

## GEOSCIENCES

## Tracking the migration of our Chinese ancestors using molecular science

Chuanlun Zhang

The Bible tells the story of Noah, who, under the direction of God, constructed a giant boat (Noah's Ark) to save his family and all the world's animals from the Great flood. In China, the hero Dayu (~4000 years ago) spent 13 years managing and fighting floods to save human lives. Yet, the wisest thing our ancestors did when facing floods was moving to higher grounds. The pattern of migration has thus been of great interest to archaeologists. However, the link between human migration and hydrological changes in ancient history has been difficult to find because of the lack of valid proxies.

Xie *et al.* [1] demonstrated that the combination of two independent proxies (the hopanoid biomarkers from aerobic bacteria living in peat bogs and the fine magnetic particles deposited in cave stalagmite) reasonably explained the events of floods associated with human migration in central China between 1000 and 13 000 years ago.

Organic biomarkers are commonly used to reconstruct paleotemperatures. They appear, however, also to be sensitive to hydrological changes in the terrestrial environment. Hopanoids can be produced by a variety of microorganisms (primarily bacteria) including both aerobic and anaerobic species [2]. Linking hopanoids to ancient hydrology is based on the idea that hopanoid-producing aerobes in peatlands will be more abundant when the water table is low and the air-saturated surface zone is thicker. Thus, periods of high hopanoids abundance should reflect less rainfall and a dry climate, whereas periods of low hopanoids

abundance should reflect greater rainfall and flooding. Indeed, Xie *et al.* observed patterns of high and low hopanoids at time scales consistent with the dry and wet periods' characteristics of the Asian monsoon system in the past 13 000 years in the Dajiuhe peatland, 600 km northwest of Wuhan. Furthermore, Xie *et al.* surveyed extensively the archaeological sites in central China and found fewer archaeological sites in the lowlands in periods of low hopanoids, indicating human migration to higher ground during wet periods.

Biomarkers are effective proxies for paleoenvironmental and paleoclimatic studies [3]. Xie *et al.* further showed that hopanoids correlated poorly with temperature inferred by other methods. They also prudently validated the hopanoid abundance—oxic water table hypothesis using molecular DNA containing the specific gene *sqhC* that is responsible for the biosynthesis of hopanoids. The results indicate that 90%–94% of the *sqhC* sequences were attributed to aerobic organisms. One assumption of this claim is that the DNA of hopanoid producing organisms has been well preserved and the organisms have not continued to grow after burial. The predominance of aerobic organisms in the tested *sqhC* sequences indicates that this might be the case. However, caution needs to be taken when interpreting DNA recovered from ancient deposits.

To validate the hopanoid proxy, Xie *et al.* employed an inorganic proxy. This proxy is based on the relative abundance of fine-grained magnetic miner-

als in total ferromagnetic particles collected from a stalagmite in the Heshang Cave in central China, ~200 km south of the Dajiuhe peatland. The term *anhysteretic remanent magnetization* (ARM) is commonly used to characterize the magnetic property of fine-grained particles having a single domain; the term *saturation isothermal remanent magnetization* (SIRM) characterizes the total magnetic property in a sample containing not only single-domain particles but also pseudo-single-domain and multidomain grains that are commonly coarser than the single-domain particles. In soil environments, fine-grained magnetic particles (e.g. magnetite and/or greigite) can be produced by microorganisms, such as magnetotactic bacteria and iron-reducing bacteria [4] or by pedogenic processes. Coarser-grained magnetic particles (magnetite, maghemite, titanomagnetite or hematite), in contrast, are commonly derived from weathering of igneous or metamorphic rocks, so-called detrital sources. Xie *et al.* were unable to identify any of these minerals from the stalagmite because of the difficulty of isolating them without chemical damage. However, the authors cleverly linked the ratio of ARM/SIRM of the stalagmite in the sub-ground to the hydrological dynamics of the soil above the ground, with low ARM/SIRM ratios indicating a high water level in the soil resulting from greater rainfall.

One caveat of the ARM/SIRM proxy is that the fine magnetic particles formed in the soil can go through transformation or degradation [5] during

transport to the sub-ground cave. Fine-grained magnetite or greigite, produced by iron- or sulfate-reducing bacteria under anoxic conditions in the soil, can be very sensitive to oxidation when exposed to air and can, thus, potentially change the magnetic property of the particles and make the ARM/SIRM value less reliable as a reflection of the soil hydrological condition. Another unresolved question lies in the lag time between a heavy rainfall event and the draining of the magnetic particles from the soil to the stalagmite deposit.

Nevertheless, Xie *et al.* made a successful attempt in using geobiological ap-

proaches to address major archaeological questions. Uncertainties of the organic and inorganic proxies raised in this study can actually promote further geobiological research in other fields. For example, the study of fossil DNA from the hopanoid-producing bacteria in the peat bog may lead to better understanding of ancient microbial community structures responsive to the paleoclimatic conditions, while the examination of the sources and mechanisms of the formation of magnetic particles in the soil may strengthen the application of the ARM/SIRM in stalagmite research.

Chuanlun Zhang

State Key Laboratory of Marine Geology, School of Ocean and Earth Sciences, Tongji University, China

**Corresponding author.** E-mail: Archaea.zhang@gmail.com

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