Supporting information

In-depth in silico search for cuttlefish (Sepia officinalis) antimicrobial peptides following bacterial challenge of haemocytes.

Louis Benoist^{1,2}, Baptiste Houyvet^{1,2,5}, Joël Henry^{1,2}, Erwan Corre⁴, Bruno Zanuttini³ and Céline Zatylny-Gaudin^{1,2,*}

¹ NORMANDIE UNIV, UNICAEN, CNRS, BOREA, 14000 CAEN, France

² Laboratoire de Biologie des Organismes et Ecosystèmes Aquatiques (BOREA) Université de Caen-Normandie, MNHN, SU, UA, CNRS, IRD, Esplanade de la Paix, 14032 Caen Cedex, France ³ Normandie Univ., UNICAEN, ENSICAEN, CNRS; GREYC, 14 000 Caen, France

⁴ Plateforme ABiMS, Station Biologique de Roscoff (CNRS-Sorbonne Université), 29688 Roscoff, France

⁵SATMAR, Société ATlantique de MARiculture, Research and Development Department, Gatteville, France

*Corresponding author: celine.gaudin@unicaen.fr

Supporting experimental section		
Supplemental Tables:		
Table S1. Twenty most expressed transcripts in c-hct	3	
Table S2. Twenty most expressed transcripts in Vs-hct	4	
Table S3. Expression pattern of selected transcripts	5	

Supporting experimental section

Detailed quality control and cDNA library preparation protocols

Total RNA was quantified using a NanoDrop Spectrophotometer ND-1000 (NanoDrop Technologies, Inc.), and its integrity was assessed on a 2100 Bioanalyzer (Agilent Technologies). Libraries were generated from 250 ng of total RNA as follows: mRNA enrichment was performed using the NEBNext Poly(A) Magnetic Isolation Module (New England BioLabs). cDNA synthesis was achieved using NEBNext RNA First Strand Synthesis and NEBNext Ultra Directional RNA Second Strand Synthesis Modules (New England BioLabs). The remaining steps of library preparation were performed using NEBNext Ultra II DNA Library Prep Kit for Illumina (New England BioLabs). Adapters and PCR primers were purchased from New England BioLabs. Libraries were quantified using the Quant-iT[™] PicoGreen® dsDNA Assay Kit (Life Technologies) and the Kapa Illumina GA with Revised Primers-SYBR Fast Universal kit (Kapa Biosystems). Average size fragment was determined using a LabChip GX (PerkinElmer) instrument.

Supplementary Tables:

			Expre		
	Name	Transcript	c-hct	Vs-hct	Fold change
1	Transferrin	TR90372 c1_g1_i1	28022.57	27562.43	0.98
2	Neurofilament	TR19485 c1_g1_i1	26823.13	23315.72	0.87
3	Chitin deacetylase	TR33375 c0_g1_i1	16019.63	14894.69	0.93
4	Structural polyprotein	TR42824 c0_g1_i1	14678.55	10635.02	0.72
5	Polyubiquitin	TR38732 c0_g23_i1	7339.71	5075.77	0.69
6	Filamin-A	TR33303 c3_g1_i1	6632.45	5638.52	0.85
7	Unknown 1	TR41826 c5_g19_i2	6351.18	10524.84	1.66
8	Ferritin	TR34156 c1_g1_i1	5373.48	3223.95	0.60
9	Unknown 2	TR39529 c1_g1_i1	4465.00	6042.63	1.35
10	Tropomyosin	TR38640 c3_g1_i7	4452.91	3596.50	0.81
11	Unknown 3	TR42689 c4_g10_i1	4086.45	2463.57	0.60
12	Matrix metalloproteinase	TR35643 c1_g1_i1	3933.39	2220.67	0.56
13	Matrilin-2°	TR5676 c0_g1_i1	3770.58	1647.49	0.44
14	Actin	TR377331c5_g10_i2	3672.30	2996.36	0.82
15	Matrilin-3	TR42669 c4_g1_i1	3612.10	2030.77	0.56
16	Riboflavin kinase	TR58606 c1_g1_i1	3441.99	4689.02	1.36
17	Dynein light chain	TR42526 c19_g12_i4	3329.41	2603.44	0.78
18	Unknown 4	TR36711 c0_g3_i2	2752.47	2320.78	0.84
19	Unknown 5°	TR74858 c0_g1_i1	2630.99	1100.13	0.42
20	Perivitellin	TR38132 c1_g1_i1	2420.55	2693.39	1.11

Table S1. Twenty most expressed transcripts in c-hct (°: c-hct-specific transcripts)

			Expre		
	Name	Transcript	c-hct	Vs-hct	Fold change
1	Transferrin	TR90372 c1_g1_i1	28022.57	27562.43	0.98
2	Neurofilament	TR19485 c1_g1_i1	26823.13	23315.72	0.87
3	Chitin deacetylase	TR33375 c0_g1_i1	16019.63	14894.69	0.93
4	Structural polyprotein	TR42824 c0_g1_i1	14678.55	10635.02	0.72
5	Unknown 1	TR41826 c5_g19_i2	6351.18	10524.84	1.66
6	Unknown 2	TR39529 c1_g1_i1	4465.00	6042.63	1.35
7	Filamin-A	TR33303 c3_g1_i1	6632.45	5638.52	0.85
8	Polyubiquitin	TR38732 c0_g23_i1	7339.71	5075.77	0.69
9	Riboflavin kinase	TR58606 c1_g1_i1	3441.99	4689.02	1.36
10	Histone H1*	TR41094 c2_g12_i1	2280.01	4563.54	2.00
11	Tropomyosin	TR38640 c3_g1_i7	4452.91	3596.50	0.81
12	Ferritin	TR34156 c1_g1_i1	5373.48	3223.95	0.60
13	Actin	TR37733 c5_g10_i2	3672.30	2996.36	0.82
14	Perivitellin	TR38132 c1_g1_i1	2420.55	2693.39	1.11
15	Unknown 6*	TR38730 c4_g1_i1	2123.73	2653.98	1.25
16	Dynein light chain	TR42526 c19_g12_i4	3329.41	2603.44	0.78
17	Unknown 3	TR42689 c4_g10_i1	4086.45	2463.57	0.60
18	Unknown 4	TR36711 c0_g3_i2	2752.47	2320.78	0.84
19	Matrix metalloproteinase	TR35643 c1_g1_i1	3933.39	2220.67	0.56
20	Matrilin-3	TR42669 c4_g1_i1	3612.10	2030.77	0.56

Table S2. Twenty most expressed transcripts in Vs-hct (*: Vs-hct-specific transcripts)

Transcript ID	Expression (TPM)					
	Vs-hct	c-hct	EB	ISF	ISM	S
TR42258 c1_g1_i1	7.566	8.928	36.498	4.556	3.755	23.107
TR27534 c0_g1_i1	23.786	17.388	3.984	1.758	1.58	10.381
TR36613 c0_g1_i1	17.011	20.28	19.871	5.199	6.307	20.806
TR42563 c7_g3_i1	0.775	1.992	0	0	0	0.319
TR5654 c0_g1_i1	17.331	9.773	59.912	42.483	30.16	61.859

Table S3. Expression patterns of selected transcripts. (ED: embryo, ISF: ink sac female, ISM: ink sac male, S: skin).