
Unveiling the importance of mule breeding in antiquity using minimal DNA data

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Résumé

The members of the *Equus* genus, which includes horses, asses and zebras, can develop first generation (F1-) hybrids, despite their striking karyotypic and phenotypic differences. These hybrids are viable but mostly infertile, and often present characters of considerable interests for breeders with mules – the offspring of a mare and a jack – showing stronger working capacities, longer life spans, and better resistance to diseases than horses. They were extremely valued in antiquity, especially for trade, transport and warfare, and are relatively commonly represented in art. However, taxonomic identification of such hybrids in archaeological assemblages based solely on morphological data remains problematic. This is mostly due to the often fragmentary nature of the material available as well as the relative scarcity of the comparative morphological panel. Using high-throughput DNA sequencing technologies, we developed a full, accurate and automated methodological procedure capable of identifying F1-equine hybrids from minute amounts of sequence data. Our procedure thus

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limits experimental costs while remains compatible with samples showing extremely limited DNA preservation levels. We apply our procedure to the most extensive equine sample panel hitherto characterized and provide insights into the extent to which mules were essential to management strategies of different past empires and societies, including the Romans and the Byzantines.

Mots-Clés: horse, mule, species identification, ancient DNA