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MOLECULAR DETECTION OF CORONAVIRUSES (*CORONAVIRIDAE*) BY RT-qPCR IN BATS FROM A WILDLIFE REHABILITATION CENTRE IN ROMANIA

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Abstract

Bats are recognized as natural reservoirs for numerous viruses, including the family Coronaviridae. The aim of this study was to investigate the presence of coronaviruses related to the Sarbecovirus subgenus in bats admitted to the Wildlife Rescue and Rehabilitation Center. A total of 22 samples from 18 bats were analyzed, including 14 intestinal samples and 8 oral swabs. For two larger individuals, three intestinal segments were analyzed separately. RNA extraction was performed using the Auto-Pure32 system with the Nucleic Acid Extraction or Purification Reagent (MedicalSystem), followed by RT-qPCR detection (CFX96 Touch Real-Time PCR Detection System) using the STAT-NAT-SARS-CoV-2 kit (Sentinel-Diagnostics) targeting the E gene common to Sarbecovirus and the N and RdRp genes specific to SARS-CoV-2. Testing with the 2019-nCoV kit (PrimerDesign) confirmed the absence of SARS-CoV-2. Four bats (22.2%), identified as Pipistrellus kuhli, Nyctalus noctula, and Vespertilio murinus, were positive for the E gene (4/14 intestinal samples and 2/8 oral swabs). These findings indicate the presence of Sarbecovirus in bats from the Bucharest-Ilfov and Prahova region, highlighting the importance of continued molecular surveillance within a One Health framework.

Key words*: Chiroptera, coronaviruses, Sarbecovirus, RT-qPCR, wildlife surveillance.*

INTRODUCTION

Bats (order *Chiroptera*) comprise approximately 1,690 species with a broad geographic distribution and represent the second most diverse group of mammals after rodents (Burgin et al., 2018). Their social organization, particularly the formation of large multispecies colonies, facilitates the maintenance and transmission of viral pathogens within bat populations (Kerth, 2008). In addition to their essential ecological roles in insect control, pollination, and seed dispersal, bats have attracted increasing scientific interest due to their capacity to act as natural reservoirs for numerous viruses, including members of the family *Coronaviridae* (Woo et al., 2006; Wang & Anderson, 2019).

Interest in bat-associated coronaviruses (CoVs) increased considerably following major global outbreaks such as Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS) (Lelli et al., 2013), and, more recently, the COVID-19 pandemic (Pisoschi et al., 2022; Marchi et al., 2024). Phylogenetic analyses demonstrated that the viruses responsible for these outbreaks are closely related to coronaviruses detected in bats, suggesting that bats are important natural reservoirs for viruses in the subgenus *Sarbecovirus* (Lau et al., 2005; Zhou et al., 2020). Extensive studies have highlighted the remarkable diversity of bat coronaviruses and their important role in coronavirus evolution (Woo et al., 2006).

Coronaviruses are enveloped positive-sense single-stranded RNA [(+), ssRNA] viruses classified within the order *Nidovirales*, family *Coronaviridae*, and subfamily *Orthocoronavirinae* (Woo, De Groot et al., 2023). They are divided into four genera: *Alphacoronavirus* (α-CoV), *Betacoronavirus* (β-CoV), *Gammacoronavirus* (γ-CoV) and *Deltacoronavirus* (δ-CoV). All mammalian coronaviruses, including those detected in bats, belong to the α-and β-CoV genera (Balboni et al., 2011). Importantly, highly pathogenic

human coronaviruses such as SARS-CoV, MERS-CoV, and SARS-CoV-2 belong to the β-CoV genus. Previous studies identified bats from the genus *Rhinolophus* as natural hosts of SARS-CoV and SARS-like coronaviruses (Gouilh et al., 2018), while more recent investigations suggested that *Rhinolophus ferrumequinum* populations in Italy may act as reservoirs for SARS-CoV-2-related viruses (Briggs et al., 2023).

In Europe, surveillance studies have reported the presence of coronaviruses in several bat genera, including *Pipistrellus*, *Nyctalus*, *Vespertilio*, and *Rhinolophus* (Lelli et al., 2013), and have identified both α-CoVs and β-CoVs in bat populations from Italy, significantly expanding knowledge of bat-CoV ecology in Europe. Additional studies from Sardinia and other European regions further confirmed the circulation of β-CoVs in bat populations and emphasized the importance of bats as wildlife hosts for coronaviruses within the "One Health" framework (Lecis et al., 2019; Leopardi et al., 2023; Mira et al., 2025). However, data regarding the circulation of bat-associated coronaviruses in Eastern Europe, particularly in Romania, remains limited.

The present study aimed to investigate the presence of coronaviruses belonging to the family *Coronaviridae*, subgenus *Sarbecovirus*, in bats admitted to the Wildlife Rescue and Rehabilitation Centre of the "Visul Luanei" Foundation using RT-qPCR-based molecular detection methods. Intestinal samples were collected post-mortem from bats that died naturally during rehabilitation, while oral swabs were obtained from live individuals during routine examinations; therefore, no animals were euthanized or otherwise distressed for this study. Although the study is limited by the relatively small sample size and the absence of genomic sequencing, the results contribute to the current understanding of coronavirus circulation in Romanian bat populations and highlight the importance of continued wildlife surveillance for emerging zoonotic pathogens.

MATERIALS AND METHODS

Study Design and Sample Collection

This study investigated the presence of viral RNA belonging to the family *Coronaviridae*, genus *Betacoronavirus*, subgenus *Sarbecovirus*, in samples collected from bats admitted to the Wildlife Rescue and Rehabilitation Centre of the "Visul Luanei" Foundation, Romania. The bats originated from different regions of the country and were brought to the centre for rehabilitation and veterinary care. A total of 22 biological samples were collected from 18 bats, including 14 post-mortem intestinal samples from 10 bats that died naturally during rehabilitation (Table 1), while oral swabs were obtained from 8 live bats during routine clinical examination and care procedures (Table 2). For two larger individuals, three intestinal segments (jejunum, ileum, and colon) were sampled separately. All samples were collected under appropriate biosafety conditions. Oral swabs were immediately immersed in 350 µL RNA Stabilization Solution (ELK-Biotechnology), while intestinal tissues were preserved in 500 µL of the same solution and stored at −80°C until analysis. No animals were euthanized for the purposes of this study.

Table 1. Description of the bat group from which intestinal mass samples were collected (original photos)

ID & Species	Sex	Weight (g)	Evaluation	Location	Death
25-2585 *Pipistrellus kuhlii* 	M	3.9	Emaciated, moderate dehydration	Bucharest	25.07.25
25-3092 *Pipistrellus kuhlii* 	M	6.2	Suspected septicemia (cat attack), agony, physical trauma	Ilfov (county)	04.09.25

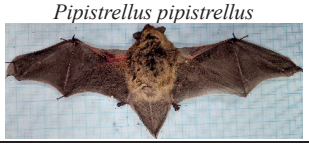
ID & Species	Sex	Weight (g)	Evaluation	Location	Death
25-2840 *Pipistrellus nathusii* 	F	3.7	Inflammation of the left radiocarpal region and the right 2nd phalanx	Bucharest	12.08.25
25-204 *Pipistrellus kuhlii* 	M	4.5	Underweight, severely dehydrated	Bucharest	16.02.25
25-547 *Vespertilio murinus* 	M	8.9	Mite infestation, severe dehydration and underweight, open fracture of the right femur	Brasov (county)	22.04.25
25-87 *Nyctalus noctula* 	M	22.1	Fracture at the level of phalanx II and II, necrotic tissue, patagium tears, right eye anophthalmia	Prahova (Sinaia)	20.01.25
24-3131 *Nyctalus noctula* 	F	27.3	Hematoma in the right-wing radio-ulnar region, inflamed right carpal joint	Brasov (county)	12.03.25
25-594 *Pipistrellus pipistrellus* 	M	5.3	Proximal open radio-ulnar fracture, right-wing	Bucharest	22.04.25
25-712 *Hypsugo savii* 	F	3.4	Missing phalanges on the right-wing	Timisoara (county)	05.05.25
25-3081 *Pipistrellus pipistrellus* 	F	4.0	Radiocarpal dislocation on the left-wing	Prahova (Ploiesti)	03.09.25

Table 2. Description of the bat group from which saliva samples were collected (*original photos*)

ID & Species	Sex	Weight (g)	Location	Diagnosis
25-3260 *Vespertilio murinus* 	F	17.0	Bucharest	Clinically healthy
25-3281 *Vespertilio murinus* 	F	12.0	Prahova (county)	Clinically healthy, slightly malnourished
25-3029 *Vespertilio murinus* 	M	14.0	Bucharest	Clinically healthy, slightly malnourished
25-852 *Nyctalus lasiopterus* 	F	58.1	Bucharest	Born in captivity, clinically healthy
25-3045 *Pipistrellus kuhlii* 	M	5.0	Bucharest	Clinically healthy
25-402 *Nyctalus lasiopterus* 	F	81.9	Bucharest	Clinically healthy

ID & Species	Sex	Weight (g)	Location	Diagnosis
25-3659 *Vespertilio murinus* 	F	14.0	Bucharest	Clinically healthy
25-3718 *Pipistrellus kuhlii* 	M	6.0	Bucharest	Old wound on the right patagium, clinically healthy

Sample Processing, RNA Extraction, and Purification

Intestinal tissues (25 mg) were mechanically homogenized in 500 µL lysis buffer (Nucleic Acid Extraction or Purification Reagent, MedicalSystem) using a Bioprep 24R homogenizer (Hangzhou Allsheng Instruments Co.) with ceramic beads. Tissue lysates were centrifuged at 10,000 × g for clarification, and the supernatants were used for RNA extraction. Following homogenization (4,000 rpm), the swab was removed from the collection tube, and 250 µL of the resulting suspension was used for RNA extraction.

Total RNA was extracted and purified using the Nucleic Acid Extraction or Purification Reagent (MedicalSystem) and the Auto-Pure32 automated extractor (Hangzhou Allsheng Instruments Co.). The method is based on magnetic bead technology and involves nucleic acid binding, washing steps, and final elution in a dedicated buffer.

To monitor extraction efficiency and detect potential PCR inhibition, an exogenous extraction control supplied with the 2019-nCoV Genesig® Advanced Kit (Primerdesign Ltd., UK) was added (10 µL/sample) during the extraction procedure. The control RNA was co-purified with the sample RNA and subsequently detected by RT-qPCR through the HEX channel. Successful amplification of the exogenous control (Ct 28 ± 3) confirmed both extraction performance and the absence of significant PCR inhibition. This approach was adopted because the internal control included in the STAT-NAT® SARS-CoV-2 MULTI Assay is based on the human *RNase P* gene and is therefore not suitable for bat-derived samples.

Molecular Detection of Coronaviruses by RT-qPCR Using the STAT-NAT® SARS-CoV-2 MULTI Assay

The STAT-NAT® SARS-CoV-2 MULTI Assay (Ref. 1N044, Sentinel Diagnostics) is a multiplex one-step RT-qPCR assay targeting the *N* and *RdRp* genes of SARS-CoV-2 (FAM and HEX channels, respectively) and the *E* gene conserved among *Sarbecovirus* members (Texas Red channel). The assay also includes a human *RNase P* internal control (Cy5 channel), which was not applicable to bat-derived samples. Reactions were prepared according to the manufacturer's instructions using 10 µL of extracted RNA in a final volume of 25 µL. Positive and no-template controls (NTC) supplied with the kit were included in each run. Amplification was performed on a CFX96 Touch Real-Time PCR Detection System (Bio-Rad Laboratories, Hercules, CA, USA). The thermal profile consisted of reverse transcription at 50°C for 10 min, followed by enzyme activation at 95°C for 2 min, 10 cycles at 95°C for 15 s and 58°C for 30 s without fluorescence acquisition, and 35 cycles under the same conditions with fluorescence detection in the FAM, HEX, Texas Red, and Cy5 channels.

Independent Confirmation Using the 2019-nCoV genesig® Advanced Kit

To independently verify the results, samples were analyzed using the 2019-nCoV genesig® Advanced Kit (Primerdesign Ltd., UK), a one-step RT-qPCR assay targeting the *RdRp* gene of SARS-CoV-2 (FAM channel), along with the exogenous extraction control (IEC, HEX channel). Reactions were prepared according to the manufacturer's instructions using the PrecisionPLUS™ OneStep 2X RT-qPCR Master Mix (Primerdesign Ltd., UK) in a final reaction volume of 20 µL, including 5 µL of extracted RNA. Positive, NTC and IEC controls were included in each run. RT-qPCR amplification was performed on a CFX96 Touch Real-Time PCR Detection System (Bio-Rad Laboratories, Hercules, CA, USA) with reverse transcription at 55°C for 10 min, enzyme activation at 95°C for 2 min, and 50 cycles of 95°C for 10 s and 60°C for 60 s, with fluorescence acquisition in the FAM and HEX channels.

Validation and Interpretation Criteria

RT-qPCR runs were considered valid when the positive control amplified within the expected Ct range, the NTC showed no amplification, and the IEC exogenous control included in the 2019-nCoV genesig® Advanced Kit amplified within the manufacturer's specified range (Ct 28 ± 5). Amplification results were expressed as cycle threshold (Ct) values generated by the instrument software. Samples with Ct values ≤ 40 were considered positive, whereas samples with Ct values > 40 or showing no amplification were considered negative.

RESULTS AND DISCUSSIONS

Validation of RT-qPCR Assays

All RT-qPCR runs met the predefined validation criteria. For the STAT-NAT® SARS-CoV-2 MULTI Assay, the positive control showed successful amplification of the *N*, *RdRp*, and *E* target genes within the expected Ct range (23.47, 23.44 and 23.12 respectively), whereas the NTC remained negative. Similarly, for the 2019-nCoV genesig® Advanced Kit, the positive control amplified within the manufacturer's specified range (Ct=15.66), while no amplification was observed in the NTC. In addition, the IEC was successfully detected in all intestinal and oral swab samples, confirming efficient RNA extraction and the absence of significant PCR inhibition. Ct values for the IEC ranged from 23 to 28 cycles in intestinal samples and from 25 to 28 cycles in oral swabs. Overall, these results confirmed the analytical validity of all RT-qPCR assays performed in this study.

Detection of *Sarbecovirus*es-Associated RNA

Using the STAT-NAT® SARS-CoV-2 MULTI Assay, amplification of the *E* gene, a target conserved among *Sarbecovirus* members, was detected in samples from four of the 18 bats analyzed (22.2%) (Table 3). Positive results were obtained in both intestinal and oral samples, with Ct values ranging from 22.0 to 23.69. Among intestinal samples, *Sarbecoviruses* associated RNA was detected in one *Pipistrellus kuhlii* individual and in all three intestinal segments (jejunum, ileum, and colon) collected from one *Nyctalus noctula* bat. In addition, two oral swab samples, obtained from *Vespertilio murinus* and *Pipistrellus kuhlii* individuals, were positive for the *E* gene. No amplification of the *N* or *RdRp* genes specific to SARS-CoV-2 was observed in any sample.

Results Obtained with the 2019-nCoV genesig® Advanced Kit

All 22 samples collected from the 18 bats included in the study were additionally analyzed using the 2019-nCoV genesig® Advanced Kit (Primerdesign Ltd., UK), which specifically targets the *RdRp* gene of SARS-CoV-2. No amplification of the *RdRp* target was detected in any of the analyzed samples. The IEC control amplified successfully in all reactions. The assay was considered valid, as the positive control amplified with a Ct value of 15.66, whereas no amplification curve was observed for the negative control. These results did not confirm the presence of SARS-CoV-2 RNA in any of the samples tested.

Table 3. Characteristics of bat samples positive for the *E* gene detected using the STAT-NAT® SARS-CoV-2 MULTI Assay

Bat ID	Species	Sample Type	Location	Ct Value
25-3092	*Pipistrellus kuhlii*	Intestinal content	Ilfov County	22.50
25-87	*Nyctalus noctula*	Jejunum	Sinaia, Prahova County	23.69
25-87	*Nyctalus noctula*	Ileum	Sinaia, Prahova County	23.15
25-87	*Nyctalus noctula*	Colon	Sinaia, Prahova County	22.66
25-3260	*Vespertilio murinus*	Oral swab	Bucharest	23.15
25-3718	*Pipistrellus kuhlii*	Oral swab	Bucharest	22.00

Correlation of Results Obtained with the Two RT-qPCR Assays

The STAT-NAT® SARS-CoV-2 MULTI Assay detected amplification of the *E* gene, a marker common to members of the subgenus *Sarbecovirus*, in samples from four bats. In contrast, no amplification of the SARS-CoV-2-specific *N* or *RdRp* genes was observed with the STAT-NAT assay, and all samples tested negative for the *RdRp* gene when analyzed using the independent 2019-nCoV genesig® Advanced Kit. Taken together, these findings indicate the presence of RNA consistent with Sarbecovirus-related coronaviruses but provide no evidence of SARS-CoV-2 circulation in the analyzed bat samples.

Discussions

The exclusive detection of the *E* gene, a molecular target conserved among members of the subgenus *Sarbecovirus*, together with the absence of amplification of the SARS-CoV-2-specific *N* and *RdRp* genes in two independent RT-qPCR assays, suggests the presence of a bat-associated *Sarbecovirus* distinct from SARS-CoV-2. This interpretation is supported by the Ct values observed in positive samples (Ct range value from 22 to 24), indicating moderated viral RNA amount, and by the detection of positive amplification curve in both intestinal and oral samples.

The analytical validation of the results was further supported by successfully amplification of the IEC positive control in all samples, with Ct values ranging from 23 to 28, indicating efficient RNA extraction and the absence of significant PCR inhibition. In addition, contamination is unlikely, as no amplification was detected in the NTC of either RT-qPCR assay, and no amplification of the SARS-CoV-2-specific *N* or *RdRp* targets was observed.

An interesting finding was the detection of *Sarbecoviruses* associated RNA in all three intestinal segments (jejunum, ileum, and colon) analyzed from a single *Nyctalus noctula* individual, supporting a genuine enteric distribution of the virus. Furthermore, two *Pipistrellus kuhlii* individuals tested positive, one in an intestinal sample and the other in an oral swab. This species is among the most common urban bats in Romania and has frequently been reported in coronavirus surveillance studies conducted across Europe.

The detection of viral RNA in both intestinal and oral samples is consistent with previous reports showing that bat coronaviruses may be shed through the gastrointestinal and respiratory tracts without causing apparent clinical disease in their hosts. The positive individuals originated from Bucharest, Ilfov County, and Sinaia (Prahova County), suggesting that *Sarbecoviruses* strains might be present in bat populations from different regions of Romania.

The overall prevalence observed in the present study (22.2%) falls within the range reported in bat coronavirus surveillance studies conducted in Europe and other geographic regions (Lelli, Papetti et al., 2013; Lecis, Mucedda et al., 2019; Kandeil, Abi-Said et al., 2023; Leopardi, Desiato et al., 2023; Mira, Gucciardi et al., 2025). The detection of viral RNA in *Pipistrellus kuhlii* and *Nyctalus noctula* is consistent with previous findings from Italy, where both α- and β-coronaviruses were identified in these species, supporting their role as hosts of bat-associated coronaviruses in Europe (Lelli, Papetti et al., 2013).

Similarly, Lecis et al. (2019) reported the presence of a bat betacoronavirus in Sardinia and demonstrated phylogenetic relationships with previously described European strains, suggesting regional circulation of related

coronaviruses among bat populations (Lecis, Mucedda et al., 2019). Within a broader One Health framework, Leopardi et al. (2023) identified bats as the vertebrate group harboring the highest coronavirus diversity in Italian wildlife, highlighting the importance of species such as *Pipistrellus kuhlii* in maintaining coronavirus diversity in European ecosystems (Leopardi, Desiato et al., 2023). Comparable findings have also been reported outside Europe. For example, Kandeil et al., (2023) detected both α- and β-CoV in bat populations from Lebanon, further emphasizing the widespread distribution and diversity of coronaviruses in chiropteran hosts (Kandeil, Abi-Said et al., 2023). Earlier studies similarly demonstrated the remarkable genetic diversity of bat coronaviruses and their importance in coronavirus evolution (Woo, Lau et al., 2006; Platto, Zhou et al., 2021).

The absence of SARS-CoV-2-specific targets in all analyzed samples is consistent with recent investigations conducted during the COVID-19 pandemic. In Sicily, Mira et al. (2025) detected bat coronaviruses but found no evidence of SARS-CoV-2 circulation despite extensive molecular screening and phylogenetic analyses (Mira, Gucciardi et al., 2025). Likewise, our results indicate that none of the bats included in the present study harbored detectable SARS-CoV-2 RNA.

Several studies have reported higher prevalence values, particularly in species of the genus *Rhinolophus*, which are considered major reservoirs of SARS-related coronaviruses (Lau, Woo et al., 2005; Balboni, Gallina et al., 2012). Such differences may reflect variation in host species composition, geographic location, sample type, and methodological approaches. Unlike those investigations, the present study included multiple bat species across different genera and focused primarily on molecular screening rather than on viral characterization.

An important limitation of the present study is the lack of genomic sequencing. Although amplification of the *E* gene strongly suggests the presence of a *Sarbecovirus*-related coronavirus, definitive taxonomic identification and phylogenetic characterization were not possible. Many surveillance studies have combined molecular detection with sequencing approaches to confirm viral identity and investigate evolutionary relationships (Lecis, Mucedda et al., 2019; Cerri, Bolatti et al., 2023). Therefore, future studies should include amplification and sequencing of conserved genomic regions, such as *RdRp*, together with larger sample sizes and broader geographic coverage.

CONCLUSIONS

This study confirms the active circulation of coronaviruses from the *Sarbecovirus* subgenus among insectivorous bats in urban and peri-urban areas of Romania, specifically in the Bucharest-Ilfov and Prahova counties.

The detection of viral RNA loads in synanthropic species, specifically *Pipistrellus kuhlii*, *Nyctalus noctula*, and *Vespertilio murinus*, highlights their likely role as local reservoirs for SARS-like coronaviruses. Furthermore, our findings suggest a dual route of potential transmission, with evidence pointing toward both an enteric tropism and viral shedding via oral secretions. While molecular screening confirmed the absence of SARS-CoV-2, the presence of related *Sarbecovirus* strains aligns with international data establishing bats as critical hosts for diverse CoV populations.

Although this study is limited by a small sample size and the absence of genomic sequencing for precise phylogenetic resolution, it provides crucial baseline data for Romania. These findings strongly emphasize the necessity of sustained, large-scale wildlife surveillance integrated within a "One Health" framework to monitor viral diversity and assess zoonotic risks in human-dominated landscapes.

REFERENCES

Balboni, A., A. Palladini, G. Bogliani & M. Battilani (2011). Detection of a virus related to betacoronaviruses in Italian greater horseshoe bats. *Epidemiology & Infection*, 139(2): 216-219.

Briggs, K., R. Sweeney, D. S. Blehert, E. Spackman, D. L. Suarez și D. R. Kapczynski (2023). SARS-CoV-2 utilization of ACE2 from different bat species allows for virus entry and replication *in vitro*. *Virology*, 586: 122-129.

Burgin, C. J., J. P. Colella, P. L. Kahn & N. S. Upham (2018). How many species of mammals are there? *Journal of mammalogy*, 99(1): 1-14.

Cerri, A., E. M. Bolatti, T. M. Zorec, M. E. Montani, A. Rimondi, L. Hosnjak, P. E. Casal, V. Di Domenica, R.

M. Barquez, M. Poljak și A. A. Giri (2023). Identification and characterization of novel alphacoronaviruses in *Tadarida brasiliensis* (Chiroptera, Molossidae) from Argentina: insights into recombination as a mechanism favoring bat coronavirus cross-species transmission. *Microbiology Spectrum*, 11(5).

Gouilh, M. A., S. J. Puechmaille, L. Diancourt, M. Vandenbogaert, J. Serra-Cobo, M. L. Roïg, P. Brown, F. Moutou, V. Caro & A. Vabret (2018). SARS-CoV related Betacoronavirus and diverse Alphacoronavirus members found in western old-world. *Virology*, 517: 88-97.

Kandeil, A., M. Abi-Said, R. Badra, R. El-Shesheny, A. A. Al-Karmalawy, R. Alnajjar, Z. Khalid, M. N. Kamel, W. Abi Habib, J. Abdallah, V. Dhanasekaran, R. Webby și G. Kayali (2023). Detection of Coronaviruses in Bats in Lebanon during 2020. *Pathogens*, 12(7): 876.

Kerth, G. (2008). Animal sociality: bat colonies are founded by relatives. *Current Biology*, 18(17): R740-R742.

Lau, S. K. P., P. C. Y. Woo, K. S. M. Li, Y. Huang, H.-W. Tsoi, B. H. L. Wong, S. S. Y. Wong, S.-Y. Leung, K.-H. Chan & K.-Y. Yuen (2005). Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. *Proceedings of the National Academy of Sciences*, 102(39): 14040-14045.

Lecis, R., M. Mucedda, E. Pidinchedda, M. Pittau & A. Alberti (2019). Molecular identification of Betacoronavirus in bats from Sardinia (Italy): first detection and phylogeny. *Virus Genes*, 55(1): 60-67.

Lelli, D., A. Papetti, C. Sabelli, E. Rosti, A. Moreno & M. B. Boniotti (2013). Detection of Coronaviruses in Bats of Various Species in Italy. *Viruses*, 5(11): 2679-2689.

Leopardi, S., R. Desiato, M. Mazzucato, R. Orusa, F. Obber, D. Averaimo, S. Berjaoui, S. Canziani, M. T. Capucchio, R. Conti, S. di Bella, F. Festa, L. Garofalo, D. Lelli, M. P. Madrau, M. L. Mandola, A. M. Moreno Martin, S. Peletto, S. Pirani, S. Robetto, C. Torresi, M. Varotto, C. Citterio & C. Terregino (2023). One health surveillance strategy for coronaviruses in Italian wildlife. *Epidemiology and Infection*, 151: e96.

Liu, Y. Chen, X.-R. Shen, X. Wang, X.-S. Zheng, K. Zhao, Q.-J. Chen, F. Deng, L.-L. Liu, B. Yan, F.-X. Zhan, Y.-Y. Wang, G.-F. Xiao & Z.-L. Shi (2020). A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*, 579(7798): 270-273.

Mira, F., F. Gucciardi, G. Schiró, R. Grasso, M. T. Spena, G. Kemenesi, C. Vaiana, D. Anzá, L. Di Paola, S. Di Bella, A. Guercio & G. Purpari (2025). Molecular Surveillance for Potential Zoonotic Pathogens in Troglophilus Bats: Detection and Molecular Characterization of Bat Coronaviruses in Southern Italy. *Pathogens*, 14(5): 457.

Pisoschi, A. M., A. Pop, F. Iordache, L. Stanca, O. I. Geicu, L. Bilteanu & A. I. Serban (2022). Antioxidant, anti-inflammatory and immunomodulatory roles of vitamins in COVID-19 therapy. *European Journal of Medicinal Chemistry*, 232: 114175

Woo, P. C. Y., S. K. P. Lau, K. S. M. Li, R. W. S. Poon, B. H. L. Wong, H.-w. Tsoi, B. C. K. Yip, Y. Huang, K.-h. Chan & K.-y. Yuen (2006). Molecular diversity of coronaviruses in bats. *Virology*, 351(1): 180-187.

Wang, L. F. & D. E. Anderson (2019). Viruses in bats and potential spillover to animals and humans. *Curr Opin Virol*, 34: 79-89.

Zhou, P., X.-L. Yang, X.-G. Wang, B. Hu, L. Zhang, W. Zhang, H.-R. Si, Y. Zhu, B. Li, C.-L. Huang, H.-D. Chen, J. Chen, Y. Luo, H. Guo, R.-D. Jiang, M.-Q. Liu, Y. Chen, X.-R. Shen, X. Wang, X.-S. Zheng, K. Zhao, Q.-J. Chen, F. Deng, L.-L. Liu, B. Yan, F.-X. Zhan, Y.-Y. Wang, G.-F. Xiao și Z.-L. Shi (2020). A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*, 579(7798): 270-273.

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