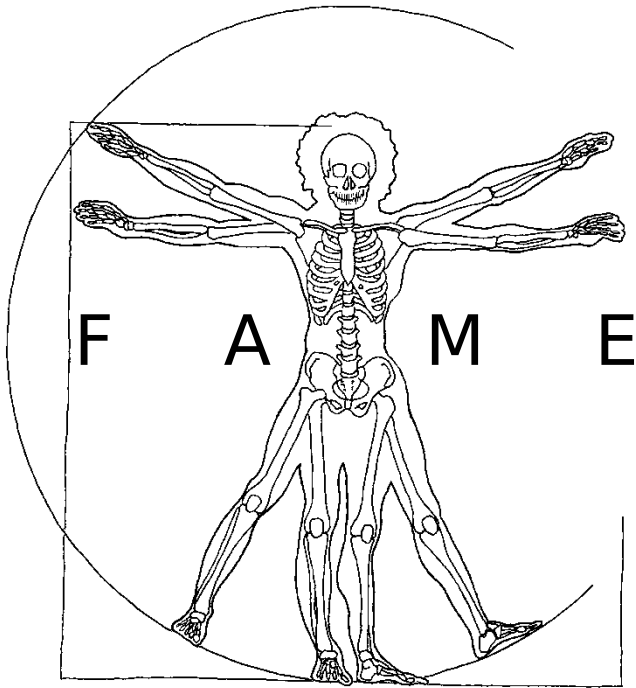


Fysisch-Anthropologische Mededelingen



Newsletter of the Dutch Association of Physical
Anthropologists

No. 28, February 2020

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Contents

From the editor	1
In memoriam	2
Najaarssymposium abstracts	3
Article	7
Abstracts of articles	10

From the editor

This issue of our newsletter starts on a sad note with an obituary of Kelly Fennema, who has been a member for over 20 years. Her enthusiasm to join in whenever she could and put in her word will be sorely missed.

This 28th issue is even bigger than the previous FAME. The number of members that contributed, however, stayed the same, or even decreased a little compared to the last issues. In contrast, the number of papers per member, and, more importantly, the number of authors that contributed to the papers increased significantly. To save you from scrolling through several pages of author affiliations, I drew a line at 10. The author affiliation sections of articles involving authors of more than 10 affiliations have been shortened. Scientifically unethical perhaps, but necessary for the FAME to remain its purpose: to give all members an overview of the research we have been involved in in 2019.

Thank you members for your useful and interesting contributions this year.

Lisette

In memoriam

Kelly Fennema-Brunner

Last year we lost one of our most remarkable members as on 23 May 2019 Kelly Fennema-Brunner sadly passed away. Her health had been problematic for several years already, which is why she had not been able to attend our meetings for some time. Her death nevertheless came unexpected.

Kelly was a member since 1996 and has ever since been active for our association almost non-stop. For nearly 20 years she edited the FAME, but she has also been treasurer, 1st and 2nd secretary and on the lustrum committee. A remarkable state of merit!

But her personality was equally remarkable. In reaction to her death I received many praising words on her: warm, witty, clever, reliable, hard-working, committed and, last but not least, very very funny with her typical dry humor. Although we miss her here dearly, I'm sure that wherever she is now, they will have a well edited newsletter and perfectly organized finances.

Thanks for all your priceless efforts Kelly, you will be remembered as a profound force of the NVFA!

Eveline Altena

Archaeological Hair Cortisol: A New Frontier?

Sarah Schrader

Laboratory for Human Osteoarchaeology, Faculty of Archaeology, Leiden University

Cortisol, a hormone associated with physical and psychosocial stress, has been examined both in modern as well as ancient human hair. In archaeological scenarios where lengths of hair are preserved, osteoarchaeologists are able to assess stress prior to an individual's death. This can provide important information about the lived experience of the individual in the weeks and months prior to death. Here, cortisol is assessed alongside skeletal indicators of non-specific stress, specifically cribra orbitalia, porotic hyperostosis, and bilateral periostitis. It is hypothesized that persistently elevated cortisol might weaken the immune response, thereby increasing the likelihood of non-specific stress indicators.

Hormone and skeletal analysis were conducted on ancient Nubian skeletal remains from the archaeological sites Abu Fatima (2500-1550 BCE) and Tombos (1550-656 BCE). These two contexts differ in socioeconomic standing, which may provide variation in cortisol levels. Preliminary analysis indicates that levels of cortisol prior to death are quite variable. There does not appear to be any connection between elevated rates of cortisol and the presence of non-specific stress indicators; however, sample size was small, owing to a limited number of archaeological hair specimens. When the osteological paradox is taken into account, another possible explanation is that some individuals may have died before non-specific stress lesions developed (i.e., frailty). Future research, incorporating a larger sample size in addition to forensic testing, is necessary.

**Towards virtual forensic anthropology**

Kerri Lee Colman

Amsterdam UMC

Most European countries lack contemporary collections and are thus unable to develop or test forensic anthropological methods. Specifically, in the Netherlands, due to legislation and the high mean age of bodies donated to the body donation, compiling a skeletal collection that is representative of the current population in the Netherlands is not a possibility. A solution to the lack of representative skeletal population samples could be the use of clinical radiological data (such as computed tomography (CT) scans) as a proxy for skeletal collections. The data from these scans might be used to build a contemporary virtual skeletal database as the data acquired is of known demographics, representative of a contemporary, residing population, and is immediately available. Ultimately, the success of a virtual skeletal database derived from clinical CT scans, depends greatly on the precise modelling of the virtual bone models from the CT images, and the accuracy with which these models represent their actual dry bone counterparts. This presentation therefore focuses on the use of 3D virtual bone models derived from clinical CT scans, and the precision and accuracy of these models. Precision concerns the reliability of virtual bones models derived from clinical CT scan data, while accuracy assesses how well the virtual bones match the actual dry bones. Since forensic anthropology estimation methods are usually based on morphological (shape) or osteometric (size) features, the accuracy is explored for both these approaches.



Cooking up Calculus: Experimental dietary research on a model calculus system

Bjørn Peare Bartholdy

Faculty of Archaeology, Leiden University

Dental calculus has become an increasingly large field of interest within biological anthropology in recent years, with researchers utilising it to explore diet, pathogens, the oral microbiome, and

more. Particularly beneficial to these studies is the ability of dental calculus to entrap and preserve plant micro-remains, proteins, and endogenous and exogenous microorganisms.

I will present my ongoing PhD research that involves developing a model calculus system, which will allow experimental research to be conducted on in vitro calculus. Oral biofilms are grown for 25 days on plastic substrata that simulate teeth. The biofilms are fed sucrose to promote bacterial growth and plaque formation, and a mineral-rich solution to promote mineralisation of the dental plaque to form calculus. The bacterial and mineral composition of the in vitro calculus will be determined in order to assess its similarity to the real thing. The biofilms are also exposed to various starch grains and solutions with medicines to examine the mode of incorporation of dietary markers and medicinal compounds into the dental calculus. This model calculus system can provide the framework to perform controlled experiments that can address fundamental questions and issues concerning dental calculus, which have yet to be explored. These include the validation of sampling techniques and extraction methods, as well as the process of incorporation of dietary and other markers into the calculus matrix, and the effects of taphonomy on these markers.



Promises and limitations of low coverage ancient DNA in studies taking whole graveyard approach

T. Kivisild

Department of Human Genetics, KU Leuven

Ancient genomic data are becoming available in increasingly larger numbers from individuals and come, often inevitably, at low coverage. The choice of material – which skeletal source to sample, the choice of sequencing methods and final data quality measures determine which questions about the past and with what confidence can be addressed. In this presentation, the promises and limitations of methods based on low coverage shotgun sequence data will be discussed in context of questions about health, genetic ancestry and relatedness within and among burial sites.



WORKSHOP 1

Opening up the casket: why and how to share your research data

Esther Plomp^{1,2}

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Data sharing is part of the recent developments in opening up scientific research, a movement also known as Open Science or Open Knowledge. The Open Science movement aims to increase the transparency of scientific research and improve the reproducibility of its results. Opening up the scientific process also promotes equitable access to resources and allows for the recognition of outputs other than the traditional scientific publication, such as data, code and analysis protocols. Many funders (e.g., Netherlands Organisation for Scientific Research (NWO), and the European Commission) and publishers now also require researchers to share their data. In this workshop you will learn how data sharing is beneficial to you, and which tools you can use to share your data.



WORKSHOP 2

Petrous bones in isotope and ancient DNA research in archaeology

Lisette Kootker¹ & Eveline Altena²

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After the first successful use of the petrous bone (pars petrosa) in ancient DNA research in 2014, the human inner ear became of

paramount importance in the field of palaeogenomics, and is in many cases now the material of choice. In that same period, the use of the so-called otic capsule within the petrous portion of the temporal bone was also explored in archaeological isotope research. Research showed the potential of the pars petrosa as a tracer for childhood residence in cases where the preferred dental enamel is lost or absent, as is always the case in cremated material.

In order to guarantee a successful use of the pars petrosa in both aDNA and isotope research it is essential to understand the basics of the anatomy of the petrous bone and to recognize the fundamental elements that need to be accurately targeted for strontium isotope and ancient DNA analysis. In this workshop we will highlight the scientific value of the petrous bone for ancient DNA and isotope studies using actual (cremated) samples, and discuss peer reviewed literature on methods for dealing with the petrous bone in isotope and DNA studies

Article

In de gezegende drup Het graf van een pasgeboren kind uit de opgraving Gouda- Westerkade

Nico van der Feest

In 2018 voerde Aeres Milieu een kleinschalig archeologisch onderzoek op een locatie aan de Westerkade in Gouda. Het terrein werd gerekend tot de tuin van het middeleeuwse leprozenhuis. Tijdens het onderzoek werden de fundamenteen gevonden van de kapel van het huis. Buiten de kapel lag een houten kistje. De zorgvuldige studie ervan in het laboratorium leverden de resten op van een pasgeboren kind.

Fundament

In de meeste gevallen vindt archeologisch onderzoek plaats in de context van grootschalige ruimtelijke ontwikkelingen. Soms is er echter reden om ook bij kleinschalige ingrepen archeologen mee te laten kijken bij de uitvoering van de werkzaamheden. Zo was de aanleg van een liftschaft op het terrein van het middeleeuwse leprozenhuis aanleiding voor een archeologische begeleiding door Aeres Milieu. Binnen een opgraving van niet meer dan 20m² werd onder verschillende sterk geroerde ophogingspakketten met een kleine hoeveelheid laat-middeleeuws en vroegmodern vondstmateriaal een uit bakstenen opgetrokken fundament gevonden (afbeelding 1). Gelet op de aard en omvang van de muur en de aanwezigheid van een steunbeer is het vrijwel zeker dat het hier gaat om een gedeelte van de fundering van de kapel van het leprozenhuis. Rond het fundament werd veel menselijk botmateriaal aangetroffen maar in geen enkel geval was sprake van begravingen in ongeroerde grond. Een eerste blik op het materiaal maakt duidelijk dat bij diverse botten sporen te zien zijn van een eenzijdige consumptie van voedsel.

Kind

Onder de ophogingspakketten boven en naast de kapelfundering werd een veenpakket aangetroffen. Van menselijk ingrijpen in deze natuurlijke ondergrond werden geen sporen gevonden, met één uitzondering, dicht bij de kapelmuur: een klein houten kistje (afbeelding 2). Hoewel het kistje op het eerste gezicht leeg leek, werd het in zijn geheel gelicht en naar het laboratorium gebracht. Daar werden in het kistje zeer kleine botresten aangetroffen waarvan een fysisch antropoloog duidelijk kon maken dat ze behoorden tot een pasgeboren, vermoedelijk doodgeboren kind.

In de christelijke traditie vormen doodgeboren kinderen een bijzondere categorie. Ze zijn immers ongedoopt. Door het ontbreken van dit heilig sacrament worden zij niet verlost van de zondigheid die ieder mens door zijn geboorte aankleeft als gevolg van de zondeval van het eerste mensenpaar (de erfzonde). Ze mochten daarom niet op gewijde grond begraven worden: die was gereserveerd voor de mensen die door de doop christen waren geworden. Dat betekende echter niet dat ongedoopte kinderen op willekeurige plekken werden begraven; meestal gebeurde dit binnen een strook grond naast de gewijde begraafplaats, de limbus

infantium, letterlijk de overgang tussen gewijde en ongewijde aarde, meer figuurlijk het voorgeborchte – noch hemel, noch hel - waar de zielen van ongedoopte kinderen een natuurlijke gelukzaligheid genoten.

Het is goed voorstelbaar dat de aan de Goudse Westerkade aangetroffen pasgeborene, zo dicht tegen de kapelmuur aan, halverwege gewijde en ongewijde grond is begraven. Wellicht meenden men dat het ontbreken van persoonlijke zonden deze nabijheid niet in de weg stond. Of gelovigen waren er van overtuigd dat het regenwater dat via de dakrand van een kerk of kapel naar beneden viel gezegend was door God. In de gezegende drup werd het kind eigenlijk alsnog gedoopt! Door Engelse onderzoekers wordt dan ook gesproken van het 'dakrand-druppelritueel' (eaves-drip ritual) en door Duitse van doopbegraving (Taufbestattung). Of de Goudse begraving een poging was om het doodgeboren kind alsnog een plek in de hemel te geven, zullen we echter nooit weten.



Afbeelding 1. Gouda-Westerkade. Fundament van de kapel van het middeleeuwse leprozenhuis van Gouda.



Afbeelding 2. Gouda-Westerkade. In het veen ingegraven kistje met de resten van een pasgeboren kind.

Craig-Atkins, E., 2014: Eavesdropping on short lives: Eaves-drip burial and the differential treatment of children one year of age and under in early Christian cemeteries, in: Hadley, D.M./ K.A. Hemer (eds) Medieval Childhood: Archaeological Approaches, Oxford, pp. 95-113.

Hausmair, B., 2017: Topographies of the afterlife. Reconsidering infant burials in medieval mortuary space, in Journal of Social Archaeology, pp. 1-27.

Kok, H.L., 1970: De geschiedenis van de laatste eer in Nederland, Utrecht

Abstracts of articles

The Dutch Y-chromosomal landscape

Eveline Altena¹, Risha Smeding¹, Kristiaan van der Gaag^{1,*}, Maarten H.D. Larmuseau^{2,3,4}, Ronny Decorte^{2,5}, Oscar Lao^{6,#}, Manfred Kayser⁶, Thirsa Kraaijenbrink¹, Peter de Knijff¹

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European Journal of Human Genetics, published online September 5 2019.

Previous studies indicated existing, albeit limited, genetic-geographic population substructure in the Dutch population based on genome-wide data and a lack of this for mitochondrial SNP based data. Despite the aforementioned studies, Y-chromosomal SNP data from the Netherlands remain scarce and do not cover the territory of the Netherlands well enough to allow a reliable investigation of genetic-geographic population substructure.

Here we provide the first substantial dataset of detailed spatial Y-chromosomal haplogroup information in 2085 males collected across the Netherlands and supplemented with previously published data from northern Belgium. We found Y-chromosomal evidence for

genetic-geographic population substructure, and several Y-haplogroups demonstrating significant clinal frequency distributions in different directions. By means of prediction surface maps we could visualize (complex) distribution patterns of individual Y-haplogroups in detail.

These results highlight the value of a micro-geographic approach and are of great use for forensic and epidemiological investigations and our understanding of the Dutch population history. Moreover, the previously noted absence of genetic-geographic population substructure in the Netherlands based on mitochondrial DNA in contrast to our Y-chromosome results, hints at different population histories for women and men in the Netherlands.



Histologic and radiological analysis on bone fractures: Estimation of posttraumatic survival time in skeletal trauma

Cappella A.¹, de Boer H.H.², Cammilli P.³, De Angelis D.³, Messina C.⁴, Sconfienza L.M.⁴, Sardanelli F.⁵, Sforza C.⁶, Cattaneo C.³.

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In antemortem fractures, the estimation of the amount of time that has lapsed between the traumatic event and eventual death (the so-called 'posttraumatic survival time' or PTST) can have substantial implications in legal proceedings. It might for instance help to corroborate witness testimonies, to reconstruct the chain of events leading to eventual death or to establish a sequence when multiple traumata in a single individual are encountered. However, PTST estimation of bone trauma is impeded by a myriad of theoretical and practical issues, and is therefore almost invariably considered challenging. A few years ago, a method that combines radiological and histological analysis of fractures to estimate the minimum amount of lapsed PTST in skeletonized remains was proposed. This study aims to test its accuracy on a set of five rib fractures and four skull lesions fractures with known and varying amounts of posttraumatic survival time. In addition, it explores the differences between the assessment on ribs and skull bones and it expands on the proposed method by including computed tomography (CT) scanning. Using conventional radiology and histology, the minimum amount of PTST was accurately estimated in 8 out of 9 of the cases (89%). The one discrepancy between the estimated and known PTST was minimal, being just one day. The precision of the method diminishes as healing advances. It was noted that skull lesions showed less advanced and less well-developed healing features than the lapsed PTST would suggest. Of the three used modalities, conventional radiology proved to be the least accurate. CT scanning proved to be a valuable, sometimes even superior alternative to conventional radiology. Histology was superior to both conventional radiology and CT scanning. The results of our study illustrate the potential of the combined application of radiology and histology to estimate the PSTS in skeletonized human fractures.

★

The Status of Forensic Anthropology in Europe and South Africa: Results of the 2016 FASE Questionnaire on Forensic Anthropology

Zuzana Obertová, Pascal Adalian, Eric Baccino, Eugenia Cunha, Hans H De Boer, Tony Fracasso, Elena Kranjoti, Philippe Lefèvre, Niels Lynnerup, Anja Petaros, Ann Ross, Maryna Steyn, Cristina Cattaneo

Journal of forensic sciences 2019/2/9

One of the goals of the Forensic Anthropology Society of Europe (FASE) is to map the existing education and practice opportunities in the field of forensic anthropology in order to support the development of the discipline and to optimize the training courses provided by the Society. To address this goal, an online questionnaire was sent to European and South African practitioners of forensic anthropology and related disciplines in 2016. The results of the questionnaire showed that the status and roles of forensic anthropologists vary depending on the national legal systems, education, and employment status of the practitioners. Despite the fact that the expertise of forensic anthropologists has been increasingly requested in a variety of investigations and the spectrum of tasks has become broader, including identification of living persons, specialized education is still restricted to a few graduate and postgraduate programs in European countries and to annual FASE courses.



The role of forensic anthropology in disaster victim identification (DVI): recent developments and future prospects

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Forensic anthropological knowledge has been used in disaster victim identification (DVI) for over a century, but over the past decades, there have been a number of disaster events which have seen an increasing role for the forensic anthropologist. The experiences gained from some of the latest DVI operations have provided valuable lessons that have had an effect on the role and perceived value of the forensic anthropologist as part of the team managing the DVI process. This paper provides an overview of the ways in which forensic anthropologists may contribute to DVI with emphasis on how recent experiences and developments in forensic anthropology have augmented these contributions. Consequently, this paper reviews the value of forensic anthropological expertise at the disaster scene and in the mortuary, and discusses the way in which forensic anthropologists may use imaging in DVI efforts. Tissue-sampling strategies for DNA analysis, especially in the case of disasters with a large amount of fragmented remains, are also discussed. Additionally, consideration is given to the identification of survivors; the statistical basis of identification; the challenges related to some specific disaster scenarios; and education and training. Although forensic anthropologists can play a valuable role in different phases of a DVI operation, they never practice in isolation. The DVI process requires a multidisciplinary approach and, therefore, has a close collaboration with a range of forensic specialists.



DNA identification of human remains in Disaster Victim Identification (DVI): An efficient sampling method for muscle, bone, bone marrow and teeth

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In disaster victim identification (DVI), DNA profiling is considered to be one of the most reliable and efficient means to identify bodies or separated body parts. This requires a post mortem DNA sample, and an ante mortem DNA sample of the presumed victim or their biological relative(s). Usually the collection of an adequate ante mortem sample is technically simple, but the acquisition of a good quality post mortem sample under unfavourable DVI circumstances is complicated due to the variable degree of preservation of the human remains and the high risk of DNA (cross) contamination. This paper provides the community with an efficient method to collect post-mortem DNA samples from muscle, bone, bone marrow and teeth, with a minimal risk of contamination. Our method has been applied in a recent, challenging DVI operation (i.e. the identification of the 298 victims of the MH17 airplane crash in 2014). 98,2% of the collected PM samples provided the DVI team with highly informative DNA genotyping results without the risk of contamination and consequent mistyping the victim's DNA. Moreover, the method is easy, cheap and quick. This paper provides the DVI community with a step-wise instructions with recommendations for the type of tissue to be sampled and the site of excision (preferably the upper leg). Although initially designed for DVI purposes, the method is also suited for the identification of individual victims.

★

Virtual forensic anthropology: The accuracy of osteometric analysis of 3D bone models derived from clinical computed tomography (CT) scans

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Clinical radiology is increasingly used as a source of data to test or develop forensic anthropological methods, especially in countries where contemporary skeletal collections are not available. Naturally, this requires analysis of the error that is a result of low accuracy of the modality (i.e. accuracy of the segmentation) and the error that arises due to difficulties in landmark recognition in virtual models. The cumulative effect of these errors ultimately determines whether virtual and dry bone measurements can be used interchangeably. To test the interchangeability of virtual and dry bone measurements,

13 male and 14 female intact cadavers from the body donation program of the Amsterdam UMC were CT scanned using a standard patient scanning protocol and processed to obtain the dry os coxae. These were again CT scanned using the same scanning protocol. All CT scans were segmented to create 3D virtual bone models of the os coxae ('dry' CT models and 'clinical' CT models). An Artec Spider 3D optical scanner was used to produce gold standard 'optical 3D models' of ten dry os coxae. The deviation of the surfaces of the 3D virtual bone models compared to the gold standard was used to calculate the accuracy of the CT models, both for the overall os coxae and for selected landmarks. Landmark recognition was studied by comparing the TEM and %TEM of nine traditional inter-landmark distances (ILDs). The percentage difference for the various ILDs between modalities was used to gauge the practical implications of both errors combined. Results showed that 'dry' CT models were 0.36-0.45mm larger than the 'optical 3D models' (deviations -0.27mm to 2.86mm). 'Clinical' CT models were 0.64-0.88mm larger than the 'optical 3D models' (deviations -4.99mm to 5.00mm). The accuracies of the ROIs were variable and larger for 'clinical' CT models than for 'dry' CT models. TEM and %TEM were generally in the acceptable ranges for all ILDs whilst no single modality was obviously more or less reliable than the others. For almost all ILDs, the average percentage difference between modalities was substantially larger than the average percentage difference between observers in 'dry bone' measurements only. Our results show that the combined error of segmentation- and landmark recognition error can be substantial, which may preclude the usage of 'clinical' CT scans as an alternative source for forensic anthropological reference data.

★

The accuracy of 3D virtual bone models of the pelvis for morphological sex estimation

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It is currently unknown whether morphological sex estimation traits are accurately portrayed on virtual bone models, and this hampers the use of virtual bone models as an alternative source of contemporary skeletal reference data. This study determines whether commonly used morphological sex estimation traits can be accurately scored on virtual 3D pelvic bone elements. Twenty-seven intact cadavers from the body donation program of the Amsterdam UMC, University of Amsterdam, were CT scanned; this data was used to produce virtual bone models. Thereafter, the dry bones were obtained. Three traits by Kiales (2012) and five traits from the Workshop of European Anthropologists (WEA) (1980) were scored on the virtual bone models and their dry skeletal counterparts. Intra- and inter-observer agreement and the agreement between the scores for each virtual bone model-dry bone pair were calculated using weighted Cohen's kappa (K). For all Kiales (2012) traits, intra- and inter-observer agreement was substantial to almost perfect for the virtual- and dry bones (K = 0.62-0.90). The agreement in scores in the virtual-dry bone pairs ranged from moderate to almost perfect (K = 0.58-0.82). For the WEA (1980) traits, intra-observer agreement was substantial to almost perfect (K = 0.64-0.91), but results were less unambiguous for inter-observer agreement (K = 0.24-0.88). Comparison of the scores between the virtual bone models and the dry bones yielded kappa values of 0.42-0.87. On one hand, clinical CT data is a promising source for contemporary forensic anthropological reference data, but the interchangeability of forensic

anthropological methods between virtual bone models and dry skeletal elements needs to be tested further.



Estimating sex from the calcaneus: applications for forensic anthropological identification in the Netherlands

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The estimation of sex is considered to be one of the fundamental steps in the forensic identification of human skeletal remains and typically involves scoring various features of the pelvis and the cranium. Though this method has proven to be highly accurate, in practice it fails to take into account aspects such as fragmentation due to post-depositional processes and taphonomy. It is therefore essential to consider a variety of methods for sex estimation that take into account factors such as these.

The calcaneus, or heel bone, is the largest bone in the foot and is often recovered fairly intact. This is mainly due to it being a weight bearing bone with a dense and compact structure, as well as it being protected from taphonomic changes with the use of footwear. Previous studies have established the potential of using the calcaneus in sex estimation, as well as recognized the validity of metric-based methods in sex estimation to be population specific.

Extending the current line of research on calcaneus-based metric sex estimation methods, the present study introduces binomial logistic function as a statistical method in calcaneus-based sex estimation and computes several models based on a set of seven calcaneal measurements from a known 19th-century osteological collection from the Netherlands (n=96). This study thereby introduces a valid adjunctive method for sex estimation in Dutch individuals, which could be vastly beneficial in the forensic identification of human skeletal remains in the Netherlands.



Delayed physical development in a first generation enslaved African woman from Pietermaai, Curaçao

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There is still much to be learned about enslavement in Curaçao, where little archaeological investigation into the historical era has been carried out. This article contributes to our knowledge on this subject through the analysis of a female individual buried in Pietermaai, an 18th century suburb of Willemstad. Excavated in the 1980s by the Archaeological-Anthropological Institute of the Netherlands Antilles, the remains are only now attracting osteological attention. Isotopic analysis has shown that this individual spent her childhood in West Africa, supporting morphological and metric analyses identifying her African ancestry. At the time of death, she had an adult chronological age (over 18 years), but her physical development indicated a non-adult biological age (possibly between 12 and 15 years). Such delayed development can occur due to many factors, including hard labour and disease. In the case of this individual, evidence such as enamel hypoplasia, osteochondritis dissecans, and periostitis may indicate stressful episodes throughout the life course. Clearly defined entheses and enthesal changes at muscle attachment sites on the arms and legs may indicate a physically demanding occupation. A variety of factors could therefore have contributed to her developmental delay. In the future, further analysis of buried populations in Curaçao will help to increase our understanding of the lifeways of enslaved people here. Meanwhile, the analysis of this isolated individual is important because it situates enslavement in a real body and indicates the value of reanalysis of human remains from existing archaeological collections in the Caribbean.



WORKSHOP: Replacing Curacao's 'mild slavery' thesis: From critique to new findings

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Thursday 21 November 201, Leiden

Slavery on the island of Curacao did not conform to the general patterns of slave-holding in the Americas. As a dry and infertile island with an excellent natural harbor the Dutch West India Company and private firms primarily used the island as a nodal point that tied together licit and illicit lines of trade. Slavery was nevertheless central to its economy.

Comparison to emblematic American slave societies such as Suriname have triggered historians in the past to characterize Curacao slavery as 'mild'. Although few would use this characterization in an unqualified manner today, historians still lack an adequate way to conceptualize Curacao as a slave society.

During this workshop historians and archeologists will have an interdisciplinary conversation about their most recent findings regarding Curacao slavery and aim to develop new ways to conceptualize it.



West Asian sources of the Eurasian component in Ethiopians: a reassessment

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The presence of genomic signatures of Eurasian origin in contemporary Ethiopians has been reported by several authors and estimated to have arrived in the area from 3000 years ago. Several studies reported plausible source populations for such a signature, using haplotype based methods on modern data or single-site methods on modern or ancient data. These studies did not reach a consensus and suggested an Anatolian or Sardinia-like proxy, broadly Levantine or Neolithic Levantine as possible sources. We demonstrate, however, that the deeply divergent, autochthonous African component which accounts for ~50% of most contemporary Ethiopian genomes, affects the overall allele frequency spectrum to an extent that makes it hard to control for it and, at once, to discern between subtly different, yet important, Eurasian sources (such as Anatolian or Levant Neolithic ones). Here we re-assess pattern of allele sharing between the Eurasian component of Ethiopians (here called "NAF" for Non African) and ancient and modern proxies. Our results unveil a genomic legacy that may connect the Eurasian genetic component of contemporary Ethiopians with Sea People and with population movements that affected the Mediterranean area and the Levant after the fall of the Minoan civilization.



The Genomic Impact of European Colonization of the Americas

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The human genetic diversity of the Americas has been affected by several events of gene flow that have continued since the colonial era and the Atlantic slave trade. Moreover, multiple waves of migration followed by local admixture occurred in the last two centuries, the impact of which has been largely unexplored. Here, we compiled a genome-wide dataset of ~12,000 individuals from twelve American countries and ~6,000 individuals from worldwide populations and applied haplotype-based methods to investigate how historical movements from outside the New World affected (1) the genetic structure, (2) the admixture profile, (3) the demographic history, and (4) sex-biased gene-flow dynamics of the Americas. We revealed a high degree of complexity underlying the genetic contribution of European and African populations in North and South America, from both geographic and temporal perspectives, identifying previously unreported sources related to Italy, the Middle East, and to specific regions of Africa.

★

Phylogeography of the second plague pandemic revealed through analysis of historical *Yersinia pestis* genomes

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The second plague pandemic, caused by *Yersinia pestis*, devastated Europe and the nearby regions between the 14th and 18th centuries AD. Here we analyse human remains from ten European archaeological sites spanning this period and reconstruct 34 ancient *Y. pestis* genomes. Our data support an initial entry of the bacterium through eastern Europe, the absence of genetic diversity during the Black Death, and low within-outbreak diversity thereafter. Analysis of post-Black Death genomes shows the diversification of a *Y. pestis* lineage into multiple genetically distinct clades that may have given rise to more than one disease reservoir in, or close to, Europe. In addition, we show the loss of a genomic region that includes virulence-related genes in strains associated with late stages of the pandemic. The deletion was also identified in genomes connected with the first plague pandemic (541-750 AD), suggesting a comparable evolutionary trajectory of *Y. pestis* during both events.



Population structure of modern-day Italians reveals patterns of ancient and archaic ancestries in Southern Europe

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European populations display low genetic differentiation as the result of long-term blending of their ancient founding ancestries. However, it is unclear how the combination of ancient ancestries related to early foragers, Neolithic farmers, and Bronze Age nomadic pastoralists can explain the distribution of genetic variation across Europe. Populations in natural crossroads like the Italian peninsula are expected to recapitulate the continental diversity, but have been systematically understudied. Here, we characterize the ancestry profiles of Italian populations using a genome-wide dataset representative of modern and ancient samples from across Italy, Europe, and the rest of the world. Italian genomes capture several ancient signatures, including a non-steppe contribution derived ultimately from the Caucasus. Differences in ancestry composition, as the result of migration and admixture, have generated in Italy the largest degree of population structure detected so far in the continent, as well as shaping the amount of Neanderthal DNA in modern-day populations.

★

Shifts in the Genetic Landscape of the Western Eurasian Steppe Associated with the Beginning and End of the Scythian Dominance

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The Early Iron Age nomadic Scythians have been described as a confederation of tribes of different origins, based on ancient DNA evidence [1-3]. It is still unclear how much of the Scythian dominance in the Eurasian Steppe was due to movements of people and how much reflected cultural diffusion and elite dominance. We present new whole-genome sequences of 31 ancient Western and Eastern Steppe individuals, including Scythians as well as samples pre- and postdating them, allowing us to set the Scythians in a temporal context (in the Western, i.e., Ponto-Caspian Steppe). We detect an increase of eastern (Altaian) affinity along with a decrease in eastern hunter-gatherer (EHG) ancestry in the Early Iron Age Ponto-Caspian gene pool at the start of the Scythian dominance. On the other hand, samples of the Chernyakhiv culture postdating the Scythians in Ukraine have a significantly higher proportion of Near Eastern ancestry than other samples of this study. Our results agree with the Gothic source of the Chernyakhiv culture and support the hypothesis that the Scythian dominance did involve a demic component.

★

East Anglian early Neolithic monument burial linked to contemporary Megaliths

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In the fourth millennium BCE a cultural phenomenon of monumental burial structures spread along the Atlantic façade. Megalithic burials have been targeted for aDNA analyses, but a gap remains in East Anglia, where Neolithic structures were generally earthen or timber. An early Neolithic (3762-3648 cal. BCE) burial monument at the site of Trumpington Meadows, Cambridgeshire, UK, contained the partially articulated remains of at least three individuals. To determine whether this monument fits a pattern present in megalithic burials regarding sex bias, kinship, diet and relationship to modern populations, teeth and ribs were analysed for DNA and carbon and nitrogen isotopic values, respectively. Whole ancient genomes were sequenced from two individuals to a mean genomic coverage of 1.6 and 1.2X and genotypes imputed. Results show that they were brothers from a small population genetically and isotopically similar to previously published British Neolithic individuals, with a level of genome-wide homozygosity consistent with a small island population sourced from continental Europe, but bearing no signs of recent inbreeding. The first Neolithic whole genomes from a monumental burial in East Anglia confirm that this region was connected with the larger pattern of Neolithic megaliths in the British Isles and the Atlantic façade.



Ancient *Yersinia pestis* genomes from across Western Europe reveal early diversification during the First Pandemic (541-750)

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The first historically documented pandemic caused by *Yersinia pestis* began as the Justinianic Plague in 541 within the Roman Empire and continued as the so-called First Pandemic until 750. Although paleogenomic studies have previously identified the causative agent as *Y. pestis*, little is known about the bacterium's spread, diversity, and genetic history over the course of the pandemic. To elucidate the microevolution of the bacterium during this time period, we screened human remains from 21 sites in Austria, Britain, Germany, France, and Spain for *Y. pestis* DNA and reconstructed eight genomes. We present a methodological approach assessing single-nucleotide polymorphisms (SNPs) in ancient bacterial genomes, facilitating qualitative analyses of low coverage genomes from a metagenomic background. Phylogenetic analysis on the eight reconstructed genomes reveals the existence of previously

undocumented *Y. pestis* diversity during the sixth to eighth centuries, and provides evidence for the presence of multiple distinct *Y. pestis* strains in Europe. We offer genetic evidence for the presence of the Justinianic Plague in the British Isles, previously only hypothesized from ambiguous documentary accounts, as well as the parallel occurrence of multiple derived strains in central and southern France, Spain, and southern Germany. Four of the reported strains form a polytomy similar to others seen across the *Y. pestis* phylogeny, associated with the Second and Third Pandemics. We identified a deletion of a 45-kb genomic region in the most recent First Pandemic strains affecting two virulence factors, intriguingly overlapping with a deletion found in 17th- to 18th-century genomes of the Second Pandemic.



The Arrival of Siberian Ancestry Connecting the Eastern Baltic to Uralic Speakers further East

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In this study, we compare the genetic ancestry of individuals from two as yet genetically unstudied cultural traditions in Estonia in the 30

context of available modern and ancient datasets: 15 from the Late Bronze Age stone-cist graves (1200-400 BC) (EstBA) and 6 from the Pre-Roman Iron Age tarand cemeteries (800/500 BC-50 AD) (EstIA). We also included 5 Pre-Roman to Roman Iron Age Ingrian (500 BC-450 AD) (InglA) and 7 Middle Age Estonian (1200-1600 AD) (EstMA) individuals to build a dataset for studying the demographic history of the northern parts of the Eastern Baltic from the earliest layer of Mesolithic to modern times. Our findings are consistent with EstBA receiving gene flow from regions with strong Western hunter-gatherer (WHG) affinities and EstIA from populations related to modern Siberians. The latter inference is in accordance with Y chromosome (chrY) distributions in present day populations of the Eastern Baltic, as well as patterns of autosomal variation in the majority of the westernmost Uralic speakers [1-5]. This ancestry reached the coasts of the Baltic Sea no later than the mid-first millennium BC; i.e., in the same time window as the diversification of west Uralic (Finnic) languages [6]. Furthermore, phenotypic traits often associated with modern Northern Europeans, like light eyes, hair, and skin, as well as lactose tolerance, can be traced back to the Bronze Age in the Eastern Baltic.



A Transient Pulse of Genetic Admixture from the Crusaders in the Near East Identified from Ancient Genome Sequences

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During the medieval period, hundreds of thousands of Europeans migrated to the Near East to take part in the Crusades, and many of them settled in the newly established Christian states along the Eastern Mediterranean coast. Here, we present a genetic snapshot of these events and their aftermath by sequencing the whole genomes of 13 individuals who lived in what is today known as Lebanon between the 3rd and 13th centuries CE. These include nine individuals from the "Crusaders' pit" in Sidon, a mass burial in South Lebanon identified from the archaeology as the grave of Crusaders killed during a battle in the 13th century CE. We show that all of the Crusaders' pit individuals were males; some were Western Europeans from diverse origins, some were locals (genetically indistinguishable from present-day Lebanese), and two individuals were a mixture of European and Near Eastern ancestries, providing direct evidence that the Crusaders admixed with the local population. However, these mixtures appear to have had limited genetic consequences since signals of admixture with Europeans are not significant in any Lebanese group today-in particular, Lebanese Christians are today genetically similar to local people who lived during the Roman period which preceded the Crusades by more than four centuries.



Ancestry-Specific Analyses Reveal Differential Demographic Histories and Opposite Selective Pressures in Modern South Asian Populations

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Genetic variation in contemporary South Asian populations follows a northwest to southeast decreasing cline of shared West Eurasian ancestry. A growing body of ancient DNA evidence is being used to build increasingly more realistic models of demographic changes in the last few thousand years. Through high-quality modern genomes, these models can be tested for gene and genome level deviations. Using local ancestry deconvolution and masking, we reconstructed population-specific surrogates of the two main ancestral components for more than 500 samples from 25 South Asian populations and showed our approach to be robust via coalescent simulations. Our f3 and f4 statistics-based estimates reveal that the reconstructed haplotypes are good proxies for the source populations that admixed in the area and point to complex interpopulation relationships within the West Eurasian component, compatible with multiple waves of arrival, as opposed to a simpler one wave scenario. Our approach also provides reliable local haplotypes for future downstream analyses. As one such example, the local ancestry deconvolution in South Asians reveals opposite selective pressures on two pigmentation genes (SLC45A2 and SLC24A5) that are common or fixed in West Eurasians, suggesting post-admixture purifying and positive selection signals, respectively.



The genetic legacy of continental scale admixture in Indian Austroasiatic speakers

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Sci Rep. 2019 Mar 7;9(1):3818. doi: 10.1038/s41598-019-40399-8.

Surrounded by speakers of Indo-European, Dravidian and Tibeto-Burman languages, around 11 million Munda (a branch of Austroasiatic language family) speakers live in the densely populated and genetically diverse South Asia. Their genetic makeup holds components characteristic of South Asians as well as Southeast Asians. The admixture time between these components has been previously estimated on the basis of archaeology, linguistics and uniparental markers. Using genome-wide genotype data of 102 Munda speakers and contextual data from South and Southeast Asia, we retrieved admixture dates between 2000-3800 years ago for different populations of Munda. The best modern proxies for the source populations for the admixture with proportions 0.29/0.71 are Lao people from Laos and Dravidian speakers from Kerala in India. The South Asian population(s), with whom the incoming Southeast Asians intermixed, had a smaller proportion of West Eurasian genetic component than contemporary proxies. Somewhat surprisingly Malaysian Peninsular tribes rather than the geographically closer Austroasiatic languages speakers like Vietnamese and Cambodians show highest sharing of IBD segments with the Munda. In addition, we affirmed that the grouping of the Munda speakers into North and South Munda based on linguistics is in concordance with genome-wide data.

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Y Chromosome Sequences Reveal a Short Beringian Standstill, Rapid Expansion, and early Population structure of Native American Founders

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The Americas were the last inhabitable continents to be occupied by humans, with a growing multidisciplinary consensus for entry 15-25 thousand years ago (kya) from northeast Asia via the former Beringia land bridge [1-4]. Autosomal DNA analyses have dated the separation of Native American ancestors from the Asian gene pool to 23 kya or later [5, 6] and mtDNA analyses to ~25 kya [7], followed by isolation ("Beringian Standstill" [8, 9]) for 2.4-9 ky and then a rapid expansion throughout the Americas. Here, we present a calibrated sequence-based analysis of 222 Native American and relevant Eurasian Y chromosomes (24 new) from haplogroups Q and C [10], with four major conclusions. First, we identify three to four independent lineages as autochthonous and likely founders: the major Q-M3 and rarer Q-CTS1780 present throughout the Americas, the very rare C3-MPB373 in South America, and possibly the C3-P39/Z30536 in North America. Second, from the divergence times and Eurasian/American distribution of lineages, we estimate a Beringian Standstill duration of 2.7 ky or 4.6 ky, according to alternative models, and entry south of the ice sheet after 19.5 kya. Third, we describe the star-like expansion of Q-M848 (within Q-M3) starting at 15 kya [11] in the Americas, followed by establishment of substantial spatial structure in South America by 12 kya. Fourth, the deep branches of the Q-CTS1780 lineage present at low frequencies

35

throughout the Americas today [12] may reflect a separate out-of-Beringia dispersal after the melting of the glaciers at the end of the Pleistocene.

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Evaluating macroscopic sex estimation methods using genetically sexed archaeological material: The medieval skeletal collection from St John's Divinity School, Cambridge

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OBJECTIVES

In tests on known individuals macroscopic sex estimation has between 70% and 98% accuracy. However, materials used to create and test these methods are overwhelming modern. As sexual dimorphism is dependent on multiple factors, it is unclear whether macroscopic methods have similar success on earlier materials, which differ in lifestyle and nutrition. This research aims to assess the accuracy of commonly used traits by comparing macroscopic sex estimates to genetic sex in medieval English material.

MATERIALS AND METHODS

Sixty-six individuals from the 13th to 16th century Hospital of St John the Evangelist, Cambridge, were assessed. Genetic sex was determined using a shotgun approach. Eighteen skeletal traits were examined, and macroscopic sex estimates were derived from the os coxae, skull, and os coxae and skull combined. Each trait was tested for accuracy to explore sex estimates errors.

RESULTS

The combined estimate (97.7%) outperformed the os coxae only estimate (95.7%), which outperformed the skull only estimate (90.4%). Accuracy rates for individual traits varied: Phenice traits were most accurate, whereas supraorbital margins, frontal bossing, and gonial flaring were least accurate. The preauricular sulcus and arc compose showed a bias in accuracy between sexes.

DISCUSSION

Macroscopic sex estimates are accurate when applied to medieval material from Cambridge. However, low trait accuracy rates may relate to differences in dimorphism between the method derivative sample and the St John's collection. Given the sex bias, the preauricular sulcus, frontal bossing, and arc compose should be reconsidered as appropriate traits for sex estimation for this group.



An isotopic perspective on the socio-economic significance of livestock in Bronze Age West-Frisia, the Netherlands (2000-800 BCE)

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The Bronze Age is increasingly characterised as a period in which the search for and trade in metals dominates mobility and exchange in Europe. Chiefs travelled the lands and seas and dominated the acquisition and possession of critical resources. Most research focuses on the provenance and distribution of metals and on the mobility of people. Yet, the mobility of one the most obvious sources of social and economic wealth in the Bronze Age has got little attention: livestock. This study explores the possible social role of

livestock of cattle and sheep, both in the household sphere and in the sphere of exchange as a means of ‘connecting people’. Here, strontium isotope data are presented from 58 cattle and sheep from settlement contexts from Bronze Age West-Frisia (2000–800 BCE), the Netherlands, with the aim to gain an isotopic perspective on the socio-economic significance of livestock. The data provide evidence for long-distance trade or exchange of livestock. Besides their monetary value, we suggest that livestock, and in particular cattle, may have been perceived as equal to people in terms of labour and production and as members of the household. Their mobility and exchange therefore signal more than just economic trade, it signals a social practice. By changing our perspective towards the social ideology of farming life, we will move closer to understanding Bronze Age societies in more diverse and inclusive ways. Research into livestock mobility is therefore considered fundamental for a more diverse understanding of Bronze Age farming life.



Animals and People in the Netherlands’ Past: >50 Years of Archaeozoology in the Netherlands

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More than fifty years ago, Anneke T. Clason published the first English-language archaeozoological study on Dutch faunal assemblages. Inspired by the anniversary of this landmark publication, this paper presents a status overview of Dutch archaeozoology organized in twelve themes (e.g. rituals, Mesolithic-Neolithic transition, medieval period). The paper also discusses the common methods applied in Dutch archaeozoology, and includes extensive supplementary material that summarizes data from gray literature in Dutch. Our aim is to provide a guide to archaeozoological questions pertaining to the Netherlands and open a window for researchers working outside the Netherlands to the highly active world of Dutch archaeozoology.



Beyond isolation: understanding past human-population variability in the Dutch town of Oldenzaal through the origin of its inhabitants and its infrastructural connections

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This study presents a first attempt to assess the mechanisms and potential controls behind past residential mobility through the integration of isotopic data from human inhumations and spatial

infrastructural information pertaining to the settlement containing these inhumations. Strontium ($^{87}\text{Sr}/^{86}\text{Sr}$) and oxygen ($\delta^{18}\text{O}_{\text{PDB}}$) isotope data are derived from 200 (post)medieval individuals from the town of Oldenzaal in the present-day Netherlands. Reconstructions of historical route networks show that Oldenzaal was well-connected interregionally throughout the Middle Ages and early-modern times (ca. AD 800-1600). Although the working hypothesis was that in the past a high degree of spatial connectivity of settlements must have been positively related to a highly-variable geographical origin of its inhabitants, the isotopic data from Oldenzaal indicate a population characterized by a low variability in terms of their origin. This unexpected result may be caused by (a combination of) various factors, related to: 1) biases in the isotopic dataset, 2) interpretative limitations regarding the results of isotopic analyses, and 3) the impact of broader socio-cultural factors that cannot be traced through isotopic analyses, such as infrastructural connectivity, socio-economics, and political factors. The human oxygen isotope dataset presented here provides a first step towards a $\delta^{18}\text{O}_{\text{PDB}}$ reference dataset, against which future samples can be compared without the need to convert the data. This paper establishes that although in archaeology a biomolecular approach potentially provides a detailed reconstruction of the development of past populations in terms of palaeodemography and geographical/cultural origin, such studies should be performed in a transdisciplinary context in order to increase the understanding of the wider controlling factors of past population change.



Spatial variations in $^{87}\text{Sr}/^{86}\text{Sr}$ ratios in modern human dental enamel and tap water from the Netherlands: implications for forensic provenance studies

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Podium presentation 7th FIRMS, 16-19 September 2019 San Michele all'Adige (TN) Italy

Strontium isotope research is an established tool in archaeology to infer information about human and faunal geological provenances. The accuracy of the interpretations, however, strongly depends on the quality and quantity of bioavailable Sr background data. In recent years, variations in $^{87}\text{Sr}/^{86}\text{Sr}$ ratios in either modern biosphere or archaeological background data have been published for different parts of Europe (e.g., United Kingdom, the Netherlands, France, Sweden) and America. Due to the continental 'supermarket diet', however, the range of $^{87}\text{Sr}/^{86}\text{Sr}$ ratios in modern humans are not expected to display a high correlation with the local biosphere, but rather to represent a mix of local (water), national and international food sources. Consequently, the applicability of these isoscapes for forensic investigations is debatable. This study aims to evaluate this issue through an extensive isotope study of modern human dental enamel (n=97) and tap water (n=127) samples from the Netherlands. The range of $^{87}\text{Sr}/^{86}\text{Sr}$ ratios in human dentition is relatively limited (0.70853-0.70997), while the $^{87}\text{Sr}/^{86}\text{Sr}$ ratios of tap water samples have greater variation (0.70839-0.71278). Moreover, no strong relationship was found between the geographical location of the individuals sampled and the geology they lived during enamel mineralisation, pointing towards a random distribution of modern human $^{87}\text{Sr}/^{86}\text{Sr}$ ratios in the Netherlands. The Sr isotope ratios of tap water samples, however, are strongly dependent on the water source. As a result, there is a distinct correlation between geographical location of the water source and tap water $^{87}\text{Sr}/^{86}\text{Sr}$ ratios. In conclusion, the range of Dutch human and tap water Sr isotope ratios is more variable than expected, making an accurate determination of geolocation of human individuals within the Netherlands challenging. Nevertheless, the presented database is highly valuable in determining a Dutch or non-Dutch provenance in forensic contexts.



The Heul Girl murder case: a new step towards identification through stable and radiogenic isotope research

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In 1976, the partially skeletonised remains of a female adolescent were found in former parking lot “the Heul” along the A12 near Maarsbergen, the Netherlands. For 30 years, she was misidentified as 18-year old Monique Jacobs, who was reported missing the previous year: Jacobs contacted her family in 2006. After exhumation in 2012, conventional human identification and DNA research failed to identify the girl. Although the Dutch statute of limitations on murder had expired, a stable (C-N-H-O) and radiogenic (Sr-Pb) isotope study was commissioned (dental enamel, mandible and femur bone, and hair). The dental enamel and bones display significantly lower $^{87}\text{Sr}/^{86}\text{Sr}$ ratios (0.7077-0.7086) than the modern Dutch reference dataset (avg. 0.7093 ± 0.0003), indicative of geolocations with a component of young volcanism or limestone. The Pb isotope data point towards a possible eastern European origin, but residence in western Europe during the last period of life (third

molar). The $^{87}\text{Sr}/^{86}\text{Sr}$, and $\delta^2\text{H}$ data of eleven 2-cm hair segments record stepwise variations. The Sr data are compatible with the Netherlands, while the Pb (~ 1.13) and H (avg. -65‰) data are more challenging to interpret due to the lack of a comprehensive European reference data. Nevertheless, the data point toward residential mobility in Europe, certainly in a different part of Europe compared to her first years or life. Moreover, the C and N isotope data of the hair sections undoubtedly reflect a period of malnutrition or starvation prior to death. Unfortunately, despite the new insights in possible childhood geolocations, media attention in the Netherlands and Germany, and recently received tips, the girl remains unidentified. In 2016, following the Dutch judiciary, the

German judiciary approved a large-scale DNA kinship study with the aim to identify the girl through a family member.



Mapping a dynamic landscape. A critical review on the accuracy of the Dutch Sr isoscape

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Podium presentation 1st CRUMBEL Workshop - Cremation, Urns and Mobility: Population Dynamics in Belgium Brussels, 16-18 October 2019

Strontium isotope analysis has been successfully applied to reconstruct past mobility patterns for more than three decades. Although the underlying principle may appear to be straightforward, the interpretation of the obtained human or faunal isotope data is complicated, and requires a vast amount of baseline data. Hence, a thorough understanding of the patterns of spatial environmental isotopic variations is key to obtain a full understanding of variations in archaeological samples for migration studies. Following approaches applied to other parts of Europe, a preliminary archaeological bioavailable strontium map of the Netherlands was published in 2016. The diversity of the Dutch geological subsurface is directly reflected in the spatial distribution of $^{87}\text{Sr}/^{86}\text{Sr}$ ratios, and six isoscapes or isotope packages could be defined with $^{87}\text{Sr}/^{86}\text{Sr}$ ranging from 0.7074 to 0.7113. This presentation covers the sampling and analytical methodology behind of the current archaeological strontium isoscape map. In addition, results of an applicability assessment of the map for reconstructing past mobility patterns will be presented. These results show the importance of encompassing all aspects of (pre)historic life, as well as the dynamics of the environment to allow for a more accurate interpretation of human Sr isotope data.



Colourimetric analysis of thermally altered human bone samples

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At this moment, no method is available to objectively estimate the temperature to which skeletal remains have been exposed during a fire. Estimating this temperature can provide crucial information in a legal investigation. Exposure of bone to heat results in observable and measurable changes, including a change in colour. To determine the exposure temperature of experimental bone samples, heat related changes in colour were systemically studied by means of image analysis. In total 1138 samples of fresh human long bone diaphysis and epiphysis, varying in size, were subjected to heat ranging from room temperature to 900 °C for various durations and

in different media. The samples were scanned with a calibrated flatbed scanner and photographed with a Digital Single Lens Reflex camera. Red, Green, Blue values and Lightness, A-, and B-coordinates were collected for statistical analysis. Cluster analysis showed that discriminating thresholds for Lightness and B-coordinate could be defined and used to construct a model of decision rules. This model enables the user to differentiate between seven different temperature clusters with relatively high precision and accuracy. The proposed decision model provides an objective, robust and non-destructive method for estimating the exposure temperature of heated bone samples.



Comment on 'A DNA extraction method for small quantities of bone for high-quality genotyping' by Caputo et al.

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The extraction of sufficient DNA for subsequent amplification is becoming increasingly important in the field of forensic science. For the identification of the deceased, especially in cases involving severe fragmentation of skeletal elements, it is of utmost

importance to base laboratory procedures on scientifically obtained, preferably empirical, data. When laboratory procedures are based on flawed data or conclusions, this can lead to missed opportunities, and thus to failure in identifying a deceased which is problematic for the relatives and the authorities.



Bilateral symmetry of the subtalar joint facets and the relationship between the morphology and osteoarthritic changes

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There is a paucity in the literature regarding bilateral symmetry between the facets of the subtalar joint. Often surgeons use the contralateral side as a reference when dealing with a fracture or other joint pathology. Moreover, the presence of osteoarthritic (OA) changes in the subtalar joint is suggested to have a relation with its morphology. In this study, we addressed both these issues. Forty pairs of cadaveric tali and calcanei were analyzed by dissection and measurement. Twenty pairs of asymptomatic calcanei were morphologically analyzed by computer tomography imaging. In the cadaveric feet, the length and width of the facets, the number and interfacet connections, the intersection angle, and the presence of OA changes were registered. In the healthy feet, the orientation and

curvature of the posterior facet were analyzed based on cylinder fittings. Bilateral symmetry was tested with paired Student's t tests. Significant associations between morphometric parameters and the presence of OA changes were tested with generalized estimating equation logistic regression models. The morphometric data demonstrated a high degree of bilateral symmetry. The types of tali and calcanei between left and right differed in about one-fifth of the individuals. No significant interactions were found between morphological parameters and the presence of OA changes. Only age had a significant association. There was a high degree of symmetry in the subtalar joints facets. No significant associations were found between OA changes and morphological features, whereas other studies did. Further research is needed to explore this relationship in further detail. *Clin. Anat.*, 2019.



Relationship between bullet diameter and bullet defect diameter in human calvariums

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Existing literature on the relationship between bullet diameter and bullet defect diameter in the human calvarium is summarized and discussed. The hypothesis, derived from the literature, that bullet deformation influences bullet defect diameter was studied in a small controlled experiment. The mean defect size caused by non-

deforming projectiles was found to be smaller than the mean defect size caused by deforming projectiles of equal original mass and size. The p value of the difference between the two means, measured in two different ways, was found to be 0.002 for both in a Mann-Whitney U test and was significant if the confidence level is set at 5%.



Estimation of the postmortem interval based on the human decomposition process

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J Forensic Leg Med. 2019 Feb;61:122-127. doi: 10.1016/j.jflm.2018.12.004. Epub 2018 Dec 13.

Postmortem interval (PMI) estimations which are used as evidence in Dutch court are sometimes solely based on the experience of the forensic physician without a scientific background. The aim of this study was to investigate the degree of agreement between forensic physicians and their PMI estimations. Fifteen cases were selected from 1534 external postmortem investigations. Photographs of the human remains were presented to 89 forensic physicians in the Netherlands with the instruction to estimate the PMI based on their

experience, knowing the remains were found indoors and in which season. Data analysis was conducted by using an interclass correlation (ICC) and Spearman's rank correlation coefficient. This study shows a poor correlation (ICC=0.254) between the PMI estimations of the 89 forensic physicians. It is therefore not advised that PMI estimations based on experience be used as evidence in court.



Study on the three-dimensional orientation of the posterior facet of the subtalar joint using simulated weight-bearing CT

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J Orthop Res. 2019 Jan;37(1):197-204. doi: 10.1002/jor.24163. Epub 2018 Nov 29.

The purpose of this study was to describe the normal 3D orientation and shape of the subtalar calcaneal posterior facet. This is not adequately described in current literature. In a supine position both feet of 20 healthy subjects were imaged in a simulated weight-bearing CT. A cylinder and plane were fitted to the posterior facet of the surface model. The orientation of both shapes was expressed by two angles in (1) the CT-based coordinate system with the axis of the foot aligned with the sagittal axis and (2) a coordinate system

based on the geometric principal axes of the subject's calcaneus. The subtalar vertical angle was determined in the intersection in three different coronal planes of the cylinder. The cylinder's axis oriented from supero-postero-laterally to infero-antero-medially. The plane's normal directed supero-antero-medially in the CT-based coordinate system, and supero-antero-laterally in the other coordinate system. The subtalar vertical angle was significantly different ($p < 0.001$) between the three defined coronal planes and increased from anterior to posterior. The mean diameter of the fitted cylinder was 42.0 ± 7.7 mm and the root mean square error was 0.5 ± 0.1 mm. The posterior facet can be modelled as a segment of a cylinder with a supero-postero-lateral to infero-antero-medial orientation. The morphometry of the posterior facet in a healthy population serves as a reference in identifying abnormal subtalar joint morphology. More generally this study shows the need to include the full 3D morphology in assessing the orientation of the subtalar posterior facet.



Evaluation of neodymium isotope analysis of human dental enamel as a provenance indicator using $10^{13}\Omega$ amplifiers (TIMS)

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Human provenance studies employing isotopic analysis have become an essential tool in forensic and archaeological sciences, with multi-isotope approaches providing more specific location

estimates compared to single isotope studies. This study reports on the human provenancing capability of neodymium isotopes (Nd), a relatively conservative tracer in the environment. Neodymium isotope ratios have only recently been determined on human remains due to low concentrations in human dental enamel (ppb range), requiring thermal ionisation mass spectrometry (TIMS) using $10^{13} \Omega$ resistors. Dental elements (third molars) from 20 individuals born and raised in the Netherlands were analysed for Nd concentration ($n = 12$) and Nd isotope ratios ($n = 15$). The geological control on Nd isotope composition was examined using coupled Nd-Sr isotope analysis of the same third molar. Teeth from different geological environments were also analysed (Caribbean, Columbian, and Icelandic, $n = 5$). Neodymium elemental concentrations in dental elements ranged between 0.1 and 7.9 ppb (median 0.5 ppb). The Dutch $^{143}\text{Nd}/^{144}\text{Nd}$ ratios of the provinces of Limburg and Friesland were between 0.5118 and 0.5121, with Dutch $^{87}\text{Sr}/^{86}\text{Sr}$ ratios in agreement with the previously established local range (0.708–0.710). The current findings were compared to previously published results on Nd concentration and composition from Dutch individuals. The concentration of Nd and $^{143}\text{Nd}/^{144}\text{Nd}$ ratios were weakly correlated ($R = 0.47$, $n = 17$) in Dutch human dental enamel. The majority ($n = 25$, 83.3%) of individuals had Nd and Sr isotope values isotopically indistinguishable from the geological environment in which their third molars formed and mineralised. However, the Nd isotope ratios of the Icelandic individual and several Dutch individuals ($n = 4$) suggested that Nd in enamel is not solely influenced by geological environment. In order for neodymium isotopes to be quantitatively applied in forensic and archaeological settings further analyses of individuals from various geographical regions with well-defined dietary Nd isotope data are required.



Following laboratory protocols: Filling in the gaps using protocols.io

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Laboratory protocols lie at the heart of the study of the chemical composition of human teeth. The isotopes in human teeth are linked to the geographic location of an individual during tooth formation, enabling researchers to examine human mobility in modern and ancient societies. Without proper documentation of the samples, reagents used and all the steps taken to chemically extract the isotopes of interest, we cannot appropriately interpret the information that is locked within a tooth.

Despite the key role that laboratory protocols play in research, the publication of full protocols that can easily be re-used by researchers is rare. A summarised version of the protocol can usually be found in the method section of articles, but this short description leaves out the details that are required to reproduce experiments.

The online platform protocols.io (<https://www.protocols.io/>) provides the possibility to share the full protocol and administers a Digital Object Identifier (DOI) to the protocol which allows you to claim credit for the method development. Through protocols.io you can create and modify protocols in a structured, detailed and efficient way, saving time and preventing loss of expertise. The platform enables efficient collaboration as you can easily share your protocols with selected individuals or reviewers. The functionalities and services of protocols.io stimulate reproducible research protocols, allowing more reliable interpretations of, for example, the mobility patterns in human societies.



Activity, Diet, and Social Practice: Addressing Everyday Life in Human Skeletal Remains

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Day-to-day activities are important in the development of social identities, the establishment of social standing, and the communal understanding of societal rules. This perspective is broadly referred to as practice theory and relates to the power of an overarching social structure and the individual actors that exist within it. Practice theory has made an important contribution to anthropological and archaeological research as these fields are particularly interested in daily life and the importance of these actions.

This volume argues that practice theory can also be used in a bioarchaeological context through the examination of human skeletal remains and the archaeological context in which they were excavated. Bioarchaeology offers a unique perspective on these day-to-day experiences—skeletal tissue is constantly undergoing a process of change and, as a living biological system, it can adapt to external forces. Furthermore, bioarchaeological studies are multi-scalar and can examine individuals, groups, or entire populations.

Using osteological indicators of activity patterns (entheseal changes, osteoarthritis) and dietary isotopes (carbon, nitrogen) as examples, this book addresses patterns of everyday life in the ancient past. Physical activities and food consumption are actions that are carried out on a daily basis. While bioarchaeology does not have the ability to recreate specific day-to-day activities, we can assess broad trends in everyday life. The volume illustrates these points using examples from the Ancient Nile Valley. Through the examination of over 800 Egyptian and Nubian individuals from five different archaeological sites, the research addresses patterns of everyday life as they relate to social inequality, agency, and practice.

Beyond osteological indicators of activity and dietary patterns, this book also discusses additional methods that can be pursued to draw attention to daily life. Lastly, this book also highlights the applicability of and potential contribution that practice theory can make to this area of research.



Intraregional $^{87}\text{Sr}/^{86}\text{Sr}$ Variation in Nubia: New Insights from Third Cataract

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Previous research of $^{87}\text{Sr}/^{86}\text{Sr}$ variability in human dental tissue from the Nile Valley has shown diversity in bioavailable strontium across the landscape. Local ranges, determined from faunal sampling, have been suggested for several sites in Nubia, including Tombos (Third Cataract, Sudan). This study builds on previous research by testing human and faunal dental enamel samples from three sites in the Third Cataract region: Tombos, Hannek, and Abu Fatima. The addition of Abu Fatima and Hannek into the assessment of the Third Cataract region brings new temporal and socioeconomic juxtapositions that can shed light on migration and locality in Bronze Age Nubia.

Two faunal samples, a sheep from Abu Fatima and a horse from Tombos, had $^{87}\text{Sr}/^{86}\text{Sr}$ values that were consistent with the previously established local Third Cataract strontium range. Seven of the 29 human samples tested for Abu Fatima are suggestive of non-local origin and consistent with the Second Cataract region. One of the four individuals tested from Hannek may have migrated to the region from Egypt or the Second Cataract region. Lastly, four of the 30 samples from Tombos indicate possible non-local origin; the $^{87}\text{Sr}/^{86}\text{Sr}$ values may suggest Egypt, the Second Cataract, or the Fourth Cataract as places of origin. These findings suggest complex human migration networks were present in the Nile Valley during the Bronze Age. We support the continued examination of migration using strontium while acknowledging that further research needs to be done.

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Stressed to Death: An Analysis of Hair Cortisol and Non-Specific Stress Indicator

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Podium presentation, British Association for Biological Anthropology and Osteoarchaeology

Cortisol, a hormone associated with physical and psychosocial stress, has been examined both in modern as well as ancient human hair. In archaeological scenarios where lengths of hair are preserved, osteoarchaeologists are able to assess stress prior to an individual's death. This can provide important information about the lived experience of the individual in the weeks and months prior to death. Here, cortisol is assessed alongside skeletal indicators of non-specific stress, specifically cribra orbitalia, porotic hyperostosis, and bilateral periostitis. It is hypothesized that persistently elevated cortisol might weaken the immune response, thereby increasing the likelihood of non-specific stress indicators.

Hormone and skeletal analysis were conducted on ancient Nubian skeletal remains from the archaeological sites Abu Fatima (2500-1550 BCE) and Tombos (1550-656 BCE). These two contexts differ in socioeconomic standing, which may provide variation in cortisol levels. Preliminary analysis indicates that levels of cortisol prior to death are quite variable. There does not appear to be any connection between elevated rates of cortisol and the presence of non-specific stress indicators; however, sample size was small, owing to a limited number of archaeological hair specimens. When the osteological paradox is taken into account, another possible explanation is that some individuals may have died before non-specific stress lesions developed (i.e., frailty). Future research, incorporating a larger sample size in addition to forensic testing, is necessary.

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The four-minute approach revisited: accelerating MRI-based multi-factorial age estimation

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OBJECTIVES

This feasibility study aimed to investigate the reliability of multi-factorial age estimation based on MR data of the hand, wisdom teeth and the clavicles with reduced acquisition time.

METHODS

The raw MR data of 34 volunteers—acquired on a 3T system and using acquisition times (TA) of 3:46 min (hand), 5:29 min (clavicles) and 10:46 min (teeth)—were retrospectively undersampled applying the commercially available CAIPIRINHA technique. Automatic and radiological age estimation methods were applied to the original image data as well as undersampled data to investigate the reliability of age estimates with decreasing acquisition time. Reliability was investigated determining standard deviation (SSD) and mean (MSD) of signed differences, intra-class correlation (ICC) and by performing Bland-Altman analysis.

RESULTS

Automatic age estimation generally showed very high reliability (SSD < 0.90 years) even for very short acquisition times (SSD ≈ 0.20 years for a total TA of 4 min). Radiological age estimation provided highly reliable results for images of the hand (ICC ≥ 0.96) and the teeth (ICC ≥ 0.79) for short acquisition times (TA = 16 s for the hand, TA = 2:21 min for the teeth), imaging data of the clavicles allowed for moderate acceleration (TA = 1:25 min, ICC ≥ 0.71).

CONCLUSIONS

FAME 28

The results demonstrate that reliable multi-factorial age estimation based on MRI of the hand, wisdom teeth and the clavicles can be performed using images acquired with a total acquisition time of 4 min.

