

Genomics, bears, fruit

The origins of three species and the adaptive evolution of their genomes under natural and agricultural selection are investigated in this issue.

When life gives you lemons, make lemonade. When it presents you with sweet oranges, mandarins, pummelos, watermelons and 34 giant pandas, it is time to party. In this new year, the celebration is for the ideas of Alfred Russel Wallace, the discoverer of evolution by natural selection, who was born on 8 January 1823 and died 100 years ago.

In *The Panda's Thumb* (Norton, New York, 1980), Stephen Jay Gould noted the marvelous evolutionary adaptation of the panda's radial sesamoid bone that converges on the grasping function of our opposable thumbs. The panda's tongue is no less remarkable, as this is the bear that lost the taste for meat. Its umami taste receptors have degenerated to nonfunctional pseudogenes. And, on page 67 of this issue, Fuwen Wei and colleagues report that two taste receptor genes homologous to human bitter receptors are under directional selection in one of the three distinct populations of pandas, with one, *Tas2r49*, being positively selected. The authors note that the panda eats shoots and leaves. In different geographic regions of China, distinct populations consume these bamboo foods in different proportions. These observations raise a hypothesis that should be tested: namely, that the bitter cyanogenic glycoside in bamboo, taxiphyllin (<http://www.chemspider.com/Chemical-Structure.96890.html>), might be a ligand for one or both of the two selected taste receptors, with alleles conferring greater or lesser sensitivity that is used by the leaf-eating pandas to select less toxic food.

Although the pandas are the poster bears for endangered wildlife, they do not lack genetic diversity and are unlikely to become extinct because of a shallow gene pool. Their genetic diversity is sufficient to model the way in which the effective population of prehistoric pandas fell and rose with cycles of climate cooling and warming, respectively, finally declining in the last few

thousand years as a result of habitat fragmentation associated with human activities. This rollercoaster history is corroborated by the climate record of pollen deposits and fossil pandas of three extinct species. One in 50 of the wild pandas alive today participated in this study, a recruitment rate of which human geneticists in much of the world can only dream.

Watermelon and orange are highly valued crop fruits, each with a distinctive history of agricultural selection, which is demonstrated by genome sequencing projects published in this issue that go far beyond the basic strategy of assembling a first reference genome. In the case of melon (p. 51), 20 wild and cultivated accessions were used to assess the genetic diversity of the species, with the finding that selection for nutritional and taste characteristics has left the crop with a poor repertoire of disease resistance variants with respect to wild relatives. By assembling markers for breeding improvement, it should now be relatively straightforward to reintroduce some of this variation while retaining the fruit's sweet and colorful virtues. The sweet orange is here shown to be a lucky accident (p. 59), with its hybrid genome frozen in time by the citrus tree's clonal mode of reproduction. Each cultivar consequently accumulates distinctive local genetic variation, sets of mutations that would have to be introduced and propagated rather laboriously from one variety to another.

We do not have to just believe in the process of evolution by natural selection. We can see mutation and selection produce varieties and species of crop plants. We can see the process at work in the wild and admire the way it creates and shapes species and populations of animals and plants. And, the most wonderful thing of all is that you can test the predictions of the idea with your own experiments, with your own eyes. ■