

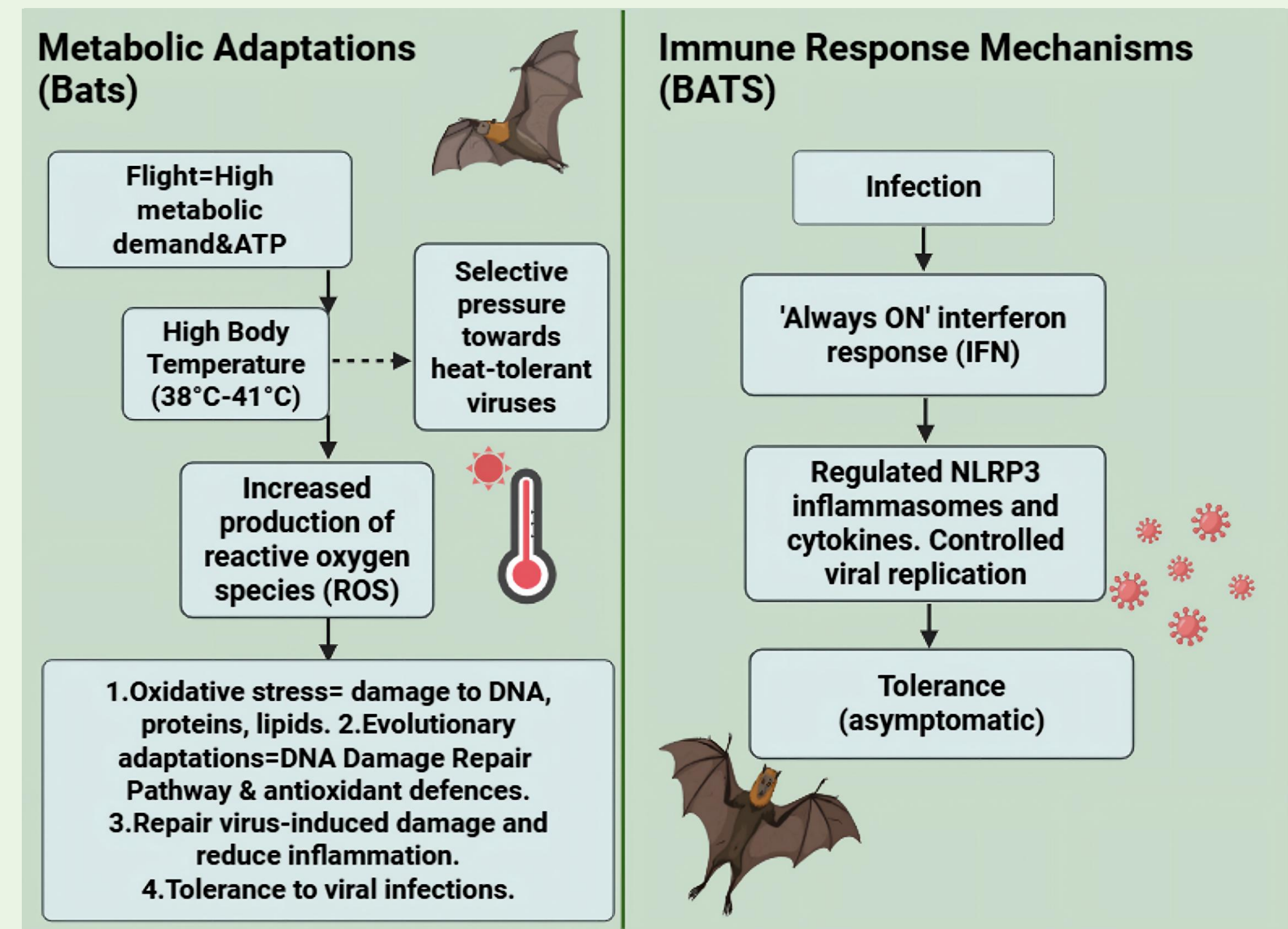
## 1. Abstract

- Bats act as asymptomatic reservoirs for highly pathogenic viruses, including Nipah virus (NiV) and Ebola virus (EBOV).
- This project analyses the evolutionary adaptations enabling bat viral tolerance and compares the molecular pathways of NiV and EBOV to evaluate their pandemic potentials and proposes a ferret-model study to identify respiratory mutations in NiV, aiming to prevent future pandemics.

## 2. Introduction

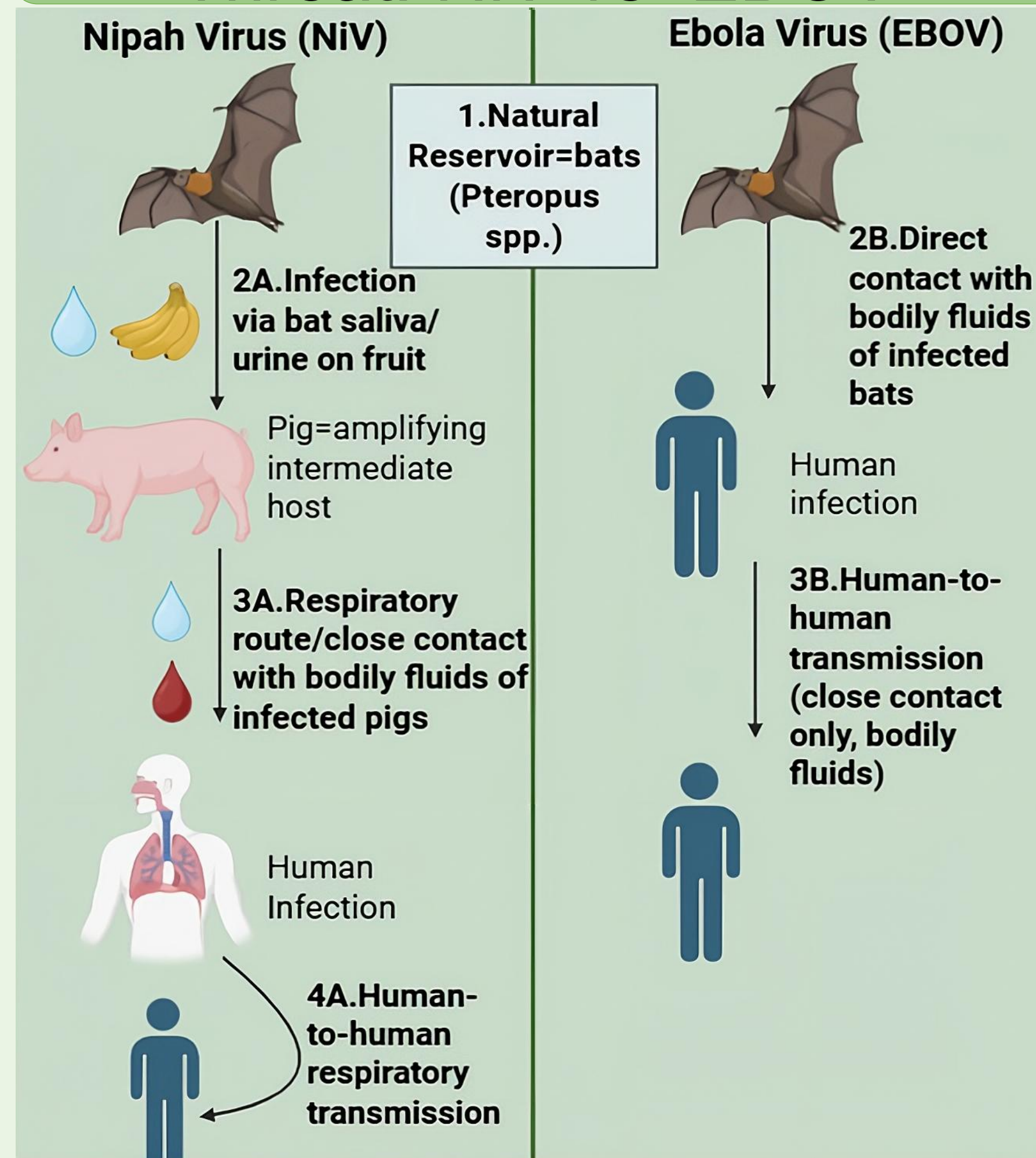
- Zoonotic bat viruses are a growing global threat due to habitat loss and spillover to humans.
- While EBOV causes regional endemics, NiV is a high-priority pathogen with up to 70% fatality rate and respiratory spread potential<sup>1</sup>.

## 3. Viral Tolerance in Bats



- 'Flight as Fever'- flight metabolism raises bat temperatures up to 41°C, naturally selecting for heat-tolerant viruses. These viruses are stable against human inflammation.
- DNA Damage Repair Pathway and antioxidant defenses.
- 'Always ON Immunity'- bats constantly express IFN- $\alpha$ . This controls viruses without triggering the fatal hyperinflammation seen in humans.

## 4. Evaluating the Pandemic Threat: NiV vs. EBOV

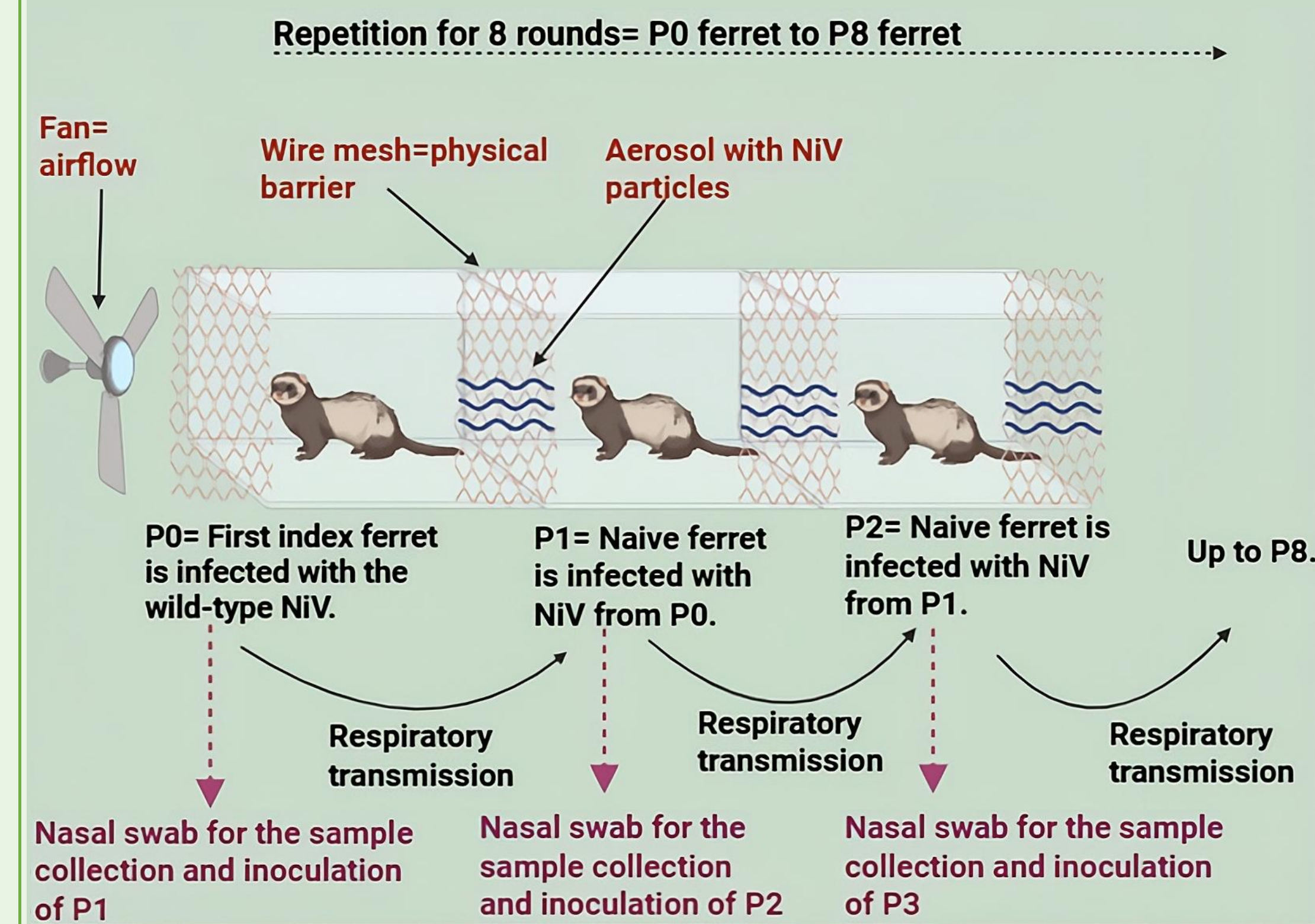


## NiV vs. EBOV Transmission

Feature	NiV	EBOV
Cellular Receptor	Ephrin-B2/3 (Broad tropism) <sup>2</sup>	NPC1 (via GP cleavage)
Transmission Route	Respiratory droplets, contaminated food, and intermediate hosts (pigs)	Direct contact with infected bodily fluids/ secretions
Pandemic Potential	High (Due to respiratory capability and human-to-human spread)	Low / Regional (Restricted by contact-dependent transmission) <sup>3</sup>

## 5. Anticipating NiV Mutations

- We lack data on which specific NiV mutations enable efficient human respiratory spread.
- Method= 8 rounds of *in vivo* serial passage using ferrets (physically separated by wire mesh to isolate aerosol transmission)<sup>4</sup>.
- Reverse genetics will be used to synthesise and confirm the high-risk nature of the identified mutations.



## 6. Conclusion

- NiV's respiratory capacity makes it a significantly higher global threat than EBOV.
- Proactively identifying airborne mutations before they emerge naturally enables targeted surveillance and proactive antiviral design.

## 7. Acknowledgements

I would like to thank Dr John Barr for his incredible support and guidance.

## 8. References

- Sun, B., et al., 2018. Phylogeography, Transmission, and Viral Proteins of Nipah Virus. *Virologica Sinica*. 33(5), pp.385–393.
- Negrete, O.A., et al., 2005. EphrinB2 is the entry receptor for Nipah virus, an emergent deadly paramyxovirus. *Nature*. 436(7049), pp.401–405.
- Vetter, P., et al., 2016. Ebola Virus Shedding and Transmission: Review of Current Evidence. *Journal of Infectious Diseases*. 214(suppl 3), pp.177–184.
- Rockx, B. and Mire, C.E. 2023. Ferret Models for Henipavirus Infection. *Methods in molecular biology*. 2682, pp.205–217.
- The figures were created using BioRender.com.