Potential Zoonotic Pathogens Hosted by Endangered Bonobos

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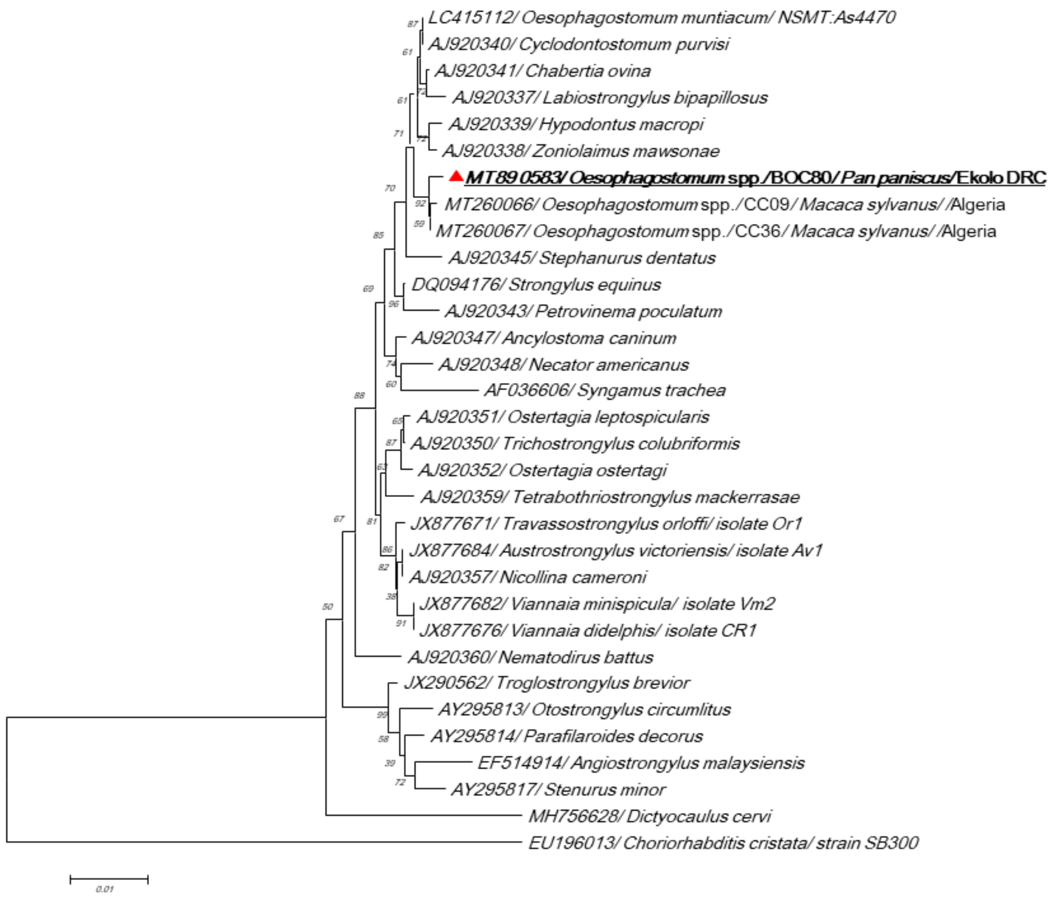

Fig. S1 Phylogenetic tree for *Nematoda* sp. detected on bonobo samples. The evolutionary history based on the *18S rRNA* partial gene, was inferred using the Neighbor-Joining method. Sequences are identified as follows: accession number/species/ strain/ host/ country. Sequences identified in this study showed >99.2 identity with *Oesophagostomum* spp.; sequences almost similar were also detected on Barbary macaques from Algeria. There were a total of 1083 positions in the final dataset. Evolutionary analyses were conducted in MEGA7.

Table S1. Primer and probe sequences used in this study for the bacteria

Bacteria	**Target gene**	**Primer name**	**Sequence (5'- 3')**	**Source**
Acinetobacter spp.	rpoB	Acineto-rpoBF	TACTCATATACCGAAAAGAAACGG	Bouvresse et al. 2011
		Acineto-rpoBR	GGYTTACCAAGRCTATACTCAAC	
		AcinetorpoB	6-FAM-CGCGAAGATATCGGTCTSCAAGC-TAMRA	
A. baumannii	*OmpA/MotB*	R	CGCTCTTGCCAGCATAAAGA	Ly et al. 2019
		F	TCAACATCACAATCTTTAGTAGCTGA	
		P	FAM_AAGTCGCCAAGAAACCTTGA-TAMRA	
Anaplasmataceae	23S	TtAna_F	TGACAGCGTACCTTTTGCAT	Dahmani et al. 2015
		TtAna_R	GTAACAGGTTCGGTCCTCCA	
		TtAna_P	6FAM- GGATTAGACCCGAAACCAAG-TAMRA	
Wolbachia spp.	16S	all.Wol.16S.301-F	TGGAACTGAGATACGGTCCAG	Laidoudi et al. 2020
		all.Wol.16S.301-R	GCACGGAGTTAGCCAGGACT	
		all.Wol.16S.301-P	6FAM-AATATTGGACAATGGGCGAA-TAMRA	
Bartonella spp.	ITS	Barto_ITS3_F	GATGCCGGGGAAGGTTTTC	Mourembou et al. 2015
		Barto_ITS3_R	GCCTGGGAGGACTTGAACCT	
		Barto_ITS3_P	6FAM- GCGCGCGCTTGATAAGCGTG-TAMRA	
Borrelia spp.	16S	Bor16S3F	AGC CTT TAA AGC TTC GCT TGT AG	Parola et al. 2011
		Bor16S3R	GCC TCC CGT AGG AGT CTG G	
		Bor16S3P	6FAM-CCG GCC TGA GAG GGT GAA CGG-TAMRA	
Coxiella burnetii	IS1111A	CB_IS1111_0706F	CAAGAAACGTATCGCTGTGGC	Mediannikov et al. 2010
		CB_IS1111_0706R	CACAGAGCCACCGTATGAATC	
		CB_IS1111_0706P	6FAM- CCGAGTTCGAAACAATGAGGGCTG-TAMRA	
Chlamydia spp.	23S	CHL23SUP	GGGGTTGTAGGGTYGAGRAIAWRRGATC	DeGraves et al. 2003
		CHL23SDN	GAGAGTGGTCTCCCCAGATTCARACTA	
		CHL23LCR	6FAM- CCTGAGTAGRRCTAGACACGTGAAAC-TAMRA	
Atopobium vaginae	16S	Atop_F	CCCTATCCGCTCCTGATACC	Fenollar et al. 2008
		Atop_R	CCAAATATCTGCGCATTTCA	
		Atop_P	VIC-GCAGGCTTGAGTCTGGTAGGGGA-TAMRA	
Neisseria gonorrhoeae	Hypothetical proteine	Ngono_2F	CATCAGCGCAATCCCTATGA	Hopkins et al. 2010
		Ngono_2R	TGGTTGTCCTCAACCGTGTC	
		Ngono_2 P	6FAM- CCACGGCGCTTCCTGATGGG-TAMRA	
	PorA	Pap-Tm-F	CAGCATTCAATTTGTTCCGAGTC	
		Pap-Tm-R	GAACTGGTTTCATCTGATTACTTTCCA	
		Pap-Tm-P	6FAM- CGCCTATACGCCTGCTACTTTCACGC	
Gardnerella vaginalis	Cpn60	Gvaginalis_F	CGCATCTGCTAAGGATGTTG	Fenollar et al. 2008
		Gvaginalis_R	CAGCAATCTTTTCGCCAACT	
		Gvaginalis_P	VIC-TGCAACTATTTCTGCAGCAGATCCT-TAMRA	
Helicobacter pylori	23S rRNA	HPY_F	AGGTTAAGAGGATGCGTCAGTC	Menard et al. 2002
		HPY_R	CGCATGATATTCCCATTAGCAGT	
		HPY_P	6FAM-TGGGAGCTGTCTCAACCAGAGATTCAGTG-TAMRA	
Leptospira spp.	16S	Lepto 171F	CCCGCGTCCGATTAG	Smythe et al. 2002
		Lepto 258R	TCCATTGTGGCCGRA/GACAC	
		Lepto P	6-FAM- CTCACCAAGGCGACGATCGGTAGC-TAMRA	
Mycoplasma spp.	ITS1	Mycop_ITS1_F	GGGAGCTGGTAATACCCAAAGT	Cohen et al. 2011
		Mycop_ITS1_R	CCATCCCCACGTTCTCGTAG	
		Mycop_ITS1_P	6FAM- GCCTAAGGTAGGACTGGTGACTGGGG-TAMRA	
Mycobacterium spp.	ITS	Mycob_ITS_F	GGGTGGGGTGTGGTGTTTGA	Bruijnesteijn et al. 2004
		Mycob_ITS_R	CAAGGCATCCACCATGCGC	
		Mycob_ITS_P	6FAM- TGGATAGTGGTTGCGAGCATC-TAMRA	

	ITS	Mtub_ITS_P	6FAM- GCTAGCCGGCAGCGTATCCAT-TAMRA	
M. genitalium	*FusA*	Mgen_fusA_F	CTGGGAAAACCACCACATCA	Edouard et al. 2017
		Mgen_fusA_R	CACTGAAGTGGCTGCAGAGG	
		Mgen_fusA_P	6FAM-TGGTGAATCAGTGATGGACTGGATGGA-TAMRA	
Rickettsia felis	*bioB*	Rfelis_0527_F	ATGTTCGGGCTTCCGGTATG	Mourembou et al. 2015
		Rfelis_0527_R	CCGATTCAGCAGGTTCTTCAA	
		Rfelis_0527_P	6FAM- GCTGCGGCGGTATTTTAGGAATGGG-TAMRA	
Salmonella spp.	*invA*	invA_F	TCTGTTTACCGGGCATACCA	Mourembou et al. 2015
		invA_R	CACCGTGGTCCAGTTTATCG	
		invA_P	6FAM- CCAGAGAAAATCGGGCCGCG-TAMRA	
	sipC	sipC_F	GTCAGGCGTCGTAAAAGCTG	Mourembou et al. 2015
		sipC_R	ACGTCGACTGGTGGTACTGG	
		sipC P	6FAM- CTCCAGGCGCGAACAGCTGG-TAMRA	
Salmonella typhi	*hypothetical protein*	Styphi_put_F	TCTCATGCTGCGACCTCAAA	
		Styphi_put_R	TTCATCCTGGTCCGGTGTCT	
		Styphi_put_P	6FAM- GCTTTTTGTGAAGCAACGCTGGCA-TAMRA	
Salmonella typhi/paratyphi	*narG*	Styphi_narG_F	GCGCCACATCTTCATCAGAC	
		Styphi_narG_R	CCCGTCCTGATATGCCAAAC	
		Styphi_narG_P	6FAM- AGTAACTTGCCCCGCGCGGG-TAMRA	
Staphylococcus aureus	*NucA*	Saur_NucA_F2	GTTGTGGATGGTGATACATTTATTGC	Mourembou et al. 2015
		Saur_NucA_R2	CCAAATGGTTGTACAGGCGTATTC	
		Saur_NucA_P2	6FAM- AGGCTTATAGGGGTTGATACGCCAGAAACGG-TAMRA	
	Amidohydrolase	Saur_Amido_F	CCTCGACAGGTAACGCATCA	
		Saur_Amido_R	AAACTCCTATCGGCCGCAAT	
		Saur_Amido_P	6FAM- TGCAATGGTAGGTCCTGTGCCCA	
Treponema spp.	23S	forw2570	CGCCGTCACTTAACGGAYA	This study
		rev2660	GATGCGATGAGCCGACAT	
		sonde2620	6FAM- CCCCAAGAGTTCACATCGAC-TAMRA	
Treponema pallidum	PolA	polA SyphT_F1	GTCGAGACTGAAAAGGAGTGCA	Leisli et al. 2007
		SyphT_R1	GTGAGCGTCTCATCATTCCAAAG	
		SyphT_P1	FAM- TGCTGTGCAGGATCCGGCATATGTCC-TAMRA	
	Fla A	Tpal_flaA_F	GCGGTTGCACAGTGGGAG	Salazar et al. 2007
		Tpal_flaA_R	CAGCATGGGCGACAGGAT	
		Tpal_flaA_P	FAM- TTGTGCTGAATTCTTCCGCGCG-TAMRA	
Tropheryma whipplei	WiSP family protein (whi 2)	T_whi2_F	TTGTGTATTTGGTATTAGATGAAACAG	Fenollar et al. 2010
		T_whi2_R	CCCTACAATATGAAACAGCCTTTG	
		T_whi2_P	6FAM- GGGATAGAGCAGGAGGTGTCTGTCTGG-TAMRA	
	WiSP family protein (whi 3)	T_whi3_F	TTGTGTATTTGGTATTAGATGAAACAG	
		T_whi3_R	CCCTACAATATGAAACAGCCTTTG	
		T_whi3_P	6FAM-GGGATAGAGCAGGAGGTGTCTGTCTGG-TAMRA	
Listeria monocytogenes	hlyQ	Lmo_hlyQ_F	CATGGCACCACCAGCATC	Fal et al. 2019
		Lmo_hlyQ_R	ATCCGCGTGTTTCTTTTCGA	
		Lmo_hlyQ_P	6FAM- CGCCTGCAAGTCCTAAGACGCCA-TAMRA	
Clostridium difficile	C. difficile Toxine A	Cdiff_tcdA_F	GGTAATAATTCAAAAGCGGCT	Luna et al. 2011
		Cdiff_tcdA_R	AGCATCCGTATTAGCAGGTG	
		Cdiff_tcdA_P	6FAM- AGCCTAATACAGCTATGGGTGCGAAG-TAMRA	
	C. difficile Toxine B	Cdiff_tcdB_F	GAAAGTCCAAGTTTACGCTCAAT	
		Cdiff_tcdB_R	GCTGCACCTAAACTTACACCA	
		Cdiff_tcdB_P	VIC- ACAGATGCAGCCAAAGTTGTTGAATT-TAMRA	
Yersinia pestis	pLA	YPpla S	GTAATAGGTTATAACCAGCGCTT	

		YPpla R	AGACTTTGGCATTAGGTGTG	Riehm et al. 2011
		YP pla TM	6FAM-ATGCCATATATTGGACTTGCAGGCCAGT-BBQ	
Vibrio cholerae	toxR	toxR-F1	CCGAATAACCACCCTGATCTTT	Greig et al. 2018
		toxR-R1	ACCTGTGGCAATGACTTCTATC	
		toxR-Pr	6FAM -ACTGGCTACCGTCAATCGAACTGT- TAMRA	

Table S2. Primer and probe sequences used in this study for the parasites

Parasites	**Target gene**	**Primer name**	**Sequence (5'- 3')**	**Source**
Ancylostoma duodenale	ITS2	Ad125F	GAATGACAGCAAACTCGTTGTTG	Verweij et al. 2007
		Ad195R	ATACTAGCCACTGCCGAAACGT	
		Ad155-XS	6FAM-ATCGTTTACCGACTTTAG-MGB	
Ascaris lumbricoides	ITS1	Alum96F	GTAATAGCAGTCGGCGGTTTCTT	Wiria et al. 2010
		Alum183R	GCCCAACATGCCACCTATTC	
		Alum124T	6FAM- TTGGCGGACAATTGCATGCGAT-TAMRA	
Cryptosporidium parvum; C. hominis	hsp70 gene	1PSF	AACTTTAGCTCCAGTTGAGAAAGTACTC	Garcés-Sanchez et al. 2002
		1PSR	AACTTTAGCTCCAGTTGAGAAAGTACTC	
		Crypt P	6FAM-AATACGTGTAGAACCACCAACCAATACAACATC-TAMRA	
Cyclospora cayetanensis	18s	Cyclo250F	TAGTAACCGAACGGATCGCATT	Verweij et al. 2003
		Cyclo350R	AATGCCACGTAGGCCAATA	
		Cyclo281T	6FAM-CCGGCGATAGATCATTCAAGTTTCTGACC-TAMRA	
Entamoeba histolytica	18S	Ehf	AACAGTAATAGTTTCTTTGGTTAGTAAAA	Roy et al. 2005
		Ehr	CTTAGAATGTCATTTCTCAATTCAT	
		Ehp	6FAM-ATTAGTACAAAATGGCCAATTCATTCA-TAMRA	
Enterobius vermicularis	5S	EnterF	TTTCCAAGCCACAGACTCAC	Sow et al. 2017
		EnterR	ATTGCTCGTTTGCCGATTAT	
		EnterP	TCATGTCTGAGCCGGAACGAGA	
Filariae	28S	qFil-28S-F	TTGTTTGAGATTGCAGCCCA	Laidoudi et al. 2019
		qFil-28S-R	GTTTCCATCTCAGCGGTTTC	
		qFil-28S-S	6FAM-CAAGTACCGTGAGGGAAAGT-TAMRA	
Giardia lamblia (intestinalis or duodenalis)	18S	Giardia-80F	GACGGCTCAGGACAACGGTT	Verweij 2004
		Giardia-127R	TTGCCAGCGGTGTCCG	
		Giardia-105T	6FAM-CCCGCGGCGGTCCCTGCTAG-TAMRA	
Kinetoplastida spp.	28S	F. 24a.5198	AGTATTGAGCCAAAGAAGG	Medkour et al. 2020
		R. 24a.5412	TTGTCACGACTTCAGGTTCTAT	
		P. 24a.5345	6FAM-TAGGAAGACCGATAGCGAACAAGTAG-TAMRA	
Leishmania spp.	18S	F	GGTTTAGTGCGTCCGGTG	Medkour et al. 2020
		R	ACGCCCCAGTACGTTCTCC	
		P	6FAM- CGGCCGTAACGCCTTTTCAACTCA-TAMRA	
Loa loa	LL20 15kDa ladder antigen	15r3-5	CGAAAAATTATAGGGGGAAAC	Touré et al. 1997
		15r3-6	TCGTAGACCAAACTGCGAAC	
		15r3-P	6FAM- TCAAGAGCCGATATACTGAAAGCTATC-TAMRA	
Mansonella spp.	ITS1	Forward	CCTGCGGAAGGATCATTAAC	Bassene et al. 2015
		Reverse	ATCGACGGTTTAGGCGATAA	
		Probe	6FAM-CGGTGATATTCGTTGGTGTCT-TAMRA	
Mansonella perstans	ITS1	Forward	AGGATCATTAACGAGCTTCC	
		Reverse	CGAATATCACCGTTAATTCAGT	
		Probe	6FAM-TTCACTTTTATTTAGCAACATGCA-TAMRA	
Necator americanus	ITS2	Na58F	CTGTTTGTCGAACGGTACTTGC	Verweij 2007
		Na158R	ATAACAGCGTGCACATGTTGC	
		Na81T	6FAM- CTGTACTACGCATTGTATAC -MGB	
Nematoda	5S	qNem.5S.1f	ACCACGTTGAAAGCACGMC	

		qNem.5S.110r	TGTCTACAACACCTSGRATTCC	Laidoudi et al. 2020
		qNem.5S.38p	6FAM-AGTTAAGCAACGTTGGGCC-TAMRA	
Plasmodium spp.	Cox	Plasmo_cox_15_F	AGGAACTCGACTGGCCTACA	Mourembou et al. 2015
		Plasmo_cox_16_R	CCAGCGACAGCGGTTATACT	
		Plasmo-cox_P	6FAM- CGAACGCTTTTAACGCCTGACATGG-TAMRA	
Strongyloides stercoralis	18S	Stro-1530F	GAATTCCAAGTAAACGTAAGTCATTAGC	Verweij et al. 2009
		Stro-1630R	TGCCTCTGGATATTGCTCAGTTC	
		Stro-1586T	6FAM-ACACACCGGCCGTCGCTGC-TAMRA	
Physaloptera spp.	12S	Phy.12S.f.204	GAATTGGATTAGTACCCAAGTAAGTG	Laidoudi et al. 2020
		Phy.12S.r.305	TGTTCCAAAAATCTTTCTAAGATCAG	
		Phy.12S.242p	VIC-GCGGGAGTAAAGTTAAGTTTAAACC-TAMRA	
Taenia saginata	ITS	Tsol_ 145F	ATGGATCAATCTGGGTGGAGTT	Praet et al. 2013
		Tsol_ 230R	ATCGCAGGGTAAGAAAAGAAGGT	
		Tsol_169Tq	6FAM-TGGTACTGCTGTGGCGGCGG-TAMRA	
Taenia solium	ITS	Tsag_F529	GCGTCGTCTTTGCGTTACAC	
		Tsag_R607	TGACACAACCGCGCTCTG	
		Tsag_581Tq	6FAM-CCACAGCACCAGCGACAGCAGCAA-TAMRA	
Toxoplasma gondii		Tgon_ITS1_F	GATTTGCATTCAAGAAGCGTGATAGTA	Jauregui et al. 2001
		Tgon_ITS1_R	AGTTTAGGAAGCAATCTGAAAGCACATC	
		Tgon_ITS1_P	6FAM-CTGCGCTGCTTCCAATATTGG-TAMRA	
Trichuris trichiura	18S	TrichF	TTGAAACGACTTGCTCATCAACTT	Liu 2013
		TrichR	CTGATTCTCCGTTAACCGTTGTC	
		TrichP	6FAM-CGATGGTACGCTACGTGCTTACCATGG-TAMRA	

Table S3. Primer and probe sequences used in this study for viruses

Virus	Target gene	Primer name	Sequence (5'- 3')	Source
DNA Extraction control	Phage T4	T4F	CCATCCATAGAGAAAATATCAGAACGA	Ninove et al. 2011
		T4R	TAAATAATTCCTCTTTTCCCAGCG	
		T4P	VIC- AACCAGTAATTTCATCTGCTTCTGATGTGAGGC-TAMRA	
RNA Extraction control	Phage MS2	MS2F	CTCTGAGAGCGGCTCTATTGGT	
		MS2R	GTTCCCTACAACGAGCCTAAATTC	
		MS2P	VIC- TCAGACACGCGGTCCGCTATAACGA-TAMRA	
Adenovirus (Adv.)	hexon gene	AQ1	GCCACGGTGGGGTTTCTAAACTT	Heim et al. 2003
		AQ2	GCCCCAGTGGTCTTACATGCACATC	
		AP	6FAM-TGCACCAGACCCGGGCTCAGGTACTCCGA-TAMRA	
Coronavirus	The ARGENE kit of the HCoH / HPIV r-gene complex, which allows the detection of 4 species of HCoH (NL63, 0C43, HKLU1 and 229E) and of HPIV (HPIV-1, HPIV2, HPIV3 and HPIV4), was used according to the manufacturer's recommendations (ARGENE, HCoH / HPIV r-gene, Biomerieux SA, France). (bioMérieux, https://www.biomerieux-diagnostics.com)			
Sarbecovirus	ORF1b-nsp14	HKU-ORF1b-nsp14F	TGGGGYTTTACRGGTAACCT	WHO, Korea
		HKU- ORF1b-nsp14R	AACRCGCTTAACAAAGCACTC	
		HKU-ORF1b-nsp141P	6FAM-TAGTTGTGATGCWATCATGACTAG-TAMRA	
	N	HKU-NF	TAATCAGACAAGGAACTGATTA	
		HKU-NR	CGAAGGTGTGACTTCCATG	
		HKU-NP	6FAM-GCAAATTGTGCAATTTGCGG- TAMRA	
Sars-Cov 2	E	E_Sarbeco_F1	ACAGGTACGTTAATAGTTAATAGCGT	Corman et al. 2020
		E_Sarbeco_R2	ATATTGCAGCAGTACGCACACA	
		E_Sarbeco_P1	FAM-ACACTAGCCATCCTTACTGCGCTTCG-QSY	
Enterovirus (EV)	5' UTR	HevFwd356	GCTGCGYTGGCGGCC	Tapparel et al. 2009
		EV PICO R	GAAACACGGACACCCAAAGTAGT	

		EV PICOPro	6FAM -CTCCGGCCCCTGAATGYGGCTAA-TAMRA	
Hepatitis A virus (HAV)	VP1	HavMrsRTfwd	GGTAGGCTACGGGTGAAAC	Motte et al. 2009
		HavMrsRTRev	GCGGATATTGGTGAGTTGTT	
		HavMrsPr	6FAM-CTTARGCTARTACTTCTATGAAGAGATGC-TAMRA	
Hepatitis E virus (HEV)	ORF3	HEVORF3-S	GGT GGT TTC TGG GGT GAC	Izopet et al. 2012
		HEVORF3-AS	AGG GGT TGG TTG GAT GAA	
		HEVORF3-P	6FAM -TGATTCTCAGCCCTTCGC- TAMRA	
Herpes simplex virus (HSV)	DNA polymerase gene	HSV DNA POL sens	CATCACCGACCCGGAGAGGGAC	Kessler et al. 2000
		HSV DNA POLrev	GGGCCAGGCGCTTGTTGGTGTA	
		HSV DNA POL PROBE	6FAM-CCGCCGAACTGAGCAGACACCCGCGC-TAMRA	
Norovirus GG2	ORF1 and ORF2	NV117	TCGACGCCATCTTCATTCA	Höhne et Schreier, 2004
		NV107a	AGCCAATGTTCAGATGGATG	
		NoroGGII_TM3	6FAM-TGGGAGGGCGATCGCAATCTGGC-TAMRA	
Parechovirus (HPeV)	Polyprotein gene	PeV_F	CTGGGGCCAAAAGCCA	Benschop et al. 2010
		PeV_R	GGTACCTTCTGGGCATCCTTC	
		PeV_P	6FAM- AAACACTAGTTGTAWGGCCC-TAMRA	
Rotavirus	NSP3	Rota-2-F	ACCATCTWCACRTRACCCTCTATGAG	Zeng et al. 2008
		Rota-2-R	GGTCACATAACGCCCCTATAGC	
		Rota-2-P	6FAM -AGTTAAAAGCTAACACTGTCAAA-TAMRA	
Simian immunodeficiency virus (SIV)	gag	SIVsmE660 Forward	GCAGAGACATCTAGTGGTGGAAAC	Monjure et al. 2014
		SIVsmE660 Reverse	GTAATTTCCTCCTCTGCCACTAGG	
		SIVsmE660 Probe	6FAM-AATGCCAGCAACAAGCAGACCAACAGCA IA-BKFQ	
Poxvirus	Humagglitunin	OPV_HA_F	TGATGCAACTCTATCATGTARTCG	Andreani et al. 2019
		OPV_HA_R	CAAGACGTCGCTTTTRGCAG	
		OPV_HA_P	6FAM- TGCTTGGTATAAGGAGCCCAATTCCA	
Sapovirus	Polymerase/ capsid junction	sapo.fwdA	ACC AGG CTC TCG CCA CCT A	Logan et al. 2007
		sapo.fwdB	ATT TGG CCC TCG CCA CCT A	
		sapo.rev	GCC CTC CAT YTC AAA CAC TAW TTT	
		sapo.probeA	6FAM -CTG TAC CAC CTA TGA ACC A-TAMRA	
		sapo.probeB	6FAM -TTG TAC CAC CTA TGA ACC A-TAMRA	
		sapo.probeC	6FAM -TGT ACC ACC TAT AAA CCA-TAMRA	
		sapo.probeD	6FAM -TGC ACC ACC TAT GAA C-TAMRA	

Table S4. Primers used in standard PCRs and sequencing.

Microorganisms	**Target gene**	**Primer name**	**Sequence (5'- 3')**	**Length and Tm**	**Source**
Papillomavirus (HPV)	L1 gene	MY09	GCMCAGGGWCATAATAATGG	2 runs of PCR, the first at Tm: 52°C; the second at Tm: 55°C.	Tamalet C et al. 2010
		MY11	CGTCCMARRGGAWACTGATC		
EMCV	3D Protein	P1	CCCTACCTCACGGAATGGGGCAAAG	Nested PCR: P1/F1 (400 bp) at 55°C; then F2/R2 (250 bp) at 55°C	This study
		F1	TTATWATTAGGGCIGGYTTG		
		F2	CTAGCAAAGACAGGRTAYAA		
		R2	ACGRAAIGGGGCAAAGAG		
ECMV64SPU/03 (Congo)		ECMV64SPU/03 F	CGCAAAGACAGGATATAAGATAACAC		
		ECMV64SPU/03 R	ACTCTTGCTTGCCAGAATGTA		
Adenoviruses (AdVs)	DNA polymerase	Fw Outer	TGATGCGYTTCTTACCTYTGGTYTCCATGAG	Nested PCR, ≈1400 bp at 58°C ≈250 bp at 55°C	Roy et al. 2009
		Rw Outer	AGTTYTACATGCTGGGCTCTTACCG		
		Fw inner	GTGACAAAGAGGCTGTCCGTGTCCCCGTA		

		Rw inner	TCACGTGGCCTACACTTACAAGCCAATCAC		
Metazoans	Cox1	dgLCO-1490	GGTCAACAAATCATAAAGAYATYGG	708 bp, Tm: 44°C	Folmer et al. 1994
		dgHCO-2198	TAAACTTCAGGGTGACCAAARAAYCA		
Nematoda	18S	Fwd.18S.631	TCGTCATTGCTGCGGTTAAA	1127–1155 bp at 54°C	Laidoudi et al. 2019
		Rwd.18S.1825r	GGTTCAAGCCACTGCGATTAA		
Helminth	28S	Hspec.28S. 5748f	GGTAAGGGAAGTCGGCAAAT	400 bp at 56°C	Medkour et al. 2020
		Hspec.28S.6394r	AGGGACAGTGGGAATCTCG		
Oesophagostomum spp.	ITS2	NC1	TTAGTTTCTTTTCCTCCGCT	1) NC1/ NC2 (280 - 400 bp), Tm: 50°C 2) NC2/ OesophITS2-21 (260 bp), Tm: 55°C	Ghai et al. 2014
		NC2	ACGTCTGGTTCAGGGTTGTT		
		OesophITS2-21	TGTRACACTGTTTGTCGAAC		
Kinetoplastida	18S	F720	GTTAAAGGGTTCGTAGTTGAA	750 bp, Tm: 50°C	Keita et al. 2020
		R1495	GACTACAATGGTCTCTAATCA		
Leptospira spp.	Adk	F	GGGCTGGAAAAGGTACACAA	531 bp, Tm: 53°C	Ahmed et al. 2006
		R	ACGCAAGCTCCTTTTGAATC		
	icdA	F	GGGACGAGATGACCAGGAT	674 bp, Tm: 53°C	
		R	TTTTTTGAGATCCGCAGCTTT		
	LipL41	F	TAGGAAATTGCGCAGCTACA	520 bp, Tm: 53°C	
		R	GCATCGAGAGGAATTAACATCA		
	rrs2	F	CATGCAAGTCAAGCGGAGTA	541 bp, Tm: 53°C	
		R	AGTTGAGCCCGCAGTTTTC		
	SecY	F	ATGCCGATCATTTTTGCTTC	549 bp, Tm: 53°C	
		R	CCGTCCCTTAATTTTAGACTTCTTC		
	LipL32	F	ATCTCCGTTGCACTCTTTGC	474 bp, Tm: 53°C	
		R	ACCATCATCATCATCGTCCA		
	16S	F 16S 37-56	CGGCGCGTCTTAAACATGCA	1125 pb, Tm: 53°C	This study
		F2 16S 397-419	GAAGGTCTTCGGATTGTAAAGT		
		R 16S 857-877	CACTCTTGCGAGCATAGTCC		
		R2 16S 1162-1183	ACATAAAGGCCATGAGGATTTG		
	23S	F 23S 1326-1345	CGGCGCGTCTTAAACATGCA	1100 bp, Tm: 53°C	
		F2 23S 1745-1764	TAAGGAACTCGGCAAATTAC		
		R 23S 1942-1962	AGCTTCGCATTGCTGCTAAC		
		R2 23S 2409-2434	GTCTCACAGTTAAGCTCCCTTATGCC		
	LipL32	F LipL32 34-53	GCACTCTTTGCAAGCATTAC	620 bp, Tm: 53°C	
		R LipL 32 653-673	ATCCTTTCACTTCACCTGGTT		
	LipL 41	F LipL41 83-103	ATCCGGTATTCCCGAAAGATA	600 bp, Tm: 50°C	
		R LipL41 682-700	CTTCRTCCAAWCCTTGTCC		
	LipL 71	F LipL71 437-456	CGAACCACATAACGTTTCCA	645 bp, Tm: 45°C	
		R LipL71 1073-1092	AAACAACAAYTAATCGATTC		
	Yidc	F Yidc 49-68	GGAATTTGGATGGGAGTGAA	880 bp, Tm: 51°C	
		F2 Yidc 348-363	TTCAAGTTGCTCGTAA		
		R Yidc 920-942	ATAAAATAACGAGAACCMGTTCC		
Treponema spp.	23S	F1- 3274	GGGAGTGAGACTGCGIGCG	F1/R2: ≈900 bp, Tm: 57°C	This study
		F2- 3592	GAGAATGCAGGYATAAGTA		
		R1- 3671	CCGRCTTACCCTGRGSAGAT		
		R2- 4163	GGTGTCASCMCCTATACGTCYCAT		
Mycobacterium spp.	rpoB	MycoF	GGCAAGGTCACCCCGAAGGG	764 bp, Tm: 64°C	Adékombi et al. 2003
		MycoR	AGCGGCTGCTGGGTGATCATC		

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Supplementary material S1. Sequences used for primer design.

A. Sequences used for design of primers for *Treponema* spp.:

NR_076531.1_Treponema_pallidum_subsp._pallidum_strain_SS14;
JX120546.1_Treponema_paraluiscuniculi_strain_Cuniculi_A ; NR_076899.1_Treponema_caldarium_strain_H1 ;
NR_076709.1_Treponema_primitia_strain_ZAS-2 ; NR_076878.1_Treponema_brennaborense_strain_DD5/3 ;
NR_076766.1_Treponema_paraluiscuniculi_strain_Cuniculi_A ; NR_076212.1_Treponema_denticola_strain_ATCC_35405;
NR_076708.1_Treponema_azotonutricium_strain_ZAS-9; NR_103187.1_Borrelia_hermsii_HS1_strain_DAH;
NR_103185.1_Borrelia_turicatae; NR_076567.1_Borrelia_recurrentis_strain_A1;
NR_103181.1_Borrelia_crocidurae_strain_Achema; NR_103969.1_Borrelia_burgdorferi;
NR_103964.1_Leptospira_biflexa_serovar_Patoc_strain_Patoc_1;
NR_076199.1_Leptospira_interrogans_serovar_Copenhageni_strain_Fiocruz_L1-130; X14249.1_Leptospira_interrogans;
NR_103021.1_Brachyspira_intermedia_strain_PWS/A; NR_076731.1_Brachyspira_murdochii_strain_56-150;
NR_076624.1_Brachyspira_hyodysenteriae_strain_WA1

B. Sequences used for design of primers for *EMCV*:

KM269482.1_ Encephalomyocarditis_virus_strain_ATCC_VR-129B;
JQ864080.1_Encephalomyocarditis_virus_isolate_HB10 ; GU181317_strain_SPU_64/03_Bonobo_RDC ;
DQ835185_strain_1086C_Rattus_Belgium;
AJ235731.1_Encephalomyocarditis_virus_mRNA_for_3D_pigs_rodents_in_Europe;
AJ235728.1_EEncephalomyocarditis_virus_mRNA_for_3D_pigs_rodents_in_Europe;
DQ294633.1_Mengo_virus_isolate_in_cell_culture; L22089.1_Mengo_virus_isolate_M;
DQ835185.2_Encephalomyocarditis_virus_strain_1086C; KU955338.1_Mengo_virus_strain_AnrB-3741;
AJ235733.1_Encephalomyocarditis_virus_mRNA_for_3Dpol_protein_strain_ITL-135/86;
AY296731.1_Encephalomyocarditis_virus_EMCV-30; X87335.1_Encephalomyocarditis_virus;
M37588.1_Encephalomyocarditis_virus_diabetogenic_variant_(D_variant_ifp-_phenotype);
M22457.1_Encephalomyocarditis_(EMC)_virus_EMC-B; KC310738.1_Encephalomyocarditis_virus_isolate_Sing-M105-02; KC310737.1_Encephalomyocarditis_virus_isolate_Sing-M100-02;

C. Sequences used for design of primers for *Leptospira* spp.:

As the same manner, we used sequences available in GenBank databases of *Leptospira* spp., and we designed primers targeting all of 16S, 23S, LipL 32, LipL 41, LipL 71 and YidC genes.