

Spatial and Ecological Drivers of Grassland Soil Viral Communities and Their Biogeochemical Implications

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Viruses have the potential to influence soil nutrient cycling by infecting, reprogramming, and killing microorganisms central to biogeochemical processes. However, viruses exhibit strong spatial structuring over meter-scale distances, whereas their prokaryotic hosts do not, making it challenging to link viruses to hosts and complicating the integration of viral contributions into biogeochemical cycles. To investigate the ecological mechanisms shaping viral distributions and better attempt to characterize virus-host dynamics, we employed a multi-omic approach to examine viral and microbial communities across scales of activity, functionality, and spatial distance in two California grasslands. We generated 64 viromes, metagenomes, metatranscriptomes, and metabolomes across spatial scales ranging from 10 cm to 100 m. Our analyses revealed that total prokaryotic hosts (derived from metagenome-assembled genome [MAG] relative abundances) follow a positive occupancy-abundance relationship, whereas viruses displayed a more complex trend, where low-abundance viruses were found in few samples, but high-abundance viruses exhibited variable spatial occupancy. While all measured datasets significantly predicted viral communities at the field-scale, random forest models revealed spatial distance as the most important variable predicting viral community composition in both sites. At the smallest spatial scales (10 cm to 1 m), viral community composition was only predicted by all measured datasets in one-third of the small-scale sampling areas, indicating that more nuanced processes drive viral production when increasing spatial resolution. These findings challenge traditional assumptions regarding virus-host spatial coupling and suggest that additional ecological mechanisms may underlie observed patterns. Future analyses incorporating metatranscriptomes could reveal if active viral populations and hosts (not just DNA-based presence) show different occupancy-abundance trends, supporting the boom-and-bust hypothesis. Additionally, metabolite profiles will be leveraged to clarify whether viral occupancy correlates with shifts in functional microbial activity, indicating environmental filtering or metabolic dependency. Our study advances the integration of viral dynamics into microbial ecology frameworks and biogeochemical models, emphasizing the need for spatially explicit analyses to accurately capture viral contributions to ecosystem functioning.