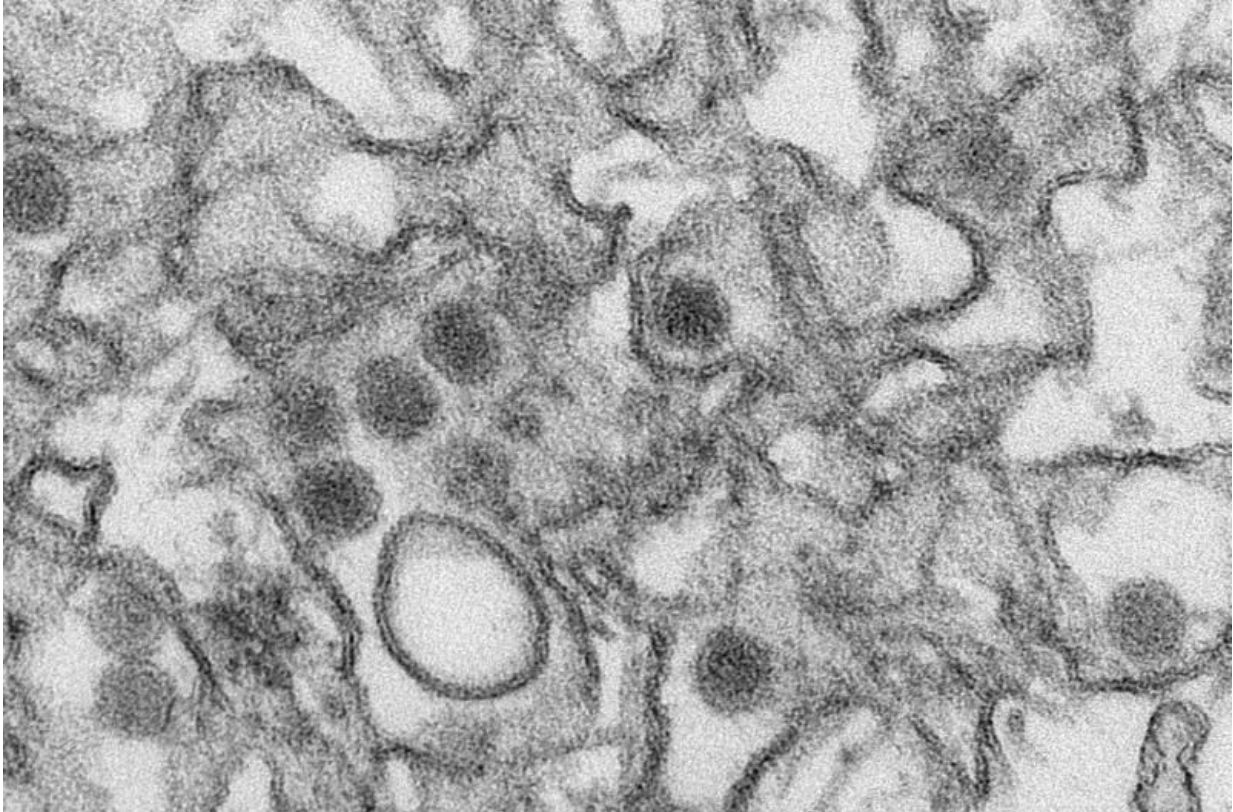


# Clues in Zika's genome

August 12 2016

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Transmission electron micrograph (TEM) of Zika virus. Credit: Cynthia Goldsmith/Centers for Disease Control and Prevention

University of Utah chemists have found that the Zika virus contains genetic structures similar to other viruses in the Flaviviridae family, and that these structures may serve as potential antiviral drug targets.

In the study, accepted for publication in *ACS Infectious Diseases*, Aaron Fleming, Cynthia Burrows and colleagues at the U searched for patterns in the Zika genome called G-quadruplexes, which are regions of DNA rich in guanine, one of the four basic building blocks of genes. With four sequences of multiple guanines, DNA can fold into a G-quadruplex structure. G-quadruplexes can serve as landmarks when comparing genomes, so Fleming and Burrows compared locations of G-quadruplexes in 78 strains of the Zika virus with other viruses in the Flaviviridae family, of which Zika is a member. Flaviviridae viruses include the [dengue virus](#), the yellow fever virus, and the West Nile virus.

Zika shares seven G-quadruplexes with its viral cousins, the researchers found. In addition, they found a G-quadruplex structure unique to, but consistent within, the Zika virus strains. The consistent G-quadruplexes across the viral family suggests that they are evolutionarily conserved, and may thus be important to viral function. Studying the folding patterns of the quadruplexes, the team found that they could be disrupted by G-quadruplex-binding compounds, suggesting a possible drug target for this rapidly-growing disease.

**More information:** Aaron M. Fleming et al, Zika Virus Genomic RNA Possesses Conserved G-Quadruplexes Characteristic of the Flaviviridae Family, *ACS Infectious Diseases* (2016). [DOI: 10.1021/acsinfecdis.6b00109](#)

Provided by University of Utah

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