

Could genetic diversity in eastern North Pacific gray whales reflect global historic abundance?

To the Editor: Alter *et al.* (1) use estimates of genetic diversity in eastern North Pacific gray whales, *Eschrichtius robustus*, to infer historic levels of abundance of this species in the North Pacific. However, the expected level of genetic diversity within local populations connected by gene flow to other populations is that of the global population (2). Alter *et al.* (1) assessed the possible effect of gene flow by computer simulations. The assessment was based on a model assuming gene flow between North Atlantic and North Pacific populations up until the Sangamonian Interglacial period some 100 kya after which gene flow was zero. Subfossil records of gray whales have so far been limited to the North Atlantic, where this species was present until the mid-18th century (3). However, given that all extant baleen whales (except bowheads and the pygmy right whale) have global distributions, it is quite plausible that gray whale populations existed in the Southern Hemisphere during the last 100 kya. In such a case, gene flow into the North Pacific could have occurred via the Southern Hemisphere after the Sangamonian Interglacial period, as has been the case in other baleen whales (4, 5). There are bones available from North Atlantic gray whale specimens. Provided that DNA sequence data can be collected from these bones, the population divergence time and current migration rates between North Atlantic and North Pacific

gray whales may be estimated (6). Indications of current migration and/or a population divergence time dating after the Sangamonian Interglacial period would imply gene flow into the North Pacific from the Southern Hemisphere. In such a case, the abundance estimate derived by Alter *et al.* (1) would represent historic abundance globally rather than in the North Pacific.

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The authors declare no conflict of interest.

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