

Cave Bear ancestors

Los antepasados del oso de las Cavernas

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ABSTRACT

The lineage of the cave bear *Ursus deningeri* --> *U. spelaeus* is well known, but to draw a limit in this evolution is not easy. The real difficulty is met when this cave bear lineage has to be linked to its ancestors... Dating physical methods, paleoclimatic and paleo environmental data, works on teeth and bones morphology, progress in paleogenetics are means our disposal to give essential information to phylogeny. A large collaboration is needed. Practical information are given about a possible discussion group.

Key words: Cave Bear, phylogeny

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1. INTRODUCTION

The topic of cave bear ancestors is seldom discussed. And yet it's an important question which partly conditions our research. The aim of this communication is to review the subject and above all to launch a debate and a discussion.

2. A PRECISE EXAMPLE

Circumstances have made me study four important paleontological sites, rich in Ursids remains, spanning a long period of time, and well grouped together geographically (Europe scale) (figure 1).

The elimination of some variable parameters (geology, hydrology, major climatic zone) is due to the geographic proximity, well knowing that at the time scale used, some factors likely to vary always exist ; such are the local climate (different environments), the variations of the conditions of fossilization and preservation specific to each place, etc...

How to establish the phyletic links between the four Ursids populations ? What are the means currently at disposal to scientists to base their research ? Most of the studies are done on dental material for classical reasons. Teeth which are harder and more resistant are well preserved ; their determination and comparison (morphology, measurement) are easier, explaining the large number of studies which use them.

The lineage of the cave bear *Ursus deningeri* --> *U. spelaeus* is well known: *U. spelaeus* obviously succeeds without discontinuity or break to *U. deningeri*. The only difficulty encountered by the paleon-

tologist is to draw a limit in this evolution to distinguish two chrono-species. The *U. deningeri* from Château (Saône-et-Loire), the *U. spelaeus* from Azé and the one, very typical from the Balme à Collomb (Entremont-le-Vieux, Savoie) constitute a good illustration of this evolution. The ancient form, *U. deningeri*, presents a combination arctoid and etruscoid features time and again reported, but already marked spelean features. The real difficulty is met when this cave bear lineage has to be linked to its ancestors.

The large group of Ursids from the Early Plio-Pleistocene, *U. etruscus*, widely spread on a vast area, logically constitutes the genetical reservoir from which the two great species *U. arctos* and *U. deningeri-spelaeus* have their direct or indirect origin. The basic question is to know if these two lineages diverge from the *U. etruscus* form in a distinct way, or if the lineage of the brown bears emerges alone, and then, in the process of evolution, sees some of its populations evolve towards the cave bear.

U. etruscus is mainly found in open sites. Probably, it didn't use caves to hibernate. This explains the rarity of its remains and sites. From the Saint-Vallier bear to the Château bear, time is far too long to reveal a direct link. The intermediate forms between *U. etruscus* and *U. deningeri* are lacking. This can be applied to the whole Europe. This gap is easily explained by several reasons : rarity of sites, lack or scarceness of paleontological material, or difficulty or poor reliability of datings. This is why so many hypothesis are always difficult to back up for the early Pleistocene, almost one million years.

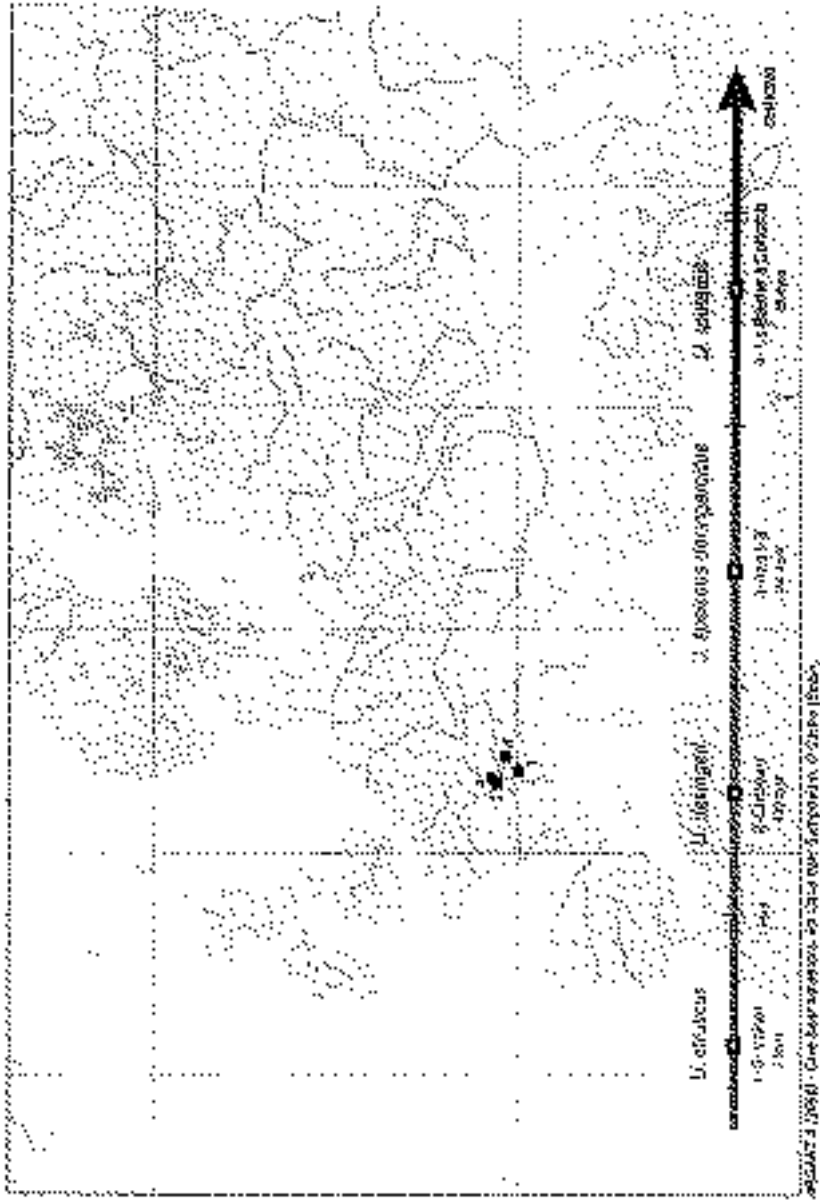


Figure 1. Location map of the four plio-pleistocene sites mentioned

3. DIFFERENT CURRENT PHYLETIC APPROACHES

The main phylogenetic interpretations, which are currently met dealing with the Eurasian bears, are summed up in the tree diagrams of figure 2. They correspond to ideas which were suggested a long time ago and abundantly debated. Diagram 1, that I approve, seems to be nowadays widely accepted, without any absolutely decisive arguments, particularly about the relation between *U. etruscus*/ *U. arctos*/ *U. spelaeus*

4. SOME REMARKS

Why can't we conclude for so long ?

Three main reasons can be put forward:

- The rarity of Early and Middle Pleistocene sites.
- The difficulty of dating these sites.
- The rarity of usable paleontological material, since many of these ancient bears didn't systematically use caves to hibernate.

Which reliable tracers record the Ursid evolution and their phyletic links ?

The greatest importance has been given up till now to dental studies. It seems to me that we must go beyond that stage and use all the available recorded information : metapods, carpus, tarsus... Fortunately, they have been used more often for some years.

Which new means are our disposal ?

- First, improvements of dating physical methods. They are more numerous and performing for the ancient periods and some of them are more and more reliable.
- Then, all the paleoclimatic and paleo

environmental data now systematically in the scientifically led excavations.

- The works of G. Rabeder since 1983, using the teeth as precise tracers of the cave bear evolution which is quantified by morphodynamic index, a useful tool (RABEDER, 1983, 1989, 1990, 1992, 1999...; RABEDER, *et al.*, 2000; ARGANT, 1995).

- Progress in paleogenetics, due to improved techniques in mitochondrial DNA analysis which can be traced back up to 130,000 years.

5. CONCLUSION

The preceding remarks allow us to reconsider phylogenetics on current basis. A methodical and coordinate research can already be organized at the European scale. It must associate the two lineages *Ursus spelaeus* and *Ursus arctos* which are historically linked, and maybe the *Ursus stehlini/thibetanus* one ? It's impossible to ignore paleogenetic information which is brought by the mitochondrial DNA, within its application chronological limits.

They are the only ones able to give this kind of essential information to phylogeny. They should be carefully considered and always controlled by paleontological data.

The question is so wide that a large collaboration is needed, on equal footing and with mutual respect between the teams dealing with Ursids.

As a discussion basis, I propose the following phyletic tree (figure 3) which includes the current information of the mitochondrial DNA (LOREILLE, *et al.* 2001). The genetic distances suggest a

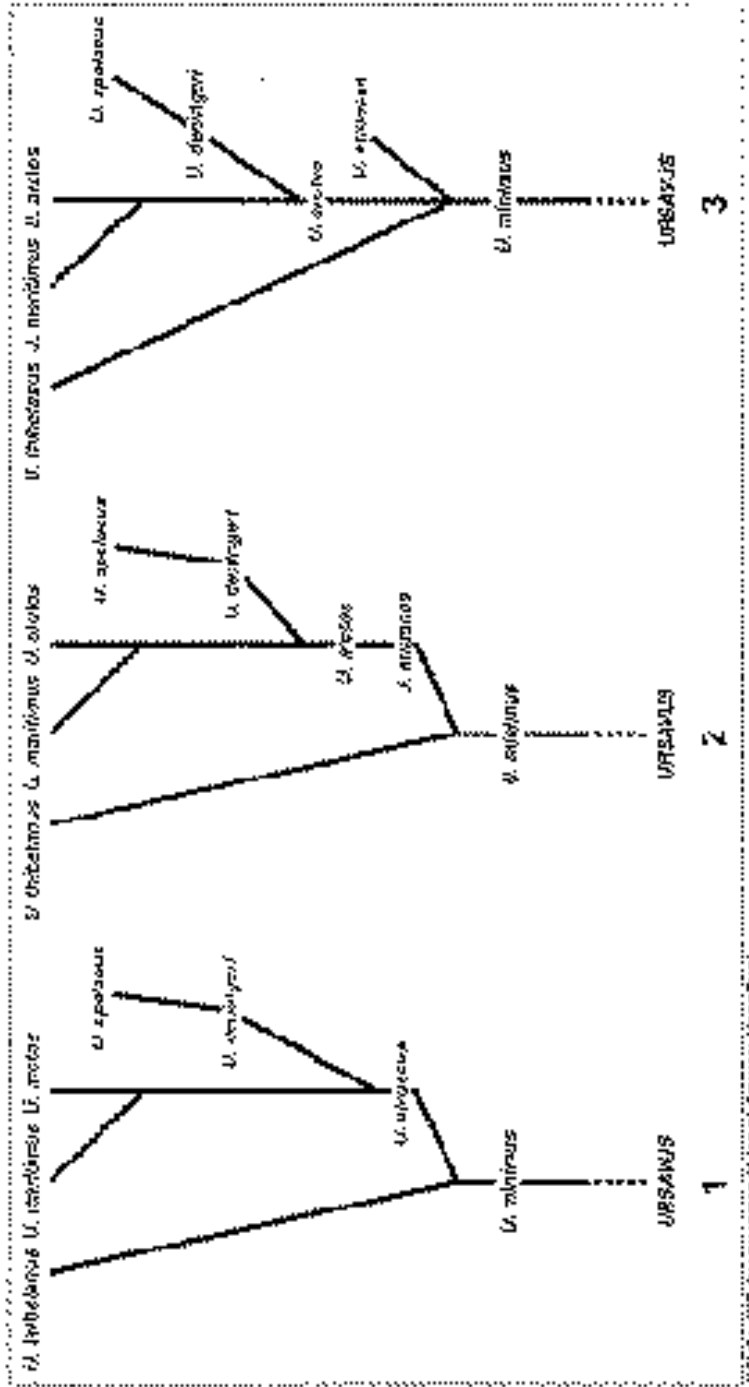


Figure 2. Main phylogenetic interpretations for Eurasian bears.

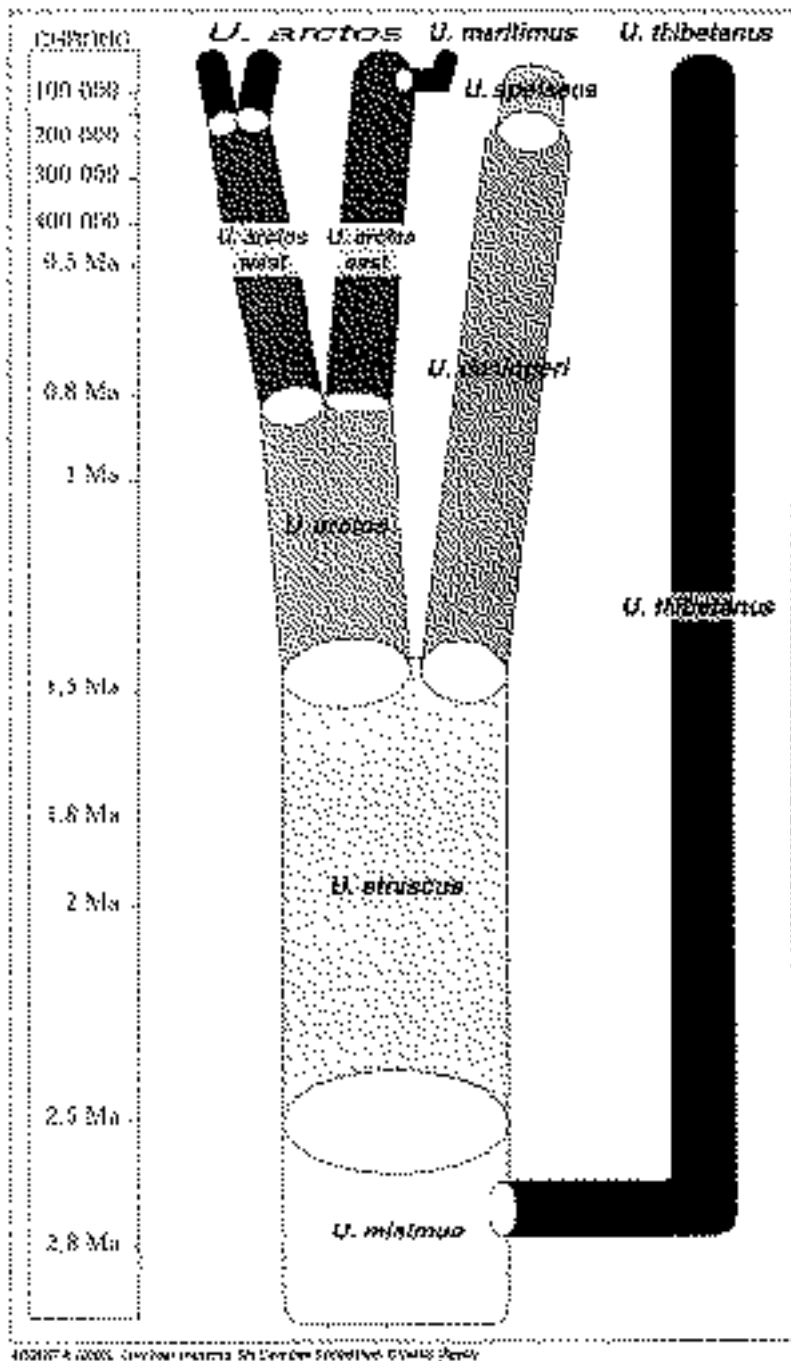


Figure 3 : phyletic tree proposed for discussion

divergence between *U. spelaeus* and *U. arctos* between 1.2 et 1.6 million years, prior to the divergence of the two Eastern and Western lineages of *U. arctos* (TABERLET & BOUVET, 1994). This allows us to rule out the model of diagram 2 and reinforce diagram 1 (figure 2).

It seems important to me that a dis-

cussion group, which could be called "URSID", should set up on the Internet. Then, more structured and official consultations should follow on the interest and the results. But, please, at first, contact <a.argant@wanadoo.fr> to express your opinion about creating such a discussion group. So long.

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