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IIT-D study reveals mechanisms driving SARS-CoV-2 evolution in humans

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The results lay the necessary groundwork for future studies



A team of researchers at the Indian Institute of Technology Delhi (IIT-D) has discovered the existence of temporal variations in selection pressures during SARS-CoV-2 evolution and adaptation to the human host.

CpG (or CG; i.e. a cytosine followed by a guanine) numbers in virus genomes has been linked to host-switching, efficiency of virus replication, immune evasion and the ability of a virus to cause disease.

Zinc-finger antiviral protein (ZAP), a host protein that can bind to CpG-rich regions in SARS-CoV-2 (and other RNA viruses) and recruits other host proteins to degrade the viral RNA. Several viruses including HIV-1, Influenza A virus and SARS-CoV-2 prefer to reduce their CpG content (by losing CpGs) to minimize the host immune response, thus allowing better virus replication and survival.

The team analyzed over 1.4 million full-length SARS-CoV-2 sequences from across the world. They found that the rate of CpG depletion from SARS-CoV-2 genomes rapidly decreases after the first few months of evolution in humans. Furthermore, most SARS-CoV-2 variants of concern had lower CpG content. This work highlights the existence of selection pressures apart from ZAP that may lead to CpG depletion in SARS-CoV-2 genomes.

Dr. Sonam Dhamija, a co-author on the paper, said, “This work has relevance to our current understanding of SARS-CoV-2 pathogenesis, immune evasion and emergence of variants of concern”.