

**REPORT OF THE FIFTH SCIENTIFIC MEETING OF THE A&G ICAZ WORKING GROUP**

4<sup>th</sup>-6<sup>th</sup> June 2012, Basel, Switzerland

The A&G ICAZ working group was founded at Durham (UK), during the 7<sup>th</sup> ICAZ meeting (August 2002), by J.-D. Vigne, M. Zeder and D. Bradley. It held its four first meetings in Paris (2004), Cambridge (2005), Tallinn (2008) and Paris (2010). The working group aims to promote exchange and collaboration between archaeo(zoo)logists and (palaeo)geneticists. The fourth scientific meeting was held on the 4<sup>th</sup>-6<sup>th</sup> June 2012, in Basel, at the Old University, ably organised by Angela Schlumbaum, Jörg Schibler and Julia Elsner of the IPAS (Institute of Prehistory and Archaeological Science) of the University of Basel.

Attendance of the 2008 meeting in Tallinn was reduced relative to previous meetings, and, more worrying, it was mostly composed of geneticists, with a very poor participation of osteoarchaeologists. In order to re-stimulate the later, the WG decided to organize the next meeting in the frame of the 11<sup>th</sup> ICAZ conference in Paris, in the form of a special session. This strategy was successful, since the attendance at the Paris session was very high, and the Basel meeting was more similar to those held originally in Paris (2004) and Cambridge (2005), with sixty scientists, from 16 countries<sup>1</sup> and a well balanced proportion of geneticists and osteo-archaeologists present. Young PhD students were numerous, as well as a good number of scientists who never participated to the WG before.

After a short introduction by the organizers and by the correspondent of the ICAZ WG and a stimulating introductory presentation by D. Y. Yang and C. Speller (Vancouver-Cagliari), who promoted the value of collaboration between the disciplines, there followed 25 excellent oral presentations, complemented by 8 posters. There was also mostly good time for questions and discussions after each paper and session. The presentations were organised in four sections: Domestication and related issues (8 talks), Expansions and migrations (6), Diversity (6) and Miscellaneous (5). Young researchers, geneticists and archaeozoologists as well, successfully chaired the sessions.

The first section (Domestication) was characterized by a large diversity of taxa (pig, cattle, sheep, dog, chicken, turkey), regions (North America, Arctic, Europe, SE Asia) and periods. B. Krause-Kyora & A. Nebel (Kiel) demonstrated that the domestication of local European wild boars started as early as the Early LBK, and discussed the presence of early pigs in the Ertebølle. A. Evin and coll. (mainly Aberdeen-Paris-Durham) presented extensive morphometric and ancient mtDNA data for a long duration in the Eastern Mediterranean, showing how the lineages of pigs which were previously domesticated in Europe were re-introduced to the Near East during the Bronze Age, and finally replaced the local Near eastern domestic pigs. A. Scheu and coll. (Mainz-Paris-Berlin) gave an extensive overview of the aDNA data for European early domestic bovids, including original data from the Balkans, analysed the haplotype diversity in connection with the unequal speed of diffusion through the continent and emphasized the recent results regarding the estimation of the number of females contributing to modern cattle lineages. L. Girdland Flink, G. Larson and coll. (Durham-Uppsala-Munich) based on modern and ancient DNA data connected with the colour of the legs to decipher the history of the domestic chickens in Europe. C. Speller and coll. (Calgary-

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<sup>1</sup> Switzerland (19), UK (11), France (6), Germany (4), Canada (3), Estonia (3), Portugal (2), Finland (2), USA (1), Australia (1), Belgium (1), Denmark (1), , The Netherlands (1), Spain (1), Sweden (1), Rumania (1).

Mexico City) analysed mitochondrial aDNA in turkeys and concluded that there were likely two independent centers of domestication in North America. S. Brown and coll. (California Univ.) analysed the genetic diversity of 24 North American Arctic dogs. M. Ollivier and coll. (Lyon-Paris-Rennes-Bucharest) presented aDNA results about coat colour of dogs which allowed them to formulate hypotheses on the diffusion of these populations throughout Eurasia. L. Ø. Brandt (Copenhagen) investigated the development of wool in Danish prehistoric sheep with both genetic and osteological techniques. The poster presented by A. Evin and coll. (Paris-Aberdeen) about the differentiation between wild and domestic pigs through the molar size and shape was also connected to this session.

Following the tradition of this ICAZ WG, two presentations involved botanical research.. They were grouped into the second session (Expansion, migration) and presented very exciting, extensive and original synthesis about the genetics of the modern tetraploid wheats of the Mediterranean (H. Oliveira and coll.; Cambridge UK – Harvard) and about the phylogeography of the edible African bananas (L. Vrydaghs and coll.; Brussels) based on phytoliths and DNA analyses. They were complemented by a poster presenting the work of a major ERC funded project on food globalization in prehistory, focusing upon the origins of cereals (D. Lister and coll.; Cambridge, UK). With the exception of a poster about the origins of the Roman cattle in the Iberian peninsula using osteometric and molecular analyses (L. Colominas et coll. Barcelona-Basel), the other presentations in this session were all focused on the dispersal of domesticates (pigs and chickens, again) and commensals (rats and gekkos) in SE Asia and Oceania. O. Lebrasseur (Durham-Aberdeen) analysed the mtDNA diversity of modern chickens from the Philippines to the remote Santa Cruz Islands in the scope of the dispersal of the Lapita societies into Oceania. A. Linderholm and coll. (Durham-Aberdeen-Paris) revisited the “Out of Taiwan” hypothesis linked to the Austronesian dispersal of pigs based on combined dental morphology and genetic signatures. A. Trinks and coll. (Durham-Aberdeen) also explored the migration patterns of human dispersal in SE Asia and the Indian Ocean through the genetics of the small common gecko, *Hemidactylus frenatus*. A. Hulme-Beaman and coll. (Aberdeen-Paris-Durham) presented impressive mtDNA and geometric morphometric data on the Polynesian rat (*R. exulans*), which also appears to retain a detailed signature of Oceanic colonisation linked with Polynesians.

The fourth session (Diversity) dealt with cattle, dogs, sheep, goat and equids, mostly in the Near East and Europe. C. Ginja and coll. (Lisbon-Lyon-Uppsala) presented preliminary data about the paleogenetics and morphometric diversity of the Chalcolithic Iberian bovids, which confirm that aurochs belong to the P haplogroup, evidence of a diversity of T3 and T1 haplogroups in the Iberian Peninsula, as well as the presence of T1 in Morocco at least since the Roman times.. A. E. Pires and coll. (Lisbon-Lyon) gave original archaeozoological and genetic data about Portuguese Mesolithic and Chalcolithic dogs. J. Elsner and coll. (Basel) revealed a large genetic diversity in Early Upper Palaeolithic horses from Switzerland, based on a large and original dataset of well preserved mtDNA, including data from waterlogged sites. This presentation was completed by a poster presented by J. Granado and coll. (Basel-Bern) about genotyping ancient horses using *Illumina* systems, and by another poster by J. Lira and coll. (Madrid) on the genetic diversity of the Iberian asses. E. Rannamäe and coll. and M. Niemi, J. Kantanen and coll. (Tartu-Helsinki-Tallinn) investigated the morphological and genetic diversity of modern sheep in Estonia and Finland, respectively, and showed the peculiarity of endangered local heritage breeds. A. Bennett and coll. (Paris-Munich) brought substantial original information about the limits of the osteological discrimination of *Equus hemionus* and *E. hydruntinus*, and presented a large panel of aDNA data which allows them to update the phylogenetical relationships between the different groups of Asiatic wild ass, and

to show that the equids of the 3<sup>rd</sup> millennium elite burials at Umm el-Marra (Syria) were actually hybrids of females of *E. asinus* and males of *E. hemionus syriacus* (the earliest known evidence for animal hybridization). In addition, a poster by S. Hughes and coll. (Lyon-Paris-Grenoble) presented the genetic diversity of the medieval Corsican goats and its meaning in terms of herding practices.

The last session (Miscellaneous) opened large and diversified perspectives. JTD Owen and coll. (Durham-Aberdeen-Paris) investigated the phylogeny of suids of the Old World, and emphasized and discussed the discrepancies between the molecular and morphological evidence, exploring ancestral traits and morphological convergence in different lineages as well. U. Strand Vidarsdóttir and coll. (Durham-Aberdeen-Paris) compared the ontogenetic morphological change in European wild boar and domestic pigs, based on a geomorphometric description of the skull, and concluded that the differences are not mainly due to pedomorphy, but that they result from both genetic of epigenetic prenatal structural differences and differences in the ontogenetic trajectory. R. Barnett and coll. (Durham) presented an impressive historical and genetic dataset about the diversity of lions and their geographical restriction during the last centuries and decades. J. Soubrier, A. Cooper and coll. (Adelaide) investigated the genomic diversity of European and American bison, and in doing so have identified a new species of bison in Eurasia, and clarified the biogeographical evolution of the bison in Europe since the Eemian. Exploring commensal microbes trapped in the dental calculus of humans and animals, C. Adler, K. Dobney and coll. (Adelaide-Aberdeen-Mainz) opened large perspectives on the history of oral pathologies, and concluded that the European farming communities had higher oral microbe diversity compared to modern populations, and that the frequency of caries-forming bacteria is potentially a result of the Industrial Revolution. Finally, the poster by A. Krüttli and coll. (Zurich) recalled that archaeozoology and genetics together are addressing big historical and anthropological questions such as the beginning of milk exploitation in Europe.

This conference was not only marked by a good participation of both archaeozoologists and geneticist and by a very high level of quality of talks, posters and exchanges, but by its wonderful organisation. As we already suspected during the meeting of the WG in Paris in 2010, even if mtDNA is still the dominant tool currently used by archaeogeneticists, it is now being quickly overtaken by nuclear markers, through new “next generation” techniques. It is good to see that this extraordinary development of molecular techniques does not widen the gap between archaeo(zoo)logists and geneticists. Conversely, it appears to be strengthening their collaborations, both by increasing and diversifying the number of common scientific issues, and by stimulating the emergence of young scientists who are specialising in this domain of interactions. However, the rich discussions during the meeting also revealed that the latter do not necessarily yet possess a sufficient critical approach towards the key archaeological issues and data, and that archaeologists are not geneticists. This makes this working group more useful than ever.

Another important evolution is the increasing use of combined (complementary) techniques and approaches – specifically those of (paleo)genetics and morphometrics, leading to much more refined and informative results. As is visible in the summary above, this is namely due to the recent development of geometric morphometrics applied to archaeozoology, an emergent technique which should be widely supported and promoted by ICAZ. In the final discussion, it was agreed that this marriage of genetics and morphometrics should be formally driven forward as a future key component of the Archaeozoology and Genetics working group. As seen in the various presentations from the recent Basel meeting,

much of the work in these areas is revealing how complementary these techniques are, both of them exploring similar questions about genotypic and phenotypic expression. Often, the population level distinctions revealed by DNA analyses are mirrored by GM analyses. This correspondence allows the result of one technique to be used as a proxy for the other in the event that both sets cannot be retrieved from the same specimen. Secondly, the GM data will likely possess signatures of both deeper evolutionary divergence, hybridization and the impact of e.g. domestication. Testing these issues at two different levels of biological organization will therefore ensure that significantly more robust conclusions may be drawn from such datasets.

Finally, following discussions and a direct vote during the Basel meeting, the next meeting of the working group will now take place in Lisbon during the winter 2014, and will be organized by Catarina Ginja, Cleia Detry and Ana Elisabete Pires.

June 27, J.-D. Vigne  
(with contributions of A. Schlumbaum and K. Dobney)