Severe zoonotic viruses carried by different species of bats and their regional distribution

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FACULTAD DE
MEDICINA
UASLP

QFB PU Vega-Méndez
Dr. SE Guerra-Palomares
Dr. CA García-Sepúlveda

Laboratorio de Genómica Viral y Humana
Facultad de Medicina
Universidad Autónoma de San Luis Potosí

Introduction

Bats comprise over 1200 species belonging to 20 families.

Approximately 20% of all mammalian species.

Optimal environment for the transmission and persistence of pathogens.

Seasonal migration.

> 4100 bat-associated animal viruses detected from 196 bat species in 69 countries worldwide.

Important hosts, efficient transmitters, or directly responsible for transmission.

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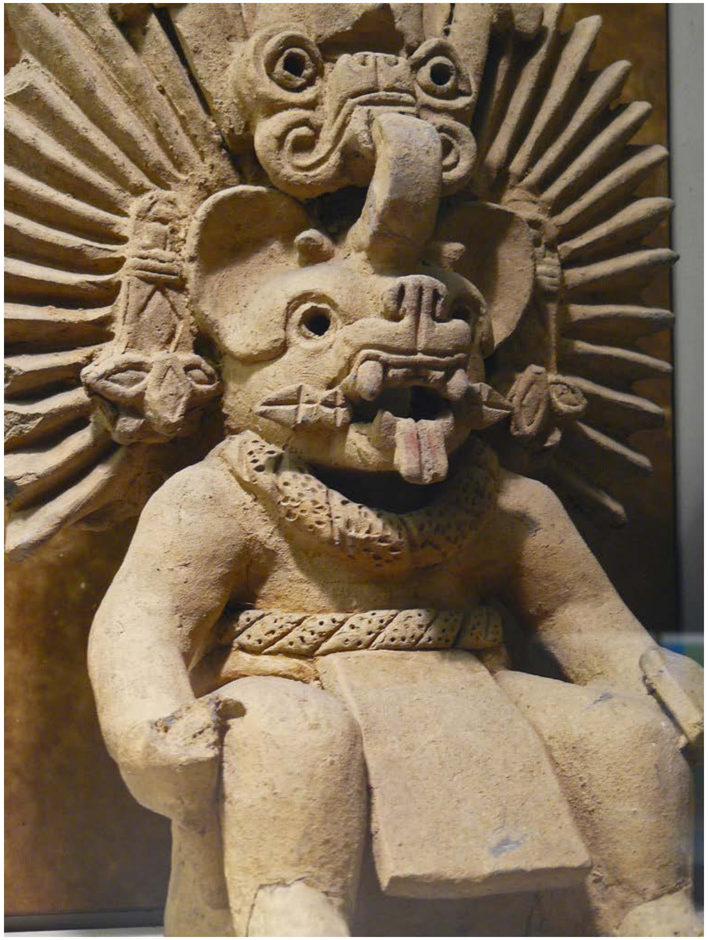


Bat god sculpture from Zapotec art dated between 200 B.C and 200 A.D.

Rabies virus

First detection and identification of zoonotic viruses in bats (California,1955. Enright et. al detected rabies virus in *Tadarida brasiliensis).*

Researchers pay more attention to it due to high mortality rate. Human deaths in Latin America.

20 bat species from 4 families: *Molossidae*, *Phyllostomidae*, *Pteropodidae*, and *Vespertilionidae.* Most bat samples are from countries in the Americas, primarily Brazil.

Tadarida brasiliensis
(Free tailed bat)
Family: Molossidae
Insectivorous

Vampirum spectrum
(Spectral bat)
Family: Phyllostomidae
Carnivorous

Pteropus scapulatus
(Little red flying fox)
Family: Pteropodidae.
Nectarivorous

Flaviviridae

1966, Texas. Sulkin et al. isolated the St. Louis encephalitis virus in *Tadarida brasiliensis.*

Japanese encephalitis virus. 8 species from 3 families. Mainly from China and Indonesia.

Dengue. 7 bat species, all from *Phyllostomidae* family.

West Nile virus. 5 species from 4 families: *Phyllostomidae*, *Pteropodidae*, *Rhinolophidae*, and *Vespertilionidae*. United States, México, India and Malaysia.

Zika virus and **St. Louis encephalitis virus** in *Artibeus jamaicensis* (México) and *Tadarida brasiliensis* (United States).

Desmodus rotundus
(Common vampire bat)
Family: Phyllostomidae
Haematophagus

Artibeus jamaicensis
(Fruit-eating bat)
Family: Phyllostomidae
Frugivorous

Bunyaviridae

1994, Korea. Kim et al identified Hantaviruses of *Rhinolophus ferrumequinum*.

Crimean Congo haemorrhagic fever virus. 12 species from 4 families. Gabon, Ghana, Congo, and Germany.

Hantaviruses. 5 species from 3 families. China, Korea, Brazil and Sierra Leone.

Novel hantavirus. 4 bat species widely distributed: Czech Republic, the Philippines, Malaysia, and China.

Rift Valley fever virus. Lack of research, only has been found in two bat species in Egypt and Guinea.

Rhinolophus ferrumequinum
(Greater horseshoe bat)
Family: Rhinolophus
Insectivorous

Rousettus amplexicaudatus
(Geoffroy´s Rousette)
Family: Pteropodidae
Frugivorous/Nectarivorous

Paramyxoviridae

Same bat-carrying Paramyxoviridae virus may also carry various other zoonotic viruses.

Nipah virus. 2 bat species both belonging to the family *Pteropodidae* from India, Malaysia, and Indonesia.

Tioman virus. 3 bat species, all belonging to the family *Pteropodidae,* also from India, Malaysia, and Indonesia.

Hendra virus. 3 bat species all from Australia.

Menangle virus. Has only been found in *Pteros Alecto* from Australia.

Pteropus vampyrus
(Large flying fox)
Family: Pteropodidae
Frugivorous/Nectarivorous

Pteropus scapulatus
(Little red flying fox)
Family: Pteropodidae
Frugivorous

Filoviridae

Rousettus aegyptiacus may be the primary natural host of Marburg virus.

Marburg virus. Has been found in *Rousettus aegyptiacus* from Sierra Leone, Gabon, Uganda, Kenya, the Republic of South Africa, and Zambia

Bombali virus. Lack of studies. Has been found in *Mops condylurus* from Guinea and Kenya.

Ebola virus. Has been found in 3 bats species from Gabon and Congo, all belonging to the family *Pteropodidae*.

Rousettus aegyptiacus
(Egyptian fruit bat)
Family: Pteropodidae
Frugivorous

Hypsignathus monstrosus
Hammer-headed fruit bat
Family: Pteropodidae
Frugivorous

Influenza A virus

Influenza A virus is the most important virus causing disease in humans, bats have been relatively poorly studied for carrying and transmitting influenza A virus.

Six bat species have been found to carry influenza A, belonging to three families: *Vespertilionidae*, *Phyllostomidae*, and *Pteropodidae*, these bats come from all over the word, including Peru, Brazil, Guatemala, Kazakhstan, Egypt, and Ghana.

Further exploration is necessary.

Nyctalus noctula
(Noctule bat)
Family: Vespertillionidae
Insectivorous

Sturnira lilium
(Little yellow-shouldered bat)
Family: Phyllostomidae
Frugivorous

Hepatitis B virus and E virus

It was believed that only humans were natural hosts for Hepatitis B and E viruses. However,…

In 2013, Drexler et al. detected Hepatitis B virus DNA in *Hipposideros ruber* from Gabon.

Hepatitis B virus. 7 bat species belonging to the families *Hipposideridae* and *Vespertilionidae,* from Gabon, Panamá, China, and Vietnam.

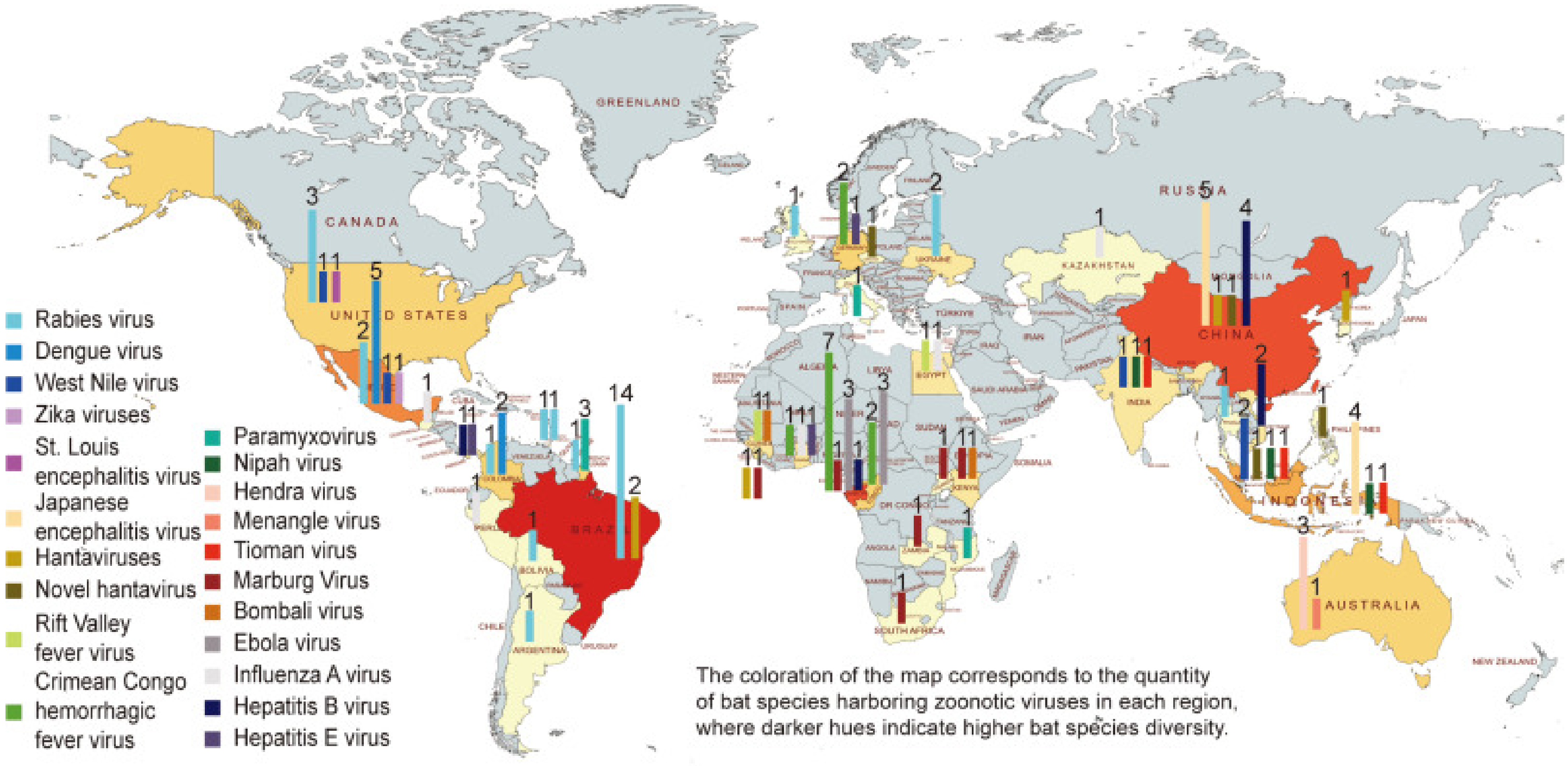
Hepatitis E virus. 3 species belonging to the families Hipposideridae, Phyllostomidae, and Vespertilionide from Germany, Ghana, and Panama.

Vampyrodes Caraccioli
(Great stripe-faced bat)
Family: Phyllostomidae
Frugivorous

Eptesicus serotinus
(Serotine bat)
Family: Vespertilionidae
Insectivorous

Different species carry severe zoonotic viruses.

Regional distribution of bats carrying severe zoonotic viruses. The numbers on the bar graph represent the number of bat species in the area that carry the corresponding zoonotic virus.



The coloration of the map corresponds to the quantity of bat species harboring zoonotic viruses in each region, where darker hues indicate higher bat species diversity.

Coronaviridae

2013. Ge et al. and Hu et al. detected SARS-like coronavirus in *Rhinolophus sinicus* and *Rhinolophus pusillus* from China.

After the SARS-CoV-2 outbreak in 2019, Zhou et al. reported that the **RaTG13 virus** shared 96.2% similarity with SARS-CoV-2.

2022. It was found that **BANAL virus** isolated from 3 different species of the *Rhinolophus* genus, shared 96.8% similarity with SARS-CoV-2.

These results imply that both SARS pandemics that occurred in humans most likely originated from bats.

SARS-like coronavirus. 4 species all belonging to the family Rhinolophidae. From Russia, Thailand, and China.

Coronaviridae

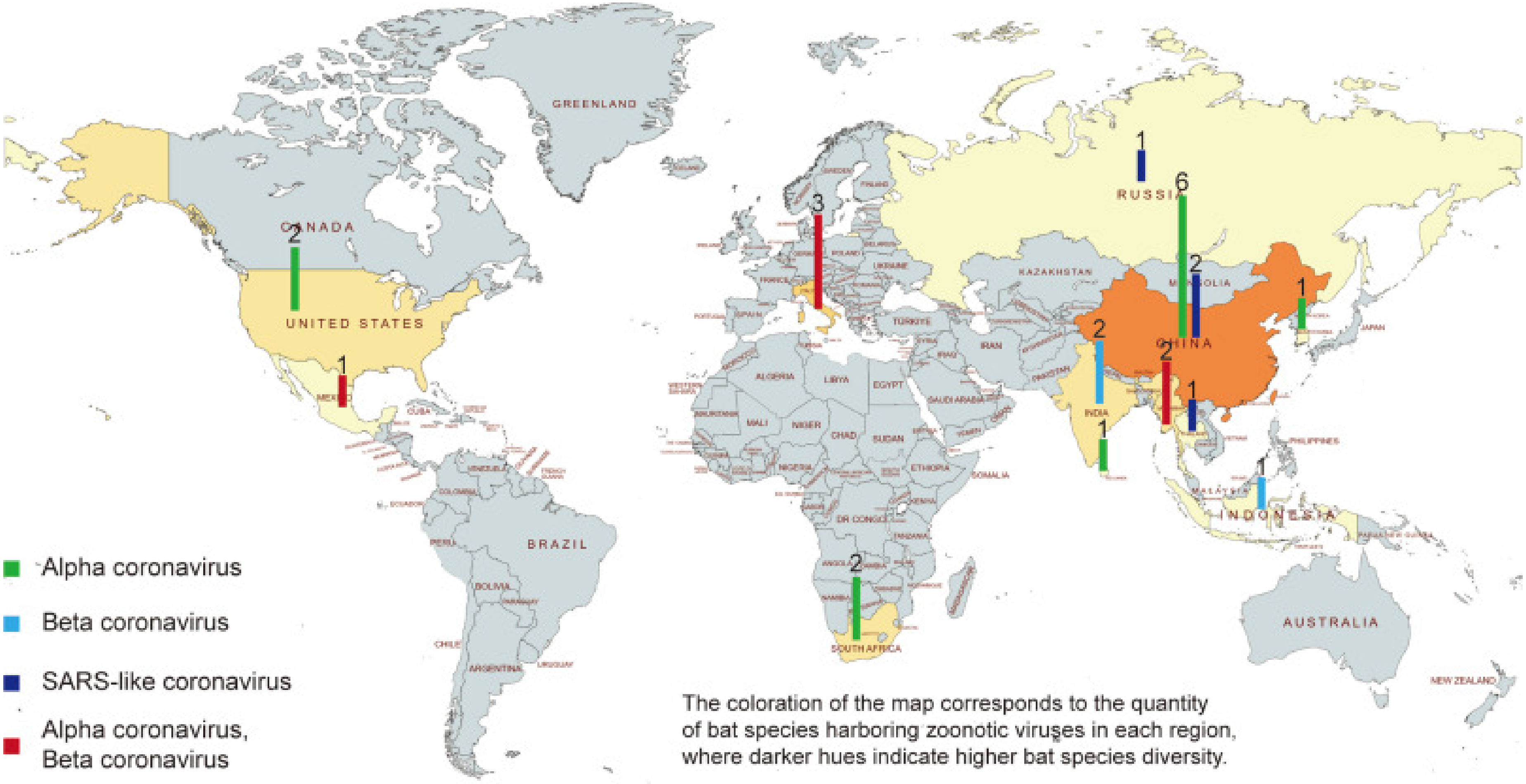
Alpha coronavirus and/or Beta coronavirus detected in 18 bat species belonging to 5 families from United States, Mexico, India, China, South Korea, Indonesia, Italy, the Republic of South Africa, Sri Lanka, Myanmar and Russia.

The same bat species was found to carry multiple types of Alpha coronavirus and Beta coronavirus this may promote an increase in the frequency of virus mutations.

Nyctinomops laticaudatus
(Broad-eared bat)
Family: Molossidae
Insectivorous

Nyctalus noctula
(Noctule bat)
Family: Vespertillionidae
Insectivorous

Coronaviridae



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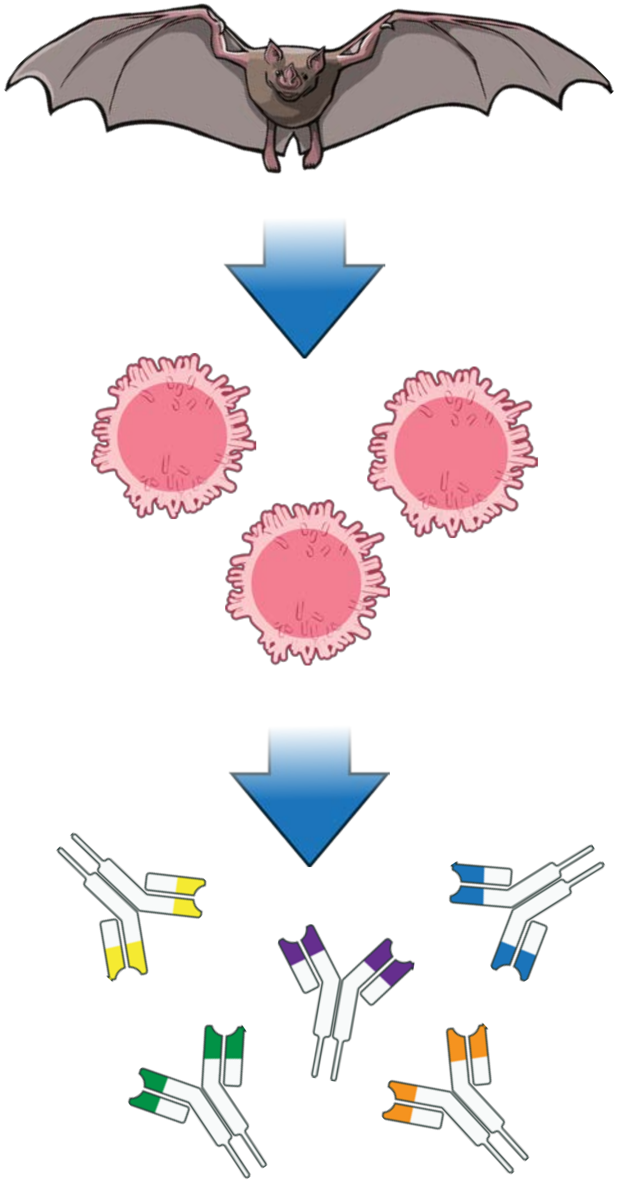
Antibody responses and B - cell molecules



There are more studies on rabies virus antibodies, Hendra virus antibodies, and Nipah virus antibodies.

There are fewer studies on antibodies to other viruses like Marburg virus antibodies, Ebola virus antibodies, West Nile virus and Japanese encephalitis virus.

Mammalian-like B lymphocytes are present in bats and are functional.

Study on B cell receptor (BCR) genes are very limited.

It is difficult to understand the conservation and variation of the BCR genes within diverse bat population.

Materials and methods

24 search terms (sources of abstract) combined with the Boolean operators, AND and OR.

Searches were carried out in PubMed. 3698 references were obtained.

Screening criteria:
- Direct isolation of the virus from bats.
- Detection of viral nucleic acids.
- Specific antibodies, etc.

By reading abstract and full text, 147 references were obtained

111 were included in the bat-carrying viruses section of the summary.

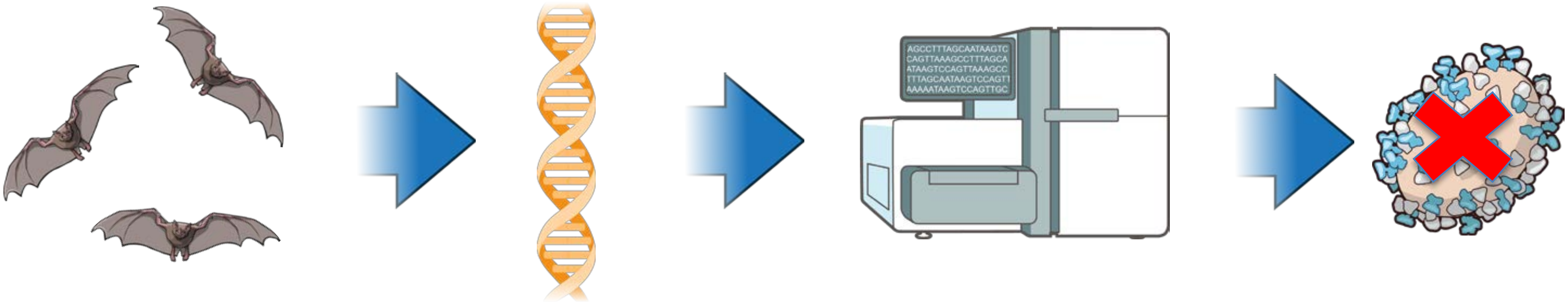
Conclussion and prospects

Rapid development of bat genome sequencing, models such as the study from viral gene fusion to the bat genome will provide new ideas for the synergistic evolution of both.

Bat species can secrete multiple antibodies to different viruses and one type of virus antibody can be produced in different bat species.

Common mechanism for virus tolerance in bats?

As more bat genomes are sequenced and assembled, there is an opportunity to annotate and compare the BCR VDJC gene composition of different bat species.



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Christian A. García-Sepúlveda — Laboratorio de Genómica Viral & Humana, Facultad de Medicina UASLP
Sandra E. Guerra-Palomares — Laboratorio de Genómica Viral & Humana,Facultad de Medicina UASLP
Juan Carlos Cuevas Tello — Grupo de Bioinformática, Facultad de Ingeniería UASLP
Ignacio Amezcua Osorio — Comité Estatal para el Fomento y Protección Pecuaria de San Luis Potosí (CEFPP)
Guillermo Espinosa Reyes — Centro de Investigación Aplicada en Ambiente y Salud (CIAAS), Facultad de Medicina UASLP
Fernando Díaz-Barriga Martínez — Centro Colaborador OMS/OPS CIAAS, Facultad de Medicina UASLP
Andreu Comas García — Epidemiología y virología molecular, Depto. Microbiología, Fac. de Medicina UASLP

Dulce Ma. Hernández Piña — Lab manager, LGVH UASLP
J. Manuel Mendoza Méndez — Hantavirus americanos en roedores silvestres, LGVH UASLP
Nidya Jurado-Sánchez — Vigilancia de vectores y arbovirus, LGVH UASLP
Mariel Pacheco-Cortez — Hantavirus SEOV en personal biomédico, LGVH UASLP
Samuel Mora-Andrade — Bat collection research, LGVH UASLP
Carolina Escalante Vargas — Bat collection research, CEFPP

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