However, those bryozoans have a complex form (morphology), and must therefore have already had a long evolutionary history. In addition, molecular studies estimating when bryozoans originated point to a time 44 million years earlier than these fossils, in the early part of the Cambrian[5,6].

Many fossils were suggested previously to be candidate Cambrian bryozoans, but ultimately proved to be something else. Now Zhang and colleagues describe a fossil species as being the oldest known bryozoan. The species is named *Protomelission gatehousei*, and it is assigned to the early Cambrian of Australia and south China. The remains represent millimetre-sized skeletons of a modular animal that has characteristics best known in bryozoans. The skeletons of this fossil have features that are associated in particular with a bryozoan suborder called the Ptilodictyina, which was present in the Ordovician.

*Protomelission gatehousei* does not show any kind of variation in the forms of the zooids that would indicate a division of labour in the colony. The zooids are uniform in shape and size and are arranged in simple linear series of rows. This animal is assumed to have been unmineralized, and was preserved because of other changes (a chemical modification called secondary phosphatization) to its body walls. Such mineralization is common in the Cambrian because the waters of this period were highly enriched in the phosphorus ions required for this modification. In the Ordovician, the level of dissolved calcium carbonate in seawater increased, and these conditions enabled the rapid diversification of animals and plants that contained calcite in their skeletons. Bryozoans acquired carbonate skeletons and diversified, together with many other phyla, as part of what is called the Great Ordovician Biodiversification Event.

Zhang and colleagues' study shows that bryozoan evolution had a notable, previously hidden history in the early Cambrian. Although this was assumed by many researchers, only now is there reliable evidence for it. The absence of hard skeletal parts in *P. gatehousei* explains why bryozoans were previously missing from the fossil record of the Cambrian.

Among modern bryozoans, groups called the Ctenostomata and the Phylactolaemata are unmineralized, and both, predictably, have poor fossil records. Stenolaemata — the group of calcite-skeleton-containing bryozoans that is most abundant and diverse in the Palaeozoic — are assumed to have been derived from an unknown, soft-bodied ancestor described as being ctenostome-like, with an unmineralized body wall and a box-shaped zooecia (the compartment surrounding the animal's zooids). *Protomelission gatehousei* shares features with both ctenostomes (an unmineralized body wall and a box-shaped zooecia) and

stenolaemates (a budding pattern of zooecia and a two-sided colonial structure, similar to a leaf, with zooids on each side), and fits well as a candidate for one of the early ancestors of bryozoans. Now that this ancestral mystery has been solved, attention can move to filling in the story of bryozoan evolution from the early Cambrian to the early Ordovician.

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## Genomics

# The unexpected ancestry of Inner Asian mummies

## Paula N. Doumani Dupuy

The genomes of Bronze Age mummies from the Tarim Basin in northwest China suggest that these individuals were descended from an ancient Asian population that was genetically isolated, despite extensive cultural interactions in the region. **See p.256**

Discoveries of 4,000-year-old naturally mummified individuals in the remote deserts of the Tarim Basin in the south of present-day Xinjiang, northwest China, have prompted decades of speculation about the individuals' ancestry. On page 256, Zhang *et al.*[1] resolve the question of the genetic origins of the mummies, and suggest that they were descended from an ancient, genetically isolated population. The authors' conclusions have implications for future studies of Inner Asian prehistory that must address the complex relationship between cultural exchange and genetic ancestry.

Natural preservation of organic material in ancient archaeological sites of Inner Asia is usually poor, thus limiting the scope of prehistoric research. The arid environment of the Tarim Basin is exceptional because it enabled the preservation of its inhabitants after burial, through natural mummification. The basin holds several intact Bronze Age cemeteries of a founding population known as the agropastoral Xiaohe culture, which formed around 2100 BC in what were then freshwater environments (the Bronze Age spanned from about 3000 to 1000 BC). The individuals' paddleboat-shaped wooden coffins, covered by cattle hides, are unlike any other type of burial custom from Inner Asia. Notably, the mummies have a 'Western' physical appearance, and wear colourful clothing made from the wool of west Eurasian sheep breeds. Their

graves also contain a mix of preserved foods — including cheese, wheat and millet — that suggest wider trans-Eurasian interactions.

The cosmopolitan character of this ancient civilization has resulted in various hypotheses that mostly favour migration from other regions as underlying the emergence of the Xiaohe culture. Zhang *et al.* set out to test three such hypotheses, named on the basis of the proposed source population of these migrations (Fig. 1). The first is the steppe hypothesis, which proposes that herders with Afanasievo (west Eurasian) ancestry made their way south from the Altai and Sayan mountains in south Siberia, through the Dzungarian Basin, to the Tarim Basin[2]. The second proposal, the oasis hypothesis, suggests that oasis farmers from the Bactria and Margiana regions in southern Central Asia moved eastward to the Tarim Basin[3]. The third proposed account, the Inner Asian Mountain Corridor (IAMC) island-biogeography hypothesis, posits that the Xiaohe culture emerged from mobile agropastoral communities along the Tianshan and Altai mountains that border Xinjiang to the west[4].

To investigate these hypotheses, the authors analysed the DNA of 18 individuals in Xinjiang: 13 from the Xiaohe culture in the Tarim Basin, dated to the Middle Bronze Age (2100–1700 BC), and 5 from the Dzungarian Basin in northern Xinjiang, dated to the Early Bronze Age (3000–2800 BC). The proteins in

the mineralized plaque (calculus) on the teeth of seven of the Tarim Basin individuals were also examined, to reconstruct their diets.

Zhang and colleagues retrieved ancient genome sequences from these 18 individuals, and compared this information with data from existing ancient and modern DNA databanks to place the studied individuals in the context of Eurasian population genetics. The authors also modelled several scenarios of the combination of genes from different populations, known as admixture, allowing them to identify potential source populations and their relative contributions to the Early and Middle Bronze Age societies of the Dzungarian and Tarim basins.

None of the 18 individuals examined was descended from Bronze Age populations that inhabited regions of southern Central Asia or the IAMC, ruling out the oasis and IAMC island-biogeography hypotheses. Notably, the authors' findings support previous population-genetics work[5] that demonstrated considerable transfer of gene variants between populations along the IAMC by individuals, but found no substantial migrations.

This left the steppe hypothesis, which proposes that the mummified individuals of the Xiaohe culture were descended from Afanasievo-related dairying pastoralists who settled in the Altai–Sayan mountains after migration from the Pontic–Caspian steppe in the Early Bronze Age (Fig. 1). This movement is supported by the archaeology[6], diet[7] and genetics[5] of individuals at Afanasievo sites in south Siberia that collectively point to cultural affinities and shared DNA along this steppe route. Moreover, the authors' dental-calculus analysis showed that Xiaohe culture individuals around 2100 BC consumed dairy products, suggesting that their diet, like that of earlier Afanasievo pastoralists, depended on milk products.

However, the genetic-admixture models could not confirm the presence of DNA of Afanasievo individuals in the Tarim Basin, suggesting that the steppe hypothesis is also incorrect. Instead, the authors' models fitted when two genetic groups of ancient Asian people were included as the main source. The uncovered mixed Asian ancestry was derived mainly from hunter-gatherers who inhabited the north Eurasian steppe and Siberia, with a smaller contribution from hunter-gatherers from the Lake Baikal region in northeast Asia (Fig. 1). The authors estimate that this north Eurasian group formed more than 9,000 years ago, long before the Bronze Age pastoral communities emerged.

Traces of this ancient genetic family were previously detected among several Bronze Age steppe and IAMC populations, showing that it was once widespread[5]. The authors found that descendants of this ancient population persisted in the Tarim Basin into the Bronze



**Figure 1 | Determining the ancestry of Bronze Age mummies from the Tarim Basin.** The ancestry of the naturally mummified Bronze Age individuals who lived about 4,000 years ago in the Tarim Basin of present-day southern Xinjiang, China, has been unclear. Zhang *et al.*[1] examined the complete genomes of 18 Bronze Age mummies from the Tarim and Dzungarian basins, to test various hypotheses of the ancestry of these populations. The steppe hypothesis suggests that the source population comprised dairying pastoralists (whose west Eurasian ancestors crossed the Eurasian steppe) who had moved south from the Altai–Sayan mountains. The Inner Asian Mountain Corridor island-biogeography (IAMC-IB) hypothesis proposes that the Tarim Basin individuals were descended from agropastoralists of the Inner Asian mountains. The oasis hypothesis posits that farmers from the Bactria–Margiana region were the source population. The authors' genetic models did not support any of these proposed scenarios. Instead, their modelling suggests that the Tarim Basin individuals were descended from a local population that was formed about 9,000 years ago from two genetic groups of ancient Asian people, and that became genetically isolated in southern Xinjiang.

Age. They explain that a population 'bottleneck' scenario accounts for its predominance in the mummies' DNA, whereby a small group entered the Tarim Basin — possibly during the Early Bronze Age — and became genetically, but not culturally, isolated. If, as Zhang and colleagues suggest, the Tarim mummies are the best representative of the descendants of a pre-pastoralist Asian population, then some revisions to the models of genetic admixture across Eurasia should be expected.

Afanasievo cemeteries have been found in the Dzungarian Basin[1], and Zhang and co-workers found that individuals from some Dzungarian cemeteries share a close genetic relationship to west Eurasian (Afanasievo) populations. But a more complex picture than simple 'colonization' by the Afanasievo dairying pastoralists emerged in their admixture models, which attributed a proportion of the ancestry of the Dzungarian Basin individuals to the two genetic groups from Asia detected in the Tarim Basin mummies. The authors conclude that the Dzungarian Basin population genetics of the Early Bronze Age is consistent with social interactions and genetic mixing between newly arrived (west Eurasian) and pre-existing (Asian) local people.

Zhang *et al*. tackle long-standing disagreements about the ancestry of the Xiaohe culture

mummies, and their study therefore contributes discoveries worthy of attention. Notably, Middle Bronze Age populations of the Tarim Basin contain no genetic ancestry consistent with substantial migrations from west Eurasian populations. But the same cannot be said for their neighbours in the Dzungarian Basin, where incoming steppe herders and descendants of long-established hunter-gatherers together contributed to the genetics and culture of these individuals.

Until now, DNA studies of Xinjiang's early populations focused on the DNA of cellular organelles called mitochondria[8–10]. Although Zhang and co-workers obtained complete genomic data for two key regions of Xinjiang, the cosmopolitan populations mummified in the Tarim Basin still retain some of their ambiguity. Several new questions must shape future research. Do the mummies represent a population confined to the basin from an earlier point in the past, or did they enter only during the Bronze Age? What knowledge and traditions did those groups bring, and why did they settle in this extreme environment?

Resolving these questions will require more-specific archaeological and genetic data for the preceding periods in underexplored regions of Xinjiang and its surroundings. A handful of archaeological sites with dates

earlier than the middle of the third millennium BC (refs 11–13) already open avenues to investigate the initial dispersal of agro-pastoral communities into Xinjiang and along the mountains at its edge. It will be crucial to know how the Tarim Basin individuals were connected with those earlier groups, or with other groups as yet undiscovered by scientists, to understand the social origins of this ancient culture.

The two disparate stories of southern and northern Xinjiang demonstrate that even the most comprehensive analysis of ancient DNA cannot fully divulge the cultural practices and choices that contribute to the archaeological past. Zhang and colleagues' description of the unique and cosmopolitan Xiaohe culture of the Tarim Basin alongside the Dzungarian Basin populations provides an example supporting previous arguments[4,14] that cultural ideas and new technologies moved fluidly through Inner Asia and took on assorted iterations in each society they touched.

Future research must consider the social mechanisms that account for the varied choices individuals made regarding food, clothing and the people with whom they settled, as well as their traditions of burying their dead. Zhang and co-workers have answered the question of the genetic origins of the Xiaohe culture. Now it is up to the collaborative input of scholars to further explain the dynamic and varied patterns of cultural exchange that define the Bronze Age of Inner Asia.

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Tumour biology

# Diet analysis suggests lipid imbalance slows cancer

## Giulia Salvadori & Valter D. Longo

Understanding how diet affects tumour growth could lead to better treatments. Analysis in mice reveals that a low-calorie diet, but not a ketogenic diet, slows the growth of pancreatic cancer. This effect is mediated by lipid changes. **See p.302**

Various diets, such as those that periodically restrict calorie intake and thereby drive metabolic changes associated with fasting (periodic fasting-mimicking diets)[1], or ones that are low in carbohydrates and high in fat (ketogenic diets), are emerging as nutritional interventions that can delay cancer growth and perhaps boost the effect of anticancer drugs[1,2]. Whereas long-term calorie restriction is not feasible for people on most cancer therapies because it leads to weight loss and lean body mass[3], ketogenic diets and periodic fasting-mimicking diets are beginning to be tested in a series of clinical trials, and are particularly promising when used in combination with standard therapies[1,2,4–6]. On page 302, Lien *et al.*[7] fill in some of the missing details about how diet affects cancer growth.

Animal studies provide evidence suggesting that various dietary interventions can be potent in combination with standard anticancer drugs[4]. But the results also underline the importance of both the relative levels of calories, proteins, fats and carbohydrates in a diet, and the duration and frequency of the diet's administration. What makes the implementation of certain diets in the clinic even more complex is that they can be highly effective in combination with one drug, but ineffective with another. Thus, understanding the molecular mechanisms that enable dietary interventions to result in toxicity to cancer cells, or to increase the effectiveness of standard drugs, is essential to the development of standard-of-care (treatments routinely recommended by clinicians) cancer therapies that include a dietary component.

Lien and colleagues' study contributes molecular insights (Fig. 1) into how the effectiveness of different diets in slowing the growth of various cancers depends on how the diets affect the lipids in the blood and tumour. The authors examined mice that had one of two types of cancer: pancreatic
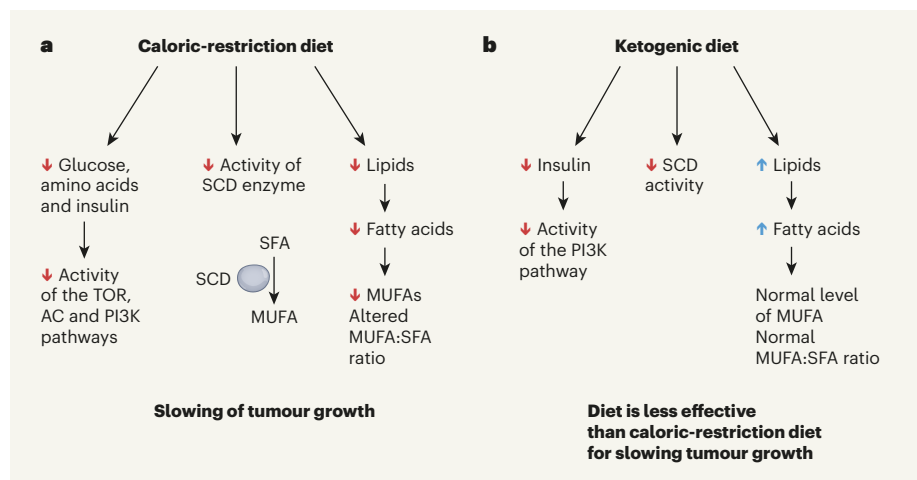


**Figure 1 | How diet affects tumour growth in mice. a**, A low-calorie diet slows tumour growth by lowering glucose, amino acids and the hormone insulin and thereby inhibiting various tumour-promoting signalling pathways (the TOR, AC and PI3K pathways)[4]. Lien *et al.*[7] report that this diet also inhibits the enzyme SCD, which can convert a saturated fatty acid (SFA) to a monounsaturated fatty acid (MUFA). The perturbed balance of fatty acids slows the growth of pancreatic tumours. **b**, A ketogenic diet, high in fat but of normal calorie content, also influences the insulin pathway as Lien *et al.* report. However, it does not alter the SFA:MUFA ratio, and it enables pancreatic tumours to grow.