The Relationships Between Host Life-History Traits and Viral Richness in Birds

Helen M. Chen | Department of Ecology, Evolution, and Environmental Biology, Columbia University

Kevin J. Olival, Ph. D | EcoHealth Alliance

Jenna M. Lawrence, Ph. D | Department of Ecology, Evolution, and Environmental Biology, Columbia University

Abstract

There are over 10,000 species of birds, and many aspects of their natural history could make them particularly effective viral reservoirs. Studies conducted on mammals have identified several host life-history traits that may be predictors for viral richness, and experiments on birds have demonstrated relationships between life history and immunocompetence. Within some bird orders, migratory species carry a wider array of nematodes than nonmigratory species. This project updates an existing database of avian host-virus associations compiled in 2011, now containing 1,907 associations involving 142 viral species and 929 host species. The updated database also incorporates host life-history traits. Database analysis includes descriptive statistics and generalized linear models; analysis identified diet type, host research effort, and reproductive effort as predictors of viral richness. These analyses contribute to a more complete picture of viral richness across the animal kingdom and suggest more targeted viral detection efforts in response to potential conservation and public health threats.

Introduction

Nonhuman-animal viral reservoirs
- Viruses from nonhuman animal reservoirs comprise disproportionate amount of pathogens responsible for emerging and remerging infectious diseases (EIDs and RIDs)
- **Identifying potential reservoirs greatly impacts conservation and public health outcomes**
- Studies conducted on viral host range in mammals suggest certain life history traits

Avian hosts
- 10,000+ bird species
- Cosmopolitan distribution in varied
- Longer co-evolutionary lineage with viruses compared to mammals
- **Reservoirs for several well-researched EIDs/RIDs; e.g. West Nile Virus (WNV), Avian Influenza (AI)**

Host life history and viral richness
- Body mass, diet positively correlated in mammals
- Bats: fever hypothesis indicating metabolic rate as predictor (O'Shea et. al., 2014)
- Avian immunocompetence studies suggest clutch size, clutch frequency, mating system (Norris and Evans, 2000).

Research question: Is there a relationship between bird species' life history traits (physiological, behavioral, reproductive) and their viral richness?

Hypotheses: basal metabolic rate, body mass, maximum longevity, publication effort, reproductive effort are positively correlated with viral richness; carnivory increases exposure risk but herbivory increases volume consumed; migration increases exposure.

Methods

Data collection
- Literature review for associations, e.g."bird AND virus"
  - Web of Science
  - PubMed
- Acquiring avian host life history trait databases
- Host taxonomy from BirdLife International, v8
- Viral taxonomy from International Committee on the Taxonomy of Viruses (ICTV) 2015 online database
- Host phylogeny from BirdTree, Ericson backbone including all species

Analysis
- Descriptive
  - R package *ggplot2*
  - R package *dplyr*
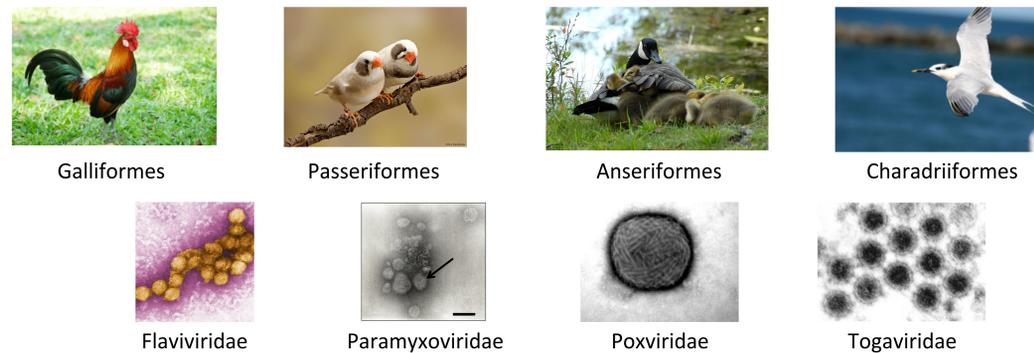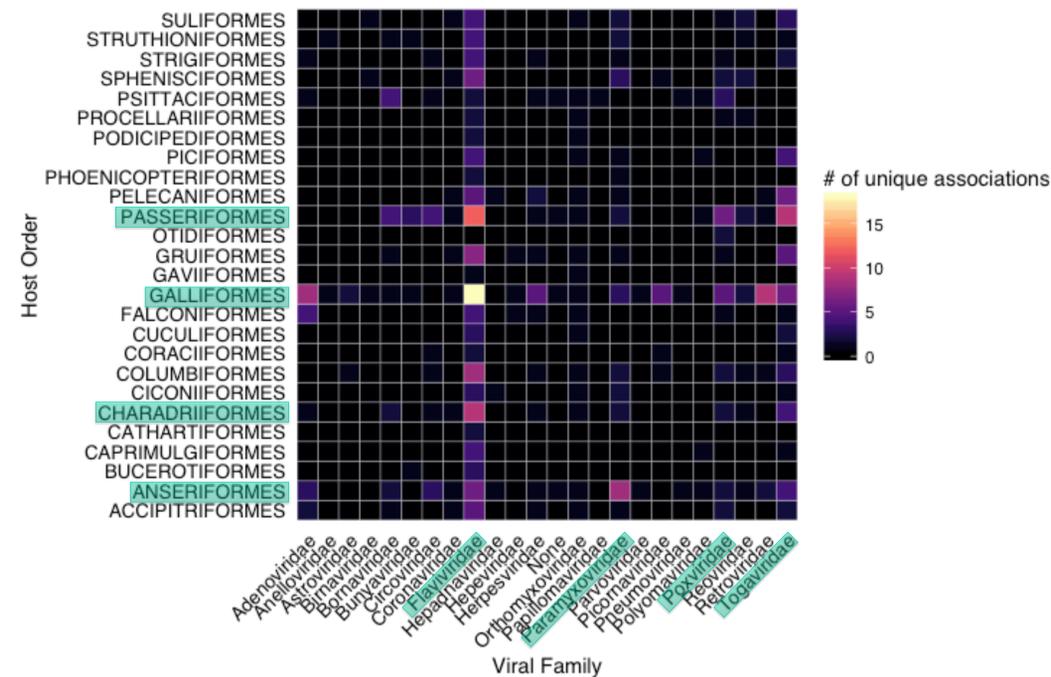- Parametric testing
- Generalized linear models (GLMs)

Figure 1. Heat map of unique associations by viral family and host order. Mean hosts per virus = 13.7, SD = 46.2, max = 469, n = 142 viruses. Mean viruses per host = 2.0, SD = 2.5, max = 53, n = 929 hosts. Photos are example species within host orders and viral families exhibiting high viral richness as indicated in the heat map.

Photo credits: purelypoultry.com, amadinai.ucoz.com, fineartamerica.com, hdwallpapersbuzz.com, cdc.gov, intechopen.com, ct.gov
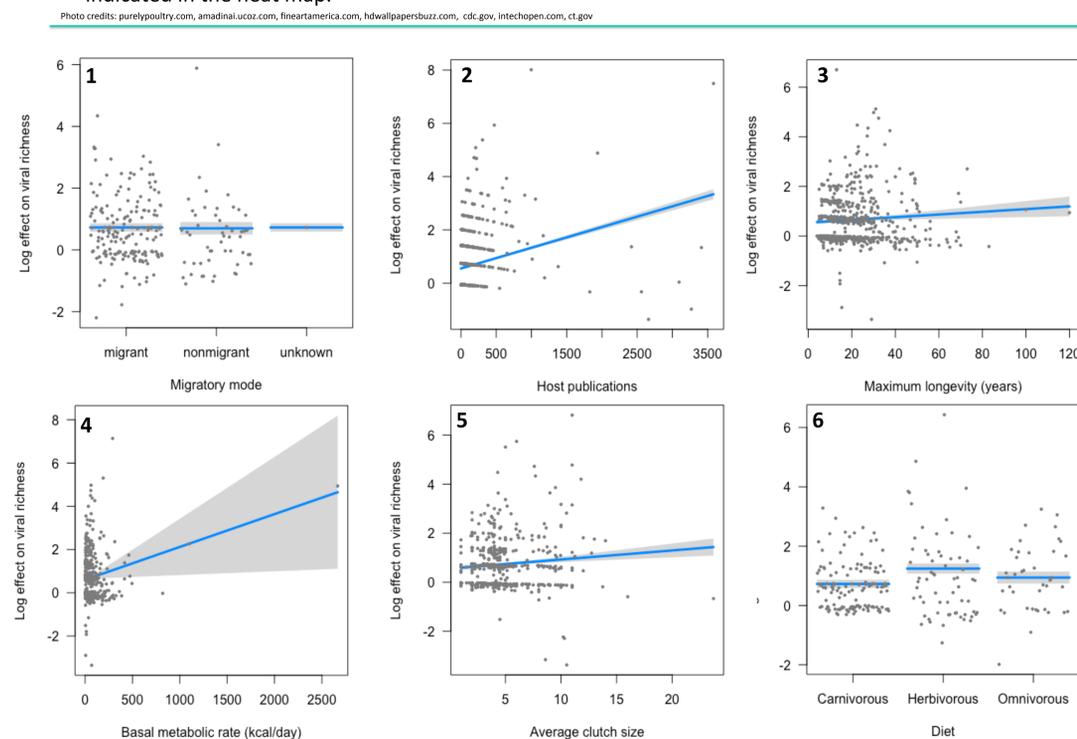

Figure 2. Scatterplots of hosts across five life history traits and publication effort, and corresponding viral richness. Plots 1 and 6 are from the behavioral GLM, 3 and 4 from the physiological, 5 from the reproductive, and 2 from host publications alone. Lines indicate values predicted by GLMs, grey shading indicates confidence at 95%. AICc values: Host publications alone = 3062.4, v = 2; behavioral traits = 951.2, v = 9 (690/929 missing observations); physiological traits = 2234.5, v = 5 (295/929 missing observations); reproductive traits = 2062.8, v = 4 (365/929 missing observations).
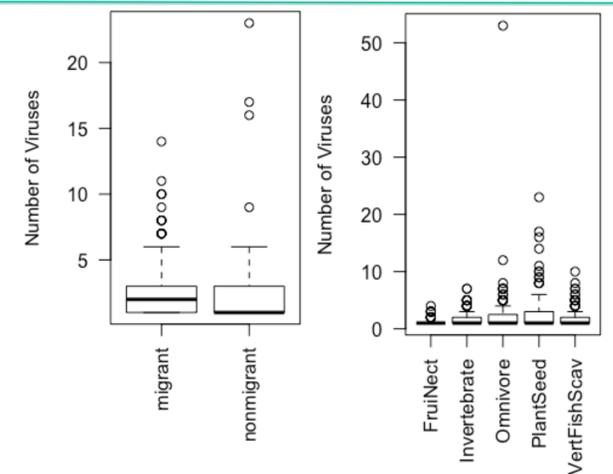

Figure 3. Boxplots of viral richness per host between migrants and nonmigrants and five diet categories. T-test for migratory mode = -0.020, P = 0.9837 (512/929 missing observations). F-test for diet categories = 4.905, P = 0.000648 (46/929 missing observations).

Discussion

Descriptive analyses
- **Lack of surveillance effort or successful surveillance** for many host orders and viral families
- *Gallus gallus* has 53 associations alone, next greatest with 23 is *Meleagris gallopavo*; WNV has 469, next greatest is AI with 231.
- Strong Poisson distribution for both hosts per virus and viruses per host, with **high-value outliers**

Inferential analyses
- **Migratory mode, like in bats, not associated with significant increase in viral richness**
- Diet category associated with significant difference in viral richness

Generalized linear models (GLMs)
- **Host publications alone was least fit model**
- Behavioral GLM was best fit of models run but missing the most observations
- **Physiological model was a poorer fit** than behavioral and reproductive models
- **Bat fever hypothesis not supported** by basal metabolic rate (BMR) results

Conclusions
- Physiological traits not strong predictors of viral richness
- Support for energetic tradeoff between reproduction and immunocompetence given number of clutches per year as stronger predictor of viral richness than publication effort alone; also evidence for behavioral risk factors
- Many viral families and host orders with few associations

Recommendations
- Need for more surveillance for many viral families and avian orders
- Controlling for effect of phylogeny
- Targeted surveillance for host species in certain range of predictor traits

References

O'Shea, T. J., Cryan, P. M., Cunningham, A. A., Fooks, A. R., Hayman, D. T. S., Luis, A. D., . . . Wood, J. L. N. (2014). Bat Flight and Zoonotic Viruses. *Emerging Infectious Diseases, 20*(5), 741-745. doi:10.3201/eid2005.130539

Norris, K., & Evans, M. R. (2000). Ecological immunology: life history trade-offs and immune defense in birds. *Behavioral Ecology, 11*(1), 19-26.