

# Surveillance for Coronaviruses in Bats, Lebanon and Egypt, 2013–2015

## Technical Appendix 1

### Laboratory Methods

#### Screening

Viral RNA was extracted by using the Qiaamp viral RNA minikit (QIAGEN, Hilden, Germany). The RNA was eluted in 60  $\mu$ L AVE buffer and was used as a template for further detection by a pan-coronavirus nested PCR targeting the *RNA-dependent RNA polymerase* (*RdRp*) gene. First-round reverse transcription PCR (RT-PCR) was conducted by using forward primer 5-GGKTG–GGAYTAYCCCKAARTG-3 and reverse primer 5-TGYTGTSWRCA-RAAYTCRTG-3 and QIAGEN 1-step RT-PCR kit. A 25- $\mu$ L reaction mixture contained 5  $\mu$ L of 5X reaction buffer, 1  $\mu$ L dNTPs, 1  $\mu$ L enzyme mix, 1.5  $\mu$ L (10 Pmole) forward primer, 1.5  $\mu$ L (10 Pmole) reverse primer, 10  $\mu$ L ddH<sub>2</sub>O, and 5  $\mu$ L of sample RNA. The PCR cyclers conditions for the amplification were 50°C for 30 min (reverse transcription) then 95°C for 15 min, 45 cycle of 94°C for 15 s (denaturation), 48°C for 30 s (annealing), 72°C for 40 s (extension), then 72°C for 10 min (final extension). The PCR product was then put through a second round PCR by using a new set of primers (forward primer 5-GGTTGG-GACTATCCTAAGTGTGA-3, reverse primer 5-CCATCATCAGATAG-AATCATCAT-3) which amplify a final PCR product of 440 bp. Using Phusion High Fidelity PCR Master Mix Kit (Thermo Scientific, Waltham, MA, USA), a 25- $\mu$ L reaction contained 12.5  $\mu$ L of 2X phusion master mix, 1.5  $\mu$ L (10 Pmole) forward primer, 1.5  $\mu$ L (10 Pmole) reverse primer, 7.5  $\mu$ L H<sub>2</sub>O, and 2  $\mu$ L of PCR product. The PCR cyclers conditions were 98°C for 2 min then 45 amplification cycles (98°C for 15 s, 48°C for 15 s, 72°C for 30 s), then 72°C for 2 min. The final PCR amplicons were gel purified using the

QIAquick gel purification kit (QIAGEN) and analyzed by sequencing (1). The *upE* quantitative reverse transcription PCR was performed as previously described (2).

### **Sequencing**

The second round forward and reverse primers were to sequence the purified DNA amplicons using a BigDyeR Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Foster City, CA, USA) according to manufacturer's instructions and were further amplified for 26 cycles at 95°C for 30 s, 50°C for 15 s, and 60°C for 4 min. The reaction product was purified by exclusion chromatography in CentriSep columns (Princeton Separations, Adelphia, NJ, USA). The recovered materials were sequenced by using a 96-capillary 3730xl DNA Analyzer (Applied Biosystems). Sequences were assembled by using SeqMan DNA Lasergene 7 software (DNASTAR, Madison, WI, USA). Sequence analysis was performed by using BioEdit 7.0 and MEGA 6.0 for multiple sequence alignment and phylogenetic tree construction of applying the neighbor-joining method with Kimura's 2-parameter distance model and 1,000 bootstrap replicates (3,4).

An RT nested PCR designed specifically for this study was used for amplifying N gene sequences of HKU9-like viruses. Reaction conditions of this assay were same as the *RdRp* assay above except for the 1-step RT-PCR with outer forward primer 5-ATGTCTGGAMGGAATAAGCCCCG-3 and inner reverse primer 5-TTATTAGGATTACGDGTGCCCAT-3, and nested PCR with inner forward primer 5-GTTCAAGCAAGAATCTGACGGTT-3 and inner reverse primer 5-ACCTTCTTCACCCACCCAGTATA-3. The expect size of the second PCR product was 400 bp.

GenBank accession nos.: KT220528–KT220562, KT368821, KT581588–KT581603.

### **Serology**

A pseudo-particle neutralization assay was used to test bat serum against MERS-CoV as previously described (5).

### **Ethical Statement**

Ethics approval was obtained from St. Jude Children's Research Hospital Institutional Animal Use and Care Committee (Memphis, TN, USA). Swabs and tissues were tested by RT-PCR, and positive samples were sequenced.

## References

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5. Perera RA, Wang P, Gomaa MR, El-Shesheny R, Kandeil A, Bagato O, et al. Seroepidemiology for MERS coronavirus using microneutralisation and pseudoparticle virus neutralisation assays reveal a high prevalence of antibody in dromedary camels in Egypt, June 2013. *Euro Surveill.* 2013;18:20574. [PubMed http://dx.doi.org/10.2807/1560-7917.ES2013.18.36.20574](http://dx.doi.org/10.2807/1560-7917.ES2013.18.36.20574)

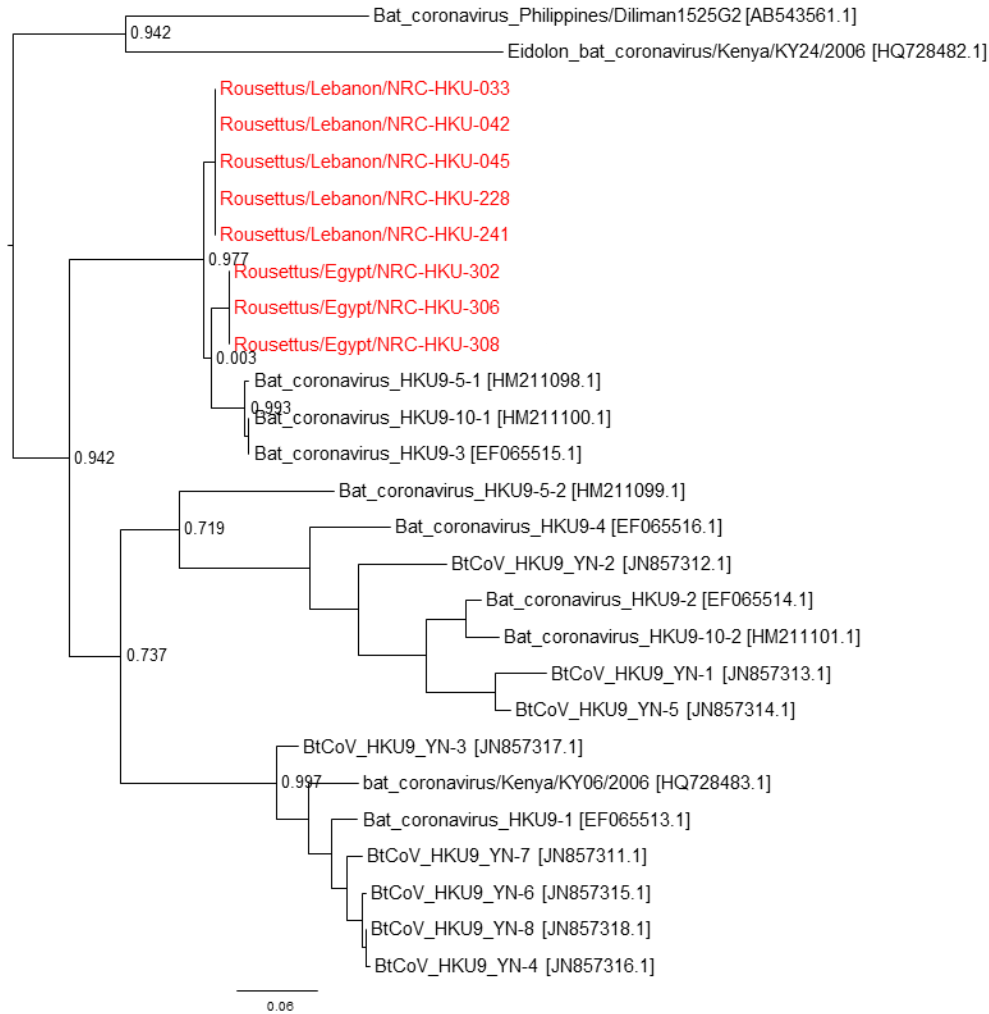
**Technical Appendix 1 Table 1.** Screening for coronaviruses in bats, Egypt, 2013–2015

Species	No bats	No. samples., type	Results	Location	Date
<i>Taphozous perforatus</i>	5	5 Serum 5 Oral 5 Lung 5 Liver		Abu-Rawwash, 13 km west of Cairo	Feb 2013
<i>T. perforatus</i>	52	52 Serum 52 Oral 52 Rectal		Abu-Rawwash, 13 km west of Cairo	Aug 2013
<i>T. perforatus</i>	25	24 Serum 25 Oral 25 Rectal		Abu-Rawwash, 13 km west of Cairo	Oct 2013
<i>Pipistrellus deserti</i>	29	29 Serum 29 Oral 29 Lung 29 Liver	1 (HKU9-like)	Abu-Rawwash, 13 km west of Cairo	Feb 2013
<i>P. deserti</i>	2	1 Serum 2 Oral 2 Rectal		Abu-Rawwash, 13 km west of Cairo	Oct 2013
<i>Rousettus aegyptiacus</i>	14	14 Serum 14 Oral 14 Lung	1 (murine hepatitis viru-like)	Cairo	Feb 2013
<i>R. aegyptiacus</i>	24	24 Serum 24 Oral 24 Lung 24 Liver	3 (HKU9-like) 2 (HKU9-like) 5 (HKU9-like)	Abu-Rawwash, 13 km west of Cairo	Feb 2013
<i>R. aegyptiacus</i>	5	4 Serum 5 Oral 5 Rectal	4 (HKU9-like)	Abu-Rawwash, 13 km west of Cairo	Oct 2013
<i>R. aegyptiacus</i>	102	101 Serum 102 Oral	2 (HKU9-like)	Abu-Rawwash, 13 km west of Cairo	Oct 2014
<i>R. aegyptiacus</i>	112	112 Serum	1 (HKU9-like)	Abu-Rawwash, 13 km west of Cairo	Nov 2014

Species	No bats	No. samples., type	Results	Location	Date
		112 Oral 112 Rectal			
Total	370		19 positive samples (5.14%)		

**Technical Appendix 1 Table 2.** Screening for coronaviruses in bats, Lebanon, 2013–2015

Species	No bats	Sample no. ,type	Result	Location	Date
<i>Rhinolophus hipposideros</i>	4	4 Serum 4 Rectal		Zgharta, North Lebanon	Oct 2013
<i>Rhinolophus ferrumequinum</i>	1	1 Serum 1 Rectal	1 (HKU9-like)	Aley, Mount Lebanon	Oct 2013
<i>Rhinolophus ferrumequinum</i>	2	2 Serum 2 Rectal		Amchit, North Lebanon	Oct 2013
<i>Miniopterus schreibersii</i>	6	6 Serum 6 Rectal		Amchit, North Lebanon	Oct 2013
<i>Rousettus aegyptiacus</i>	50	50 Serum 50 Rectal	4 (HKU9-like)	Akkar, North Lebanon	Oct 2013
<i>Rousettus aegyptiacus</i>	1	1 Serum 1 Rectal	1 (HKU9-like)	Amchit, North Lebanon	Oct 2013
<i>Rousettus aegyptiacus</i>	51	51 Serum 51 Rectal	1 (HKU9-like)	Bisri, South Lebanon	Oct 2013
<i>Rousettus aegyptiacus</i>	34	34 Serum 34 Rectal	3 (HKU9-like)	Antelias, Mount Lebanon	Oct 2013
<i>Rousettus aegyptiacus</i>	21	21 Serum 21 Rectal	5 (HKU9-like)	Ras Keefa, North Lebanon	Apr 2014
<i>Rousettus aegyptiacus</i>	5	5 Serum 5 Rectal		Berqayel, North Lebanon	Jun 2014
<i>Rousettus aegyptiacus</i>	75	72 Serum 75 Rectal	7 (HKU9-like)	Tripoli, North Lebanon	Jun 2014
<i>Rousettus aegyptiacus</i>	34	34 Serum 34 Rectal	3 (HKU9-like)	Antelias, Mount Lebanon	Sep 2014
<i>Rousettus aegyptiacus</i>	101	101 Serum 101 Rectal		Bisri, South Lebanon	Jun 2014
<i>Rousettus aegyptiacus</i>	30	30 Serum 30 Rectal		Jbeil, Mount Lebanon	Jun 2014
<i>Rousettus aegyptiacus</i>	32	32 Serum 32 Rectal		Edde, Mount Lebanon	Oct 2014
<i>Rousettus aegyptiacus</i>	4	4 Serum 4 Rectal		Karm Saddeh, North Lebanon	Apr 2015
Total	451		25 positive samples (5.54%)		



**Technical Appendix 1 Figure.** Phylogenetic tree of the coronavirus N gene. This tree was constructed on the basis of sequence alignment of 400 bp of the N gene and neighbor-joining method. Sequences in red are those found in this study. Scale bar indicates nucleotide substitutions per site.