**Spillover of RNA viruses between *A. mellifera* and *Bombus* spp. through shared flowers diluted by floral diversity**

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**Abstract:**

Evidence is mounting that RNA viruses, likely originating from honeybees, have been spilling over into wild bee populations. While transmission of disease between bee species likely occurs through the use of shared flowers, only two published studies have directly examined this floral transmission route and no study has yet examined their role in RNA virus dissemination. Previous work in this system has shown that flowers can harbor viruses and that prevalence varies across species. In the field of disease ecology, the dilution hypothesis examines the idea that host diversity can dampen the effectiveness of a pathogen reducing the prevalence of the disease. Though there is evidence to support this hypothesis, the underlying mechanisms are still undetermined and the debate over its existence persists. In this study, we experimentally demonstrate how flowers may be facilitating the spillover of Deformed Wing Virus (DWV) from honey bees into bumble bee communities. In addition, through a combination of experimentation and mathematical modeling, we propose a mechanism for the dilution of transmission through increased floral diversity. Clean bumble bees were allowed to forage on hand inoculated and naturally infected artificial and natural flowers. Viral load was measured using RT-qPCR. We measured the viral load that can be picked up by a bee from a flower as a function of foraging time, determined the potential rate at which the route might work in reverse (bumble bees to honeybees) and determined how much virus is required to cause a replicating infection. We found that DWV can be picked up by bumble bees from field realistic hand-inoculated flowers and that foraging time increased viral load only during the first 10 seconds of visitation. Our mathematical model showed that the parameter estimates for viral deposition and probability of infection are able to drive a simulated spillover event that mirrors empirical data from field surveys. The inclusion of floral diversity with differential viral harboring potential dampened overall disease prevalence. Spillover of diseases into naïve bumble bee populations has been implicated as one of the factors responsible for their losses. The demonstration of this transmission route and the proposed floral dilution mechanism may be used to inform recommendations for responding to future emerging infectious disease outbreaks. Future work should look to optimized tolerance (HOT) models, which might be used to determine ideal floral composition for human-made pollinator gardens and crop buffers to maximize floral diversity and minimize disease spillover risk.