

Scientific Report

for the Exploratory ESF Workshop

“Archaeology and Genetics: towards (integrated) Archaeogenetics”

Trans-Committee-LESC / SCH:

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Title: *Archaeology and Genetics: towards (integrated) Archaeogenetics*

Dates: Wednesday 02 June 2004 – Saturday 05 June 2004

Location: Centre International de Séjours,
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1. Executive summary

The aim of the Workshop was to bring a limited number of archaeologists and geneticists together in order to openly discuss the achievements and limitations of current methods to unravel the history of human populations. The organisation of the Workshop was intended to promote discussion and critical appraisal of the two fields involved (archaeology and population genetics), and to encourage future collaborations.

The general structure of the Workshop was as follows:

1. An introductory session organized on the day of arrival allowed participants to make a short presentation of their research interests and institutes. This clearly facilitated contact between invitees from the first day on.
2. During the first two days, a series of review talks on relevant archaeological and genetic theories, methods and case-studies accessible to both archaeologists and geneticists were organized, followed by extended discussion periods. Most of the first day was devoted to general methodological and data problems. The end of the first day and the whole second day were devoted to case studies.
3. The last morning was devoted to short talks on recent developments in both archaeology and genetics and perspectives for the future.

Details of this structure, including talk titles and summaries can be found in section two ("*Scientific content of the event*") and section 4 ("*Final programme*"). Below is a summary of the Workshop

The first morning was devoted to genetics. The first two talks aimed at presenting reviews of the current knowledge on the two most used genetic systems, namely, the Y chromosome (Mark Thomas) and the mitochondrial DNA (Lluis Quintana-Murci). These two talks were done in order to help archaeologists to become familiar with the terminology that would be used throughout the meeting. The different types of genetic markers were presented together with a summary of the current knowledge on the distribution of mutations in the world population. The following talk was presented by Rosalind Harding. She presented in simple terms the necessary background to understand population genetics modelling. In particular, R. Harding insisted in showing that it is not trivial to link ancestral *population* demography to present-day *genetic* patterns. This issue was to become the centre of many discussions throughout the Workshop and it proved very important to have addressed it at this early stage. The following talk was given by Toomas Kivisild. During this talk T. Kivisild presented other methods used to analyse population genetics data. In particular he explained the principles behind "median-network" methods. These methods use the structure of mitochondrial or Y chromosome DNA networks to infer demographic events such as population bottlenecks or migration events. After T. Kivisild and R. Harding's talks, most participants were able to realise that the disagreement among geneticists present at the Workshop was on whether they agreed with the first or second talk.

The first session of the afternoon was devoted to archaeology, with two review talks. The first was given by Stephen Shennan who discussed the difficulties in defining prehistoric populations using archaeological artefacts. In this talk S. Shennan discussed also the possibilities of using population genetics theory in the framework of archaeological artefacts. This was the first talk trying to explicitly link archaeological and population genetics models, to improve the understanding of the transmission of cultural traits such as pottery decorative attributes, which are sometimes used to define "populations". The following talk by Evzen Neustupny was a review of available data on the demography of prehistoric populations. Unless better estimates of past demography are available, it will be difficult to develop specific models to analyse the genetic data of present-day populations. E. Neustupny showed that the current data are unfortunately not very precise.

The following session, was the first of a series of talks aimed at providing reviews on particular case-studies, which were to continue on Friday. For all these case studies, both a geneticist and a non-geneticist (archaeologist, anthropologist, etc.) were asked to provide a talk. During this first session, James Steele provided an account of the controversies related to the colonization of the Americas from an archaeological point of view, whereas Peter Forster gave a summary of the genetic data available on Amerindian populations, with some possible interpretations. Both talks provided material for discussion notably regarding the possible early colonization of the Americas.

Case studies continued on the following day. Marta Lahr and Laurent Excoffier provided reviews on the origins of modern humans from a biological anthropologist and a geneticist point of view. Their talks were followed by a talk by Francesco d'Errico and Marian Vanhaeren on the origin and emergence of modern human symbolic behaviour. This set of three talks covered a lot of material and provided an occasion to discuss the origins of our species, the morphological differences between modern humans and many of our possible ancestors, the possibility that Neandertals had similar cognitive and symbolic behaviour to those of our direct ancestors.

The three following talks concentrated on the origins of Europeans from an archaeological (Colin Renfrew), a genetic (Guido Barbujani) and a bio-anthropological (Eric Crubézy and Jaroslav Bruzek) viewpoint. This issue is highly controversial and relates to the estimation of the relative genetic and demographic contributions of the early hunter-gatherers and the first farmers who entered Europe during the Neolithic transition. Many discussions took place after the talks. In particular controversies exist regarding the best methodologies to analyse genetic data to answer questions related to this issue.

The second day finished with a talk by Luca Cavalli-Sforza, who can be considered as one of the founding fathers of Archaeogenetics, years before the term was coined by C. Renfrew. He reviewed first the history of his involvement in the genetic study of human populations. He then presented some of his most recent results on the use of mutations geographic distribution to determine the location of their origin.

The final morning was devoted to recent methodological developments such as the use of strontium isotopes to detect prehistoric movements (Alexander Bentley) or the use of ancient DNA to infer past demography (Ian Barnes). Mike Weale showed how recent statistical modelling methodology can be used to test hypotheses regarding the demographic history of the British Isles.

Shorter talks followed during which Daniel Falush showed how human gut bacteria can be used to infer human past demography provided that proper statistical modelling is used. Franz Manni showed that surnames can be used to improve the sampling of Y chromosome data. This sampling is currently done using the place of birth of grand-fathers. F. Manni showed using Dutch surname data that this can be misleading. Martin O'Hely discussed the importance of prior distributions on the results obtained using Bayesian methods. In particular he discussed this issue in relation to a method developed to estimate admixture between populations. Finally, Shuichi Matsumura showed preliminary results of simulations to determine whether it is possible to date demographic events using genetic data.

In conclusion, this proved to be a very intensive Workshop. Review and methodological talks were followed by long discussions. This allowed archaeologists; anthropologists, and geneticists to argue, ask questions and appreciate the disagreements and controversies existing in the disciplines involved. **One of our aims** was to convince the non-geneticists that genetic data carry much more uncertainty than is usually believed.

One of the key points to emerge was the importance to both archaeologists and geneticists of obtaining evidence of demographic patterns over time. Such data, which archaeology can potentially provide, would supply valid parameters for genetic models. Modelling population history using some of these data would allow the geneticists to test scientifically a number of hypotheses which are currently not properly tested.

This should be a major area for future cooperation between archaeologists and geneticists and it was agreed that the next step arising from the workshop should be the development of collaborative European projects in this area. In fact, some collaboration has already begun.

2. Scientific content of the event

2.1 Background and Origins

Genetic data from studies on ancient and modern DNA have greatly contributed to our understanding of the human past. Starting from Cavalli-Sforza's seminal studies, projects involving geneticists, anthropologists and archaeologists have clarified previously elusive aspects of human evolution and prehistory and have opened new avenues for research. However, most specialists involved in the emerging field of "Archaeogenetics" would agree that there still exists conflict on how genetic data should be used to address problems raised in archaeology. Disagreements appear to stem from a lack of communication between geneticists and archaeologists, but also, and perhaps more crucially, among geneticists. How much information can be extracted from genetic data for archaeological purposes seems to be the focus of the current debate. As genetic data are likely to play an increasing role in the interpretation of archaeological data, there is a crucial need to discuss how the two types of evidence can be integrated into congruent models.

The fact that archaeological artefacts and genes do not share the same modes of transmission, while widely recognised, is often overlooked. Indeed, why should archaeological and genetic evidence be easily reconciled when sets of genetic markers can generate different patterns leading to different conclusions (e.g. mitochondrial versus Y chromosome DNA) ?

Genetic data are often presented as being "more scientific", "less prone to over-interpretation" and thus as representing "harder" evidence than archaeological data. While this may contain some truth, one possible reason for this impression is that the assumptions underlying genetic studies are not often clearly specified. This has made some conclusions sound stronger than they actually are.

In fact, archaeologists are increasingly aware that genetic data cannot be interpreted in a simple and straightforward manner. We can, *in extremis*, consider that there are currently two major schools of thought regarding the use of genetic data for unravelling ancient human history. The first can be related to Phylogeography, in which phylogenetic and geographical information are analysed together. Patterns are identified and used to infer colonisation events, demographic expansions, etc. The Nested Clade Analysis methodology is the most widely used method of this school. In Europe, Median Network related methods are very popular among human geneticists.

The second school is more closely related to classical population genetics and stresses the importance of statistical modelling to estimate demographical parameters of interest (gene flow, population increase rates, etc.). There are a number of methods developed to estimate different parameters. Usually these methods are tested using computer simulations.

Both methodological approaches have limitations. While the first tends to neglect statistical uncertainty in building scenarios, statistical inferences from the second school are too often limited to unrealistically simple models. Consequently, controversies between adherents of the two schools have generated legitimate frustration among archaeologists and geneticists alike.

This situation led us to organize the Workshop in which participants belonging to different schools of thought were invited. One of the aims was to ask archaeologists to directly challenge geneticists to more fully consider ways of testing their models with genetic data. We also wanted to persuade geneticists to listen more to archaeologists rather than argue amongst themselves.

We thought that these discussions among scientists from all the fields involved would favor a closer integration and a better understanding of the two disciplines' methodologies and assumptions. If that was achieved, Archaeogenetics would be more than a word.

As explained in the Executive summary, the Workshop's aim was to bring a limited number of archaeologists and geneticists together for a few days in order to openly discuss the achievements and limitations of current methods to unravel the past.

2.2 The event

The main sessions on the following two days took the form of a series of review talks on relevant archaeological and genetic theories, methods and case-studies accessible to both archaeologists and geneticists, followed by extended discussion periods. The last morning was devoted to talks on recent developments and perspectives for the future.

Thursday June 3rd

Mark Thomas reviewed the state of Y chromosome research in relation to the possibilities of reconstructing population history. He pointed out the high global variation in the distribution of Y chromosome haplotypes, with a high level of population differentiation. Factors that could explain this large population structure include selection and the small male effective population sizes which can itself be explained by a high variance in male reproductive success, lower migration movements as compared to female (i.e. patrilocality in some human groups). This variation among human populations makes the Y chromosome interesting from the point of view of phylogeography because different haplogroups have different distributions. This is intuitively attractive for interpretation in terms of population processes and events, and it is clearly possible to use this information to infer past population processes.

However, high evolutionary variance in the Y chromosome makes such inferences much more problematic than usually believed: small differences in demographic history can produce large differences in the shape of the gene genealogy. Similarly, the same genealogy can potentially be explained by a range of different demographic scenarios. Phylogeographic interpretations tend to be post-hoc and alternative hypotheses cannot be formally tested. The alternative is population genetic modelling, which can be used to formally test alternative demographic hypotheses but which is difficult to implement and requires the modelling of assumptions that may not be correct. An example is provided by Mike Weale's talk on the last day, to which M. Thomas contributed.

Lluis Quintana-Murci reviewed global variation and its distribution in mtDNA, noting that its high mutation rate has the advantage of being able to identify short-term changes relevant to female population history. However, the high mutation rate can result in homoplasy – i.e. the same changes occurring independently of one another in different populations may be interpreted in terms of population movement or ancient migration events. He pointed out that the deepest roots of the human mtDNA phylogeny continue to be in Africa, implying the existence of larger more diverse populations there and possibly the location of modern human origins. Current estimates of the time to the most recent common ancestor (TMRCA) of extant human mtDNA are $171,500 \pm \text{BP}$ and for 'out of Africa' mtDNA $52,000 \pm \text{BP}$. A case-study of the Makrani population in Southern Pakistan population thought to have African ancestry was presented, comparing patterns in mt and Y DNA and linking the higher proportion of African mtDNA in the present-day population to a postulated female bias in the import of slaves from Africa. This led to a discussion of the relations between present-day gene distributions and past population contributions.

Rosalind Harding reviewed the role of the coalescent in genetic demography. The coalescent is a probabilistic model used in population genetics to describe gene genealogies. It has had a huge success in population genetics because it is explicitly sample-based. Due to this property it provides a statistical framework to estimate parameters conditional on the data observed. It is also extremely efficient in terms of computing time as it is not necessary to simulate the whole population. Coalescent modelling has been extensively used to make inferences from genetic data by simulating different demographical histories to see what to expect in polymorphism data (where there is more than one version (allele) of a gene in a given population). Rosalind Harding emphasized the importance of the demographical history of a population in shaping the structure of genealogical trees. She reminded the audience that the ages of the nodes in a genealogical tree rarely coincide with demographic events of interest. For instance, she reminded the participants that the famous "mitochondrial Eve" is not a very interesting concept. Indeed, it is a "moving target". Any population at any time has its own "mitochondrial Eve". This is true today and will be true in 50 000 years, except that they will be different due to the properties or gene genealogies.

She also reminded the audience of the huge variance that exist in the genealogical processes. This means that estimates based on mitochondrial or Y chromosome DNA should not be trusted unless this uncertainty is explicitly accounted for. She concluded that to improve 'phylo-

geographic' inference we need implementations of the structured coalescent appropriate for a colonization/extinction demography.

Toomas Kivisild reviewed the relationship between median network methods of analysis and phylogeographic inferences, including a critique of the 'founder analysis' technique. In this talk T. Kivisild, explained how networks, rather than genealogical trees, can be constructed between molecules of DNA. These networks have edges that represent the links between the DNA sequences obtained in present-day populations. He showed that the structure of these networks can be used to detect and infer population demographical events. He showed the limitations of the so-called "founder-analysis".

After these two talks, much discussion took place around the fact that network-related methods do not account for the uncertainty generated by the genealogical processes. Thus, while the networks could prove useful as representations of the data, there was disagreement on whether they should be used to make inferences on demographic events or parameters.

In the afternoon Stephen Shennan outlined a proposal for improving the links between archaeological and population genetic models and interpretations by treating cultural attributes as traits passed on by transmission, just as genes are, but following different transmission routes. He argued that just as some genes are neutral, unaffected by selection, and therefore the best indicators of population histories, so it is possible to establish cultural traits which are (nearly) neutral. If this can be done, then the mathematical theory of neutral genetic evolution can be applied to explaining patterning in cultural traits, and patterning in those traits will stem from variation in the degree of interaction between people and the size of the interacting population. These ideas were illustrated with examples from the changing frequencies of pottery decorative attributes in Neolithic South West Germany and from the phylogenetic analysis of basketry descriptive attributes from California.

Evžen Neustupny reviewed the available sources of evidence for prehistoric population sizes and densities, including cemetery data and settlement distributions, pointing out the problems that arise with all these different sources as far as demographic estimation and chronological resolution are concerned.

The following two papers presented archaeological and genetic views of the colonisation of the Americas. James Steele outlined the history of the controversy concerning the antiquity of the presence of humans in the Americas. He presented the results of a recent radiocarbon-dating programme in South America which produced no evidence of anything substantially pre-Clovis and also showed that there was no sign of a gradient in the dates from north to south. In addition he presented the results of some diffusion modelling work demonstrating ways in which this could occur, and also potentially accounting for the greater density of early archaeological material well away from the assumed entry point at the Bering Strait. In contrast, Peter Forster suggested that some genetic mutations that, in his view, could only have originated in populations that were already in North America must be substantially older than the Clovis date, thus indicating an earlier colonisation. This led to major discussion. A number of the geneticists present did not agree with the methodology used by P. Forster in dating the colonization. They did not agree that the dates given necessarily corresponded to demographic events posterior to the colonization of the Americas. They insisted that until simulations were performed to test alternative hypotheses, such conclusions were premature. On the other side, some archaeologists did not agree with J. Steele's dismissal of the South American pre-Clovis dating. These discussions were very interesting for all participants as they demonstrated that apparently solid statements were actually more controversial than expected from non specialists.

Friday June 4th

Marta Lahr presented a biological anthropologist's view of modern human origins and the relation between variation in present-day populations and that which would have existed in the Pleistocene. She pointed out that all present-day modern humans share features that differentiate them from the earliest known fossil anatomically-modern humans at 160,000 BP, so the common ancestor must be more recent. The history of human populations has been one of extinctions and dispersals. In particular, inter-group diversity has decreased markedly since the beginning of the Holocene, not least as a result of the expansion of farming and the

assimilation of foragers by farmers in many areas. She suggested that present-day human genetic variation cannot be taken as representative of the range that would have existed in the past.

Laurent Excoffier reviewed the genetic evidence for modern human origins, pointing out that autosomal genetic variation, like Y chromosome and mtDNA, points to an African origin. He also noted that the fact that some autosomal markers are very old suggests that there was not a strong African bottleneck ca.150,000 BP, as some have argued. He also showed recent simulation work modelling the range expansion of modern humans. He showed how such simulations could be used to address issues such as the possible inter-breeding of modern humans with Neanderthals. He showed that in this case, they were able to demonstrate that the maximum possible amount of inter-breeding would have been minute. Previous studies, while minimising the possible contribution of Neanderthals, had not been able to dismiss contributions as high as 25%. A discussion followed regarding the modelling assumptions and how they could influence the final results.

Francesco d'Errico and Marian Vanhaeren examined the cultural evidence for modernity, emphasising the importance of distinguishing modern human biological origins from the emergence of modern human behaviour. They discussed the lack of qualitative distinctions in terms of probable symbolic behaviour between Middle Stone Age (MSA) and Upper Palaeolithic/Late Stone Age, especially in Africa. They showed that symbolic behaviours did emerge in the African MSA, but not everywhere, and some of them disappeared again. Many similar ones emerged at the same time or later among the Neanderthals. They suggested that patterns in the distribution of personal ornaments in the European early Upper Palaeolithic may indicate ethnic group boundaries.

Papers by Colin Renfrew, Guido Barbujani and Eric Crubézy/Jaroslav Bružek looked at the spread of farming from the Near East to Europe. Despite years of controversy, it appeared that the estimation of the relative contributions of early hunter-gatherers and incoming farmers, were still debated. Both C. Renfrew and G. Barbujani emphasised the importance of the archaeological evidence. The classic genetic clines from SE to NW Europe do not carry a date. Gene genealogies do, argued Barbujani, but it's the wrong one, because the split in a gene genealogy will be earlier, possibly much earlier, than the population split.

Finally, Luca Cavalli-Sforza's paper reviewed the history of his involvement in the genetic study of population history and described recent simulation work demonstrating that mutations on an expanding demographic wave front will have a much greater chance of spreading than ones behind the wave, which will remain localised and unlikely to spread. He showed that mutations that did spread could be used to determine their place of origin.

Saturday June 5th

The morning was divided into two sections with three medium-sized talks (45 mn, including discussion) and four short papers (15 mn). These talks emphasized current work rather than reviews.

Alexander Bentley showed how the study of strontium and other isotopes in prehistoric human and animal bone could give a direct indication of prehistoric mobility patterns, which could potentially be related to genetic evidence.

Ian Barnes described the contamination problems associated with the study of ancient human DNA and described a case-study involving the collection of ancient bison DNA from frozen late Pleistocene remains in Siberia and Alaska. The results revealed the great range of genetic variation in Pleistocene populations. Present-day populations do not exhibit this variation any longer as a result of subsequent population bottlenecks. This emphasised Lahr's earlier point about loss of variation in the Holocene.

Mike Weale outlined issues arising from responses to, and subsequent work on, the published study of Y chromosome variation on a transect across England and North Wales which he and colleagues had carried out. This had suggested that the Roman to Anglo-Saxon transition may have been accompanied by a 50% male population replacement from Friesland in England, although Wales was unaffected. Subsequent work had emphasised the uncertainties in these inferences, not least the date of the suggested population/gene influx.

After the break Daniel Falush described inferences about human population history that could be made by looking at genetic variation in human gut bacteria. Franz Manni presented an analysis of Dutch surname distributions showing how much mobility there had been in the last 200 years and the problems this posed for standard procedures of Y chromosome population sampling. Presence of a grandfather in the same area as an individual is usually taken as a justification that sampling that individual will give an indication of long-term family occupation of that place, and thus of local population history. Martin O'Hely described Bayesian models he is developing to estimate admixture among three populations, taking into account drift. He discussed the problems existing in defining prior probabilities in a Bayesian framework. Finally, Shuichi Matsumura described his current simulation work exploring the limits of precision of some genetic dating methods.

3. Assessment of the results, contribution to the direction of the field and outcome.

The lack of a 1:1 correspondence between gene genealogies and populations was emphasised throughout the meeting, as was the problematical nature of genetically-based dates arising from their lack of precision. Archaeology in general provided better dates but transferring archaeological dates to genetic questions and using archaeologists' questions as the basis for genetic analysis raised their own problems of potential circularity.

For the archaeologists present the extensive disagreements between the geneticists in terms of appropriate methods and the conclusions which can legitimately be drawn from different types of analysis were a revelation. Equally striking was the importance of overcoming the problems with ancient DNA studies so that valid assessments of prehistoric genetic variation can be obtained. The present-day genetic composition of human populations is not adequate for this, while the comparison between ancient and modern variation would in itself be enormously informative of human population history.

It was clear that the development of better genetic models depends crucially on having independent evidence of demographic patterns over time, which can supply valid model parameters. Archaeology has its methodological problems in making population estimates but in order-of-magnitude terms this can certainly be achieved. This should be a major area for future cooperation between archaeologists and geneticists and it was agreed that the workshop convenors should take the archaeogenetics theme further by developing collaborative European projects in this area between those present, and also with others. In fact, some collaboration has already begun.

4. Final programme

Below is the final version of the programme, which includes names of presenters and facilitators.

FINAL PROGRAMME

Presenters are indicated in **bold**, facilitators in *red* and between brackets

Wednesday 2 June 2004

*Arrival in Toulouse throughout the day
Bus leaving Toulouse airport at 17h00
Arrival at the Maison du Haut Salat at 19h00-19h30*

20h00

Introduction of Invitees and “Apéritif”

Presentation of the European Science Foundation (ESF)

Zeljko Kucan (Standing Committee for Life, Earth and Environmental Sciences)

20h30

Dinner at the Maison du Haut Salat

Thursday 3 June 2004

08h30-09h30

On genetic markers in humans (Chaired by **Toomas Kivisild**)
The case of the Y chromosome
Mark Thomas
A global view of mtDNA phylogeny and phylogeography
Lluís Quintana-Murci

09h30-10h30

Coalescent models for genetic demography: what can the coalescent do for you? (Chaired by **Guido Barbujani**)
Rosalind Harding

10h30-11h00

Coffee break

11h00-12h00

Median networks and phylogeographic inferences (Chaired by **Giorgio Bertorelle**)
Toomas Kivisild

12h00-12h30

Discussion (**Lounès Chikhi** and **Stephen Shennan**)

12h30-14h00

Lunch

14h00-15h00

Prehistoric cultures and populations: Explaining cultural trait distributions (Chaired by **Francesco d’Errico**)
Stephen Shennan

15h00-16h00	Prehistoric demography (Chaired by Francesco d'Errico) Evzen Neustupny
16h00-16h30	<i>Coffee break</i>
16h30-17h30	Colonization of the Americas (Chaired by Marta Lahr) James Steele
17h30-18h30	Colonization of the Americas (Chaired by Marta Lahr) Peter Forster
18h30-19h00	General Discussion (Chaired by Henry Harpending) <i>Dinner</i>

Friday 4 June 2004

08h30-09h30	Modern human origins (Chaired by Francesco d'Errico) Marta Lahr
09h30-10h30	Modern human origins inferred from genetic data (Lounès Chikhi) Laurent Excoffier
10h30-11h00	<i>Coffee break</i>
11h00-12h00	Origin of modern behaviour and identification of ethnolinguistic groups of the Upper Palaeolithic (Chaired by Marta Lahr) Francesco d'Errico and Marian Vanhaeren
12h00-12h30	Discussion (Chaired by Marta Lahr)
12h30-14h00	<i>Lunch</i>
14h00-15h00	Neolithic transition in Europe: an archaeologist's point of view (Chaired by João Zilhão) Colin Renfrew
15h00-16h00	Neolithic transition in Europe: Genetic evidence on European prehistoric gene flow (Chaired by João Zilhão) Guido Barbujani
16h00-16h30	<i>Coffee break</i>
16h30-17h30	Neolithic transition in Europe: an anthropological viewpoint (Paolo Biagi) Eric Crubézy and Jaroslav Bruzek
17h30-18h30	Overview Talk (Chaired by Henry Harpending) Luca Cavalli-Sforza
18h30-19h00	General Discussion (Chaired by Stephen Shennan) <i>Dinner</i>

Saturday 5 June 2004

- 08h00-08h45 Strontium isotopes: Tracking prehistoric human mobility directly from the skeletons (Chaired by Colin Renfrew)
Alex Bentley
- 08h45-09h30 Ancient DNA and humans (Chaired by Mark Thomas)
Ian Barnes
- 09h30-10h00 *Archaeogenetics: lessons from British genetic history studies* (Chaired by Mark Thomas)
Mike Weale
- 10h00-10h30 *Coffee break*
- 10h30-11h30 Short talks on recent methods (Chaired by Mark Beaumont)
Anthropological genetics: lessons from Helicobacter pylori **Daniel Falush**
A new method for surname studies of ancient patrilineal population structures and its possible application to the improvement of Y chromosome sampling
Franz Manni
On priors in a bayesian framework with examples from estimating admixture and drift.
Martin O'Hely
Genetic dating methods: some simulation results
Shuichi Matsumura
- 11h30-13h00 *Lunch*
- 13h15** Departure by Bus to Toulouse

5. Final list of participants.

The final list of participants is only slightly different from the “pre-final” list. The main difference is that a number of colleagues were allowed to come as “observers” at the very last stages of the organisation. Indeed, three of the “observers” originally suggested were not able to come due to overlap of the Workshop with other duties.

In order to account for the comments of the referees of the original proposal, and who suggested that we invite at least an American scientist, we decided to contact Professor Henry Harpending, a leading scientist in the field of anthropological and population genetics. His presence at the meeting was extremely beneficial.

While we expected to have 30 participants, the final number was 39. However, as agreed, funding was offered only to those originally invited, including Prof. Harpending.

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The list of all participants is given below by country of “origin” (meaning the country in which they worked at the time of the Workshop).

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6. Statistical information on participants

Overall, 39 scientists attended the Workshop. Institutes and Universities from eight European countries were represented (Austria, Czech Republic, Estonia, France, Italy, Portugal, United Kingdom, Switzerland) with scientists originating from 14 countries (on top of the previously cited countries, the following states were represented: Argentina, Australia, Belgium, Japan, Spain, USA). Approximately half of the participants were archaeologists or anthropologists and the other half were geneticists. Six of the participants were female.

One linguist and a physicist were also present. Both contacted us during the last stages of the organisation and funded themselves.

The youngest participants were in their late twenties or early thirties (Elise Belle, Marian Vanhaeren, Ian Barnes and Murray Cox, are doing their first or second post-docs). The oldest participant was Professor Cavalli-Sforza. Born in 1922 he is turning 82 this year and remains as productive as ever, as his talk reminded us (see above).