

Rearing effect of biofloc on antioxidant and antimicrobial transcriptional response in *Litopenaeus stylirostris* shrimp facing an experimental sub-lethal hydrogen peroxide stress

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Abstract :

This study compares the antioxidant and antimicrobial transcriptional expression of blue shrimps reared according to two different systems, BioFloc Technology (BFT) and Clear sea Water (CW) and their differential responses when facing an experimental sublethal hydrogen peroxide stress. After 30 days of rearing, juvenile shrimps were exposed to H₂O₂ stress at a concentration of 30 ppm during 6 hours. The oxidative stress caused by H₂O₂ was examined in the digestive glands of the shrimp, in which antioxidant enzyme (AOE) and antimicrobial peptide (AMP) gene expression were analysed by quantitative real-time PCR. Results showed that rearing conditions did not affect the expression of genes encoding AOE or AMPs. However, H₂O₂ stress induced a differential response in expression between shrimps from the two rearing treatments (BFT and CW). Comparative analysis of the expression profiles indicates that catalase transcripts were significantly upregulated by H₂O₂ stress for BFT shrimps while no change was observed for CW shrimps. In contrast, H₂O₂ caused down-regulation of superoxide dismutase and glutathione transferase transcripts and of the three AMP transcripts studied (penaeidin 2 and 3, and crustin) for CW shrimps, while no effect was observed on BFT shrimp transcript levels. These results suggested that BFT shrimps maintained antioxidant and AMP responses after stress and therefore can effectively protect their cells against oxidative stress, while CW shrimp immune competence seems to decrease after stress.

Highlights

► Contrasted rearing conditions, biofloc and clear water, did not affect the expression of genes encoding antioxidant enzymes and antimicrobial peptides. ► Biofloc shrimps maintained antioxidant and antimicrobial peptide responses after H₂O₂ stress while the immune competence of clear water shrimp seemed to decrease after stress. ► Biofloc seems to improve the immune resistance of animals against stress.

Keywords : biofloc, shrimps, antimicrobial peptides, antioxidant enzymes

1. Introduction

In shrimp aquaculture, intense interest has focused on biofloc technology (BFT). BFT is a rearing system with zero or minimal water exchange. Conglomerates of microbes, algae, protozoa and other organisms, together with detritus and dead organic particles, develop in the water column ([Avnimelech, 2009](#)). The intensive microbial community present in this system can be used as a water quality treatment system for the pond and microbial protein can serve as a feed additive. At the present time, when shrimp production faces many losses due to disease outbreaks, the use of BFT can restrain the development of shrimp diseases. One explanation is that, with zero or minimal water exchange, BFT improves biosecurity because the exclusion of pathogens is enhanced by limiting contact with water from external aquatic ecosystems ([Taw, 2013](#)). Another explanation is that the microbial proteins assimilated by shrimp are believed to confer beneficial effects on well-being and shrimp immune status ([Avnimelech, 2009](#)). Nevertheless, the influence of biofloc on shrimp immune status has been poorly documented ([Xu and Pan, 2013, 2014](#); [Kim *et al.*, 2013](#); [Ekasari *et al.*, 2014](#)).

Because of their lack of acquired immunity, marine invertebrates' defence against invading pathogens relies solely on innate immune mechanisms ([Mitta *et al.*, 2000](#)). In shrimp these include: 1) pattern recognition receptors (PRR) ([Wang and Wang, 2013](#)); 2) humeral

62 responses characterized by the expression of antimicrobial peptides (AMPs), (Destoumieux *et*
63 *al.*, 1997) but also coagulation and melanisation by so-called clotting (Omori *et al.*, 1989; Yeh
64 *et al.*, 1998; Chen *et al.*, 2005) and prophenoloxidase activating systems (Sritunyalucksana
65 and Söderhäll, 2000; Lee *et al.*, 2002; Charoensapsri *et al.*, 2011); 3) cellular responses,
66 mainly performed by haemocytes, such as phagocytosis (Song *et al.*, 1994), chemotaxis with
67 haemocyte migration into inflammatory foci (Munoz *et al.*, 2002), release of humeral defence
68 components (agglutinins, coagulation and phenoloxidase enzymes, antimicrobial peptides),
69 encapsulation and nodule formation (Holmblad and Söderhäll, 1999).

70 Animal stress induced by sub-lethal H₂O₂ concentration is a method rarely used to induce
71 stress and therefore original. It seemed interesting to study the response of animals to H₂O₂
72 stress because, although oxygen radical stress and antioxidant protection are coming
73 increasingly into focus in physiological research on marine invertebrates, only a few studies
74 have considered the effects of elevated concentrations of reactive oxygen species (ROS) on
75 invertebrate physiology (Abele-Oeschger *et al.*, 1997). Among commonly used biomarkers of
76 immunity, antioxidant enzymes (AOEs) are directly involved in scavenging ROS and play
77 pivotal roles in preventing damage generated by oxidative stress. ROS have been identified as
78 major initiators of tissue damage and can upregulate enzyme activity, signal transcription, and
79 gene expression (Massafra *et al.*, 2000). The antioxidant defence and immune systems are
80 closely linked to responses to pathogens and other stress-related issues that might lead to
81 respiratory burst (Holmblad and Söderhäll, 1999). Measuring AOE expression after
82 environmental stressors such as pH (Wang *et al.*, 2009), temperature, salinity, hypoxia (De
83 Zoysa *et al.*, 2009) and H₂O₂ stress (De Zoysa *et al.*, 2008) has proven to be a very good tool
84 to study the responses of aquatic invertebrates. In contrast, very few studies have used
85 antimicrobial peptide (AMP) analysis to investigate the impact of environmental stress on
86 invertebrate immunology (Mitta *et al.*, 2000, Cellura *et al.*, 2007; Li *et al.*, 2009). The major
87 studies on AMPs have focused on their identification, characterization, and regulation
88 following pathogen infection (Bachère *et al.*, 2004). However, investigating AMPs can
89 provide a unique opportunity to greatly advance current understanding in the field of
90 ecological immunology and especially the impact of environmental stressors (Ellis *et al.*,
91 2011).

92 In our study, we explore the transcriptional responses of genes coding either for AOEs or
93 AMPs in shrimp during contrasted rearing conditions, biofloc *versus* clear seawater, and
94 experimentally induced stress produced by a sub-lethal dose of hydrogen peroxide.

95

96 **Materials and method**

97 **Shrimps**

98 The 12 day-old shrimps post-larvae *Litopenaeus stylirostris* used in this experiment were
99 supplied by the hatchery of the Aquaculture Technical Centre of Tahiti (French Polynesia).
100 Shrimps acclimated during 15 days in a 25 m³ clear seawater tank (300% water renewal per
101 day) and were fed three times per day with commercial feed at 20% of the shrimp biomass
102 (SICA grower 40).

103 **Biofloc production**

104 The biofloc culture was established before the experiment in 4 tanks (250 L) with sub-adult
105 shrimps (mean weight: 20 g, biomass: 500 g.m⁻²) and fed twice per day with commercial
106 shrimp feed (SICA grower 40) during 30 days. The shrimps were removed before the
107 beginning of the experiment. Aeration was delivered continuously via an air stone in each
108 tank. No water exchange was performed. Tanks were covered with a shade net to control the
109 sunlight (70% inhibition of light).

110

111 **Experimental design**

112 Shrimps were caught in clear water tanks using a cast net and randomly distributed into 8
113 tanks (250 L). One hundred individuals (0.07±0.02g) were put into each tank (400 shrimps.
114 m⁻²). Each tank was continuously aerated with an air stone. No water was exchanged during
115 the experimental period in the biofloc rearing system and a water renewal rate of 300% per
116 day was applied in the clear seawater rearing system.

117 Two treatments with four replicate tanks for a period of 30 days were tested: clear seawater
118 (CW) and biofloc (BFT). Shrimps were fed *ad libitum* 3 times per day (07:00 am, 01:00 pm
119 and 05:00 pm) with commercial shrimp feed (SICA® grower 40). The pellet given to shrimp
120 was the only source of carbon. It is equivalent to a C/N ratio of 8/1.

121 **H₂O₂ stress, sampling and conservation**

122 To achieve H₂O₂ stress, water renewal was operated in the biofloc tank during 12 hours to
123 place the shrimp in sea clear water. During stress, all shrimps were maintained under the same
124 conditions (clear seawater, temperature = 26.3°C, salinity = 34.5‰, pH = 8.20).

125 Then, all shrimps remaining in the tanks were stressed by immersion for 6 hours with a sub-
126 lethal concentration of H₂O₂ (30 ppm) added directly to the rearing tank.

127 Only shrimps in the inter-molt phase were sampled for molecular analysis. Molting stages
128 were determined by microscopic examination of antennal scales according to the method of
129 Drach and Tchernigovtzeff (1967). This was to minimize variations, because changes in
130 physiological parameters are generally observed during the molting cycle in crustaceans.

131 The sampling was performed before and after 6 hours of stress; ten shrimps per tank were
132 caught and put directly in iced seawater (0°C). Because of their small size, only digestive
133 gland tissues were sampled.

134 The digestive glands of 10 intermolt shrimps per tank (before and after H₂O₂ stress) were
135 removed. The tissues were immediately pooled in RNA Later (Sigma[®]), refrigerated at 4°C
136 for 12 hours and kept at – 80 °C until analysis.

137 **Antioxidant and AMP gene expression analysis by relative quantitative real-time PCR** 138 **(q-PCR)**

139 Total RNA from the digestive glands was extracted using the Trizol method (Invitrogen,
140 USA) according to the manufacturer's instructions. The quantity and quality of each RNA
141 were assessed by measuring their absorbance at 260 and 280 nm using a Nanodrop 1000
142 Spectrophotometer (Thermo Scientific) associated with ND-1000 V3 7.0 software. A DNase
143 treatment to remove residual DNA was carried out using the Ambion DNase free kit,
144 following the manufacturer's instructions.

145 First-strand cDNA was synthesized with 500 ng of total RNA in each reaction system using
146 the Roche[®] transcriptor first strand cDNA synthesis system according to the manufacturer's
147 protocol. All cDNAs were diluted 1/100 with nuclease-free water and stored at -20 °C until
148 used as templates in real-time quantitative PCR (qRT-PCR).

149 Specific primers for Catalase (CAT), Glutathione peroxidase (GPX), Super oxide dismutase
150 (SOD), and glutathione transferase (GSHT) were obtained by alignment of the most
151 conserved regions from those sequences registered in Genbank. Primers for AMP genes,
152 lysozyme (Lyso), Peneaidin 2 and 3 (Pen 2, Pen 3) and Crustin (Cru) were obtained from De
153 Lorgeril *et al.* (2008). The primer sequences are shown in table 1.

154 Real-time qRT-PCR was carried out in a Stratagene Mx3000P machine (Agilent
155 Technologies) using Brilliant® II SYBR® Green QPCR Master Mix following the
156 manufacturer's recommendations. The reactions were mixed in a volume of 25 µL containing
157 12.5µL SYBR Premix, 10 µL cDNA (diluted 1/100), and 1.25 µL each of the 4 µM forward
158 and reverse primers. After initial denaturation at 95°C for 10 min, 40 cycles of amplification
159 were carried out starting at 95 °C for 30 s, followed by 45 s at 57 °C and 45 s at 72 °C, with a
160 final extension at 95°C for 1 min, 30 sec at 55°C and at 95°C for 30 sec followed by a final
161 cycle for differentiation curve analysis.

162 To determine the RT-PCR efficiencies of each primer pair used, standard curves were
163 generated using five serial dilutions (one log of dilution) of a pool of one hundred cDNA
164 samples from the hepatopancreas. The primers' ability was validated when the amplification
165 efficiency varied between 90 and 110%.

166 Then, all samples collected during the experiment were run in duplicate. Relative gene
167 expression levels were normalized against two specific house-keeping genes, Elongation
168 factor (EF) and glyceraldehyde-3-phosphate-deshydrogenase (GADPH), and each value was
169 calculated in reference to CW shrimps before stress (relative expression = 1) according to the
170 $2^{-\Delta\Delta C_t}$ method (Livak and Schmittgen, 2001).

171 **Statistical analysis**

172 Statistical analysis of the data was carried out using XLSTAT software 2012. Percent data
173 (survival rate) were normalized using an arcsine transformation before analysis. The
174 normality of the data distribution and homogeneity of variance were tested for all
175 zootechnical and molecular analysis data using the Shapiro-Wilk test and F-test, respectively.
176 The zootechnical data were normally distributed and variances were homogenous. Hence, the
177 effects of the rearing treatments were tested using a one-way analysis of variance. The
178 molecular results were not normally distributed; the effects of the rearing treatments were
179 tested using the Kruskal-Wallis test.

180 **Results**

181 **Survival and growth**

182 After 30 days of rearing, BFT shrimp presented a significantly higher survival rate compared
183 to CW shrimp (99.30 ± 1.30 % vs. 42.17 ± 15.35 %, $p < 0.01$). The mean body weight of the

184 BFT shrimp at the end of rearing (0.88 ± 0.19 g) was significantly higher than in the CW
185 treatment (0.21 ± 0.04 g) ($p=0.001$).

186 **Expression profiling of antioxidant enzyme genes**

187 For all genes studied, the rearing period did not induce a difference of expression between the
188 two conditions. However, H_2O_2 stress did cause different patterns of expression between the
189 two conditions (Figure 1). As a reminder, relative gene expression levels were normalized
190 with two specific housekeeping genes, Elongation factor (EF) and glyceraldehyde-3-
191 phosphate-dehydrogenase (GADPH), and each value was calculated in reference to CW
192 shrimps before stress. SOD and GSHT for CW shrimps showed a significantly decreased
193 relative transcript abundance 6 hours after stress, 0.39 ± 0.03 and 0.31 ± 0.12 , respectively
194 ($p=0.03$ for both genes), while no significant change was observed for BFT shrimps ($0.84 \pm$
195 0.26 and 0.97 ± 0.65 , $p>0.05$). The difference between BFT and CW shrimps after stress was
196 significantly different for SOD and GSHT ($p<0.01$ and $p=0.04$, respectively). Nevertheless,
197 no effect of stress was observed on GPX expression for animals under either condition. CAT
198 showed a distinct pattern compared to other antioxidant enzymes. BFT shrimps displayed a
199 significant increase in relative RNA abundance after stress ($p=0.04$) compared to CW
200 shrimps, in which the relative abundance of CAT RNA did not change (2.39 ± 1.49 vs. $0.76 \pm$
201 0.28 , $p=0.02$).

202 **Expression profiling of antimicrobial peptide genes**

203 As for antioxidant enzyme genes, for all AMPs genes studied, the rearing period did not
204 induce differences in expression between the two conditions. However, H_2O_2 stress caused
205 different patterns of expression under both conditions (Figure 2). For the penaeidin family, the
206 relative transcript abundance of Pen 2 and Pen 3 decreased significantly after stress in CW
207 shrimps ($p=0.03$ for both genes). On the contrary, in the BFT shrimps, no change in Pen 2
208 and Pen 3 transcript abundance was detected after stress compared to before stress ($p>0.05$).
209 However, significant differences were observed between rearing conditions after stress;
210 respectively, for CW and BFT, 0.15 ± 0.08 vs. 0.94 ± 0.40 ($p=0.03$) for Pen 2 and 0.14 ± 0.06
211 vs. 0.88 ± 0.53 ($p=0.02$) for Pen 3. Similar to the penaeidin family, another AMP (Cru)
212 transcript showed a significant decrease in RNA abundance 6 hours after stress in CW
213 shrimps, (0.12 ± 0.04 , $p=0.03$), but not in BFT shrimps (0.41 ± 0.23 , $p>0.05$). The difference

214 between BFT and CW shrimps was significant ($p=0.03$). No effect of induced stress was
215 observed on lysozyme expression in animals from the two conditions.

216 **Discussion**

217 At the present time, when shrimp production faces many losses due to disease outbreaks, the
218 use of BFT can restrain the development of shrimp diseases. It has been hypothesized that the
219 biofloc allowed the shrimp to better withstand environmental stress or infection by pathogenic
220 bacteria or viruses by stimulating non-specific immunity. Recently, several authors
221 determined that BFT stimulated the non-specific immunity of shrimp (Kim *et al.*, 2013; Xu
222 and Pan, 2013, 2014; Ekasari *et al.*, 2014) and one recent work showed that BFT improved
223 shrimp resistance to infectious myonecrosis virus infection (Ekasari *et al.*, 2014). In this
224 research, the antioxidant and antimicrobial transcriptional responses before and after
225 experimental sub-lethal hydrogen peroxide stress in blue shrimps reared according to two
226 different systems, BFT and CW, were compared in order to improve our understanding of
227 BFT's action on antioxidant defences and the humeral immune system of shrimps at the
228 transcriptional level. We undertook, for the first time, to monitor AOE and AMP gene
229 expression in shrimps under different rearing conditions, BFT and CW, and after induced
230 stress.

231 **Biofloc rearing conditions improves shrimp growth and survival**

232 Our results showed that the BFT system promotes better growth (x 4.2) and survival (x 0.4) of
233 *Litopenaeus stylirostris* juvenile shrimps compared to the CW system. Such results have
234 already been described (Moss and Pruder, 1995; Cohen *et al.*, 2005; Azim and Little, 2008;
235 Mishra *et al.*, 2008). According to these authors, the improved performances can be related to
236 the consumption of biofloc by the shrimp, as a source of bacteria, microalgae and
237 zooplankton, which could enhance shrimp nutrition and immunity. In the biofloc system, its
238 natural productivity plays an important and complementary nutritional role for the shrimp in
239 addition to the artificial pellets (Moss and Pruder 1995; Epp *et al.*, 2002; Tacon *et al.*, 2002;
240 Burford *et al.*, 2004). Biofloc is known to be an important source of proteins (Wasielesky *et*
241 *al.*, 2006) and also of lipids (Crab *et al.*, 2010). Moreover, biofloc can contain microbially
242 bioactive components such as carotenoids, vitamins (Ju *et al.*, 2008) and glutathione (Cardona
243 *et al.*, in prep.). Major nutrients like proteins, lipids, antioxidant and vitamins, carotenoids and

244 minerals are known to participate, in different ways, in nutritional modulation of immune
245 responses (Trichet, 2010).

246 **Shrimp AOE and AMP gene expression are not modified by rearing conditions**

247 However, in the absence of any particular stressful conditions, we showed that the
248 transcriptional responses of AOE and AMP genes of shrimp were not different between the
249 different rearing conditions. With the significantly different growth and survival results
250 obtained, we could expect a differential response between animals from the two conditions, as
251 shown by others authors. Indeed, Kim *et al.* (2013) showed that biofloc rearing improved
252 immune-related gene expression in *L.vannamei* post-larvae. Nevertheless, these authors used
253 different biomarkers of shrimp immunity than those used in this study. Indeed, the genes
254 targeted were involved in prophenoloxidase (ProPo) cascade activation (6 studied genes:
255 prophenoloxidase 1, prophenoloxidase 2, prophenoloxidase activating enzyme, serine
256 protease, and masquerade-like serine protease). The ProPo cascade can be activated by
257 components of the cell wall like β -1,3-glucan, lipopolysaccharide, and peptidoglycan, elicitors
258 found abundantly on biofloc particles (Johansson & Söderhäll, 1985; Van de Braak *et al.*,
259 2002; Amparyup *et al.*, 2013). Indeed, bacteria were one of the principal constituents
260 identified in biofloc particles, with a high concentration ranging from 10^6 to 10^9 cell.mL⁻¹
261 (Otoshi *et al.*, 2006; Burford *et al.*, 2003; Avnimelech, 2009; Kim *et al.*, 2013).

262 Moreover, in addition to activating the ProPo cascade, earlier studies have revealed that
263 biofloc led to an increase in both total haemocyte count and the phagocytic response in shrimp
264 hemolymph, whereas respiratory burst, antibacterial and bacteriolytic activities were not
265 affected (Xu and Pan, 2013; Ekasari *et al.*, 2014). The presence and digestion of the biofloc
266 ingested by the shrimp may release substances in the gastrointestinal tract that could
267 potentially stimulate cellular defences (phagocytosis and the proPo cascade) and the release of
268 more haemocytes into the circulation without a noticeable effect on humeral defence factor
269 (such as AMPs and lysozyme) production (Xu and Pan, 2013). Our results are in accordance
270 with these assertions and confirm that at the gene expression level there is no effect of the
271 BFT condition by comparison to CW.

272 **Differential AOE and AMP responses induced by H₂O₂ stress between shrimps from** 273 **BFT and CW**

274 After a H₂O₂ stress treatment, a strong effect of the rearing condition was noticed in AOE and
275 AMP gene expression levels. The antioxidant defence system is inducible at a moderately
276 high concentration of H₂O₂, which is hypothesized to also act as a messenger of signal
277 transduction by regulating the mRNA level through activation of signal pathways (Ji, 1995;
278 Sen and Packer, 1996). In this study, the expression of CAT was significantly increased in the
279 digestive gland after 6 hours under H₂O₂ exposure for animals reared in BFT, while no
280 change in RNA transcript abundance was recorded for CW shrimps. This result suggested that
281 H₂O₂ stimulated the expression of CAT in BFT animals. AOE's function is to catalyse the
282 conversion of H₂O₂ into water and molecular O₂ to protect the organism from peroxidation
283 (Zhang *et al.*, 2008). This result seems to show that excess H₂O₂ that penetrates cells and
284 tissues would be more easily detoxified and neutralized in the cytosol by catalase in BFT
285 shrimp than in CW shrimp. The increase in CAT RNA expression in BFT shrimp could
286 correspond to an adaptive antioxidant stress response (Bigot *et al.*, 2010). In contrast, the
287 absence of a response in the CW shrimps could reflect an inappropriate response of the
288 organism to neutralize peroxides and their potential involvement in oxidative cellular damage
289 (Meng *et al.*, 2014). GPX also catalyses the conversion of H₂O₂ into H₂O and O₂. The absence
290 of significant differential expression before and after 6 hours under stress could be explained
291 by it being too short a time for the animals to react or to the paucity of biological replicates
292 (n=4) to draw out significant differences. Indeed, Fu *et al.* (2012) showed that GPX mRNA
293 transcription increased significantly between 8 h and 12 h after H₂O₂ injection. Stress induced
294 significant down-regulation of SOD and GSHT in CW animals only. Similar to our findings
295 on CAT genes, this could be explained by a diminished capacity for the CW organism to
296 protect itself against oxidative stress (Bigot *et al.*, 2010) and the degradation of cells by H₂O₂.
297 All together, the difference in response between animals from the two rearing conditions
298 suggests that CW shrimp did not seem able to abolish cytotoxic effects due to H₂O₂-induced
299 oxidative stress, while BFT shrimp seemed to present an adaptive antioxidant stress response.
300 For information, we had measured SOD and CAT enzymatic activities. However, the
301 observed standard deviations of the results were very important. Thus, it was very difficult to
302 define correlations with the molecular data. These observations could be explained by the fact
303 that it is not so easy to measure and interpret enzymatic activities on crude extract. Many
304 activity inhibitors could be present in the extract. Therefore, we have decided not to show
305 these biochemical results.

306 In addition to AOE production, haemocytes are able to synthesize soluble antimicrobial
307 peptides (AMPs). Measuring humeral immunity offers a further insight into the impact of
308 stressors on haemocyte functionality, associated with an organism's immunocompetence
309 (Ellis *et al.*, 2011). This study shows differences in AMP gene expression levels according to
310 the rearing conditions of *L. stylirostris* facing a H₂O₂ stress. The transcript levels of three out
311 of four AMP genes studied (Pen 2 and 3, Crustin) appeared to be significantly modified after
312 stress in CW shrimps only. The reported modulations in mRNA quantities were distributed in
313 circulating haemocytes present in the digestive gland, since in invertebrates AMPs are
314 produced mostly by haemocytes (Bachère *et al.*, 2004). In our experiment, no cell counts were
315 performed before RNA extraction. Total RNA quantities were adjusted before reverse
316 transcription and cDNA concentrations were adjusted another time in order to use identical
317 template quantities in qPCR. Meanwhile, we have no data on the quantitative and qualitative
318 composition of the various haemocytes sampled. The decreases in the AMP transcripts of CW
319 shrimps could be explained by two phenomena: (i) a decrease in the relative number of
320 haemocytes expressing the considered mRNA (Cellura *et al.*, 2007) induced by H₂O₂
321 cytotoxicity and (ii) a migration of haemocytes from the digestive gland towards exposed
322 tissue to H₂O₂ as is often observed after infection by a pathogen or by injury (Bachère *et al.*,
323 2004). However, the observed differences in AMP transcript level could be compared to the
324 data observed for shrimp survival under the BFT and CW conditions. We can suppose that the
325 differential AMP transcriptional response after stress could be related to an improved immune
326 ability of BFT animals facing a H₂O₂ stress. Nevertheless, further study is needed to confirm
327 this assumption.

328 **Conclusion**

329 The rearing condition, BFT or CW, did not affect gene expression encoding antioxidant
330 enzymes and antimicrobial peptides, although BFT significantly improved the growth and
331 survival of animals. However, H₂O₂ stress induced a differential response in AOE and AMPs
332 between shrimp from BFT and CW. Biofloc shrimps seem to maintain their antioxidant and
333 antimicrobial peptide responses after H₂O₂ stress, while clear water shrimp immune
334 competence seemed to decrease after stress.

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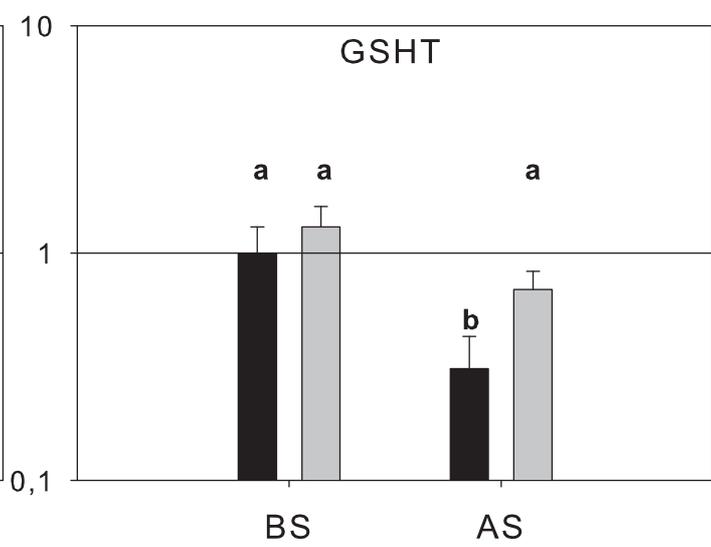
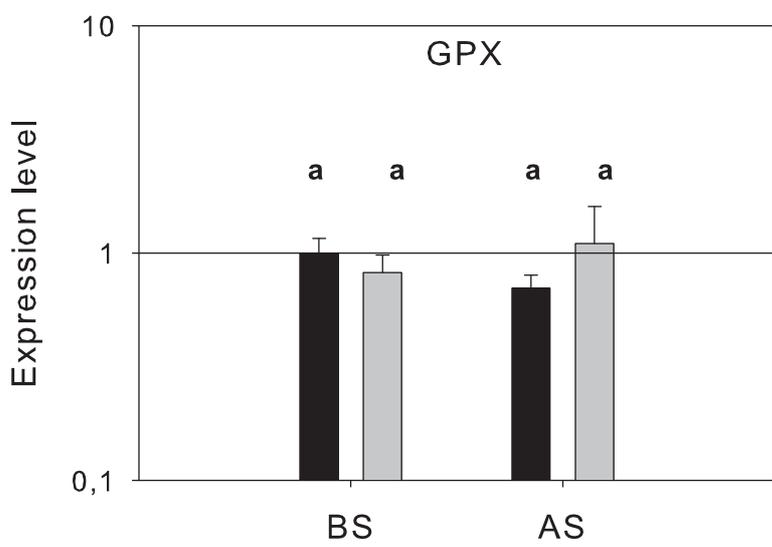
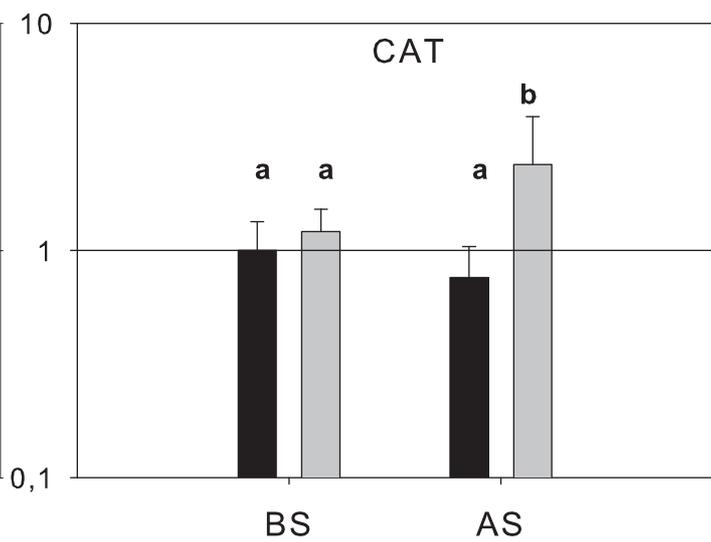
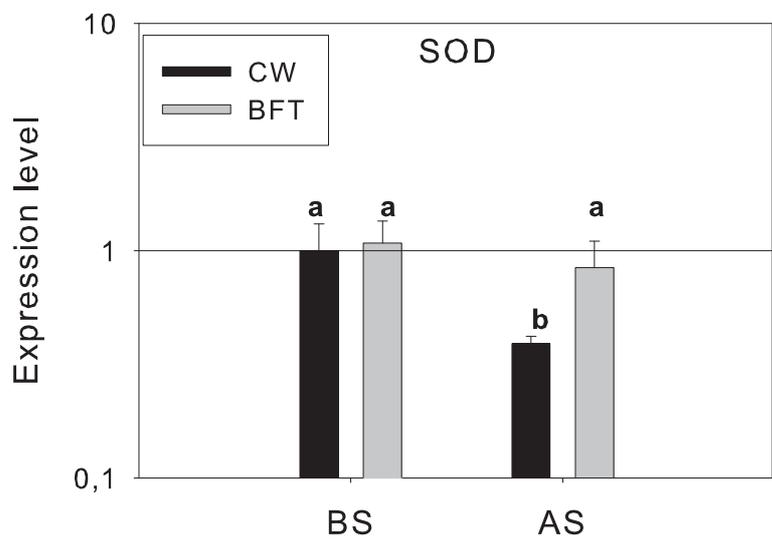
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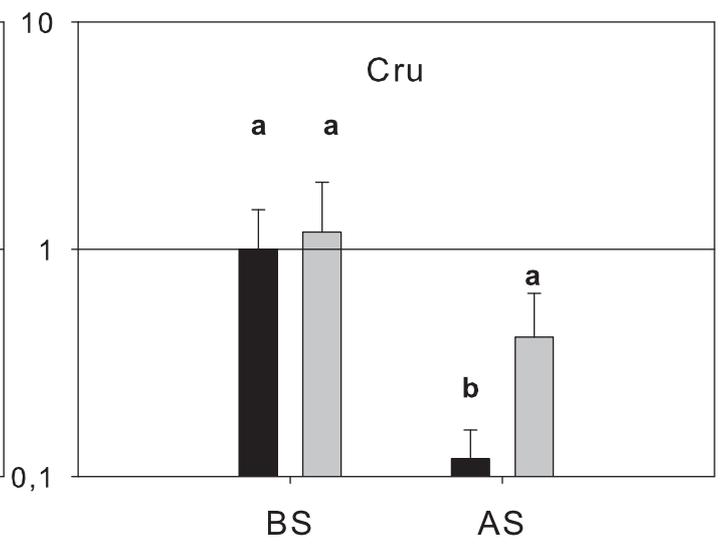
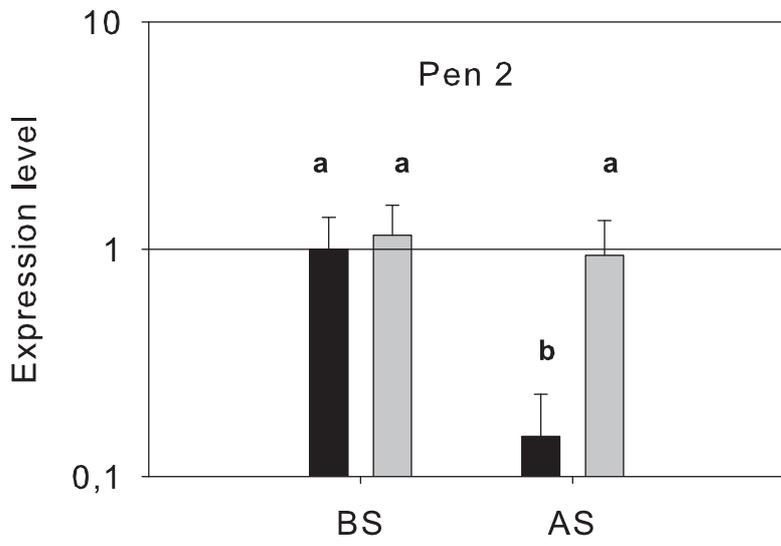
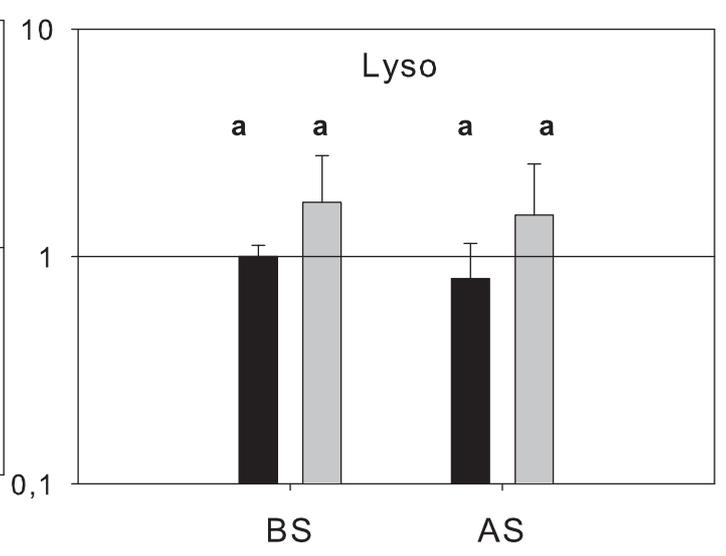
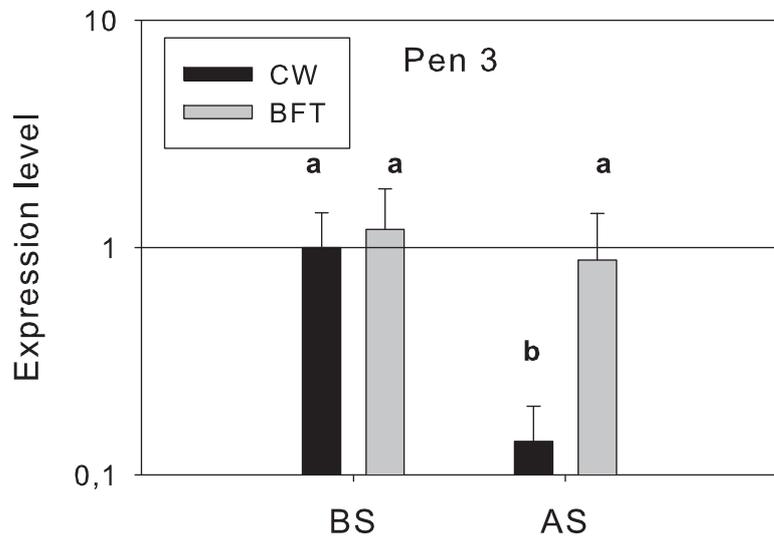
Table 1. PCR primers (F: Forward, R: Reverse) used to amplify antimicrobial peptides (Pen3, Pen2, Lyso, Cru), antioxidant enzymes (GPX, SOD, GSHT, CAT) and house-keeping genes (GADPH, EF) of the shrimp *Litopenaeus stylirostris* in a real-time PCR procedure.

Figure 1. Expression profiles of genes coding for the antioxidant enzymes Super oxide dismutase (SOD), Catalase (CAT), Glutathione peroxidase (GPX) and Glutathione transferase (GSHT) in animals under both conditions both before (BS) and after stress (AS).

Figure 2. Expression profiles of genes coding for AMPs, Lysozyme (Lyso), Peneaidin 2 and 3 (Pen 2 and Pen 3) and Crustin (Cru) in animals from both conditions both before (BS) and after stress (AS).

Name	Gene name	Sequence 5' - 3'	Size	Primer size	Tm	GeneBank
Pen 2 - F	Peneaidin 2	GTCTGCCTGGTCTTCTTGG	178pb	19	60	AY351655
Pen 2 - R	Peneaidin 2	CGAACCTGCTGCAGCAATTG		20	62	
Pen 3 - F	Peneaidin 3	CCATGCGCCTCGTGGTCTG	211pb	19	64	AY351656
Pen 3 - R	Peneaidin 3	GAACGCGCTTGTAAAGGTGGTAA		22	64	
Lyso - F	Lysozyme	GGCTTGGCACCAGGGTTACC		20	59	CV699332
Lyso - R	Lysozyme	CGTCTGCACGTCAGCTGTG		20	59	
Cru - R	Crustin	GTGATTCTGTGCGGCCTCTT	395pb	30	63	
Cru - F	Crustin	TCTTGCACCAATACCTGCAG		30	60	
GPX - F	Glutathione peroxidase	TCAACAGCTGATCCCCTCT	157pb	19	59	
GPX - R	Glutathione peroxidase	CCTTGCCGATGAGGAATTT		19	60	
SOD - F	Super oxide dismutase	GCAATGAATGCCCTTCTACC	247pb	20	60	
SOD - R	Super oxide dismutase	CAGAGCCTTTCCTCAACG		21	60	
GSHT - F	Glutathione transferase	CTGGAGAAGCTGCACGAAG	198pb	19	60	
GSHT - R	Glutathione transferase	GTCACGTTCCCTGTGCTTGC		19	60	
CAT - F	Catalase	TACTGCAAGTTCCATTACAAGACG	285pb	24	61	
CAT - R	Catalase	GTAATTCCTTGGATTGCGGTCA		22	61	
EF - F	Elongation factor 1 α	CGTTCGGTGATCATGTTCTTGATG	382pb	35	60	AY117542
EF - R	Elongation factor 1 α	GGTGCTGGACAAGCTGAAGGC		31	60	
GADPH - F	Glyceraldehyde-3-phosphate-deshydrogenase	CGTTGGACACCACCTTCA	146pb	18	59	AI770197
GADPH - R	Glyceraldehyde-3-phosphate-deshydrogenase	GTGTGCGGTGTCAACATGGA		30	55	





Highlights

- Contrasted rearing conditions, biofloc and clear water, did not affect the expression of genes encoding antioxidant enzymes and antimicrobial peptides.
- Biofloc shrimps maintained antioxidant and antimicrobial peptide responses after H₂O₂ stress while the immune competence of clear water shrimp seemed to decrease after stress.
- Biofloc seems to improve the immune resistance of animals against stress.