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Genetic barcode for malaria could help contain outbreaks

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A new genetic 'barcode' for malaria parasites has been found which could be used to track and contain the spread of the disease, according to new research published in *Nature Communications*.

Malaria kills around 600,000 people per year, and increased population mobility through international air travel carries risks of re-introducing parasites to elimination areas and dispersing drug-resistant varieties to new regions. A simple genetic marker that quickly and accurately identifies the geographic origin of infections would be a valuable tool for locating the source of outbreaks, and spotting the spread of drug-resistant parasites from Asia to Africa.

New research, led by the London School of Hygiene & Tropical Medicine, has found a highly predictive barcode in the genetic sequence of the malaria parasite *Plasmodium falciparum* which can be used to identify the geographic origin of a parasite from a blood sample and monitor its spread.

The researchers analysed the DNA of over 700 *P. falciparum* malaria parasites taken from patients in 14 countries in West Africa, East Africa, South East Asia, Oceania and South America. They found several short genetic sequences which were distinct in the DNA of parasites from certain geographic regions, which allowed them to design a genetic 'barcode' to be used in identifying the source of new infections.

Lead author [Dr Taane Clark](#), Reader in Genetic Epidemiology and Statistics at the London School of Hygiene & Tropical Medicine, said: "Being able to determine the geographic origin of malaria parasites has enormous potential in containing drug-resistance and eliminating malaria. Our work represents a breakthrough in the genetic barcoding of *P. falciparum*, as it reveals very specific and accurate sequences for different geographic settings. We are currently extending the barcode to include other populations, such as India, Central America, southern Africa and the Caribbean, and plan to include genetic markers for other types malaria, such as *P. vivax*."

Genetic markers have proved extremely valuable in tracking and eradicating diseases, such as polio. However, previous candidates for malaria genetic barcodes have relied on identifying DNA markers found in the parasite's cell nucleus, which shows too much genetic variation between individual parasites to be used accurately.

Now for the first time, the researchers studied the DNA found in two parts of the parasite's cells outside of the nucleus. The mitochondria (the 'power houses' of the cell) and the apicoplasts (used in the cell's metabolism) are only inherited through maternal lines and so their genes remain much more stable over generations, and have therefore often been used as tools to explore the origins of humans.

By identifying short sequences in the DNA of the parasite's mitochondria and apicoplasts which were found to be specific for different geographic locations, the team were able to design a highly accurate genetic barcode (92% predictive) which is stable and geographically informative over time.



Study co-author [Dr Cally Roper](#), Senior Lecturer in Malaria Genetics at the London School of Hygiene & Tropical Medicine, said: “By taking finger-prick bloodspots from malaria patients and using rapid gene sequencing technologies on small amounts of parasite material, local agencies could use this new barcode to quickly and accurately identify where a form of the parasite may have come from, and help in programmes of malaria elimination and resistance containment.”

The authors say this barcode is limited as the current study lacks representation of the Indian sub-continent, Central America, southern Africa and the Caribbean, owing to the scarcity of sequence data from these regions. In addition, there is a need to study more samples from East Africa, a region of high genetic diversity, high migration and poor predictive ability.

Publication

Mark D. Preston et al. [A barcode of organellar genome polymorphisms identifies the geographic origin of *Plasmodium falciparum* strains](#). *Nature Communications*. DOI: 10.1038/ncomms5052

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