Over the past decade, most countries endemic for *Plasmodium falciparum* malaria have shifted their national treatment policies to artemisinin-based combination therapies (ACTs), although many of these countries still do not conduct routine therapeutic efficacy studies. The development of parasite resistance to artemisinin – the key compounds in ACTs – is a major public health concern.

Resistance is occurring as a consequence of several factors, including poor treatment practices, inadequate patient adherence to prescribed antimalarial regimens, and the widespread availability of oral artemisinin-based monotherapies and substandard forms of the drug.

*Plasmodium falciparum* resistance to artemisinin derivatives in Southeast Asia threatens malaria control and elimination activities worldwide. To monitor the spread of artemisinin resistance, a molecular marker is urgently needed.

Using whole-genome sequencing of an artemisinin-resistant parasite line from Africa and clinical parasite isolates from Cambodia, mutations in the PF3D7\_1343700 kelch propeller domain ('K13-propeller') with artemisinin resistance in vitro and in vivo were associated.

K13-propeller polymorphism constitutes a useful molecular marker for large-scale surveillance efforts to contain artemisinin resistance in the Greater Mekong Sub region and prevent its global spread.

## **Read more**

## A molecular marker of artemisinin- resistant Plasmodium falciparum malaria

## **Related links**

Emergency response to artemisinin resistance in the Greater Mekong sub region (ERAR) – a regional framework for action to guide an emergency scale-up of containment efforts in affected countries [pdf 1.7Mb]

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