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Marine and Freshwater Research

Supplementary Material

Multi-gene insights into the taxonomy and conservation of Tasmania's galaxiid fishes

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Table S1. Allozyme profiles of all taxa in the original 1985 overview study.

	Pe 2 (6)	B 10,23,24 (14)	N 5 (6)	J 26 (6)	F 14 (6)	O 32 (6)	Pa 2 (6)	A 19 (6)	Tr 9,24 (18)	Ta 21 (6)	M 7,13 (12)	NC 9,12 (10)	PM 21 (6)	PJ 24 (6)	PE 23 (6)	PD 23 (6)
Locus																
<i>Acon1</i>	e	e	e	e	e	a	b	d	d	d	d ⁷⁵ ,e	c	d	c	d	d
<i>Acp</i>	b	b	b	b	c	a	a	b	b	b	b	a	a	a	b	a
<i>Ada</i>	i ⁶⁷ ,h ¹⁷ ,k	h ⁶⁴ ,i ²⁹ ,k	i	k ⁸³ ,m	k	g	d	d ⁶⁷ ,b	d ⁸⁹ ,b	d	j ⁹² ,l	b	a	b	a ⁶⁷ ,c	e ⁶⁷ ,f
<i>Adh</i>	b	b	b	b	d	a	d	a	a	a	a	b	d	d	d	d
<i>Akl</i>	a	a	a	a	a	a	a	a	a	a	b	a	a	a	a	a
<i>Ak2</i>	c	c	c	c	c	c	c	b	b	b	e	d	c	a	c	c
<i>Ald1</i>	b	b	b	b	b	b	a	b	b	b	b	b	a	a	a	a
<i>Ald2</i>	b	b	b	b	b	a	b	b	b	b	b	a	a	a	a	a
<i>Ca</i>	a	a	a	a	a	a	a	a	a	a	b	b	c	c	c	c
<i>Ck1</i>	a	a	a	a	b	b	b	b	b	b	b	b	b	b	b	b
<i>Ck2</i>	b	b	b	b	b	b	a	b	b	b	b	b	d	d	d	d
<i>Ck3</i>	b	b	b	b	b	b	b	b	b	b	b	-	b	b	b	b
<i>Enol</i>	b	b	b	b	b	d	d	a	a	a	b	b	b	d	d	d
<i>Fdp</i>	d	d	d	d	d	c	c	c	c	c	b	e	e	e	f	
<i>Fum</i>	b	b	b	b	d	b	a	d	d	d	d	e	d	d	d	d
<i>G6pd</i>	c	c	c	c	a	c ⁸³ ,d	b	d	d	d	a	d	c	c	c	a
<i>Gda</i>	c	c	c	c	b ⁶⁷ ,c	b	d ⁸³ ,b	f ⁶⁷ ,g	h ⁷⁸ ,i ¹⁶ ,e	e	d	c	a	a	a	a
<i>Glo</i>	b	b ⁷⁹ ,c	b	c	b	c	c	c	c	c ⁸³ ,a	c	c	c	c	c	c
<i>Got1</i>	b	b	b	b	b	b	c	b	b	b	b	a	b	b	b	b
<i>Got2</i>	b ⁸³ ,c	b ⁹³ ,d	b	b	b	a	c	b	b	b	f	a	d	e	e	e
<i>Gpi1</i>	c	c	c	a	c	c	c	c	c ⁶⁷ ,b	c	c	c	d	d	d	d
<i>Gpi2</i>	g	g	g	g ⁶⁷ ,h	g ⁸³ ,h	d ⁶⁷ ,b ¹⁷ ,f	h	d	d	d	c	e ⁹⁰ ,c	a	a	a	a
<i>Gsr</i>	d	d	d	c	f	c	c ⁸³ ,d	d	c	c	f	a	d	b	d	d
<i>Idh1</i>	d	d	d	d	d	a	a	a	a	a	d	-	c ⁸³ ,b	b	b	b
<i>Ldh1</i>	d	d	d	d	d	d	d	b ⁸³ ,d	b	b	d	d	e	e ⁶⁷ ,c	e	e
<i>Ldh2</i>	c	c	c	c	c	c	c	c	c	c	c	c	b	b	b	b
<i>Mdh1</i>	c	c ⁹³ ,a	d ⁸³ ,c	d	e	d	c	c	c	c	d	b	d	d	d	d
<i>Mdh2</i>	b	b ⁵⁷ ,a	b	b ⁸³ ,a	d	b	b ⁸³ ,d	b	b	a ⁸³ ,b	b	d	d	d	d	d

	Pe 2 (6)	B 10,23,24 (14)	N 5 (6)	J 26 (6)	F 14 (6)	O 32 (6)	Pa 2 (6)	A 19 (6)	Tr 9,24 (18)	Ta 21 (6)	M 7,13 (12)	NC 9,12 (10)	PM 21 (6)	PJ 24 (6)	PE 23 (6)	PD 23 (6)
<i>Me2</i>	b	b	b	b	b	b	b	b	b	b	b ⁵⁰ ,c	b	b	a	b	b
<i>Mpi</i>	c	c ⁹³ ,f	c	c	c	c	a	a	a	a	f	e ⁵⁰ ,c ⁴⁰ ,b	b	b	d	b
<i>PepA</i>	b	b ⁹³ ,c	b	b	b	a	a	a	a	a	a	c	a	a	a	a
<i>Pgam</i>	a	a	a	a	a	a	b	a	a	a	a	a	a	a	a	a
<i>6Pgd</i>	a	a	a	a ⁸³ ,c	c ⁶⁷ ,a	a ⁸³ ,b	a	a	a	a	c ⁹² ,a	d	b	d	c ⁸³ ,d	c ⁸³ ,a
<i>Pgk</i>	a	a	a	a	a	b	b	b	b	b	b	b	d	d	d	d
<i>Pgm1</i>	b	b	b ⁸³ ,d	c	c	a	f ⁸³ ,d	c	d ⁸³ ,c	d	d	d	g	e	e ⁸³ ,g	e
<i>Pgm2</i>	d	d	d	a	b	b	f ⁸³ ,e	e	d ⁴² ,f ³³ ,b	e	d ⁹² ,c	e	-	-	-	-
<i>Pk1</i>	c	c	c	c	a	a	b	c	c	c	b	d	d	d	d	d
<i>Pk2</i>	b	b	b	b	b	e	c	c	c	c	c	b	c	c	d	c
<i>Sordh</i>	b ⁵⁰ ,c ³³ ,a	c ⁵⁰ ,b ⁴⁰ ,a	a	c	b	b ⁷⁵ ,a	c	a	a	a	-	a	b	b	b	b
<i>Tpi1</i>	a	a	a	a	a	a	b	a	a	a	a	a	c	c	c	c
<i>Tpi2</i>	b	b	b	b	a	b	b	b	b ⁵⁶ ,c ³³ ,a	b	b	b ⁹⁰ ,c	c	b	b	b
<i>Ugpp</i>	b	b	b	b	a	b	b	b	b ⁸³ ,c	b	c	c	c	-	c	

Where multiple allozymes were present in a population, superscripts indicate the frequency of the most or more common allozyme(s). Taxa are identified using the code employed in Table 2. The sites sampled are also shown below each taxon, with the number of haploid genomes sampled shown in parentheses. Invariant locus: *Ald3*.

Table S2. Allozyme frequencies for populations sampled in the 2012 allozyme study.

Locus	Tr8	Tr11	Tr13	Tr17	Tr30	Tr31	Tr34	Tr35	Tr36	Tr37	Tr38	Tr39	Tr33	Tr22	Ta21	A19
<i>Acon2</i>	c	c	c	c	c ⁹⁰ ,d	c	c	c	c	c ⁹² ,a	c ⁹⁰ ,b	c ⁹¹ ,b	c	c ⁸⁷ ,a	a ⁸³ ,c	c
<i>Acyc</i>	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁹⁴ ,a
<i>Ada</i>	a ⁵⁰ ,b	b ⁸¹ ,a	b ⁶⁷ ,a	b	b	b ⁵⁶ ,a	b ⁵⁰ ,a ⁴⁴ ,c	b ⁶⁹ ,a	a ⁵⁰ ,b	b ⁵⁸ ,a	b	b ⁹⁵ ,a	b	b	b	b ⁸⁷ ,a
<i>Adh1</i>	a	a ⁶⁹ ,c	c ⁶⁷ ,a	a	a ⁶⁰ ,c	a ⁵⁰ ,c	a ⁶⁹ ,c	a ⁶⁹ ,c	a	c ⁷⁵ ,a	c ⁹⁵ ,b	c	c	c	c	c
<i>Adh2</i>	b	b ⁹⁴ ,a	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁸¹ ,c
<i>Est2</i>	b	b	b	b ⁵⁰ ,c	b	b ⁹⁴ ,c	b ⁹⁴ ,c	b	b	b ⁹² ,c	b ⁹⁵ ,a	b ⁷⁷ ,a	b	b	b	b ⁸⁷ ,a
<i>Est3</i>	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁸³ ,a	b
<i>Glo</i>	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁸³ ,a	b
<i>Got2</i>	b	b	b	b	b ⁹⁰ ,a	b	b	b	b	b ⁹² ,c	b ⁸⁵ ,d	b ⁸² ,d	b	b ⁹⁴ ,a	b	b
<i>Gp1</i>	a	a	a	a	a	a	a	a	a	a	a	a	a ⁷⁵ ,b	a	a	a
<i>Gpd2</i>	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁶² ,a	b ⁶⁷ ,c	b
<i>Gpi1</i>	a	a	a	a	a	a ⁹⁴ ,b	a	a	a	a	a	a	a	a	a	a
<i>Gpi2</i>	b	b	b	b	b	b ⁸⁷ ,a	b	b	b	b	b	b	b	b	b ⁶⁷ ,c	b
<i>Gsr</i>	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a	b
<i>Idh1</i>	b	b	b	b	b	b ⁸⁸ ,c	b ⁹⁴ ,d	b	b ⁹² ,a	b	b	b	b	b	b	b
<i>Ldh1</i>	a	a	a	a	a ⁹⁰ ,b	a	a	a	a	a	a	a	a	a	a	a ⁸⁸ ,b
<i>Mdh2</i>	b	b	b	b	b	b	b	b	b	b ⁹² ,a	b	b	b	b ⁸¹ ,a	a	b ⁹⁴ ,c
<i>Me1</i>	a	a	a	a	a	a	a	a	a	a ⁹² ,b	a	a	a	a	a	a
<i>Me2</i>	a	a	a	a	a	a ⁹⁴ ,b	a	a	a	a	a	a	a	a	a	a
<i>Mpi</i>	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁹⁴ ,a
<i>PepA2</i>	b	b	b	b	b	b	b	b	b	b ⁹² ,a	b	b	b	b	b	b
<i>PepC</i>	b	b	b ⁸³ ,a	b	b	b	b ⁹⁴ ,a	b	b	b ⁸³ ,a	b	b	b	b ⁹⁴ ,c	a	a
<i>PepD</i>	b	b ⁹⁴ ,a	b	b	b	b	b	b	b	b ⁹² ,a	b	b	b	b	b	c
<i>6Pgd</i>	a	a	a	a	a	a ⁹⁴ ,b	a ⁹⁴ ,c	a ⁶³ ,b	a	a ⁹² ,b	a	a	a ⁵⁰ ,b	a	a	a
<i>Pgm1</i>	c ⁵⁰ ,e	c ⁸¹ ,e	e ⁶⁶ ,bc ¹⁷	c ⁵⁰ ,e	c ⁶⁰ ,e	c ⁶³ ,e ³¹ ,b	e ⁶² ,c	c ⁵⁰ ,e	c ⁵⁰ ,e	c ⁹² ,b	a	a ⁷⁵ ,c	e ⁹⁴ ,c	e ⁸³ ,d	c ⁹⁴ ,a	
<i>Pgm2</i>	c	c ⁸⁸ ,be ⁶	c	c	c ⁹⁰ ,e	c ⁸¹ ,e ¹³ ,d	c ⁸⁸ ,e	c ⁸¹ ,a	c ⁵⁰ ,e	c	c	c	e	a ⁵⁰ ,b ³⁸ ,ce ⁶	c ⁸³ ,a	c
<i>Sordh</i>	a	a	a	a	a	a	a	a ⁹⁴ ,b	a	a	a	a	a	a	a	a
<i>Tpi2</i>	c	c ⁸⁸ ,ab ⁶	c	c	c ⁹⁰ ,b	c ⁸⁷ ,b	c ⁸⁸ ,ab ⁶	c ⁷⁵ ,a	b ⁵⁰ ,c	c ⁹² ,b	c	c	c	b ⁴³ ,a ³⁸ ,c	c	c

General format as for Table S1. Populations are identified by their taxon plus site codes. The two landlocked populations of *G. truttaceus* are shown in red. Invariant loci: *Acon1*, *Acp*, *Ak*, *Ald1*, *Ald2*, *Ca*, *Ck*, *Dia*, *Enol1*, *Enol2*, *Fdp*, *Fum*, *Gapd1*, *Gapd2*, *Got1*, *Gp2*, *Gpd1*, *Idh2*, *Ldh1*, *Ndpk1*, *Ndpk2*, *PepA1*, *PepB*, *Pgk*, *Pk2*, *Tpi1* and *Ugpp*.

Table S3. Allozyme frequencies for populations sampled in the ‘2022’ integrated allozyme dataset.

Locus	Tr10	Tr11	Tr12	Tr13	Tr22	Tr24	Tr25	Tr30	Tr31	Tr33	Tr34	Tr35	Tr37	Tr38	Tr39	Ta20	Ta21	Ta21	A18	A19	A19
<i>Ada</i>	c ⁷⁰ ,b ²⁹ ,a	c ⁸¹ ,b	c ⁶² ,b	c ⁶⁷ ,b	c	c	c	c ⁵⁶ ,b	c	c ⁵⁰ ,b ⁴⁴ ,d	c ⁶⁹ ,b	c ⁵⁸ ,b	c	c ⁹⁵ ,b	c	c ⁸³ ,b	c	c ⁹¹ ,b ⁸ ,e	c ⁶⁷ ,b	c ⁸⁷ ,b	
<i>Est2</i>	b ⁹⁹ ,c	b	b	b	b	b	b	b ⁹⁴ ,c	b	b ⁹⁴ ,c	b	b ⁹² ,c	b ⁹⁵ ,a	b ⁷⁷ ,a	b	b	b	b ⁹⁷ ,a	b	b ⁸⁷ ,a	
<i>Fum</i>	b ⁹⁹ ,a	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁹⁸ ,c	b	b	
<i>Glo</i>	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁸³ ,a	b ⁸³ ,a	b ⁸³ ,a	b	b	
<i>Got2</i>	c ⁹³ ,a ⁶ ,b	c	c ⁹⁹ ,a	c	c ⁹⁴ ,a	c	c	c ⁹⁰ ,a	c	c	c	c ⁹² ,d	c ⁸⁵ ,e	c ⁸² ,e	c	c	c	c	c	c	
<i>Gpd2</i>	b ⁹⁹ ,a	b	b	b	b ⁶² ,a	b ⁷⁵ ,a	b ⁵⁴ ,a	b	b	b	b	b	b	b	b	b	b	b ⁶⁷ ,c	b	b	
<i>Gpi1</i>	b	b	b	b	b	a ⁵⁰ ,b	b ⁷⁷ ,a	b	b	b ⁹⁴ ,c	b	b	b	b	b	b	b	b	b	b	
<i>Gpi2</i>	d ⁹⁸ ,ac ¹	d	d ⁹⁸ ,bf ¹	d	d	d	d	d ⁸⁷ ,b	d	d	d	d	d	d	d	e ⁶⁷ ,d	d ⁶⁷ ,e	d	d	d	
<i>Gsr</i>	a	a	a ⁹⁹ ,b	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a ⁹⁸ ,ac ¹	b	b	
<i>Ldh1</i>	a ⁹³ ,b ⁶ ,c	a	a ⁹⁸ ,b	a	a	a	a	a ⁹⁰ ,b	a	a	a	a	a	a	a	a	a	a ⁸⁶ ,b	a ⁸³ ,b	a ⁸⁸ ,b	
<i>Ldh2</i>	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁹⁹ ,a	b	b	
<i>Mdh1</i>	b	b	b ⁹⁹ ,a	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	
<i>Mdh2</i>	b	b	b	b	b ⁸¹ ,a	b	b	b	b	b	b	b	b	b ⁹² ,a	b	b	a ⁸³ ,b	a	a	b ⁹⁴ ,c	
<i>Mpi</i>	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁹⁹ ,c	b	b ⁹⁴ ,a	
<i>PepA2</i>	b ⁹⁸ ,ac ¹	b	b	b	b	b	b	b	b	b	b	b	b	b ⁹² ,a	b	b	b	b	b	b	
<i>PepD</i>	b	b ⁹⁴ ,a	b ⁹⁹ ,a	b	b	b	b	b	b	b	b	b	b	b ⁹² ,a	b	b	b	b	c	c	
<i>Pgm1</i>	c ⁵⁸ ,e	c ⁸¹ ,e	c ⁵⁸ ,e ⁴¹ ,b	e ⁶⁶ ,bc ¹⁷	e ⁹⁴ ,c	e	e ⁷⁹ ,c	c ⁶⁰ ,e	c ⁶³ ,e ³¹ ,b	e ⁷⁵ ,c	e ⁶² ,c	c ⁵⁰ ,e	c ⁵⁰ ,e	c	c	e	e ⁸³ ,d	e ⁸³ ,d	c ⁸⁵ ,a ¹⁴ ,d	c	c ⁹⁴ ,a
<i>Pgm2</i>	c ⁸⁴ ,e ¹⁰ ,ab ³	c ⁸⁸ ,be ⁶	c ⁸¹ ,e ⁹ ,ab ⁵	c	a ⁵⁰ ,b ³⁸ ,ce ⁶	b ⁴² ,e ³³ ,a	a ⁴⁸ ,b ⁴⁰ ,e	c ⁹⁰ ,e	c ⁸¹ ,e ¹³ ,d	e	c ⁸⁸ ,e	c ⁸¹ ,a	c	c	c	c	c	c ⁸³ ,a	c ⁹⁹ ,e	c	c
<i>Tpi2</i>	e ⁸² ,d ¹³ ,b	e ⁸⁸ ,bd ⁶	e ⁸² ,d ¹¹ ,b ⁵ ,af ¹	e	d ⁴³ ,b ³⁸ ,e	b ⁶⁷ ,d	d ⁵² ,b	e ⁹⁰ ,d	e ⁸⁷ ,d	e	e ⁸⁸ ,bd ⁶	e ⁷⁵ ,b	e ⁹² ,d	e	e	e	e	e	e ⁹⁷ ,c	e	e
<i>Ugpp</i>	b	b	b ⁹⁸ ,a	b	b	b	b	b	b	b	b	b	b	b	b	b	b ⁸³ ,c	b	b	b ⁹⁹ ,c	

General format as for Tables S1 and S2. Blue text, 1985 study; red text, 1988 study; black text, 2012 study.