

Viruses: More survival tricks than previously thought

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Among eukaryotes with modified nuclear genetic codes, viruses are unknown. Until now it had been believed that the modifications to the genetic code effectively prevented new viral infections. However, researchers have now reported the first example of a virus that can be shown to have crossed the boundary from organisms using the standard genetic code to those with an alternate genetic code.

"The finding is significant because it means that virus-host co-evolution after a genetic code shift can be more extensive than previously thought", said researcher Derek J. Taylor, professor of [biological sciences](#) at the University at Buffalo.

"It shows that these viruses can overcome what appears to be an insurmountable change in the [host genome](#)," Taylor said. "So the fact that we haven't previously seen any viruses in these species with a modified genetic code may not be because the viruses can't adapt to that shift. It may be that we haven't looked hard enough."

The study, titled "Virus-host co-evolution under a modified nuclear genetic code," was published on Tuesday, March 5th in *PeerJ*, a peer-reviewed, open-access journal in which all articles are freely available. The team of scientists, all from the University of Buffalo, discovered the highly adapted virus—a totivirus—in the [yeast species](#) *Scheffersomyces segobiensis* (a distant relative of [human pathogens](#) in the genus [Candida](#)).

In most living things, the genetic code comprises 64 elements called

codons, most of which instruct the body to produce a certain amino acid, the basic building block of a protein. In *S. segobiensis*, however, the genetic code has been modified - a codon that usually stands for the amino acid leucine codes instead for serine (an amino acid change that can affect how proteins function). It had been thought that such a radical change in the genome may help [host species](#) evade viruses.

However, the presence of the totivirus in *S. segobiensis* shows that viruses may be more nimble than previously thought, able to overcome even this enormous hurdle. Intriguingly, the totivirus the researchers discovered has only one C-U-G codon left in its genome, suggesting that it may have purged that sequence as it adapted to the yeast host.

The research team found other odd and interesting evidence pointing to a history of co-evolution between totiviruses and yeasts with the modified code. For instance, the modified yeasts appeared to have incorporated genetic material from totiviruses into their genomes on at least four occasions. In total, evidence was found of past, or present, viral infection in five lineages of yeasts with a modified [genetic code](#).

In the yeast *Scheffersomyces stipitis*, the scientists even identified a former totivirus gene that the host is now using to produce a protein.

"It's a non-retroviral RNA virus gene being kidnapped and expressed as a protein by a cellular host in the absence of a current viral infection" Taylor said. The function of this protein is unknown, but the result is further evidence of the unexpected co-evolution between viruses and hosts with modified nuclear code.

More information: peerj.com/articles/50

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