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APPENDICES

APPENDIX A

I Genes homologues identified of *P. monodon* by DD-PCR

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S1	2-hydroxyacid dehydrogenase	Mesorhizobium loti MAFF303099	NP_106146.1	1.00E-34	120/214 (56%)	DD43
S2	acyl-Coenzyme A oxidase 1, palmitoyl	Gallus gallus	NP_001006205.1	8.00E-75	105/143 (73%)	DD61
S3	adducin-like protein R1 isoform	Drosophila melanogaster	AAG01377.1	6.00E-07	34/43 (79%)	DD52
S4	AF263243_1 SocE	Myxococcus xanthus	AAF91388.1	7.00E-19	69/115 (60%)	DD83
S5	unknown gene	-	-	-	-	DD32 DD33
S6	ATP-dependent RNA helicase	Aedes aegypti	EAT44187.1	5.00E-94	186/219 (84%)	DD58 DD70
S7	B4galt3-prov protein	Xenopus laevis	AAH77601.1	4.00E-04	33/44 (75%)	DD57
S8	carbonic anhydrase	Aedes aegypti	EAT43649.1	2.00E-53	133/199 (66%)	DD53 DD55
S9	ced-6 CG11804-PC, isoform C	Apis mellifera	XP_392026.2	4.00E-74	167/206 (81%)	DD63
S10	cell wall-associated hydrolase	Actinobacillus succinogenes 130Z	ZP_00731820.1	1.00E-51	104/127 (81%)	DD65

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S11	CG14476-PB	Apis mellifera	XP_623603.1	6.00E-60	141/208 (67%)	DD52 DD59
S12	CG14982-PB	Apis mellifera	XP_001121606.1	8.00E-13	82/176 (46%)	DD54 DD56 DD57
S13	CHK1 checkpoint homolog (S. pombe)	Xenopus tropicalis	CAJ83813.1	4.00E-10	35/45 (77%)	DD71
S14	corin isoform 2	Pan troglodytes	XP_001153181.1	3.00E-06	24/31 (77%)	DD95
S15	cytochrome c oxidase subunit I	Marsupenaeus japonicus	YP_238256.1	5.00E-55	118/140 (84%)	DD85
S16	cytokinesis protein 1	Rattus norvegicus	XP_001055442.1	2.00E-34	100/161 (62%)	DD59
S17	ENSANGP00000017400	Anopheles gambiae str. PEST	EAA01290.4	2.00E-06	39/62 (62%)	DD59
S18	fibulin-1, isoform D precursor	Strongylocentrotus purpuratus	XP_001189248.1	1.00E-40	121/215 (56%)	DD57
S19	Gcap1 gene product	-	AAA68426.1	1.00E-05	34/54 (62%)	DD80
S20	hypothetical protein RSc1364	Ralstonia solanacearum GMI1000	NP_519485.1	1.00E-45	94/102 (92%)	DD13

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S21	integrin alpha-ps	Aedes aegypti	EAT34371.1	1.00E-17	118/227 (51%)	DD55
S22	karyopherin (importin) alpha 4	Tribolium castaneum	XP_975030.1	1.00E-118	234/262 (89%)	DD42 DD49 DD79
S23	LacOPZ-alpha peptide from pUC9	Cryptosporidium hominis TU502	XP_664835.1	5.00E-20	52/62 (83%)	DD83
S24	MGC83562 protein	Xenopus laevis	AAH73100.1	3.00E-05	32/43 (74%)	DD77
S25	NIMA-family kinase Nek7	Xenopus laevis	AAT45117.1	1.00E-74	140/147 (95%)	DD55
S26	ORF2	Drosophila melanogaster	AAA70222.2	5.00E-13	94/203 (46%)	DD58
S27	putative senescence-associated protein	Pisum sativum	BAB33421.1	2.00E-32	75/108 (69%)	DD83
S28	ribosomal protein L10	Callinectes sapidus	AAV71145.1	1.00E-49	94/96 (97%)	DD29 DD30
S29	ribosomal protein L7a	Argopecten irradians	AAN05607.1	4.00E-45	111/146 (76%)	DD90
S30	ribosomal protein Rps16	Mus musculus	AAH82286.1	6.00E-50	110/121 (90%)	DD35
S31	ribosomal protein S27E	Homarus americanus	AAB46716.1	2.00E-35	70/70 (100%)	DD27

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S32	ribosomal protein S4	Bombyx mori	NP_001037257.1	1.00E-111	216/253 (85%)	DD95
S33	ribosomal protein L11.2	Caenorhabditis elegans	NP_508413.1	3.00E-29	69/79 (87%)	DD3 DD4 DD28
S34	sarcolemmal associated protein-2	Aedes aegypti	EAT46394.1	3.00E-54	144/199 (72%)	DD70
S35	small nuclear ribonucleoprotein protein F	Bombyx mori	ABF51434.1	3.00E-26	66/71 (92%)	DD65
S36	solute carrier family 7, member 6	Mus musculus	NP_001007568.1	4.00E-04	60/116 (51%)	DD90 DD91
S37	ubiquitin-protein ligase	Aedes aegypti	EAT42542.1	7.00E-72	154/176 (87%)	DD88
S38	vacuolar protein sorting 18	Tribolium castaneum	XP_974055.1	6.00E-04	25/33 (75%)	DD69
S39	unknown gene	-	-	-	-	DD10
S40	unknown gene	-	-	-	-	DD41
S41	unknown gene	-	-	-	-	DD41
S42	unknown gene	-	-	-	-	DD42

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S43	unknown gene	-	-	-	-	DD42
S44	unknown gene	-	-	-	-	DD43
S45	unknown gene	-	-	-	-	DD43
S46	unknown gene	-	-	-	-	DD44
S47	unknown gene	-	-	-	-	DD44
S48	unknown gene	-	-	-	-	DD45
S49	unknown gene	-	-	-	-	DD45
S50	unknown gene	-	-	-	-	DD47
S51	unknown gene	-	-	-	-	DD49
S52	unknown gene	-	-	-	-	DD19
S53	unknown gene	-	-	-	-	DD19
S54	unknown gene	-	-	-	-	DD50
S55	unknown gene	-	-	-	-	DD21
S56	unknown gene	-	-	-	-	DD51

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S57	unknown gene	-	-	-	-	DD21
S58	unknown gene	-	-	-	-	DD52
S59	unknown gene	-	-	-	-	DD55
S60	unknown gene	-	-	-	-	DD56
S61	unknown gene	-	-	-	-	DD27
S62	unknown gene	-	-	-	-	DD27
S63	unknown gene	-	-	-	-	DD27
S64	unknown gene	-	-	-	-	DD28
S65	unknown gene	-	-	-	-	DD28
S66	unknown gene	-	-	-	-	DD28
S67	unknown gene	-	-	-	-	DD60
S68	unknown gene	-	-	-	-	DD30
S69	unknown gene	-	-	-	-	DD62
S70	unknown gene	-	-	-	-	DD63

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S71	unknown gene	-	-	-	-	DD64
S72	unknown gene	-	-	-	-	DD64
S73	unknown gene	-	-	-	-	DD65
S74	unknown gene	-	-	-	-	DD69
S75	unknown gene	-	-	-	-	DD69
S76	unknown gene	-	-	-	-	DD72
S77	unknown gene	-	-	-	-	DD72
S78	unknown gene	-	-	-	-	DD74
S79	unknown gene	-	-	-	-	DD76
S80	unknown gene	-	-	-	-	DD76
S81	unknown gene	-	-	-	-	DD77
S82	unknown gene	-	-	-	-	DD81
S83	unknown gene	-	-	-	-	DD81
S84	unknown gene	-	-	-	-	DD81

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S85	unknown gene	-	-	-	-	DD84
S86	unknown gene	-	-	-	-	DD85
S87	unknown gene	-	-	-	-	DD85
S88	unknown gene	-	-	-	-	DD86
S89	unknown gene	-	-	-	-	DD86
S90	unknown gene	-	-	-	-	DD86
S91	unknown gene	-	-	-	-	DD87
S92	unknown gene	-	-	-	-	DD88
S93	unknown gene	-	-	-	-	DD88
S94	unknown gene	-	-	-	-	DD90
S95	unknown gene	-	-	-	-	DD90
S96	unknown gene	-	-	-	-	DD91
S97	unknown gene	-	-	-	-	DD91
S98	unknown gene	-	-	-	-	DD91

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S99	unknown gene	-	-	-	-	DD95
S100	unknown gene	-	-	-	-	DD95
S101	unknown gene	-	-	-	-	DD97
S102	unknown gene	-	-	-	-	DD97
S103	unknown gene	-	-	-	-	DD37
S104	unknown gene	-	-	-	-	DD18
S105	unknown gene	-	-	-	-	DD39
S106	unknown gene	-	-	-	-	DD1 DD2
S107	unknown gene	-	-	-	-	DD54 DD81
S108	unknown gene	-	-	-	-	DD15 DD16

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S109	unknown gene	-	-	-	-	DD11 DD76
S110	unknown gene	-	-	-	-	DD7 DD19
S111	unknown gene	-	-	-	-	DD83 DD84
S112	unknown gene	-	-	-	-	DD93 DD95
S113	unknown gene	-	-	-	-	DD96 DD97
S114	unknown gene	-	-	-	-	DD92 DD94
S115	unknown gene	-	-	-	-	DD37 DD39

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S116	unknown gene	-	-	-	-	DD37 DD39
S117	unknown gene	-	-	-	-	DD78 DD80
S118	unknown gene	-	-	-	-	DD47 DD48 DD49
S119	unknown gene	-	-	-	-	DD21 DD22 DD23
S120	unknown gene	-	-	-	-	DD17 DD18 DD27

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S121	unknown gene	-	-	-	-	DD66 DD67 DD74
S122	unknown gene	-	-	-	-	DD21 DD23 DD24
S123	unknown gene	-	-	-	-	DD24 DD25 DD26
S124	unknown gene	-	-	-	-	DD68 DD71 DD82

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S125	unknown gene	-	-	-	-	DD79 DD80 DD81
S126	unknown gene	-	-	-	-	DD60 DD61 DD62 DD63
S127	unknown gene	-	-	-	-	DD14 DD20 DD23 DD28

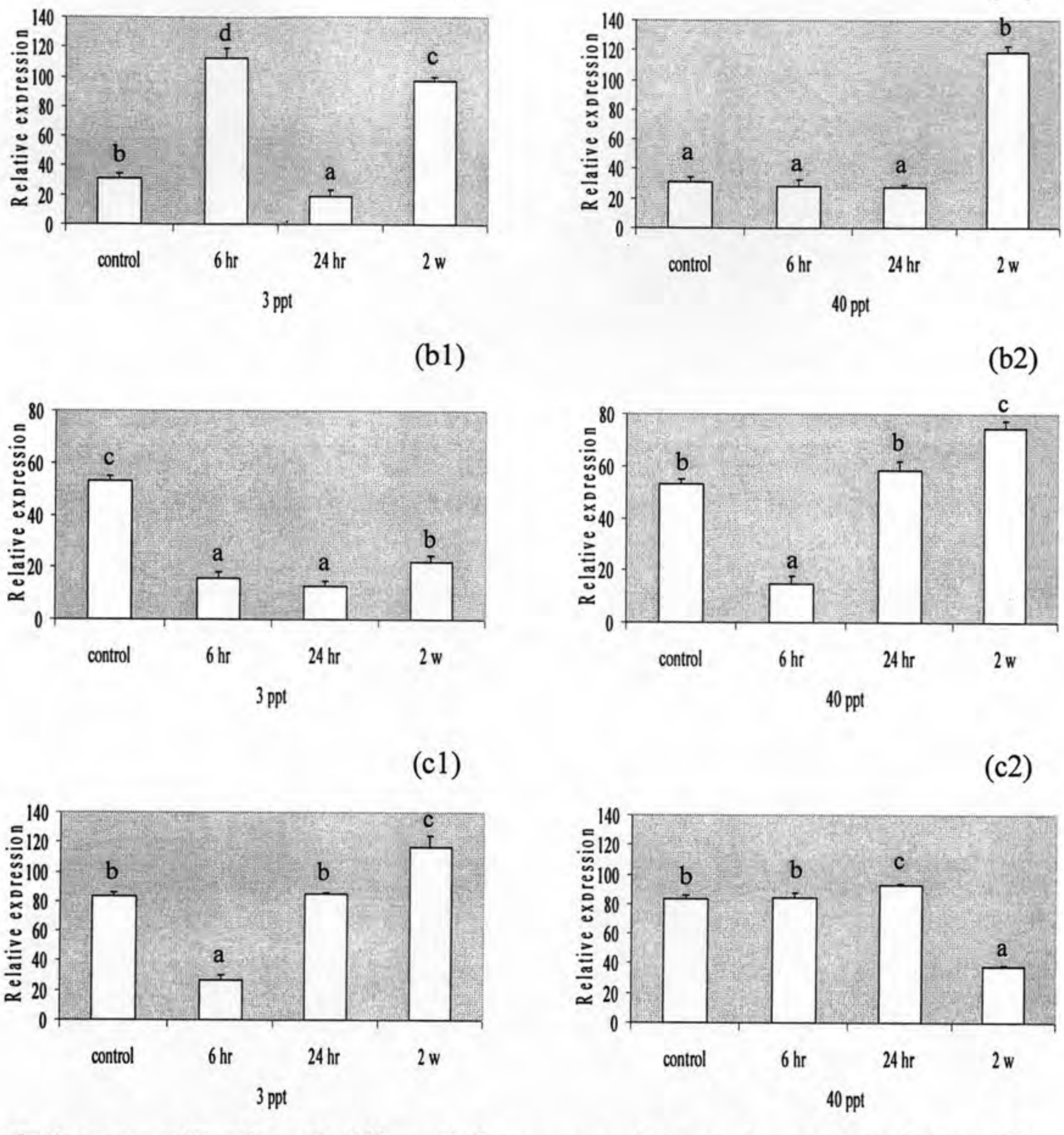
I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S128	unknown gene	-	-	-	-	DD5 DD12 DD14 DD16 DD19 DD20

I (continued)

Sequence	Sequence homology	Closest species	Accession no. of closest species	Expected value	Positive	Differentially expressed band
S129	unknown gene	-	-	-	-	DD9 DD10 DD11 DD31 DD32 DD34 DD35 DD36 DD38 DD40 DD46 DD48 DD50 DD73 DD75 DD89

APPENDIX B

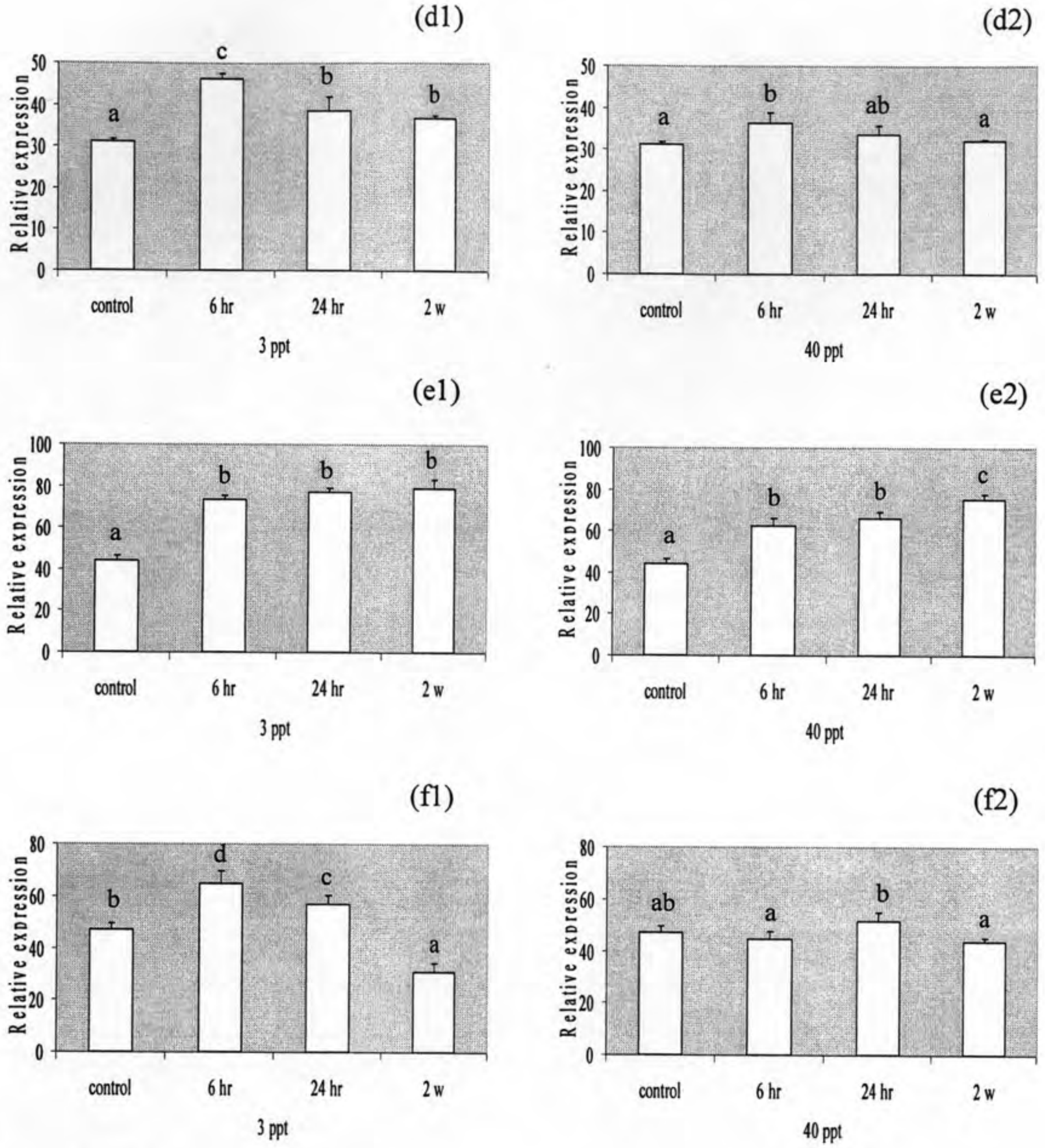


I Relative quantification of differentially expressed genes in control shrimp (25 ppt) compared to stressed shrimp shrimp (3 and 40 ppt salinities) by semi-quantitative RT-PCR. Different letters indicate significant (p < 0.05) difference in the mean expression level of the salinity expressed gene.

(a1, a2) The gill template was amplified with P-S5 primer.

(b1, b2) The epipodite template was amplified with P-S8 primer.

(c1, c2) The gill template was amplified with P-S8 primer.

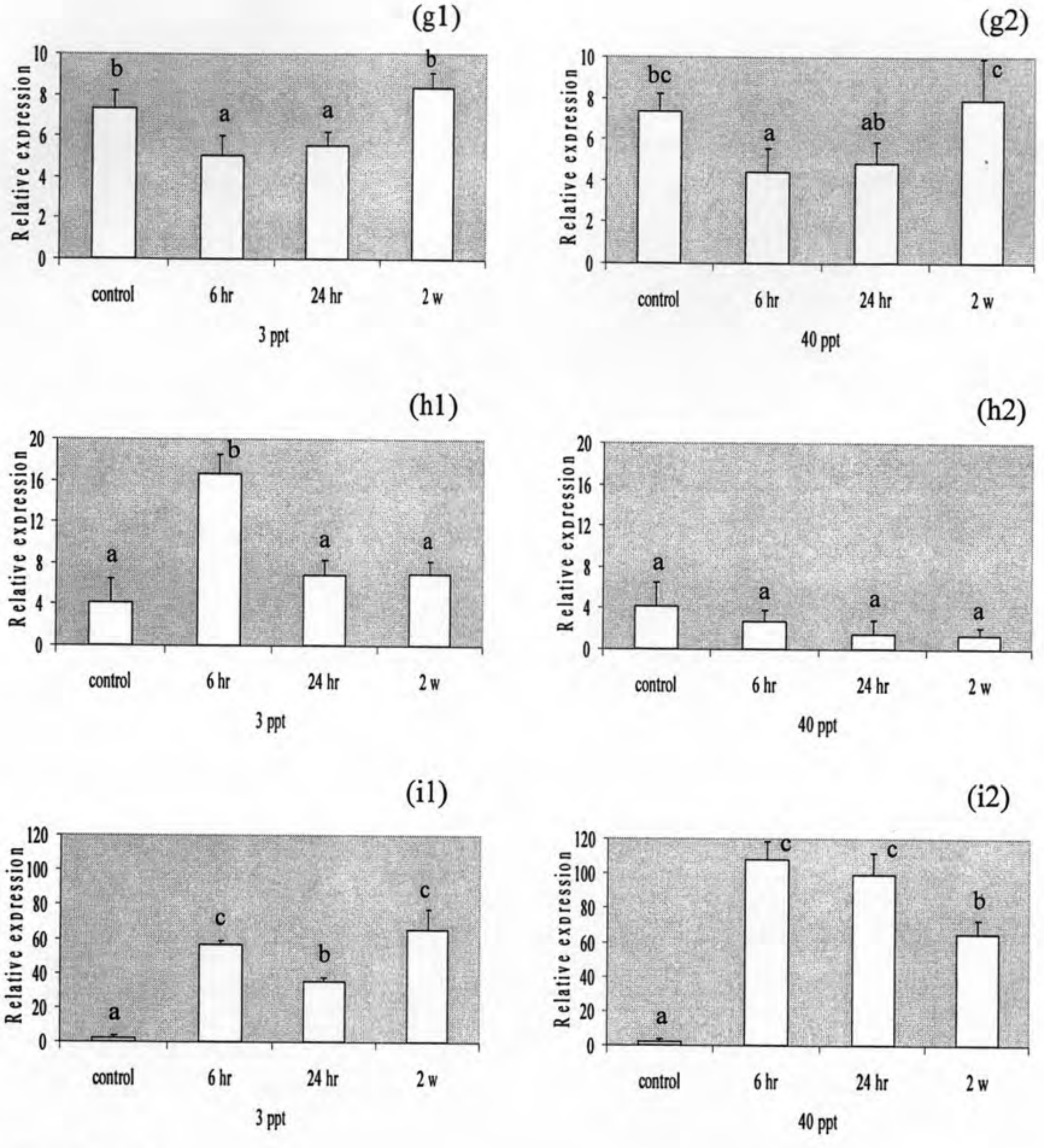


I (continued)

(d1, d2) The gill template was amplified with P-S9 primer.

(e1, e2) The antennal gland template was amplified with P-S11 primer.

(f1, f2) The gill template was amplified with P-S11 primer.

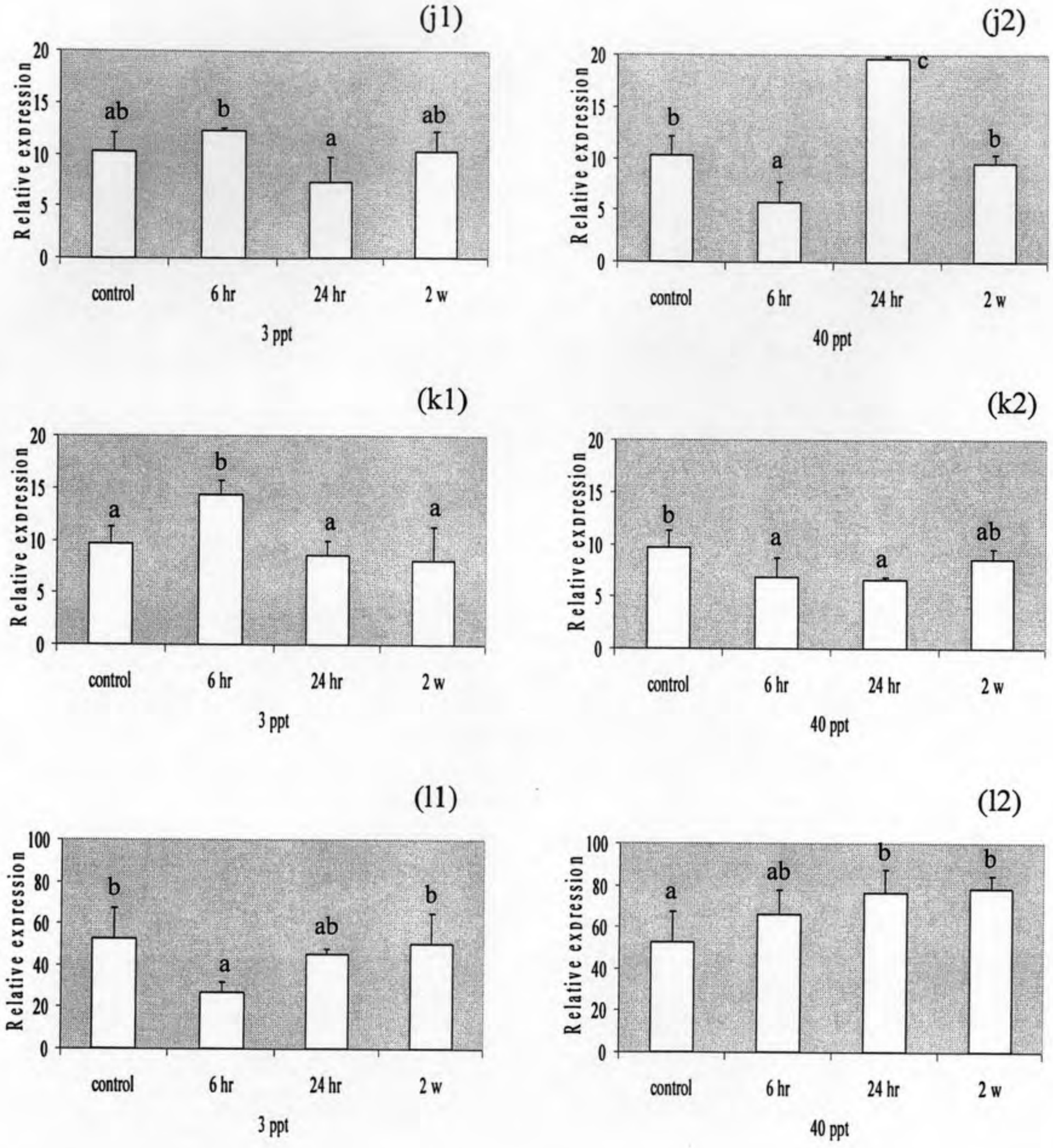


I (continued)

(g1, g2) The epipodite template was amplified with P-S12 primer.

(h1, h2) The gill template was amplified with P-S12 primer.

(i1, i2) The gill template was amplified with P-S13 primer.

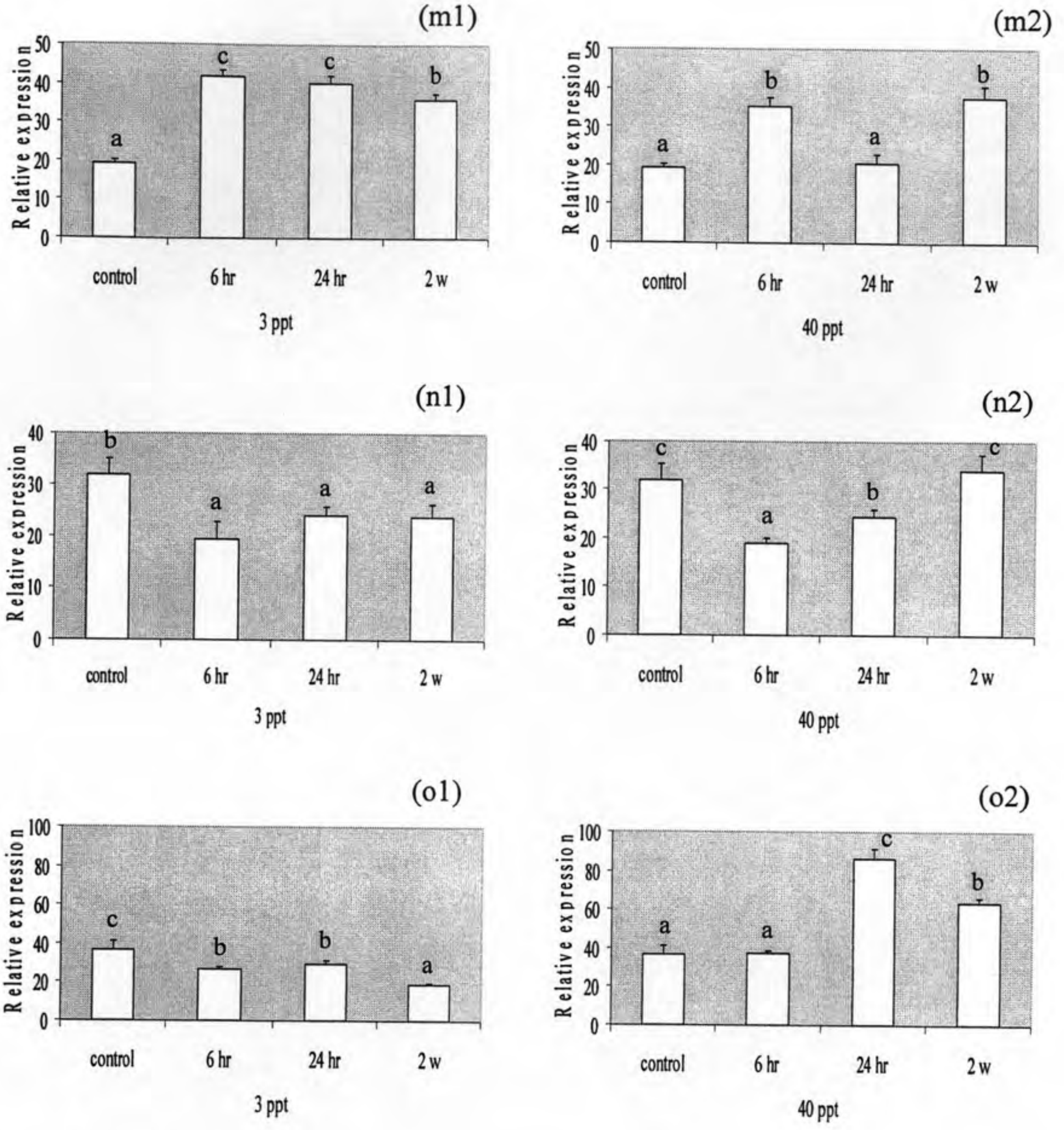


I (continued)

(j1, j2) The gill template was amplified with P-S14 primer.

(k1, k2) The gill template was amplified with P-S17 primer.

(l1, l2) The gill template was amplified with P-S21 primer.

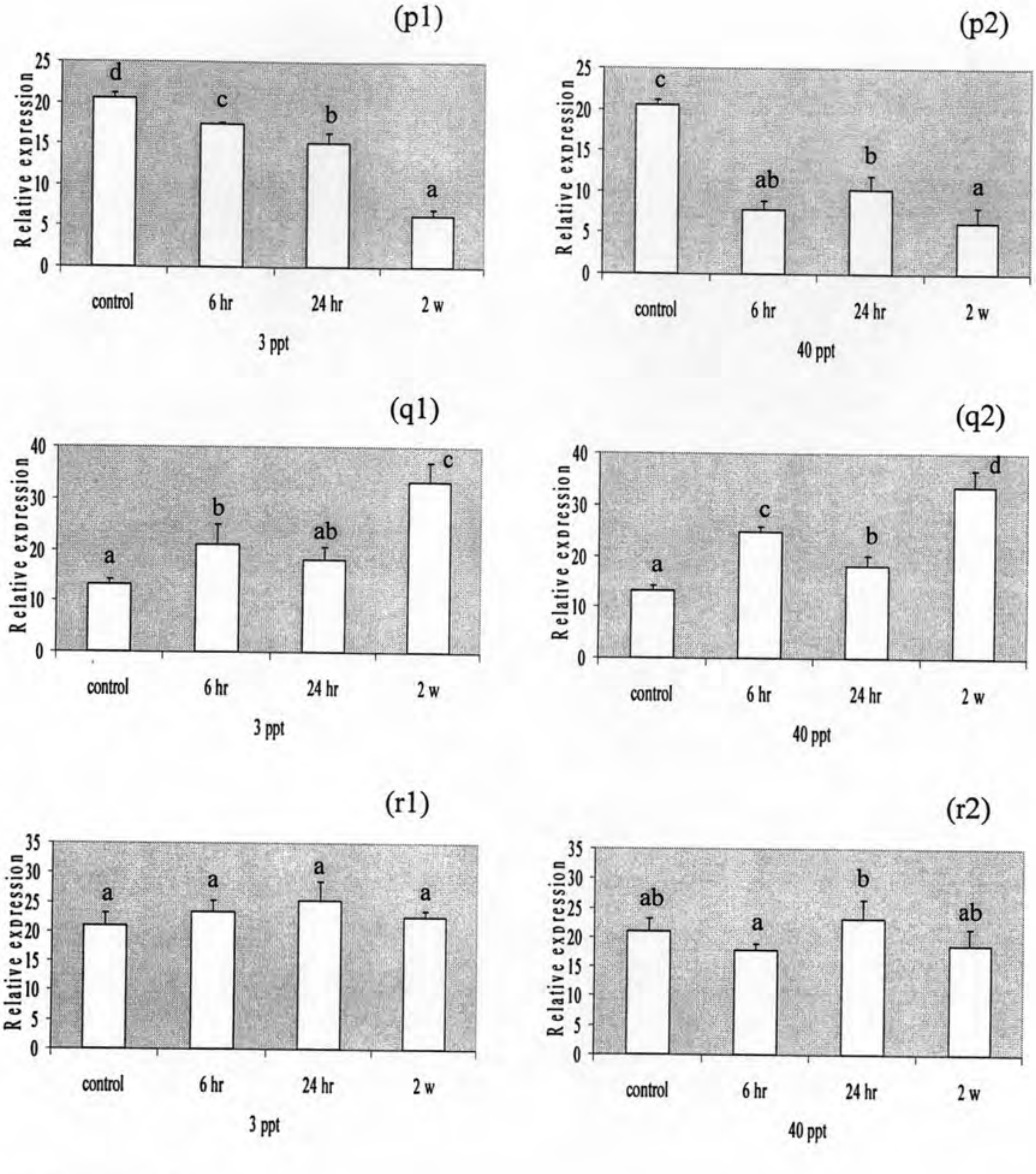


I (continued)

(m1, m2) The antennal gland template was amplified with P-S22 primer.

(n1, n2) The epipodite template was amplified with P-S22 primer.

(o1, o2) The gill template was amplified with P-S25 primer.

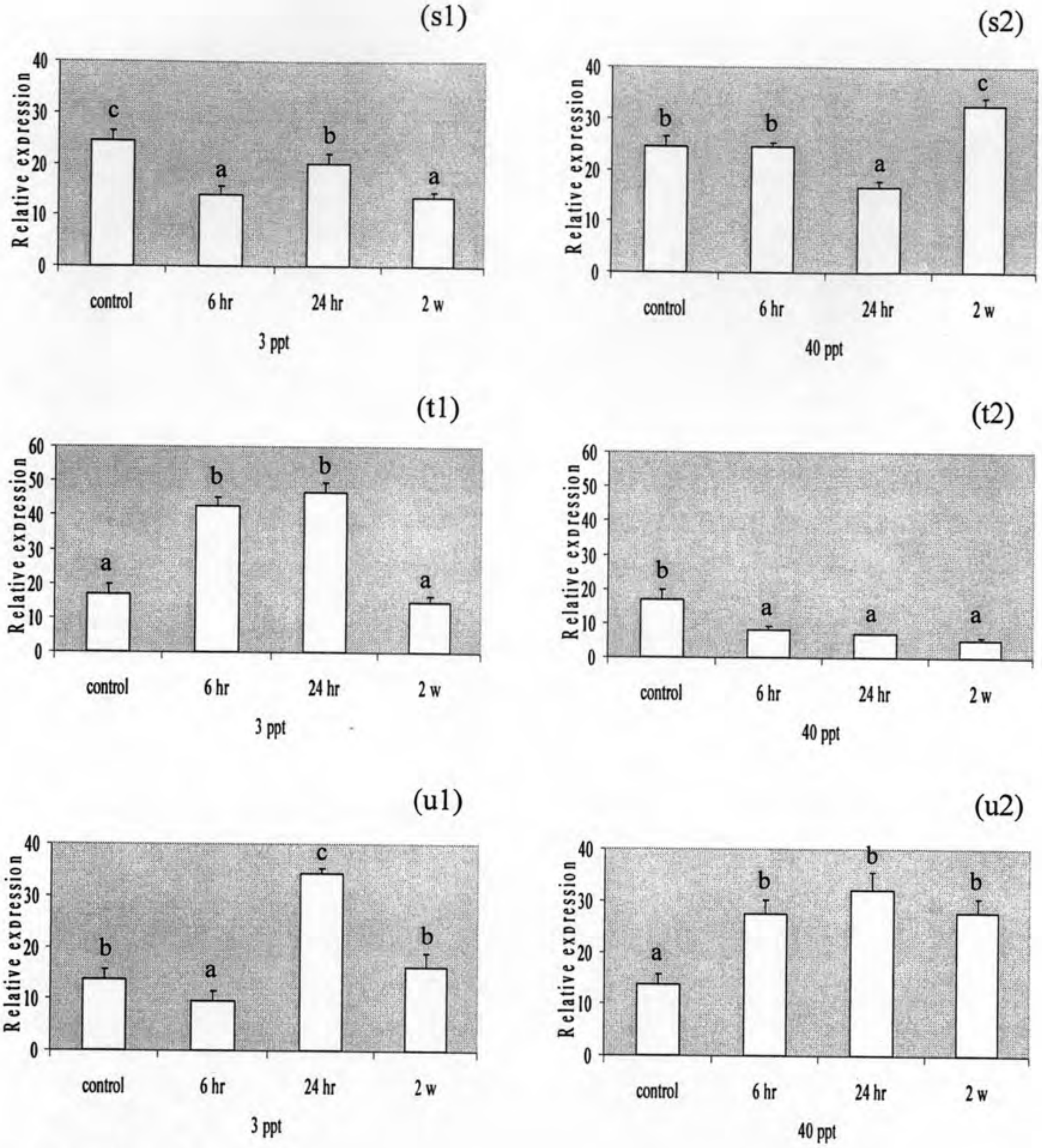


I (continued)

(p1, p2) The gill template was amplified with P-S26 primer.

(q1, q2) The antennal gland template was amplified with P-S30 primer.

(r1, r2) The gill template was amplified with P-S34 primer.

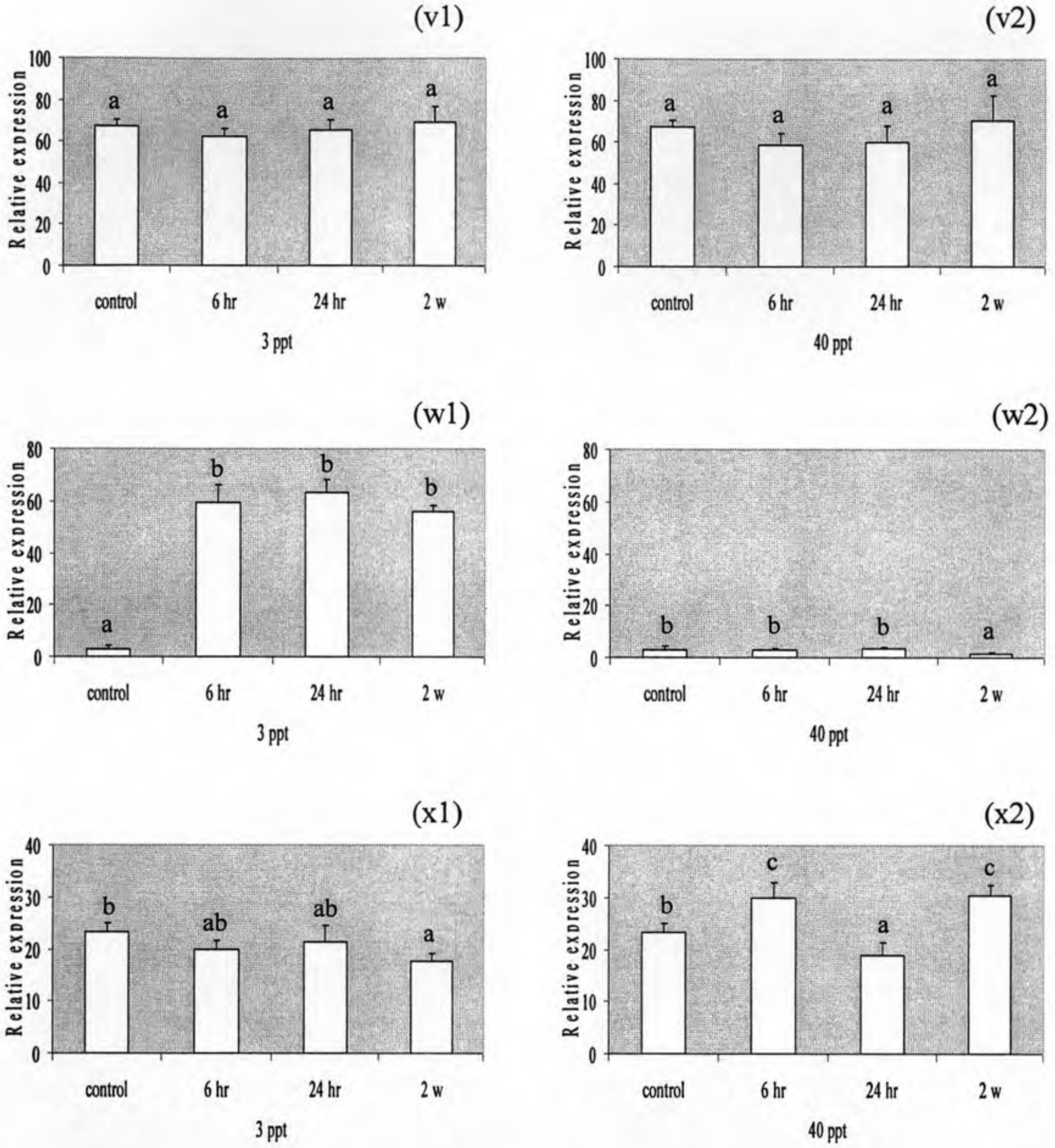


I (continued)

(s1, s2) The epipodite template was amplified with P-S38 primer.

(t1, t2) The gill template was amplified with P-S56 primer.

(u1, u2) The gill template was amplified with P-S71 primer.

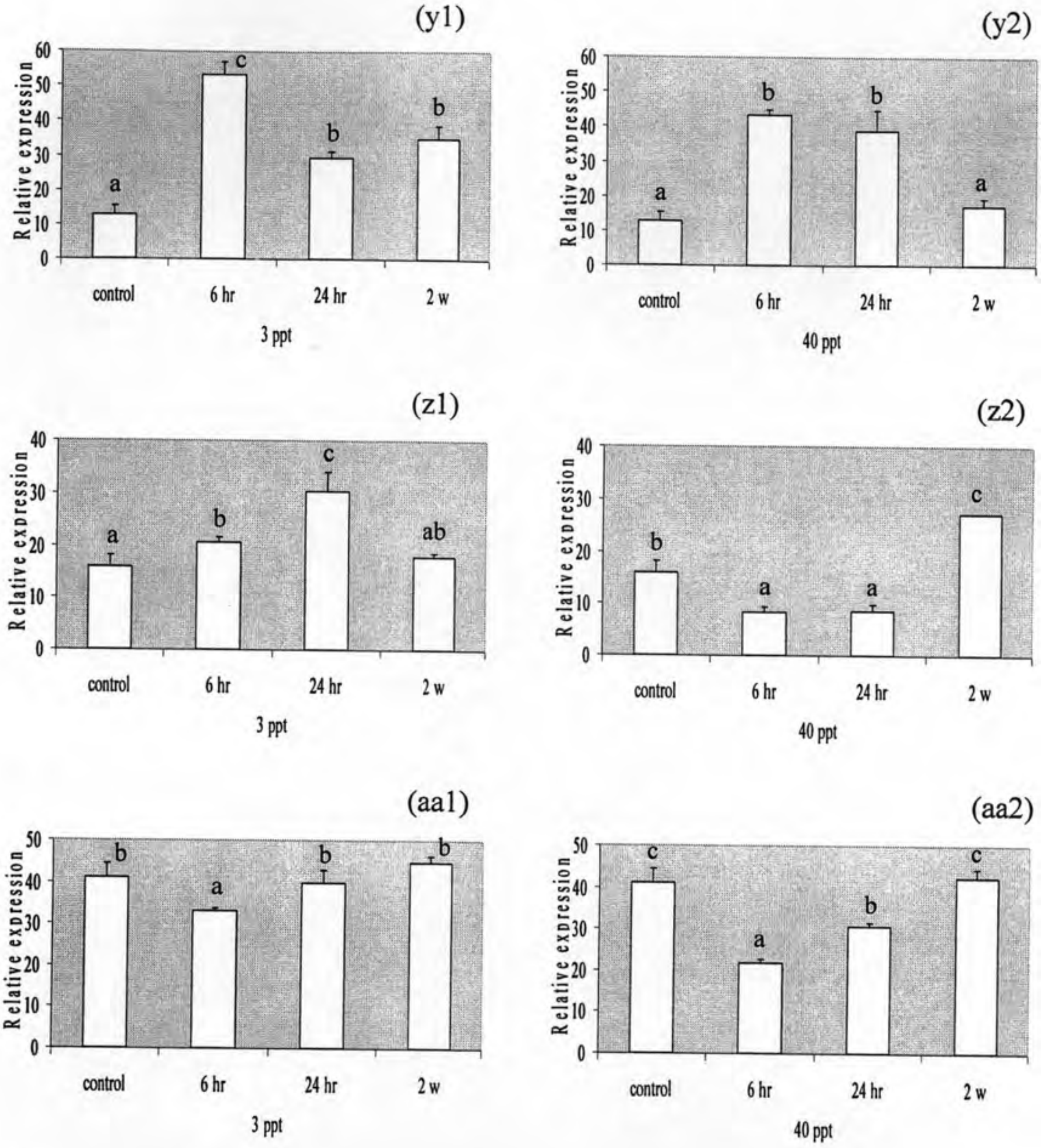


I (continued)

(v1, v2) The antennal gland template was amplified with P-S111 primer.

(w1, w2) The gill template was amplified with P-S112 primer.

(x1, x2) The gill template was amplified with P-S114 primer.

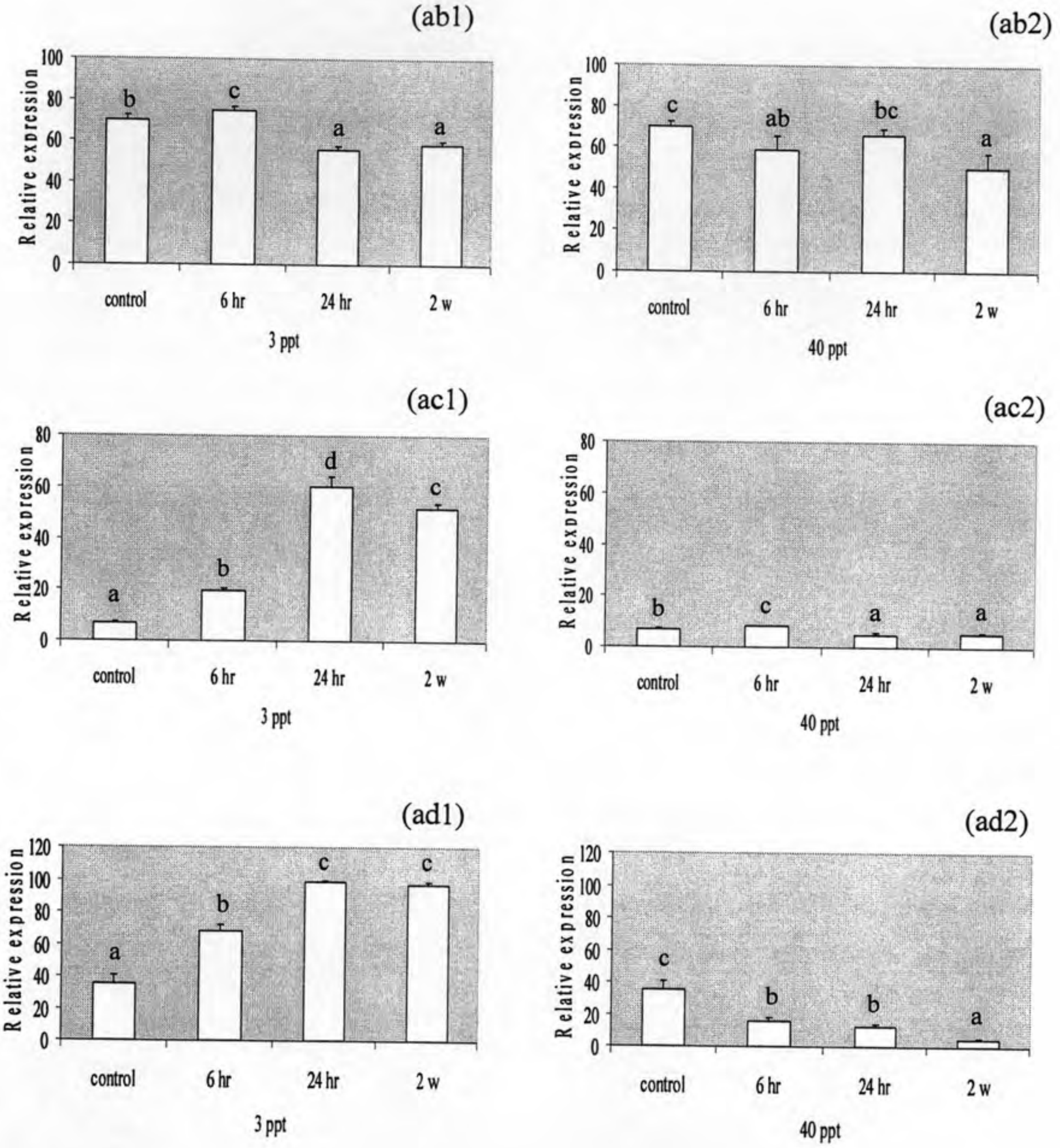


I (continued)

(y1, y2) The gill template was amplified with P-S114 primer.

(z1, z2) The antennal gland template was amplified with P-S118 primer.

(aa1, aa2) The epipodite template was amplified with P-S118 primer.

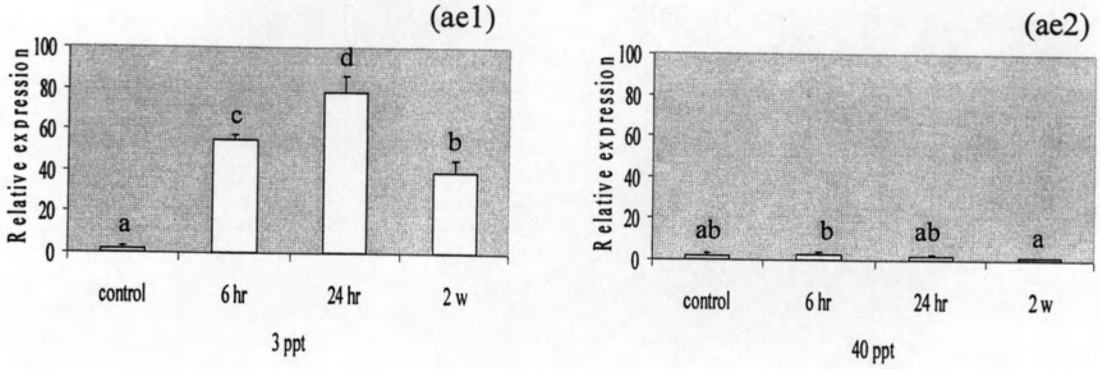


I (continued)

(ab1, ab2) The gill template was amplified with P-S126 primer.

(ac1, ac2) The antennal gland template was amplified with P-S129 primer.

(ad1, ad2) The epipodite template was amplified with P-S129 primer.



I (continued)

(ae1, ae2) The gill template was amplified with P-S129 primer.

BIOGRAPHY

Miss Suchonma Udomlertpreecha was born on February 9, 1982 in Nakhon Ratchasima. She graduated with the degree of Bachelor of Science from the Department of Biotechnology, Faculty of Science, Thammasat University in 2004. She has studied for the degree of Master of Science at the department of Biotechnology, Chulalongkorn University since 2004.