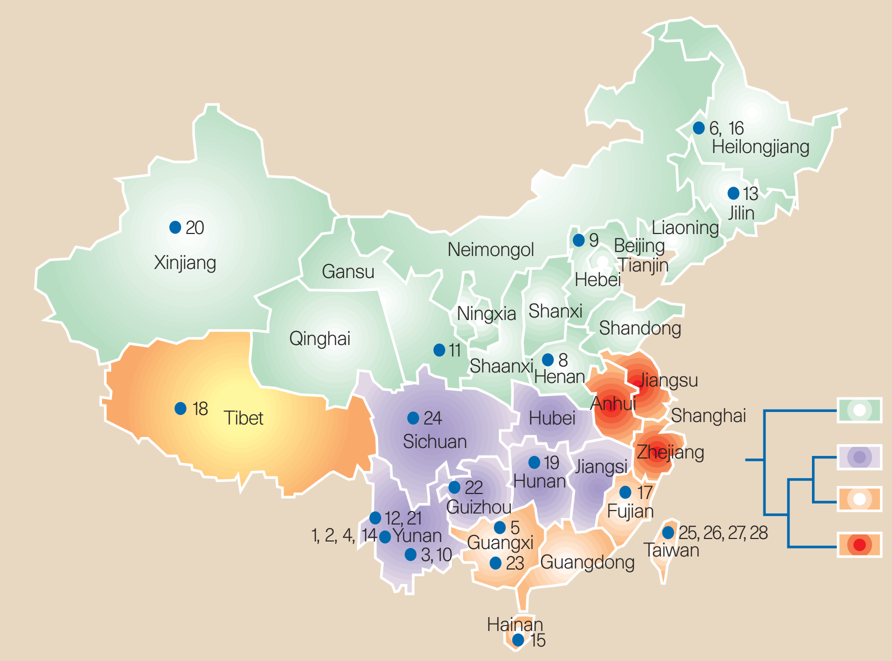

Figure 2 **Map of China showing locations of the sampled populations, and geographical display of a phylogenetic tree based on Han surnames (from ref. 9). Sampled populations are numbered 1–28, but sample 7 is not shown as it is Han from the Bay area of California.**

genetically different — at least from the relatively few samples tested by blood-group and protein-marker polymorphisms. But this heterogeneity, supported by anthropological, environmental, archaeological, prehistoric and historical evidence, was far from a robust result derived from well-planned genetic surveys at a micro-geographical level. Physical appearance, as anywhere and at any time, was an important factor in recognizing these differences. The northern Chinese tend to be taller and paler, with smaller eyes that seem more 'slanted'. Moreover, old skeletons differ, the southern ones being more similar to contemporary South-east Asian types, especially those with a darker skin (such as the so-called Negritos)[3].

Chu *et al.*[1] used 15 to 30 microsatellites to test genetic variability in 28 samples from the different provinces of China. Microsatellites are repeats of short DNA segments, widely distributed in our genome, that are commonly used in evolutionary analyses because they are numerous, inherited in Mendelian fashion, highly variable and easy to handle. The Chinese government officially recognizes 56 different ethnic groups. The Han (from the name of the great Han dynasties, 206 BC to AD 220) is the most important in terms of numbers (1.1 billion people) and historical tradition. The other 100 million Chinese people are found mostly in southern China, nearly half of them in one province, Yunnan.

Chu and colleagues sampled four Han groups and 24 minority groups. They also tested four East Asian, two American Native, one Australian, one New Guinean, four Caucasoid and three African samples with the same set of microsatellites, as non-Chinese control populations. They summarize the genetic differences in two phylogenetic trees, the main features of which are shown in Fig. 1. This tree is robust (as measured by the 'bootstrap' reproducibility test[4]) only where it represents populations that are very distant from one another both geographically and genetically (that is, populations outside East Asia). There are much smaller genetic differences between East Asian populations, and historical records document many incidents of possible gene flow between them. So a tree model of evolution may not be the best one to describe the genetic history of China — as has been repeatedly pointed out in the genetic analysis of European populations[5].

The main structure of the tree agrees closely with previous results using classical, non-DNA genetic markers[6]. Its root separates African from non-African populations, and all East Asian populations cluster together, their nearest genetic neighbours being American Natives, followed by Australian aborigines and New Guineans. These results agree with the subsequent settlement times of Australia (about 60,000 to 50,000 years ago) and the Americas (from 30,000 to 15,000 years ago). The southern group of Chinese samples is distributed in three genetically related clusters, called S1, S2 and S3 (Fig. 1). The clusters differ in the number of minority groups that inhabit the Yunnan region, and in the language distribution; only one Han Chinese-speaking group is included (in S2) from the province of Henan.

▶

Behavioural ecology

Pick out a penguin

It's party time. The hi-fi is booming, and people are chattering loudly. Yet you can readily hear a couple talking at the other side of the room. This is the 'cocktail party effect', a phenomenon familiar to attentional psychologists. And penguins.

Breeding colonies of king penguins (*Aptenodytes patagonicus*) on subantarctic islands can number up to 300,000 birds. Penguin chicks, of course, need feeding, and must find the parent that has been foraging at sea on the latter's return. It is known that the initial detection is by vocal cues rather than sight or smell. But how good are chicks at identifying the parent's call when it is masked by the background din of the colony and screened by intervening bodies?

T. Aubin and P. Jouventin have tackled the question (*Proc. R. Soc. Lond. B* 265, 1665–1673; 1998). They measured the amplitude and other acoustic properties of parental calls and the ambient noise of a king-penguin colony; they then assessed the propagation of the call in the centre of the feeding area, as compared to an open area, to quantify the screening effect of bodies. In playback experiments, a chick reacted only to calls made by its own parent, turning and then running towards the source. Further experiments involved 'jamming' the calls of one parent by mixing in the calls of other adults, mimicking the true situation in the feeding zone.


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The authors' calculations suggest that the maximum distance at which the chick should be able to detect its parent against the background cacophony should not exceed 8–9 metres. But even when the parent's calls were jammed, chicks picked them out at nearly twice that distance. This remarkable feat of auditory discrimination is yet to be explained.

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