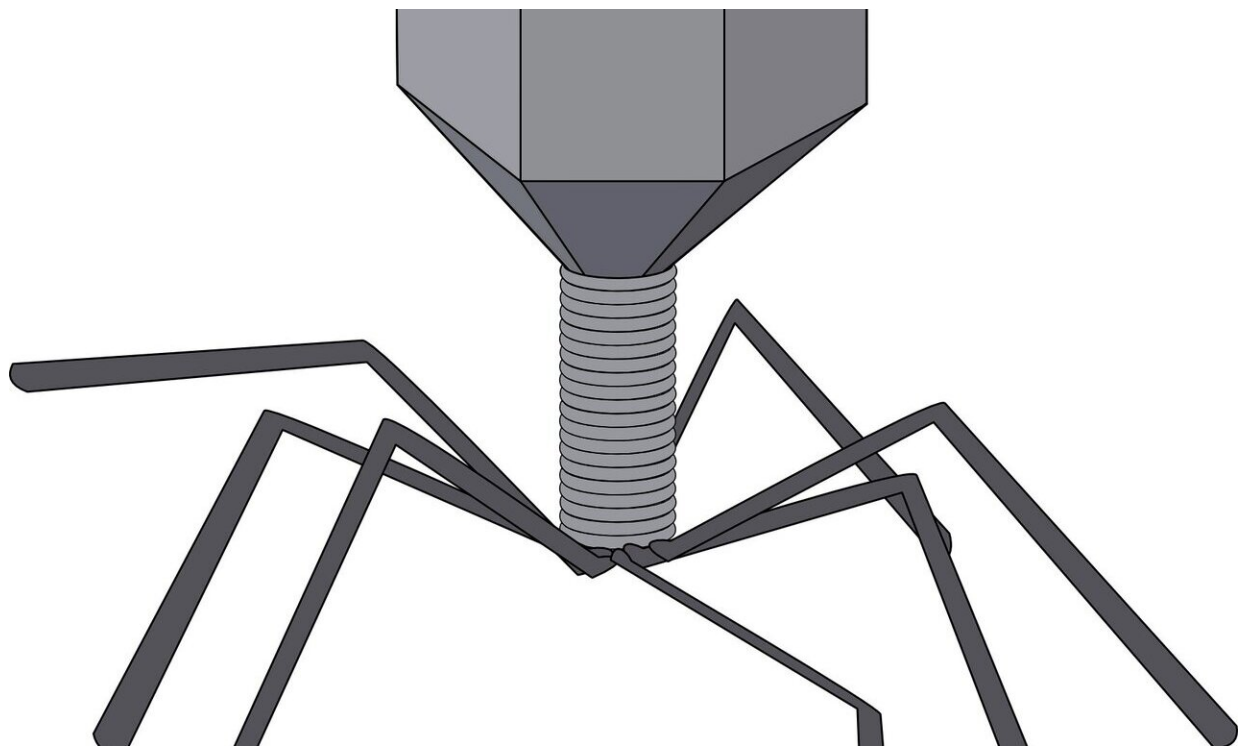


Three new studies suggest Z-genome is much more widespread in bacteria-invading viruses than thought

April 30 2021, by Bob Yirka



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Three teams working independently have found evidence that suggests the Z-genome in bacteria-invading viruses is much more widespread than thought. All three of the groups have used a variety of genomic

techniques to identify parts of the pathways that lead development of the Z-genome in bacteria-invading viruses known as bacteriophages. The first team was made up of researchers from several institutions in China and one in Singapore, the second with members from several institutions in France; the third was an international effort. All three teams have published their results in the journal *Science*. Michael Grome and Farren Isaacs with Yale University have also published a Perspectives piece in the same journal issue outlining the work of all three teams.

The genomic DNA of most living things has four distinct nucleotides: adenine, thymine, cytosine and guanine, respectively labeled ATCG. But back in 1977, scientists learned that most bacteriophages have a slightly different alphabet, one that typically omits adenine and adds diaminopurine, which has subsequently been labeled Z. After this discovery, it was thought that the alphabet was so rare little work was done to learn more about it; thus, little is known about how bacteriophages function without adenine in their genome. In this new effort, all three teams sought to learn more about the Z [nucleotide](#) and how it works in bacteriophages.

In the first, effort, the researchers studied the composition of a phage called Vibrio and discovered that it had the Z nucleotide rather than A. They also described the structure of an enzyme that is encoded by a gene similar to one known as PurA, which they called PurZ. They then showed that it functioned in ways much like the Z pathway in PurA. The second team found phage genes that encode DNA polymerases that select for diaminopurine rather than [adenine](#). And the third team found an enzyme that plays a main role in putting together DNA molecules from parent molecules. They also discovered that it worked as a gate, excluding A nucleotides and instead adding Zs.

The work by the three teams suggests that the Z nucleotide is much more prevalent in bacteriophages than thought—further study could lead to

new and improved ways to combat bacterial infections.

More information: Yan Zhou et al. A widespread pathway for substitution of adenine by diaminopurine in phage genomes, *Science* (2021). [DOI: 10.1126/science.abe4882](https://doi.org/10.1126/science.abe4882)

Dona Sleiman et al. A third purine biosynthetic pathway encoded by aminoadenine-based viral DNA genomes, *Science* (2021). [DOI: 10.1126/science.abe6494](https://doi.org/10.1126/science.abe6494)

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