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Climate-driven Changes To Host Nutrition May Impact The Emergence And Phenotype Of Viral Variants

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Deficits in host nutrition can increase the virulence and evolution rate of viruses. In particular, selenium (Se) deficiency decreases host immune response, increases susceptibility to viral infection, and can accelerate the rate of viral evolution and emergence of variants. Se deficiency has been associated with higher CoVID-19 and influenza morbidity and mortality. Global climate change is expected to decrease nutritional Se bioavailability to humans and the zoonotic hosts of viruses especially in drought-stricken regions. Understanding the health impacts of these environmentally driven changes will be critical to mitigate vulnerabilities to emergent viral diseases. We propose to address this urgent and inevitable scenario by defining the impact of Se deficiency on viral evolution and vaccine efficacy for SARS CoV-2 and influenza virus. Differences in viral evolution will be defined in mouse models including vaccinated and unvaccinated mice fed a Se deficient (Se def) or normal diet. We will use deep sequencing of the viral genome to identify variant emergence, and immunological profiling of host response to determine direct health effects, and effect of Se def on vaccine efficacy. Emergent viral variants will be characterized for changes in phenotype using computational protein structure modeling and synthetic biology. Mutations generated by these in vivo models will be compared to mutations that emerged globally during global transmission to gauge the predictive capacity of this model for variant emergence. Understanding the role of nutrient availability on vaccine efficacy, viral variant emergence, and the severity of emergent phenotypes will enable targeted intervention for ecosystems and human populations that are most affected by these changes.