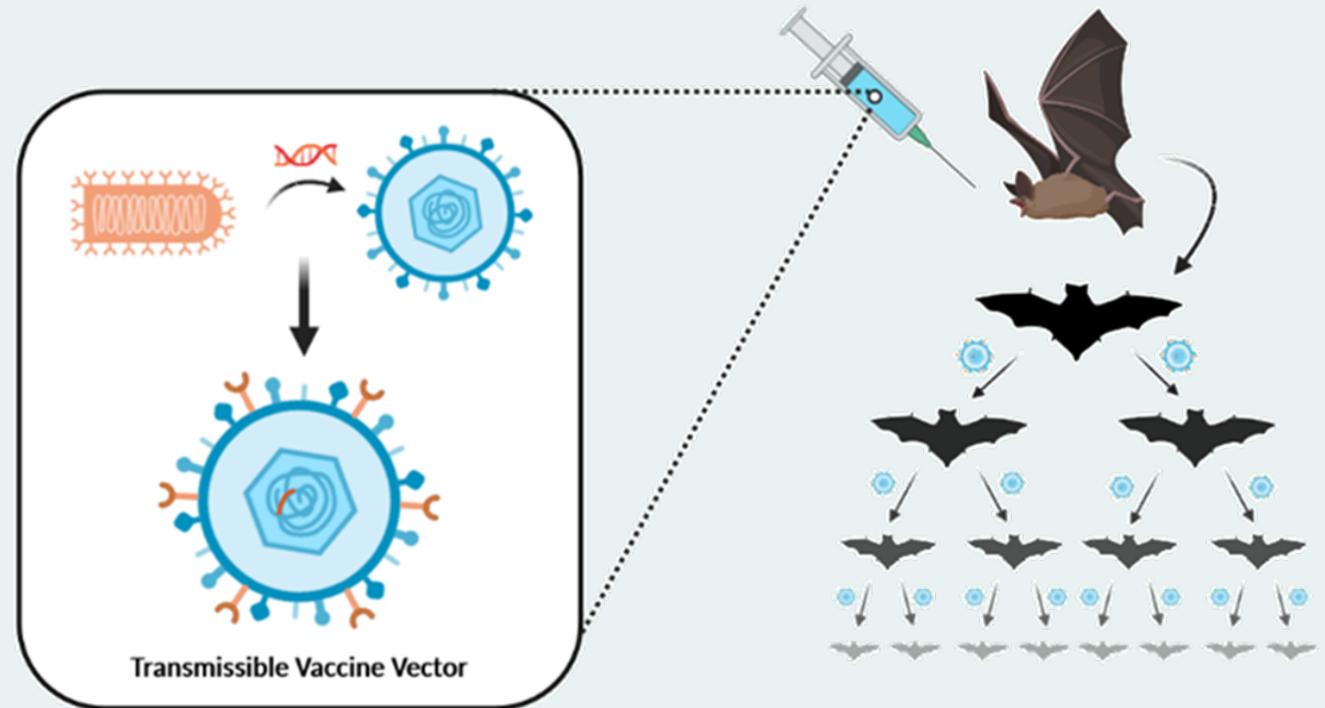


Investigating a **betaherpesvirus** of vampire bat *Desmodus rotundus* as a transmissible vaccine vector against rabies virus

Aims:

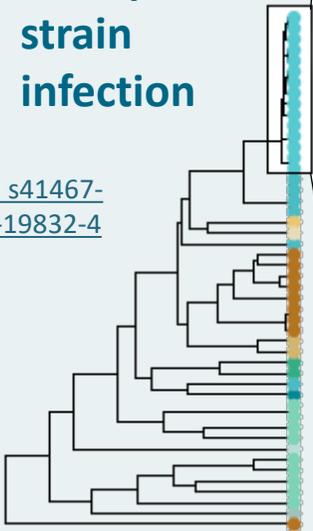
- (1) Evaluate DrBHV for **key characteristics of a transmissible vaccine**.
 - (i) Host specificity
 - (ii) Transmissibility
 - (iii) Super-infection
- (2) Use **deep sequencing** and **longitudinal samples** to explore intra- and inter-host transmission dynamics.
- (3) Model DrBHV transmission and **simulate the effects of vaccination** on rabies virus outbreaks (ongoing).



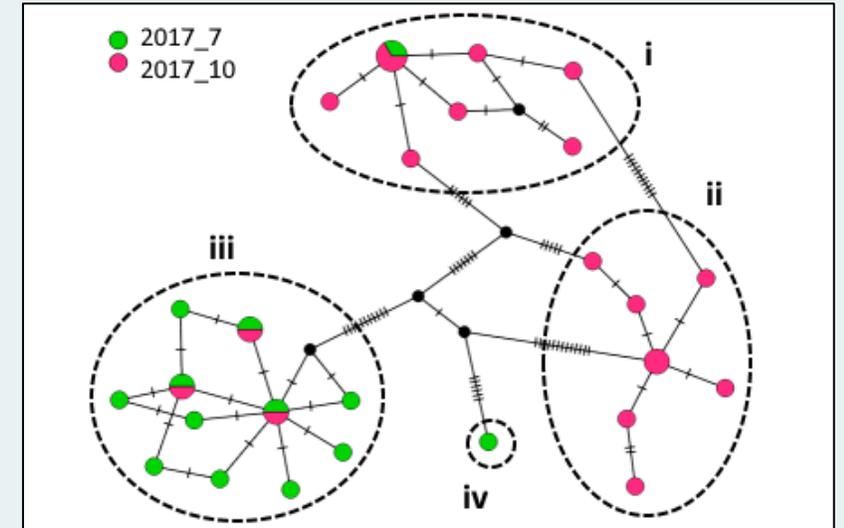
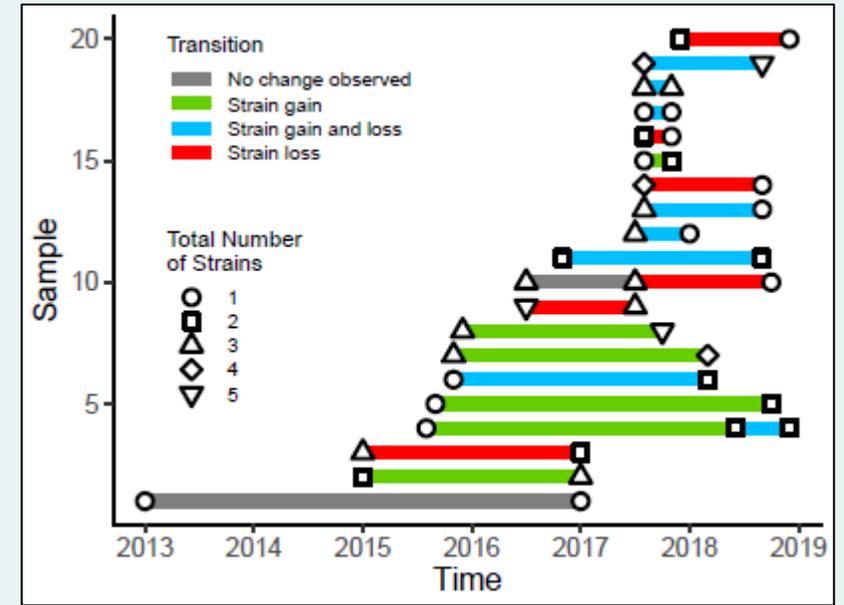
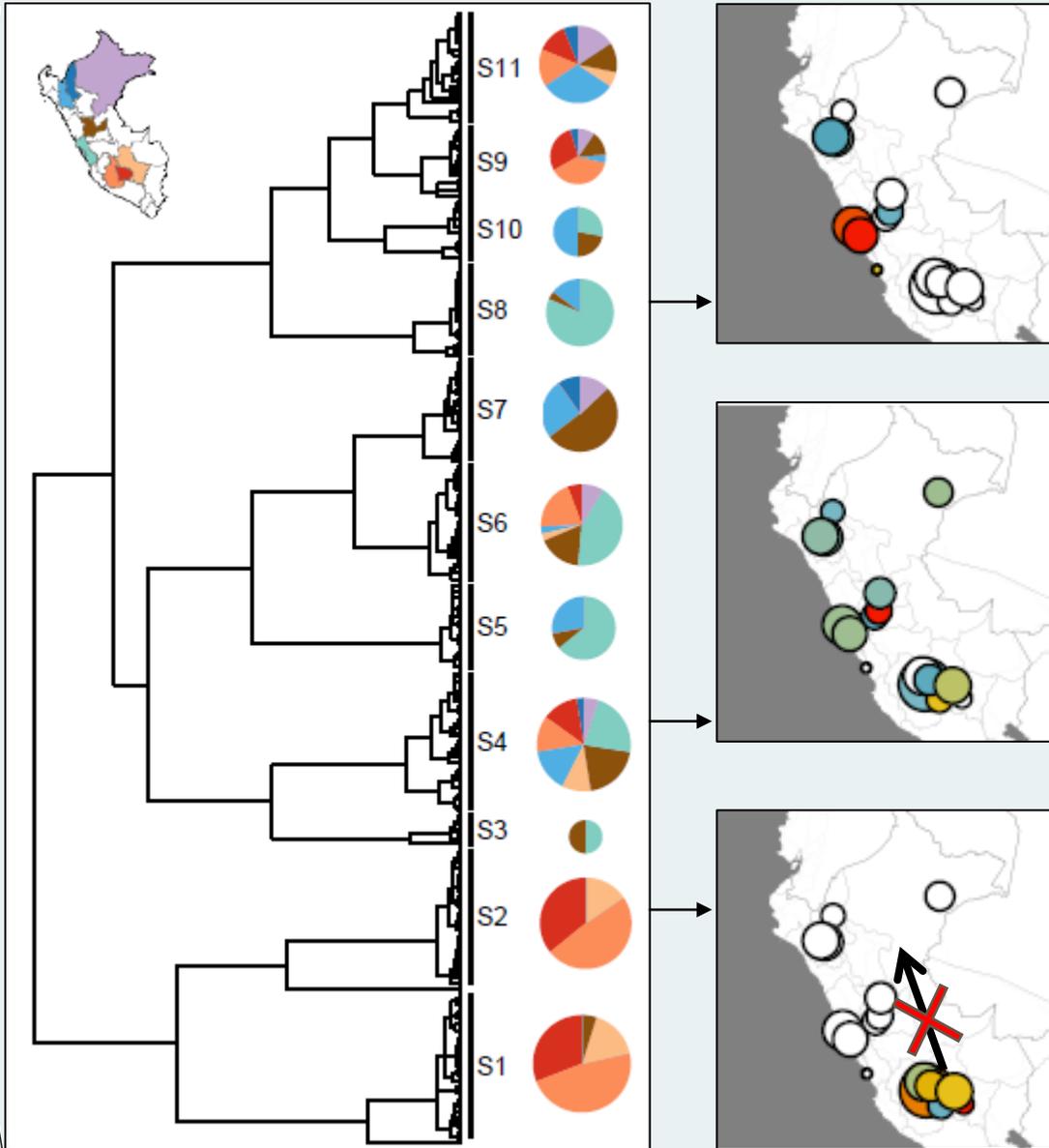
***Desmodus rotundus* betaherpesvirus:**
key characteristics

- **Host specific** at the bat family level
- **97%** overall prevalence in all bats
- ~230kbp genome
- **Multiple strain infection**

DOI: s41467-020-19832-4



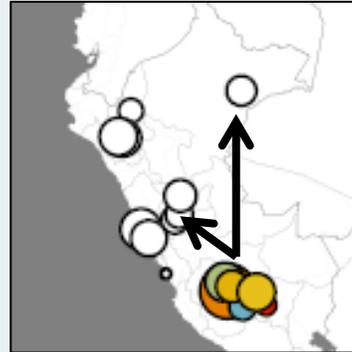
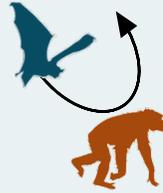
Between host dynamics: 11 strains with unique geographic profiles. Unidirectional transmission in some areas. Strain prevalence influenced by strain age.



Within host dynamics: longitudinal sequencing shows evidence of strain gain, loss, and long term infection with latency and reactivation.

Conclusions:

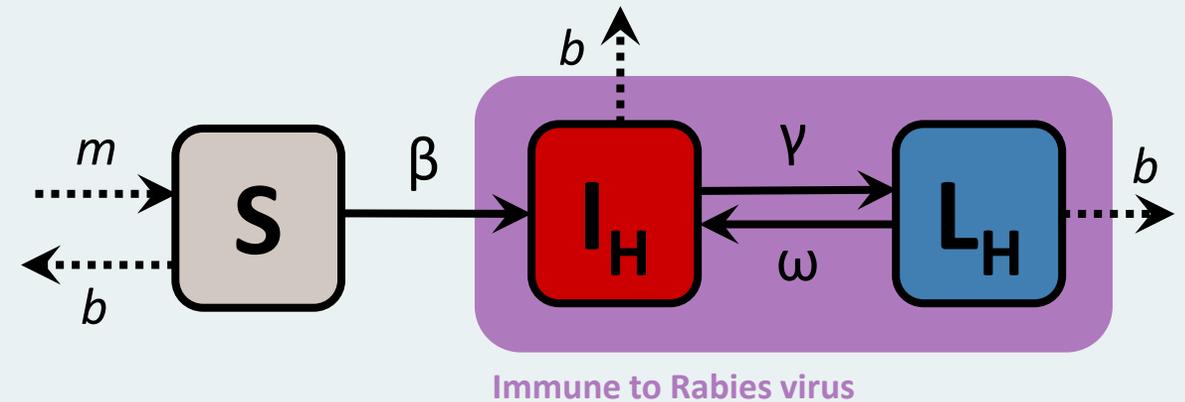
- ✓ **Host specific** – unlikely to transmit outside of the target family
- ✓ **Transmissible** – can reach even strain specific prevalences of up to 65%.
- ✓ **No interference with wildtype** – can't show same strain superinfection, but can use strains from different areas



Future work:

Model the equilibrium levels of DrBHV, and the impact of vaccination on **rabies outbreaks**.

Identify the **most important parameters** that we don't currently have data for, e.g. **how long vaccination lasts**.



- Realistic strain-specific prevalence of **30-50%**.
- Active infection in **20-40%** of samples.
- Latent period could be as short as 5 months.

