On the origin of Wisent, again

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Comment on the papers:


And


Something impressive has happened. Simultaneously, two different papers (Soubrier et al 2016 and Massilani et al. 2016) appeared, dealing with the same subject that interests zoologists and palaeontologists, namely “the obscure question on the origin of the Wisent (Bison bonasus),” as put by Emma Marris (Nature/News from 18 October 2016). Besides, they use the same methods: ancient DNA analysis and paleo-depictions evidences. This coincidence brings to mind the concept of the noosphere (the sphere of human though), introduced by Pierre Teilhard de Chardin and Vladimir Ivanovich Vernadsky in the beginning of the past century, simultaneously on top of it all.

Both teams support their paleogenetic conclusions with analyses of prehistoric depictions, in which they find evidence for the parallel existence and even co-occurrence of Bison bonasus and Bison priscus in the Upper Palaeolithic. The idea of the parallel existence (though not necessarily at the same pace) by these two species, by the way, has been published before, and so is the approach of using analysis of prehistoric rock art in studying the origin of wisent. These two subjects are dealt with in detail by Spassov & Stoychev (2003).
As for the conclusions on wisent origin by the two teams (Sourbier et al. 2016 and Massilani et al. 2016) based on ancient DNA analysis, they are radically different in the two mentioned papers. Often zoologists and palaeontologists unfamiliar in details with the methods of molecular phylogenetics are much in awe of geneticists’ taxonomic conclusions. Contradictions such as those above, however, show that those methods, too, have their limits, not always being more valid than comparative morphology approach, and that science is eventually dependant not on the methods but on the ability to interpret results.

Sourbier et al (2016) reach the impressive conclusion that modern wisent “is the product of hybridization between the extinct steppe bison (Bison priscus) and ancestors of modern cattle (aurochs, Bos primigenius) before 120 kya, and contains up to 10% aurochs genomic ancestry”. This, however, is not supported by the analysis of the exterior and skeletal morphological characters of the – indeed very close – Bison and Bos. With closely related species, occasional crosses are possible, and a weak gene flow signal might be recognized in the genome of the descendent population. Yet, in the cases of interbreeding between species resulting in hybrid populations, there are always intermediary characters, or characters from one or the other ancestor (simple examples of animals with intermediary characters are mules and tigons, hybrids between a tiger and a lion). Nothing similar is seen in the wisent characters. Its exterior clearly puts it next to bison (Flerov, 1979), same goes for the skull and horn-cores (Godina et al., 1962), as well as the bones of the skeleton (Bibikova, 1958; Burchak-Abramovich & Vekua, 1980; Spassov, 1992). Today the wisent is compelled by man to live only in wooded habitats. However, large number of comparative data indicate that both, wisent and aurochs are forest-steppe animals, but the wisent is more specialized towards forest habitats (Spassov, 1992 and references herein). It is difficult to accept that crossing long-horned steppe forms such as the aurochs and Bison priscus would result in the short-horned and largely forest- and mountain-dwelling wisent. Thus, I find more logical the explanation by Massilani et al. (2016) that incomplete lineage sorting of mitogenomes in a metapopulation of the Bos and Bison ancestors during the period of divergence of these forms could account for the affiliation patterns of these mitogenomes without the need to postulate a more recent post-speciation gene flow. It could be supposed that the aurochs genome preserved the most of the common ancestor’s characters, and that of B. bison – the least. The “typically” aurochs characters in the wisent genome might actually represent remnants of the ancestor’s genome rather than indicate hybridization.

Massilani et al.’s claim of bifurcation between the Bison bonasus and Bison priscus/ bison mitogenome lineages about 1.0 million years ago sound rather logical considering the available palaeontological data on the evolution of the genus close to the early / middle Pleistocene boundary. That node corresponds more or less to the time of probable split of long- and short- horned lineages, the latter possibly being the wisent ancestral lineage. Spassov & Stoychev (2003) reminded that as early as the beginning of the 20th century Hilzheimer (1918) noted the possibility that already in the Mindel-Riss in Europe there could be two lineages occurring in parallel: the steppe long-horned bison Bison priscus in the open landscapes, and,
in the more southern and forested areas, the descendants of the short-horned *Bison schoetensacki*. Spassov & Stoychev (2003) noted also that the images from France and Spain, where *Bison priscus mediator* is depicted contemporaneously with and later than wisent-like bisons, seem to support the hypothesis for the parallel occurrence of the steppe long-horned form *Bison priscus* and a forest (southern) short-horned form of genus *Bison* during the Late Pleistocene (and probably from the Middle Pleistocene).

The latest studies discussed here (Soubrier et al 2016 and Massilaniet al. 2016) in no way invalidate the conclusions by Spassov & Stoychev (2003). It could be supposed, judging from modern wisent’s ecology and distribution area, that the short-horned phylogenetic lineage evolved probably into *Bison bonasus* somewhere in the area between South (South-Eastern) Europe and the Middle East much before the end of the Pleistocene. To the present day, this area remains insufficiently studied from the viewpoint of Pleistocene – Holocene bison history.

References


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Отново за произхода на зубъра

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Обсъждат се изводите в трудовете на SOURBIER et al. (2016) и MASSILANI et al. (2016) за произхода на европейския бизон (зубъра).