another explanation would be that different geographical origins – subalpine or midland farms and pastures – and thus different management (feeding) conditions led to different habitus.

Genetic approach

Overview

The ability to extract and amplify DNA specific for the X- and Y-chromosomes means it is possible to directly identify an archaeological animal's genetic sex. Ancient DNA (aDNA) does not need to be recovered from a specific element but can be extracted from any bone. aDNA has previously been used to confirm osteometric sexing of archaeological cattle metapodia (Svensson et al., 2008) and mortality profiles compiled based upon the limited ageing data available from these bones (Telldahl et al., 2011), the method was also successfully used in three other recent publications (Davis et al., 2012; McGrory et al., 2012; Telldahl et al., 2012). In the 119 bones analysed in these studies where both morphological and genetic information about sex have been available the correlation between genetics and morphology has been complete (Svensson et al., 2008; Davis et al., 2012; Telldahl et al., 2012). Based upon this background an in-depth analysis of the Bern material therefore seemed promising.

Material and Methods

All 108 complete cattle metapodials, 65 metacarpals (MC) and 43 metatarsals (MT) from the late 13th century used in said osteometric analysis (Rehazek and Nussbaumer, 2012) were sent to the ancient DNA lab in Uppsala. From each bone, approximately 100 mg of bone powder were sampled for DNA extraction in a dedicated aDNA facility at the Evolutionary Biology Centre. Extraction was carried out based on a method developed by Yang et al. (1998), with the addition of urea to the extraction buffer and an amicon-filtration step (Malmström et al., 2007). This extraction protocol has been shown to be effective on archaeological material (Yang et al., 1998; Malmström et al., 1998; Svensson et al., 2007). For each bone included in the analysis, DNA was extracted on at least two separate occasions and at least one negative extraction control was included for every four extractions. All pre- and post-PCR work was done in physically separated areas. To assess the molecular preservation of the samples all extracts were screened using a 70 bp mitochondrial DNA fragment that contain a variable position that separates human and cattle and can thus be used to assess the level of authentic to human contaminating DNA in the extracts (Malmström et al., 2007). A pair of primers targeting a cattle-specific 63 bp sequence of the ZFX and ZFY genes was used to amplify DNA from the sample extracts. The region targeted by these primers includes

20 Originalarbeiten/Original contributions

the C243T SNP that can be used to discriminate between the X- and Y-chromosomes (Svensson et al., 2008). Successful amplification was confirmed by electrophoresis on 2% agarose gel. Genotyping was done using pyrosequencing as in Svensson et al. (2008). A subset of the samples was also sequenced for a SNP in the Y-chromosomal intron *UTY19* that separate modern taurine cattle in two major haplogroups Y1 and Y2 (Götherström et al., 2005). Y1 is common in northern European breeds, and Y2 is more common in Southern Europe (Götherström et al., 2005; Edwards et al., 2011). The same protocol as described in Svensson et al. (2008) was used. The melanocortin receptor 1 (*MC1R*) influences coat colour; the U39469.2:c.296T>C SNP results in dominant black coat colour (Klungland et al., 1995) and the c.296T is the wild-type allele, the same protocol described in Svensson et al. (2007) was used.

Results

Success rate: Out of the 108 bones, 90 produced definitive reliable and reproducible genetic results for sex, another 13 samples produced inconclusive results due to poor quality of the DNA, and 5 of the samples yielded no nuclear DNA (Tab. 1). This is a high success rate for retrieval of nuclear aDNA, and higher or comparable to datasets of similar age (Svensson et al., 2007; Telldahl et al., 2011). The good preservation bodes well for further genetic studies of material from the same site.

Allelic dropout: Allelic dropout, that is the typing of a heterozygous individual as homozygous due to the amplification of only one allele, is a common problem in genetic analysis of degraded material. It can be overcome by repeating the PCRs and genotyping multiple times. Here we found that the risk of not detecting a male is $p = 0.0282$ with four typings.

Damages and contamination: DNA molecules from ancient specimens often suffer from damages. There are many types of damages and several processes that can cause them. Chemical degradation can lead to altered bases, and may thus result in an erroneous genotype. However, repeated PCRs and genotypings may overcome the problem. In this dataset, 5 female samples show signs of nucleotide damage. These samples have all been extensively typed as females, 5–20 times, with just one typing as CT, or CC. Another 8 samples also show signs of either damages or low-level background contamination, it was not possible to determine the sex for these samples with confidence; they were therefore excluded from the analysis. Leonard et al. (2007) found a 5% level of contamination due to contaminated reagents; the sporadic putative contamination found here is within that range. With the high number of typings for samples in this dataset, we can be sure to detect both background contamination and damaged bases, the genotypes included in the analysis are thus determined with high confidence. It was not possible to genotype any of the negative controls, so the

level of possible background contamination must have been low.

Sex identification: Morphologically the metatarsals were separated into four clusters. Genetic sexing shows that cluster 4 are male. The bones that have produced results in cluster 3 are male, with one exception; sample MT-114 is female. Both clusters 1 and 2 are female, except for one sample in each cluster. The metacarpals morphologically cluster in three groups. Males are found in both clusters 2 and 3 and females in both cluster 1 and 2.

Y-haplogroups: 13 males were found to belong to haplogroup Y2 and one to Y1. The Y1 male is found in cluster three of metatarsals (MT-102). The low frequency of Y1 is similar to that found in mediaeval Northern European cattle (Svensson and Götherström, 2008).

Coat colour: The majority of samples successfully genotyped (24/28) for the *MC1R* SNP have the wild homozygous TT genotype (red-brown or light coat colour); while 4 are heterozygous (CT, dominant black). Another 31 samples yielded partial genetic results (too few typings for a conclusive genotype); here too, the TT genotype is most common (27) along with 3 CT and 1 homozygous CC sample.

Historical approach and discussion

Unfortunately, no contemporary sources on the cattle and meat economies of the 13th century in Bern are available in writing. However, the sources from subsequent centuries and the results of historical research do allow some conclusions to be drawn. A description of this area of the Swiss confederation originating from the 16th century reveals that the Bernese Oberland was extraordinarily rich in cattle (Stumpf, 1548; Fig. 5). This may also be assumed to have applied to the 13th century, due to the existence of several official documents on the land tenures including pastures from this area (Rechtsquellen, 1912). Bern had around 2500 inhabitants in the middle of the 13th century. As a custom typical of mediaeval towns, Bern exerted its right to hold weekly markets for livestock and foods of all kinds. Many of the city inhabitants reared their own pigs, sheep, goats and poultry. A few may have even held cattle in order to feed themselves. Yet this did not suffice to fully cover the market demand for meat. For that reason, the butcher's guild was commissioned by the town to provide the population with meat of good quality in sufficient quantities, with fair prices, and produced under hygienic conditions (Häsler, 2010). Assuming that the annual meat consumption (cattle, sheep, goat, pig, poultry) per inhabitant was 50 kg, 20 kg of which stemmed from cattle acquired from outside the town, and assuming an average slaughter weight of 100 kg, Bern will have most likely required 500 beef cattle per year. The meat was sold at market stalls (Latin: *scala*, German: *Schaal*) at the city's conduit in what is today called the Kramgasse and the Gerechtigkeitsgasse. In both these streets, the cattle market was held too. Where the animals were slaugh-



Figure 5: Cattle on the alps in the Simmental, 19th century, oil painting, unknown artist. (in private ownership).

tered in the 13th century is not known. Presumably, in the same streets where the trade took place. As far as the later centuries are concerned it is known that the lesser part of the beef cattle came from the close surroundings and the greater part came from the area of today's Bernese Oberland, which may have also been the case in the 13th century (Gerber, 1999; Schläppi, 2006; Fig. 6). Already in the first half of the 13th century, the City of Bern had formed alliances with the castle owners in the close surroundings and in 1224, it took over the patronage over the Abbey of Interlaken, which owned big estates in the Bernese Oberland (Zahnd, 2003). These political treaties had the objective of creating an economic basis, particularly aiming at gaining an advantage over the other towns of the Swiss Midlands (e.g. Burgdorf, Solothurn) with regard to the buying up of cattle. By the end of the 14th century, Bern completely prohibited the selling of cattle to foreign traders. This not only had to do with the supply of meat, but also with the raw material leather (Rechtsquellen, 1971).

The interpretation of the morphological finds of the metapodials enables a good overview of the shape of the animals destined to be slaughtered. With a withers height of 100 to 120 cm they were, compared to today, fairly small animals (original Simmentaler Fleckvieh: 130 to 153 cm; Herdbook, 2013). As most of the metapodials investigated had no cut marks we can conclude that dur-



Figure 6: Butcher buys livestock. Draft for glass panel, 16th century. Ascribed to Hans Funk. (Bernisches Historisches Museum, Inv. 3591).

22 Originalarbeiten/Original contributions

Table 1: Results from the genetic analysis of metapodials. Numbers refer to number of times a genotype was obtained in the pyrosequencing. Genotype in capital letters is statistically certain, while genotype in lower case letters is likely but not certain, due to too few repeated typings.

Cluster	Sample Name	ZFX Y number of typings			DNA SEX	MC1R	UTY19
		CC	CT	TT	ZFX Y result		
1	MT-92		1	4	?		
1	MT-101	3	2	3	male	TT	
1	MT-127						
1	MT-115			4	female	tt	
1	MT-112			6	female	TT	
1	MT-88			8	female		
1	MT-81			6	female	CT	
1	MT-77			5	female	TT	
1	MT-107			4	female	ct	
1	MT-113	1		2	?		
1	MT-79			6	female	TT	
2	MT-125			6	female	tt	
2	MT-87			4	female		
2	MT-109			9	female	TT	
2	MT-116			8	female	tt	
2	MT-110			9	female	TT	
2	MT-96			4	female	cc	
2	MT-99			6	female	TT	
2	MT-111			6	female	CT	
2	MT-117			5	female	tt	
2	MT-118			5	female		
2	MT-78			1	no		
2	MT-80			4	female	TT	
2	MT-89			5	female	tt	
2	MT-90			6	female	TT	
2	MT-93			6	female		
2	MT-95			6	female	TT	
2	MT-98			4	female		
2	MT-100			4	female	tt	
2	MT-119			6	female	CT	
2	MT-108	2		2	male		
3	MT-97	1		4	?	tt	
3	MT-102	2	2	6	male	TT	Y1
3	MT-106		2	2	male	tt	
3	MT-126		10	2	male	TT	Y2
3	MT-83	2	1	3	male		
3	MT-124	2		5	male		
3	MT-85	3		1	male	tt	Y2
3	MT-104	1	2	5	male	tt	Y2
3	MT-114			7	female		
4	MT-86		5		male	CT	Y2
4	MT-120	2		2	male	TT	
4	MT-123		2	1	male		
1	MC-51			6	female	tt	
1	MC-2			3	?	tt	
1	MC-15			4	female	tt	
1	MC-66			4	female	TT	
1	MC-44			5	female		

Table 1: Results from the genetic analysis of metapodials. Numbers refer to number of times a genotype was obtained in the pyrosequencing. Genotype in capital letters is statistically certain, while genotype in lower case letters is likely but not certain, due to too few repeated typings. (Continuation)

Cluster	Sample Name	ZFX Y number of typings			DNA SEX	MC1R	UTY19
		CC	CT	TT	ZFX Y result		
1	MC-37			4	female	tt	
1	MC-60			4	female		
1	MC-53			4	female		
1	MC-68			8	female		
1	MC-40			4	female	tt	
1	MC-122			5	female		
1	MC-21			4	female		
1	MC-14	2	5	10	male		
1	MC-18			5	female		
1	MC-24			4	female		
1	MC-3			9	female		
1	MC-50			4	female		
1	MC-5		1	10	damaged female		
1	MC-11						
1	MC-57						
1	MC-43			1	no		
1	MC-46			4	female		
1	MC-45	1		20	damaged female		
1	MC-49			15	female		
1	MC-27						
1	MC-26			4	female		
1	MC-75			4	female		
1	MC-54			6	female		
1	MC-20			4	female		
1	MC-36			9	female		
2	MC-6	1		2	?	tt	
2	MC-52			5	female		
2	MC-39	1	3		male	TT	
2	MC-63	2	1	4	male		
2	MC-47			1	?		
2	MC-65	1	1	2	male		Y2
2	MC-38				?		
2	MC-28	1	6	13	male	tt	
2	MC-67	6			male		
2	MC-74	4		2	male	tt	
2	MC-23	2	2	9	?	TT	
2	MC-61		1	13	damaged female	tt	
2	MC-25	2		4	?	tt	
2	MC-42			4	female		
2	MC-34			4	female	tt	
2	MC-13	4	3	8	male	TT	
2	MC-7	3	5	5	male	TT	
2	MC-16	1		6	damaged female	tt	
2	MC-56	3	1	2	male	tt	
2	MC-48	1		4	?		
2	MC-64	5	2	6	male	ct	
2	MC-33	2	1	5	?		
3	MC-73	4		2	male	tt	

24 Originalarbeiten/Original contributions

Table 1: Results from the genetic analysis of metapodials. Numbers refer to number of times a genotype was obtained in the pyrosequencing. Genotype in capital letters is statistically certain, while genotype in lower case letters is likely but not certain, due to too few repeated typings. (Continuation)

Cluster	Sample Name	ZFX Y number of typings			DNA SEX	MC1R	UTY19
		CC	CT	TT	ZFX Y result		
3	MC-55	5	2	4	male	TT	Y2
3	MC-35	6	2	11	male	TT	Y2
3	MC-41	2	5	11	male	ct	Y2
3	MC-62	1	4	6	male	TT	Y2
3	MC-1	2	2	7	male	tt	
3	MC-8	1		3	male	tt	
3	MC-10	1	1	1	male		
3	MC-32	1	1	2	male		Y2
3	MC-59		5	1	male	TT	Y2

ing the slaughter process the limbs were severed at the carpus or the tarsus, as is done today, and that the distal part thus had no nutritional purpose. In what way does this historical background help us with the interpretation of the putative morphologically distinguishable clusters mentioned in the introduction? Whereas practically all the bone samples could be sexed, the genetic analysis yielded two male morphological groups and – as far as the metatarsi are concerned – two female groups. The first can most likely be attributed to bulls (Fig. 1 and 3, cluster 3) and oxen (Fig. 3, cluster 4). The latter are anecdotally mentioned in an anthem to the treaty of 1243 between Bern and Freiburg (Switzerland). The two cities are compared to two oxen, which graze on the same pasture and remain invincible, as long as they stay together (Zahnd, 2003).

However, the reasons that have led to the formation of the two morphological groups in cows (Fig. 3, cluster 1 and 2) are less obvious. Since one can only speak of racial breeding in the modern sense from the beginning of the 19th century, we consider the following tentative explanation as the most plausible: the variety of the growth forms of the two female cattle groups are most likely explained by the different husbandry conditions, where the range of feed and its quantity and quality (alpine pastures, grass, foliage, hay ...) were the crucial factors. In a geographically tightly confined area such as, for example, the close surroundings of Bern, there could not have been great differences in feeding. Taking into account the historical background of the supply area reaching from the town of Bern to the Bernese Oberland, we presume that the two cattle types may be of different geographical origin. We hypothesise that the slightly bigger and more robust cows stem from the Oberland, which has been a centre of cattle breeding and dairy farming since the High Middle Ages. The smaller and more delicate type on the other hand may have lived on the outskirts of Bern where less luscious pasture may have been available due to intensive grain cultivation. No satisfactory explanation can be found for the few outliers in which the genetic and os-

teometric sexing do not agree. Possibly the two robust female metacarpi 34 and 52 in the male cluster 2, which are classified osteometrically as male, could originate from cows which had a stronger bone structure due to their use as draft animals.

The genetic analysis of the *MC1R* allele determining the coat colour of the cattle revealed that practically all the cattle were of red-brown colour (TT, see Tab. 1) and only a couple of heterozygotes and one – equivocal – homozygous black animal. Based on the random distribution of these genetic types found among our samples no conclusion can be drawn as to any kind of grouping, neither with regard to gender nor with regard to cluster affiliation.

Only in the second half of the 19th century did the coat colour acquire the significance of a selection criterion in the area, which is the canton of Bern today. Around 1825 a well-known cattle breeder writes that the colour of a calf can be forced. Thus, wrote the breeder, cows mated in daylight would give birth to white calves, and cows mated in the dark would give birth to dark calves. Nevertheless, he continued, "... the colour belongs to the secrets of nature, since it occurs that in a twin birth one calf is red and the other black" (Zahler, 1825). Then in 1856 it is stated that in the (by definition) black-and-white Freiburger breed every now and again red-marked animals appear and with the red-marked Bernese breed black-marked individuals occur (Zangger, 1861). The first illustrations in colour from mediaeval times show cattle mostly in a single light brown colour (Fig. 7). The present analysis of coat colour thus shows very clearly the agreement between genetic results and contemporary illustration sources.

Since in mediaeval times the alpine passes were important trade routes and, thanks to the then higher snowline, suitable for transits on foot. These migration movements are historically recorded. The "Walser"-people, for example, walked from the Bernese Oberland to the Valais and from there in a southerly and easterly direction and also back north (Zinsli, 1968). In history and fables, one tells of conflicts over the possession of alpine pastures lying

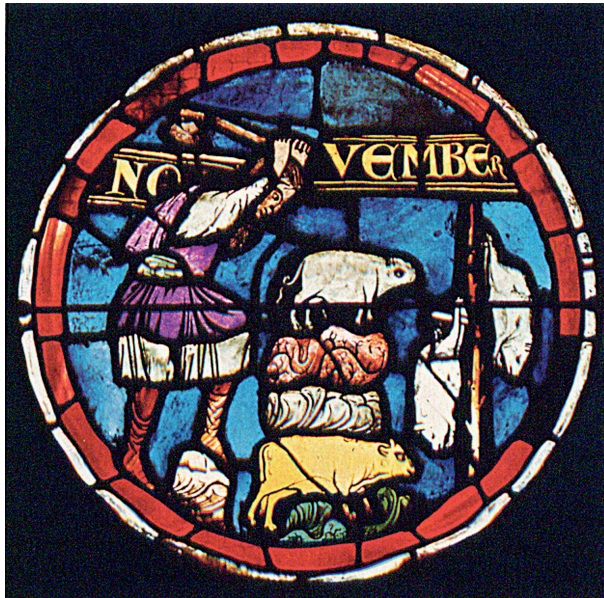


Figure 7: The slaughter of cattle, sheep and pig. Glass panel, 13th century, Lausanne Cathedral. (Nationalbibliothek, KLb 105).

on the border between the Valais and the Bernese Oberland, thus hinting at a genetic connection between cattle on either side of the Alps. Finally we may note that modern Swiss cattle breeds, such as Braunvieh, Evolène and Simmental, show similar genetic patterns to the investigated mediaeval Bernese bones in respect of the *MC1R* allele (Svensson, unpublished) as well as the Y (Edwards et al., 2011). Our research seems to confirm a certain continuity from the Middle Ages to modern times. However, until further genetic analysis has been carried out this must remain speculation.

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