News

Sunlight Adaptation Region of Neanderthal Genome Found in up to 65% of Modern East Asian Populations

With the Neanderthal genome now published, for the first time, scientists have a rich new resource of comparative evolution. For example, recently, scientists have shown that humans and Neanderthals once interbreed, with the accumulation of elements of Neanderthal DNA found in up to 5% in modern humans.

Are there any advantages to the retention of Neanderthal DNA that favors modern humans? In a new article published in Molecular Biology and Evolution, Ding et al. (2013) present evidence for the accumulation of a Neanderthal DNA region found on chromosome 3 that contains 18 genes, with several related to ultraviolet (UV)-light adaptation, including the Hyal2 gene. Their results reveal that this region was positively selected and enriched in East Asians, ranging from up to 49% in Japanese to 66% in southern Chinese.

Interestingly, the authors note the geographic distribution of the Neanderthal genomic region suggests that UV-light mutations were shown to be lost during the exodus of modern human from Africa and reintroduced to Eurasians from Neanderthals. “Overall, it is still very controversial whether there is more Neanderthal DNA contributions to Asians than Europeans, as we have evidence to argue against this,” said Lin. “Although in the case of the Hyal2 variant, it did indeed have a higher frequency in Asians.”

From 45,000 to 5,000 years BP, effective population sizes of the Neanderthal region increased at a steady rate. Notably, the growth rate of the effective population size increased at around 5,000–3,500 years BP, which suggests a population expansion event. This Asian-specific Neanderthal evolutionary event is also consistent with previous reports of higher levels of Neanderthal ancestry in East Asians than in Europeans.

Reference

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How a Scorpion Gets Its Sting

Defensins, as their name implies, are small proteins found in plants and animals that help ward off viral, bacterial, or fungal pests. One fascinating question of invertebrate evolution is how these proteins evolved into venoms to attack their prey.

Based on structural similarity, it was proposed that scorpion toxins and antimicrobial invertebrate defensins could have a common ancestor. To address how a nontoxic protein develops into a toxin, authors Zhu et al. (2014) studied the evolution of scorpion venom-derived neurotoxins, known as α-KTx.

In a recent study, published in Molecular Biology and Evolution, they analyzed the α-KTx family sequences to extract the conserved amino acid sites associated with neurotoxin structure and function (called “scorpion toxin signature,” abbreviated as STS). They searched for insect defensins that contain a STS to unlock the molecular mechanisms behind STS evolution. Their results show that a STS-containing insect defensin can be converted to the scorpion α-KTx-like neurotoxin through just a single genetic deletion event. The study provides the first functional evidence for an connection between insect defensins and scorpion α-KTxs, and how one small genetic mutation leads to a new protein function to give scorpions their deadly sting.

“The most significant findings of our paper are the predictability of scorpion toxicity evolution—arising via structural deletion of a loop on an ancestral defensin scaffold recruited into the venom to remove steric hindrance of peptide-channel interaction,” said lead author Dr Shunyi Zhu. “Our work represents an excellent example of divergent evolution, where structural alteration in an ancestral scaffold led to functional shift of proteins from fighting against microbes to attacking prey.”

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