

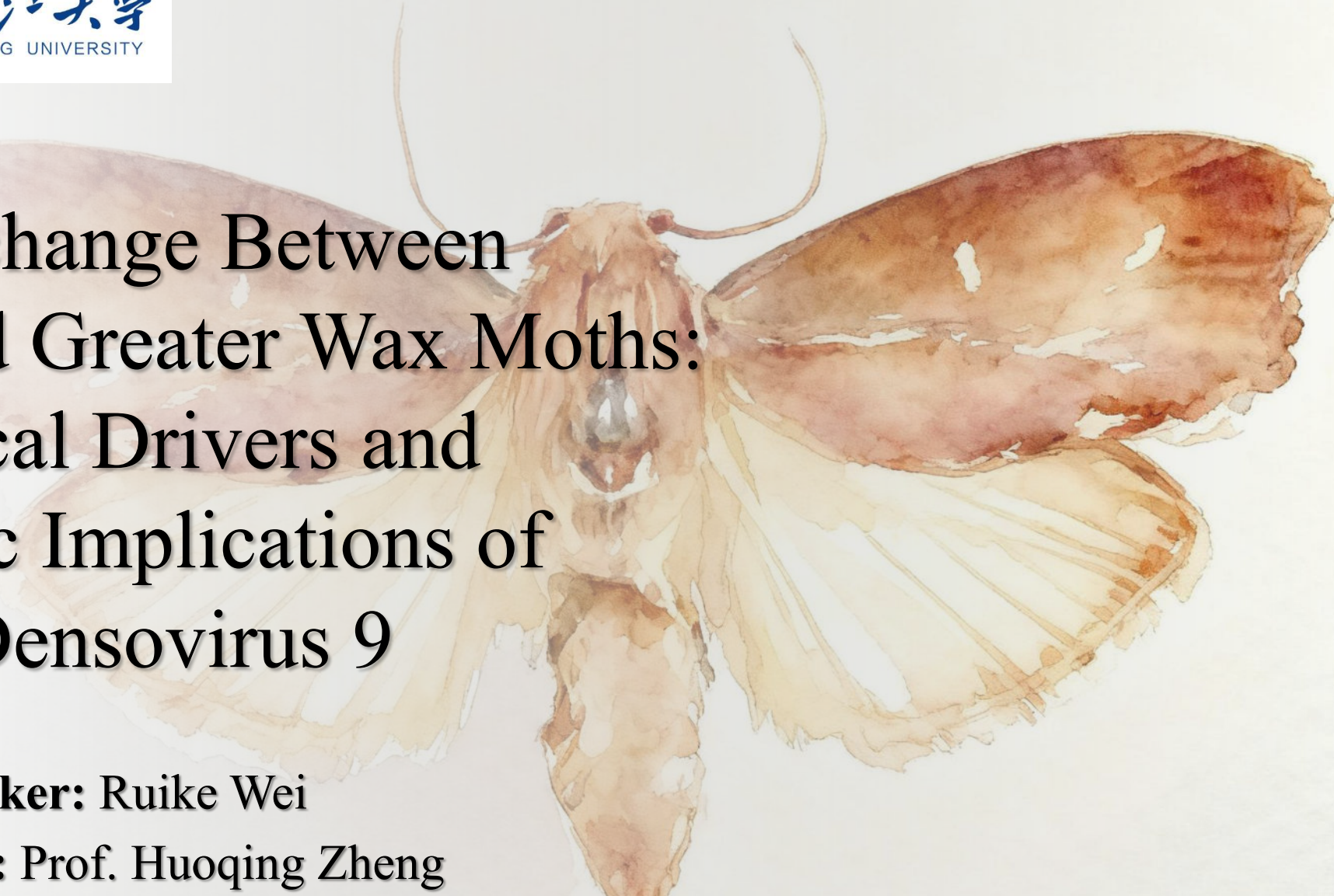
Viral Exchange Between Honeybees and Greater Wax Moths: Ecological Drivers and Pathogenic Implications of Bee Densovirus 9

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Cross-species viral transmission between honeybees and their pests poses significant risks to pollinator health. However, the ecological drivers and host-pathogen interactions underlying viral spillover remain poorly characterized. The greater wax moth (*Galleria mellonella*), a pervasive hive pest sharing ecological niches with Eastern honeybees (*Apis cerana*), may facilitate virus host-shifting between phylogenetically distant species. While viral spillover from bees to non-bee hosts has been documented, the virome interface between *G. mellonella* and *A. cerana*, and its implications for disease ecology, remain largely unexplored. Here, we characterized the virome of *G. mellonella* and *A. cerana* under laboratory and field conditions to assess viral sharing dynamics and the infectivity of a novel densovirus, Bee densovirus 9 (BDV9), initially identified in Czech *A. mellifera* colonies in 2024.

Virome analysis demonstrated significantly higher viral diversity in *G. mellonella* (3.13–4.44% of reads mapping to viral genomes) versus *A. cerana* (0.02–0.08%), with 25–33 viral species shared between cohabiting groups. Strikingly, BDV9 exhibited 100% prevalence in *G. mellonella* populations across 12 Chinese regions. Experimental inoculation demonstrated BDV9-induced mortality in both *A. cerana* ($p < 0.001$) and *A. mellifera* ($p = 0.021$), though viral replication was transient, declining sharply by day 14 post-infection. Quantitative PCR confirmed shared upregulation of four antiviral peptides across both species, with species-specific statistical significance (Defensin1 and Hymenoptaecin in *A. cerana*; Apidaecin and Defensin2 in *A. mellifera*), suggesting convergent antiviral strategies limiting viral persistence.

Our findings redefine the ecological interplay between wax moths and honeybees. Beyond physical hive damage, *G. mellonella* may act as a viral reservoir host, leveraging its high viral diversity and colony ubiquity to facilitate cross-species transmission. The delayed pathogenicity and low replication efficiency of BDV9 imply an evolutionary trade-off favoring coexistence, yet its pervasive prevalence in *G. mellonella* underscores underestimated risks to apiculture. This study highlights the need to integrate pest-virus ecology into pollinator conservation strategies, emphasizing that wax moth management is critical not only for hive integrity but also for mitigating emerging viral threats.



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Sep 26th 2025

Background

Common name: Greater wax moth

Current scientific name: *Galleria mellonella*

Threat:

A significant pest to honeybees (especially *Apis cerana*).

Knowledge Gap:

Viral community and role in interaction are poorly understood.

Opportunity:

By studying the viruses present in wax moth, we can better understand the full scope of their threat to bees, and support the development of targeted, sustainable control methods.



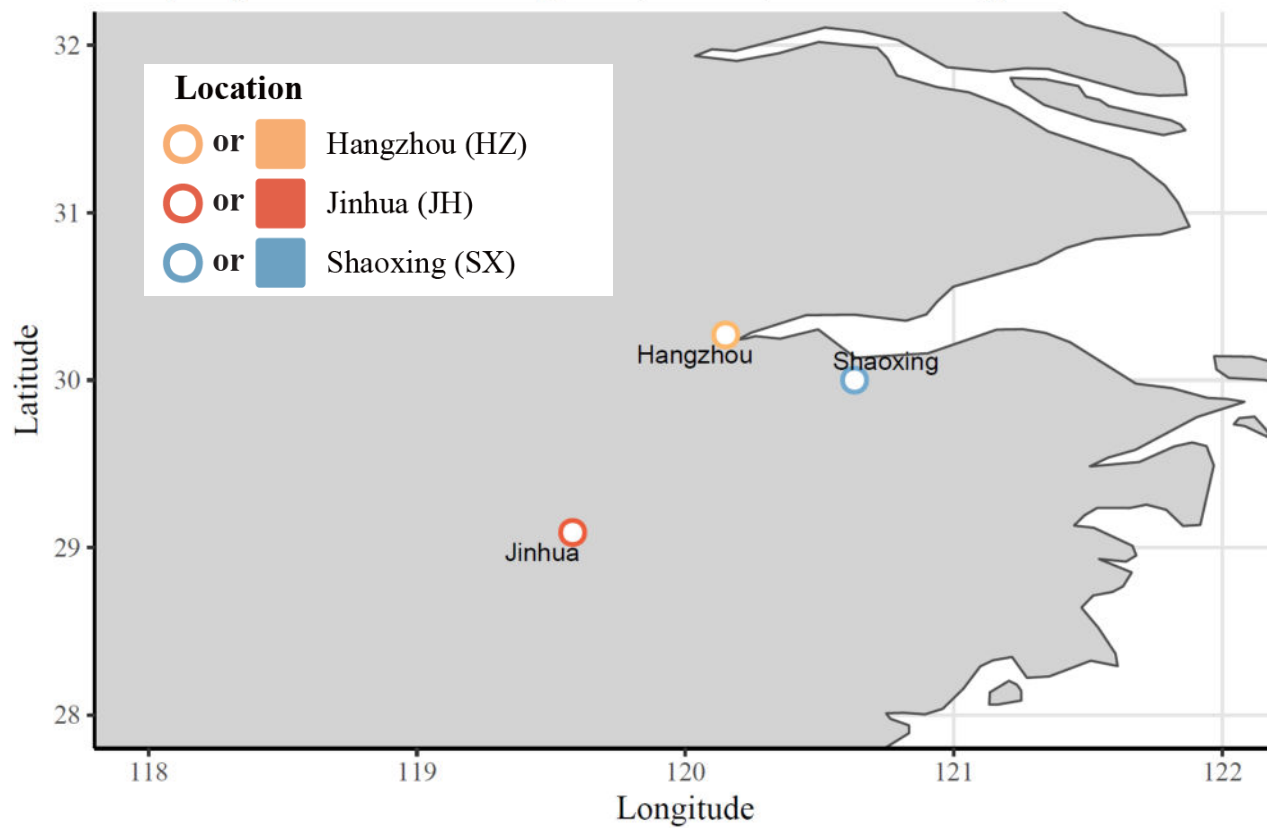
(NCBI 2025, Taxonomy ID: 7137)



(Photograph by Yanling Xie)

Sample collection

Sampling Locations in Hangzhou, Jinhua, and Shaoxing



4 colonies / location



Western honeybee
(*A. mellifera*)
AM



Greater wax moth
(*G. mellonalla*)
GM(AM)

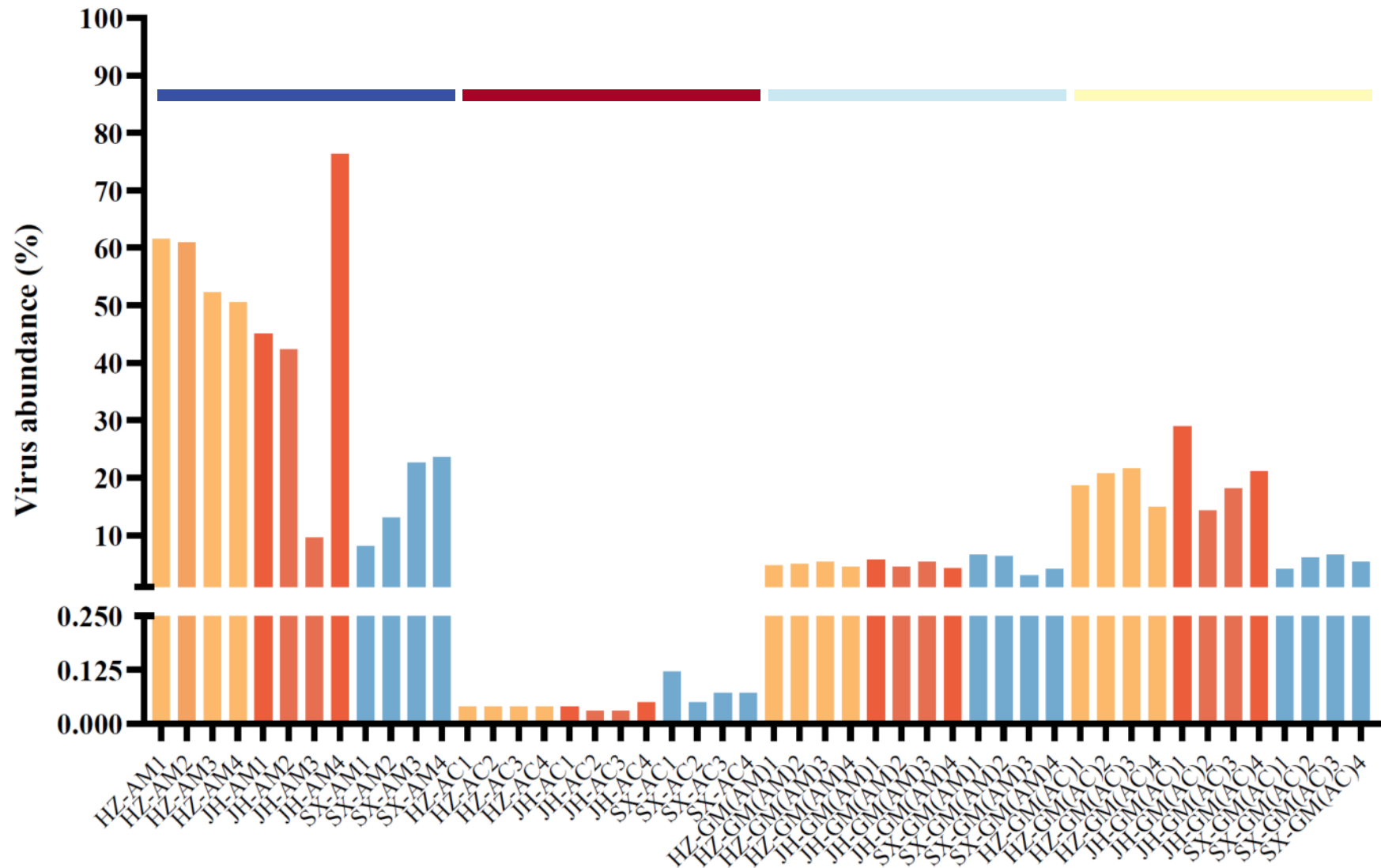


Eastern honeybee
(*A. cerana*)
AC



Greater wax moth
(*G. mellonalla*)
GM(AC)

Virus abundance



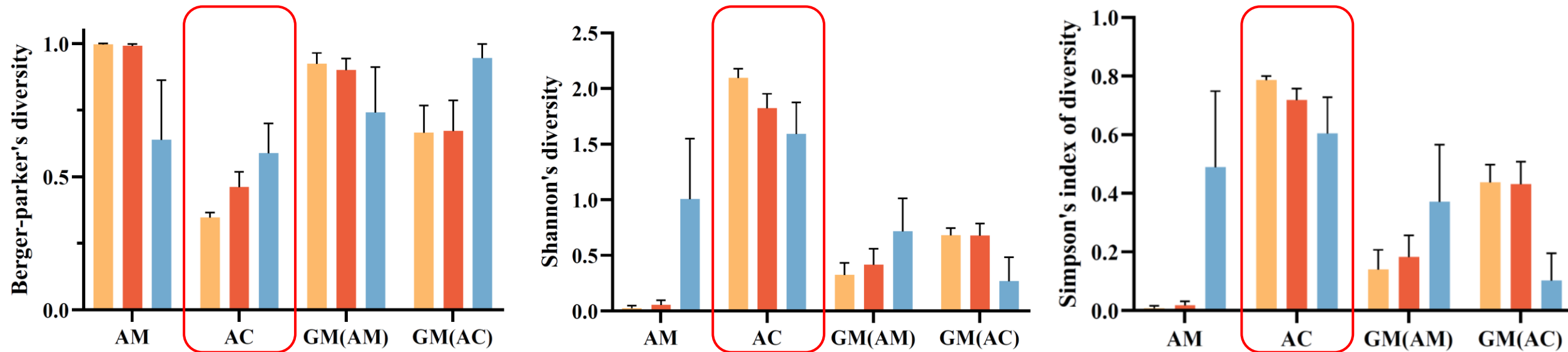
AM: $38.82 \pm 22.85\%$

AC: $0.05 \pm 0.03\%$

GM(AM): $4.93 \pm 1.01\%$

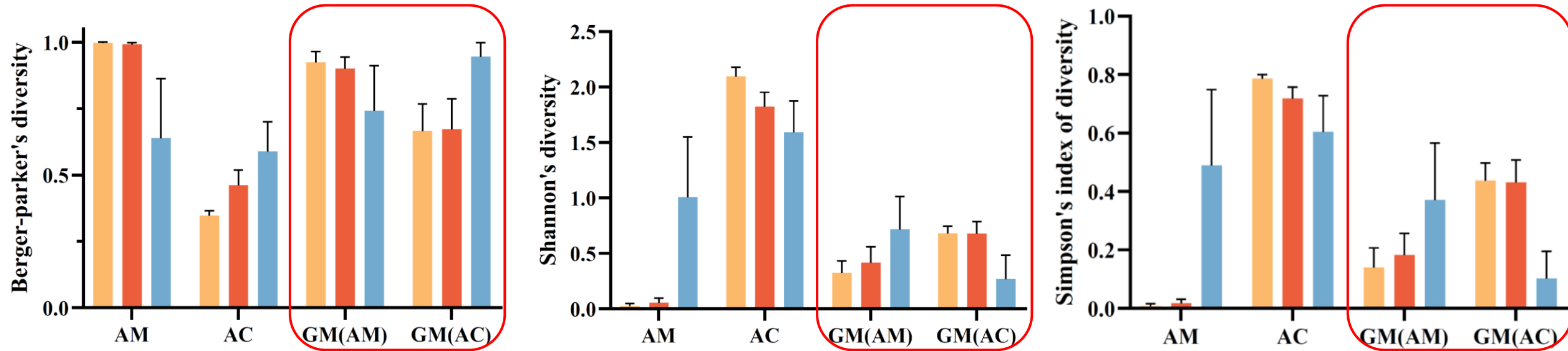
GM(AC): $15.03 \pm 7.95\%$

Alpha diversity



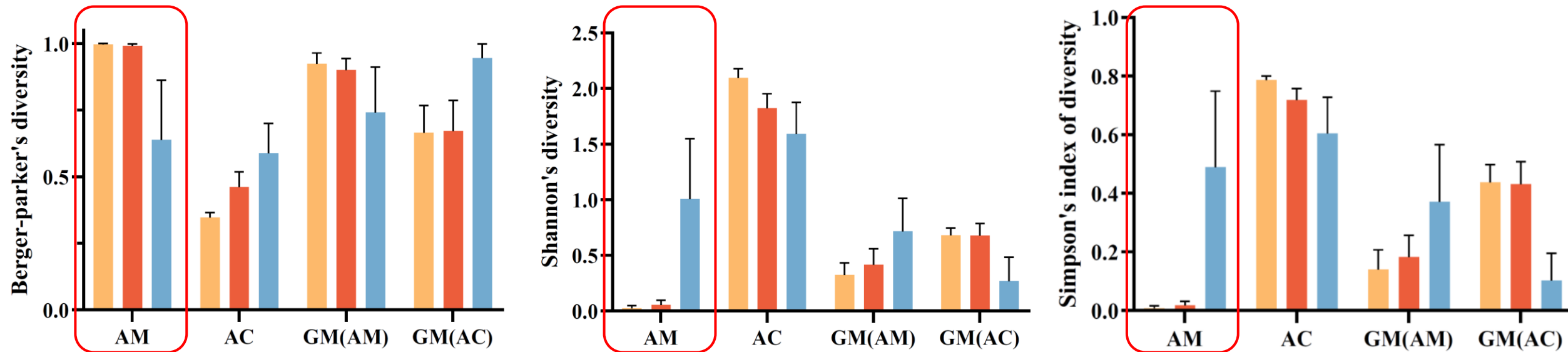
A. cerana exhibited higher viral alpha diversity, while *A. mellifera* and *G. mellonella* communities were characterized by higher dominance of a few core viruses.

Alpha diversity



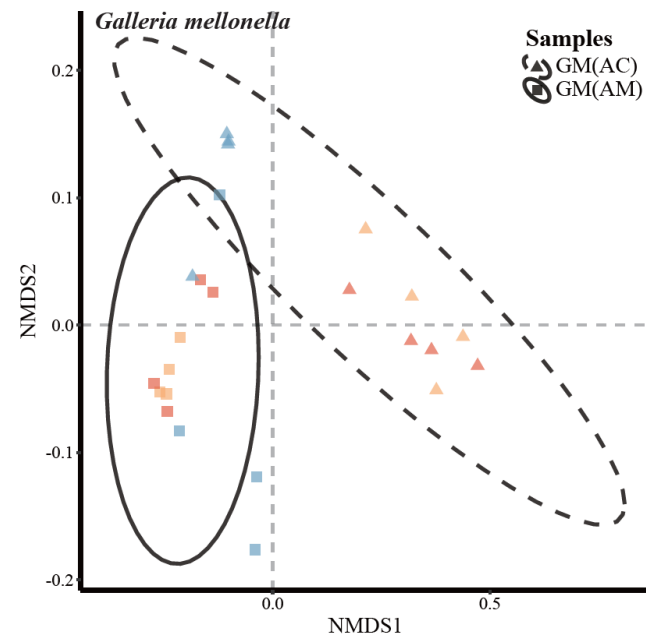
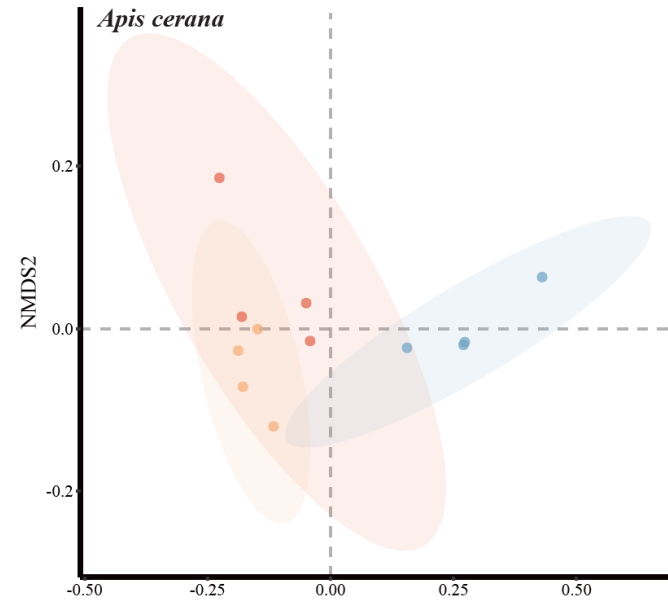
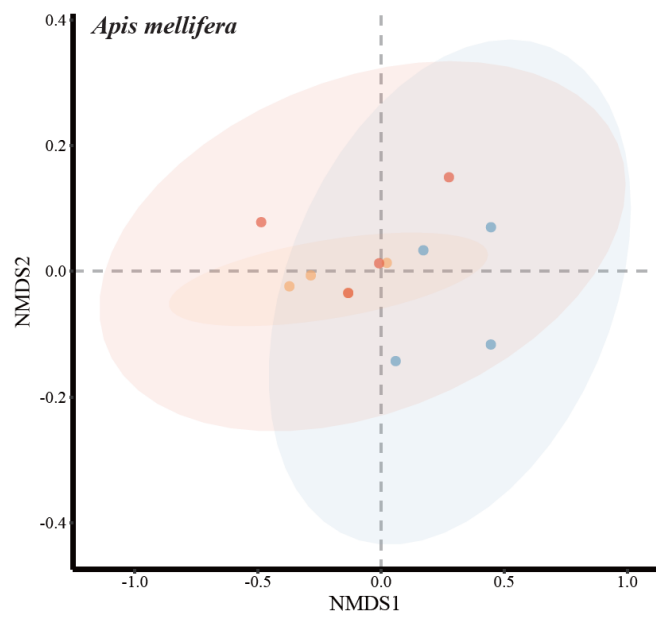
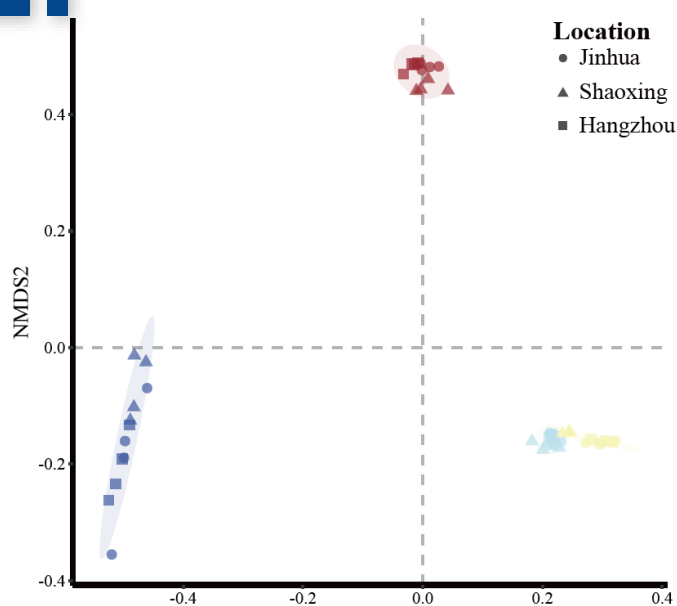
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Alpha diversity



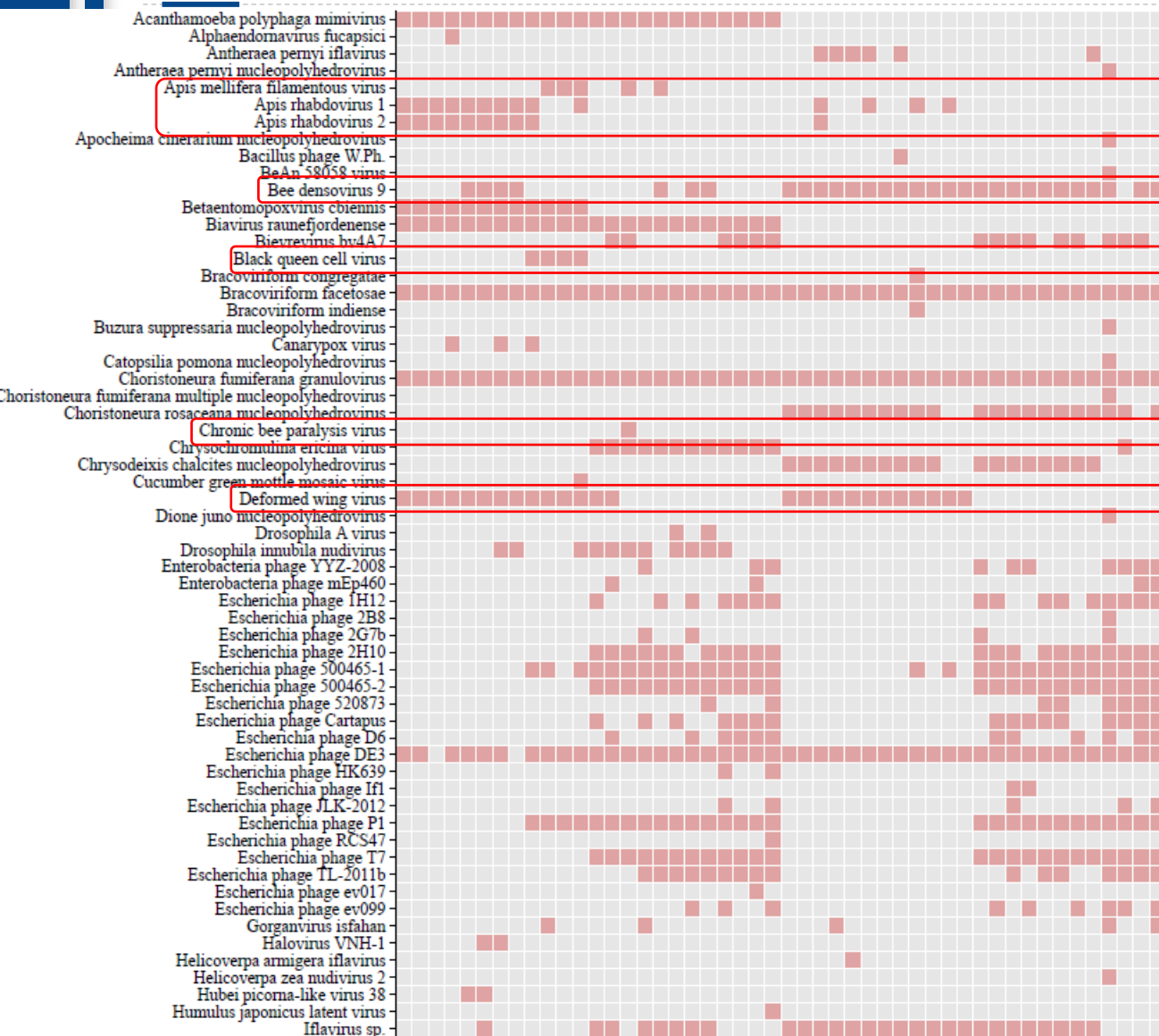
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Beta diversity



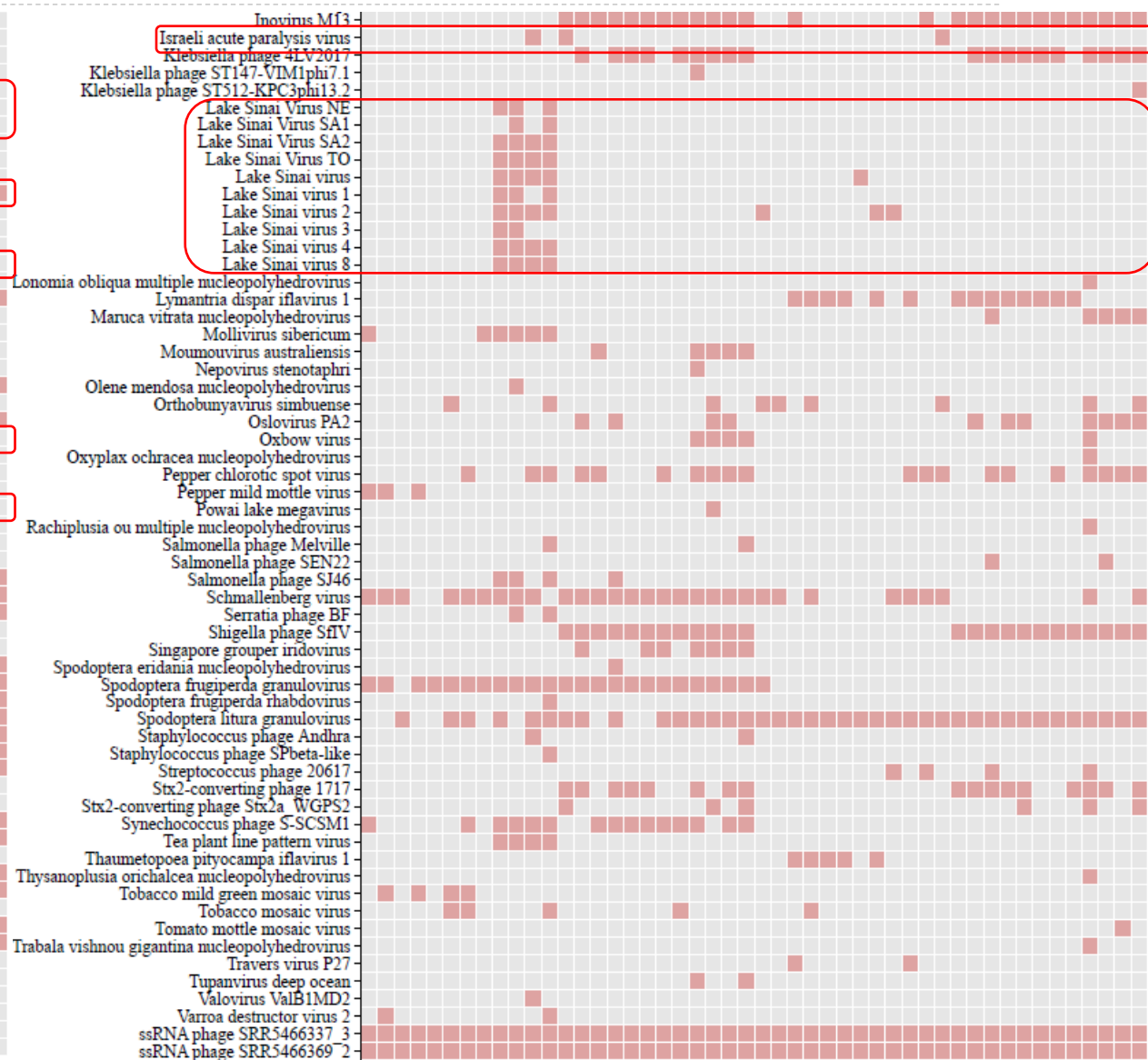
Viral communities differed significantly among the three host species (interspecific variation). Notably, the virome of *G. mellonella* further separated based on its hive host (*A. cerana* vs *A. mellifera*), revealing a clear intraspecific pattern that was not driven by geographic location.

Viral Reads Detection



Present

Absent



AM&AC

• • •

All groups

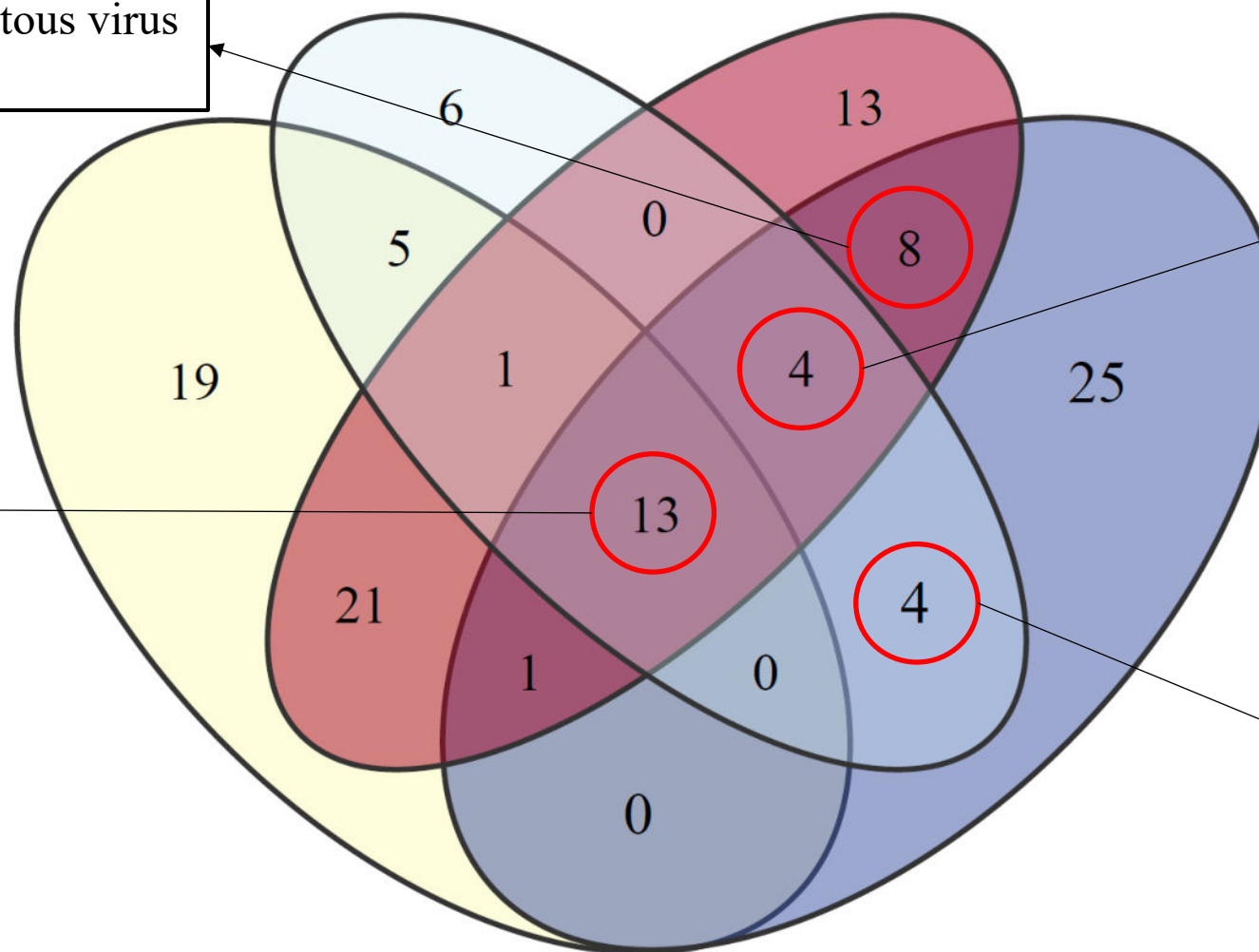
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AM&AC&GM(AM)

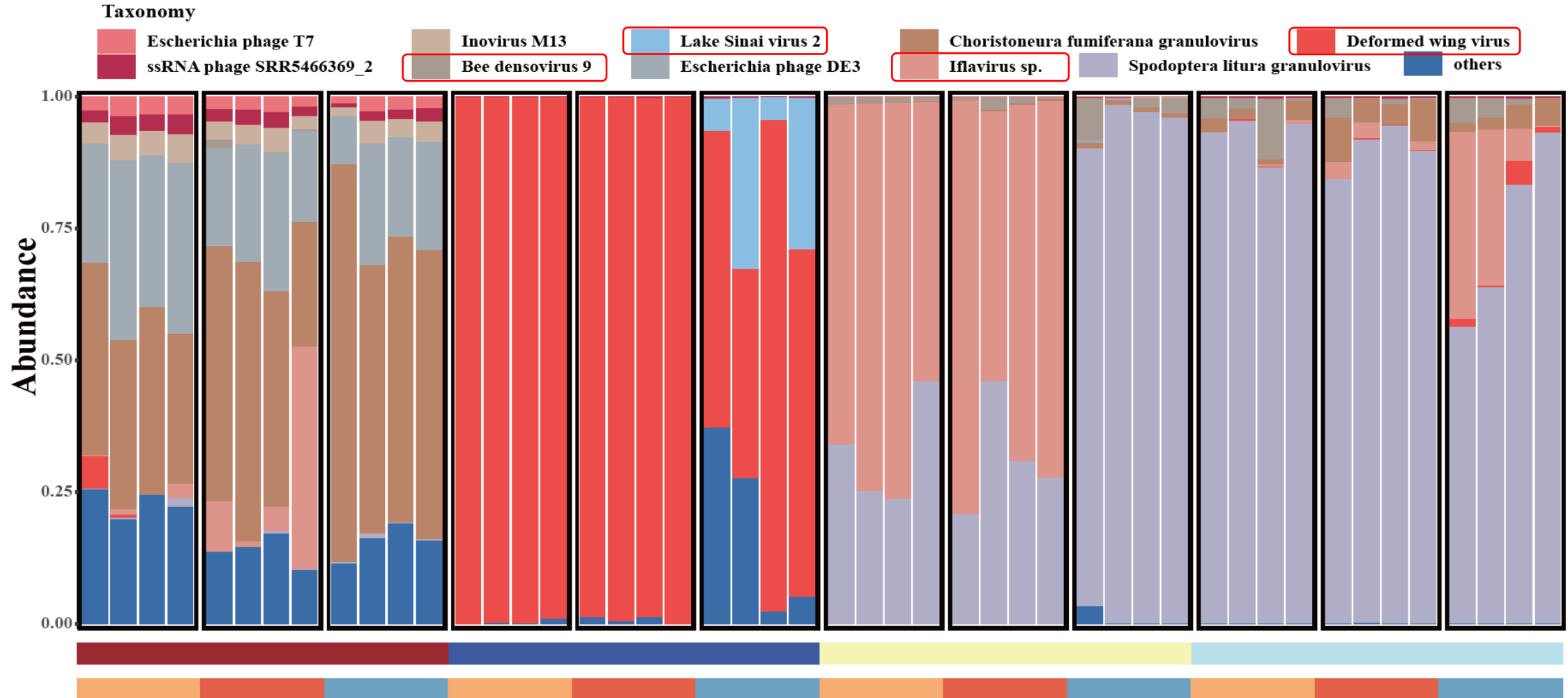
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AM&GM(AM)

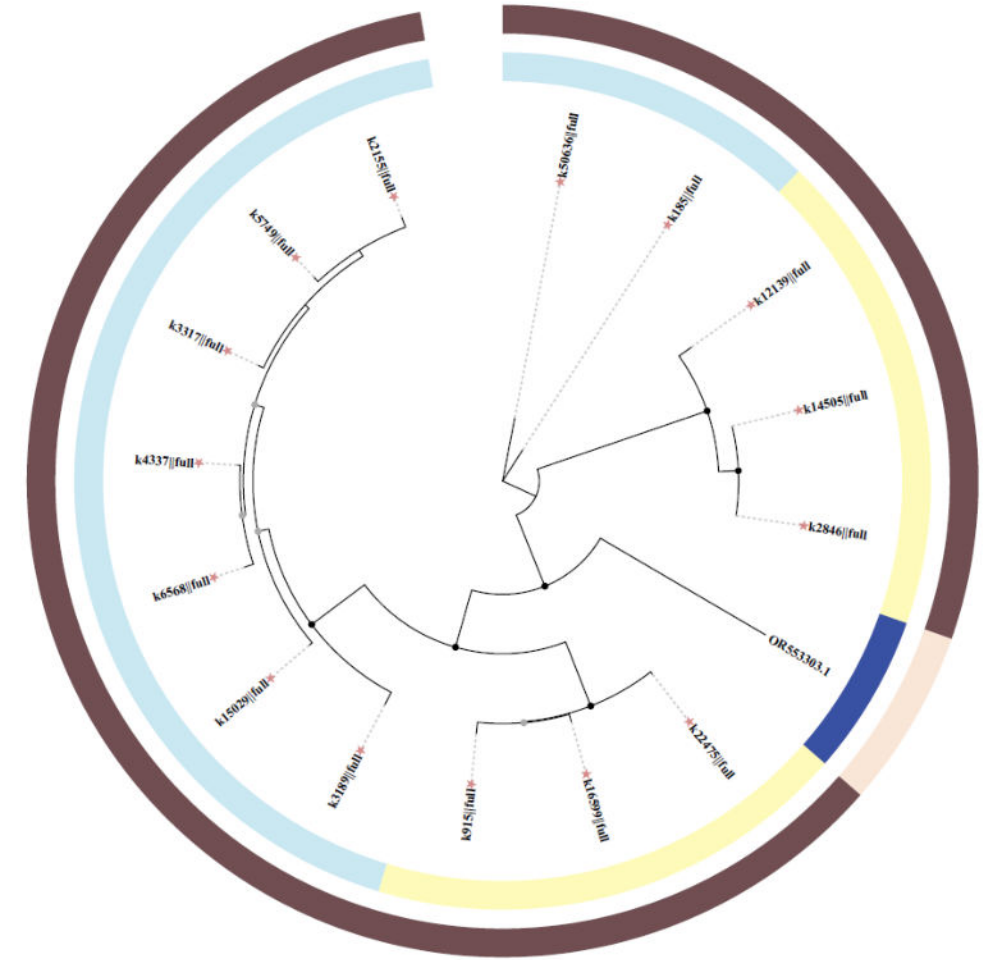
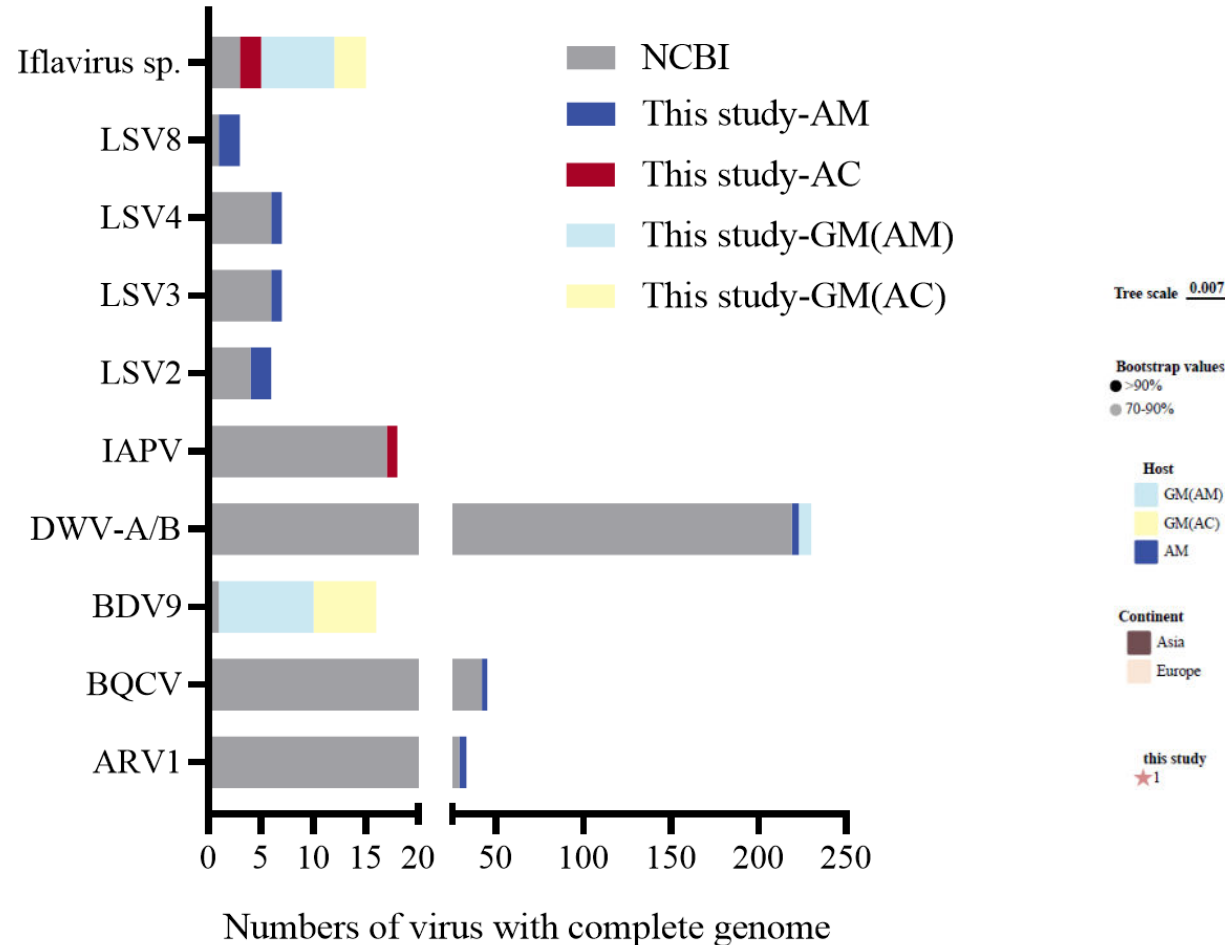
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Relative abundance

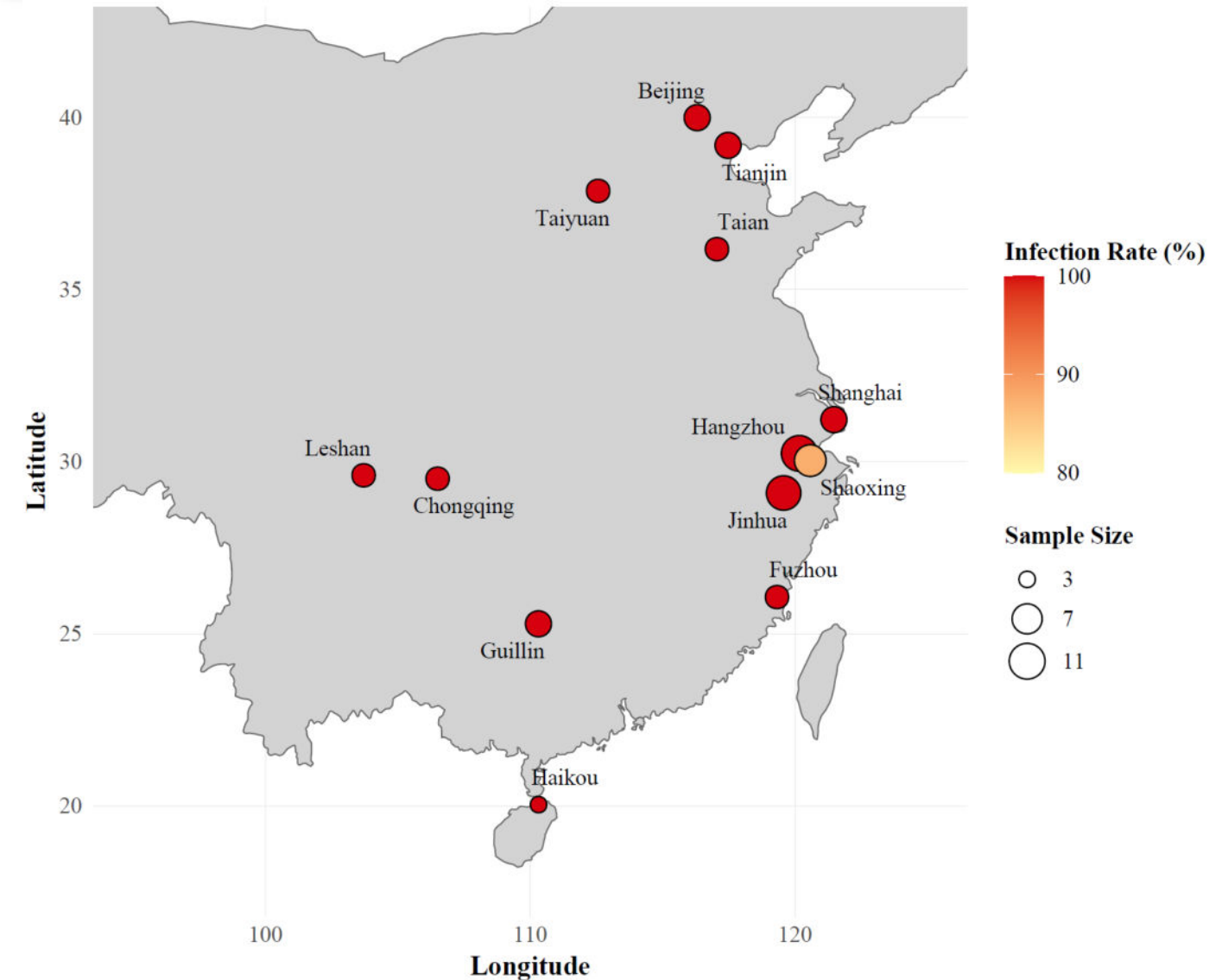


Complete genome sequence



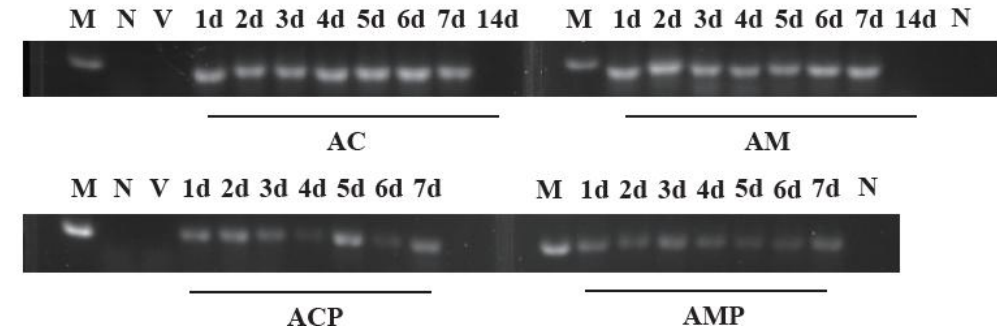
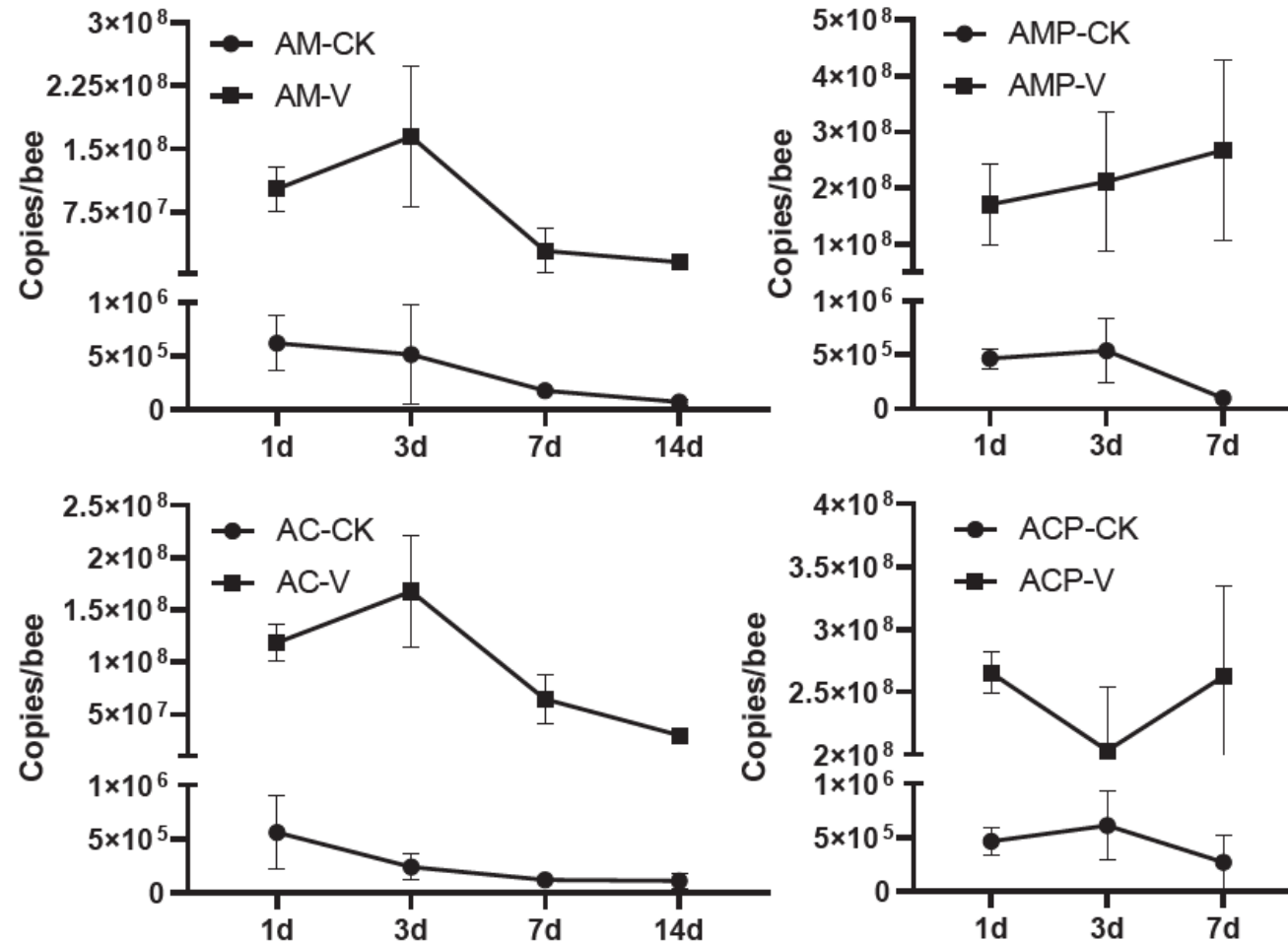
We assembled a total of **52 complete viral genomes**. Among these, key findings include the first complete genomes of **BDV9** and **DWV-A** from *G. mellonella*, and novel **Iflavirus sp.** from *A. cerana*.

Prevalence rate of Bee densovirus 9 (BDV9)



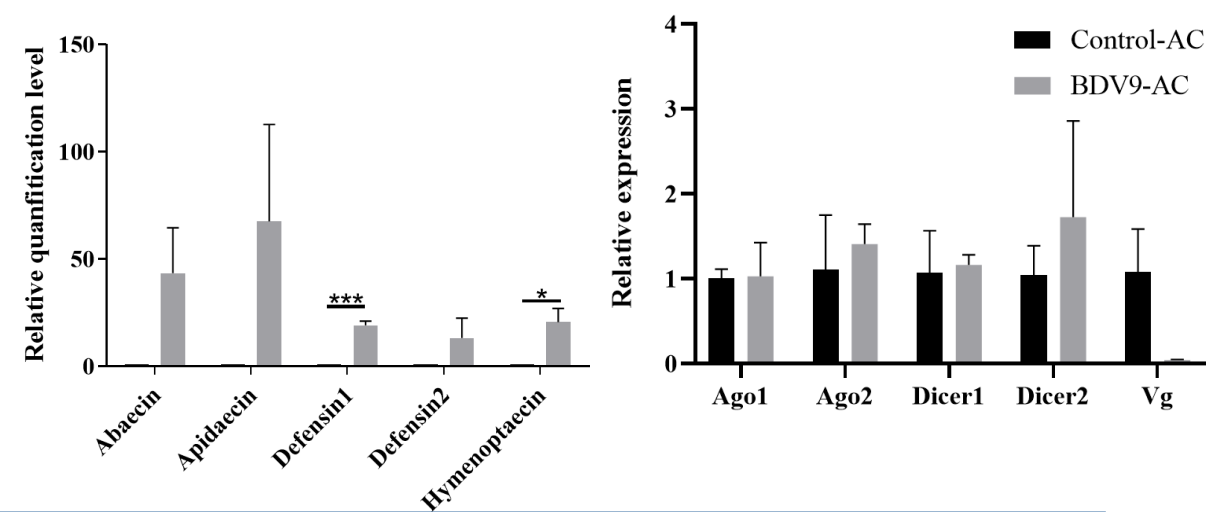
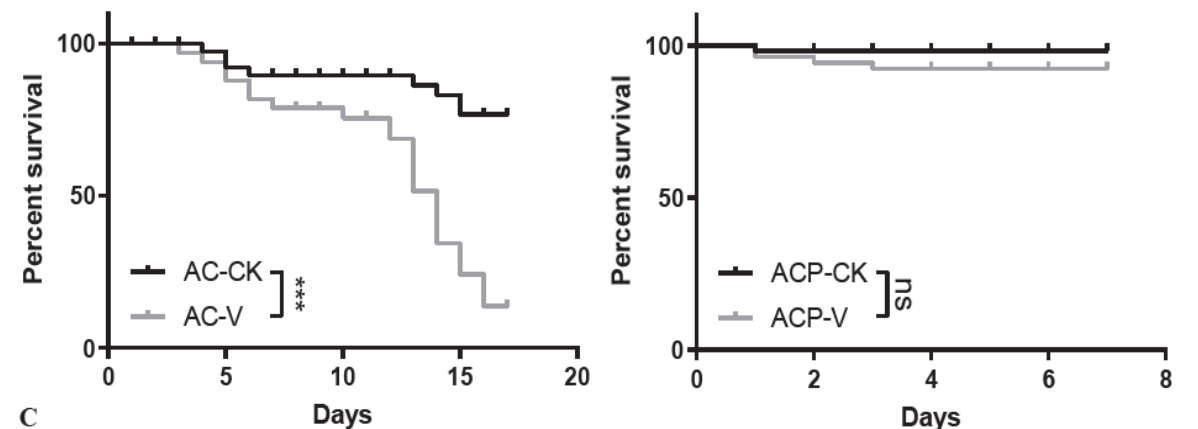
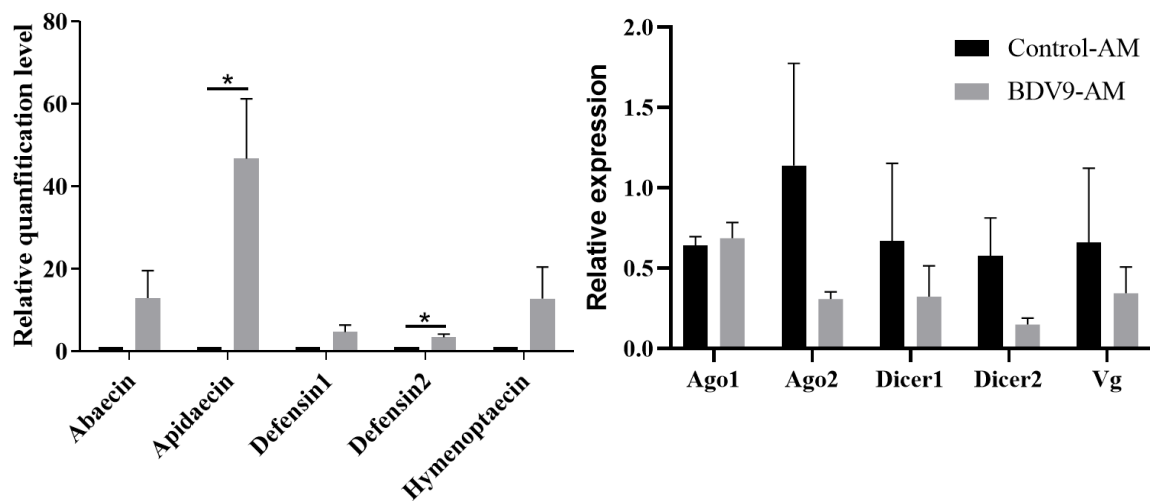
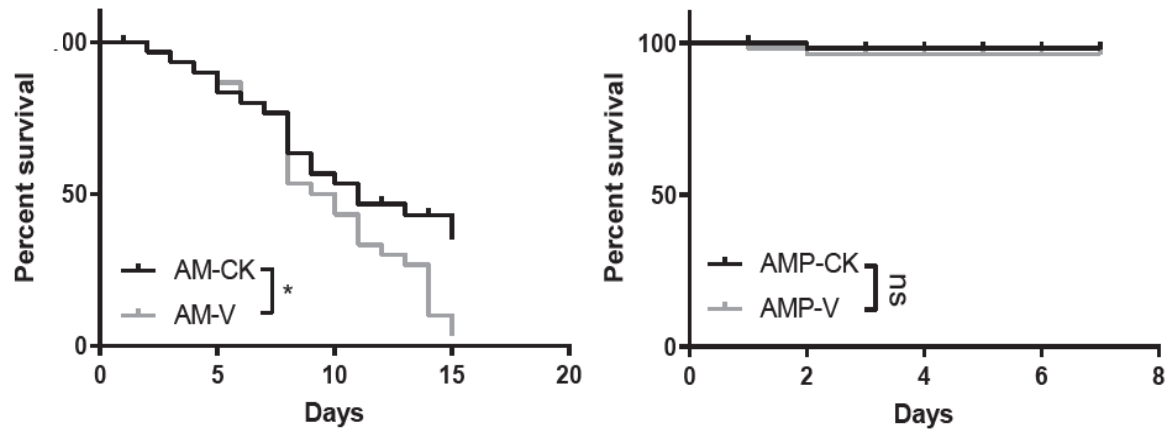
Our extensive survey across 13 cities revealed a near-universal presence of **BDV9 in *G. mellonella***, with an infection rate of **98.6% (71/72 colonies)**.

BDV9 Replication Dynamics in Honey Bees



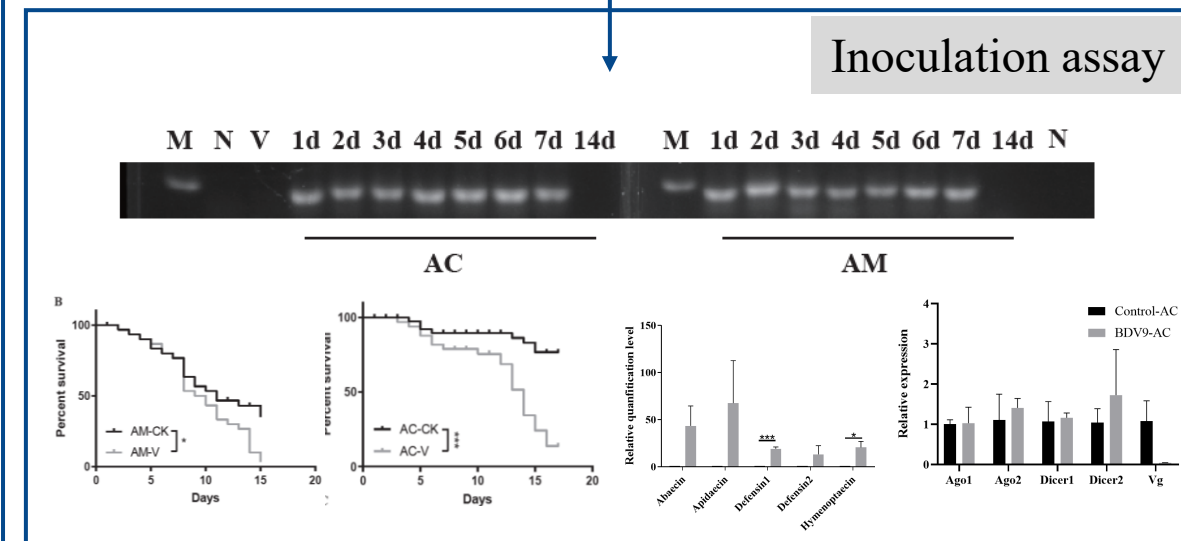
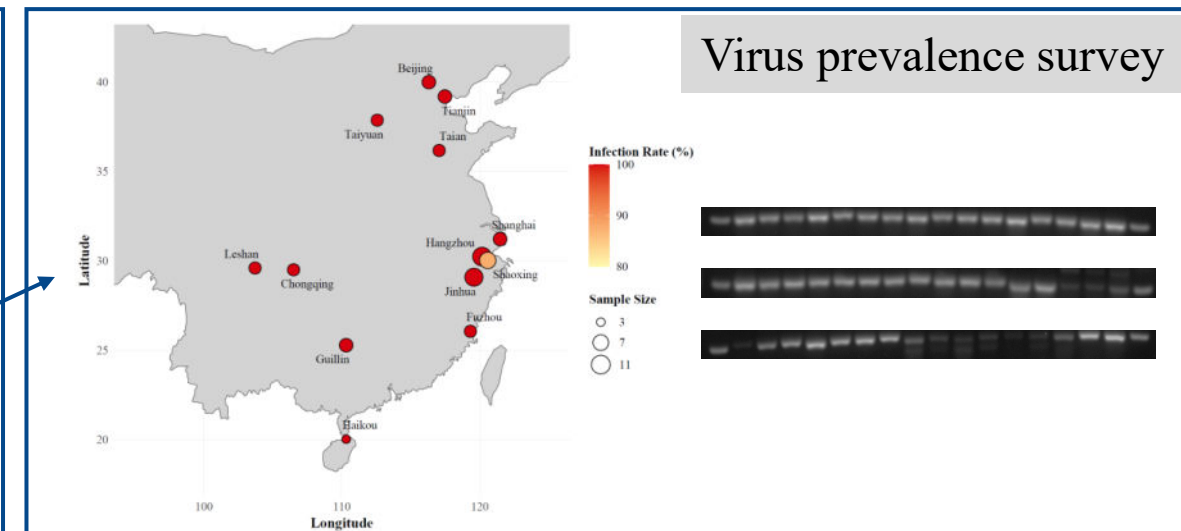
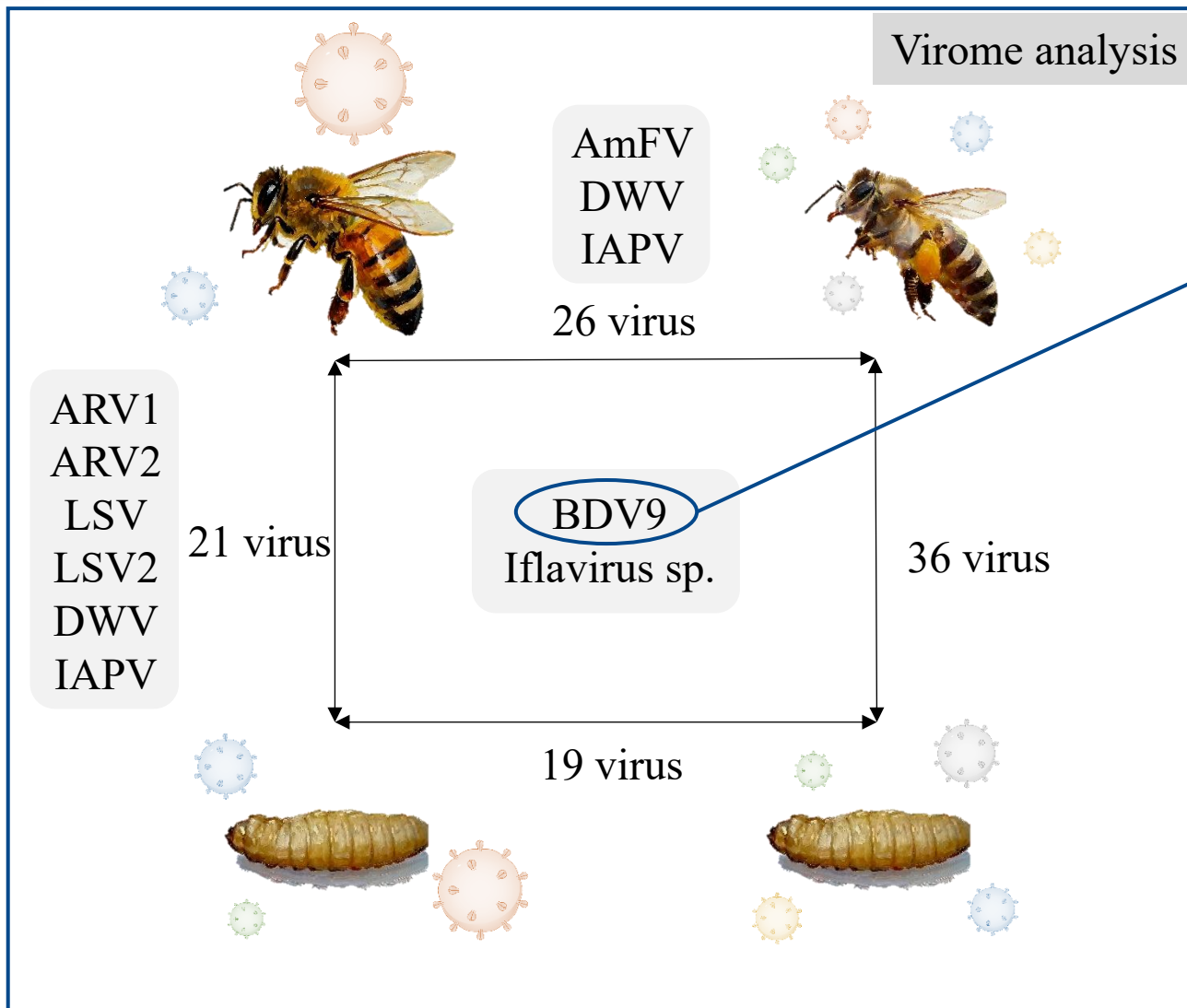
While viral titer peaked transiently at day 3 before declining, viral RNA was detectable for 7 days but was cleared by day 14.

BDV9-Induced Mortality and Immune Gene Expression



- BDV9 infection caused no visible pupal defects but **significantly impaired adult survival** in both bee species.
- The observed mortality was associated with a strong **upregulation of antimicrobial peptide** genes at D14.¹³

Conclusion



Acknowledgements



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Thank You

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