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Vaccination shapes evolutionary trajectories of SARS-CoV-2

The large-scale evolution of the SARS-CoV-2 virus has been marked by successive turnover of genetic clades. New variants show intrinsic functional changes, notably increased transmissibility, as well as antigenic changes that reduce the cross-immunity conferred by previous infections or vaccinations. How this functional variation shapes the global evolutionary dynamics has remained unclear. Here we show that antigenic fitness induced by vaccination is the strongest force driving the recent evolution of SARS-CoV-2; other forces include intrinsic fitness and antigenic fitness induced by previous infections. To obtain this result, we build a fitness model with parameters inferred from sequence data, epidemiological records, and cross-neutralisation assays. The model establishes a computable fitness ranking of viral clades, sets conditions for the invasion of new variants, and predicts the feedback of vaccine changes on future viral evolution.

Tuesday, Mai 31, 2022, 17:30
Institute for Biological Physics Room S0.03
and online via Zoom

Hosted by Michael Lässig