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Dramatic evolution within human genome may have been caused by malaria parasite

March 23, 2017 - - - A genetic mutation that protects people from a common form of malaria spread like wildfire in sub-Saharan Africa about 42,000 years ago, according to a new study. Today, it’s nearly impossible to find somebody from this region who doesn’t have it. That makes the mutation one of the swiftest, strongest changes to the human genome yet seen—though it remains a mystery why this particular disease sparked such a dramatic evolutionary response.

The world’s most widespread type of human malaria is caused by *Plasmodium vivax*, a single-celled parasite transmitted by mosquitoes. Although less deadly than other strains, *P. vivax* malaria remains a disruptive disease: It infected some **16 million people** across the globe in 2013. Yet across much of sub-Saharan Africa, *P. vivax* accounts for fewer than 5% of all reported malaria cases. That’s because about 99% of Africans living here have a variant of a gene called *DARC*, which shuts off a particular protein receptor on the surface of red blood cells that the parasite needs to gain entry.

To learn more about how and when this mutation spread, Omar Cornejo, a population geneticist at Washington State University in Pullman, and colleagues analyzed full genome sequences from 1000 modern individuals from 21 population centers in Africa, Asia, and Europe. The researchers then employed a computer-based simulation that predicts how certain genetic variants spread throughout a population over time given the region’s known demographics and various selective pressures.

For more information, see http://www.sciencemag.org/news/2017/03/dramatic-evolution-within-human-genome-may-have-been-caused-malaria-parasite

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