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PP-606 [Bee Health]

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INTERSPECIFIC TRANSMISSION OF BEE PATHOGENS IN WILD POLLINATORS IN NATIONAL PARKS

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INTRODUCTION & AIM

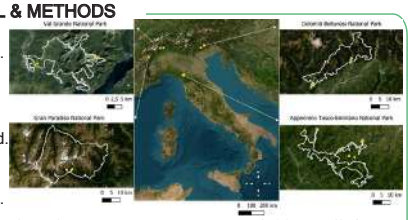
Pollinators, especially **bees** and **hoverflies**, are essential for ecosystems but are experiencing alarming declines due to habitat loss, climate change, and pathogens. While bee pathogens are well studied, their effects on hoverflies remain poorly understood.

Transmission can occur through shared flowers, contaminated food or water, or direct contact, with hoverflies acting mainly as potential mechanical vectors via floral visitation.

This study investigates 10 bee-associated pathogens in bees and hoverflies from four Italian mountain parks, evaluating environmental, seasonal, and biological factors influencing infection.

MATERIAL & METHODS

In 2024, 16 sites across four National Parks in Northern Italy were sampled from May to September. Sites included grazed pastures and ungrazed meadows, with collections performed only on spontaneous vegetation.



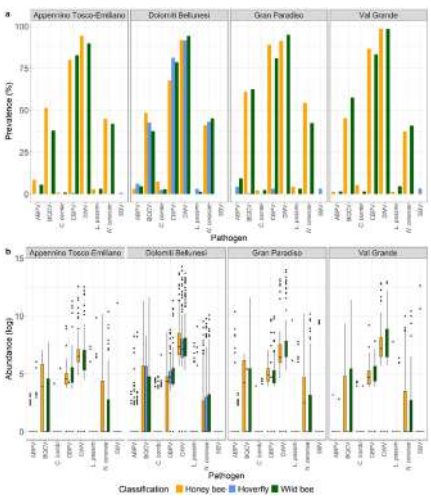
Honey bees, wild bees, and hoverflies were collected. Nucleic acids were extracted from each individual, and qPCR was used to detect and quantify 10 pathogens (viruses, microsporidia, trypanosomatids).

Normalised Difference Vegetation (NDVI) was derived from Copernicus satellite images (500 m buffer) to assess vegetation cover and habitat complexity.

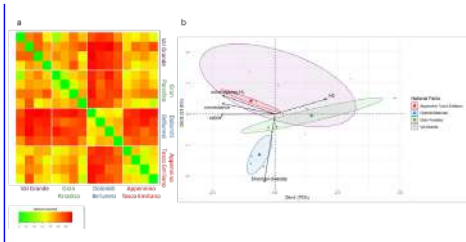
Prevalence and abundance patterns were analyzed with GLMMs. Factors included altitude, NDVI, land management, season, and host traits (diet, voltinism, sex).
Host-pathogen networks were explored with bipartite metrics.

RESULTS

A total of 1,688 specimens were collected: 388 honey bees, 632 wild bees, and 668 hoverflies.
Overall, 76.3% of individuals were positive for at least one pathogen. The most prevalent pathogens were DWV (70.4%) followed by CBPV (60.4%), BQCV (35.2%) and *N. ceranae* (32.5%). DWV showed the highest abundance (5.2×10^{11} copies).



Prevalence patterns differed among hosts and parks: wild bees were positive for nearly all pathogens except SBV, and honey bees never carried SBV, ABPV in Gran Paradiso, or *L. passim* in Dolomiti Bellunesi. Hoverflies were particularly noteworthy, as they hosted multiple pathogens, including SBV, which appeared exclusively in Syrphidae in several parks. Notably, in Dolomiti Bellunesi, hoverflies exhibited prevalence and abundance levels comparable to those of honey bees and wild bees, underlining their potential role as overlooked pathogen reservoirs.



The network analysis revealed clear differences in pathogen-host interactions among parks. The dissimilarity matrix showed that sites within the same park were generally more similar, while Dolomiti Bellunesi stood out as the most distinct compared to all others. The PCA confirmed this pattern: Val Grande sites appeared more scattered and weakly structured. Gran Paradiso sites showed intermediate network characteristics, while Appennino Tosco-Emiliano sites were more connected, with pathogens displaying similar interaction patterns across hosts.

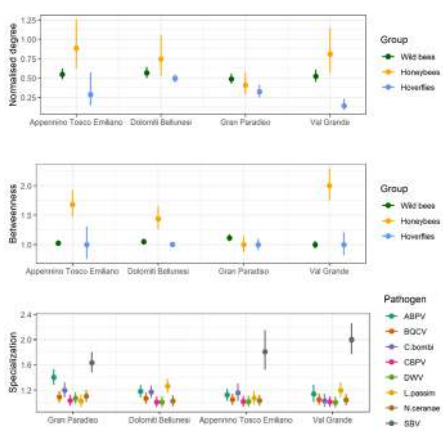
Linear models showed that honey bees were the main epidemiological "bridges," carrying the highest number of pathogens and connecting different host groups, except in Gran Paradiso where wild bees played this role.

SBV emerged as the most specialized pathogen, infecting only hoverflies and being absent in the Dolomiti Bellunesi.

Environmental factors strongly influenced pathogen risk: infection decreased with altitude but increased with NDVI and grazing, and peaked in July.

Hoverflies had lower infection risk overall compared to bees. Within hoverflies, risk was shaped by biological traits: zoophagous larvae, females, and bivoltine species were more often infected, while univoltine species showed the lowest prevalence.

At the genus level, *Melanostoma* and *Episyrphus* were the most susceptible, highlighting important intra-group variability.



CONCLUSION

This study reveals widespread pathogen circulation in mountain pollinator communities, even in protected National Parks. Pathogens were found not only in bees but also in hoverflies, highlighting their emerging role as potential hosts and mechanical carriers in pollinator pathogen networks. Environmental factors (altitude, vegetation, land use, seasonality) and host traits (species, sex, larval diet, and life cycle) significantly influence infection risk, with seasonal peaks in pathogen load observed in summer

These findings underscore the complexity of pathogen dynamics in wild pollinators, the important role of hoverflies in pathogen spread, and the need for integrated "One Health" approaches to safeguard pollination services and ecosystem health.

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Interspecific transmission of bee pathogens in wild pollinators in National Parks

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The health of pollinators has garnered significant attention due to their essential role in maintaining biodiversity and supporting ecosystem services. However, habitat destruction, environment fragmentation, pollution, and diseases pose serious risks to their populations. One key factor affecting pollinator health is pathogen spillover, a process in which infectious agents transfer between different species. This transmission can occur through shared resources (food and water) or direct contact, leading to increased pathogen prevalence among pollinators from different taxa. Among the most studied cases of pathogen spillover in pollinators, honey bee and bumblebee pathogens have been found to infect wild bees and hoverflies. This transmission not only amplifies the spread of diseases but can also have sublethal consequences, affecting the fitness and survival of affected hosts. This study focuses on evaluating the presence of bee pathogens in wild pollinators by conducting a field survey in four National Parks located in Northern Italy. In total, 852 hoverflies, 764 wild bees and 424 honey bees were sampled and individually analysed through qPCR to assess the abundance of 11 bee pathogens. Field sampling was carried out during the summer months. The main objective is to assess the extent of pathogen spillover and identify the taxa most vulnerable to infections. The research also examines various factors influencing pathogen transmission, contributing to a deeper understanding of disease dynamics in pollinator communities. Although no visible symptoms of infection were observed among the collected pollinators, the qPCR analysis revealed prevalence and abundance in each investigated target insect. Additionally, instances of co-infection were detected, indicating varying levels of susceptibility to pathogens among different wild pollinator species. The findings of this study offer valuable insights into the ecology and health status of wild pollinators. By identifying the risks associated with pathogen spillover, the research underscores the need for effective conservation strategies. These measures are particularly relevant within the One-Health approach, which emphasizes the interconnectedness of human, animal, and environmental health. Understanding the mechanisms of pathogen transmission in pollinators is crucial for developing policies aimed at mitigating disease risks, preserving biodiversity, and ensuring the sustainability of pollination services critical for ecosystems and agriculture.