

What can sequence-based analyses of natural selection of SARS-CoV-2 tell us about the past, present, and future evolution of the virus?

Insights from selection analysis of complete genomes

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Key drivers of adaptation in rapidly evolving pathogens

- Zoonoses and transmission to new hosts (both species and individuals)
- Immune selection (CTL, innate, antibody)
- Development of drug resistance
- Virulence/transmissibility
- Host/pathogen arms-races, e.g. host antiviral factors
- **Most** of the time, **most** of the viral genome is conserved
- **Most** of the **observed variation** is “neutral”
- Changes that are **not neutral** are important to **detect early**, and, ideally, **predict**