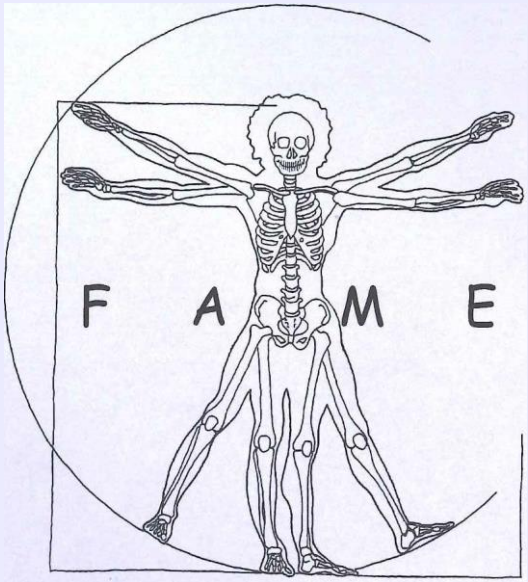
Fysisch-Anthropologische Mededelingen



Newsletter of the Dutch Association of Physical Anthropologists

No. 22, February 2014

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February 2014

From the editor

Last year we celebrated the 30th anniversary of the NVFA. We did this in style of course and organised a very interesting and successful symposium on various aspects of DNA research. Three foreign and three Dutch speakers entertained an audience of well over 100 people. We are opening this new issue of Fame with the abstracts of the talks in case you were not able to come or would like to read them again.

Although the deadline for submission of contributions for this issue of Fame went out repeatedly, only a handful of authors responded. Hence a slightly thinner issue than usual.

The colourful publication concludes with a short calendar of forthcoming events and an up-to-date address list of our members.

Mark Thomas

Research Dept. of Genetics, Evolution and Environment
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The Co-Evolution of Lactase Persistence and Dairying

Most Europeans take drinking milk for granted; it's the everyday consumption of an everyday drink. But for most adult humans, indeed, for most adult mammals, milk is very far from an everyday drink. Milk is something that we have specifically evolved to be able to consume in the relatively recent past. The ability to digest the sugar in milk is called Lactase Persistence and Darwin's engine of evolutionary change, natural selection, has probably worked harder on this trait than on any other biological characteristic of Europeans in the last **10,000** years. In this presentation we will see how Genetics, Archaeology, Anthropology, Physiology, ancient DNA and computer simulations can be combined to understand where, when and how Lactase persistence co-evolved with the culture of dairying in Europeans.

Eveline Altena

Forensic Laboratory for DNA Research, LUMC

The Dutch genetic landscape from past to present

For several decades population genetic research on modern human populations has been used to infer large scale (pre)historic human

demographic events all over the world. Mainly due to recent technical advances in the field of DNA sequencing it is now also possible to analyse large sample collections of ancient individuals. By incorporating data from archaeological populations in population genetics we will be able to test many more hypotheses and get a detailed insight in past demographic events.
Since 2006 archaeological DNA research is carried out on several large and small scale human skeletal collections across the Netherlands. The majority of these samples date from the medieval and post-medieval periods. They enable us to reconstruct (part of) the genetic history of the Netherlands.
This presentation mainly focuses on the results of the male specific Y-chromosome. By comparing Y-chromosomal information of Dutch archaeological sites and an extensive survey study on modern Dutch males, we are now able for the first time to get a glimpse of not only the regional, but also the temporal genetic variation of the Y-chromosome in the Netherlands. This will be a useful tool in understanding the extent and complexity of historical demographic processes that took place and shaped the present Dutch genetic landscape.

Peter de Knijff

Forensic Laboratory for DNA research, LUMC

STR genotyping 3.0: a new human identification method

Forensic DNA research is, strictly speaking, a relatively simple kind of genetic research made complex because results are used to, sometimes, convict suspects of serious crimes (meaning that simple science has to be explained to notoriously difficult students such as judges and lawyers or members of a jury, one of the most difficult teaching tasks

one can imagine). The basic scientific principle is easy enough. You make DNA profiles from biological samples found at crime scenes and compare these with similar profiles from suspects and victims of crime. If, subsequently, a profile from a crime scene sample matches with a suspect, it seems likely (note: not proven!) that this suspect is the donor of that sample and can at least be linked to the crime. Ideally, DNA profiles should be easy to detect in very small DNA quantities. They should be so unique that each profile is only found in a single human individual and the method to detect these profiles should be fast and robust.

It was therefore extremely fortunate that, in 1991, Al Edwards and Tom Caskey from Baylor College of Medicine, Houston, Texas, USA, were the first to describe the use of short tandem repeats (STRs, also called microsatellites), for a number of different genetic diagnostic purposes (1). STRs represent small pieces of DNA that can be found in different lengths in different human individuals, and since we, humans, have always been very good in measuring lengths, with or without the help of complex technology, these STRs caused the most important revolution in forensic DNA research of the past 50 years. To illustrate its importance, there are now worldwide at least 50,000,000 STR-DNA profiles in criminal DNA databases.

Since 1991, in just four years, the initial genotyping method (using different gel-type separation techniques and various band staining protocols) was replaced by the multiplex, fluorescent based capillary separation method using the ABI 310 in 1995. STR genotyping 2.0, in vogue for close to 20 years, did not improve substantially, and it is about time to move on. With the introduction of a new generation of DNA sequence technologies, starting with the Roche-454 massive parallel sequence platform in 2005 (2), it seems that we are very close to the introduction of STR genotyping 3.0, that will revolutionize routine STR genotyping. Exactly how will be explained and shown in detail in this presentation.

(1) Edwards A, Civitello A, Hammond HA and Caskey CT (1991) DNA typing and genetic mapping with trimeric and tetrameric tandem repeats. Am J Hum Genet 49: 746-756.
(2) Margulies M, et al. (2005) Genome sequencing in microfabricated high-density picolitre reactors. Nature 437: 326-327.

Toineke Westen

Netherlands Forensic Institute

Who is in my sample? Identifying multiple contributors and phenotypic traits with SNPs

Apart from medicine, human DNA typing is performed in forensic cases to determine the cell donor of a stain, in kinship analysis and in human identification cases. DNA typing is usually based on the analysis of short tandem repeats (STRs). STRs are characterised by differences in length, due to a difference in the number of repeated DNA elements. STRs are the "golden standard" in forensic DNA typing, and national DNA databases are based on STR data. However, other types of markers, such as single nucleotide polymorphisms (SNPs), are also available for forensic use. SNPs are characterised by a change in the DNA sequence of only one nucleotide (i.e. DNA building block) in length. Even though SNP information is not available in the national DNA database, SNPs possess several characteristics that make them interesting for one-to-one comparisons between a reference sample and a stain. As these markers are very small, they are suited for the analysis of (highly) degraded DNA. Additionally, SNPs may be used to predict someone's bio-geographical ancestry or externally visible characteristics. The potential of the use of SNPs to obtain information on the donor of a sample will be explained in this presentation.

Kirsten Bos

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Science, Eberhard-Karls-Universiteit Tubingen

Ancient Pathogen Genomics: What we can learn from historic **Pathogens**

Genome-wide data from ancient microbes may help to uncover mechanisms of pathogen evolution and adaptation for many diseases. Using high throughput DNA sequencing in combination with targeted DNA enrichment we have reconstructed medieval bacterial genomes of *Yersinia pestis* and *Mycobacterium leprae* from skeletal remains. Phylogenetic analyses indicate that the ancient *Y.pestis* strain from the Black Death pandemic is ancestral to most extant strains, and falls very close to the ancestral node of many Y. *pestis* bacteria. Temporal estimates suggest that the Black Death of 1346 — 1351 was the main historical event responsible for the worldwide dissemination of most currently circulating Y. *pestis* strains. In contrast, the medieval *M. leprae* strains fall within current genetic diversity and are found on at least two main branches in the phylogenetic tree of leprosy bacteria. Dating analyses reveal a most recent common ancestor of both *Y.pestis* and *M.leprae* within the last 4000 years, suggesting that both diseases may have a Neolithic origin. The extraordinary preservation of the *M.leprae* DNA allowed for the first *de novo* genome assembly of an ancient organism and indicates that some bacterial DNA may survive longer than vertebrate DNA in ancient remains This may permit tracing the history of many infectious organisms back to their prehistoric origins.

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Christos Economou

Dept. of Archaeology and Classical Studies, Stockholm University

Health in ancient Scandinavia: infections and genetic diseases

Infectious diseases have always played a major role in shaping the history of the societies of the past and Palaeopathology is the scientific field that approaches their occurrence and effects on human populations through the use of archaeological remains. Ancient-DNA has proven to be of invaluable assistance to such studies as it can provide answers not only for the mere presence of the pathogens in the remains but it can shed light on their geographical distribution, evolution and host's immunity as well. Leprosy and Plague had been two of the most talked-about diseases in Middles-Ages Europe, either due to the social stigma that they carried or the high mortality rate. The main purpose of our current studies is to molecularly analyse human remains from Medieval Sweden that had been infected by those two diseases (using osteological or historical evidence) and make a map of the health conditions in Scandinavia of that period. Apart from the molecular identification of the pathogens in the remains, the infected individuals were also tested for the presence or absence of alleles that are thought to provide immunity to those particular diseases. A connection between the bacteria and the host's immune system during that particular period of time is therefore tackled and comparisons with published modern data can be made.

Abstracts of articles

MOISTURE INHIBITS THE DECOMPOSITION PROCESS OF TISSUE BURIED IN SEA SAND: A FORENSIC CASE RELATED STUDY

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In: Journal of Forensic Research 3: 176 (2012)
doi:10.4172/2157-7145.1000176

Many aspects influence the decomposition process of a body and, as such, are important in forensic science for estimation of the post mortem interval. In a recent forensic case, a missing man was found buried in sea sand. The post mortem interval estimation as obtained at autopsy was quite different to the actual period this man was missing. In the present study, we have set up an artificial decomposition model to study the effect of sea soil and moisture, relevant to this particular case, on the decomposition mode.
Pig *(Sus domesticus)* legs were buried in 50 litres of sea sand and control sand (woodland sand) respectively, within containers for 1, 2

and 3 months. The sand was evaluated using routine pedological analysis. The legs were analysed using AZAN staining and microscopically scored for their decomposition grade. In the second part of the study, the effect of moisture hereon was analysed.
Pedological analysis did not show significant differences in composition between the sea- and woodland sand. Although an increase in decomposition grade was found in both soils over time, no differences in decomposition grade was found. In the second part of the study, however, we found a significant decrease in decomposition score in legs buried in wet, soaked sea sand compared to those buried in dry sea sand. Soaked means a small layer of water was seen on the container's surface.
We have successfully developed an *in vitro* decomposition model in order to address taphonomic questions related to a forensic case and have found that moisture inhibited the process of decomposition in sea sand.

BLOOD AMMONIA, A POSSIBLE PREDICTIVE ANALYTE FOR ESTIMATING THE EARLY POSTMORTEM INTERVAL

Krap, Tristan', Tom van Sundert[2], Sjaak Reumkes[3], and Wilma Duijst[1-4]

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Poster abstract KAMG congress 28-11-2013

Keywords: Decomposition, forensic, biochemistry, postmortem interval.

The early postmortem interval in medico-legal investigations is currently being estimated by the use of HenBge's nomogram, a mathematical temperature model with a minimal time frame of 5.6 hours. The cry for a more reliable and specific method comes not only from the coroner's office, but other parties involved also demand at least a second reliable method for admitting a conclusion into the courthouse. Based on a previously published article in 1956, postmortem blood ammonia levels might be strongly correlated to the time since death, but some irregularities could not be explained at that time. Now much more is unraveled about the physiological processes involving ammonia. Furthermore, measuring ammonia in the blood has become easier, more specific and more sensitive. These reasons led to a reinvestigation of the relation between blood ammonia and the time since death for use in medico-legal death investigations. The in-vitro rise of blood ammonia and the dependence on both temperature and time were investigated. Blood was drawn of sixty volunteers, of whom the sex ratio was equally divided over three age categories (18-34, 35-60, and 50+). The EDTA treated blood was divided over three temperature lines, scilicet 4°C - 24°C and 37°C, and the serum was analysed after 6h/12h/18h/24h and 30h by using a precise enzymatic method. There was a marked positive correlation between time and the ammonia level at the different temperatures, with a mean correlation coefficient of 0.997 at 4°C, 0.973 at 24°C and 0.986 at 37°C. The results confirm the predictive value of blood ammonia for use in estimating the postmortem interval.

HISTOLOGICAL CHANGES IN HUMAN CORTICAL BONE DUE TO HEAT (AND A FORENSIC CASE STUDY OF SUSTAINED HUMAN COMBUSTION)

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Abstract: Oral presentation at the Forensic Anthropology Society Europe Conference (26-28/9/2013 — Heidelberg, Germany)

Keywords: Bone histology, burned human remains, case study, forensic, sustained human combustion.

In a previous study the first author showed that both temperature and time are important variables for histological changes of the organic component in human cortical bone. Defleshed radii and ulnae from dissection room cadavers where exposed to temperatures up to 400 degrees Celsius, for varying lengths (10, 20 and 30 minutes). These results proved to be useful in a forensic case study in which a body was discovered in a small local house fire with disintegrated radii, ulnae and partially the humeri. The main questions in the forensic case were: what was the duration and extent of the fire, considering such local destruction? To answer these questions multiple reconstructions were carried out. As a part of these reconstructions bone fragments were heated in animal fat *(Sus scrofa domesticus).* Surprisingly the histological findings differed from the previous study, suggesting that the thermal conductivity of the medium is an important variable as well. These results lead to new research questions regarding the changes the (organic component of) bone undergoes when exposed to heat in different media.

CLINAL DISTRIBUTION OF HUMAN GENOMIC DIVERSITY ACROSS THE NETHERLANDS DESPITE ARCHAEOLOGICAL EVIDENCE FOR GENETIC DISCONTINUITIES IN DUTCH POPULATION HISTORY

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Investigative Genetics 2013, 4:9. doi:10.1186/2041-2223-4-9

Background: The presence of a southeast to northwest gradient across Europe in human genetic diversity is a well-established observation and has recently been confirmed by genome-wide single nucleotide polymorphism (SNP) data. This pattern is traditionally explained by major prehistoric human migration events in Palaeolithic and Neolithic times. Here, we investigate whether (similar) spatial patterns in human genomic diversity also occur on a micro-geographic scale within Europe, such as in the Netherlands, and if so, whether these patterns could also be explained by more recent demographic events, such as those that occurred in Dutch population history.
Methods: We newly collected data on a total of 999 Dutch individuals sampled at 54 sites across the country at 443,816 autosomal SNPs using the Genome-Wide Human SNP Array 5.0 (Affymetrix). We

studied the individual genetic relationships by means of classical multidimensional scaling (MDS) using different genetic distance matrices, spatial ancestry analysis (SPA), and ADMIXTURE software. We further performed dedicated analyses to search for spatial patterns in the genomic variation and conducted simulations (SPLATCHE2) to provide a historical interpretation of the observed spatial patterns. Results: We detected a subtle but clearly noticeable genomic population substructure in the Dutch population, allowing differentiation of a north-eastern, central-western, central-northern and a southern group. Furthermore, we observed a statistically significant southeast to northwest dine in the distribution of genomic diversity across the Netherlands, similar to earlier findings from across Europe. Simulation analyses indicate that this genomic gradient could similarly be caused by ancient as well as by the more recent events in Dutch history.
Conclusions: Considering the strong archaeological evidence for genetic discontinuity in the Netherlands, we interpret the observed clinal pattern of genomic diversity as being caused by recent rather than ancient events in Dutch population history. We therefore suggest that future human population genetic studies pay more attention to recent demographic history in interpreting genetic clines. Furthermore, our study demonstrates that genetic population substructure is detectable on a small geographic scale in Europe despite recent demographic events, a finding we consider potentially relevant for future epidemiological and forensic studies.

Keywords: Population substructure, Genetic cline, Genome-wide diversity, SNP, Europe, Netherlands

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U-SERIES AND RADIOCARBON ANALYSES OF HUMAN AND FAUNAL REMAINS FROM WAJAK, INDONESIA

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In: Journal of Human Evolution 64, 356-365 (2013)

Laser ablation U-series dating results on human and faunal bone fragments from Waj ak, Indonesia, indicate a minimum age of between 37.4 and 28.5 ka (thousands of years ago) for the whole assemblage. These are significantly older than previously published radiocarbon estimates on bone carbonate, which suggested a Holocene age for a human bone fragment and a late Pleistocene age for a faunal bone. The analysis of the organic components in the faunal material show severe degradation and a positive $8^{13}C$ ratio indicate a high degree of secondary carbonisation. This may explain why the thermal release method used for the original age assessments yielded such young ages.

While the older U-series ages are not in contradiction with the morphology of the Wajak human fossils or Javanese biostratigraphy, they will require a reassessment of the evolutionary relationships of modern human remains in Southeast Asia and Oceania. It can be expected that systematic direct dating of human fossils from this area will lead to further revisions of our understanding of modern human evolution.

Forthcoming events

March 14, 2014
36th Kroon-voordracht
Prof. dr André F.L. van Dijk, Prof. dr Jerzy G. Gawronski,
Prof. dr Jon Adams, and Drs Henk Dessens
on Maritime Archaeology
KNAW, Kloveniersburgwal 29, Amsterdam
www.snmap.nl

July 12, 2014
Barge Forum
Speaker, title and exact venue to be announced
LUMC, Leiden

August 25-29, 2014
European Anthropological Association
19th Congress of EAA
Moscow, Russia
http://19eaa-moscow.ru/

August 26-29, 2014
Paleopathology Association
European Meeting
Lund, Sweden

September 12-14, 2014
British Association for Biological Anthropology and
Osteoarchaeology
Annual Conference
Department of Archaeology
Durham, U.K.