

The transcriptome-wide effects of exposure to a pyrethroid pesticide on the Critically Endangered delta smelt *Hypomesus transpacificus*

Ken M. Jeffries*, Lisa M. Komoroske, Jennifer Truong, Inge Werner, Matthias Hasenbein, Simone Hasenbein, Nann A. Fanguie, Richard E. Connon

* Corresponding author: kenmjeffries@gmail.com

Endangered Species Research 28: 43–60 (2015)

Supplement.

Table S1. Gene descriptions, gene symbols and relative log₂ fold changes for the 69 microarray features that were significantly different between the lowest exposure concentration (0.69 µg l⁻¹) and the control group (ANOVA; q < 0.05) after 96 h of exposure to permethrin. Features that were significantly different from the control group are in bold. The order of the genes in the table is the same as in the heat map.

Probe ID	Gene Symbol	Gene	Mean Fold Change				q-value	Process
			0.69 µg l ⁻¹ vs Control	1.37 µg l ⁻¹ vs Control	2.56 µg l ⁻¹ vs Control	4.84 µg l ⁻¹ vs Control		
CUST_2580_PI428861894	PSMA1	Proteasome subunit alpha type 1	-1.56	1.29	1.22	1.82	9.74E-03	Proteosomal breakdown
CUST_2582_PI428861894	PSMA1	Proteasome subunit alpha type 1	-1.58	1.19	1.18	1.77	1.02E-02	Proteosomal breakdown
CUST_24424_PI428861894	PRPF6	Pre-mRNA-processing factor 6-like	-1.19	1.10	-1.07	-1.12	1.16E-02	Protein Synthesis
CUST_27697_PI428861894	EPD1	Ependymin-1 precursor	-2.22	-1.18	1.08	1.51	1.16E-02	Cell-Matrix adhesion; Calcium binding
CUST_2579_PI428861894	PSMA1	Proteasome subunit alpha type 1	-1.55	1.18	1.13	1.78	1.16E-02	Proteosomal breakdown
CUST_4110_PI428861894	PSMB3	Proteasome subunit beta type 3	-1.48	1.30	1.17	1.83	1.19E-02	Immune response; Proteosomal breakdown
CUST_19401_PI428861894	CDK9	Cell division protein kinase 9	-1.20	1.18	1.17	1.11	1.21E-02	Protein Synthesis
CUST_27696_PI428861894	EPD1	Ependymin-1 precursor	-2.19	-1.36	1.09	1.49	1.27E-02	Cell-Matrix adhesion; Calcium binding
CUST_24688_PI428861894	EIF1	Translation factor sui1-like	-1.46	1.01	1.30	1.19	1.38E-02	Protein Synthesis
CUST_2583_PI428861894	PSMA1	Proteasome subunit alpha type 1	-1.62	1.07	1.11	1.52	1.77E-02	Proteosomal breakdown
CUST_2584_PI428861894	PSMA1	Proteasome subunit alpha type 1	-1.63	1.12	1.14	1.50	1.88E-02	Proteosomal breakdown
CUST_22625_PI428861894	RRS1	Ribosome biogenesis regulatory protein homolog	-1.24	-1.08	1.07	1.07	2.09E-02	Ribosome biogenesis

CUST_18247_PI428861894		CI085 protein	-1.61	-1.47	-1.11	-1.07	3.67E-02	
CUST_16023_PI428861894	NMT1	Glycylpeptide N-tetradecanoyltransferase 1	-1.48	-1.19	-1.19	-1.16	4.70E-02	Immune response
CUST_546_PI428861894	ZNF106A	Zgc:100799	-1.39	-1.45	-1.21	-1.46	4.20E-02	Metal ion binding
CUST_13502_PI428861894	NOP10	H/ACA ribonucleoprotein complex subunit 3	-1.21	-1.33	-1.21	-1.21	4.43E-02	Ribosome biogenesis; Telomere maintenance
CUST_31531_PI428861894	DB-1	TPA: defensin-like protein 1	-1.25	-1.34	-1.27	-1.47	1.13E-02	Immune response
CUST_21758_PI428861894	PCDH2AB6	Protocadherin 2 alpha b 6 precursor	-1.30	-1.29	-1.43	-1.52	1.43E-02	Cell Adhesion; Calcium Binding
CUST_25131_PI428861894	MYCT1	myc target protein 1 homolog	-1.33	-1.33	-1.33	-1.45	1.62E-02	Transcription regulator of MYC genes
CUST_25218_PI428861894	SEZ6	Seizure protein 6 homolog	-1.23	-1.30	-1.22	-1.00	1.64E-02	Cell signalling
CUST_2995_PI428861894	TRA2A	Transformer-2 protein homolog alpha-like	-1.38	-1.24	-1.34	-1.48	2.06E-02	Protein Synthesis
CUST_11537_PI428861894	NDUFS8	NADH dehydrogenase iron-sulfur protein 8, mitochondrial precursor	-1.88	-1.82	-1.79	-1.61	2.52E-02	Metabolism
CUST_14617_PI428861894	BAP18	Potential DNA-binding protein C17orf49 homolog	-1.32	-1.43	-1.36	-1.46	2.53E-02	DNA Binding
CUST_11708_PI428861894	MRPS16	28S ribosomal protein S16, mitochondrial precursor	-1.17	-1.24	-1.28	-1.27	2.78E-02	Protein Synthesis
CUST_28636_PI428861894	METTTL21A	FAM119A	-1.21	-1.24	-1.20	-1.17	3.38E-02	Protein binding; Stress Response
CUST_544_PI428861894	ZNF106A	Zgc:100799	-1.44	-1.49	-1.23	-1.49	3.92E-02	Metal ion binding
CUST_543_PI428861894	ZNF106A	Zgc:100799	-1.39	-1.45	-1.20	-1.42	3.93E-02	Metal ion binding
CUST_19927_PI428861894	Unknown		-1.45	-1.20	-1.54	-1.34	1.51E-02	Unknown
CUST_34910_PI428861894		Hypothetical protein BRAFLDRAFT_96790	-1.26	-1.28	-1.25	-1.26	4.93E-02	Unknown
CUST_18873_PI428861894		Unnamed protein product	-1.45	1.36	1.40	1.81	7.42E-03	Unknown
CUST_24774_PI428861894	CAND1	Cullin-associated and neddylation-dissociated 1	-1.40	1.35	1.32	1.78	7.42E-03	Proteosomal breakdown
CUST_10645_PI428861894	ELOF1	Transcription elongation factor 1 homolog	-1.16	1.10	1.15	1.32	7.42E-03	Protein Synthesis
CUST_6302_PI428861894	HPD	4-hydroxyphenylpyruvate dioxygenase	-1.14	1.05	1.14	1.25	7.42E-03	Tyrosine Catabolism
CUST_1795_PI428861894	OCIAD1	OCIA domain-containing protein 1	-1.26	1.12	1.03	1.52	7.66E-03	Endosome
CUST_2581_PI428861894	PSMA1	Proteasome subunit alpha type 1	-1.52	1.22	1.18	1.78	8.69E-03	Proteosomal breakdown
CUST_23791_PI428861894	MTERFD3	mTERF domain-containing protein 3, mitochondrial-like	-1.77	1.27	1.42	1.90	8.77E-03	Protein Synthesis
CUST_36638_PI428861894	PSMD6	26S proteasome non-ATPase regulatory subunit 6	-1.72	1.31	1.47	2.54	9.12E-03	Proteosomal breakdown
CUST_2441_PI428861894	NDFIP2	NEDD4 family-interacting protein 2	-1.31	1.16	1.22	1.48	9.21E-03	Endosome; Proteosomal breakdown
CUST_25194_PI428861894	RNF10	RING finger protein 10	-1.48	1.26	1.35	1.66	9.21E-03	Protein Synthesis
CUST_7406_PI428861894		Hypothetical protein	1.19	-1.07	-1.23	-1.19	8.88E-03	
CUST_30798_PI428861894	PEBP1	Phosphatidylethanolamine-binding protein 1-like	1.35	-1.12	-1.16	-1.39	9.01E-03	ATP-binding

CUST_16287_PI428861894	ADD3	Gamma-adducin-like	1.23	-1.14	-1.01	1.15	1.94E-02	Cytoskeleton; Calmodulin binding
CUST_14100_PI428861894	PHPT1	14 kDa phosphohistidine phosphatase	2.15	-1.39	-1.02	-1.48	2.78E-02	Cell signalling; Calcium channel inhibitor activity; Ion channel binding
CUST_13956_PI428861894		Hypothetical protein LOC793702	1.30	1.04	-1.04	1.55	2.93E-02	
CUST_926_PI428861894	Unknown		1.54	-1.02	1.13	-1.15	3.18E-02	
CUST_22712_PI428861894	CEP192	Centrosomal protein of 192 kDa-like	1.21	1.10	1.00	-1.02	3.54E-02	
CUST_34469_PI428861894		Molecular identification of Poly A binding protein	1.38	-1.13	-1.08	-1.00	3.87E-02	Protein Synthesis
CUST_34468_PI428861894		Molecular identification of Poly A binding protein	1.49	-1.02	-1.02	1.05	4.74E-02	Protein Synthesis
CUST_16994_PI428861894	SPAST	Spastin-like	1.20	1.53	1.27	1.36	8.88E-03	Cytoskeleton; Cell Division
CUST_1248_PI428861894	ATG101	Autophagy-related protein 101	1.30	1.52	1.49	1.54	2.02E-02	Autophagy; Protein binding
CUST_1247_PI428861894	ATG101	Autophagy-related protein 101	1.38	1.60	1.45	1.58	3.29E-02	Autophagy; Protein binding
CUST_36767_PI428861894	ATG101	Autophagy-related protein 101	1.36	1.60	1.52	1.61	3.55E-02	Autophagy; Protein binding
CUST_13657_PI428861894		Hypothetical protein LOC100690156	1.51	1.68	1.45	1.42	3.55E-02	
CUST_30296_PI428861894	ORF2P	ORF2-encoded protein	1.28	1.34	1.24	1.16	2.01E-02	Protein synthesis
CUST_5595_PI428861894	BDH2	3-hydroxybutyrate dehydrogenase type 2	1.21	1.21	-1.11	-1.26	5.92E-03	Iron homeostasis
CUST_24047_PI428861894	CHL1	Neural cell adhesion molecule L1-like protein isoform 3	1.36	1.51	1.04	1.22	7.42E-03	Cell adhesion
CUST_2293_PI428861894	SLC22A2	Solute carrier family 22 member 2	1.40	1.60	1.26	1.41	2.02E-02	Ion transport; Transport
CUST_27636_PI428861894	Unknown	Hypothetical protein LOC100698035	1.14	1.17	-1.11	-1.16	7.42E-03	Unknown
CUST_17196_PI428861894	HOXC9	Homeobox protein Hox-C9-like	1.25	1.23	-1.13	1.09	7.42E-03	Protein Synthesis
CUST_17057_PI428861894	SLC27A2	Solute carrier family 27 member 2	1.31	1.38	-1.19	-1.35	8.22E-03	Fatty acid metabolism
CUST_19185_PI428861894		Hypothetical protein LOC100710905	1.41	1.71	-1.20	-1.10	8.22E-03	
CUST_24048_PI428861894	CHL1	Neural cell adhesion molecule L1-like protein isoform 3	1.37	1.36	-1.01	1.21	1.52E-02	Cell adhesion
CUST_25481_PI428861894	DDRGK1	DDRGK domain-containing protein 1	1.18	1.16	1.01	-1.01	1.93E-02	Protein binding; ER
CUST_15052_PI428861894	PDXP	Pyridoxal phosphate phosphatase	1.50	1.60	1.09	1.18	1.97E-02	Cytoskeleton; Cell Division
CUST_10187_PI428861894	CUTC	Copper homeostasis protein cutC homolog	1.20	1.24	1.07	1.06	2.75E-02	Copper ion homeostasis
CUST_5229_PI428861894	NSMAF	Protein FAN, partial	1.29	-1.06	-1.37	-1.27	8.62E-03	Cell signalling
CUST_5957_PI428861894	MRPS25	Mitochondrial 28S ribosomal protein S25	1.10	-1.05	-1.12	-1.12	8.69E-03	Ribosome
CUST_31170_PI428861894	IGSF10	Immunoglobulin superfamily member 10-like	1.28	-1.05	-1.13	-1.46	8.88E-03	Osteogenesis; Differentiation
CUST_15047_PI428861894		Hypothetical protein LOC560010	1.99	-1.31	-1.17	-2.84	1.05E-02	

Table S2. Summary of the number of significant microarray features that were different between all treatment groups as determined by ANOVA followed by a Student Newman-Keuls (SNK) post-hoc test ($q < 0.05$).

	Control	0.69 $\mu\text{g l}^{-1}$	1.37 $\mu\text{g l}^{-1}$	2.56 $\mu\text{g l}^{-1}$	4.84 $\mu\text{g l}^{-1}$
Control		69	430	776	1993
0.69 $\mu\text{g l}^{-1}$	69		571	1147	2377
1.37 $\mu\text{g l}^{-1}$	430	571		345	959
2.56 $\mu\text{g l}^{-1}$	776	1147	345		401
4.84 $\mu\text{g l}^{-1}$	1993	2377	959	401	