

Phenotypic and gene expression profiles of embryo development of the ascidian *Ciona robusta* exposed to dispersants

Maria Concetta Eliso ^{1,*}, Ilaria Corsi ², Loredana Manfra ^{3,4,*} and Antonietta Spagnuolo ^{1, ‡}

¹ Department of Biology and Evolution of Marine Organisms, Stazione Zoologica Anton Dohrn, Naples, Italy; mariaconcetta.eliso@szn.it; antonietta.spagnuolo@szn.it

² Department of Physical, Earth and Environmental Sciences, University of Siena, Siena, Italy; ilaria.corsi@unisi.it

³ Department of Marine Biotechnology, Stazione Zoologica Anton Dohrn, Naples, Italy;

⁴ Institute for Environmental Protection and Research (ISPRA), Rome, Italy; loredana.manfra@isprambiente.it

* Correspondence: M.C.E.: mariaconcetta.eliso@szn.it; L.M.: loredana.manfra@isprambiente.it

‡ equal contributors

Table S1. Accession number and/or Gene Model ID, sequences and length of PCR fragments are listed for the analyzed genes.

Gene Name	Acronym	Accession Name and or Gene Model ID	Primer	Sequence (5' → 3')	Amplicon length (bp)
Superoxide dismutases_a	<i>soda</i>	XM_002121064.4 KH2012:KH.S1012.1	CiSODa_F	CCACAAAATATAGACGAAGGCGAC	95
			CiSODa_R	GACAACGCACTATTCAACGGG	
Superoxide dismutases_b	<i>sodb</i>	XM_002122490.5 KH2012:KH.L50.19	CiSODb_F	AAGTGAGAGTGTGAGTGGGAC	89
			CiSODb_R	CAGCCAACCCTGTAAGCGA	
Glutathione peroxidase	<i>gpx</i>	NM_001190351.1 KH2012:KH.C9.698	CiGPx7_F	TTGAGAAGAAGCACGGGGCAA	93
			CiGPx7_R	GGATGGCCCCCACTCATTT	
Glutathione S-transferase	<i>gst</i>	XM_002128135 KH2012:KH.C2.852	CiGST_F	CCAAGCGATGCTAATGCGAG	94
			CiGST_R	CGGCGGGATTGAGGTATGT	
Glutathione Reductase	<i>GluR</i>	XM_002119519.5 KH2012:KH.C7.514	CiGRed_F	AGCACTTCTTACACCAGTTGC	130
			CiGRed_R	CCCAATGGGTGGATGACTGA	
Cytochrome p450	<i>cyp450</i>	NM_001128875 KH2012:KH.C11.63	CiCyP450_F	CCCAACCAGATGTTCTGTCC	156
			CiCyP450_R	CTGCCTGTCTGGGGAATGTAG	
Heat shock protein 60 kDa	<i>hsp60</i>	XM_018812296.2 KH2012:KH.C6.85	CiHSP60_1F	AGACGAACAAGTTGGGGTTG	196
			CiHSP60_1R	GACTTTCGTTGGGTCCAGAA	
Heat Shock Protein 70 kDa	<i>hsp70</i>	NM_001033834.1 KH2012:KH.L46.6	CiHSP70_2F	TCTCTGTGCTCACCATCGAC	241
			CiHSP70_2R	GCTTTTTCGACAGGGTCAAG	
Superoxide dismutase, mitochondrial	<i>MnSOD</i>	XM_002128454.4 KH2012:KH.C12.466	CiMSOD_2F	TCAAGGTTCTGGCTGGAGTT	175
			CiMSOD_1R	GTAATCTGGCCGCACATTTT	
p38 mitogen-activated protein kinases	<i>p38 MAPK</i>	NM_001078490.1 KH2012:KH.C11.76	CiP38_1F	GACGACCACGTCCAGTTTTT	172
			CiP38_1R	CGGTCATTTGGTCATCTGTG	
Cytochrome b	<i>cytB</i>	ENSCINT00000037367.1	CiCytb_1F	TTATCGGTTACCGGCTCCTA	151
			CiCytb_1R	ATGGTTCACAGAAGAAAAAGCTA	

Caspase 8	<i>cas8</i>	XM_002122812.4 KH2012:KH.C8.550	CiCas8_2F	GGTCATGTCTCATGGGCTCT	184
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Table S2. E(L)C₅₀ values (µg mL⁻¹) calculated for dispersant A and B.

	Dispersant A E(L)C₅₀ (95%CI)	Dispersant B E(L)C₅₀ (95%CI)	References
<i>Phaeodactylum tricornutum</i> (72 h)	6.60 (4.40–8.80)	82.70 (63.40–102.00)	Manfra et al., 2017
<i>Tigriopus fulvus</i> (96 h)	5.89 (4.86–7.04)	49.66 (40.36–62.42)	
<i>Artemia franciscana</i> (96 h)	1.60 (1.20–1.97)	–	
<i>Dicentrarchus labrax</i> (96 h)	16.19 (13.75–19.07)	71.18 (65.34–77.55)	
<i>Ciona robusta</i> (22 h)	160 (150.4 to 171.2)	44.30 (39.92 to 49.15)	

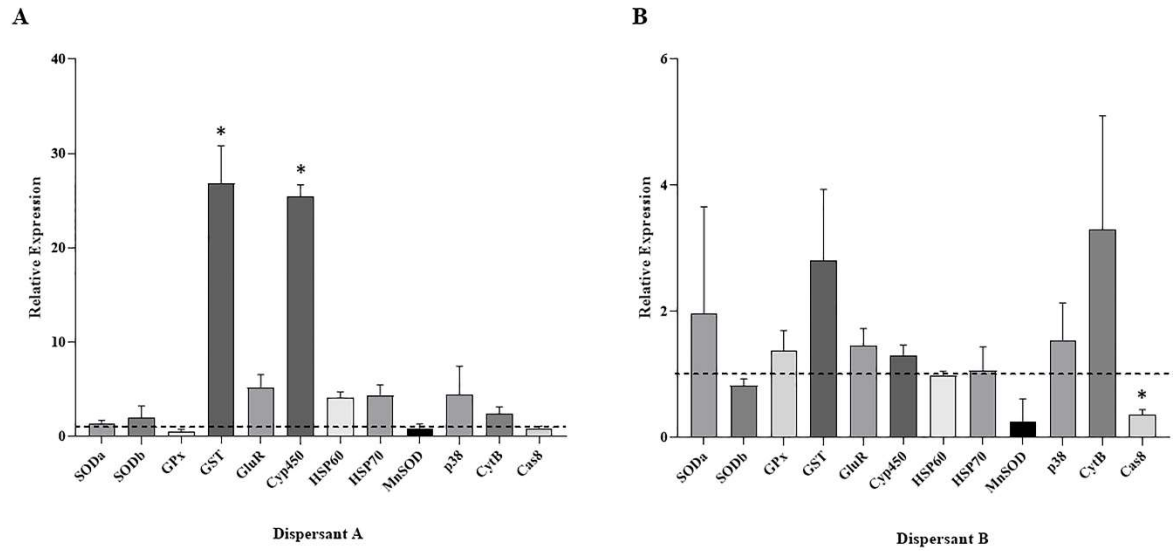


Figure S1. Expression of *soda*, *sodb*, *gpx*, *gst*, *GluR*, *Cyp450*, *hsp60*, *hsp70*, *MnSod*, *cytB*, *p38 MAPK* and *cas8* genes by comparative RT q-PCR with total RNA isolated from control and exposed embryos to dispersant A (A) and dispersant B (B) after 22 hpf. Results are expressed as fold increase compared to controls assumed as 1, using cytoskeletal actin as reference gene for normalization. Each bar represents the mean of three independent experiments \pm SEM. * indicates a significant difference (t-test, $p < 0.05$) respect to controls.