



Questioning new answers regarding Holocene chicken domestication in China

Xiang et al. (1) assert that chickens were domesticated on the North China plain 10,000 y ago. Although a great deal remains unknown about the temporal and geographic origins of poultry husbandry, this claim is extraordinary. We welcome the increasing application of modern bioarcheological techniques to questions pertaining to animal domestication in China, but we are skeptical about these conclusions for several reasons.

Firstly, their claim that chickens were domesticated on the North China plain is problematic because this region is currently climatically unsuitable for their wild ancestor (the red jungle fowl). In support of this assertion, they point to the abundance of tropical animals at the sites of Nanzhuangtou and Cishan. High-resolution paleoclimatic records (2) suggest, however, that before the mid-Holocene, cooler temperate conditions prevailed between 35°N and 40°N (hence the dominance of Palaearctic species at Nanzhuangtou). Although higher (+2–4 °C) average temperatures in the mid-Holocene supported the presence of an Indomalayan mammalian complex, the species identified are present today above 30°N. In contrast, red jungle fowl populations in China do not exist north of 23°N. This evidence suggests that an environment suitable for thermophile red jungle fowl did not exist at the sites of Cishan or Wangyin. In addition, although cooler temperatures would allow for enhanced DNA preservation, the predicted (thermal-age.eu) mean fragment lengths of 23 bp and 31 bp for Nanzhuangtou and Cishan, respectively, appear at odds with the described looped PCR protocol.

Secondly, identifying Galliform bones to genus on the basis of their morphology is straightforward (3). In fact, studies of phasianid remains from across China (4) have revealed that although pheasants were identified at Neolithic Cishan and Wangyin, *Gallus* was only present in the Warring States Period tomb (476–221 B.C.) at Jiuliandun.

More recent work has confirmed this assessment.* Xiang et al. instead rely on mtDNA sequences obtained from bones to conclude that the earlier morphological identifications were mistaken. They include photographs of bones (without a scale) in their study, which reinforces concerns regarding the DNA identifications, because the bones on the bottom right of figure 1B in ref. 1 are not chickens but clearly canids, and likely dogs.

There are also numerous errors that undermine confidence in the study overall. For instance, although Xiang et al. claim there are no post-Neolithic cultural deposits from which chicken bones could have originated, both Nanzhuangtou and Cishan possess definitive later occupation deposits (5), allowing for the possibility that some of the recovered bones are intrusive. Although other *Gallus* species contributed to the gene pool of domestic chickens, this is neither supported nor illustrated by their data. Finally, we have concerns about the DNA sequencing. Not only does one of the forward primer sequences align as a reverse primer but, also, none of the primers were excluded from submitted sequences. As a result, all of the reported haplotypes possess an artifactual thymine base introduced by the CRI-F primer.

The conclusions reported by Xiang et al. are unexpected and exciting and may be valid. Given the numerous concerns mentioned above, however, a robust reappraisal of all of the available evidence is required before these conclusions can be fully accepted.

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