



# Abstract book

Sunday, October 11<sup>th</sup>

## KEYNOTE TALKS – ARCHAEOLOGY & GENETICS

### **The Steppe Hypothesis and the Archaeology of Indo-European Migrations**

David W. Anthony and Dorcas Brown, Hartwick College, New York

Ancient DNA allows archaeologists to detect with much greater confidence prehistoric migrations, and to define the degree of population admixture associated with them. Migration and admixture analysis are relevant to detecting the spread of languages and understanding the mechanisms of language spread. A sequence of prehistoric migrations from the Russian-Ukrainian steppes were congruent in direction and sequence with the sequence of splits and geographic locations for the Indo-European daughter branches.

### **Indo-Europeans and Archaeology: some questions**

Jean-Paul Demoule, Institut Universitaire de France & Université de Paris I, Paris

Finding the movements of the original Indo-European people (“Urvolk”), requires two conditions: 1) observation of a migratory movement from a given region (the “Urheimat”), a movement then branching out to end up in the geographical locations of the various historically documented peoples speaking Indo-European languages; 2) proof that the populations living in the supposed region of origin had “something” Indo-European about them. While the recent results of aDNA analyses seem to show an East-West migratory movement in the 3rd millennium, it would be premature to consider that all the conditions have initially been met to identify this as the departure of the “Urvolk”. So much so that one can also question the starting point, which takes the existence of a unique language that can be entirely reconstructed (“Ursprache”) as the only model possible.





## **Ancient DNA suggests a major migration from the steppe as the source for Indo-European languages in Europe**

David Reich, *Harvard Medical School & Broad Institute, Boston*

This talk will present a genome-wide analysis showing that Europeans today largely derive from three highly differentiated ancestral populations: (1) West European Hunter-Gatherers, who derive from the Upper Paleolithic indigenous population of Europe and contributed ancestry to all Europeans but not to Near Easterners; (2) Ancient North Eurasians related to Upper Paleolithic Siberians, who contributed to both Europeans and Near Easterners; and (3) Early European Farmers, who were mainly of Near Eastern origin. However, our analysis of ancient genomes shows that the Ancient North Eurasian ancestry that is ubiquitous in Europe today was rare or absent at the time of the arrival of the Early European Farmers. To understand when the Ancient North Eurasian ancestry arrived, we generated genome-wide data from 69 Europeans who lived between 8,000-3,000 years ago by enriching ancient DNA libraries for a target set of almost four hundred thousand polymorphisms. This strategy decreases the sequencing required for genome-wide ancient DNA analysis by about 250-fold, allowing us to produce a dataset of genome-wide ancient DNA that is more than double the size of the entire preceding literature. We show that the populations of western and far eastern Europe followed opposite trajectories between 8,000- 5,000 years ago. At the beginning of the Neolithic period in Europe, ~8,000-7,000 years ago, closely related groups of early farmers appeared in Germany, Hungary, and Spain, different from indigenous hunter-gatherers, whereas Russia was inhabited by a distinctive population of hunter-gatherers with high affinity to a ~24,000 year old Siberian. By ~6,000-5,000 years ago, a resurgence of hunter-gatherer ancestry had occurred throughout much of Europe, but in Russia, the Yamnaya steppe herders of this time were descended not only from the preceding eastern European hunter-gatherers, but also from a population of Near Eastern ancestry. Western and Eastern Europe came into contact ~4,500 years ago, as the Late Neolithic Corded Ware people from Germany traced ~3/4 of their ancestry to the Yamnaya, documenting a massive migration into the heartland of Europe from its eastern periphery. This steppe ancestry persisted in all sampled central Europeans until at least ~3,000 years ago, and comprises about half the ancestry of today's northern Europeans. These results support the theory of a steppe origin of at least some of the Indo-European languages of Europe, and show the power of genome-wide ancient DNA studies to document human migrations.





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## Population genomics of Bronze Age Eurasia

Morten E. Allentoft, Centre for GeoGenetics, Natural History Museum, University of Copenhagen

The Bronze Age of Eurasia (around 3000–1000 BC) was a period of major cultural changes. However, there is debate about whether these changes resulted from the circulation of ideas or from human migrations, potentially also facilitating the spread of languages and certain phenotypic traits. We investigated this by using new, improved methods to sequence low-coverage genomes from 101 ancient humans from across Eurasia. We show that the Bronze Age was a highly dynamic period involving large-scale population migrations and replacements, responsible for shaping major parts of present-day demographic structure in both Europe and Asia.

Our findings are consistent with the hypothesized spread of Indo-European languages during the Early Bronze Age. We also demonstrate that light skin pigmentation in Europeans was already present at high frequency in the Bronze Age, but not lactose tolerance, indicating a more recent onset of positive selection on lactose tolerance than previously thought.

## On the pleasures and perils of being a (Bayesian) phylolinguist

Russell Gray, Max Planck Institute for the Science of Human History, Jena

In this talk I will outline the way in which Bayesian language phylogenies can be constructed from lexical data. I will focus on ways in which the inferences can be validated and the conditions under which the trees reliably track population histories. Simulations and Austronesian and Indo-European examples will be used to illustrate these points. I will argue that with careful attention to data quality, and appropriate model selection, Bayesian phylogeographic methods provide a powerful way of integrating inferences from linguistics, genetics and archaeology.





## Asking the Right ‘Indo-European Question’: What Language Data Do and Do Not Say About the Population Prehistory of Eurasia

Paul Heggarty, Max Planck Institute for the Science of Human History, Jena

The ‘Indo-European question’ first gave rise to the science of linguistics in 1786, and thereby contributed to the early development of other disciplines too, not least archaeology and (evolutionary) biology. For over two centuries, the question itself remained unresolved — but modern archaeogenetics now suddenly holds out the prospect of a definitive answer at last.

Ancient DNA data indicate a major role for populations from the Steppe in reshaping the population prehistory of significant parts of Europe, at least. Superficially, that may seem to support the ‘Steppe hypothesis’ of Indo-European origins, as recent genetics papers have duly suggested.

But the new data do not yet resolve the *real* Indo-European question, whose scope goes much wider and deeper. Above all, this talk will clarify what that question really is. Was the Steppe the *primary* source of *all* Indo-European, everywhere? Or was it just an intermediate source, of a secondary spread, that accounts only for *some* branches of Indo-European (and of Uralic), in parts of Europe? If the latter, then the family as a whole would still go back to a primary expansion with agriculture, as per the leading rival hypothesis. This talk will set out in detail this ‘A<sub>2</sub>’ version of the farming hypothesis.

Also, for the purposes of geneticists and archaeologists, I will clarify what the linguistics both *does* and does *not* definitively say. I will assess the nature of the linguistic ‘evidence’ — and what within it may seem superficially convincing, but is in fact subjective interpretation. And I will pinpoint the outstanding research questions that linguistics raises, and aDNA may be able to answer.

On each level of the why, when and where of Indo-European origins, this talk will explore how the main linguistic analyses correspond with the latest genetic and archaeological data, for or against each of the two leading hypotheses.

See also:

*Ancient DNA and the Indo-European Question*, at <http://dlc.hypotheses.org/807>.





# Abstract book

Monday, October 12<sup>th</sup>

## LINGUISTICS, ARCHAEOLOGY & GENETICS

### **The Neolithic and the Indo-European: Some Issues**

James P. Mallory, Queen's University, Belfast

My paper will briefly examine three issues concerning attempts to associate the expansion of the Indo-Europeans with the beginning of the Neolithic. These will comprise: 1) the ramification of applying a Neolithic time depth to the formation of the Indo-European branches; 2) the quest to recover the language of Europe's first farmers; and 3) the association of the earliest Neolithic centres in Southwest Asia with the Indo-European language family.

### **From Yamnaya to Bell Beakers: Mechanisms of Transmission in an Interconnected Europe, 3500–2000 BC**

Volker Heyd, Universtiy Bristol, Bistol and University of Helsinki, Helsinki

Yamnaya Peoples in the East and Bell Beakers Users in the West are rightly seen as the apogees in a long-term process of individualisation, gender differentiation, warrior display and internationalisation/unification that fundamentally change the face of the European Continent from the mid fourth and throughout the third millennium BC. We can only approach the reasons why prehistoric peoples and cultures from regions across Europe, which were no more than marginally in touch before, join in the same emblematic pottery, new drinking habits, similar burial customs, anthropomorphic stelae, ostentatious display of weapons and other paraphernalia, and thus common values. However rather than seeing this development as an internal European progress I want to point to the importance of the Pontic-Caspian steppes, and a 2000 years lasting interaction scenario of infiltrating Suvorovo-Novodanilovka, Nizhnemikhailovka-Kvityana and Yamnaya peoples and populations with their more sedentary contemporaries in southeast Europe, the Carpathian basin and northeast of the Carpathian bow. A crucial part of this interaction –besides migrations and the exchange of genes and goods as recently highlighted in several publications not only in Nature and Science– is the forwarding of innovations in the sphere of subsistence economy. We see this archaeologically in a further importance of animal husbandry, with larger herds, specialised breeding and new forms of herd-





ing management in particular for cattle. This obviously sets in motion a substantial shift in general mobility patterns and of communication networks.

It is easily conceivable that this interaction must also have had a profound impact on the whole settlement organisation and people's way-of-life, in consequence probably fundamentally affecting the basics of societies and thus challenging the whole system of ideas, imaginations, morale, symbols and terms – a new world-view and ultimately the base for a new language.

### **Health, population history and language: from the Neolithic to the Bronze Age in Europe**

Kristian Kristiansen, Göteborgs Universitet, Göteborg

In this presentation I provide a brief survey of population histories from the Neolithic until the beginning of the Bronze Age. It is argued that there existed a close connection between demography, economy/diet and health, which goes some way to explain population changes, and following from that also language change. Language expansion and/or contraction is considered a secondary variable to these more basic historical processes.





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## **The East European Steppe in the Discussion about the Expansion of the Indo-European Language**

Elke Kaiser, Institut für Prähistorische Archäologie, Freie Universität Berlin, Berlin

Ever since the late 19th century archaeologists and linguists, using methods specific to their fields, have attempted to identify the region in which the proto-Indo-European language was spoken.

However, today there is still no consensus in the many conclusions; several areas and time spans have been put forward as the “Indo-European homeland” and are yet a subject of debate.

In the past year several scientific papers were published concerning specific features that could be determined, by using population genetic methods, in the skeletal material that had been excavated and analysed from grave mounds dated to the 1<sup>st</sup> half of the 3<sup>rd</sup> millennium BCE (Yamnaya culture) in the east European steppe area.

The same features were then identified in graves of the Corded Ware culture in Central Germany, moreover in surprisingly high amounts. This population genetic shift has now been associated with processes that have been repeatedly postulated with regard to the spread of the proto-Indo-European language: namely, large population groups migrated from the east European steppe zone into Central Germany, a movement that led to marked demographic as well as cultural changes. Have we come closer to solving the puzzle about the spread of the proto-Indo-European language?

In order to better judge this issue, we should be aware of the different levels at which the various conclusions have been made. Therefore, in my contribution I will focus on the Yamnaya culture which in general terms is archaeologically described by a specific grave construction and a specific burial custom. Following this I will present a few sceptical considerations concerning the possibility of correlating archaeological evidence with the linguistic construct of the proto-Indo-European language.





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## In search for initial Indo-European gene pool from genome-wide data on IE populations as compared with their non-IE neighbors

Oleg Balanovsky, Vavilow Institute of General Genetics, Russian Academy of Sciences, Moscow

Most researchers agree that there was a proto-Indo-European population which descendants spread the derived languages over half of Eurasia. During this migration, the IE-carriers have had to assimilate the local substratum populations which might predominate in numbers, and therefore “dissolve” the initial gene pool of the proto-IE population. Then, most of present day IE populations should carry a genetic legacy of proto-IE population though it might form a small fraction of their gene pools. We tried to identify this proto-IE genetic component by genome-wide genotyping in 9 population pairs. Each pair consisted of IE population and its non-IE neighbor, for example IE French and Spanish *vs* non-IE Basque, IE Tajiks *vs* non-IE Uzbeks, and 7 other pairs. We searched for genetic markers which are shared by IE populations in contrast with their “paired” non-IE populations.

We expected this proto-IE genetic component to be small, but found it is nearby zero. For example, if one looks for a markers present in all IE but absent in all paired populations (or for markers two times more frequent in the IE population than in the corresponding non-IE paired population), no one out of 128,000 studied markers fit these criteria. When criteria are released, the common IE genetic component could be formally identified but number of markers does not exceed the one expected from random distribution. The data mining is still in progress but it is already clear that most (if not all) presentday IE populations does not carry genetic legacy of proto-IE population. Hence, this proto-IE gene pool has been completely replaced by gene pools of assimilated populations. To explain this finding, the simple predominance of assimilated substratum is not enough. Indeed, even in case of language change through elite dominance, the dominated group is expected to make some genetic contribution, which is detectable by genome-wide scans (as was recently shown for Turkic speakers). Thus, we should conclude that IE languages spread by *chain* of elite dominance events: the population acquired IE language with small portion of proto-IE gene pool then in turn transmitted the language to the next population but made only minor genetic contribution in it. After some such chain links the proto-IE gene pool is expected to be completely dissolved which we indeed see in our data.

This conclusion of the repeated language change events as a primary model for IE spread is supported by the historically recent and well documented example of Slavic languages. We studied all extant Balto-Slavic speaking populations by both, genome-wide and haploid genetic systems. The signals of substratum populations as-



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simulated by expanding Slavs were strong but there were virtually no signal of initial Slavic gene pool.

Though pan-IE genetic markers do not exist, in the restricted geographic scale the markers associated with particular phases of the IE expansion could be identified. The best example is the branch L657 of the Y-chromosomal haplogroup R1a: the branch originated in Eurasian steppe but is frequent only in the Indian IE populations. Considering this branch is 3,5-5 ky old, one may believe it as a marker of Indo-Aryan migration into South Asia. Another example is Y-chromosomal haplogroup G1 which might mark the previous phase, namely migration of (proto-)Indo-Iranians from South-West Asia into steppe areas.

Taken together, these results made me skeptical about reconstructing earlier events of IE expansion from genetic data on (present day) populations, when the later events sometimes could (Indo-Aryans) and sometimes could not (Slavs) be traced in the contemporary gene pools. Note that increasing the *number* of genetic markers often does not help much, while increasing their *information value* – like deep analysis of Y-chromosomal haplogroups or autosomal haplotypes – might be productive way for tracing ancient population events.

## Post Glacial Expansion from the Levant

Pierre Zalloua, Lebanese American University, Beirut





**Uniparental markers in the debate on Indo-European origins**

Toomas Kivisild, University of Cambridge, Cambridge

Indo-European is the most widely spoken language family in Eurasia. Multiple lines of evidence, including linguistic, archaeological and genetic, have been used to argue for a recent spread of this language family by people originating either from Anatolia or from the East European Steppe belt; or possibly from both sources albeit at different times. Significant changes in the genetic landscape of Europe have been inferred from analyses based on living populations as well as from ancient DNA of skeletal remains. This presentation will focus on the patterns that have emerged from the analyses of uniparental markers, mtDNA and Y chromosome, in the context of autosomal evidence.



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Monday, October 12<sup>th</sup>, afternoon

## GENETICS & LINGUISTICS

### **Indo-European Language Origins Re-Revisited**

Remco Bouckaert, University of Auckland, Auckland

The origin of Indo-European language has been a topic of hot debate for the last few centuries. The main contenders are the steppen in what is currently Ukraine, and part of Turkey, giving rise to the Steppen and Anatolian hypotheses. After introducing a number of methodological innovations to linguistics borrowed from phylogenetics, in 2012, we published a statistical analysis (Bouckaert et al., *Science*) that showed overwhelming support for the Anatolian hypothesis. Chang et al. (*Language*, 2015) rebutted with another set of methodological innovations and their statistical analysis showed support for the Steppen hypothesis. In this talk, we examine the assumptions underlying these analyses and conclude with a new analysis that allows us to test these assumptions. To find out which hypothesis is supported using the latest methods and with the newest data, please come to the talk.



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## Close genetic relationship of Neolithic Anatolians to early European farmers

Iosif Lazaridis<sup>1,2</sup>, Songül Alpaslan<sup>3</sup>, Daniel Fernandes<sup>4</sup>, Mario Nowak<sup>4</sup>, Kendra Sirak<sup>4</sup>, Nadin Rohland<sup>1,2</sup>, Swapan Mallick<sup>1,2,5</sup>, Kristin Stewardson<sup>1,5</sup>, Fokke Gerritsen<sup>6</sup>, Nick Patterson<sup>2</sup>, Ron Pinhasi<sup>4,\*</sup>, David Reich<sup>1,2,5,\*</sup>

<sup>1</sup>Department of Genetics, Harvard Medical School, Boston, MA USA

<sup>2</sup>Broad Institute of MIT and Harvard, Cambridge, MA USA

<sup>3</sup>Independent physical anthropologist, Netherlands

<sup>4</sup>Conway Institute of Biomolecular and Biomedical Research, University College Dublin, Dublin, Ireland

<sup>5</sup>Howard Hughes Medical Institute, Harvard Medical School, Boston, MA USA

<sup>6</sup>Netherlands Institute in Turkey, Istiklal Caddesi, Nur-i Ziya Sokak 5, Beyoğlu, Istanbul, Turkey

We study 1.2 million genome-wide single nucleotide polymorphisms on a sample of 26 Neolithic individuals (~6,300 years BCE) from northwestern Anatolia. Our analysis reveals a homogeneous population that was genetically similar to early farmers from Europe ( $F_{ST}=0.004\pm 0.0003$  and frequency of 60% of Y-chromosome haplogroup G2a). We model Early Neolithic farmers from central Europe and Iberia as a genetic mixture of ~90% Anatolians and ~10% European hunter-gatherers, suggesting little influence by Mesolithic Europeans prior to the dispersal of European farmers into the interior of the continent. Neolithic Anatolians differ from all present-day populations of western Asia, suggesting genetic changes have occurred in parts of this region since the Neolithic period. We suggest that the language spoken by the homogeneous Anatolian-European Neolithic farmers is unlikely to have been the same as that spoken by the Yamnaya steppe pastoralists whose ancestry was derived from eastern Europe and a different population from the Caucasus/Near East [Haak et al. 2015], and discuss implications for alternative models of Indo-European dispersals.

## Some things I read about early farmers

Mark Thomas, University College, London



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## **Iron Age and Anglo-Saxon genomes from East England reveal British migration history**

Stephan Schiffels, Max Planck Institute for the Science of Human History, Jena

British population history is shaped by a series of immigration periods and associated changes in population structure. It is an open question to what extent these changes affect the genetic composition of the current British population. Here we present whole genome sequences generated from 10 individuals, found in archaeological excavations in Hinxton, Oakington and Linton, close to Cambridge, and ranging from 2,300 years before present (Iron Age) until 1,200 years before present (Anglo-Saxon period). We use modern genetic samples from the 1000 Genomes Project and additional external data from Britain, the Netherlands and Denmark to characterize the relationship of these ancient samples with contemporary British and other European populations. By analyzing the distribution of shared rare variants across ancient and modern individuals, we find that samples from the Anglo-Saxon period are relatively more closely related to central northern Europe, while earlier samples and contemporary British samples are relatively more closely related to Southern European populations. To quantify this series of relationships further, we developed a new method, rarecoal, that fits a demographic model parameterized by split times, population sizes and migration rates to the distribution of shared rare variants across a large number of modern and ancient individuals. We use rarecoal to estimate the history of European population structure within the last 10,000 years and to map our ancient samples onto the European population tree. Our approach provides a unique picture of population history in Europe, and in particular helps characterizing the complex genetic impact of Anglo-Saxon immigrations into Britain.

## **The Genetic History and Structure of Britain**

Nick Patterson, Broad Institute, Boston and David Reich, Harvard Medical School and Broad Institute, Boston

The recently published paper on the genetic structure of Britain (Leslie et al. Nature 2015) has shown subtle genetic variation correlating with geography.

Here we reexamine the evidence in the light of our understanding of the genetics of Ancient Europe and comment on some implications for how Indo-Europeans spread into Europe.

## **Demigod**

Adam Powell, Max Planck Institute for the Science of Human History, Jena





Tuesday, October 13<sup>th</sup>

### ARCHAEOLOGY & LINGUISTICS

#### **Archaeological indications for Mid-Holocene migrations and interactions between immigrant and local populations in Temperate Western Eurasia**

Detlef Gronenborn, Römisch-Germanisches Zentralmuseum, Leibniz Research Institute for Archaeology

The period between the terminal eighth millennium and the onset of the fifth millennium cal BC in Western Temperate Eurasia is marked by numerous archaeological indicators for long-distance movements of technological innovations in lithic technology and pottery.

For the period when hunting and gathering predominates in Temperate Europe (Late Early Mesolithic/Late Mesolithic), these changes in material culture may be interpreted as indicators for actual migration of people if not populations.

Another data set indicates contact and exchange between immigrant farming populations (LBK), pastoral groups (La Hoguette), and hunter-gatherers. Evidence for such contact and interaction scenarios increase towards the western sphere of the LBK oikumene and may indicate an increase in local groups within immigrant farming populations. Several well-researched sites do show chronologically highly resolved archaeological indicators of the dynamics of co-habitation between immigrant farmers and local hunter-gatherers.

The relevance of these archaeological data for genetics and linguistics is discussed.





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**Pre-Indo-European speech carrying a Neolithic signature emanating from the Aegean**  
Guus Kroonen, Institute for Nordic Studies and Linguistics, Copenhagen University,  
Copenhagen

When different Indo-European speaking groups settled Europe, they did not arrive in *terra nullius*. Both from the perspective of the Anatolian hypothesis<sup>1,2,3</sup> and the Steppe hypothesis,<sup>4,5,6</sup> the carriers of Indo-European speech likely encountered existing populations that spoke dissimilar, unrelated languages. Relatively little is known about the Pre-Indo-European linguistic landscape of Europe, as the Indo-Europeanization of the continent caused a largely unrecorded, massive linguistic extinction event. However, when the different Indo-European groups entered Europe, they incorporated lexical material from Europe's original languages into their own vocabularies.<sup>7</sup> By integrating these "natural samples" of Pre-Indo-European speech, the original European linguistic and cultural landscape can partly be reconstructed and matched against the Anatolia and the Steppe hypotheses. My results reveal that Pre-Indo-European speech contains a clear Neolithic signature emanating from the Aegean,<sup>8</sup> and thus patterns with the prehistoric migration of Europe's first farming populations.<sup>9,10,11</sup> These results also imply that Indo-European speech came to Europe following a later migration wave, and therefore favor the Steppe Hypothesis as a likely scenario for the spread of the Proto-Indo-Europeans.<sup>12</sup>

<sup>1</sup> Renfrew, C. 1987. *Archaeology and Language: The Puzzle of Indo-European Origins*. Cambridge.

<sup>2</sup> Gray, R.D. & Q.D. Atkinson. 2003. Language-tree Divergence Times Support the Anatolian Theory of Indo-European Origin. *Nature* 426 (6965): 435-439.

<sup>3</sup> Bouckaert, R. et al. 2012. Report: Mapping the Origins and Expansion of the Indo-European Language Family. *Science* 337 (6097): 957-960.

<sup>4</sup> Gimbutas, M. 1956. *The prehistory of eastern Europe* (I : Mesolithic, Neolithic and Copper Age cultures in Russia and the Baltic area). Cambridge, Mass.

<sup>5</sup> Mallory, J.P. 1989. *In search of the Indo-Europeans, language, archaeology and myth*, London.

<sup>6</sup> Anthony, D.W., 2007, *The Horse, the Wheel, and Language: How Bronze-Age Riders from the Eurasian Steppes Shaped the Modern World*. Princeton, NJ [etc.].

<sup>7</sup> Schrijver, P. 1997. Animal, vegetable and mineral: some Western European substratum words. In: A.M. Lubotsky (ed.), *Sound Law and Analogy*, 293-316. Amsterdam / Atlanta.

<sup>8</sup> Kroonen, G. 2012. On the etymology of Greek ἄγλις and γέλις 'garlic': an Akkadian loanword in Pre-Greek. *Journal of Indo-European Studies* 40, no. 3/4, 289-299.

<sup>9</sup> Malmström, H. et al. 2009. Ancient DNA reveals lack of continuity between neolithic hunter-gatherers and contemporary Scandinavians. *Current Biology* 19 (20), 1758-62.

<sup>10</sup> Haak W. et al., 2010. Ancient DNA from European Early Neolithic Farmers Reveals Their Near Eastern Affinities. *Public Library of Science Biology* 8(11): e1000536. doi:10.1371/journal.pbio.1000536.

<sup>11</sup> Skoglund, P. et al. 2012. Origins and Genetic Legacy of Neolithic Farmers and Hunter-Gatherers in Europe. *Science* 336 (6080), pp. 466-469.

<sup>12</sup> Haak, W. et al., 2015. Massive migration from the steppe was a source for Indo-European languages in Europe *Nature* 522, 207–211 (11 June 2015).





**Indo-European in Atlantic Europe at the proto-historic horizon and before: some recent work and its possible implications**

John T. Koch, University of Wales, Centre for Advanced Welsh and Celtic Studies, Cardiff

The aim is to introduce briefly a few topics in current research of potential relevance for the workshop's theme. These include the following:

- the Celticity of the South-western ('Tartessian') inscriptions and their background in the SW Iberian Late Bronze Age 'warrior' stelae, Middle Bronze Age Alentejo stelae, and Copper Age anthropomorphic stelae of the north Pontic region;
- the common Palaeohispanic name *Arquius* 'bowman' and the regional survival of archery from the Beaker Copper Age;
- the recurring idea (= emerging consensus?) of Celtic as Indo-European on an Iberian and/or Aquitanian/Palaeo-Basque substrate;
- Phoenicians (together with literacy and the historical record) reaching the West by 900 BC, catalysing the break-up of the Atlantic Bronze Age and Proto-Celtic.





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## Archaeological temporal constraints make phylogenetic methods to support the steppe homeland theory of Indo-European

Igor Yanovich, Armin Buch, Johannes Dellert, Marisa Koellner, Fabrício Marcel Ferraz Gerardi, Roland Mühlenbernd, Johannes Wahle and Gerhard Jäger, Institute for Linguistics, University of Tuebingen

Until recently all authors who attempted a computational-phylogenetic study of Indo-European obtained strong support for the Anatolian theory, stemming from the temporal estimates for the root of the inferred Indo-European language-family tree. The first split was estimated at 6700 BC [Gray and Atkinson, 2003], ca. 6000-5500 BC [Nicholls and Gray, 2008], 6400 BC [Ryder and Nicholls, 2011], ca. 5900-5800 BC [Bouckaert et al., 2012] (median values), all of those much better compatible with the Anatolian theory assigning the start of Indo-European dispersal to the 7th millennium BC, as opposed to the late 5th millennium under the steppe theory. This would seem to constitute a very strong argument for the Anatolian theory.

Recently those results were challenged by [Chang et al., 2015], who replicated [Bouckaert et al., 2012]’s study with the following change: Dead Indo-European languages that are independently known to be ancestors of living languages (e.g., Latin to Romance languages) are placed as internal nodes from which the descendants speciate. Chang et al. estimate the first Indo-European split at ca. 4000 BC. This is in agreement with the steppe theory. However, Chang et al. crucially exclude six languages from the original dataset, among them Anatolian languages Luvian and Lycian. Without those, the Anatolian-family clade only contains Hittite. This exclusion by itself shaves off a thousand years from the estimate for the root. Thus though [Chang et al., 2015]’s results do indicate that the support for the Anatolian theory from phylogenetics is not unequivocal, they do not demonstrate unambiguous support for the steppe theory either.

We report results from a different modification of the analyses by [Gray and Atkinson, 2003] and [Bouckaert et al., 2012]. Existing phylogenetic analyses of Indo-European rely on historical sources for formulating calibration constraints. Not constraining the internal nodes of the tree beyond the historical period by itself may introduce a significant source of bias. To test for that, we formulated two non-controversial prehistoric calibration constraints for Indo-European. Our two new constraints are accepted by the proponents of both the Anatolian and the steppe theories. By adding them to phylogenetic analyses, we thus do not implicitly tilt the balance towards either theory:

- Indo-Iranian split. In recent years, a near-consensus emerged in archaeology identifying the Andronovo culture of northern Kazakhstan steppes with Indo-Iranian speakers. For concreteness sake, we assume that Indic speakers moved south around 1900–1800 BC. Old Indic would then have further developed in Central Asia





through 1800–1600 BC. We represent this in a constraint for the Indic-Iranian split at 1900–1600 BC.

- Tocharian split. The steppe and Anatolian theories identify the Tocharian split with different events, but fortunately, their timing almost coincides. We posit a single Tocharian-split constraint at 3400-3100 BC, common to both theories.

We replicated [Gray and Atkinson, 2003] on a larger version of the dataset they used, namely IELex as used by [Bouckaert et al., 2012]. With our two new constraints, that estimate goes down to 4660 BC, in satisfactory accordance with the steppe theory, and very far from the Anatolian theory's predictions.

Our conclusion is two-fold. Given the current data, the steppe theory now appears more likely from the phylogenetic-inference perspective. However, further testing indicated that the time estimate of our model does not show much more robustness against the addition of further constraints than those of the predecessor models. The main objective of this study is therefore to initiate a debate on the status of time constraints in Bayesian phylogenetic inference.

### **Reconstructing prehistoric language spreads on the Eurasian steppe**

Johanna Nichols, Department of Slavic Languages and Literatures, University of Berkeley, Berkeley

While genetics and archaeology can draw data bearing on steppe expansions directly from steppe locations, this is not possible in linguistics, where every major spread absorbs the previous languages, making the steppe itself linguistically uninformative. Linguistics must instead rely on data from the steppe periphery. This report shows how data from the peripheries using historical comparison and population typology can help to reconstruct, for every major language spread on the steppe beginning with the early Neolithic, the origin of the spread; its trajectory; the relative (and sometimes absolute) chronology of the beginning and end of the spread; aspects





# Abstract book

of the sociolinguistics triggering the spread; and the linguistic impact of the far periphery on the spreading language. I give an overview of the methods and the main findings, including what evidence exists for pre-Neolithic spreads.

## **Comparative linguistics as a window to prehistory: what does it tell**

Martin Joachim Kuemmel,, Friedrich Schiller University, Jena

With the foundation of Comparative and Historical Linguistics about 200 years ago a new method was introduced into research about human history, and it was soon celebrated as a really new and scientific approach that could achieve reliable results in cases where other data were not sufficiently available, especially in the absence of historical (written) records and of well-understood archeological finds. However, the connection between comparative linguistics and (pre)historical research became much weaker later, partly due to misuses of just this kind of interdisciplinary approaches. In the end of the past century the interest in this connection increased again, and in recent years this has become even stronger, as the old connection to biology was reestablished - now at the same place as where it started - here in Jena. The aim of my presentation is to ask about the current contribution of the comparative method, the "gold standard" for "genetic" linguistic research, to questions of prehistory: What does it tell us, and what can it not tell us? And what is the quality of its evidence?

## **Indo-European and Altaic landscapes: reconstructed lexics**

Anna Dybo, Russian State University for the Humanities, Moscow

It is the first part of a larger work that represents an attempt to systematize our ideas on the natural environment and material culture of the Proto-Indo-Europeans. It is based on a more or less complete selection of reconstructed words from the appropriate semantic areas and on their comparison with a similar selection performed for a protolanguage of similar time depth, whose speakers evidently inhabited a territory that was not in contact with the Proto-Indo-European one — Proto-Altaic. In this part, only the words that belong to the semantic field of landscape terms are analyzed. The main conclusion is that the hypothesis of a steppe environment is more applicable for the Proto-Altaic population, whereas for Proto-Indo-Europeans a mountainous region seems more appropriate.





**Old stories, new failures? Genetics, migration and mobility during third millennium European archaeology**

Marc Vander Linden, Institute of Archaeology, University College London, London

Over the past few years, several publications based upon the application of scientific techniques (e.g. Sr isotopes, aDNA) have revived the interest for migration, mobility and demography during the 3<sup>rd</sup> mill. cal. BC in Europe. These contributions should be welcomed by archaeologists for forcing us to revisit our data from another perspective, as well as for bringing back the spotlight on a period sometimes forgotten between the Neolithic and the Bronze Age. Yet, many archaeologists have expressed either doubt or a relative lack of interest for these papers, largely because some of their results worryingly echo interpretations which have been lurking throughout the history of the discipline for more than a century (e.g. steppe influences, Iberian homeland,...)

This paper will briefly discuss the scientific and archaeological evidence for the 3<sup>rd</sup> mill. cal. BC, with a focus on the Corded Ware and Bell Beaker complexes. This review aims at showing the complexity inherent to this period, which cannot be read as a mere suite of migratory events which would have distributed artefacts, genes and languages across Europe. On the contrary, distinct facets of the archaeological record, genetics and linguistics all seem to tell different stories. Rather than proposing a mere cautionary tale rejecting cross-disciplinary dialogue, this paper will explore alternative ways aiming at retuning together these apparently discordant voices.

