

Ancient DNA and Paleoprotein Investigation of Dairying and the Evolution of Swiss Diet

Project: 440

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Ruminant milk and dairy products are historically important food resources in many European, African, and Middle Eastern societies. These areas are also known to be associated with derived genetic variants for lactase persistence (LP). In mammals, lactase, the enzyme that hydrolyzes the milk sugar lactose, is normally down-regulated after weaning, but at least five human populations around the world have independently evolved mutations regulating the expression of the lactase (LCT) gene. These mutations result in a dominant LP phenotype and continued dietary tolerance of lactose in adulthood. A single nucleotide polymorphism (SNP) at C/T-13910 is responsible for LP in European populations, but when and where the T-13910 polymorphism originated and the evolutionary processes by which it rose to high frequency in Europe has been the subject of strong debate. A history of dairying is presumed to be a prerequisite, but archaeological evidence is lacking.

The purpose of this project was to 1) investigate allele frequencies of the European lactase persistence (LP) allele C/T-13910 in historic European populations using ancient DNA technologies, 2) investigate fossilized dental calculus as a reservoir of information about ancient diet and health, 3) apply novel mass spectrometry methods to the direct investigation of past milk consumption in fossilized dental calculus, and 4) to support student training and research. The results of this investigation were an overwhelming success.

We have determined the allele frequency of LP in Central Europe during the Medieval period (c. AD 1100) and find it to be no different than today, narrowing the period during which selection of this allele took place and confirming that the catastrophic population declines associated with the Black Death are not responsible for the high LP allele frequencies observed today. We have demonstrated that dental calculus is a long-term reservoir of both health and dietary information in archaeological populations. Using DNA and protein based approaches, as well as histochemical techniques, we have characterized the Central European Medieval oral microbiome and found it to contain a range of cariogenic and periodontal pathogens, including *Streptococcus mutans*, *Porphyromonas gingivalis*, *Treponema denticola*, and *Tannerella forsythia*. We have positively identified DNA from bread wheat (*Triticum aestivum*), cruciferous vegetables (*Brassica* sp.), pork (*Sus* sp.), and mutton (*Ovis* sp.) in dental calculus; this is the first successful demonstration of biomolecular identification of diet directly from an ancient skeleton. We have also positively identified proteins specific to ruminant beta-lactoglobulin milk proteins in the dental calculus of living Swiss volunteers and Norse Vikings in Medieval Greenland. This is the first successful identification of milk consumption directly from an ancient skeleton. Finally, the SFEFS funding supported the training and research of one Archaeology undergraduate student at the University of Zürich and two Master's students at the University of York.