

Supplementary information

**Ecology, evolution and spillover of
coronaviruses from bats**

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Supplementary Table 1. Wild bat hosts of coronaviruses reported in published studies. All coronaviruses were considered in our search, but we highlight links between bat species and key bat coronavirus subgenera associated with human infections (e.g., *Sarbecovirus*), domestic animal infections (e.g., *Rhinacovirus*), or are widespread and well characterized (e.g., *Nobecovirus*) based on sequencing information available in the associated studies.

Bat species	Bat family	Key coronavirus subgenera	Reference
<i>Emballonura alecto</i>	Emballonuridae	<i>Nobecovirus</i>	5
<i>Taphozous melanopogon</i>	Emballonuridae		1,9
<i>Taphozous perforatus</i>	Emballonuridae	<i>Merbecovirus</i>	10,11
<i>Aselliscus stoliczkanus</i>	Hipposideridae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	12,145,163,173,174
<i>Hipposideros abae</i>	Hipposideridae	<i>Duvinacovirus</i>	13
<i>Hipposideros armiger</i>	Hipposideridae	<i>Hibecovirus</i> <i>Merbecovirus</i> <i>Nobecovirus</i> <i>Rhinacovirus</i> <i>Sarbecovirus</i>	1,9,14-17,145,174
<i>Hipposideros bicolor</i>	Hipposideridae		1
<i>Hipposideros caffer</i>	Hipposideridae	<i>Duvinacovirus</i> <i>Hibecovirus</i> <i>Sarbecovirus</i>	1-4,142,163,172
<i>Hipposideros cervinus</i>	Hipposideridae		18,163
<i>Hipposideros cf. caffer</i>	Hipposideridae	<i>Duvinacovirus</i> <i>Hibecovirus</i>	19
<i>Hipposideros cf. ruber</i>	Hipposideridae	<i>Duvinacovirus</i> <i>Hibecovirus</i>	13,20-22
<i>Hipposideros cineraceus</i>	Hipposideridae	<i>Rhinacovirus</i>	23,152
<i>Hipposideros curtus</i>	Hipposideridae	<i>Duvinacovirus</i>	163,172
<i>Hipposideros diadema</i>	Hipposideridae		1,5,163
<i>Hipposideros fuliginosus</i>	Hipposideridae	<i>Hibecovirus</i>	163,172
<i>Hipposideros galeritus</i>	Hipposideridae	<i>Sarbecovirus</i>	1
<i>Hipposideros gentilis</i>	Hipposideridae		169
<i>Hipposideros khaokhouayensis</i>	Hipposideridae		169
<i>Hipposideros larvatus</i>	Hipposideridae	<i>Hibecovirus</i> <i>Nobecovirus</i> <i>Rhinacovirus</i> <i>Sarbecovirus</i>	1,9,15,26,27,152,163,173,174
<i>Hipposideros lekaguli</i>	Hipposideridae	<i>Nobecovirus</i>	1,9,163
<i>Hipposideros pomona</i>	Hipposideridae	<i>Hibecovirus</i> <i>Rhinacovirus</i> <i>Sarbecovirus</i>	28-30,145,152,163,173,174
<i>Hipposideros pratti</i>	Hipposideridae	<i>Hibecovirus</i> <i>Rhinacovirus</i> <i>Sarbecovirus</i>	1,31,145
<i>Hipposideros ruber</i>	Hipposideridae	<i>Duvinacovirus</i> <i>Hibecovirus</i> <i>Nobecovirus</i> <i>Sarbecovirus</i>	1,4,141,142,156,163,172

Bat species	Bat family	Key coronavirus subgenera	Reference
<i>Macronycteris gigas</i> (formerly <i>Hipposideros gigas</i>)	Hipposideridae	<i>Duvinacovirus</i> <i>Hibecovirus</i>	1,22,142,163,172
<i>Macronycteris vittatus</i> (formerly <i>Hipposideros commersoni</i>)	Hipposideridae	<i>Duvinacovirus</i> <i>Hibecovirus</i> <i>Nobecovirus</i>	24,25,32
<i>Cardioderma cor</i>	Megadermatidae		24,32
<i>Lyroderma lyra</i> (formerly <i>Megaderma lyra</i>)	Megadermatidae		1,9,163,174
<i>Miniopterus africanus</i>	Miniopteridae		24
<i>Miniopterus australis</i>	Miniopteridae		33
<i>Miniopterus fuliginosus</i>	Miniopteridae		1,14,30,31,34,35,140,162,171
<i>Miniopterus fuscus</i>	Miniopteridae		30,145
<i>Miniopterus inflatus</i>	Miniopteridae		1,22,24,142
<i>Miniopterus magnater</i>	Miniopteridae		1,9,36-39,163
<i>Miniopterus minor</i>	Miniopteridae		2,24,32
<i>Miniopterus mossambicus</i>	Miniopteridae		3
<i>Miniopterus natalensis</i>	Miniopteridae		7,24
<i>Miniopterus pusillus</i>	Miniopteridae		9,36-40,145,163,174
<i>Miniopterus schreibersii</i>	Miniopteridae	<i>Merbecovirus</i> <i>Rhinacovirus</i> <i>Sarbecovirus</i>	8,9,17,30,33,37,41-47,140,145,163,171,174
<i>Chaerephon plicatus</i>	Molossidae	<i>Merbecovirus</i> <i>Sarbecovirus</i>	26,31,48,49,152,169,174
<i>Chaerephon pumilus</i>	Molossidae	<i>Duvinacovirus</i> <i>Nobecovirus</i>	1-4,6,24,142,163
<i>Cynomops abrasus</i>	Molossidae		50
<i>Cynomops planirostris</i>	Molossidae		50
<i>Eumops glaucinus</i>	Molossidae	<i>Merbecovirus</i>	51
<i>Molossus currentium</i>	Molossidae		52
<i>Molossus molossus</i>	Molossidae		53-55
<i>Molossus rufus</i>	Molossidae		51,52,54,55
<i>Mops condylurus</i>	Molossidae	<i>Hibecovirus</i> <i>Nobecovirus</i>	1-3,6,142,163,172
<i>Mops midas</i>	Molossidae		3,7,163
<i>Mormopterus francoismoutoui</i>	Molossidae		3
<i>Mormopterus jugularis</i>	Molossidae		3
<i>Nyctinomops laticaudatus</i>	Molossidae	<i>Merbecovirus</i>	1,56
<i>Otomops martiensseni</i>	Molossidae		24,32,163
<i>Tadarida brasiliensis</i>	Molossidae		1,53,56,158
<i>Tadarida teniotis</i>	Molossidae	<i>Sarbecovirus</i>	8,57
<i>Pteronotus davyi</i>	Mormoopidae		54
<i>Pteronotus parnellii</i>	Mormoopidae		1,52,56
<i>Pteronotus personatus</i>	Mormoopidae		1
<i>Mystacina tuberculata</i>	Mystacinidae		58
<i>Nycteris cf. gambiensis</i>	Nycteridae	<i>Merbecovirus</i>	59
<i>Nycteris macrotis</i>	Nycteridae	<i>Merbecovirus</i>	141

Bat species	Bat family	Key coronavirus subgenera	Reference
<i>Nycteris thebaica</i>	Nycteridae	<i>Merbecovirus</i>	3
<i>Nycteris tragata</i>	Nycteridae		163
<i>Anoura caudifer</i>	Phyllostomidae		1,163
<i>Anoura geoffroyi</i>	Phyllostomidae		52
<i>Artibeus jamaicensis</i>	Phyllostomidae		1,52,56,60
<i>Artibeus lituratus</i>	Phyllostomidae		1,51,52,55,56
<i>Artibeus obscurus</i>	Phyllostomidae		1,163
<i>Artibeus planirostris</i>	Phyllostomidae		1,163
<i>Carollia brevicauda</i>	Phyllostomidae		52
<i>Carollia castanea</i>	Phyllostomidae		60
<i>Carollia perspicillata</i>	Phyllostomidae		1,51,52,56,60,61
<i>Carollia sowelli</i>	Phyllostomidae		1,56
<i>Dermanura phaeotis</i> (formerly <i>Artibeus phaeotis</i>)	Phyllostomidae		1,56
<i>Desmodus rotundus</i>	Phyllostomidae		50,62,63,143,164
<i>Glossophaga soricina</i>	Phyllostomidae		1,50,51,55,60,61
<i>Lichonycteris obscura</i>	Phyllostomidae		163
<i>Lonchorhina aurita</i>	Phyllostomidae		1,56
<i>Mesophylla macconnelli</i>	Phyllostomidae		1,163
<i>Phyllostomus discolor</i>	Phyllostomidae		52,55
<i>Sturnira erythromos</i>	Phyllostomidae		1,163
<i>Sturnira lilium</i>	Phyllostomidae		1,51
<i>Acerodon celebensis</i>	Pteropodidae	<i>Nobecovirus</i>	163
<i>Cynopterus brachyotis</i>	Pteropodidae	<i>Nobecovirus</i>	1,5,9,27,64,65,163,170
<i>Cynopterus horsfieldii</i>	Pteropodidae	<i>Nobecovirus</i>	1,163
<i>Cynopterus sphinx</i>	Pteropodidae	<i>Nobecovirus</i>	1,9,23,27,145,147,163,169
<i>Dobsonia moluccensis</i>	Pteropodidae	<i>Nobecovirus</i>	66
<i>Dyacopterus spadiceus</i>	Pteropodidae	<i>Nobecovirus</i>	1
<i>Eidolon dupreanum</i>	Pteropodidae	<i>Nobecovirus</i>	67
<i>Eidolon helvum</i>	Pteropodidae	<i>Nobecovirus</i>	1,2,4,6,10,11,24,32,68,141,142,163,172
<i>Eonycteris spelaea</i>	Pteropodidae	<i>Nobecovirus</i>	1,27,64,69-71,144,145,163,169,174
<i>Epomophorus gambianus</i>	Pteropodidae	<i>Nobecovirus</i>	1,141,156,163,172
<i>Epomophorus labiatus</i>	Pteropodidae	<i>Nobecovirus</i>	4,32
<i>Epomops buettikoferi</i>	Pteropodidae	<i>Nobecovirus</i>	163
<i>Epomops franqueti</i>	Pteropodidae	<i>Nobecovirus</i>	1,142,163,172
<i>Macroglossus minimus</i>	Pteropodidae	<i>Nobecovirus</i>	5,72,170
<i>Megaerops ecaudatus</i>	Pteropodidae	<i>Nobecovirus</i>	163
<i>Megaerops kusnotoi</i>	Pteropodidae	<i>Nobecovirus</i>	23
<i>Megaerops niphanae</i>	Pteropodidae	<i>Nobecovirus</i>	1,27
<i>Megaloglossus woermanni</i>	Pteropodidae	<i>Nobecovirus</i>	1,142,163,172
<i>Micropteropus pusillus</i>	Pteropodidae	<i>Nobecovirus</i>	1,20,142,163,172
<i>Myonycteris angolensis</i> (formerly <i>Lissonycteris angolensis</i>)	Pteropodidae	<i>Duvinacovirus</i> <i>Hibecovirus</i> <i>Nobecovirus</i>	1,4,6,141,163
<i>Myonycteris torquata</i>	Pteropodidae	<i>Nobecovirus</i>	163,172
<i>Nanonycteris veldkampii</i>	Pteropodidae	<i>Nobecovirus</i>	141
<i>Ptenochirus jagori</i>	Pteropodidae	<i>Nobecovirus</i>	5,64

Bat species	Bat family	Key coronavirus subgenera	Reference
<i>Pteropus alecto</i>	Pteropodidae	<i>Nobecovirus</i>	1,33,73
<i>Pteropus conspicillatus</i>	Pteropodidae	<i>Nobecovirus</i>	163
<i>Pteropus lylei</i>	Pteropodidae	<i>Nobecovirus</i>	74,163
<i>Pteropus medius</i> (formerly <i>Pteropus giganteus</i>)	Pteropodidae	<i>Nobecovirus</i>	1,75-77,163
<i>Pteropus rufus</i>	Pteropodidae	<i>Nobecovirus</i>	67
<i>Rousettus aegyptiacus</i>	Pteropodidae	<i>Nobecovirus</i>	1,2,4,6,24,32,78,141,163,172
<i>Rousettus amplexicaudatus</i>	Pteropodidae	<i>Nobecovirus</i>	1,5,27,64,170
<i>Rousettus leschenaultii</i>	Pteropodidae	<i>Merbecovirus</i> <i>Nobecovirus</i>	1,23,27-29,40,71,79-81,159,162,163,174
<i>Rousettus madagascariensis</i>	Pteropodidae	<i>Nobecovirus</i>	3
<i>Rhinolophus acuminatus</i>	Rhinolophidae	<i>Sarbecovirus</i>	151,163
<i>Rhinolophus affinis</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	1,12,30,47,82,83,145,146,161,163,169,174
<i>Rhinolophus blasii</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	45,163
<i>Rhinolophus cf. clivosus</i>	Rhinolophidae	<i>Duvinacovirus</i> <i>Sarbecovirus</i>	6,139
<i>Rhinolophus clivosus</i>	Rhinolophidae	<i>Duvinacovirus</i> <i>Hibecovirus</i> <i>Rhinacovirus</i> , <i>Sarbecovirus</i>	1,4,84
<i>Rhinolophus cornutus</i>	Rhinolophidae	<i>Sarbecovirus</i>	85,148
<i>Rhinolophus creaghi</i>	Rhinolophidae	<i>Sarbecovirus</i>	1,163
<i>Rhinolophus darlingi</i>	Rhinolophidae		141
<i>Rhinolophus euryale</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	8,45,86,163
<i>Rhinolophus ferrumequinum</i>	Rhinolophidae	<i>Merbecovirus</i> <i>Nobecovirus</i> <i>Rhinacovirus</i> <i>Sarbecovirus</i>	1,8,12,17,23,29,31,43-45,57,78,83,86,89-93,140,145,159,160,163,171,174
<i>Rhinolophus fumigatus</i>	Rhinolophidae		2
<i>Rhinolophus hildebrandtii</i>	Rhinolophidae	<i>Sarbecovirus</i>	32
<i>Rhinolophus hipposideros</i>	Rhinolophidae	<i>Sarbecovirus</i>	86,94,95,160,165
<i>Rhinolophus landeri</i>	Rhinolophidae		2,32
<i>Rhinolophus lepidus</i>	Rhinolophidae		163
<i>Rhinolophus lobatus</i>	Rhinolophidae	<i>Rhinacovirus</i>	3
<i>Rhinolophus macrotis</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	17,43,83,91,145
<i>Rhinolophus malayanus</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	96,152,169,174
<i>Rhinolophus marshalli</i>	Rhinolophidae	<i>Sarbecovirus</i>	169
<i>Rhinolophus megaphyllus</i>	Rhinolophidae		33
<i>Rhinolophus mehelyi</i>	Rhinolophidae	<i>Sarbecovirus</i>	45,163
<i>Rhinolophus monoceros</i>	Rhinolophidae	<i>Sarbecovirus</i>	14,17,97

Bat species	Bat family	Key coronavirus subgenera	Reference
<i>Rhinolophus pearsonii</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	17,43,91,174
<i>Rhinolophus pusillus</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	17,31,46,49,82,83,93,98,99,145,152,153,163,169,174
<i>Rhinolophus rex</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	1,17,82
<i>Rhinolophus rhodesiae</i>	Rhinolophidae	<i>Rhinacovirus</i>	3
<i>Rhinolophus rufus</i>	Rhinolophidae	<i>Nobecovirus</i>	5
<i>Rhinolophus shameli</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	1,9,27,83,150
<i>Rhinolophus sinicus</i>	Rhinolophidae	<i>Nobecovirus</i> <i>Rhinacovirus</i> <i>Sarbecovirus</i>	1,12,17,23,30,31,38,40,43,82,83,100-109,145,147,152,159,163,173,174
<i>Rhinolophus stheno</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	29,152,161
<i>Rhinolophus thomasi</i>	Rhinolophidae	<i>Rhinacovirus</i> <i>Sarbecovirus</i>	17,163
<i>Rhinolophus trifolius</i>	Rhinolophidae		18,163
<i>Rhinonycteris aurantia</i>	Rhinonycteridae	<i>Hibecovirus</i>	33
<i>Triaenops afer</i>	Rhinonycteridae	<i>Setracovirus</i>	1,3,32,142
<i>Triaenops menamena</i>	Rhinonycteridae		3
<i>Triaenops persicus</i>	Rhinonycteridae	<i>Merbecovirus</i> <i>Nobecovirus</i> <i>Setracovirus</i>	1,6,142
<i>Rhinopoma hardwickii</i>	Rhinopomatidae	<i>Nobecovirus</i> <i>Sarbecovirus</i>	10,163
<i>Bauerus dubiaquercus</i>	Vespertilionidae		1
<i>Chalinolobus gouldii</i>	Vespertilionidae		110
<i>Chalinolobus morio</i>	Vespertilionidae		110
<i>Corynorhinus townsendii</i>	Vespertilionidae		154
<i>Eptesicus fuscus</i>	Vespertilionidae		56,111-113,149
<i>Eptesicus isabellinus</i>	Vespertilionidae	<i>Merbecovirus</i>	42
<i>Eptesicus nilssonii</i>	Vespertilionidae	<i>Merbecovirus</i>	114
<i>Eptesicus serotinus</i>	Vespertilionidae	<i>Merbecovirus</i>	8,92,98,115,116,171
<i>Glauconycteris poensis</i>	Pteropodidae		163
<i>Glauconycteris variegata</i>	Pteropodidae	<i>Nobecovirus</i>	163
<i>Falsistrellus mackenziei</i>	Vespertilionidae		110
<i>Hypsugo alaschanicus</i>	Vespertilionidae		140,171
<i>Hypsugo pulveratus</i>	Vespertilionidae	<i>Merbecovirus</i>	101,159
<i>Hypsugo savii</i>	Vespertilionidae	<i>Merbecovirus</i>	42,94,117
<i>Ia io</i>	Vespertilionidae	<i>Merbecovirus</i>	1,118,145
<i>Kerivoula hardwickii</i>	Vespertilionidae		163
<i>Kerivoula pellucida</i>	Vespertilionidae		163
<i>Kerivoula titania</i>	Vespertilionidae		14
<i>Murina cyclotis</i>	Vespertilionidae		152
<i>Murina leucogaster</i>	Vespertilionidae		17,23
<i>Murina recondita</i>	Vespertilionidae		14
<i>Myotis adversus</i>	Vespertilionidae		174
<i>Myotis aurascens</i>	Vespertilionidae		171

Bat species	Bat family	Key coronavirus subgenera	Reference
<i>Myotis bechsteinii</i>	Vespertilionidae		119,120
<i>Myotis blythii</i> (includes <i>Myotis oxygnathus</i>)	Vespertilionidae		42,89,115
<i>Myotis bombinus</i>	Vespertilionidae		140
<i>Myotis brandtii</i>	Vespertilionidae		114
<i>Myotis californicus</i>	Vespertilionidae		1
<i>Myotis capaccinii</i>	Vespertilionidae		8
<i>Myotis chinensis</i>	Vespertilionidae		145,174
<i>Myotis dasycneme</i>	Vespertilionidae		116,120,121,167
<i>Myotis daubentonii</i>	Vespertilionidae	<i>Merbecovirus</i> <i>Rhinacovirus</i>	1,8,23,29,31,42,86,89,114,116,120-122,163,167
<i>Myotis davidii</i>	Vespertilionidae		17
<i>Myotis emarginatus</i>	Vespertilionidae		41,90
<i>Myotis evotis</i>	Vespertilionidae		113
<i>Myotis fimbriatus</i>	Vespertilionidae		14,98,163
<i>Myotis formosus</i> (formerly <i>Myotis flavus</i>)	Vespertilionidae		14
<i>Myotis horsfieldii</i>	Vespertilionidae	<i>Nobecovirus</i>	1,27,145,163
<i>Myotis ikonnikovi</i>	Vespertilionidae	<i>Merbecovirus</i>	171
<i>Myotis laniger</i>	Vespertilionidae	<i>Rhinacovirus</i>	152,163
<i>Myotis longipes</i>	Vespertilionidae		1,174
<i>Myotis lucifugus</i>	Vespertilionidae		113,123,124,125
<i>Myotis macrodactylus</i>	Vespertilionidae		140,171
<i>Myotis macropus</i>	Vespertilionidae		33,126
<i>Myotis muricola</i>	Vespertilionidae		152
<i>Myotis myotis</i>	Vespertilionidae		1,8,42,86,89,127,157
<i>Myotis nattereri</i>	Vespertilionidae		8,41,86,89,116,119,122
<i>Myotis nigricans</i>	Vespertilionidae		51
<i>Myotis occultus</i>	Vespertilionidae		111
<i>Myotis pequinius</i>	Vespertilionidae	<i>Merbecovirus</i>	98
<i>Myotis petax</i>	Vespertilionidae		140,171
<i>Myotis pilosus</i> (formerly <i>Myotis ricketti</i>)	Vespertilionidae	<i>Merbecovirus</i> <i>Rhinacovirus</i>	1,31,38,43,46,98,145,163,174
<i>Myotis punicus</i>	Vespertilionidae		8
<i>Myotis riparius</i>	Vespertilionidae		51
<i>Myotis siligorensis</i>	Vespertilionidae	<i>Merbecovirus</i> <i>Rhinacovirus</i>	17,163,174
<i>Myotis velifer</i>	Vespertilionidae		1,56
<i>Myotis volans</i>	Vespertilionidae		113
<i>Myotis welwitschii</i>	Vespertilionidae		163
<i>Neoromicia capensis</i>	Vespertilionidae	<i>Merbecovirus</i>	7,128,129
<i>Neoromicia cf. zuluensis</i>	Vespertilionidae	<i>Merbecovirus</i>	130
<i>Neoromicia somalica</i>	Vespertilionidae	<i>Nobecovirus</i>	163
<i>Nyctalus lasiopterus</i>	Vespertilionidae		42
<i>Nyctalus leisleri</i>	Vespertilionidae		45
<i>Nyctalus noctula</i>	Vespertilionidae	<i>Merbecovirus</i>	94,121,157
<i>Nyctalus plancyi</i>	Vespertilionidae		1,31

Bat species	Bat family	Key coronavirus subgenera	Reference
(includes <i>Nyctalus velutinus</i>)			
<i>Nyctophilus geoffroyi</i>	Vespertilionidae		110
<i>Nyctophilus gouldi</i>	Vespertilionidae		110
<i>Perimyotis subflavus</i>	Vespertilionidae		131
<i>Pipistrellus abramus</i>	Vespertilionidae	<i>Merbecovirus</i> <i>Nobecovirus</i> <i>Sarbecovirus</i>	31,38,43,92,101,118,132,145,171,174
<i>Pipistrellus cf. hesperidus</i>	Vespertilionidae	<i>Merbecovirus</i>	6,133
<i>Pipistrellus coromandra</i>	Vespertilionidae	<i>Merbecovirus</i>	1,27,163
<i>Pipistrellus hesperidus</i>	Vespertilionidae	<i>Merbecovirus</i>	1,163
<i>Pipistrellus inexpectatus</i>	Vespertilionidae		172
<i>Pipistrellus kuhlii</i> (includes <i>Pipistrellus deserti</i>)	Vespertilionidae	<i>Merbecovirus</i> <i>Nobecovirus</i>	10,42,78,89,94,117,134,168
<i>Pipistrellus nathusii</i>	Vespertilionidae	<i>Merbecovirus</i>	59,119,120
<i>Pipistrellus pipistrellus</i>	Vespertilionidae	<i>Merbecovirus</i>	1,41,43,59,89,118,121,135,157,166
<i>Pipistrellus pygmaeus</i>	Vespertilionidae	<i>Merbecovirus</i>	59,86,116,119,120,167
<i>Pipistrellus tenuis</i> (formerly <i>Pipistrellus minus</i>)	Vespertilionidae	<i>Merbecovirus</i>	118
<i>Plecotus auritus</i>	Vespertilionidae	<i>Merbecovirus</i> <i>Sarbecovirus</i>	57,89
<i>Plecotus taivanus</i>	Vespertilionidae		14
<i>Scotophilus dinganii</i>	Vespertilionidae	<i>Nobecovirus</i>	1,32,142,172
<i>Scotophilus heathii</i>	Vespertilionidae	<i>Nobecovirus</i>	9,26,163,174
<i>Scotophilus kuhlii</i>	Vespertilionidae	<i>Nobecovirus</i>	1,9,14,27,43,97,136,137,145,147,163,174
<i>Scotophilus leucogaster</i>	Vespertilionidae	<i>Nobecovirus</i>	1,172
<i>Scotophilus nux</i>	Vespertilionidae		1,163,172
<i>Submyotodon latirostris</i>	Vespertilionidae		14
<i>Tylonycteris pachypus</i>	Vespertilionidae	<i>Merbecovirus</i> <i>Rhinacovirus</i>	1,31,38,43,46,101,118,132,145,155,159,163,174
<i>Tylonycteris robustula</i>	Vespertilionidae	<i>Rhinacovirus</i>	101,174
<i>Vespadelus baverstocki</i>	Vespertilionidae		110
<i>Vespadelus pumilus</i>	Vespertilionidae		33
<i>Vespadelus regulus</i>	Vespertilionidae		110
<i>Vespertilio murinus</i>	Vespertilionidae	<i>Merbecovirus</i>	157
<i>Vespertilio sinensis</i> (formerly <i>Vespertilio superans</i>)	Vespertilionidae	<i>Merbecovirus</i> <i>Hibecovirus</i>	1,31,92,118,138,145,171

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Supplementary Table 2. Comparison of difference approaches to studying coronaviruses in bats. A total of 214 original studies on bat-associated coronaviruses were classified into study types. Study types were not exclusive, so a study may fit into multiple types depending on the sampling approach and analytical methods. All classified studies can be found in Supplementary Dataset 1.

Study type and description	Number of studies	Overview	What we can learn	Advantages	Caveats
<p>Experimental Experimental infection of individual bats or bat cell lines, or other viral manipulations in a controlled environment</p>	<p>Bat cell lines: 29 Live bats: 6</p>	<p><u>Bat cell experiments</u></p> <ul style="list-style-type: none"> • Target cells: brain, embryo, intestine, kidney, lung • Tested viruses: multiple bat SARS-related CoVs, BatCoV HKU4, BatCoV HKU9, HCoV-229E, HCoV-NL63, MERS-CoV, PEDV, Ro-BatCoV GCCDC1, SADS-CoV, SARS-CoV, SARS-CoV-2, <i>Scotophilus bat CoV</i> 512, TGEV <p><u>Live bat experiments</u></p> <ul style="list-style-type: none"> • Tested hosts and viruses: <i>Artibeus jamaicensis</i> (MERS-CoV), <i>Eptesicus fuscus</i> (SARS-CoV-2), <i>Myotis lucifugus</i> (Myl-CoV), <i>Rousettus leschenaultii</i> (BatCoV HKU9), <i>Rousettus aegyptiacus</i> (bat SARSr-CoV WIV1, SARS-CoV-2) 	<ul style="list-style-type: none"> • Characterization of newly detected viruses • Bat species susceptibility to infection and dose-response relationships • Magnitude, quality, and kinetics of immune responses to pathogens, and mechanisms of viral control or tolerance • Disease pathogenesis (or lack thereof) • Individual and within-host infection, disease, and immunological processes, especially those required for dynamic modeling (e.g., infectious periods, acute vs. latent infections, waning immunity, etc.) • Tissue tropism and routes of virus excretion and transmission 	<ul style="list-style-type: none"> • Ability to test Koch's postulates using different strains and bat species • Causal inference • Controlled environment • Rapid technological advances make diagnostic tools affordable • Relatively rapid data acquisition 	<ul style="list-style-type: none"> • Relies on existing viral isolates; cannot isolate new pathogens • No ecological context; impossible to accurately replicate environmental conditions • Lab conditions may not effectively mimic the environmental conditions that drive infections in reservoir hosts • Challenging and expensive to house and breed colonies of bats • Often requires biosafety level 3 or 4 facilities and specialized training • A bat is not a bat, and a virus is not a virus: species-specific responses to infection make it difficult to generalize across species or bat families

Study type and description	Number of studies	Overview	What we can learn	Advantages	Caveats
			<ul style="list-style-type: none"> • Receptor binding efficiency in bats and other potential hosts • Facilitative or antagonistic interactions between coinfecting viruses • Virus surface survival and sensitivity to heat or desiccation • Development of model systems, laboratory protocols, and screening tools for the field • Spillover potential to other/novel hosts 		<ul style="list-style-type: none"> • <i>In vitro</i> studies miss differences in cell recruitment and localization or cell-cell interaction • Immortalized cells behave differently from primary cells or cells in an <i>in vivo</i> context • Fundamental knowledge of bat immune systems and basic tools for probing bat immune responses are lacking • Experiments are usually time-limited (e.g., limited ability to study immune function senescence, viral recrudescence, etc.)
<p>Longitudinal Repeated sampling of individuals, single populations, or multiple populations over time; ideally, this occurs in closed populations with known individual life-histories</p>	14	<ul style="list-style-type: none"> • Countries: Australia, China, Denmark, Germany, Malaysia, Singapore, South Korea, Thailand • Serially sampled species: <i>Eonycteris spelaea</i>, <i>Hipposideros cervinus</i>, <i>Myotis daubentonii</i>, <i>Myotis macropus</i>, <i>Myotis myotis</i>, <i>Pteropus lylei</i>, 	<ul style="list-style-type: none"> • Some spatial and temporal dynamics of pathogens in populations, and maybe in individuals • Spatiotemporal patterns of infection (e.g., travelling waves) • Transmission rates and dynamics, using carefully collected 	<ul style="list-style-type: none"> • Ability to identify and isolate novel pathogens • May have ability to repeatedly collect covariate data or track life-histories of individuals • More power to exclude time-invariant differences between individuals, 	<ul style="list-style-type: none"> • May not be truly longitudinal: without known recapture of individuals, repeated longitudinal monitoring at a geographic location may instead represent multiple cross-sectional surveys of the population

Study type and description	Number of studies	Overview	What we can learn	Advantages	Caveats
		<p><i>Rhinolophus sinicus</i>, <i>Rousettus leschenaultii</i></p>	<p>age-prevalence and age-seroprevalence data</p> <ul style="list-style-type: none"> • Variation in prevalence/seroprevalence with host traits or environmental covariates • Parameters of the disease process in individuals and populations required for dynamic modeling (e.g., seasonality, maybe transmission rates, life-history traits) • Some dynamics of co-circulating viruses • Interventions that might reduce prevalence or magnitude of an epizootic or enzootic 	<p>populations, or environments</p> <ul style="list-style-type: none"> • Identification of temporal trends (e.g., seasonality) • Potential for forecasting and prediction • Intervention analysis • Relationship between time-series variables 	<ul style="list-style-type: none"> • Expensive, time-consuming, and logistically challenging; slow data acquisition • Effective implementation requires a strong ecological understanding of the study system and collection of data to determine sampling frequency and duration • May be temporally biased; sampling at regular intervals may consistently detect or consistently miss viral shedding • May be spatially biased; difficult to sample spatially replicated populations • Determining disease dynamics is difficult: requires consistent recapture of individuals, longitudinal sampling that exceeds pathogen infectious period, nonlethal

Study type and description	Number of studies	Overview	What we can learn	Advantages	Caveats
					<p>pathogen detection, and moderate prevalence</p> <ul style="list-style-type: none"> • Large sample sizes, spatially replicated populations, and short sampling intervals are needed to understand environmental drivers, and individual and population-level variation in viral shedding • Relationships that exist for groups may not apply to individuals (ecological fallacy, e.g., virus x detected in all population subgroups sampled in Habitat A; therefore, all individuals or other population subgroups in Habitat A must also carry virus x.
<p>Cross-sectional (intra-species) Sampling of a bat population or population subgroup(s) at a specific timepoint</p>	14		<ul style="list-style-type: none"> • Genetic variation of strains within host population(s) • Spatial distribution of strains within host population(s) • Some differences between 	<ul style="list-style-type: none"> • Relatively fast and inexpensive • Sampling of isolated populations can help distinguish between population-level pathogen persistence and spatiotemporally irregular transmission 	<ul style="list-style-type: none"> • No ability to detect seasonality or other temporal trends • No causal inference • Large amounts of data are required to account for variation

Study type and description	Number of studies	Overview	What we can learn	Advantages	Caveats
			<p>demographic stages (dependent on sampling time-point)</p> <ul style="list-style-type: none"> • Possible to integrate with longitudinal studies of same species • Natural routes of excretion 	<ul style="list-style-type: none"> • Can sample populations adaptively in response to spillover • Ability to isolate pathogens • Some ability to detect spatial variation or statistically analyze differences. 	<p>among individuals or populations</p> <ul style="list-style-type: none"> • Effective implementation requires a strong ecological understanding of the study system • May be temporally biased: sampling during peaks or troughs in population prevalence will over- or underestimate geographic variation in prevalence or genetic diversity • May be spatially biased: at one timepoint, different population subgroups may have peaks or troughs in prevalence • Ecological fallacy (as in longitudinal studies)
<p>Cross-sectional (inter-species) Sampling of bat assemblages or a subset of a bat assemblage (>1 species) at a specific timepoint</p>	123	<ul style="list-style-type: none"> • Sampled countries: 69 • Sampled bat families: 18 • Positive bat families: 14 • Sampled bat species: 543 	<ul style="list-style-type: none"> • Identity of potential reservoir hosts • Potential exchange of strains between hosts • Host and geographic factors that impact viral diversity 	<ul style="list-style-type: none"> • Rapid detection of viruses in multiple species • Ability to isolate pathogens • Some ability to detect species-level differences 	<ul style="list-style-type: none"> • Same caveats as intra-species cross-sectional studies • Often low sample sizes for opportunistically sampled species • Species bias: research effort may

Study type and description	Number of studies	Overview	What we can learn	Advantages	Caveats
		<ul style="list-style-type: none"> Positive bat species: 238 		<ul style="list-style-type: none"> Relatively fast and inexpensive 	<ul style="list-style-type: none"> inadvertently skew importance of a particular species as a reservoir or spillover host Ecological fallacy (as in longitudinal and intra-species cross-sectional studies)
<p>Multi-pathogen detection Detection of multiple pathogens (virus families, strains, or other parasite taxa) using metagenomic sequencing or other targeted methods on samples collected during cross-sectional or longitudinal sampling at the individual- or population-level</p>	36		<ul style="list-style-type: none"> Viral species diversity, abundance, and community dynamics Some information about periods of potential spillover risk for newly detected viruses not yet known to be zoonotic Coinfection and some insight into interactive effects of viruses on hosts 	<ul style="list-style-type: none"> Can be combined with next-generation sequencing to identify viral communities May require little to no fieldwork if samples are already available Can be relatively inexpensive with rapid data acquisition (design dependent) 	<ul style="list-style-type: none"> Same caveats as longitudinal or cross-sectional studies, depending on design May be difficult to distinguish between facilitative or antagonistic interactions between coinfecting viruses or viruses synchronously shed from a bat population; requires large sample sizes combined with simulation or experimental studies Drivers of multi-viral infection or shedding may be difficult to detect (e.g., may be driven by facilitative interaction between known or undetected coinfecting viruses, interactions with host physiology/immunity,

Study type and description	Number of studies	Overview	What we can learn	Advantages	Caveats
					<p>and/or a response to optimal environmental conditions)</p> <ul style="list-style-type: none"> • Biased detection: high titers of one virus in a sample may reduce assay sensitivity to other viruses • No causal inference • Co-detection of pathogens in pooled or population-level samples may reflect coinfection or contribution of multiple bats to the collected sample
<p>Sequencing only Viral sequencing on samples collected during longitudinal or cross-sectional sampling; little collection of data on other covariates</p>	29		<ul style="list-style-type: none"> • Comparative genomics • Mutation and evolutionary rates • Virus discovery • Effective population size and genetic diversity of virus within or across subpopulations • Some information on viral dynamics may be possible (e.g., through phylodynamics) 	<ul style="list-style-type: none"> • Requires little background knowledge of study system • Relatively inexpensive; rapid data acquisition • May require little to no fieldwork if samples are already available 	<ul style="list-style-type: none"> • No ecological or physiological context • No causal inference

