



Funded by
the European Union



SEASONAL STRUCTURING OF BAT COMMUNITIES AT A TRANSBOUNDARY HUMAN-WILDLIFE INTERFACE IN EASTERN THAILAND

Aingorn Chaiyes*, Prateep Duengkae,
Nutthinee Sirichan, Boripat Siriaroonrat

Faculty of Science, Kasetsart University,
Bangkok 10900, Thailand

*Corresponding author: E-mail:
aingorn.ch@ku.ac.th, aingorn.ch@ku.th





Funded by
the European Union

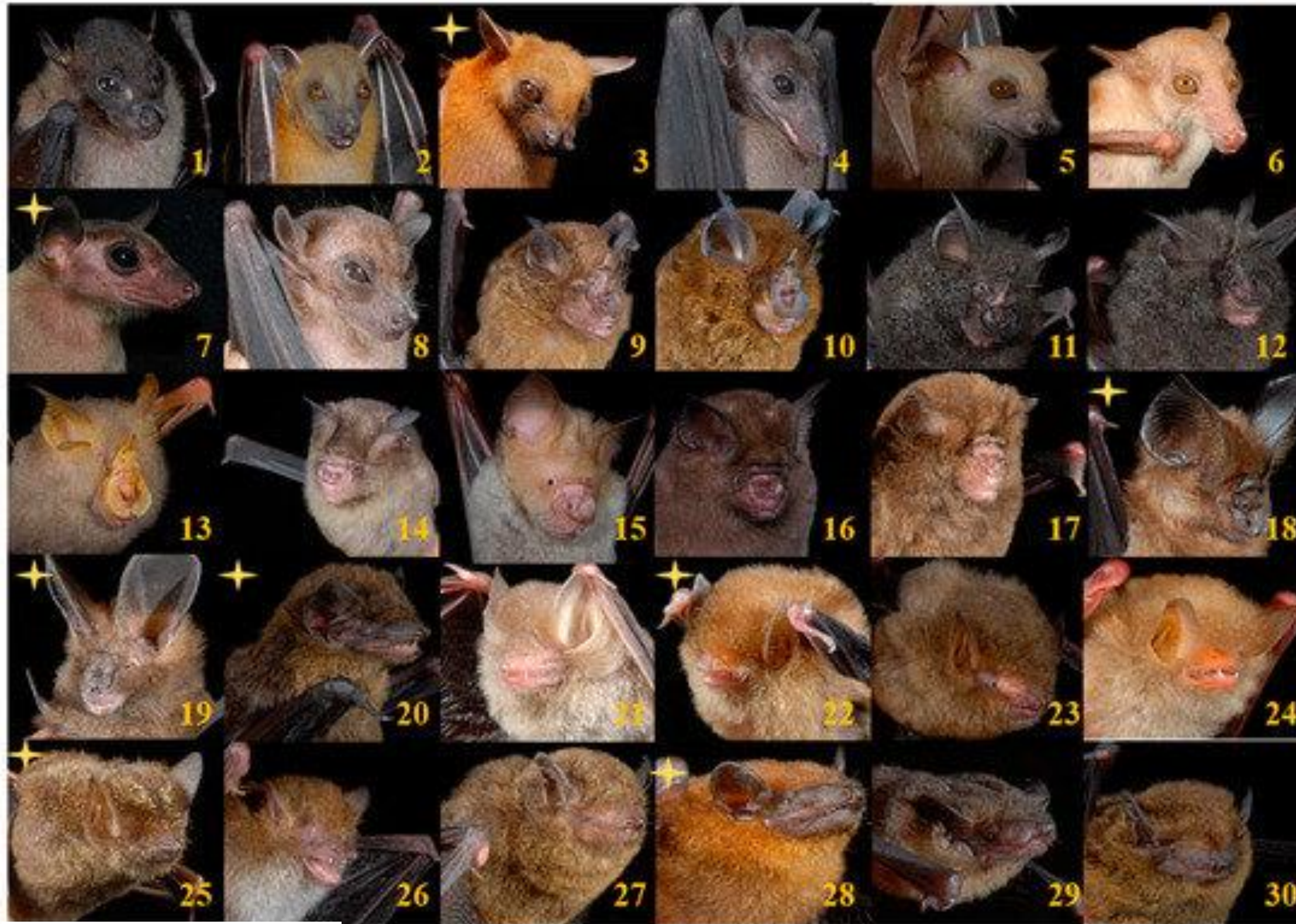


PANDASIA
PREVENTING FUTURE PANDEMICS



Thailand

How many bat species in Thailand?



Thailand is home to 148 bat species, representing 47 genera and 10 families, accounting for approximately 10% of the world's bat species (updated in 2023).

Background & One Health Context



Bat Ecological Dynamics as a One Health Pillar

Understanding the nuanced, seasonal shifts in bat communities is fundamental to predicting viral maintenance and mitigating spillover risks.

We cannot protect human health without understanding host ecology.

Study area and Habitats

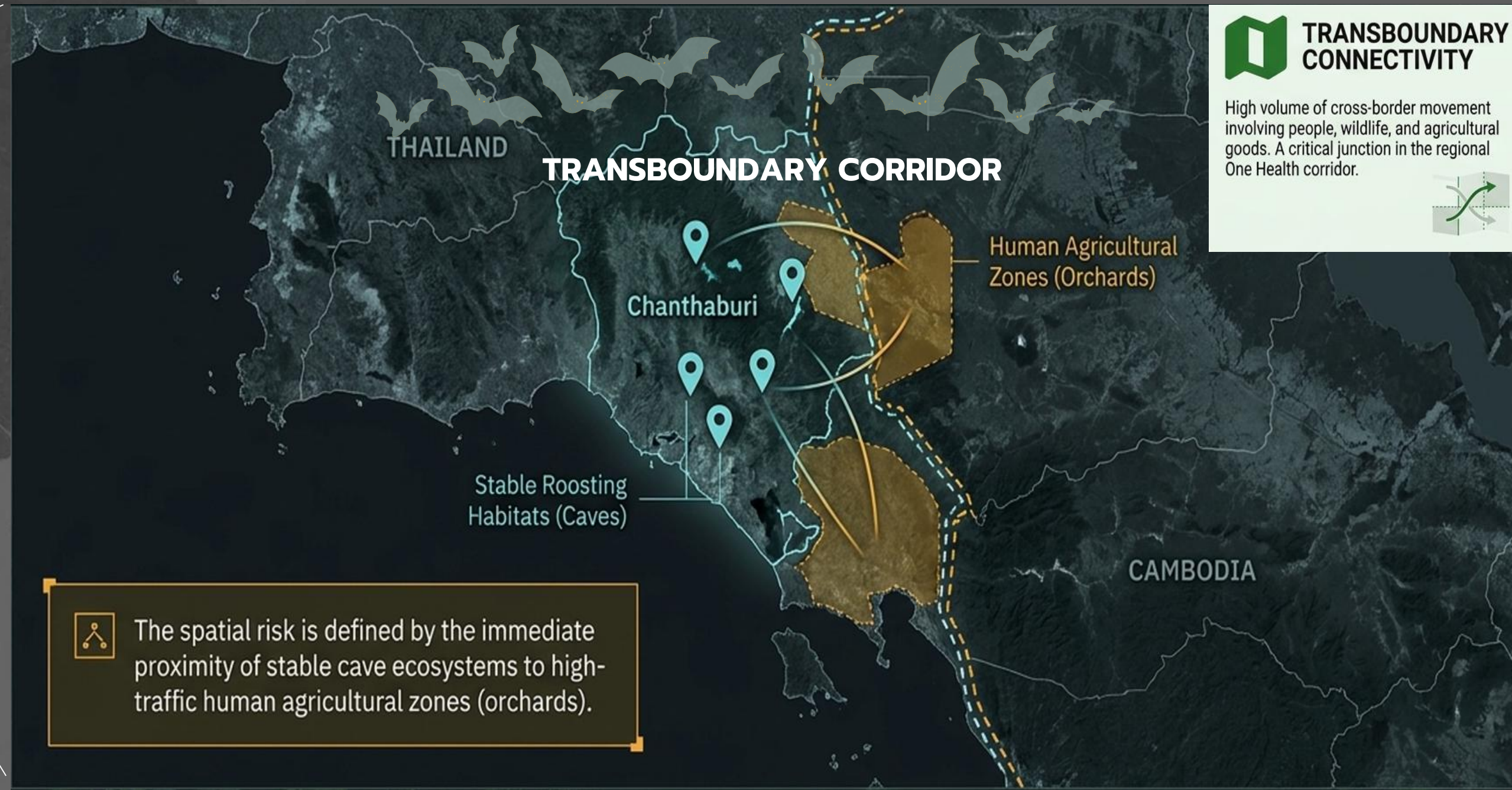
Chantaburi Province

- 1) Pong Nam Ron Sub-district
- 2) Soi Dao Sub-district

Habitat

- 1) Cave
- 2) Orchards

CHANTHABURI PROVINCE
THAILAND-CAMBODIA
BORDER REGION



METHODOLOGY: SURVEY DESIGN & HABITATS

DURATION: FULL STUDY SPANNING 2 years, (2024–2025)

COVERING DISTINCT DRY AND WET SEASONAL CYCLES.

HABITAT I : CAVE

Natural Reservoir Hubs



Wet Season Cave Surveys



Dry Season Cave Surveys

Role: Primary roosting habitats providing stable environments for year-round resident species.

Interface: Site of frequent human contact through tourism and Buddhist activities.

HABITAT II :ORCHARD

Agricultural Interface



Wet Season Orchard Surveys



Dry Season Orchard Surveys

Role: Secondary foraging and seasonal roosting habitats for transitional indicator species.

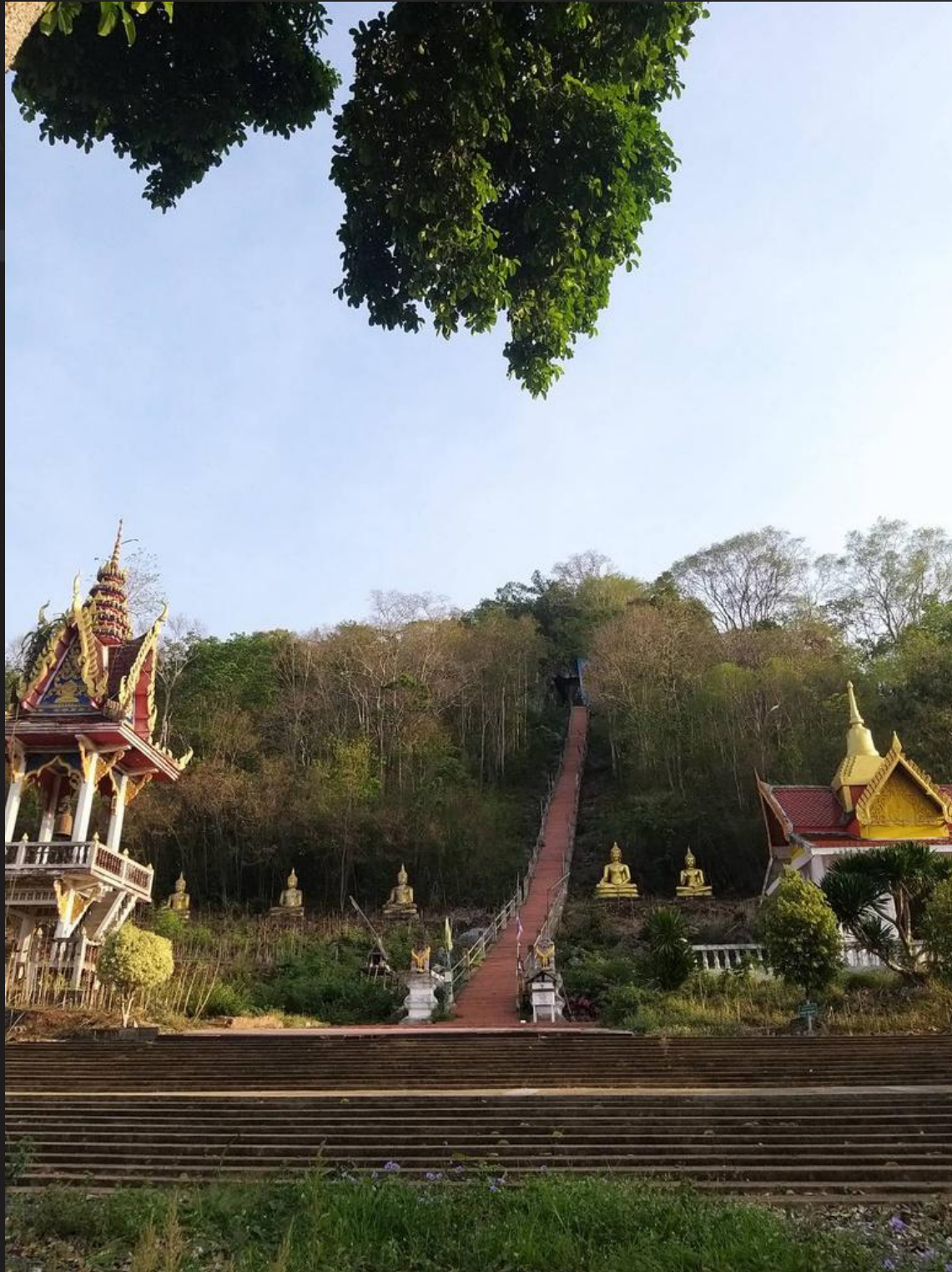
Risk: Dynamic seasonal community shifts creating periodic pulses of viral spillover potential.

Study Area and Habitats: CAVE

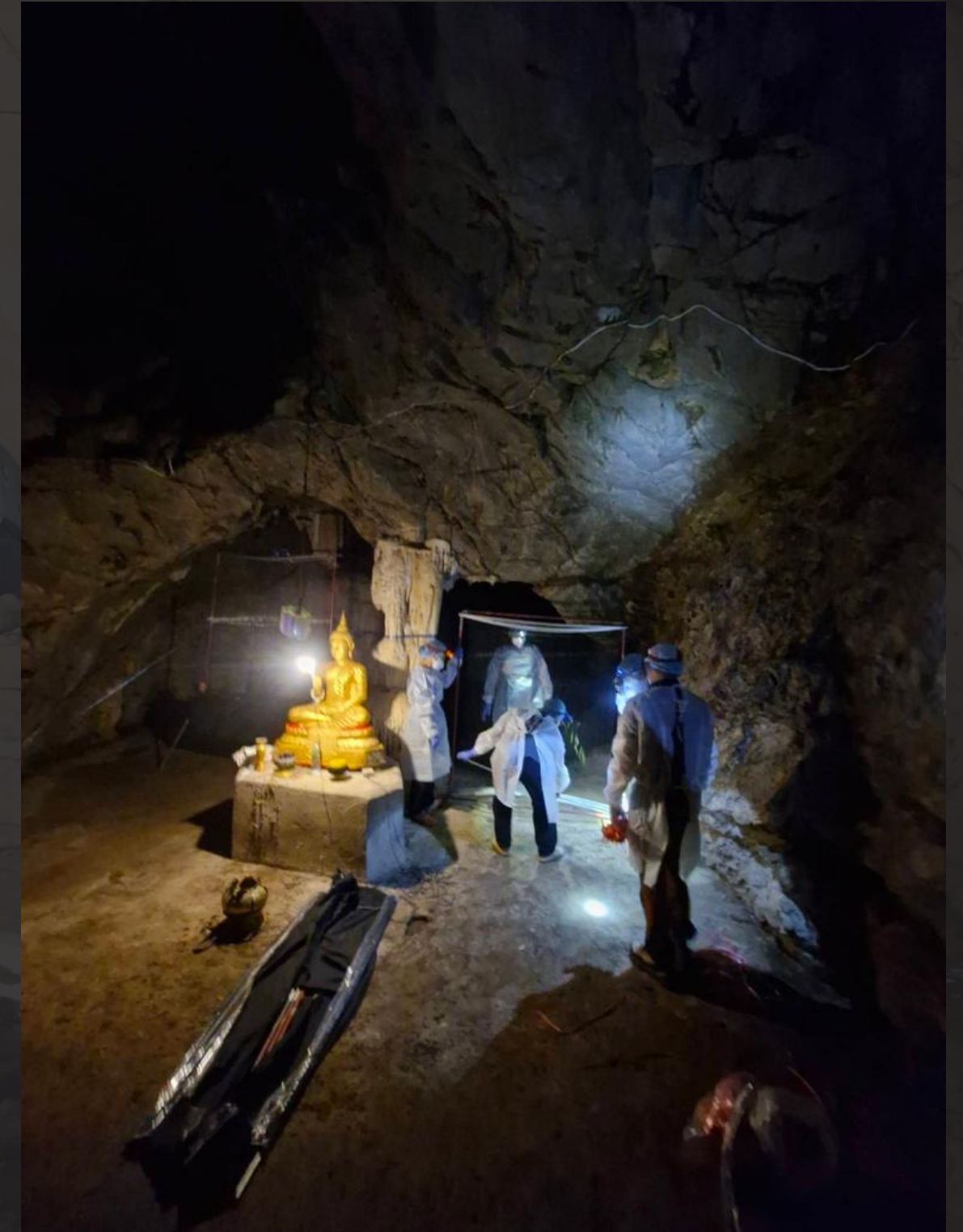
Chantaburi Province

Pong Nam Ron & Soi Dao Sub-district

1.Thum-Sarika Temple



2.Thum-Khao-Keaw Temple



Study Area and Habitats: ORCHARDS | Chantaburi Province Pong Nam Ron & Soi Dao Sub-district

1. Khao-Soi-Dao-Nue Temple

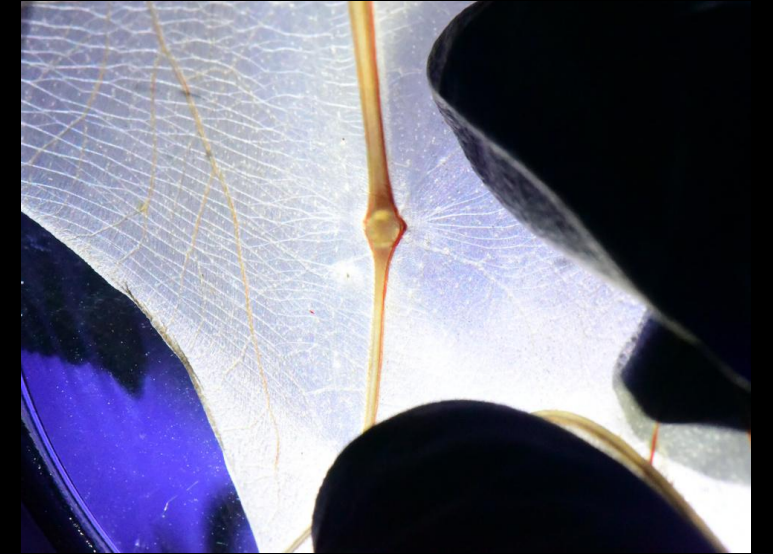
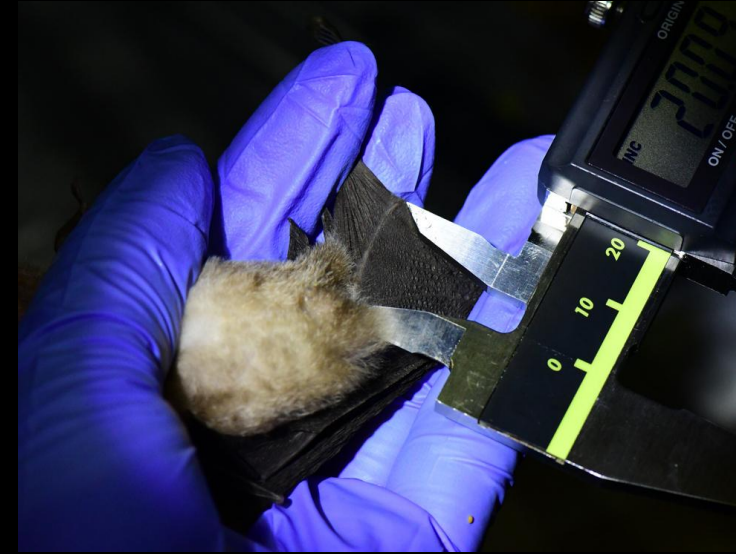


2. Durian, Logan, Mango Orchard



Measurement & Data Collection

Identify & Measurement the bat Characteristics



Equipments for collecting data



Collecting Sample

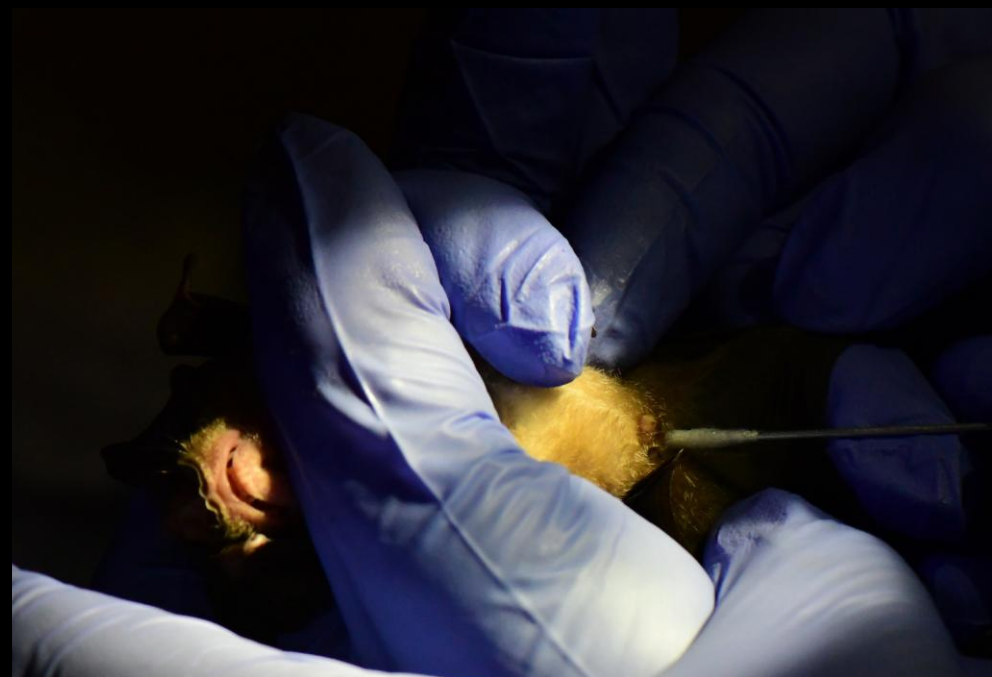
Oral Swab



Wing tissue by biopsy punch



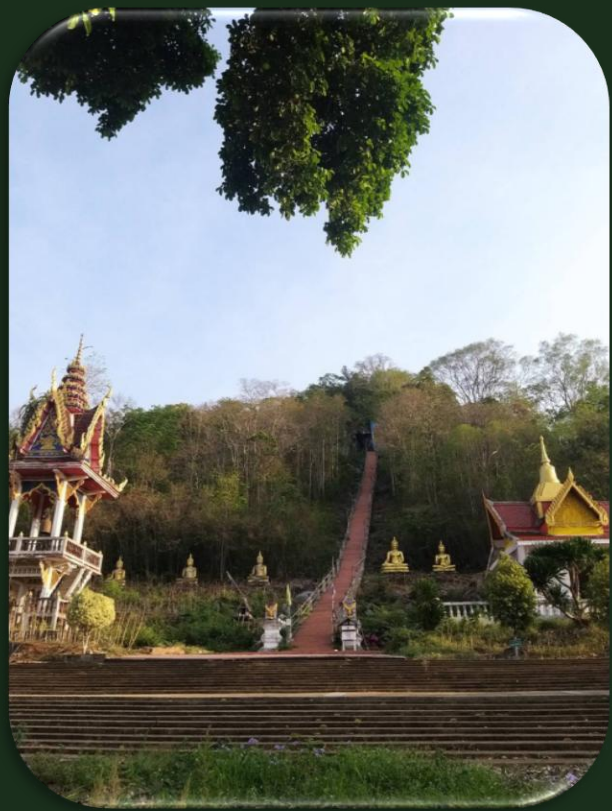
Rectal Swab



Ectoparasite

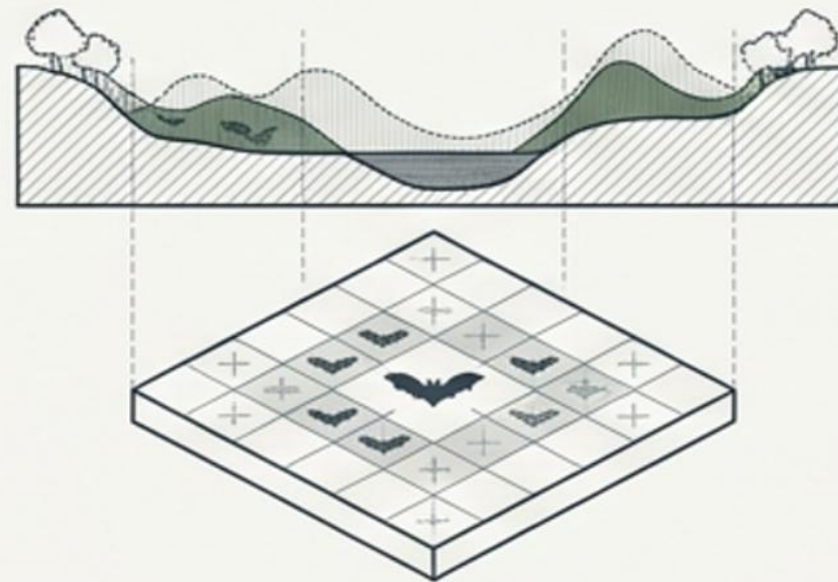


Study Framework



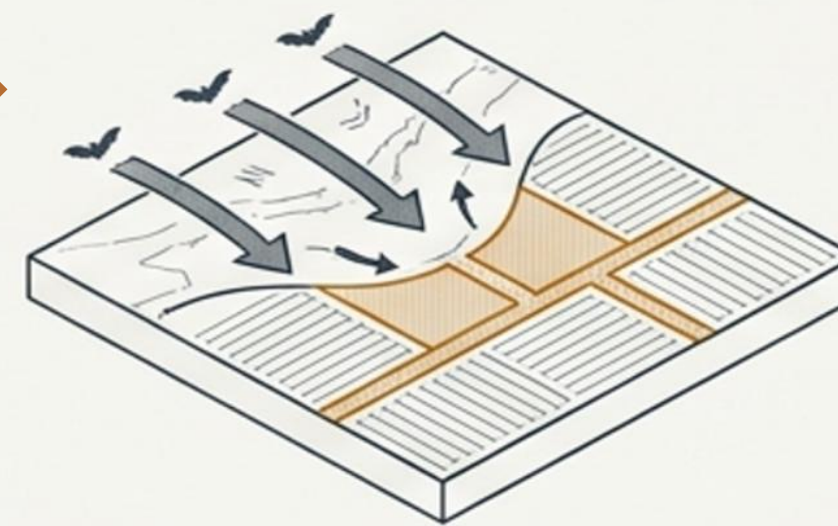
Understand (Ecology)

2024–2025 systematic surveys reveal stable **alpha diversity** but massive seasonal structuring of 16 bat species.

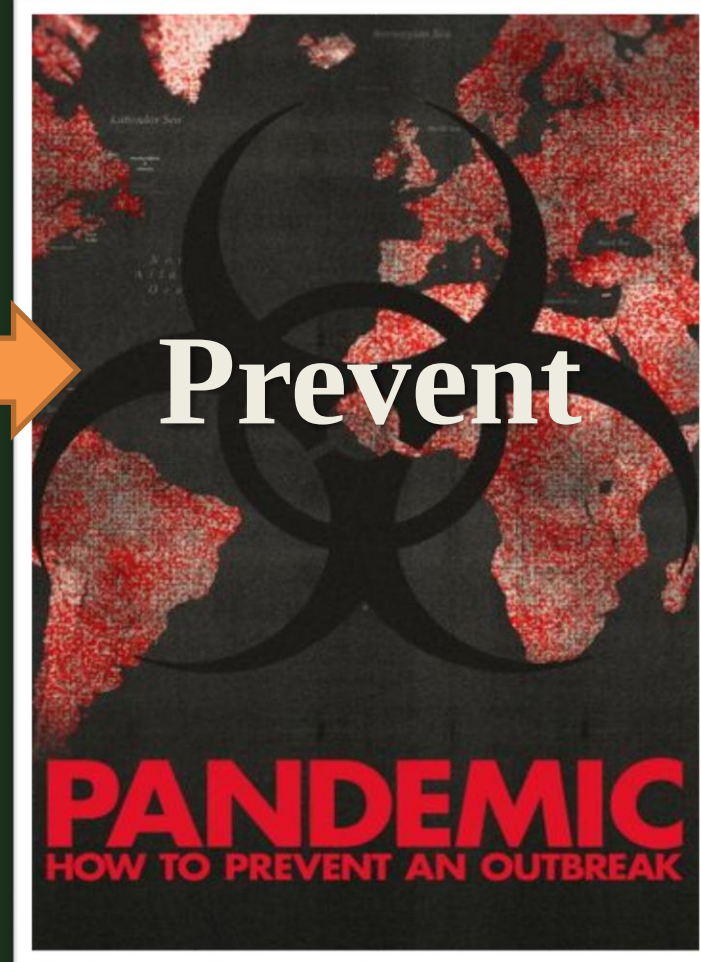


Predict (Viral Risk)

Seasonal bat influxes into agricultural zones drive highly specific viral risks (**Hantaviridae** vs. **SARS-related Betacoronaviruses**).

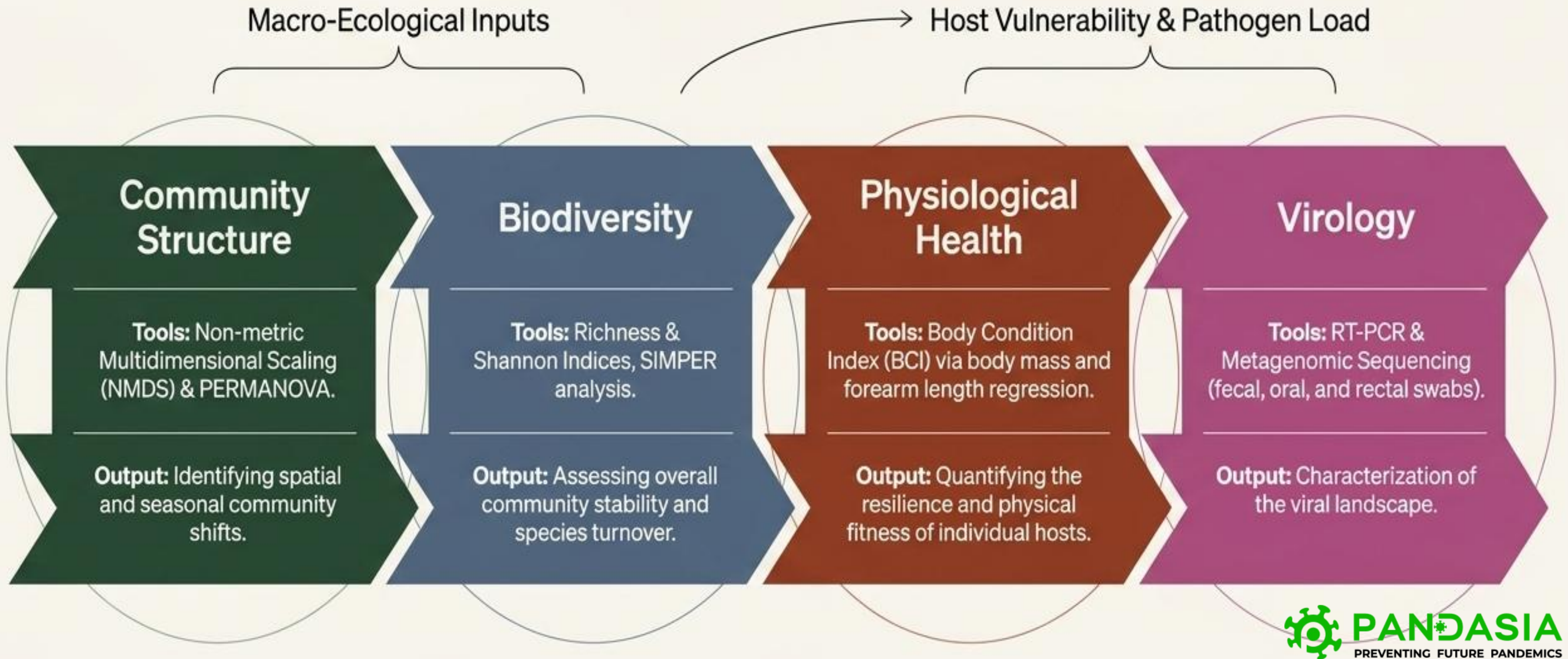


Prevent



Methodology: Analytical Framework

Ecological Assessment



Results: Species Diversity & Seasonality

Total 492 individual bats

16 Species, 8 Genera, and 5 Families



TAXONOMIC DIVERSITY

Scientific Name	Family
<i>Hipposideros armiger</i>	Hipposideridae
<i>Hipposideros cineraceus</i>	Hipposideridae
<i>Hipposideros galeritus</i> 5 sp.	Hipposideridae
<i>Hipposideros gentilis</i>	Hipposideridae
<i>Hipposideros larvatus</i>	Hipposideridae
<i>Cynopterus cf. brachyotis</i>	Pteropodidae
<i>Cynopterus sphinx</i>	Pteropodidae
<i>Eonycteris spelaea</i> 5 sp.	Pteropodidae
<i>Macroglossus sobrinus</i>	Pteropodidae
<i>Rousettus leschenaultii</i>	Pteropodidae
<i>Rhinolophus malayanus</i>	Rhinolophidae
<i>Rhinolophus pusillus</i>	Rhinolophidae
<i>Rhinolophus shameli</i> 4 sp.	Rhinolophidae
<i>Rhinolophus thomasi</i>	Rhinolophidae
<i>Myotis siligorensis</i> 1 sp.	Vespertilionidae
<i>Taphozous melanopogon</i> 1 sp.	Emballonuridae



Results: Species Diversity & Seasonality

TAXONOMIC DIVERSITY

Total 492 individual bats

1

6

Species

distinct bat species
recorded
across both
cave systems and
agricultural orchards.

8 Genera
5 Families

5 sp..

Taphozous melanopogon
Hipposideros armiger
Hipposideros larvatus
Rhinolophus pusillus
Rhinolophus shameli

3 sp..

Cynopterus cf. brachyotis
Rhinolophus malayanus
Rhinolophus thomasi

8 sp..

Hipposideros gentilis
Macroglossus sobrinus
Eonycteris spelaea
Rousettus leschenaultii
Hipposideros galeritus
Cynopterus sphinx
Hipposideros cineraceus
Myotis siligorensis

2024

Dry ☀️

Wet 💧

2025

Dry ☀️

Wet 💧

Core
Residents

Seasonal
Specialists

Intermittent
Transients

Detection Status

- Consistent Presence
- Dry Season Detection
- Wet Season Detection
- Undetected

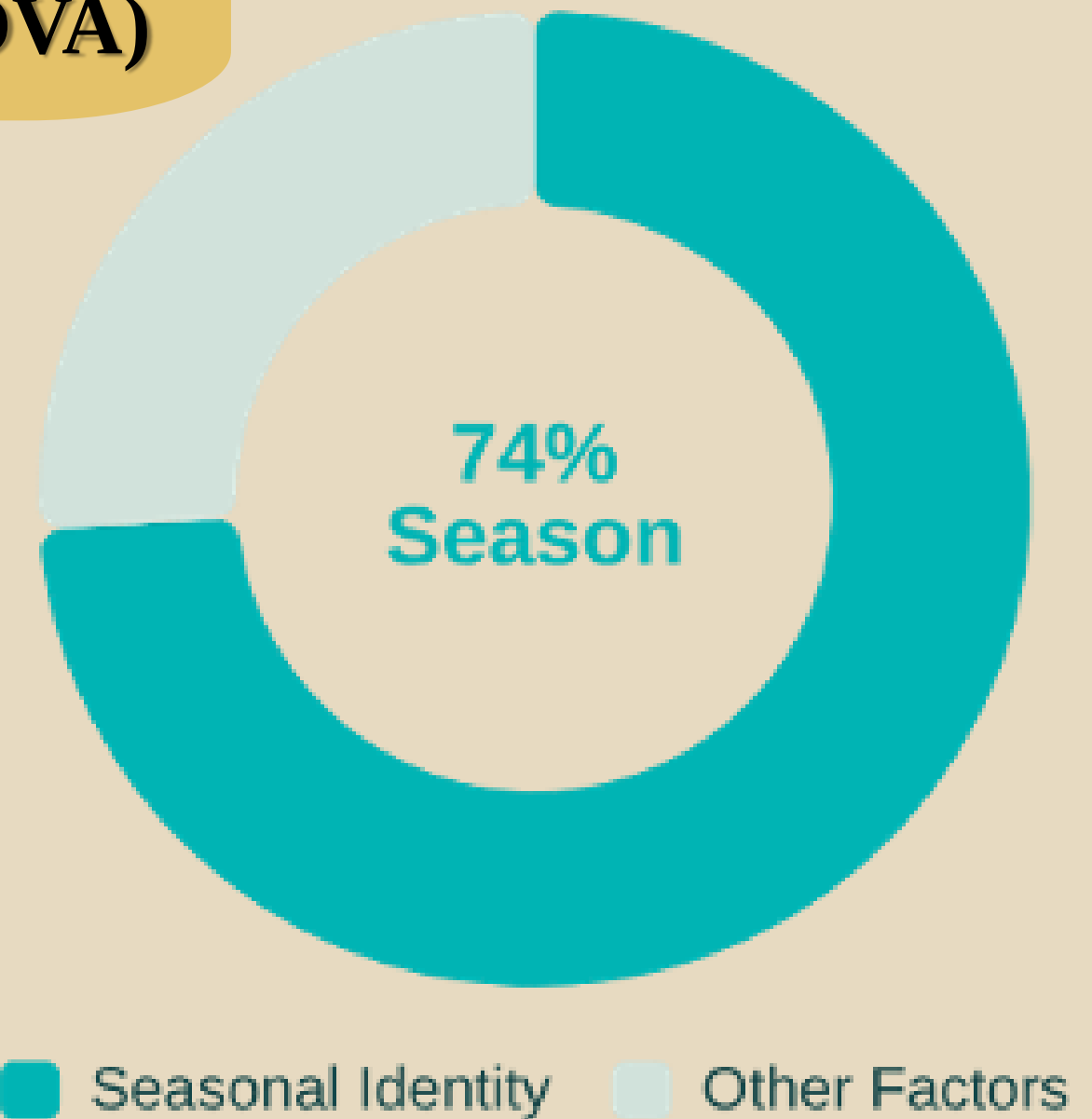
A complex ecological landscape with a vast capacity for viral maintenance

KEY RESULTS: SPECIES DIVERSITY & SEASONALITY

Permutation multivariate analysis of variance (PERMANOVA)

Seasonal Identity as a Dominant Driver

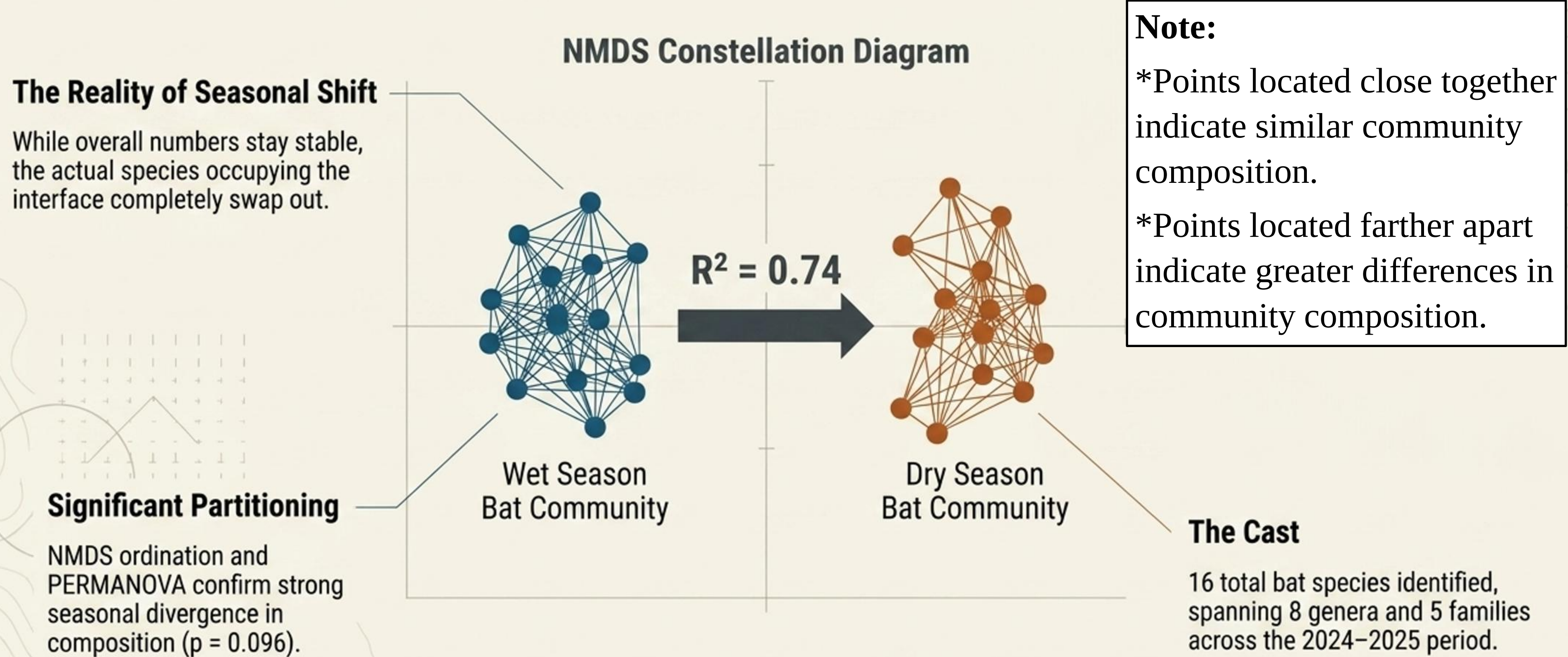
- Community composition shows clear divergence between seasons.
- Dry and wet season assemblages are significantly different.
- Temporal shifts drive the colonization of orchards by specific indicator species.



Core Ecological Link: Seasonal identity explains 74% of bat community variance ($R^2=0.74$, $p<0.001$) providing the statistical foundation for evidence-based surveillance scheduling.

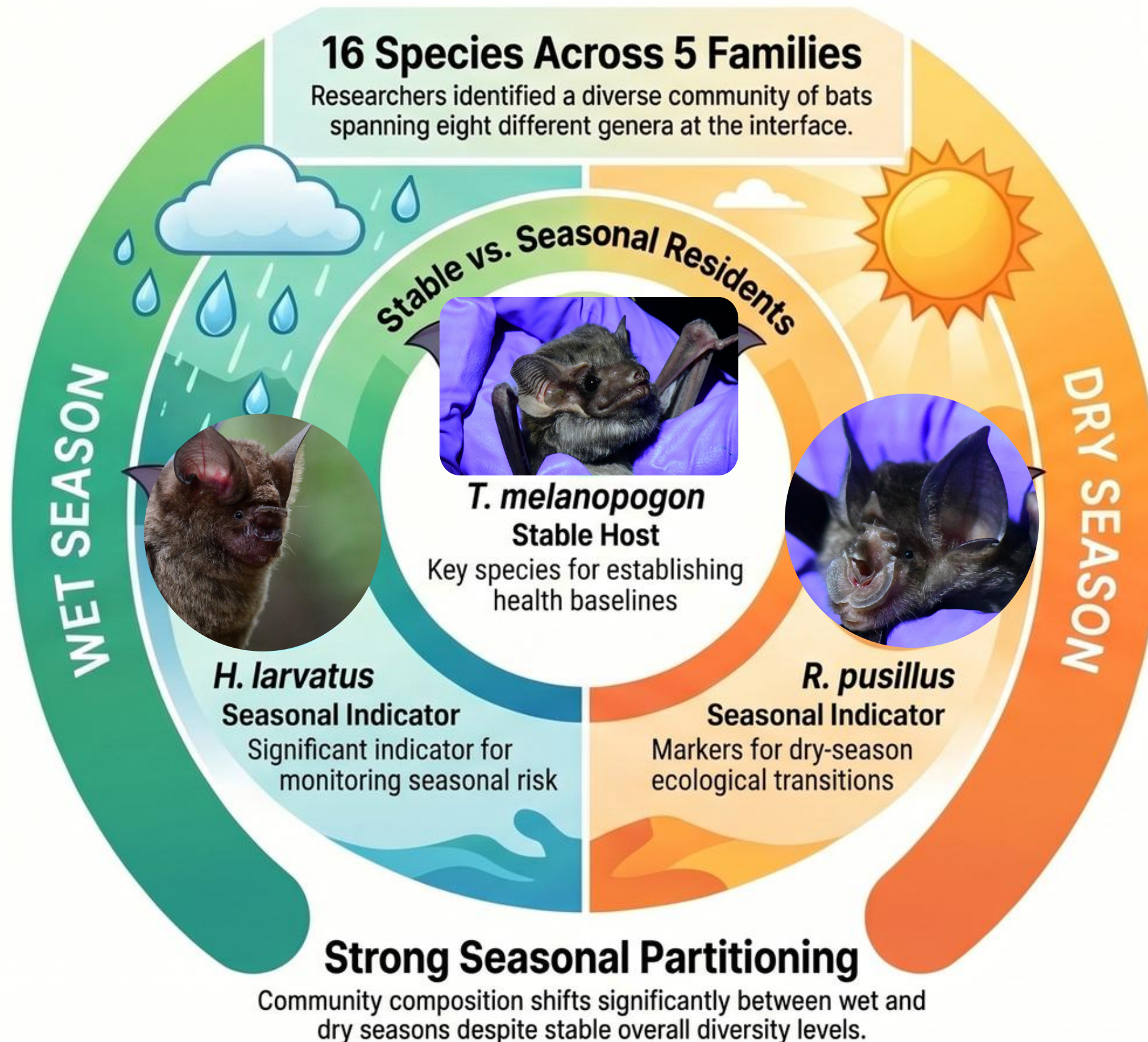
KEY RESULTS: SPECIES DIVERSITY & SEASONALITY

Non-metric Multidimensional Scaling (NMDS) is a statistical ordination method used to visualize similarities or differences in biological communities.



KEY RESULTS: SPECIES DIVERSITY & SEASONALITY

Seasonal Species Turnover



The Stability vs. Turnover Paradox

- Alpha Diversity Stability: Overall species richness remained broadly constant between wet and dry seasons.
- Beta Diversity Turnover: Significant shifts in species identities; who is present changes even if total count doesn't.
- Risk Implication: Standard richness metrics mask critical seasonal restructuring events in viral reservoirs.

KEY RESULTS:

HABITAT-BASED RISK GRADIENT

CHANTHABURI STUDY | 2024–2025

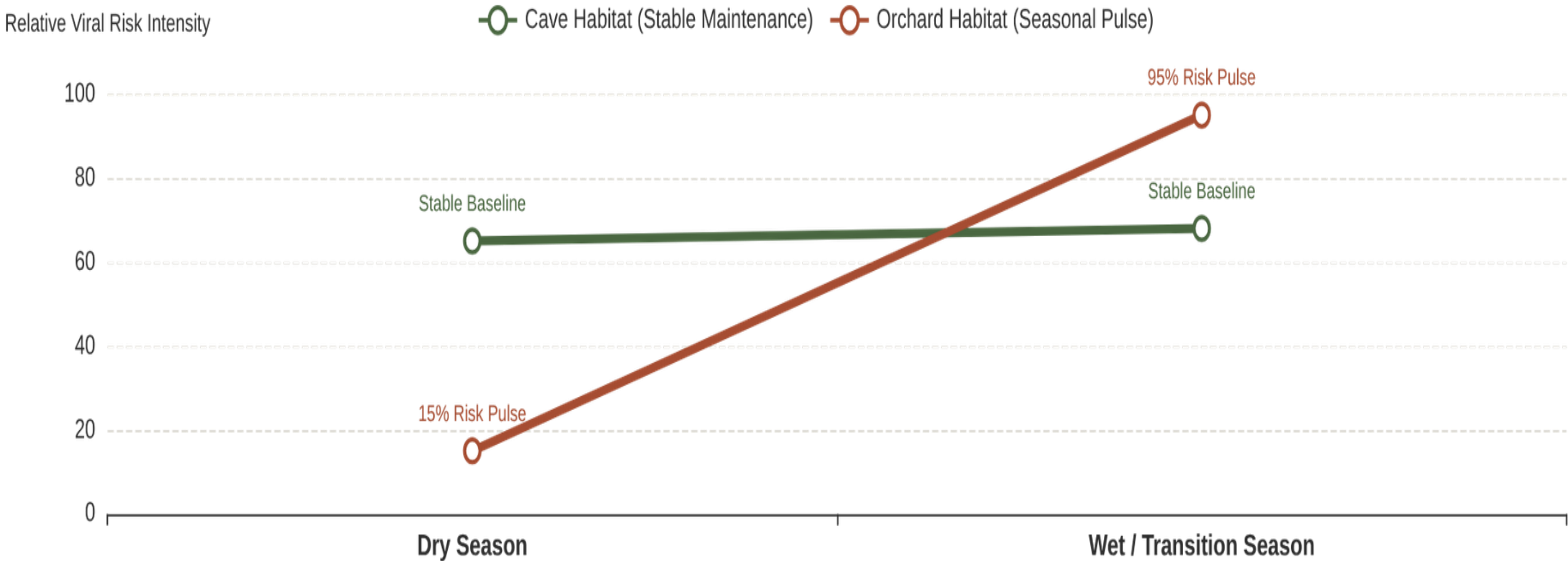
▲ Cave Systems: Stable Reservoirs

- ✓ Stable Baseline: Year-round viral maintenance by resident colonies.
- ✓ Core Species: *T. melanopogon* provides a constant viral reservoir.
- ✓ Risk Profile: Low-frequency but continuous exposure (guano collectors).

🌳 Agricultural Orchards: Seasonal Pulses

- ⚠️ Dynamic Pulse: High-intensity viral risk during seasonal influx periods.
- ⚠️ Indicator Species: *H. larvatus* and *R. pusillus* create risk spikes.
- ⚠️ Risk Profile: High-intensity windows coinciding with agricultural work.

COMPARATIVE VIRAL RISK INTENSITY BY HABITAT & SEASON

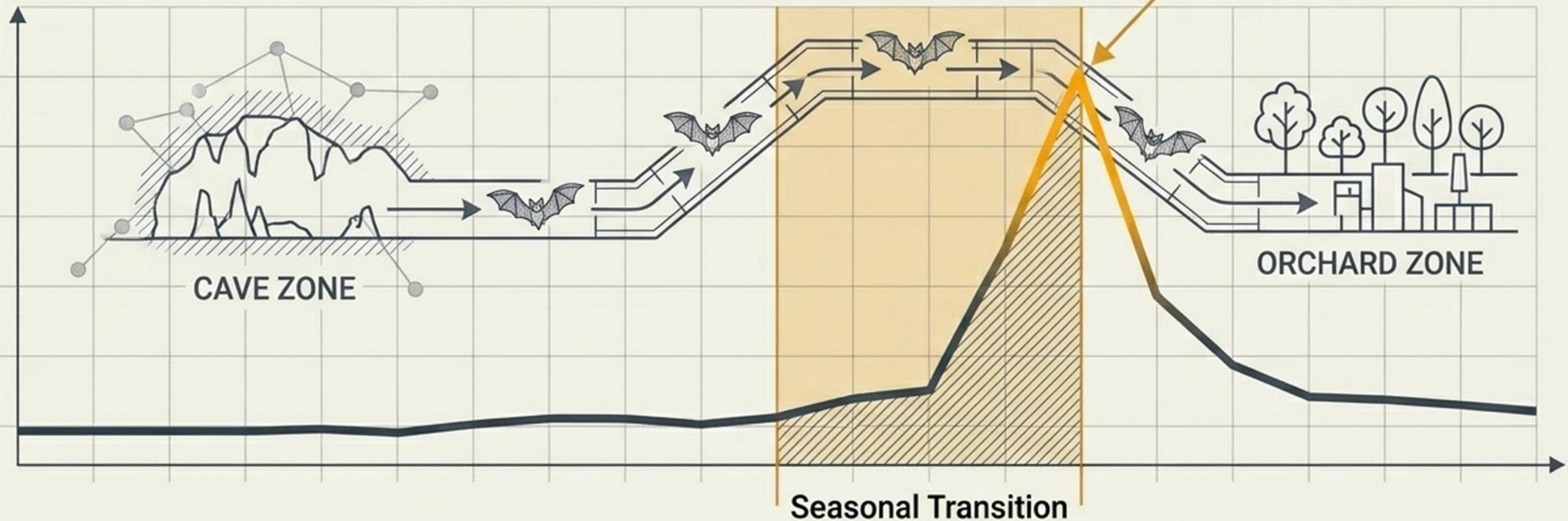


Critical Insight: Human exposure risk peaks sharply when seasonal indicator species colonize orchards, creating a **temporal spillover window** that demands targeted biosecurity interventions.

KEY RESULTS: The Seasonal Threat: Peak Spillover Risk

Hipposideros larvatus and *Rhinolophus pusillus* act as seasonal indicators. Their migration out of natural caves and into human-cultivated orchards creates temporary but extreme high-risk interfaces.

Risk Activation Curve

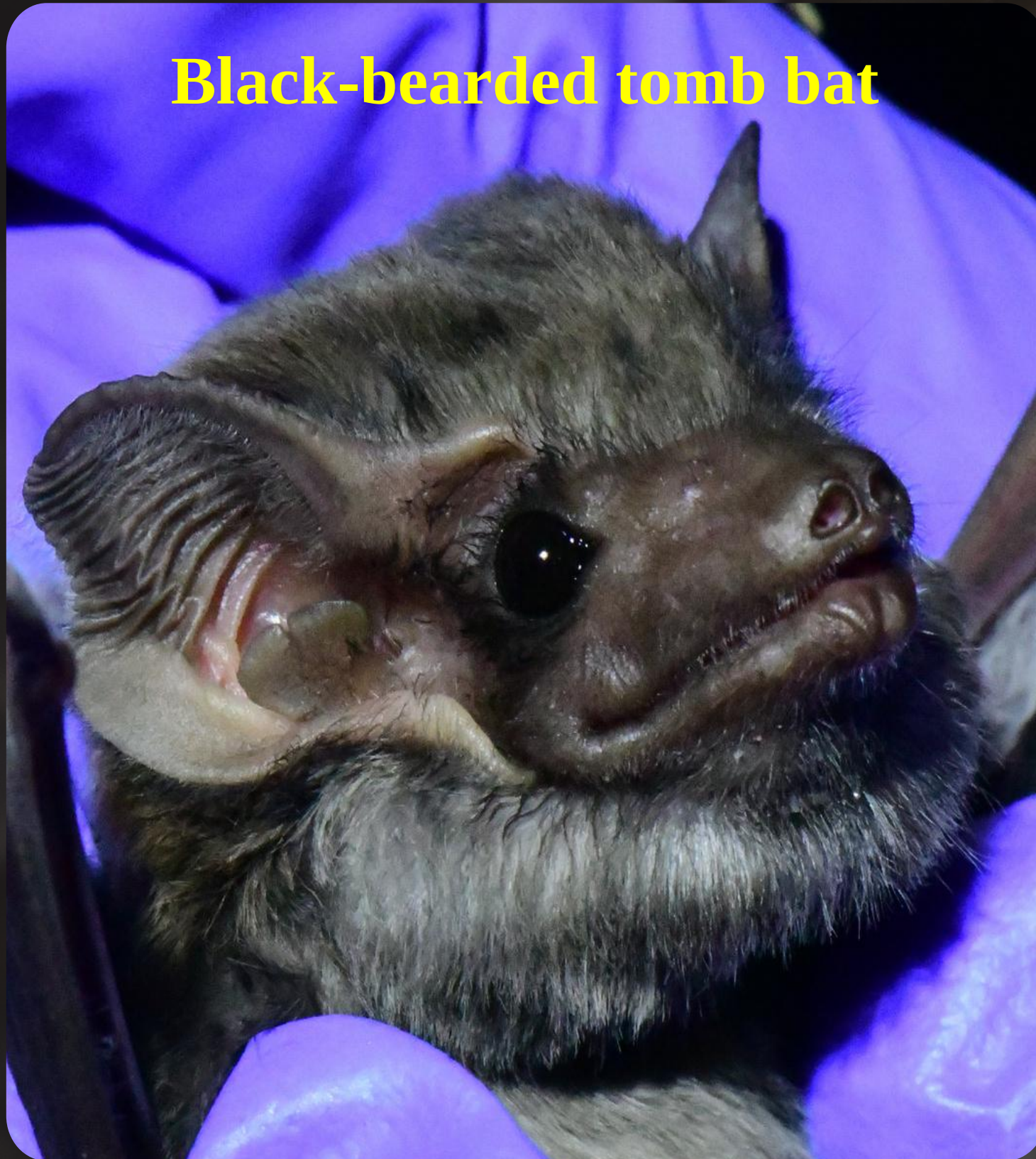


KEY RESULTS:

Taphozous melanopogon as a Stable Reservoir

CHANTHABURI STUDY | 2024–2025

Black-bearded tomb bat



Ecological Stability & Presence

Habitat Fidelity: Primary year-round resident in cave systems across Chanthaburi.

Spatial Consistency: Maintains high abundance in both dry and wet seasons within stable roosts.

Physiological Resilience (BCI)

Body Condition Index: Calculated as the residual of body mass regressed on forearm length.

Seasonal Stability: *T. melanopogon* exhibited stable BCI metrics regardless of seasonal environmental shifts.

Pathogen Association

Láibín Virus: Confirmed/candidate reservoir for this hantavirus (Family Hantaviridae). + Coronavirus

Exposure Route: Risk to tourists and Buddhist activities through contact with urine or aerosolized fecal particles.

KEY RESULTS: Seasonal Indicator Species in Orchards

CHANTHABURI STUDY | 2024–2025



Hipposideros larvatus

Intermediate Roundleaf Bat

- Primary indicator for wet/transitional season community shifts in agricultural zones.
- Utilizes an orchard area for seasonal foraging.
- Significant seasonal influx creates dense population pockets during peak fruit cycles.



Rhinolophus pusillus

Least Horseshoe Bat

- Key indicator species associated with heightened viral spillover risk windows.
- Strong temporal overlap with *H. larvatus*, intensifying the seasonal risk profile.
- Maintains high contact potential with both humans and domestic animals in orchard settings.

How many bat species reported in the project have been found to carry diseases (CoV) in Thailand?

Scientific Name	Family
1. <i>Hipposideros armiger</i>	Hipposideridae
<i>Hipposideros cineraceus</i>	Hipposideridae
<i>Hipposideros galeritus</i>	Hipposideridae
<i>Hipposideros gentilis</i>	Hipposideridae
2. <i>Hipposideros larvatus</i>	Hipposideridae
<i>Cynopterus cf. brachyotis</i>	Pteropodidae
3. <i>Cynopterus sphinx</i>	Pteropodidae
<i>Eonycteris spelaea</i>	Pteropodidae
<i>Macroglossus sobrinus</i>	Pteropodidae
<i>Rousettus leschenaultii</i>	Pteropodidae
<i>Rhinolophus malayanus</i>	Rhinolophidae
<i>Rhinolophus pusillus</i>	Rhinolophidae
4 <i>Rhinolophus shameli</i>	Rhinolophidae
<i>Rhinolophus thomasi</i>	Rhinolophidae
<i>Myotis siligorensis</i>	Vespertilionidae
5. <i>Taphozous melanopogon</i>	Emballonuridae



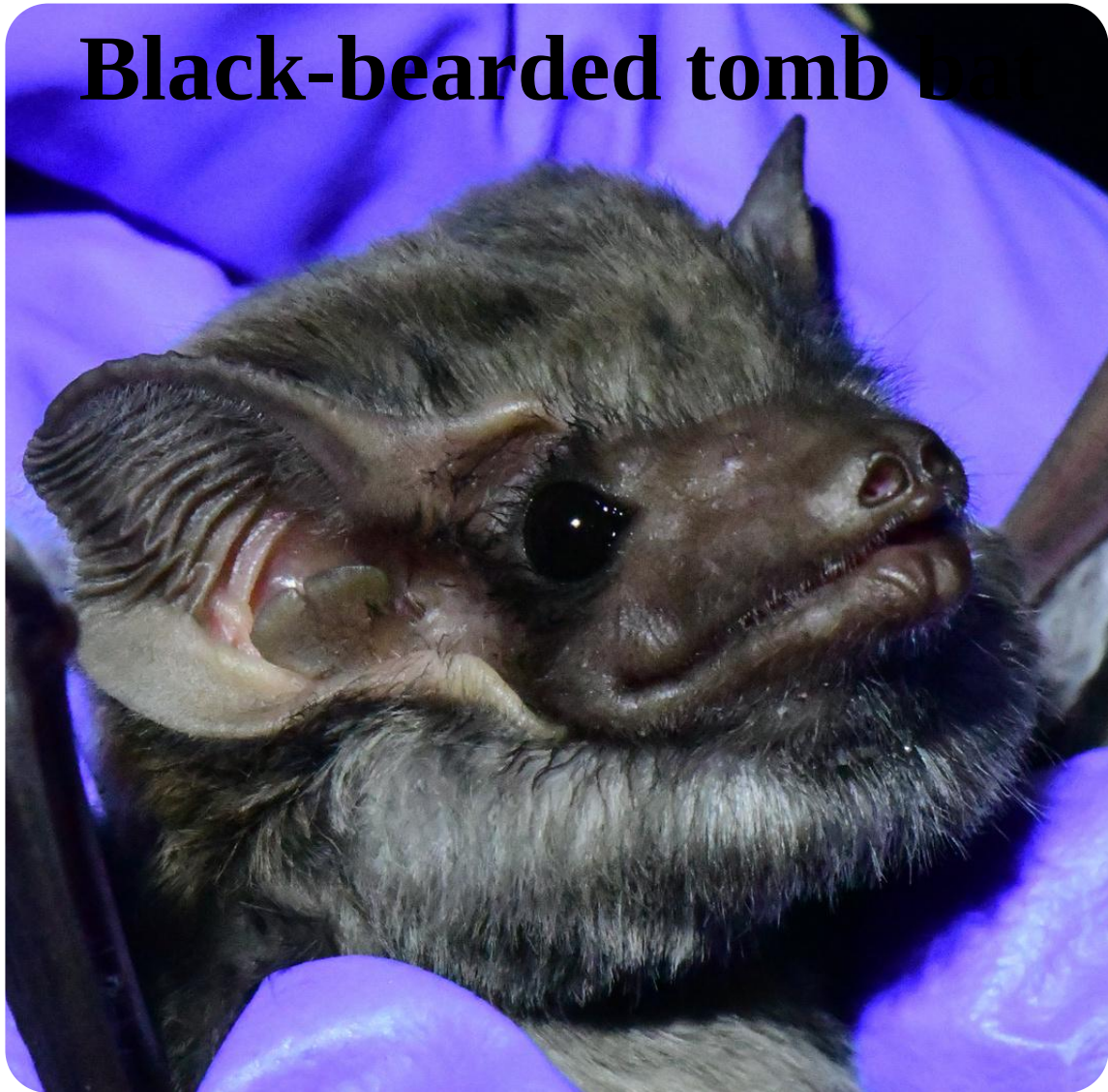
Table 1 Bat species tested for coronaviruses

Family	Species	No. of positive/total† (%)	Sampling site (year)†	
Pteropodidae	<i>Cynopterus brachyotis</i>	1/9 (11.1)	AA(2011*); TR(2011)	
	<i>Cynopterus sphinx</i>	4/14 (28.6)	AA(2011); RD(2008); TR(2011)	
	<i>Eonycteris spelaea</i>	0/11 (0)	AA(2011); TR(2011); CB(2012)	
	<i>Rousettus amplexicaudatus</i>	0/3 (0)	SK(2011)	
Emballonuridae	<i>Taphozous longimanus</i>	0/12 (0)	RD(2008/2012)	
	<i>Taphozous melanopogon</i>	2/123(1.6)	RD(2012*/2013); CK(2012); SK(2011*/2012)	2 [HKU7]/(1), 5 [HKU10]/(1)
Hipposideridae	<i>Hipposideros armiger</i>	2/140(1.4)	CK(2012); RD(2008/2012*/2013); SK(2012)	1 [CoV1A/B]/(1), 5 [HKU10]/(1)
	<i>Hipposideros cineraceus</i>	0/3	CK(2012)	
	<i>Hipposideros larvatus</i>	1/29(3.4)	CK(2012); RD(2008/2012/2013*)	9 [SARS]/(1)
	<i>Hipposideros lekaguli</i>	10/159(6.3)	CK(2008*/2012*)	1 [CoV1A/B]/(2), 5 [HKU10]/(6), 8 [HKU9]/(2)
Macroglossinae	<i>Macroglossus sobrinus</i>	0/2(0)	AA(2011); TR(2011)	
Megadermatidae	<i>Megaderma lyra</i>	1/2 (50)	RD(2012*/2013)	5 [HKU10]/(1)
Rhinolophidae	<i>Rhinolophus shameli</i>	2/20(10)	CK (2012*)	5 [HKU10]/(1), 6 [HKU2]/(1)
Vespertilionidae	<i>Miniopterus magnater</i>	6/30(20)	CK (2012*)	1 [CoV1A/B]/(5), 2 [HKU7]/(2**)
	<i>Miniopterus pusillus</i>	1/1(100)	CK(2012*)	3 [HKU8]/(1)
	<i>Miniopterus schreibersii</i>	12/53(22.6)	CK(2008*/2012)	1 [CoV1A/B]/(3), 2 [HKU7]/(1), 3 [HKU8]/(8)
	<i>Myotis horsfieldii</i>	0/4(0)	CK(2012); CB(2012)	
	<i>Scotophilus kuhlii</i>	2/3(66.7)	CB(2012*)	7 [New cluster]/(2)
	<i>Scotophilus heathii</i>	3/8(37.5)	CB(2012*)	4 [CoV 512]/(2), 7 [New cluster]/(1)
	Total	47/626(7.5)		

‡Samples were 84 fecal and 542 rectal swabs; *A positive location (and year) is indicated by an asterisk; First report of CoV in species (indicated in bold).
†AA = Ang Aed, Chataburi; CB = Chonburi; CK = Chakan, Srakaew; RD = Rad, Chachongsao; SK = Sarika, Chantaburi; TR = Trat.
**Sample No. BRT55593 (*Miniopterus magnater*) contained 2 different CoV species belong to clade 1 and 2.

Taphozous melanopogon

Black-bearded tomb bat



Short communication

Novel hantavirus identified in black-bearded tomb bats, China



Lin Xu ^{a,1}, Jianmin Wu ^{b,1}, Biao He ^{a,1}, Shaomin Qin ^b, Lele Xia ^a, Minchao Qin ^d, Nan Li ^a, Changchun Tu ^{a,c,*}

^a Military Veterinary Institute, Academy of Military Medical Sciences, Changchun, Jilin, China

^b Guangxi Veterinary Research Institute, Nanning, Guangxi, China

^c Jiangsu Co-innovation Center for Prevention and Control of Important Animal Infectious Diseases and Zoonoses, Yangzhou, Jiangsu, China

^d Laibin Center for Animal Disease Control and Prevention, Laibin, Guangxi, China



viruses



► *Viruses*. 2019 Mar 7;11(3):228. doi: [10.3390/v11030228](https://doi.org/10.3390/v11030228)

Molecular Phylogeny of Mobatviruses (*Hantaviridae*) in Myanmar and Vietnam

Satoru Arai ¹, Fuka Kikuchi ^{1,2}, Saw Bawm ³, Nguyễn Trường Sơn ^{4,5}, Kyaw San Lin ⁶, Vương Tân Tú ^{4,5}, Keita Aoki ^{1,7}, Kimiyuki Tsuchiya ⁸, Keiko Tanaka-Taya ¹, Shigeru Morikawa ⁹, Kazunori Oishi ¹, Richard Yanagihara ^{10,*}

Wacharapluesadee *et al. Virology Journal* (2015) 12:57
DOI 10.1186/s12985-015-0289-1



VIROLOGY JOURNAL

SHORT REPORT

Open Access

Diversity of coronavirus in bats from Eastern Thailand

Supaporn Wacharapluesadee^{1*}, Prateep Duengkae², Apaporn Rodpan¹, Thongchai Kaewpom¹, Patarapol Maneeorn³, Budsabong Kanchanasaka³, Sangchai Yingsakmongkon^{1,4}, Nuntaporn Sittidetboripat¹, Chaipayorn Chareesaen³, Nathawat Khlangsap², Apisit Pidthong³, Kumron Leadprathom⁵, Siriporn Ghai¹, Jonathan H Epstein⁶, Peter Daszak⁶, Kevin J Olival⁶, Patrick J Blair⁷, Michael V Callahan^{1,8} and Thiravat Hemachudha¹

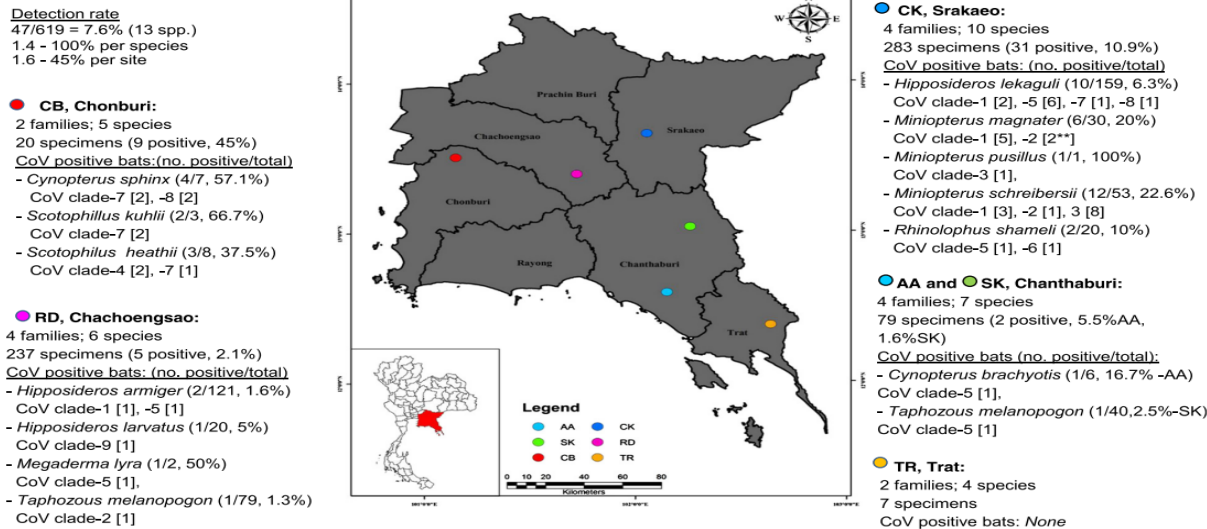


Figure 1 Areas in Eastern Thailand where samples were collected with CoV-positive bat species additionally named. Chakarn cave (CK, Dark blue) in Srakaao province; Rad cave (RD, Pink) in Chachoengsao province; Chonburi province (CB, Red); Ang Aed (AA, Pale blue) and Sarika (SK, Green) caves in Chanthaburi province; and Trat province (TR, Orange). At CK site, bats were captured 4 times: in May 2008, July 2008, January 2012 and May 2012; RD site, 5 times: May 2008, July 2008, January 2012, May 2012 and January 2013; SK site, 2 times: December 2011 and May 2012; AA site, 1 time: December 2011; TR site, 1 time: December 2011. Between January and December 2012 at CB site, bats were captured monthly at 2 local swine farms. Generally, bats were caught in mist nets or harp traps as they emerged from their roosts. At two sites (CB and TR), bats were trapped during the night as they foraged near open orchards. The number of CoV positive bats [bracket] in each clade is indicated for each site. ** Sample No. BRT55593 (*Miniopterus magnater*) contained 2 different CoV species belong to clade 1 and 2.

Hipposideros larvatus

Intermediate Roundleaf Bat



- **Coronaviruses (CoVs):** *H. larvatus* is a known host for various Alpha- and Betacoronaviruses, including the bat coronavirus HKU10. While several of these strains share genetic ancestry with SARS-related coronaviruses, studies show they are distinct from SARS-CoV-2 and are currently classified as circulating bat viruses.
- **Rhabdoviruses:** Novel rhabdoviruses (like the Yangjiang bat virus) have been genetically isolated from *H. larvatus*. These rhabdoviruses form unique genetic lineages related to the family *Rhabdoviridae*, which also includes the rabies virus.
- **Henipaviruses (e.g., Nipah):** While *H. larvatus* populations in Thailand have tested positive for Nipah virus RNA, extensive serological surveillance in countries like Cambodia indicates that they are typically negative for the antibodies, suggesting they are incidental or spillover hosts rather than the primary reservoir compared to flying foxes (*Pteropus* species).

Bat Nipah Virus, Thailand

Supaporn Wacharapluesadee,*
Boonlert Lumlertdacha,† Kalyanee Boongird,‡
Sawai Wanghongsa,‡ Lawan Chanhom,†
Pierre Rollin,§ Patrick Stockton,§
Charles E. Rupprecht,§ Thomas G. Ksiazek,§
and Thiravat Hemachudha*

Cell

CellPress
OPEN ACCESS

Article Virological characteristics of SARS-CoV-2-related coronaviruses dynamically circulating in Southeast Asia

Supaporn Wacharapluesadee,^{1,29,*} Wilaiporn Saikruang,^{2,29} Spyros Lytras,^{2,3,29} Kanata Matsumoto,⁴ Keiya Uriu,² Alfredo Hinay, Jr.,² Ziyi Guo,² Khwankamon Rattanamhi,¹ Ananporn Supataragul,¹ Sasiprapa Ninwattana,¹ Nattakarn Thippamom,¹ Tanawut Srisuk,¹ Patarapol Maneern,⁵ Kirana Noradechanon,⁵ Prateep Duengkae,⁶ Nutthinee Sirichan,⁶ Yusuke Kosugi,^{2,7} Shigeru Fujita,^{2,7} Maximilian Stanley Yo,^{2,8} Ryo Matsunaga,^{9,10} Bingjie Hu,¹¹ Lianzhao Du,¹¹ Lei Wang,^{12,13} Masumi Tsuda,^{12,13} Yoshitaka Oda,¹² Hesham Nasser,^{14,15}

Table. ELISA, PCR saliva, and PCR urine results for Nipah virus from 12 bat species, Thailand, 2002–2004*

Species	Total bats	ELISA		PCR saliva‡		PCR urine‡	
		No. analyzed	No. positive (%) †	No. analyzed	No. pool positive/total	No. analyzed	No. pool positive/total
Frugivorous							
<i>Cynopterus sphinx</i>	34	10	0	34	0/5	34	0/5
<i>Eonycteris spelaea</i>	64	54	0	64	0/7	64	0/7
<i>Pteropus hypomelanus</i>	36	26	4 (15.4)	36	0/6	35	0/6
<i>P. lylei</i>	857	813	76 (9.3)	845	1/87	845	6/87
<i>P. vampyrus</i>	39	39	1 (2.6)	39	0/4	39	0/4
<i>Rousettus leschenaulti</i>	11	4	0	6	0/3	6	0/3
Insectivorous							
<i>Emballonura monticola</i>	14	12	0	14	0/2	14	0/2
<i>Hipposideros armiger</i>	88	6	0	88	0/10	88	0/10
<i>H. larvatus</i>	95	74	1 (1.3)	94	1/10	91	0/10
<i>Megaderma spasma</i>	13	0	0	13	0/2	13	0/2
<i>Scotophilus heathi</i>	3	3	0	3	0/1	3	0/1
<i>Tadarida plicata</i>	50	13	0	50	0/5	50	0/5
Total	1,304	1,054	82 (7.8)	1,286	2/142	1,282	6/142

*ELISA, enzyme-linked immunosorbent assay; PCR, polymerase chain reaction.

†ELISA positive: titer $\geq 1:400$.

‡10 individual samples (saliva or urine) from the same species, colony, and the time of capture were saved into the same pool.

Rhinolophus pusillus

Least Horseshoe Bat



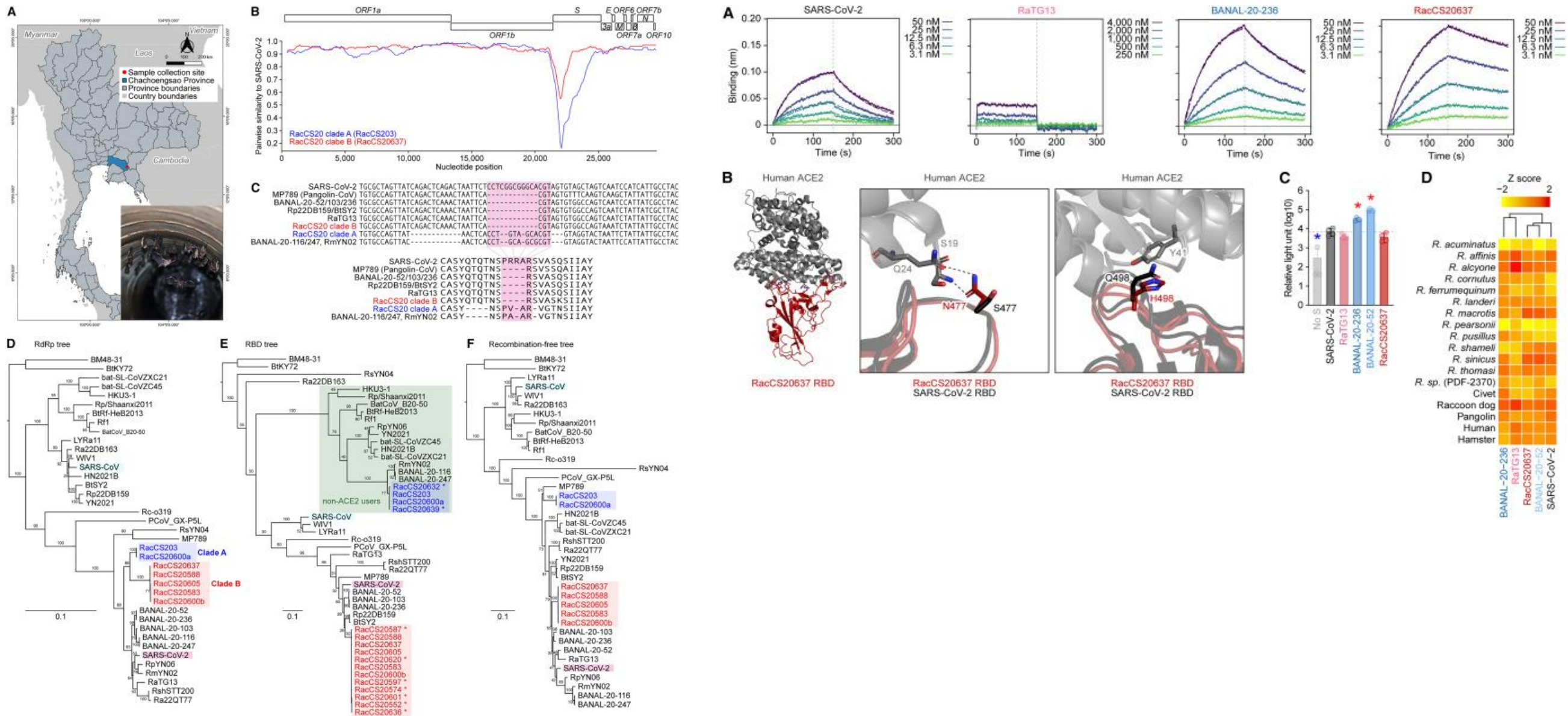
Cell

CellPress
OPEN ACCESS

Article

Virological characteristics of SARS-CoV-2-related coronaviruses dynamically circulating in Southeast Asia

Supaporn Wacharapluesadee,^{1,29,*} Wilaiporn Saikruang,^{2,29} Spyros Lytras,^{2,3,29} Kanata Matsumoto,⁴ Keiya Uriu,² Alfredo Hinay, Jr.,² Ziyi Guo,² Khwankamon Rattanatumhi,¹ Ananporn Supataragul,¹ Sasiprapa Ninwattana,¹ Nattakarn Thippamom,¹ Tanawut Srisuk,¹ Patarapol Maneeorn,⁵ Kirana Noradechanon,⁵ Prateep Duengkae,⁶ Nutthinee Sirichan,⁶ Yusuke Kosugi,^{2,7} Shigeru Fujita,^{2,7} Maximilian Stanley Yo,^{2,8} Ryo Matsunaga,^{9,10} Bingjie Hu,¹¹ Lianzhao Du,¹¹ Lei Wang,^{12,13} Masumi Tsuda,^{12,13} Yoshitaka Oda,¹² Hesham Nasser,^{14,15}



CHANTHABURI STUDY | 2024–2025

SEASON	DOMINANT BAT SPECIES	HABITAT INTERFACE	PRIMARY VIRAL THREAT	RISK DYNAMICS
 Dry Season	<i>T. melanopogon</i>	 Cave Systems	Hantavirus+CoV	BASELINE
 Wet Season	<i>H. larvatus</i> , <i>R. pusillus</i> + <i>T. melanopogon</i>	 Orchards +  Caves	Hantavirus+ Nipah virus+CoV	SEASONAL PULSE
 Year-Round	<i>T. melanopogon</i>	 Cave Systems	Hantavirus+CoV	CONTINUOUS

Cell

Article

Virological characteristics of SARS-CoV-2-related coronaviruses dynamically circulating in Southeast Asia

Supaporn Wacharapluesadee,^{1,29,*} Wilaiporn Saikruang,^{2,29} Spyros Lytras,^{2,3,29} Kanata Matsumoto,⁴ Keiya Uriu,² Alfredo Hinay, Jr.,² Ziyi Guo,² Khwankamon Rattatumthi,¹ Ananporn Supataragul,¹ Sasiprapa Ninwattana,¹ Nattakarn Thippamom,¹ Tanawut Srisuk,¹ Patarapol Maneern,⁵ Kirana Noradechanon,⁵ Prateep Duengkae,⁶ Nutthinee Sirichan,⁶ Yusuke Kosugi,^{2,7} Shigeru Fujita,^{2,7} Maximilian Stanley Yo,^{2,8} Ryo Matsunaga,^{9,10} Bingjie Hu,¹¹ Lianzhao Du,¹¹ Lei Wang,^{12,13} Masumi Tsuda,^{12,13} Yoshitaka Oda,¹² Hesham Nasser,^{14,15}

CONCLUSION:

Seasonal Bat Dynamics & Viral Spillover Risk in Eastern Thailand

BIODIVERSITY & CONSTANT RESERVOIRS

16 Bat Species Recorded

16 Bat Species Recorded

The study identified 16 species across five families within the trans-boundary human-wildlife interface.

Year-Round Viral Maintenance



Láibin virus
(Hantaviridae)

Year-Round Viral Maintenance

Taphozous melanopogon showed high physiological resilience, serving as a stable host for Lálbin virus.

High Physiological Resilience



Body Condition Index (BCI)

Consistent Body Condition Index (BCI) across seasons indicates a stable host environment for pathogens.

SEASONAL SHIFTS & SPILLOVER RISKS



H. larvatus
(*Hippoxideros larvatus*)



R. pusillus
(*Rhinolophus pusillus*)

Orchard Habitat Influx

Seasonal indicators *H. larvatus* and *R. pusillus* move into orchard habitats during specific seasons.

PREDICT AND PREVENT



Targeted, season-specific biosecurity measures at orchard interfaces are necessary to prevent viral emergence.

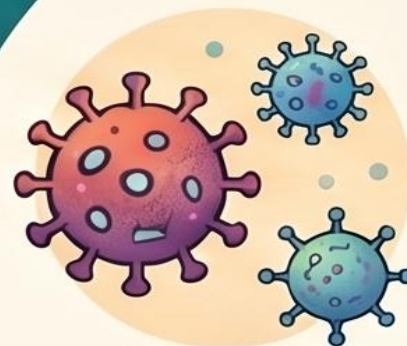
A two-year study in Chanthaburi Province identifies seasonal partitioning and host resilience to provide a framework to predict and prevent viral emergencies.

HOST STABILITY & VIRAL RISKS AMONG KEY SPECIES

BAT SPECIES	HABITAT USE	VIRAL ASSOCIATION
<i>Taphozous melanopogon</i>	 Stable Host	 HantaVirus+ CoV
<i>Hipposideros larvotus</i>	 Stable Host	 Nipah virus+ CoV
<i>Rhinolophus pusillus</i>	 Seasonal (Orchards)	 CoV

Reservoir for SARS-related Viruses

Seasonal indicator species
are known reservoirs for
Betacoronaviruses,
Adenoviruses, and Bocaviruses.



Executive Summary & Path Forward



UNDERSTAND

2024–2025 systematic surveys reveal a deeply partitioned, dynamic ecosystem of 16 bat species thriving at the transboundary interface.



PREDICT

BAT SPECIES	HABITAT USE	VIRAL ASSOCIATION
<i>Taphozous melanopogon</i>	 Stable Host	 <u>HantaVirus+</u> <u>CoV</u>
<i>Hipposideros larvotus</i>	 Stable Host	 <u>Nipah virus+</u> <u>CoV</u>
<i>Rhinolophus pusillus</i>	 Seasonal (Orchards)	 <u>CoV</u>



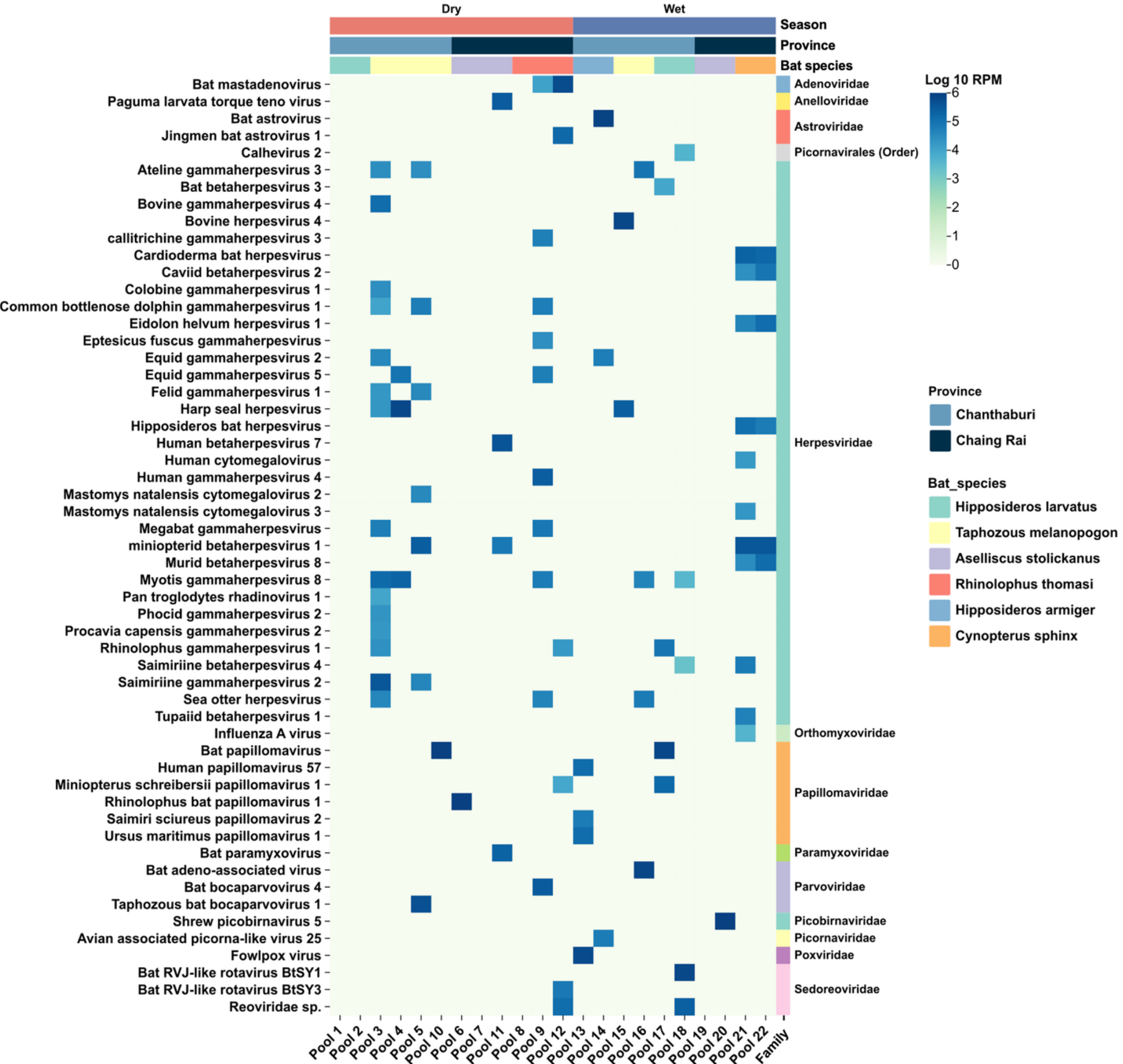
PREVENT

Mitigation must transition from blanket policies to precision, season-specific biosecurity deployed at agricultural interfaces.

Distribution of viral abundance at the family level in bat populations, categorized by virus families, genome type, geographic location, and season. Blank cell = no virus detected.

Virus families	Genome Type	Total Reads	Overall (%)	Chanthaburi (%)		Chiang Rai (%)		Season (%)	
				SD (%)	PN (%)	WK (%)	MF (%)	Dry (%)	Wet (%)
Adenoviridae	dsDNA	406	4.51			4.51		4.51	
Anelloviridae	ssDNA	26	0.29			0.29		0.29	
Astroviridae	ssRNA (+)	736	8.17		6.97	1.2		1.2	6.97
Herpesviridae	dsDNA	3,493.00	38.79		20.29	4.4	14.1	22.5	16.29
Orthomyxoviridae	ssRNA (-)	5	0.06				0.06		0.06
Papillomaviridae	dsDNA	702	7.8		7.23	0.57		0.7	7.1
Paramyxoviridae	ssRNA (-)	19	0.21			0.21		0.21	
Parvoviridae	ssDNA	429	4.76		3.01	1.75		3.3	1.47
Picobirnaviridae	dsRNA	367	4.08			4.08			4.08
<u>Picornavirales</u> (Order)	ssRNA (+)	12	0.13		0.13				0.13
Picomaviridae	ssRNA (+)	49	0.54		0.54				0.54
Poxviridae	dsDNA	150	1.67		1.67				1.67
Sedoreoviridae	dsRNA	2,610.00	28.99		27.43	1.55		1.55	27.43
Total		9,004.00	100		67.28	18.56	14.16	34.26	65.74

SD: SOI DAO, PN: PONG NAM RON, WK: WIANG KAEN, MF: MAE FAH LUANG.



Overview of mammal-associated viral species abundance detected in bats. Viral abundance in each sequencing library was calculated and normalized as reads per million (RPM) of total mapped reads and is represented using a light green-to-blue gradient scale, where darker blue indicates higher abundance. The heatmap annotations indicate bat species, sampling season, and province of sample collection.

Bat TEAM MEMBER



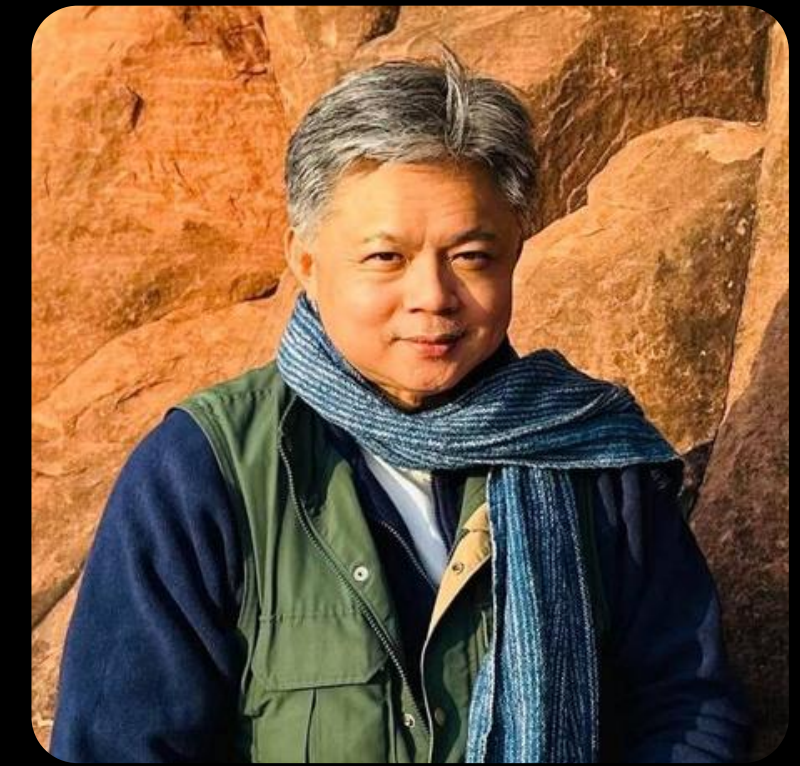
AINGORN CHAIYES (1,2*)



PRATEEP DUENGKAE (3)



NUTTHINEE SIRICHAN (3)



BORIPAT SIRIARONRAT (4)



- 1 The International Undergraduate Program in Bioscience and Technology, Faculty of Science, Kasetsart University, Bangkok 10900, Thailand
2 Animal Genomics and Bioresource Research Unit (AGB Research Unit), Faculty of Science, Kasetsart University, Bangkok 10900, Thailand
3 Special Research Unit for Wildlife Genomics (SRUWG), Department of Forest Biology, Faculty of Forestry, Kasetsart University, Bangkok 10900, Thailand
4 Faculty of Environmental and Resource Studies Mahidol University, Nakhon Pathom, 73170, Thailand
*Corresponding author: E-mail: aingorn.ch@ku.ac.th, aingorn.ch@ku.th





Funded by
the European Union



THANK YOU

