Impact of sampling strategies and reconstruction protocols in nasal airflow simulations in fossil hominins

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In their study, de Azevedo et al. (1) employ a sample of 12 individuals from Argentina of Chinese, Japanese, and Korean origin [northeastern Asians (NEA)] as representative of cold-adapted populations. However, all previous literature on the subject shows that the craniofacial morphology of these populations does not exhibit features adapted to a cold climate (e.g., refs. 2, 3). In fact, the climate of the most populated parts of China and Japan is temperate and cannot be referred to as "cold." As stated by the authors, Arctic populations drive climate-morphology correlations in many studies (4), including their own (ref. 1, p. 4).

Additionally, it is surprising that no differences in the morphology of the anterior nasal region were found between the NEA and southwestern Europeans (SWE) (figure 1 of ref. 1), despite well-established differences in craniofacial features between those groups (e.g., ref. 5). This leads to a general concern that the sample is poorly described (no sex and age distributions). More importantly, no criteria are given for choosing the two individuals who were used in the subsequent computational fluid dynamics (CFD) model (ref. 1, p. 5). Consequently, this produces the main, in our opinion, issue of this study: a lack of knowledge about the factors contributing to differences in the soft tissue airway shape of those two individuals. Indeed, the nasal mucosa is an erectile tissue; its state of congestion is affected by numerous factors (e.g., nasal cycle). Therefore, the nasal airway's shape and size can fluctuate rapidly and to a very substantial degree (e.g., ref. 6). That is the reason why the criteria for choosing the SWE and NEA individuals used in the CFD model should be stated in detail. As a result, the huge differences reported in the CFD results between these two individuals (figure 2 of ref. 1) are highly questionable.

Finally, how the nasal cavity and mucosa are modeled in the Neanderthal specimen also raises several questions. First, one SWE individual was used as the starting shape for the model (ref. 1, p. 5), and the results for the SWE and Neanderthal individuals were similar (figure 1 of ref. 1). What would have been the results if one NEA individual had been used instead? Second, the association detected by the authors (figure S7 of ref. 1) between the bone and soft tissue of the nasal cavity is too weak to predict soft tissue morphology from bone morphology. Third, it has been shown that there is no correlation between the shape of the nasal aperture and that of the choanae in humans (7). Ignoring this study, the authors performed their own study (ref. 1, p. 2 and *SI Appendix*, pp. 3–7), where they analyzed representatives of different families of primates together. While some correlations were found (figures S3–S5 of ref. 1), it remains unclear whether the pattern of association would remain the same, vary, or be absent at a lower taxonomic level. Several reconstructions of Neanderthal nasal airways based on different modern individuals would have been necessary to determine the robustness of such a protocol. Without proper quantification of nasal airway form variation, any result based on a single individual per group conflates interindividual and interpopulation variation.

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