Supplementary material

Molecular identification of *Sarcocystis halieti* n. sp., *Sarcocystis lari* and *Sarcocystis truncata* in the intestine of a white-tailed sea eagle (*Haliaeetus albicilla*) in Norway

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Table S1
Primers used to amplify the four DNA regions examined in the present study.

DNA region	Primer name	Primer sequence	References
18S rRNA gene	ERIB1	ACC TGG TTG ATC CTG CCA G	Barta et al., 1997
	S2r	CTG ATC GTC TTC GAG CCC CTA	Fischer and Odening, 1998
	S3f	TTG TTA AAG ACG AAC TAC TGC G	Fischer and Odening, 1998
	Primer BSarc	GAT CCT TCC GCA GGT TCA CCT AC	Gjerde, 2014a
	A1F	CAC ATA CCT CTT CCC TCG TG	This study
	A2F	ATC CTC CTG ATT GGT GTC ATC	This study
	A2R	AAT GAA GTG ATG ATG ACA CCA ATC	This study
ITS1	SU1F	GAT TGA GTG TTC CGG TGA ATT ATT	Gjerde, 2014b
	5.8SR2	AAG GTG CCA TTT GCG TTC AGA A	Gjerde, 2014b
28S rRNA gene	KL1	TAC CCG CTG AAC TTA AGC	Mugridge et al., 1999
	KL3	CCA CCA AGA TCT GCA CTA G	Mugridge et al., 1999
cox1	SF1	ATG GCG TAC AAC AAT CAT AAA GAA	Gjerde, 2013
	SR5	TAG GTA TCA TGT AAC GCA ATA TCC AT	Gjerde, 2013
	SF4[a]	TAC TTA CGG CNG GYA TCT TTA G	Gjerde et al., 2017
	SR8D	CAT TGC CCA TDA CTA CGC C	Gjerde, 2013

[a] The sequence of primer SF4 was unfortunately given in its reverse complementary form in Table S2 of the Supplementary material of Gjerde et al., 2017.

References for primers

Barta, J.R., Martin, D.S., Liberator, P.A., Dashkevicz, M., Anderson, J.W., Feighner, S.D., Elbrecht, A., Perkins-Barrow, A., Jenkins, M.C., Danforth, H.D., Ruff, M.D., Profous-Juchelka, H., 1997. Phylogenetic relationships among eight *Eimeria* species infecting domestic fowl inferred using complete small subunit ribosomal DNA sequences. J. Parasitol. 83, 262–271. http://dx.doi.org/10.2307/3284453.

Fischer, S., Odening, K., 1998. Characterization of bovine *Sarcocystis* species by analysis of their 18S ribosomal DNA sequences. J. Parasitol. 84, 50–54. http://dx.doi.org/10.2307/3284529.

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Mugridge, N.B., Morrison, D.A., Johnson, A.M., Luton, K., Dubey, J.P., Votýpka, J., Tenter, A.M., 1999. Phylogenetic relationships of the genus *Frenkelia*: a review of its history and new knowledge gained from comparison of large subunit ribosomal ribonucleic acid gene sequences. Int. J. Parasitol. 29, 957–972. http://doi.org/10.1016/S0020-7519(99)00062-4.

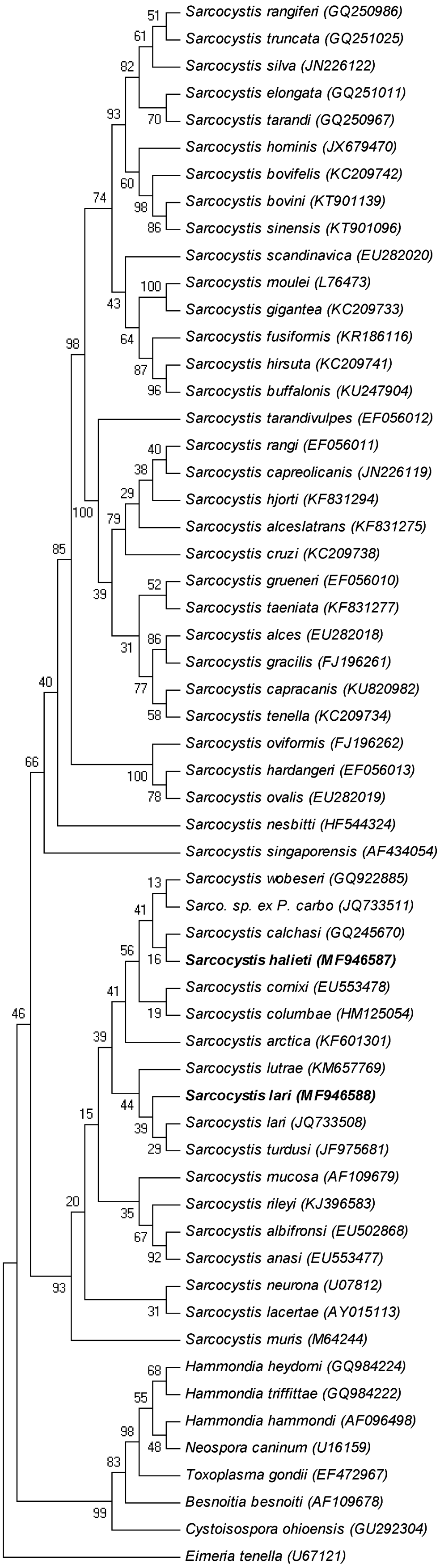
Table S2

Identity of the new *cox1* sequences of *S. halieti* (GenBank acc. no. MF946583) and *S. lari* (GenBank acc. no. MF946584) with the most similar sequences available in GenBank (as of October 2017).

Species	**GenBank acc. no.**	***S. halieti***	***S. lari***
S. halieti	MF946583		1051/1053 nt (99.8%)
S. lutrae	KM657808–KM657809; KF601326–KF601327	1051/1053 nt (99.8%)	1053/1053 (100%)
S. turdusi	KT588511–KT588518	1051/1053 nt (99.8%)	1049/1053 nt (99.6%
S. jamaicensis	KY995652	1050/1053 nt (99.7%)	1050/1053 nt (99.7%)
S. arctica	KF601318–KF601324	1045/1053 nt (99.2%)	1047/1053 nt (99.4%)
S. canis	KX721495	1044/1053 nt (99.1%)	1046/1053 nt (99.3%)
S. strixi	MF162317	1038/1045 nt (99.3%)	1040/1045 nt (99.5%)
S. speeri	KT207461	1040/1052 nt (98.9%)	1042/1052 nt (99.0%)
S. neurona	EST contig[a]	1041/1052 nt (98.9%)	1043/1053 nt (99.1%)
S. calchasi	KU220952	626/626 nt (100%)	625/626 nt (99.8%)
Sarcoystis sp. *ex A. cooperii*	KY348756	899/900 nt (99.9%)	899/900 nt (99.9%)
S. rileyi	KJ396582	1021/1053 nt (97.0%)	1021/1053 nt (97.0%)

[a] The *cox1* sequence (1,095 bp) of *S. neurona* was artificially concatenated from expressed sequence tags (ESTs) downloaded from GenBank as described by Gjerde and Schulze, 2014 (Parasitol. Res. 113, 811–821. http://dx.doi.org/10.1007/s00436-013-3711-x). The sequence is available in the Supplementary material of that paper.

Fig. S1. Phylogenetic tree for members of the Sarcocystidae based on 58 sequences of the near complete 18S rRNA gene of 56 taxa and inferred using the using the maximum likelihood method based on the Hasegawa–Kishino–Yano model with gamma distribution and invariable sites. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates) is shown next to the branches. The two new sequences from the present study are in boldface.



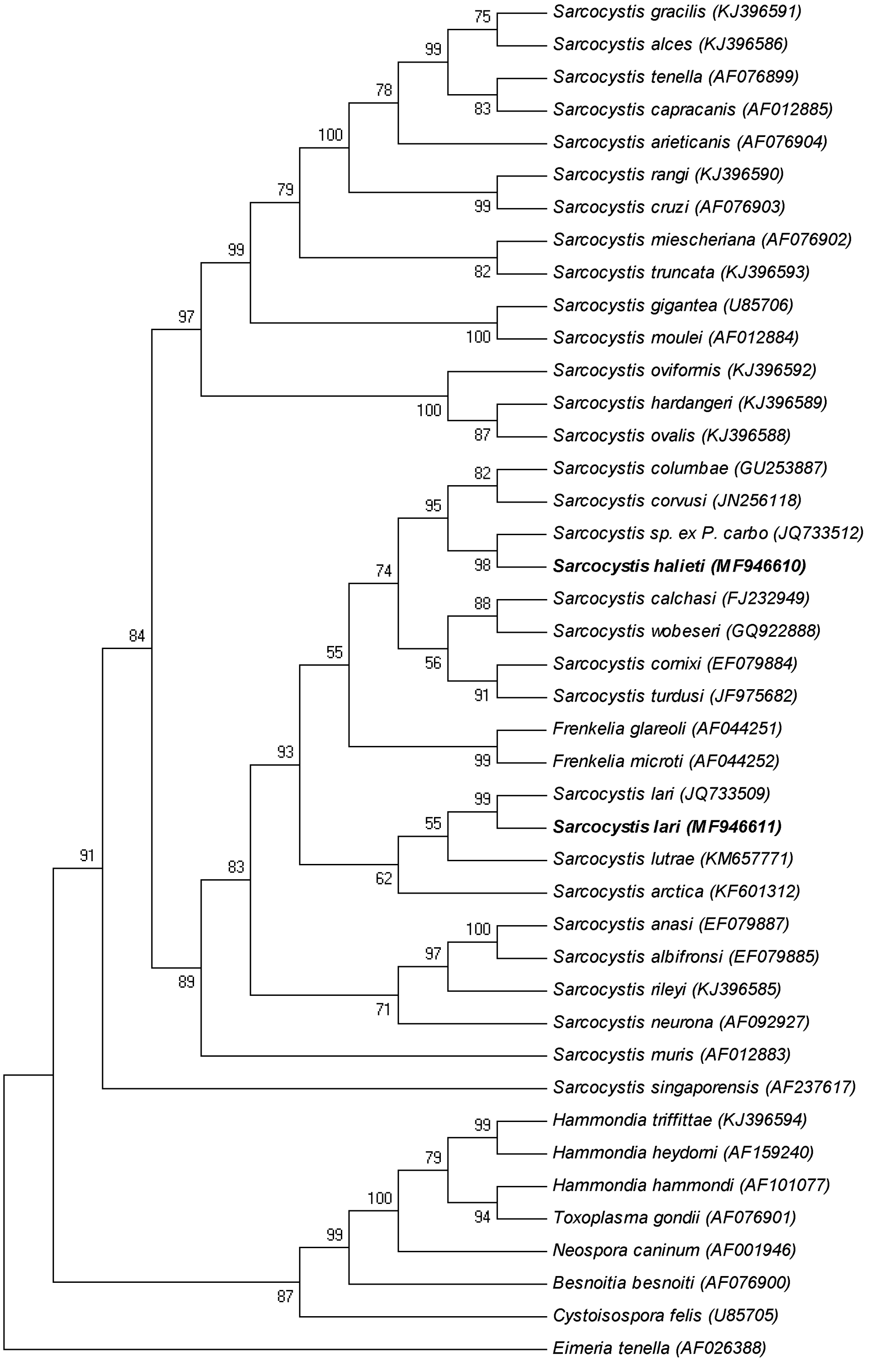


Fig. S2. Phylogenetic tree for members of the Sarcocystidae based on 42 sequences of the partial 28S rRNA gene of 40 taxa and inferred using the maximum parsimony method with the Tree–Bisection–Regrafting algorithm. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates) is shown next to the branches. The two new sequences from the present study are in boldface.