遺伝子配列解析（種判定）報告書

xxxx 年 xx 月 xx 日

株式会社 xxxxx
xxxxxxxx　様

下記のとおり、ご依頼いただきました分析が完了しておりますことをご報告致します。

1. 受入れサンプル
・ ハチクマと想定される羽、1 検体（サンプル名：hachi2-6）。
2. 解析遺伝子領域
・ ミトコンドリア cytB 領域（当社、*in silico* 解析に基づき決定）。
3. 解析結果
・ hachi2-6 に含まれる DNA は *Pernis ptilorhyncus orientalis*（ハチクマ）由来の配列と最も強い相同性があることが確認された。
・ 概要は下表のとおり（詳細は別添参照）。

サンプル名	推定同定種のランキング	最大一致スコア[1]	最大カバー率 (%)[2]	最大一致率 (%)[3]
hachi2-6	1. *Pernis ptilorhyncus orientalis*	189	100.00	100.00
	1. *Pernis ptilorhyncus philippensis*	189	100.00	100.00
	1. *Pernis ptilorhyncus ruficollis*	189	100.00	100.00
	2. *Pernis celebensis streerei*	183	100.00	99.02
	3. *Pernis celebensis winkleri*	178	100.00	98.04

解析元
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[1] DNA 配列（塩基）の一致/不一致に数値による重み付けを行い、それを積算した値。一致する残基が多いとスコアも高くなる。なお、種同定ランキングはこの値に基づく。
[2] 取得配列に対し、データベースから検索された配列が相同性を確保できる領域の割合。値が大きいほどカバーしている領域が広い。
[3] 上記の領域内で、配列が一致している塩基の割合。値が大きいほど相同性が高い。

特記事項

- サンプル中の DNA 劣化が著しい可能性があり、ユニバーサルプライマーを用いた長鎖 DNA 断片の増幅ならびに配列決定はできなかった。
- 本分析用に設計された特異的プライマーによる PCR では、約 100bp の DNA 断片が増幅された。
- 今次供試サンプルは *Pernis ptilorhyncus orientalis* のほか、*Pernis ptilorhyncus philippensis* および *Pernis ptilorhyncus ruficollis* とも 100%の相同性が確認された。これらは *Pernis ptilorhyncus orientalis* の地域亜種とみられる。
- NCBI のデータベース上で「*Pernis ptilorhyncus orientalis*」を含む遺伝子配列データは 7 件のみ。うち、すべてが cytB 遺伝子領域であった（2020 年 8 月 20 日現在）。

取得配列とBLAST searchの結果

取得配列 102 bp

CCGCAGACACAACACTAGCTTTTTCATCCGTCGCCCATACATGCCGAAACGTACAGTACGGTTGACTTATCCGCAACCTACATGCCAACGGAGCATCACTCT

BLAST searchの結果

	Description	Max Score	Total Scor	Query Cov	E value	Per. Ident	Accession
1	Pernis ptilorhyncus orientalis strain Pptiori15 cytochrome b gene, partial cds; mitochondrial	189	189	100%	2E-44	100.00%	AY424385.1
2	Pernis ptilorhyncus orientalis strain Pptiori14 cytochrome b gene, partial cds; mitochondrial	189	189	100%	2E-44	100.00%	AY424384.1
3	Pernis ptilorhyncus orientalis strain Pptiori10 cytochrome b gene, partial cds; mitochondrial	189	189	100%	2E-44	100.00%	AY424381.1
4	Pernis ptilorhyncus orientalis strain Pptiori16 cytochrome b gene, partial cds; mitochondrial	189	189	100%	2E-44	100.00%	AY424376.1
5	Pernis ptilorhyncus philippensis strain Pptiphi2 cytochrome b gene, partial cds; mitochondrial	189	189	100%	2E-44	100.00%	AY424377.1
6	Pernis ptilorhyncus ruficollis strain Pptiruf6 cytochrome b gene, partial cds; mitochondrial	189	189	100%	2E-44	100.00%	AY424375.1
7	Pernis ptilorhyncus ruficollis strain Pptiruf3 cytochrome b gene, partial cds; mitochondrial	189	189	100%	2E-44	100.00%	AY424374.1
8	Pernis celebensis streerei strain Pcelste7 cytochrome b gene, partial cds; mitochondrial	183	183	100%	9E-43	99.02%	AY424388.1
9	Pernis celebensis streerei strain Pcelste2 cytochrome b gene, partial cds; mitochondrial	183	183	100%	9E-43	99.02%	AY424386.1
10	Pernis ptilorhyncus orientalis strain Pptiori11 cytochrome b gene, partial cds; mitochondrial	183	183	100%	9E-43	99.02%	AY424382.1
11	Pernis ptilorhyncus orientalis strain Pptiori4 cytochrome b gene, partial cds; mitochondrial	183	183	100%	9E-43	99.02%	AY424380.1
12	Pernis celebensis winkleri strain Pcelwin2 cytochrome b gene, partial cds; mitochondrial	178	178	100%	4E-41	98.04%	AY424391.1
13	Pernis celebensis winkleri strain Pcelwin1 cytochrome b gene, partial cds; mitochondrial	178	178	100%	4E-41	98.04%	AY424390.1
14	Pernis celebensis streerei strain Pcelste3 cytochrome b gene, partial cds; mitochondrial	178	178	100%	4E-41	98.04%	AY424387.1
15	Pernis ptilorhyncus ruficollis strain Pptiruf2 cytochrome b gene, partial cds; mitochondrial	178	178	100%	4E-41	98.04%	AY424373.1
16	Pernis ptilorhyncus ptilorhyncus strain Pptipti3 cytochrome b gene, partial cds; mitochondrial	178	178	100%	4E-41	98.04%	AY424372.1
17	Pernis ptilorhyncus torquatus strain Pptitor6 cytochrome b gene, partial cds; mitochondrial	178	178	100%	4E-41	98.04%	AY424367.1
18	Pernis ptilorhyncus ptilorhyncus strain Pptipti2 cytochrome b gene, partial cds; mitochondrial	174	174	98%	6E-40	98.00%	AY424371.1
19	Pernis ptilorhyncus torquatus strain Pptitor7 cytochrome b gene, partial cds; mitochondrial	174	174	98%	6E-40	98.00%	AY424368.1
20	Pernis ptilorhyncus torquatus strain Pptitor1 cytochrome b gene, partial cds; mitochondrial	174	174	98%	6E-40	98.00%	AY424365.1
21	P.apivorus mitochondrial cytb gene	172	172	100%	2E-39	97.06%	X86758.1
22	Pernis apivorus strain Papi1 cytochrome b gene, partial cds; mitochondrial	172	172	100%	2E-39	97.06%	AY424396.1
23	Pernis ptilorhyncus torquatus strain Pptitor3 cytochrome b gene, partial cds; mitochondrial	172	172	100%	2E-39	97.06%	AY424366.1
24	Pernis ptilorhyncus palawanensis strain Pptipal1 cytochrome b gene, partial cds; mitochondrial	169	169	98%	3E-38	97.00%	AY424369.1
25	Pernis celebensis celebensis strain Pcelcel5 cytochrome b gene, partial cds; mitochondrial	167	167	100%	9E-38	96.08%	AY424394.1
26	Pernis celebensis celebensis strain Pcelcel2 cytochrome b gene, partial cds; mitochondrial	167	167	100%	9E-38	96.08%	AY424393.1
27	Dryotriorchis spectabilis cytochrome b (cytb) gene, partial cds; mitochondrial	145	145	100%	4E-31	92.16%	AY987255.1
28	Egretta thula cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	145	145	94%	4E-31	93.75%	AF193826.1
29	Egretta garzetta mitochondrion, complete genome	141	141	98%	6E-30	92.00%	KJ192197.1
30	Egretta garzetta mitochondrion, complete genome	141	141	98%	6E-30	92.00%	KJ190950.1
31	Calidris ferruginea cytochrome b (cytb) gene, partial cds; mitochondrial	141	141	98%	6E-30	92.00%	KC969157.1
32	Egretta garzetta mitochondrial cytb gene for cytochrome b, partial cds, isolate: k132ptr	141	141	98%	6E-30	92.00%	AB600558.1
33	Hieraaetus morphnoides voucher IPMB 5950 cytochrome b (cytb) gene, partial cds; mitochondrial	141	141	98%	6E-30	92.00%	EU345503.1
34	Calidris ferruginea specimen-voucher UAM 14401 cytochrome b (cytb) gene, partial cds; mitochondrial gene for mitochon	141	141	98%	6E-30	92.00%	AY156160.1
35	Gypaetus barbatus cytochrome b gene, partial cds; mitochondrial	139	139	100%	2E-29	91.18%	KM203403.1
36	Gypaetus barbatus haplotype GBB67 cytochrome b (cytb) gene, partial cds; mitochondrial	139	139	100%	2E-29	91.18%	EU496467.1
37	Spizaetus africanus isolate Safr3 cytochrome b (cytb) gene, partial cds; mitochondrial	139	139	100%	2E-29	91.18%	EF459637.1
38	Spizaetus africanus cytochrome b (cytb) gene, partial cds; mitochondrial	139	139	100%	2E-29	91.18%	AY987295.1
39	Gypaetus barbatus cytochrome b (cytb) gene, partial cds; mitochondrial	139	139	100%	2E-29	91.18%	AY987237.1
40	G.barbatus mitochondrial cytb gene	139	139	100%	2E-29	91.18%	X86749.1
41	Gypaetus barbatus partial mitochondrial cytb gene for cytochrome b	139	139	100%	2E-29	91.18%	AJ604494.1
42	Gypaetus barbatus mitochondrion cytochrome b gene, partial cds	139	139	100%	2E-29	91.18%	U08943.1
43	Aquila nipalensis mitochondrion, complete genome	137	137	93%	7E-29	92.63%	NC_045042.1
44	Aquila nipalensis voucher IPMB 3876 cytochrome b (cytb) gene, partial cds; mitochondrial	137	137	93%	7E-29	92.63%	EU345507.1
45	Falco longipennis voucher IPMB 8042 cytochrome b (cytb) gene, complete cds; mitochondrial	137	137	93%	7E-29	92.63%	EU233075.1
46	Falco longipennis voucher IPMB 5949 cytochrome b (cytb) gene, complete cds; mitochondrial	137	137	93%	7E-29	92.63%	EU233074.1
47	Aquila nipalensis cytochrome b (cytb) gene, partial cds; mitochondrial	137	137	93%	7E-29	92.63%	AY987287.1
48	Falco longipennis cytochrome b (cytb) gene, partial cds; mitochondrial	137	137	93%	7E-29	92.63%	AY987229.1
49	Aquila nipalensis partial mitochondrial cytb gene for cytochrome b	137	137	93%	7E-29	92.63%	AJ604489.1
50	Egretta gularis mitochondrial partial cytb gene for cytochrome b	135	135	98%	3E-28	91.00%	LN901327.1
51	Phaethon lepturus mitochondrion, complete genome	135	135	92%	3E-28	92.55%	KR349465.1
52	Egretta eulophotes mitochondrion, complete genome	135	135	98%	3E-28	91.00%	KJ190949.1
53	Gyps coprotheres mitochondrion, complete genome	135	135	95%	3E-28	91.75%	MF683387.1
54	G.coprotheres mitochondrial cytb gene	135	135	95%	3E-28	91.75%	X86751.1
55	Gyps coprotheres haplotype GC48 cytochrome b (cytb) gene, partial cds; mitochondrial	135	135	95%	3E-28	91.75%	EU496448.1
56	Gyps coprotheres haplotype GC47 cytochrome b (cytb) gene, partial cds; mitochondrial	135	135	95%	3E-28	91.75%	EU496447.1
57	Gyps coprotheres haplotype GC46 cytochrome b (cytb) gene, partial cds; mitochondrial	135	135	95%	3E-28	91.75%	EU496446.1
58	Spizaetus tyrannus voucher IPMB 7302 cytochrome b (cytb) gene, partial cds; mitochondrial	135	135	95%	3E-28	91.75%	EU345519.1
59	Phaethon rubricauda cytochrome b (cytb) gene, complete cds; mitochondrial	135	135	92%	3E-28	92.55%	EU167010.1
60	Egretta eulophotes mitochondrion, complete genome	135	135	98%	3E-28	91.00%	EU072995.1
61	Nisaetus alboniger isolate Salb4 cytochrome b (cytb) gene, partial cds; mitochondrial	135	135	95%	3E-28	91.75%	EF459654.1
62	Nisaetus alboniger isolate Salb1 cytochrome b (cytb) gene, partial cds; mitochondrial	135	135	95%	3E-28	91.75%	EF459653.1
63	Nisaetus nipalensis taiwanensis isolate Sniptai1 cytochrome b (cytb) gene, partial cds; mitochondrial	135	135	95%	3E-28	91.75%	EF459650.1
64	Phaethon rubricauda mitochondrial DNA, complete genome	135	135	92%	3E-28	92.55%	AP009043.1
65	Spizaetus nipalensis cytochrome b (cytb) gene, partial cds; mitochondrial	135	135	95%	3E-28	91.75%	AY987274.1
66	Gyps coprotheres cytochrome b (cytb) gene, partial cds; mitochondrial	135	135	95%	3E-28	91.75%	AY987262.1
67	Spizaetus alboniger mitochondrial DNA, complete genome	135	135	95%	3E-28	91.75%	AP008239.1
68	Spizaetus nipalensis partial mitochondrial cytb gene for cytochrome b	135	135	95%	3E-28	91.75%	AJ604507.1
69	Phaethon rubricauda cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product	135	135	92%	3E-28	92.55%	AF158251.1
70	Falco peregrinus brookei voucher FPE5 cytochrome b (cytb) gene, partial cds; mitochondrial	134	134	88%	9E-28	93.33%	MH837634.1
71	Tachybaptus ruficollis mitochondrion, complete genome	134	134	100%	9E-28	90.20%	KJ913674.1
72	Treron apicauda voucher YPM:63671 cytochrome b (cytb) gene, partial cds; mitochondrial	134	134	100%	9E-28	90.20%	KJ456489.1
73	Calidris minutilla cytochrome b (cytb) gene, partial cds; mitochondrial	134	134	100%	9E-28	90.20%	KC969164.1
74	Calidris melanotos cytochrome b (cytb) gene, partial cds; mitochondrial	134	134	100%	9E-28	90.20%	KC969162.1
75	Bulweria bulwerii mitochondrial cytb gene, partial (isolate 1)	134	134	100%	9E-28	90.20%	AJ004155.1
76	Bulweria bulwerii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds	134	134	100%	9E-28	90.20%	U74351.1
77	Bulweria bulwerii cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds	134	134	100%	9E-28	90.20%	U70488.1
78	Aquila rapax voucher IPMB 8079 cytochrome b (cytb) gene, partial cds; mitochondrial	132	132	93%	3E-27	91.58%	EU345510.1
79	Falco eleonorae voucher IPMB 27883 cytochrome b (cytb) gene, partial cds; mitochondrial	132	132	93%	3E-27	91.58%	EU233063.1
80	Falco cuvierii voucher IPMB 9552 cytochrome b (cytb) gene, partial cds; mitochondrial	132	132	93%	3E-27	91.58%	EU233054.1
81	Aquila rapax voucher IPMB 8079 cytochrome b (cytb) gene, partial cds; mitochondrial	132	132	93%	3E-27	91.58%	EU233028.1
82	Aquila rapax vindhiana isolate Arapvin1 cytochrome b (cytb) gene, partial cds; mitochondrial	132	132	93%	3E-27	91.58%	EF459627.1
83	Milvus migrans parasitus voucher AMNH 264858 cytochrome b (cytB) gene, partial cds; mitochondrial	132	132	93%	3E-27	91.58%	AY994412.1
84	Aquila rapax partial mitochondrial cytb gene for cytochrome b	132	132	93%	3E-27	91.58%	AJ604491.1
85	Plegadis falcinellus cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product	132	132	96%	3E-27	90.82%	AF193819.1
86	Aegotheles albertisi mitochondrial cytochrome b gene	132	132	90%	3E-27	92.39%	X95764.1
87	Pelecanoides garnotii isolate YISG12 cytochrome b gene, partial cds; mitochondrial	130	130	98%	1E-26	90.00%	MK113825.1
88	Pelecanoides garnotii isolate YISG05 cytochrome b gene, partial cds; mitochondrial	130	130	98%	1E-26	90.00%	MK113820.1
89	Pelecanoides garnotii isolate YILV06 cytochrome b gene, partial cds; mitochondrial	130	130	98%	1E-26	90.00%	MK113808.1
90	Pelecanoides garnotii isolate YIGA02 cytochrome b gene, partial cds; mitochondrial	130	130	98%	1E-26	90.00%	MK113798.1
91	Haliaeetus albicilla voucher IN1796 mitochondrion, complete genome	130	130	95%	1E-26	90.72%	NC_040858.1
92	Circus cyaneus mitochondrion, complete genome	130	130	95%	1E-26	90.72%	KU237286.1
93	Circus cyaneus mitochondrion, complete genome	130	130	95%	1E-26	90.72%	KX925606.1
94	Gyps fulvus mitochondrion, complete genome	130	130	95%	1E-26	90.72%	KX893247.1
95	Aquila heliaca mitochondrion, complete genome	130	130	95%	1E-26	90.72%	KU646835.1
96	Circus cyaneus cyaneus voucher SMNH<SWE>:856428 cytochrome b (cytb) gene, partial cds; mitochondrial	130	130	95%	1E-26	90.72%	KX453172.1
97	Circus cyaneus cyaneus voucher SMNH<SWE>:826569 cytochrome b (cytb) gene, partial cds; mitochondrial	130	130	95%	1E-26	90.72%	KX453171.1
98	Circus cyaneus cyaneus voucher SMNH<SWE>:836680 cytochrome b (cytb) gene, partial cds; mitochondrial	130	130	95%	1E-26	90.72%	KX453170.1
99	Buteo buteo burmanicus mitochondrion, complete genome	130	130	95%	1E-26	90.72%	KM364882.1
100	Aquila chrysaetos chrysaetos genome assembly, organelle: mitochondrion	130	130	95%	1E-26	90.72%	LR822062.1

・個別の「Description」のデータの詳細は、下記サイトのダイアログボックスに「Accession」を入力することで閲覧できます。
https://www.ncbi.nlm.nih.gov/nuccore/
・Max Score = 類似断片中の最大のBLASTスコア
・Total Score = 個々の類似断片の合計のBLAST スコア
・Query Cover =(データベース中の配列とアラインされている領域の長さ)/(取得配列の全長)
・E-value =検出された類似度(Score)以上の類似度を示す配列の断片が、データベース中から偶然見出される本数の期待値小さいほど偶然生じたとは考えにくい統計的有意性の指標
・Per. Identity = 配列一致度(%)
・Accession = 検出配列のデータベース中のID