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Was This Page Helpful?

Form approved OMB#: 0925-0668, EXP. DATE: 02/28/2019

When the user selects "Yes" they get an opportunity to offer suggestions to improve the page.

What can we do to improve this page?

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A brief thank you and the survey disclaimer appear when the user presses the "Finish" button.

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Your response has been recorded.

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Public reporting burden for this collection of information is estimated to average 2 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a currently valid OMB control number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden, to: NIH, Project Clearance Branch, 6705 Rockledge Drive, MSC 7974, Bethesda, MD 20892-7974, ATTN: PRA# 0925-0668. Do not return the completed form to this address.

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If a user selects "No" they are asked to select one or more reasons why.

I did not find this page helpful because the content on the page (check all that apply):

- Had too little information
- Had too much information
- Was confusing
- Was out-of-date
- Other

[Previous](#)[Next](#)

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What can we do to improve this page?

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Congressional Testimony

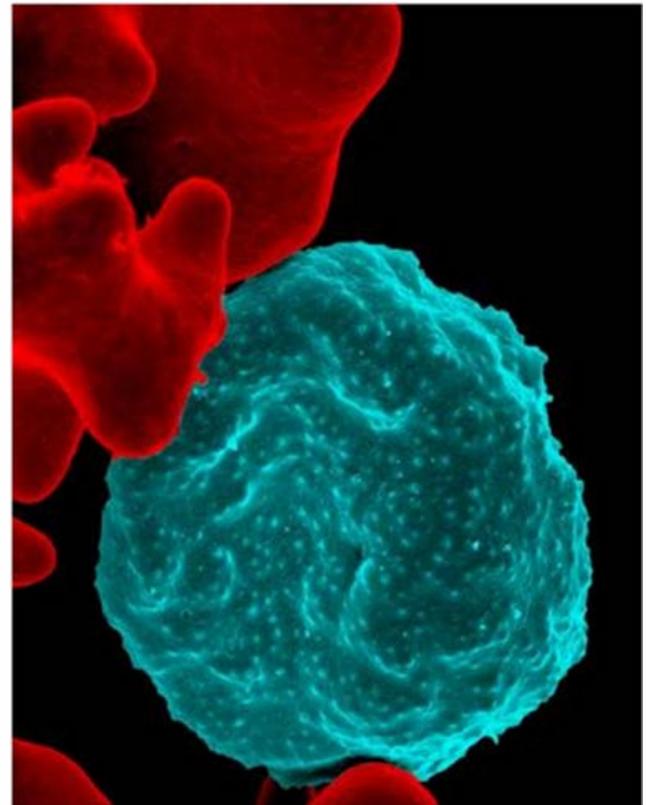
Essential Malaria Parasite Genes Revealed

NIAID-Funded Research Could Aid Antimalarial Drug Development

May 3, 2018

Researchers have exploited a quirk in the genetic make-up of the deadly malaria parasite, *Plasmodium falciparum*, to create 38,000 mutant strains and then determine which of the organism's genes are essential to its growth and survival. *P. falciparum* is responsible for about half of all malaria cases and 90 percent of all malaria deaths. New information about the parasite's critical gene repertoire could help investigators prioritize targets for future antimalarial drug development. The international research team led by John H. Adams, Ph.D., of the University of South Florida, was supported by the National Institute of Allergy and Infectious Diseases (NIAID), part of the National Institutes of Health. The study appears in the May 4 issue of *Science*. Rays H.Y. Jiang, Ph.D., of University of South Florida, and Julian C. Rayner, Ph.D., of the Wellcome Trust Sanger Institute, U.K., collaborated with Dr. Adams in this research.

The complete genetic sequence of *P. falciparum* was determined more than a decade ago, but the functions of most of its genes remain unknown, and until now only a few hundred mutant strains had been created in the lab. The difficulties in manipulating *P. falciparum* stem in part from the extremely high percentage of adenine or thymine (two of the four chemical building blocks that make up DNA) in its genome. Standard methods for creating mutants rely on more variation in gene sequences and so do not work on *P. falciparum*. In the new research, Dr. Adams and his colleagues created mutated versions of nearly all the parasite's 6,000 genes with a technique that preferentially targets areas rich in adenine and thymine, thus exploiting the very feature that had foiled previous attempts at genetic manipulation.



Colorized scanning electron micrograph of red blood cell infected with malaria parasites, which are colorized in blue. The infected cell is in the center of the image area. To the left and right are uninfected cells with a smooth red surface.

Credit: NIAID

Was this page helpful?

Yes

No

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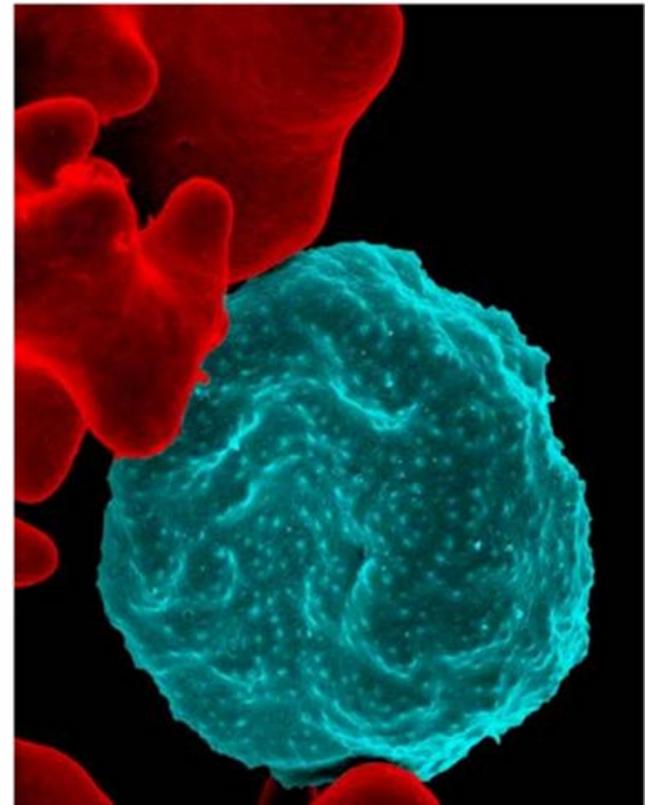
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