

1 **Depurated fish as an alternative reference for field-based biomarker monitoring**

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20 Running head: Depurated fish as reference for field based biomarker studies

21

22 **ABSTRACT**

23 The entire Swan-Canning Estuary, south-western Australia, is impacted by human activity,
24 and the selection of a reference site to assess the impact of contamination on the health of
25 biota is not possible. To determine whether the use of fish depurated under laboratory
26 conditions is a suitable substitute, adult *Acanthopagrus butcheri* were collected from the
27 estuary and maintained in clean water (24 ppk) for 3 months. A suite of biomarkers were
28 assessed, namely; mixed-function oxygenase enzymes [ethoxycoumarin-*O*-deethylase
29 (ECOD) and ethoxyresorufin-*O*-deethylase (EROD)] activities, serum sorbitol
30 dehydrogenase (s-SDH), naphthalene-, pyrene-, and benzo[*a*]pyrene-type biliary
31 metabolites, DNA strand breaks, and heat shock protein (HSP70) levels. The results were
32 compared to field captured black bream from three sites within the estuary (Ascot,
33 Claisebrook, and Riverton), and to hatchery-bred juvenile fish. Biomarker levels were
34 lower (up to 3.8 times) in depurated fish compared to field captured fish, while DNA
35 integrity was higher. EROD activity was marginally lower in the hatchery-bred black
36 bream than the depurated fish while s-SDH levels were 2 times higher in the hatchery fish,
37 comparable to levels measured in the field. From the results obtained, field captured fish
38 depurated for 3 months are suitable to determine reference/baseline levels for biomarker of
39 health studies in estuarine environments.

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43 **Keywords:** *Acanthopagrus butcheri*, alkaline unwinding assay, bile metabolites

44 biomarkers, biomonitoring, DNA strand breaks, s-SDH, HSP70

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46

47 INTRODUCTION

48 Defining the reference condition is considered to be an essential feature of ecosystem risk
49 assessment to determine a baseline against which all experimental evidence is compared
50 (Baird and Burton Jr 2001; Suter *et al.* 2007; Schmidt *et al.* 2009). However, this assumes
51 that a reference baseline exists in each ecosystem that is constant, except when influenced
52 by human activity (Kapustka 2008). Suter *et al.* (2007) defines different types of reference
53 conditions, such as historical, self-reference, local, regional natural, regional acceptable, or
54 no reference. None of these conditions can be applied to biochemical marker of fish health
55 studies in estuaries such as the Swan-Canning Estuary (SCE) in south-western Australia,
56 where anthropogenic inputs affect the whole system, with the exception of the no reference
57 definition. This is in accord with Foran and Ferenc (1999) who state that a priori definition
58 of a reference sites is not always possible especially where all sites within a study area are
59 considered impaired.

60

61 The SCE is a highly modified, wave-dominated salt wedge estuary (NLWRA 2002) with
62 an open (via training walls and dredging) connection to the ocean at Fremantle (Fig. 1).
63 Like all estuarine environments this estuary is a complex ecosystem undergoing high levels
64 of natural variability (Elliott and Quintino 2007; Schulte 2007). Physico-chemical
65 conditions are extremely variable with daily and seasonal movements of the salt wedge
66 within the estuary playing an important role in the distribution of soluble hydrocarbons at
67 the sediment/surface water interface (Thomson *et al.* 2001; Twomey and John 2001;
68 Westbrook *et al.* 2005).

69

70 The SCE is the focal point around which the city of Perth, with a population approaching
71 1.6 million people, has developed. There are no areas within its catchment that have not

72 been impacted by some form of human activity, either through urban, light industrial or
73 agricultural development. Direct discharge, surface runoff and groundwater all have the
74 potential to contribute nutrients, pesticides, fertilisers, heavy metals, and polycyclic
75 aromatic hydrocarbons (PAHs) in the form of fuel and oil into the estuary (Foulsham *et al.*
76 2009; Nice 2009; Nice *et al.* 2009).

77

78 Fish biomarker of health studies in the Swan-Canning Estuary commenced in 2000 at a
79 limited number of sites within the system (Webb and Gagnon 2002) after 170 years of
80 expanding human development throughout the catchment. A historical baseline for
81 biomarker studies in fish from this estuary is therefore not available. Estuaries similar to
82 the SCE in south-western Australia are all influenced by anthropogenic inputs from
83 agriculture, urbanisation and other human activity. Foran and Ferenc (1999) suggest
84 assessing site results based on a gradient of biochemical response from low to extremely
85 stressed. However studies to date show the proximity of major roads and stormwater
86 drains, former landfill sites and industrial precincts, significant weather events, are the
87 most significant factors affecting biomarker levels in biota. There is no evidence of
88 gradients of biomarker responses up- or downstream in the SCE (Webb and Gagnon 2002;
89 Webb *et al.* 2005a; b; c).

90

91 Depuration is a process designed to cleanse or remove contaminants from an animals gut
92 or tissue. This process is often used in purging shellfish of pathogens (Barile *et al.* 2009),
93 or to remove detritus from the gut of crustaceans (McClain 2000), to improve hygiene or
94 palatability for human consumption. Other studies use depuration techniques to determine
95 the bioaccumulation potential of lipophilic compounds in aquatic organisms (Ellgehausen
96 *et al.* 1980).

97

98 In this study black bream (*Acanthopagrus butcheri*), a fish species endemic to estuaries in
99 south-western Australia, were depurated in order to determine a baseline (reference)

100 condition for the assessment of health of fish in the estuary using biochemical markers.

101 Black bream were captured from the estuary and maintained under laboratory conditions

102 using clean water replicating the physico-chemical conditions within the estuary for a

103 period of three months. At the end of 3 months the depurated fish were sacrificed and a

104 selection of biomarkers were compared with fish, of a similar size and age, collected

105 directly from the estuary at the same time the laboratory depuration was terminated.

106 Further comparison was undertaken for several biomarkers measured in juvenile fish

107 sourced from a fish hatchery. It was hypothesised that laboratory depurated fish would be

108 suitable to use to determine a reference state for fish health biomarker studies in estuarine

109 environments.

110

111 **METHODS**

112 *Depuration of Fish*

113 Ten (10) black bream (*Acanthopagrus butcheri*) were collected from the Swan River in

114 January 2006 by a commercial fisherman using a 120 m, 100 mm monofilament haul net

115 then transferred to a 1000 litre tank at the Curtin Aquatic Research Laboratory with UV

116 sterilised recirculating water filtration. The fish were maintained at 24ppk and 20°C for 92

117 days, and fed human food quality mussels (*Mytilus* sp.). On the 92nd day the fish were

118 sacrificed and tissue and fluid biopsies taken

119

120 *Field collection*

121 In April 2006, 56 black bream were collected from two sites in the Swan River
122 (Claisebrook and Ascot; $N = 20$ respectively) and one site in the Canning River (Riverton;
123 $N = 16$; Fig 1). The fish were sacrificed within 2 hour of capture and biopsies taken.

124

125 *Hatchery-bred Fish*

126 Twenty (20) juvenile black bream, purchased from the Challenger Institute of Technology
127 hatchery Fremantle, Western Australia, had been maintained as control fish for an
128 unrelated laboratory experiment. These fish were kept in 4 x 100 litre aquariums under
129 similar conditions to the hatchery (37ppk, 20°C) in semi-static water conditions with 50%
130 daily water changes. These fish were sacrificed on day 21.

131

132 *Sample Collection*

133 Total weight, gutted weight and standard lengths were recorded for each fish. An external
134 examination was conducted for abnormalities and any sign of parasite infestation. A blood
135 sample was taken from the caudal vein using a vacutainer, which was allowed to clot on
136 ice for 15 minutes then centrifuged for 10 minutes at 3000 x g. Each fish was killed by the
137 method of ike jime, bile collected from the gall bladder, and gill and liver biopsies taken.
138 All samples were immediately placed in liquid nitrogen then later transferred to a freezer
139 and held at -80°C until analysis. Total protein content in the bile, and liver and gill
140 supernatants, was determined using the method of Lowry *et al.* (1951).

141

142 *Biomarker Analyses*

143 Ethoxyresorufin-*O*-deethylase (EROD) activity was measured in liver supernatant using
144 the methods of Hodson *et al.* (1991) adapted to black bream as detailed in Webb (2005).
145 The fluorescence of the supernatant was read on a Perkin-Elmer LS-45 Luminescence

146 Spectrometer at excitation/emission wavelengths of 535/585 nm (slit 10 ex/10 em). EROD
147 activity was expressed as picomoles of resorufin produced, per mg of total protein, per
148 minute ($\text{pmol R mg Pr}^{-1} \text{ min}^{-1}$).

149

150 Bile Metabolites - Three biliary metabolite-types were measured, naphthalene, pyrene and
151 benzo(a)pyrene (B[a]P) by fixed wavelength fluorescence (FF) using the methods of
152 Krahn *et al.* (1986) for pyrene-type metabolites and Lin *et al.* (1996) for both naphthalene-
153 type and B(a)P-type metabolites. Biliary PAHs are standardised to biliary protein
154 (metabolite mg protein^{-1}).

155

156 Serum sorbitol dehydrogenase (s-SDH) activity - The s-SDH assay was modified from the
157 Sigma Diagnostics (St Louis, USA) Sorbitol Dehydrogenase Procedure No. 50-UV as
158 described by Webb and Gagnon (2007). The linear decrease in the rate of absorbance (ΔA)
159 over one minute was read on a Pharmacia UV-Visible Spectrophotometer at 340 nm. The
160 s-SDH activity is expressed as milli-International Units (mU) mL^{-1} serum.

161

162 The following biomarkers were measured in the depurated and field captured fish only.

163 Ethoxycoumarin-O-deethylase (ECOD) activity was measured in liver supernatant using
164 methods previously detailed by Webb *et al.* (2005a). The fluorescence of the supernatant
165 was read on a Perkin-Elmer LS-45 Luminescence Spectrometer at excitation/emission
166 wavelengths of 380/452 nm. ECOD activity was expressed as picomoles of 7-
167 hydroxycoumarin produced, per mg of total protein, per minute ($\text{pmol H mg Pr}^{-1} \text{ min}^{-1}$).

168

169 DNA strand breakage - DNA strand breaks in liver supernatant was determined using the
170 alkaline unwinding assay method of Shugart (1996). Incubation times and temperatures to

171 obtain partially unwound DNA (DSS) and single stranded DNA (SS) in each sample were
172 optimized for black bream. Hoechst dye 33258 is used to bind with the isolated DNA in
173 solution. When DNA is in the single-stranded form, the intensity of fluorescence of the
174 bound dye is reduced to approximately one half of that observed for double-stranded DNA.
175 This development constitutes the basis for determining the amount of double- and single-
176 stranded DNA present in a sample of DNA during the alkaline unwinding assay (Shugart
177 1996). The fluorescence of the double stranded DNA (DS), DSS (incubated at 35°C for 5
178 mins), and SS (incubated 85°C, 30 mins) present in each sample was read on a Perkin-
179 Elmer LS-5 Luminescence Spectrometer at excitation/emission wavelengths of
180 350ex/453em nm. The ratio of double-stranded DNA in the sample (F value) was
181 calculated using the equation, $F = (DSS - SS)/(DS - SS)$. The F value is a measure of DNA
182 integrity with a high value corresponding to high DNA integrity.

183

184 Stress protein (HSP70) - Stress protein response was measured in gill supernatant using the
185 methods of Martin et al. (1996) optimized for black bream as outlined in Webb and
186 Gagnon (2009). HSP70 levels in the black bream are expressed as pixel density per μg of
187 total protein (pixels $\mu\text{g pr}^{-1}$).

188

189 *Statistical analysis*

190 Data are presented as mean \pm standard error (SE) and analysis was done using the SPSS
191 statistical package (Version 17; SPSS GmbH, Germany). Where necessary, Log_{10}
192 transformations were done for each biomarker to achieve normality and homoscedasticity.
193 Student *t*-tests were carried out to determine whether any sexual differences were present
194 for each biomarker ($\alpha = 0.05$). As no interactions were found in the data sets main effects
195 were analysed using one-way ANOVAs. Where significant differences were found ($p <$

196 0.05), a Dunnett's (2 sided) test was run to compare the field and hatchery-bred fish with
197 the depurated fish group.

198

199 **RESULTS**

200 No significant differences were detected between male and female black bream for any
201 morphological measure, physiological indices, or biomarker analysed in this study ($p \geq$
202 0.05) so the results for both sex were pooled for each variable.

203

204 The length and weights of the black bream purchased from the hatchery were significantly
205 smaller than either the depurated fish or the freshly captured fish from the estuary (field
206 captured fish; $p \leq 0.001$; Table 1). The liver somatic index (LSI) of the hatchery-bred fish
207 was also much smaller compared to the other fish in the study ($p \leq 0.001$). However, the
208 hatchery-bred fish had a significantly higher condition factor (CF) compared to both the
209 depurated fish and the field captured fish ($p \leq 0.001$; Table 1). The depurated fish and the
210 field captured fish had similar morphology and physiological indices ($p \geq 0.05$; Table 1).

211

212 No significant differences were found in EROD activity ($p = 0.21$; Fig 2a), naphthalene-
213 type biliary metabolites ($p = 0.43$; Fig 3a), pyrene-type biliary metabolites ($p = 0.52$; Fig
214 3b) and B[a]p-type biliary metabolites ($p=0.99$; Fig 3c) measured in the hatchery-bred
215 black bream when compared with the depurated fish. Compared to the depurated fish, the
216 hatchery-bred black bream measured significantly higher s-SDH activity ($p = 0.006$; Fig 4)
217 which was at similar levels to the field collected fish.

218

219 *Field-captured vs. Depurated black bream*

220 EROD activity in the black bream was lower in the depurated fish than the field captured
221 fish ($p \leq 0.001$). This difference was significant between the depurated fish and fish
222 captured from Ascot ($p = 0.01$) and Claisebrook ($p \leq 0.001$) but not Riverton ($p = 0.81$; Fig
223 2a).

224

225 All biliary metabolites measured in the depurated black bream were lower than the field
226 captured fish in this study. This difference was significant at Claisebrook for all
227 metabolites (naphthalene and pyrene-type $p \leq 0.001$; B[a] P-type $p = 0.01$; Figs 3a, b, c).
228 The fish collected from Ascot had significantly higher pyrene-type metabolites ($p = 0.016$;
229 Fig 3b) while the fish from Riverton had higher B[a] P-type ($p = 0.02$; Figs 3c) when
230 compared to the depurated fish.

231

232 The activity of s-SDH was lower in the depurated black bream compared to all field
233 captured fish in this study but this difference was only significant when compared to the
234 fish from Ascot ($p = 0.003$) and Claisebrook ($p = 0.004$; Fig 4).

235

236 ECOD activity was significantly lower in the depurated fish ($p = 0.003$) than the field
237 captured black bream. This difference was statistically significant between the depurated
238 fish and fish captured from Claisebrook ($p = 0.04$) but not Ascot ($p = 0.99$) nor Riverton (p
239 $= 0.30$; Fig 2b).

240

241 The depurated black bream displayed higher DNA integrity than the field captured fish (p
242 $= 0.01$), which was only significant compared to the fish from Riverton ($p = 0.004$). Ascot
243 ($p = 0.06$) and Claisebrook ($p = 0.07$) also had lower DNA integrity but this was not
244 statistically lower (Figure 5a).

245

246 HSP70 levels were lower in the depurated black bream compared to the field captured fish
247 ($p = 0.01$) but this difference was only significant compared to Riverton ($p = 0.02$) and not
248 Claisebrook ($p = 0.06$) or Ascot ($p = 0.93$; Fig 5b).

249

250 **DISCUSSION**

251 This study has clearly validated the use of depurated fish to establish baseline levels for a
252 suite of biochemical markers of fish health in the black bream from the Swan-Canning
253 Estuary.

254

255 The biomarkers measured in the depurated black bream are all significantly lower than
256 those measured in the fish collected directly from the field. There was an almost 50%
257 reduction in the Cytochrome (CYP) detoxification enzymes as measured by both EROD
258 and ECOD activity induction levels. Serum SDH levels in the depurated were also up to
259 50% below the levels measured in the field fish demonstrating that the lower levels of
260 EROD and ECOD levels were not due to liver damage. There was a 100 to 275%
261 improvement in the levels of biliary metabolites measured. DNA integrity was higher in
262 the depurated fish although this was only significant when compared to the fish captured
263 from the Riverton site. Finally, HSP70 expression was between 119% lower than the black
264 bream measured from Claisebrook and 155% lower than the fish analysed from Ascot
265 indicating a reduction in oxidative stress levels. These results clearly show that the
266 biomarker levels had come close to, or attained, baseline levels in the black bream which
267 compares well to the results of Ferreira *et al.* 2007 using sea mullet (*Mugil cephalus*).

268

269 Ferreira *et al.* 2007 studied long term depuration on the levels of oxidative stress
270 biomarkers in *M. cephalus*). The fish, chronically exposed to contaminants in the Douro
271 estuary, were transferred to and maintained in unpolluted seawater for periods of 1, 4, and
272 8 months. The researchers found that the mullets had the capacity to recover oxidative
273 damage following long term depuration. Mixed results were observed after 1 month
274 depuration whereas the activities of antioxidant enzymes, as well as stress induced
275 oxidative damaged proteins, had returned to normal values at 4 months.

276

277 Depurated fish also provided an improved benchmark when compared to hatchery-bred
278 fish. The fish collected for depuration were adults of comparable size/age and with similar
279 life histories as the fish sampled directly from the field whereas as the hatchery-bred fish
280 were appreciably smaller juvenile fish (Table 1) that had been bred and reared under
281 artificial conditions. Although EROD activity induction was lower in hatchery-bred fish,
282 measured s-SDH levels were comparable to the highest readings measured in the field
283 captured fish. This result suggests the possibility that some hepatocellular injury had
284 occurred in the juvenile black bream impacting the CYP1A detoxification enzymes.

285

286 3. Implications for ERM

- 287 • According to Baird and Burton Jr (2001) the establishment of an appropriate benchmark
288 or reference condition for comparison is required to assess biochemical responses of
289 fish to contaminant exposure under field conditions.
- 290 • Preston 2002 – Reference sites in ecological risk assessment used to compare an
291 impacted to a ‘pristine’ or non-impacted site. Often located in close proximity.
292 Reference may be compromised by indirect results. E.g. periodic foraging of a fish in a
293 relatively small contaminated patch may have adverse effects over a much larger

294 geographic area with adjacent areas. Adjacent non-contaminated ecosystems may still
295 be affected at a distance by contamination and therefore not suitable as reference.

296 • Elliott and Quintino 2007 – Estuarine Quality Paradox – the difficulty in separating
297 natural and anthropogenic stress in estuaries – repercussions for implementation of all
298 environmental management systems reliant on ability to detect changes based on a
299 defined reference condition.

300 • Lobry *et al.* 2006 - particularly difficult in estuarine situations to define a reference
301 condition as estuaries are complex ecosystems and fluctuate with time (seasonally).

302 • This is the case in many estuarine environments, such as the Swan-Canning Estuary
303 (SCE), where anthropogenic inputs affect the whole system.

304

305 4. Conclusions

306 From the results obtained, field captured fish depurated for 3 months are suitable to
307 determine baseline levels and therefore the reference state for biomarker of health studies
308 in estuarine environments.

309

310 **Acknowledgements**

311 This study was funded by an Australian Research Council Linkage grant to MMG and the
312 Department of Environment, Western Australia. The authors wish to extend special thanks
313 to Mr Neil Oliver, commercial fisherman, for his assistance with field collections. The
314 treatment of animals was in accordance with Curtin University Animal Experimentation
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316

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418

420 TABLE 1: Mean (\pm SEM) measurements and physiological indices of black bream
 421 collected during autumn in the Swan-Canning Estuary. Within columns, values marked
 422 with an asterisk are significantly different to the depurated fish ($p \geq 0.05$).

Site	N	Standard length (cm)	Gutted weight (g)	Condition Factor ¹	Liver Somatic Index ²
Depurated	7	26.1 \pm 1.2	534 \pm 59	2.98 \pm 0.14	1.62 \pm 0.27
Ascot	20	25.3 \pm 0.4	460 \pm 25	2.81 \pm 0.03	1.24 \pm 0.08
Claisebrook	10	24.8 \pm 0.3	439 \pm 12	2.87 \pm 0.03	1.17 \pm 0.04
Riverton	16	25.8 \pm 0.8	517 \pm 58	2.89 \pm 0.03	1.56 \pm 0.09
Hatchery bred	17	13.8* \pm 0.03	91* \pm 6	3.37* \pm 0.07	1.02* \pm 0.07
<i>p</i> -value		≤ 0.001	≤ 0.001	≤ 0.001	0.008

423 ¹Condition Factor = (gutted weight/standard length³) x 100. ²Liver Somatic Index = (Liver
 424 weight/gutted weight) x 100.

425

426 **List of Figures**

427 **Figure 1.** Field collection sites within the Swan-Canning Estuary (adapted from Swan
428 River Trust, 1999).

429

430 **Figure 2.** Mixed function oxygenase activities (mean \pm SEM) in black bream (A) EROD
431 activity (pmol R mg Pr⁻¹ min⁻¹); (B) ECOD activity (pmol H mg Pr⁻¹ min⁻¹). Bars marked
432 with an asterisk are significantly different to the depurated fish ($p \geq 0.05$).

433

434 **Figure 3.** Biliary metabolites (mean \pm SEM) in black bream; (A) naphthalene-type (mg
435 metabolite mg protein⁻¹); (B) pyrene-type (μg metabolite mg protein⁻¹); (C) B[a]p-type (μg
436 metabolite mg protein⁻¹). Bars marked with an asterisk are significantly different to the
437 depurated fish ($p \geq 0.05$).

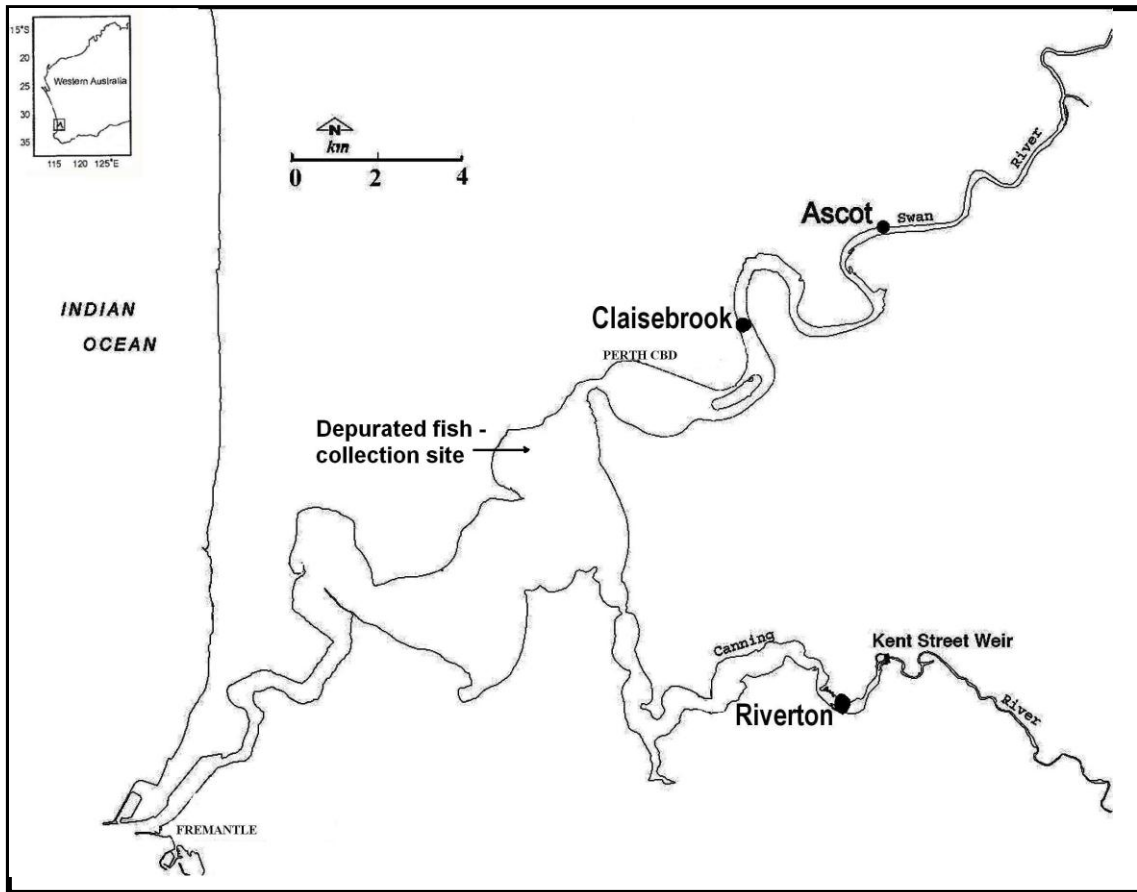
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439 **Figure 4.** s-SDH activity (mU; mean \pm SEM) in the serum of black bream. Bars marked
440 with an asterisk are significantly different to the depurated fish ($p \geq 0.05$).

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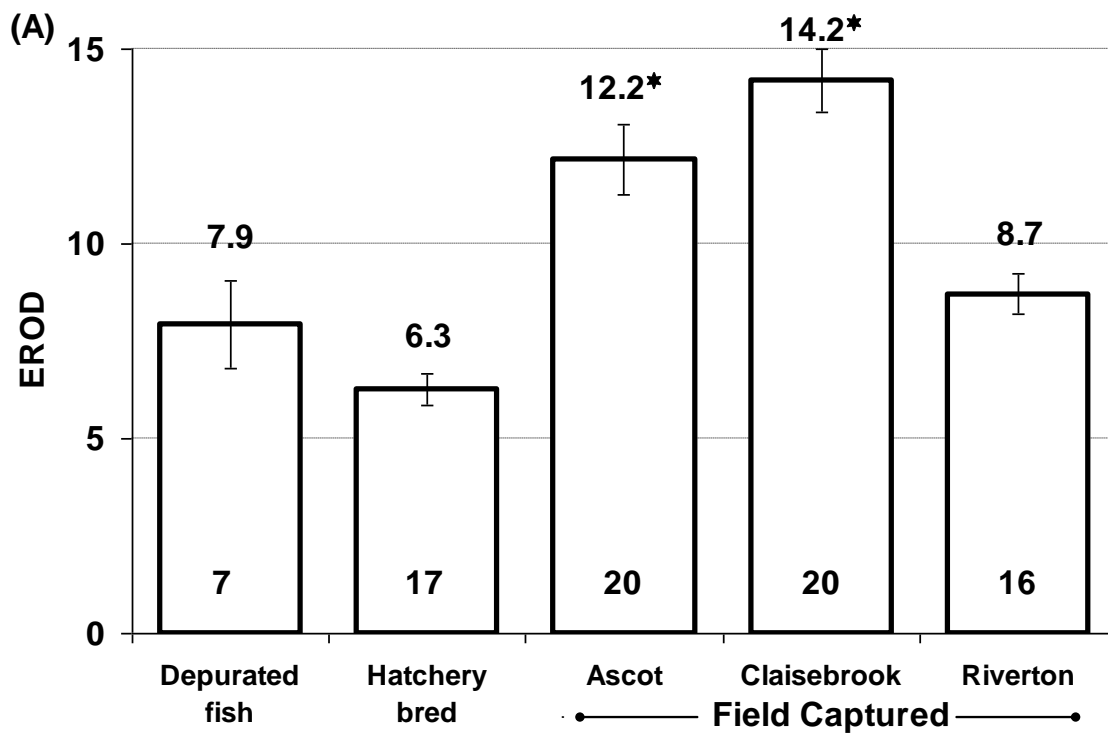
442 **Figure 5.** Biomarkers of effect (mean \pm SEM) in black bream. (A) DNA integrity (F
443 value); (B) HSP70 levels (pixels μg pr-1). Bars marked with an asterisk are significantly
444 different to the depurated fish ($p \geq 0.05$).

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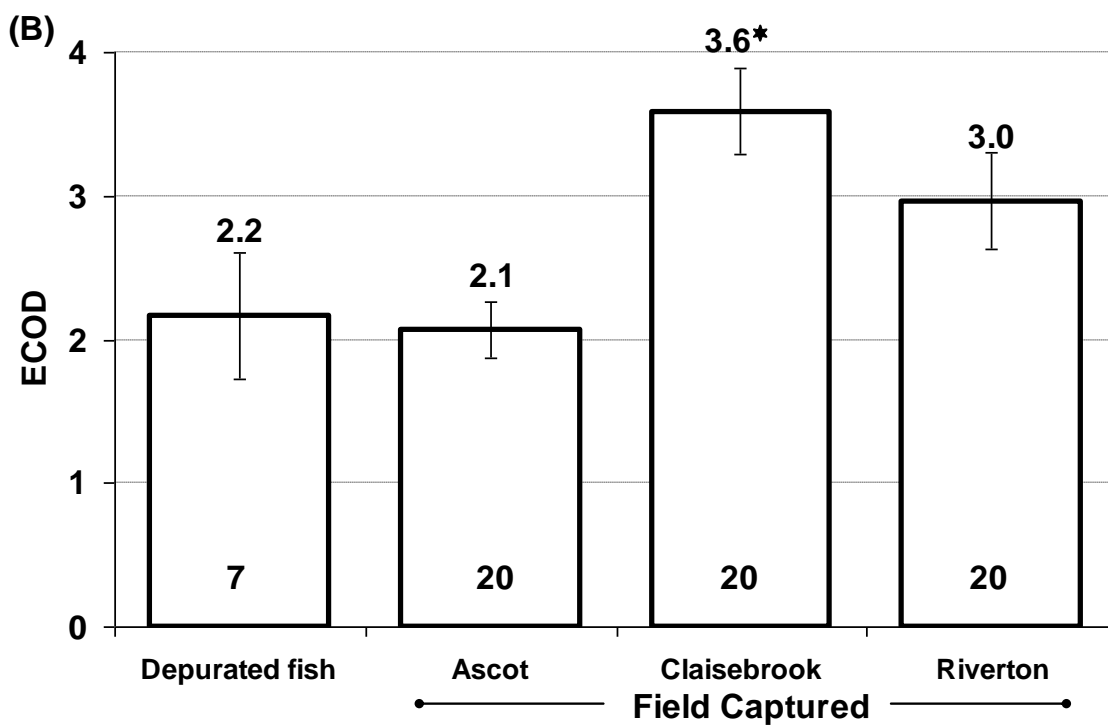


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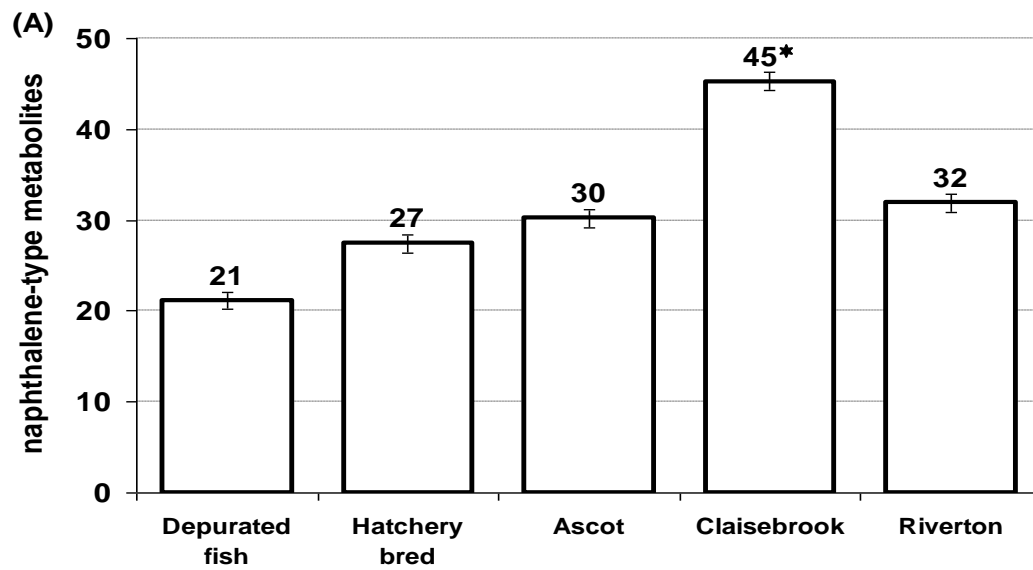
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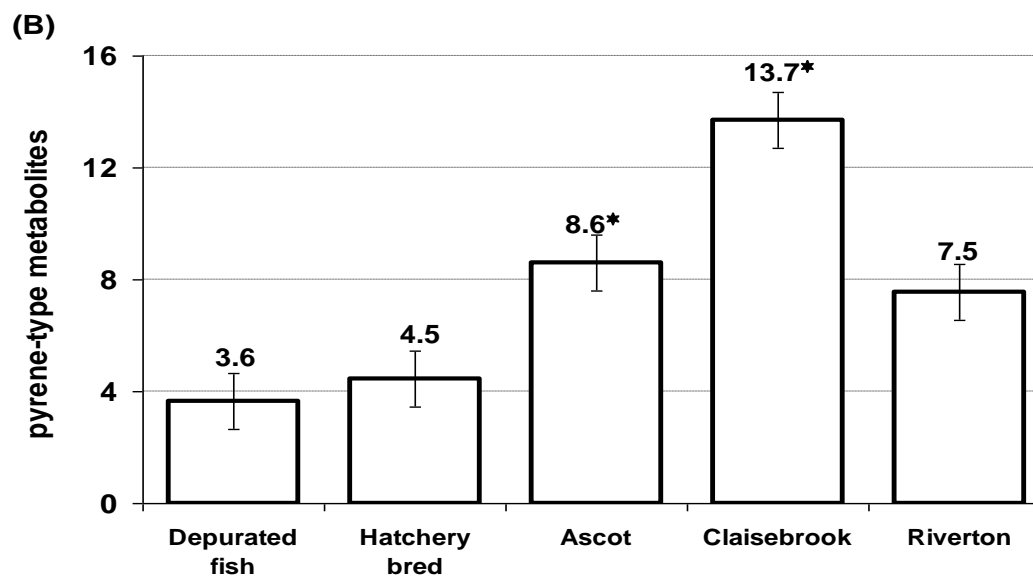
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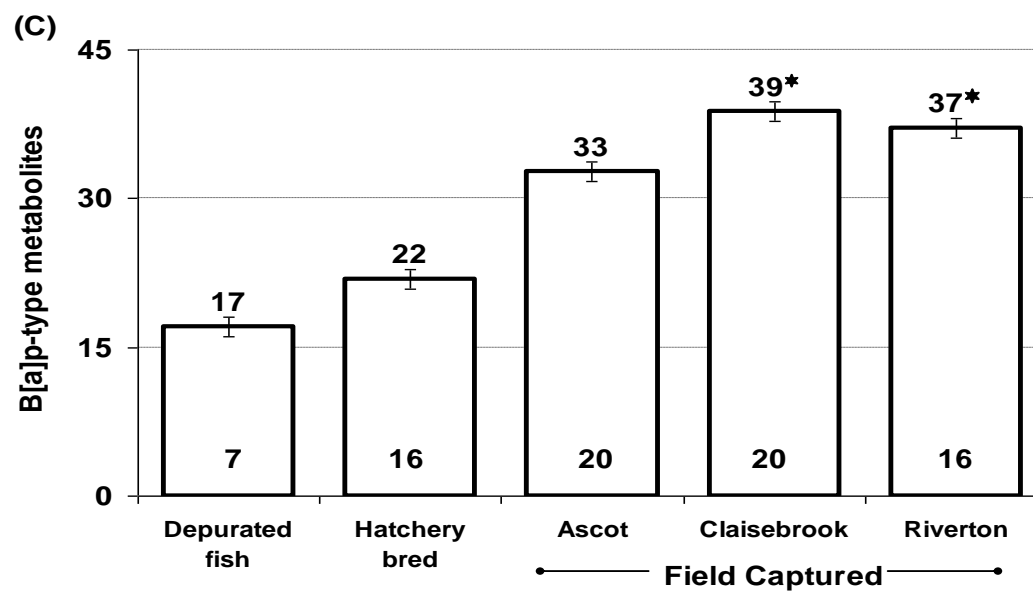
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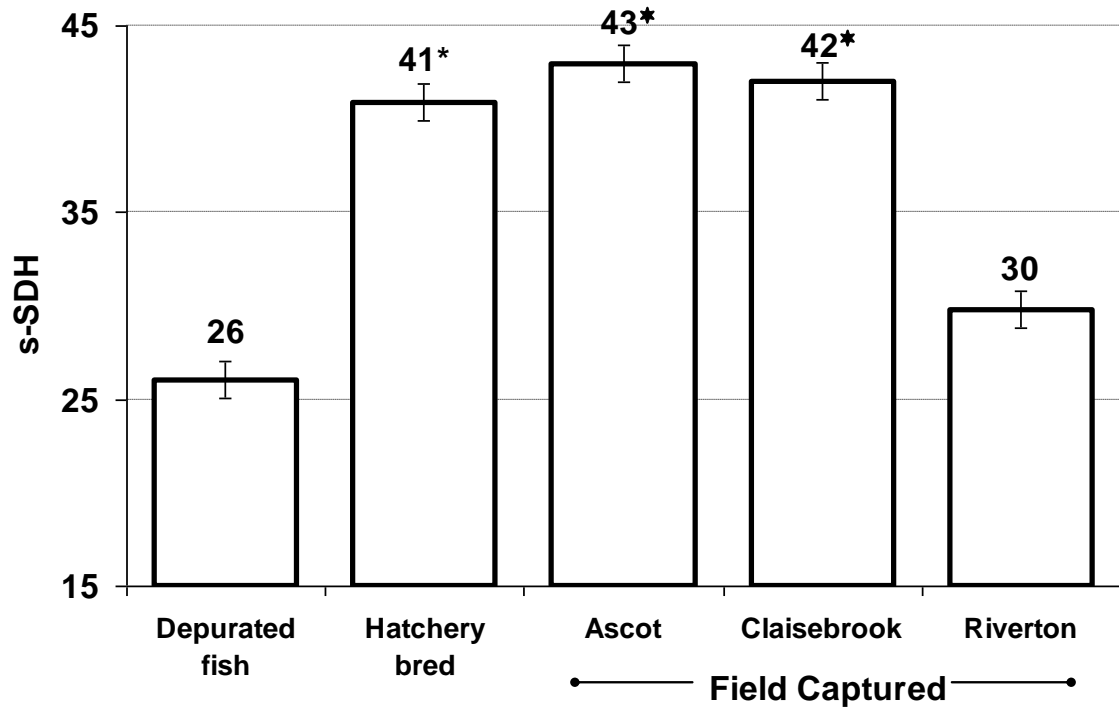


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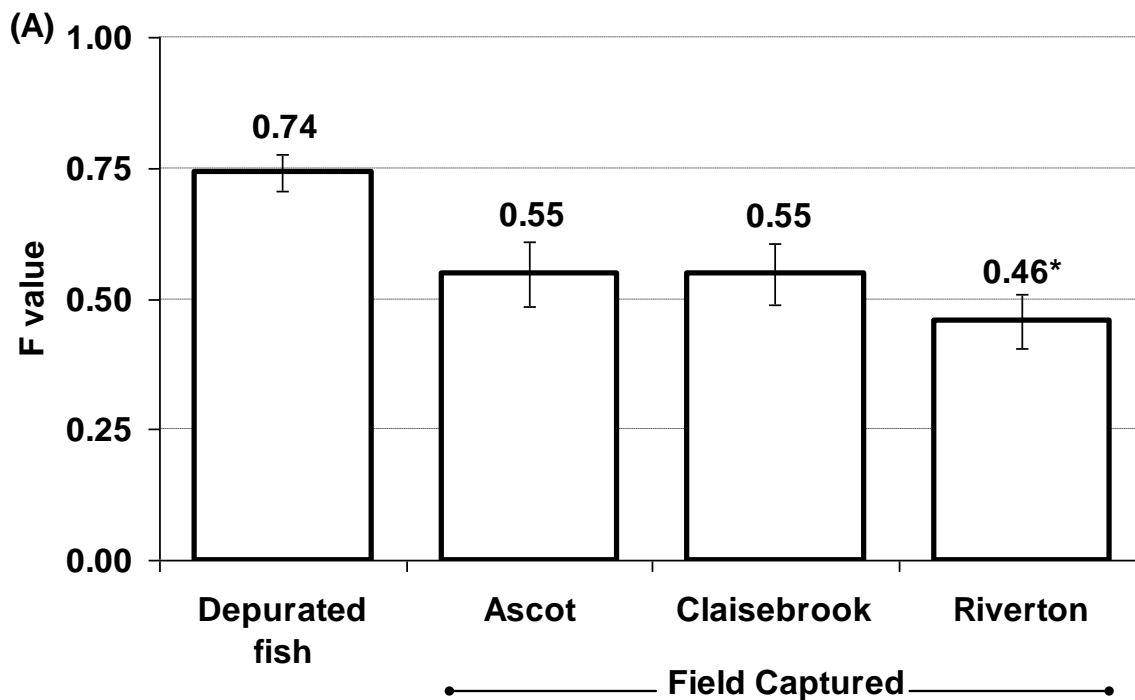


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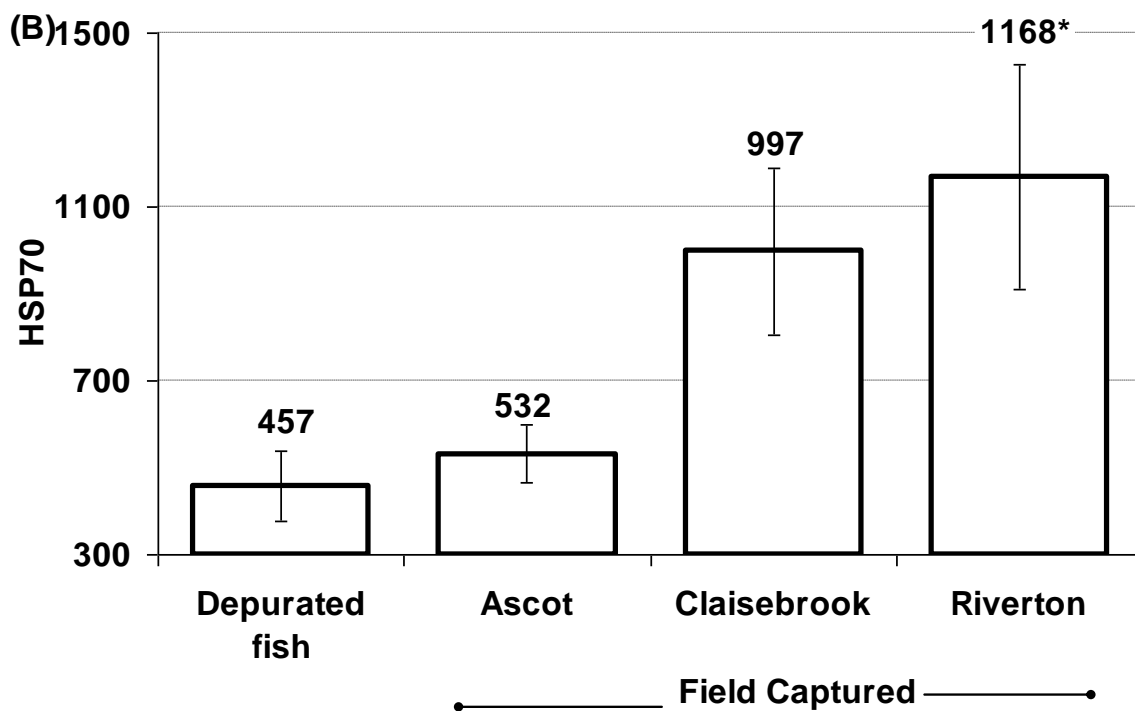
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