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Viruses: More Survival Tricks than Previously Thought

Research uncovers a virus which infects a host that has
a non-standard nuclear genetic code

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 (https://PeerJ.com). 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.

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Abstract (from the article)

Among eukaryotes with modified nuclear genetic codes, viruses are unknown. However, here we provide evidence of an RNA virus that infects a fungal host (Scheffersomyces segobiensis) with a derived nuclear genetic code where CUG codes for serine. The genomic architecture and phylogeny are consistent with infection by a double-stranded RNA virus of the genus Totivirus.We provide evidence of past or present infection with totiviruses in five species of yeasts with modified genetic codes. All but one of the CUG codons in the viral genome have been eliminated, suggesting that avoidance of the modified codon was important to viral adaptation. Our mass spectroscopy analysis indicates that a congener of the host species has co-opted and expresses a capsid gene from totiviruses as a cellular protein. Viral avoidance of the host's modified codon and host co-option of a protein from totiviruses suggest that RNA viruses co-evolved with yeasts that underwent a major evolutionary transition fromthe standard genetic code.