# 'Open science' paves new pathway to develop malaria drugs

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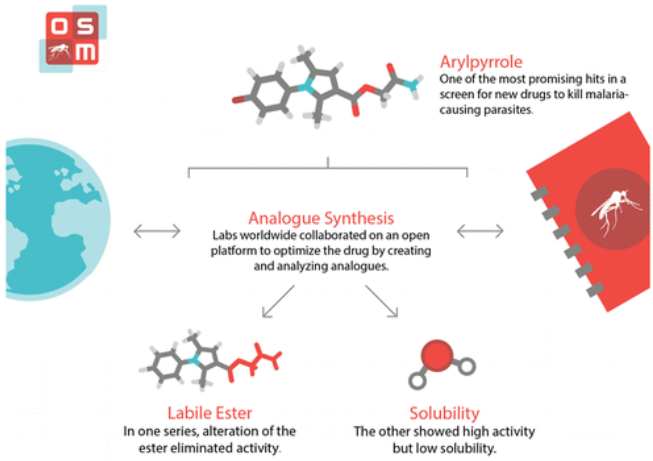


Credit: American Chemical Society

Malaria remains one of the world's leading causes of mortality in developing countries. Last year alone, it killed more than 400,000 people, mostly young children. This week in *ACS Central Science*, an international consortium of researchers unveils the mechanics and findings of a unique "open science" project for malaria drug discovery that has been five years in the making.

The current gold standard antimalarial treatments are based on artemisinin, a compound developed in the 1970s in China, combined with a partner drug. Yet, resistance to artemisinin and its partners has already emerged in some parts of the world. If the resistance spreads, there are no viable replacement treatments. Given the lack of commercial incentive for industry to develop drugs for neglected diseases such as malaria, and because academic researchers often lack resources to move compounds forward, there is a clear need for new approaches. In response, Matthew Todd from the University of Sydney together with the not-for-profit research and development organization Medicines for Malaria Venture proposed an "open source" solution akin to the open source concept used in software development.

More than 50 researchers from 21 organizations in eight countries added their research to the project, which started with a large set of potential drug molecules made public by the company GlaxoSmithKline. Anyone willing to contribute—anywhere in the world—was welcome to share data and collaborate by adding comments to an electronic notebook as part of the Open Source Malaria Consortium. Some scientists designed and synthesized new generations of the antimalarial compounds; others ran assays and interpreted results. Several rounds of research were conducted, addressing water solubility and structural issues, with all the data being made public in real time. A wide array of scientists, from professors to undergraduates, participated by choice, agreeing that no one would individually seek patents to protect their contributions. The authors note that the current results, while promising, are merely the beginning of the story. They continue to welcome additional contributions, also researched openly and collaboratively.

**More information:** Alice E. Williamson et al. Open Source Drug Discovery: Highly Potent Antimalarial Compounds Derived from the Tres Cantos Arylpyrroles, *ACS Central Science* (2016). DOI: 10.1021/acscentsci.6b00086

**Abstract**

The development of new antimalarial compounds remains a pivotal part of the strategy for malaria elimination. Recent large-scale phenotypic screens have provided a wealth of potential starting points for hit-to-lead campaigns. One such public set is explored, employing an open source research mechanism in which all data and ideas were shared in real time, anyone was able to participate, and patents were not sought. One chemical subseries was found to exhibit oral activity but contained a

labile ester that could not be replaced without loss of activity, and the original hit exhibited remarkable sensitivity to minor structural change. A second subseries displayed high potency, including activity within gametocyte and liver stage assays, but at the cost of low solubility. As an open source research project, unexplored avenues are clearly identified and may be explored further by the community; new findings may be cumulatively added to the present work.

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