Corrigendum

Park, J.-K., Kim, K.-H., Kang, S., Jeon, H. K., Kim, J.-H., Littlewood, D. T. J. and Eom, K. S. (2007) Characterization of the mitochondrial genome of *Diphyllobothrium latum* (Cestoda: Pseudophyllidea) – implications for the phylogeny of eucestodes. *Parasitology* **134**, 749–759 (Published online 11 January 2007. doi: 10.1017/S003118200600206X).

Since publication some of the gene boundaries in this paper have changed. The corrected tables are reproduced below and an updated sequence is available in GenBank.

Table 2. Mitochondrial genome organization of *Diphyllobothrium latum*

Genes/ regions	No. of		Codons		Positions (5′–3′)
	Nucleotides	Amino acids	Initiation	Termination	
trnG	66				1–66
cox3	651	216	GTG	TAG	70–720
trnH	67				711–777
cob	1107	368	ATG	TAA	781–1887
nad4L	261	86	ATG	TAA	1889–2149
nad4	1251	417	ATG	TAG	2110–3360
trnQ	63				3361–3423
trnF	67				3420–3486
trnM	67				3483–3549
atp6	510	169	ATG	TAG	3553–4062
nad2	879	292	ATG	TAG	4065–4943
trnV	64				4945–5008
trnA	63				5016–5078
trnD	64				5082–5145
nad1	891	296	ATG	TAG	5146–6036
trnN	66				6036–6101
trnP	65				6109–6173
trnI	63				6183–6245
trnK	66				6252–6317
nad3	357	118	ATG	TAG	6318–6674
$trnS1_{(AGN)}$	59				6664–6722
trnW	63				6725–6787
cox1	1566	521	ATG	TAG	6796–8361
trnT	62				8352–8413
rrnL	968				8414–9381
trnC	64				9382–9445
rrnS	740				9446–10185
cox2	570	189	ATG	TAA	10186–10755
trnE	71				10759–10829
nad6	459	152	ATG	TAG	10826–11284
trnY	65				11288–11352
NR1	222				11353–11574
$trnL1_{(CUN)}$	67				11575–11641
$trnS2_{(UGN)}$	66				11652–11717
$trnL2_{(UUN)}$	64				11730–11793
trnR	56				11794–11849
nad5	1569	522	ATG	TAA	11853–13421
NR2	187				13422–13608

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Table 3. Nucleotide composition of the mitochondrial genome of *Diphyllobothrium latum*

Description	Length (bp)	A	C	T	G	A+T
Entire sequence	13 608	23·6	12·0	44·6	19·8	68·2
Protein-coding sequence	10 071	21·6	12·0	46·4	20·0	68·0
Codon position: 1st	3357	23·5	10·7	41·6	24·2	65·1
2nd	3357	17·4	15·6	47·2	19·8	64·6
3rd	3357	23·9	9·8	50·4	15·9	74·3
Ribosomal RNA gene sequence	1708	29·2	11·7	39·9	19·2	69·1
Transfer RNA gene sequence	1418	29·6	11·2	36·6	22·6	66·2
Non-coding region	409	31·1	10·5	43·3	15·2	74·4

Table 4. Codon usage for 12 protein-coding genes of the *Diphyllobothrium latum* mitochondrial genome

NC	AA	No.	%	NC	AA	No.	%	NC	AA	No.	%	AA	Ab.	No.	%
TTT	Phe	341	10·16	CCA	Pro	17	0·51	GAT	Asp	48	1·43	Ala	A	119	3·54
TTC	Phe	46	1·37	CCG	Pro	5	0·15	GAC	Asp	19	0·57	Cys	C	116	3·46
TTA	Leu	269	8·01	ACT	Thr	69	2·06	GAA	Glu	31	0·92	Asp	D	67	1·99
TTG	Leu	107	3·19	ACC	Thr	7	0·21	GAG	Glu	36	1·07	Glu	E	67	1·99
CTT	Leu	69	2·06	ACA	Thr	33	0·98	TGT	Cys	86	2·56	Phe	F	387	11·53
CTC	Leu	10	0·30	ACG	Thr	9	0·27	TGC	Cys	30	0·89	Gly	G	233	6·94
CTA	Leu	44	1·31	GCT	Ala	78	2·32	TGA	Trp	56	1·67	His	H	51	1·52
CTG	Leu	22	0·65	GCC	Ala	9	0·27	TGG	Trp	41	1·22	Ile	I	262	7·80
ATT	Ile	149	4·44	GCA	Ala	22	0·65	CGT	Arg	46	1·37	Lys	K	52	1·55
ATC	Ile	26	0·77	GCG	Ala	10	0·30	CGC	Arg	3	0·09	Leu	L	521	15·52
ATA	Ile	87	2·59	TAT	Tyr	157	4·68	CGA	Arg	0	0·00	Met	M	86	2·56
ATG	Met	86	2·56	TAC	Tyr	50	1·49	CGG	Arg	6	0·18	Asn	N	106	3·16
GTT	Val	155	4·62	TAA	*	4	0·12	AGT	Ser	81	2·41	Pro	P	86	2·56
GTC	Val	29	0·86	TAG	*	8	0·24	AGC	Ser	24	0·71	Gln	Q	23	0·68
GTA	Val	71	2·11	CAT	His	41	1·22	AGA	Ser	42	1·25	Arg	R	55	1·64
GTG	Val	72	2·14	CAC	His	10	0·30	AGG	Ser	17	0·51	Ser	S	365	10·87
TCT	Ser	110	3·28	CAA	Gln	13	0·39	GGT	Gly	151	4·50	Thr	T	118	3·52
TCC	Ser	11	0·33	CAG	Gln	10	0·30	GGC	Gly	21	0·63	Val	V	327	9·74
TCA	Ser	69	2·06	AAT	Asn	62	1·85	GGA	Gly	19	0·57	Trp	W	97	2·89
TCG	Ser	11	0·33	AAC	Asn	18	0·54	GGG	Gly	42	1·25	Tyr	Y	207	6·17
CCT	Pro	48	1·43	AAA	Asn	26	0·77						*	12	0·36
CCC	Pro	16	0·48	AAG	Lys	52	1·55								

* Stop (termination) codon.
Ab, Abbreviation.

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