

Table S2. The conservation of amino acid identity in select codons from *cox1*, *cox2*, and *cox3* genes from the mt genomes of *Dendropoma maximum*, *D. gregarium*, *Eualetes tulipa*, and *Thylacodes squamigerus*.

	Codon ^a	<i>cox1</i>			<i>cox2</i>			<i>cox3</i>			Total		
		Conserved ^b	All ^c	Percent	Conserved ^b	All ^c	Percent	Conserved ^b	All ^c	Percent	Conserved ^b	All ^c	Percent
<i>Dendropoma maximum</i>	TGA	10	10	100.0%	5	6	83.3%	7	7	100.0%	22	23	95.7%
	ATA	15	17	88.2%	4	6	66.7%	4	4	100.0%	23	27	85.2%
	AGA	1	2	50.0%	0	0	n/a	2	3	66.7%	3	5	60.0%
	AGG	2	2	100.0%	0	0	n/a	2	2	100.0%	4	4	100.0%
	AAA	3	4	75.0%	1	3	33.3%	0	1	0.0%	4	8	50.0%
<i>Dendropoma gregarium</i>	TGA	9	9	100.0%	4	4	100.0%	8	9	88.9%	21	22	95.5%
	ATA	9	9	100.0%	5	5	100.0%	2	2	100.0%	16	16	100.0%
	AGA	0	1	0.0%	0	1	0.0%	4	7	57.1%	4	9	44.4%
	AGG	2	2	100.0%	0	1	0.0%	0	1	0.0%	2	4	50.0%
	AAA	4	4	100.0%	0	0	n/a	0	0	n/a	4	4	100.0%
<i>Eualetes tulipa</i>	TGA	12	12	100.0%	4	4	100.0%	10	10	100.0%	26	26	100.0%
	ATA	14	17	82.4%	3	7	42.9%	1	4	25.0%	18	28	64.3%
	AGA	0	0	n/a	1	2	50.0%	3	4	75.0%	4	6	66.7%
	AGG	1	1	100.0%	1	3	33.3%	1	1	100.0%	3	5	60.0%
	AAA	5	5	100.0%	2	2	100.0%	1	3	33.3%	8	10	80.0%
<i>Thylacodes squamigerus</i>	TGA	9	9	100.0%	3	3	100.0%	5	6	83.3%	17	18	94.4%
	ATA	18	21	85.7%	5	7	71.4%	3	6	50.0%	26	34	76.5%
	AGA	0	0	n/a	1	2	50.0%	2	2	100.0%	3	4	75.0%
	AGG	2	2	100.0%	1	2	50.0%	0	1	0.0%	3	5	60.0%
	AAA	3	3	100.0%	2	3	66.7%	1	1	100.0%	6	7	85.7%

^a Codons whose amino acid identity has changed in the mt genetic code of other metazoans [46] .

^b The number of codons whose corresponding amino acid occurred in a conserved position in comparison with other select caenogastropods (>50%).

^c The total number of codons within the gene.