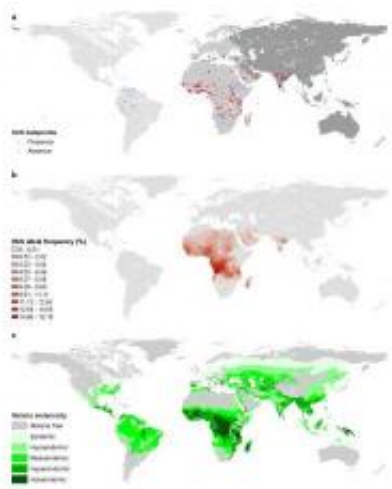


Global map of the sickle cell gene supports 'malaria hypothesis'

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These are maps showing the distribution of the HbS "sickle cell gene" and the endemicity of malaria. Credit: Malaria Atlas Project

At a global scale, the sickle cell gene is most commonly found in areas with historically high levels of malaria, adding geographical support to the hypothesis that the gene, whilst potentially deadly, avoids disappearing through natural selection by providing protection against malaria.

In a study funded by the Wellcome Trust, geographers, biologists and statisticians at the University of Oxford, together with colleagues from the KEMRI-Wellcome Trust Programme in Kenya, have produced the

first detailed global map showing the distribution of the sickle cell gene. The results are published today in open access in the journal *Nature Communications*.

Haemoglobin S (HbS) is known to cause sickle cell disease, which is usually fatal if untreated. [Natural selection](#) suggests that such a disadvantageous gene should not survive, yet it is common in people of African, Mediterranean and Indian origin.

More than sixty years ago, researchers observed that the sickle cell gene tended to be more common in populations living in, or originating from, areas of high malaria prevalence. This led to the 'malaria hypothesis', which suggested that, although deadly when inherited from both parents, the gene provided a degree of protection from malaria in children inheriting it from just one parent. This protective advantage was strong enough in areas of intense [malaria transmission](#) for the gene to survive.

The malaria hypothesis has since been supported by both population and laboratory studies, but the original observations of a geographical overlap between frequency of the gene and malaria prevalence have never been tested beyond simple visual comparisons at the global scale.

To address this, Dr Fred Piel and colleagues collated all the information currently accessible on the occurrence of the sickle cell gene in native populations worldwide and, using modern mapping techniques, created a map of the global frequency of this gene. The map was then compared with the distribution and intensity of malaria before widespread malaria control.

The study showed that the sickle cell gene is most common in sub-Saharan Africa, the Middle East and India, and that the areas of high frequency of this gene are coincident with historically high levels of malaria, thus confirming that the malaria hypothesis is correct at the

global scale.

"This study highlights the first steps in our efforts to create an open-access, online database of the frequency of various inherited blood disorders," says lead author Dr Piel, from the University of Oxford. "Such databases will help improving estimates of their public health burden and guide where resources would be best applied."

More information: The sickle frequency map was created as part of the activities of the Malaria Atlas Project, a multinational research collaboration funded primarily by the Wellcome Trust. Further information about the Malaria Atlas Project can be found at www.map.ox.ac.uk

Provided by Wellcome Trust

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