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Gene expression patterns and related enzymatic activities of detoxification and oxidative stress systems in zebrafish larvae exposed to the 2,4-Dichlorophenoxyacetic acid herbicide.

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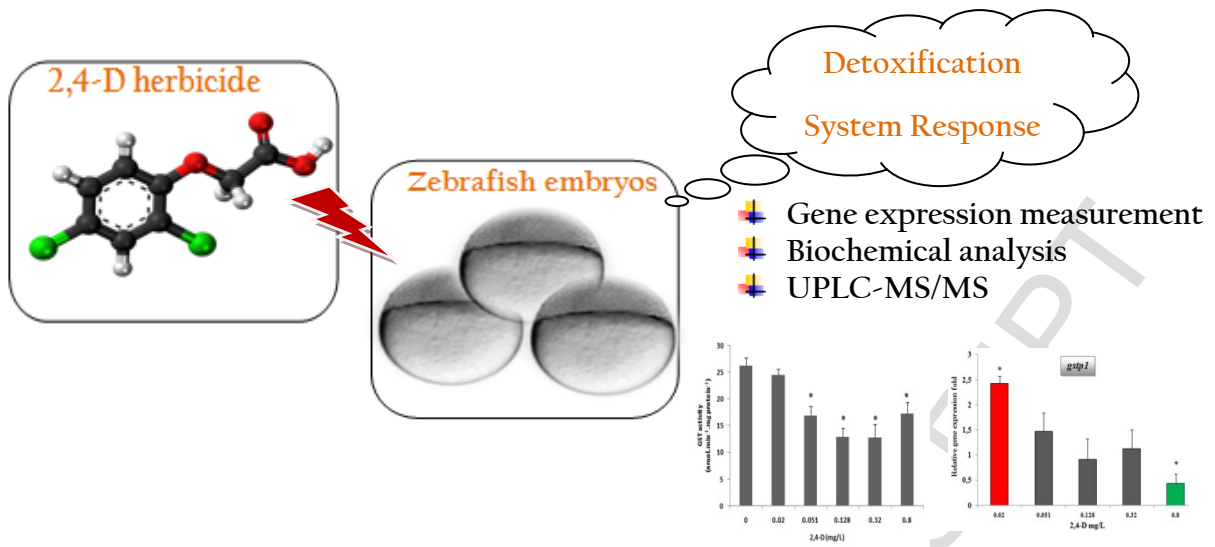
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Running title: 2,4-D affects detoxification **system in zebrafish larvae.**



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1 ABSTRACT

2 The present study aims to assess the effects of 2,4-D herbicide on biotransformation and
3 oxidative stress status of zebrafish larvae. Animals were exposed to a range of sublethal
4 concentrations (0.02 to 0.8 mg/L) and biomarkers at transcriptomic level and biochemical
5 level were assessed. Chemical analysis with showed that the bioaccumulation of 2,4-D in 96
6 hpf zebrafish larvae were increased in a concentration-dependent manner. This herbicide
7 induced significant effects at both gene expression and enzymatic activities levels after at 96
8 hpf. Results of mRNA expression showed a differential transcription regulation with all target
9 genes depending on the tested concentrations. The mRNA level of *gsr* and *cypla* were up
10 regulated at the highest dose of herbicide (0.8 mg/L). The gene expression of *gstp1* showed an
11 up regulation at lower dose (0.02 mg/L) and a down regulation at the highest dose (0.8 mg/L)
12 of 2,4-D. A significant induction of EROD activity and inhibition of GST activity were noted
13 in groups exposed to 0.8 mg/L of 2,4-D. Considering the antioxidant defenses, the activity of
14 CAT was increased in larvae exposed to 0.8 mg/L of herbicide and GPx activity was induced
15 at lower doses of 2,4-D (0.02 and 0.051 mg/L). Moreover, peroxidative damage, assessed as
16 MDA content, was markedly increased in larvae exposed to high 2,4-D concentration.
17 Overall, the present study data indicate that bioaccumulation of 2,4-D in 96 hpf zebrafish
18 larvae and alterations in detoxification and oxidative stress related parameters, likely
19 associated with ROS production, which may endanger the embryo-larval stages development
20 of fish.

21

22 Keywords: Herbicide; gene expression; biotransformation; oxidative stress; Zebrafish, early
23 life stages.

24 1. Introduction

25 Over the last decades aquatic environmental pollution has become a worldwide problem.
26 Currently, chemical discharge on freshwater systems displays high diversity and complexity
27 making this ecosystem at the center of ecotoxicological interest with the aim to prevent
28 harmful effects of toxic waste. Agricultural herbicides are among the emerging pollutants
29 contaminating the natural habitat (Konstantinou et al., 2006; Albuquerque et al., 2016; Vieira
30 et al., 2016). It may contaminate water surface, from point sources deriving from sewage or
31 industrial effluents and from diffuse sources such as agricultural and domestic activities
32 therefore endangering aquatic life (Akcha et al., 2012). 2,4-D (2,4dichlorophenoxyacetic acid)
33 is a common herbicide widely used in agriculture and forestry since 1946 and is present in
34 more than 1500 formulations (Garabrant, 2002; USEPA, 2005, Tayeb et al., 2011). It's a
35 synthetic auxin, known to kill the target weed by mimicking the plant growth hormone auxin,
36 causes uncontrolled and disorganized plant growth that leads to plant death (Tu et al., 2001;
37 Song, 2014). Applications of 2,4-D in agriculture area include barely, wheat, oats, corn,
38 soybeans, rice, and sugar cane (Akbulut et al., 2014). In Tunisia, the estimated quantities of
39 the main active compounds used in the agricultural areas surrounding the Ichkeul Lake and
40 Bizerte Lagoon was reported to be up to 2309 kg confirming its leader position in the country
41 (Ben salem et al., 2016). Extensive application of 2,4-D may induce toxicological problems in
42 non-target organisms at molecular and biochemical levels. Previous research report that
43 exposure to 2,4-D enhances the production of reactive oxygen species (ROS) in cells
44 (Atamaniuk et al., 2013; Tayeb et al., 2013). The latter's lead to the generation of oxidative
45 stress and the resulting damage is countered by a range of cellular antioxidant defenses
46 (Tayeb et al., 2012). Although 2,4-D toxicity on non-target organisms has been a topic of
47 extensive research, data concerning 2,4-D sublethal effect in zebrafish larvae remains
48 overlooked.

49 Therefore monitoring and assessing the toxicity of 2,4-D especially fish early life stage is
50 crucial in protecting the aquatic environment and to larger extend human health.

51 The early-life stage (ELS) test is being reliable for screening the toxicity of chemical
52 to aquatic organisms. Namely, the zebrafish embryo-larval assay has been suggested as a
53 replacement of adult zebrafish test (OECD., 2012, 2013). The rapid embryonic development
54 of zebrafish enables to record the sub-lethal endpoints and to evaluate toxic potential of
55 herbicides in the first days post fertilization (dpf) (Gellert and Heinrichsdorff, 2001; Wigh et
56 al., 2015). Moreover, *D. rerio* genome is almost fully sequenced (Shin & Fishman, 2002). The
57 conservation of several molecular pathways and basic cellular process, involved in the
58 response to chemicals, between zebrafish and humans (Ahmad et al., 2012; Howe et al., 2013)
59 allow the use of gene expression analysis for studying toxic mechanisms of pollutants.

60 Several pollutants are known to modulate organisms' metabolism promoting the reactive
61 oxygen molecules (ROS) inducing oxidative alterations to aquatic biota including zebrafish
62 embryos (Livingstone, 2003; Jin et al., 2013). For a better evaluation of 2,4-D effects on
63 zebrafish larvae, various markers of detoxification and oxidative stress were chosen. Firstly,
64 we studied responses at the transcriptomic level. The endpoints for gene expression related to
65 detoxification process (cytochrome P450 (*cyp1a*), glutathione-S transferase (*gstp1*)), and
66 oxidative stress responses (catalase (*cat*), glutathione peroxidase (*gpx1a*) and additionally
67 glutathione reductase (*gsr*)) were analyzed.

68 Secondly, we studied the responses at the biochemical level: enzymatic response. The
69 cytochrome P4501A, one of the main Phase (I) monooxygenase enzymes, involved in
70 metabolism of xenobiotics as well in bioactivation of pro-carcinogens. The CYP4501A
71 synthesis is inducible by multiple organic compounds and can be quantified by
72 ethoxyresorufin-O-deethylase (EROD) activity measurement. The enzymatic activity of
73 glutathione S- transferase (GST), a phase II enzymes, involved in the detoxification of

74 numerous environmental chemicals, through the conjugation of electrophilic xenobiotic and
75 oxidized metabolites with glutathione (GSH) (Hyne and Maher, 2003; Pan et al., 2009).
76 Catalase (CAT), an important antioxidant enzyme defense, prevents ROS accumulation by
77 converting hydrogen peroxide in water and oxygen (Livingstone, 2001). Glutathione redox
78 cycle enzymes: glutathione peroxidase (GPx) participates in the reduction of hydrogen
79 peroxide and glutathione reductase (GR) reduces the oxidized glutathion to GSH. Lactate
80 dehydrogenase (LDH) was indicative of anaerobic metabolism (Saravanan et al., 2011). To
81 evaluate peroxidative damage, lipid peroxidation (LPO) was used as marker of membrane
82 phospholipid oxidation (Kamel et al., 2014).

83 Therefore the major concern for this work was to assess the molecular and sub-cellular
84 responses aiming to shed the light on the molecular mechanisms by which 2,4-D may be
85 harmful on zebrafish early life stages.

86 **2. Materiel and Methods**

87 **2.1. Test chemicals and preparation of test solutions**

88 Commercial formulation of 2,4-D (Désormone lourde EC; SEPCM company) consists of 600
89 g/L 2,4-D. Working solutions were prepared by dissolving the herbicide in dimethyl sulfoxide
90 (DMSO).

91 **2.2. Adult maintenance**

92 Adults Zebrafish "*Danio rerio*" were kept in a ZebTEC (Tecniplast) recirculating
93 system established at the Department of Biology, University of Aveiro (Portugal). A
94 photoperiod cycle of 16:8 h (light:dark) was maintained. Culture water was purified by
95 reverse osmosis and activated carbon filtered tap water, complemented with 0.34 mg/L salt
96 "Instant Ocean Synthetic Sea Salt" (Spectrum Brands, USA) and automatically adjusted for

97 pH and conductivity. Water pH was 7.5 ± 0.5 , conductivity 750 ± 50 IS, salinity 0.35 ppt.
98 Temperature was 26.0 ± 1 °C and dissolved oxygen equal or above 95 % saturation. Nitrogen
99 compounds were kept below 0.01 mg/L (nitrite and ammonia) and 0.1 mg/L (nitrate). The
100 culture water was monitored daily and was used as dilution water for the preparation of the
101 test solutions. The adult fish were fed twice a day with commercially available artificial diet
102 (ZM-400 fish food; Zebrafish Management Ltd).

103 **2.3. Embryo toxicity assay**

104 The experimental was based on the Organisation for Economic Co-operation and
105 Development (OECD) draft guideline on fish embryo toxicity (FET) test (OECD, 2012).
106 Sexually mature male and female of the same size and age (between 16 and 18 weeks) were
107 selected for spawning. Marbles were used in the spawning aquariums; the zebrafish embryos
108 were collected immediately after natural mating, rinsed in water system and checked under a
109 stereomicroscope (Stereoscopic Zoom Microscope-SMZ 1500, Nikon Corporation). Only
110 fertilized and normal developed embryos (in the blastula stage; 3 hpf) were used in the tests.
111 Newly Fertilized eggs previously selected, were exposed for 96 h in static conditions to five
112 sublethal concentrations of 2,4-D (0.02, 0.051, 0.128, 0.32, 0.8 mg L⁻¹). The sublethal assay
113 design included also a negative control (water system only) and solvent control (0.3 µL/L of
114 DMSO, the maximal concentration of DMSO used in the 2,4-D treatments). The sublethal
115 concentrations tested were selected based on the LC₅₀ determined in a previous study (Gaaied
116 et al., 2019). The exposure was done with the aim of collecting material for biomarkers
117 analysis, transcriptomic analysis and chemical analysis. Eggs were exposed into small petri
118 dishes the numbers of individuals and replicates used differed according to the test. Larvae at
119 96 hpf for each biomarkers and chemicals analysis were snap frozen in microtubes and kept at
120 - 80 °C until analysis. For transcriptomic analysis larvae were frozen in RNA Later at -20 °C.

121 2.4. Chemicals analysis

122 30 larvae per experimental condition (3 biological replicates) were homogenized in 0.2 mL of
123 50% acetonitrile (diluted in ultrapure water). The chromatographic separation was performed
124 on a C18 column (ACQUITY UPLC BEH), with a gradient elution using a mobile phase
125 made of acetonitrile and 0.02 M ammonium acetate with 0.1% (v/v) formic acid (Li et al.,
126 2017). The injection volume was 5 mL and the flow rate was 0.25 mL/min. An internal
127 standard made of a serial dilution of a 2,4-D stock solution was used (0, 1, 5, 10 and 15
128 mg/mL). The extraction recovery of 2,4-D was performed using five replicates of each
129 Quality Control samples. The recoveries (mean) of 2,4-D were found to be in the range from
130 100.4% to 101.8%.

131

132 2.5. Gene expression measurements

133 Total RNA was extracted from 20 larvae (n=4 for each exposure condition) using acidphenol-
134 chloroform precipitation according to Chomczynski and Sacchi (1987) with TRI-Reagent
135 (Sigma-Aldrich). RNA was further processed as described by Banni et al (2011, 2014).
136 Relative mRNA abundances of the zebrafish genes encoding *gstp1*, *cat*, *gpx1a*, *gsr*, *Cy1a*
137 were evaluated with SYBR Green I chemistry (EvaGreen®dye; Bio-Rad Laboratories; Banni
138 et al., 2007, 2014). Primer pairs (Table 1) were designed using Beacon Designer v3.0
139 (PremierBiosoft International, Inc.).

140 The PCR efficiencies used to calculate relative fold induction levels in relation to the control
141 represent the median value obtained from at least four independent experiments, and they
142 were 2.0, 1.96 and 1.95, 1.88 and 1.92 respectively for *gstp1*, *cat*, *gpx1a*, *gsr*, *Cy1a*.
143 Moreover, the relative expression stability of the three reference genes was calculated in our
144 experimental conditions using geNorm. Our data showed expression stability values of 0.23,
145 0.37 and 0.41 respectively for *eef1a112*, β -*actin* and *gapdh*. Relative expression data were

146 geometrically normalized to *eef1a112*, β -*actin* and *gapdh* (Perrichon et al., 2016). qRT-PCR
147 was performed with four biological replicates and three technical replicates. Statistical
148 analyses were carried out on the group mean values using a random reallocation test (Pfaffl et
149 al., 2002).

150 **2.6. Biochemical endpoints**

151 GST, CAT, GR, GPx, LDH activities were analyzed from whole zebrafish larvae. Enzymatic
152 determinations were made spectrophotometrically (Labsystem Multiskan EX microplate
153 reader) using 96 well microplate. Samples were defrosted on ice in the day of enzymatic
154 analyses, homogenized in K-phosphate buffer (0.1 M, pH 7.4) using a sonicator (Branson S-
155 250A) and centrifuged (4 °C, 9000 g, 20 min) to isolate the post-mitochondrial supernatant
156 (PMS) later used for enzyme activity determinations. The protein concentration in the PMS
157 was determined based on the Bradford method (1976), using a wavelength of 595 nm and γ -
158 globulin as standard.

159 CAT, GST, CAT, GR, GPx, LDH activities and LPO content were determined respectively
160 according to Clairborne (1985), Habig and Jakoby (1981), Athar and Iqbal (1998), Lima et al.
161 (2007), Diamantino et al. (2001) and Livingstone et al., (1993).

162 In vivo EROD activity measurements were performed according to Le Bihanic et al. (2013)
163 with some modifications. Measurements were conducted on living larvae at 96 hpf. Larvae
164 were randomly distributed into 48 well plates and incubated in 1 μ M 7-ethoxyresorufin
165 solution for 1 h at 28 ± 0.5 °C in obscurity. Then the old 7-ER was removed and replaced
166 with 600 μ L fresh 1 μ M 7-ER solution. The microplate was then incubated for 4 h at 28°C
167 and protected from light with aluminum foil Process fluorescence reading was conducted with
168 the microplate reader exc./em.: 560/590 nm and EROD activity was expressed as
169 pmol/well/larvae.

170 2.7. Statistics analysis

171 Statistically significant effects were assessed using SPSS 20.0 software package. Differences
172 between controls (negative and solvent) were carried out using a Student t-test ($p < 0.05$). The
173 normality of the distribution was tested using the Shapiro–Wilk test. Significant differences
174 between the control and experimental groups were assessed by the parametric one-way
175 analysis of variance (ANOVA) with Tukey’s test. All values were expressed as the mean \pm
176 standard deviation (SD). Values were considered statistically significant when p was less than
177 0.05.

178 3. Results

179 3.1. The concentration of 2,4-D in the exposure medium

180 Chemical analysis results of 2,4-D in the exposure medium are presented in table 2. The
181 exposure medium showed stable concentrations and within 95.13–110 % of the nominal
182 concentrations in what refers the sublethal test (0.02–0.8 mg/L).

183 3.2. The concentration of 2,4-D in larvae after 96 h of exposure

184 The loads of 2,4-D in zebrafish larvae after the exposure period are reported in Table 2. 2,4-D
185 concentrations were significantly increased in dose-dependent manner in 96 hpf larvae when
186 compared to control. The 2,4-D accumulation reached a maximum in the group exposed to
187 0.8 mg/L with up to 54.44 ± 4.78 ng/mg dry weight.

188 3.3. Effects of 2,4-D on detoxification and oxidative stress-related gene transcription:

189 Expression analysis of genes was performed by real time quantitative PCR on zebrafish larvae
190 transcripts using *eef1a1l2*, *β -actin*, and *gapdh* mRNA as reference genes. The mRNA
191 expression levels are expressed in relation to the average expression of the 3 reference genes.

192 Overall the mRNA level of various genes encoding detoxification proteins (*cyp1a* and *gstp1*)
193 and antioxidant proteins (*cat*, *gpx1a* and *gsr*) were altered after 96 h of exposure to 2,4-D (Fig
194 1 and 2). The results demonstrated that the relative mRNA level of *cyp1a* was up-regulated in
195 larvae exposed to a concentration equal or above 0.128 of 2,4-D. The transcription level of the
196 gene encoding *gstp1* significantly increased at lower dose (0.02 mg/L) however significantly
197 decreased at higher dose (0.8 mg/L). In addition, a significant up-regulation of *cat* expression
198 was observed in larvae exposed to 0.02 and 0.051 mg/L. The relative mRNA level of *gpx1a*
199 was significantly increased in groups exposed to 0.128 and 0.32 mg/L of 2,4-D. Moreover,
200 The transcripts of *gsr* in zebrafish larvae was significantly up regulated after 96 h of exposure
201 at concentration equal or above to 0.32 mg/L.

202

203 3.4. Effect of 2,4-D on detoxification and oxidative stress enzyme activities:

204 Enzymes involved in detoxification process are presented in figure 3. A significant increase in
205 EROD activity was found in groups exposed to (0.02, 0.051, 0.128 and 0.8 mg/L) compared
206 to the control. GST activity showed an inhibition for all tested concentrations (0.02 to 0.8
207 mg/L) compared to control and results were statistically significant at concentration equal or
208 above 0.051 mg/L ($p < 0.05$). Enzymes involved in oxidative stress process are presented in
209 figure 4. GR activity was not statistically significant in all tested concentrations compared to
210 the control group. However, a significant ($p < 0.05$) increase in the activity of GPx was found
211 in groups exposed to (0.02 and 0.051 mg/L) when compared to the control. The activity of
212 CAT was significantly higher ($p < 0.05$) in groups exposed to the highest tested dose of 2,4-D
213 (0.8 mg/L) compared to the control group. Regarding LDH activity no significant differences
214 were found when compared to the control.

215 3.5. Effect of 2,4-D on lipid peroxidation:

216 Lipid oxidative damage was investigated by the evaluation of the MDA accumulation in
217 larvae tissues. Results shows a significant increase ($p < 0.05$) in MDA levels in groups
218 exposed to (0.02, 0.051, 0.128 and 0.8 mg/L) compared to control group (Fig. 5).

219

220 4. Discussion

221 Oxidative stress has become an interesting parameter in aquatic toxicology assessment
222 and is known to occur when the rate of ROS production exceeds the activities of antioxidant
223 systems (Livingstone, 2003; Adeyemi et al., 2015). Previous studies reported that pesticides
224 are able to enter redox cycles by accepting/donating electrons and consequently they may
225 increase ROS level causing oxidative damage in fish (Slaninova et al., 2009; Lushchak,
226 2011). Thus, the effects of pro-oxidant chemicals in fish can be used to assess water pollution
227 through monitoring the modification of the antioxidant activity or the expression of the
228 encoding gene. From this idea, we aimed to investigate, for the first time, the impact of 2,4-D
229 herbicide on mRNA expression of target genes associated with biotransformation and
230 oxidative stress and their related enzyme activities in 96 hpf *D. rerio* larvae.

231 In this study, transcriptomic analysis provided considerable evidence that exposure to
232 sublethal concentrations of 2,4-D modulate mRNA levels of genes encoding detoxification
233 (*cyp1a* and *gstp1*) and antioxidant proteins (*cat*, *gsr* and *gpx1a*) in zebrafish embryos after 96
234 h. Nonetheless, there is no dose response expression in targeted genes, we can conclude that
235 this compound contribute to oxidative stress in zebrafish larvae.

236 In this work, we evaluated the *cyp1a* gene expression, a subfamily of *cyp 450* known to serve
237 as bioindicators of environmental stress in fish (Brammell and Andrew, 2010; Xing et al.,
238 2014). Relative gene expression analyses revealed that, compared to the control, *cyp1a* was
239 significantly up-regulated in response to 2,4-D at concentrations equal or above to 0.128
240 mg/L. Similar enhanced expression of *cyp1a* gene was reported in zebrafish larvae after
241 exposure to chlorpyrifos and diuron (Jeon et al., 2016; Velki et al., 2017). Considering the
242 mechanism associated in *cyp1a* gene expression, the up regulation of *cyp1a* gene may be
243 dependent on the response of Pregnane X receptor (PXR), a member of nuclear receptor (NR)
244 family. PXR plays a pivotal role in regulation of xenobiotic metabolism enzymes (Timsit and

245 Negishi, 2007) and any change of PXR signaling pathway may be linked with the
246 biotransformation and detoxification of xenobiotic (Wang et al., 2019). It is well documented
247 that the gene expression of *cyp1a* is regulated partly by PXR (Kamenickova et al., 2012) and
248 according to Kojima et al. (2010) the 2,4-D represent an agonist to PXR. Thus, the *cyp1a*
249 regulation in this study seems to be partly controlled by the PXR. Upon activation, the PXR
250 displace to the nucleus and bind to DNA response elements in promoters generating the
251 expression of several metabolizing enzymes including cytochrome P4501A (Staudinger et al.,
252 2010). Regarding *gstp1* the gene expression pattern was up regulated at lower concentration
253 of herbicide (0.02 mg/L) however a significant decrease of *gstp1* mRNA expression was
254 observed in larvae exposed to the highest concentration (0.8 mg/L). It is possible that in the
255 present work, the increase in the transcription of the detoxifying and anti-oxidative stress
256 genes would contribute to the elimination of ROS from the cell (Banni et al., 2014). However,
257 the reduced mRNA level demonstrated a transcriptional regulation of gene expression in
258 larvae. The gene expression of *cat* and *gpx1a* was up regulated at lower (0.02 and 0.051
259 mg/L) and medium concentrations (0.128 and 0.32 mg/L) respectively. However, a clear
260 return to baseline expression of reference genes was noted with *cat* and *gpx1a* genes in larvae
261 exposed to the highest concentration (0.8 mg/L). Thus, the change in the expression of *cat* and
262 *gpx1a* indicates the implication of oxidative stress in the toxicity mechanism of 2,4-D. Li et
263 al. (2017) found a down regulation of *gpx1a* and *cat* 2,4-D in zebrafish embryos exposed to
264 25 mg/L of 2,4-D. The up regulation of *cat* and *gpx1a* genes observed in this study was also
265 reported in other studies with pesticides, Jiang et al. (2015a; 2015b and 2016) also found that
266 carbendazim, acetochlor and pretilachlore induced an up-regulation of *cat* and *gpx* genes in
267 zebrafish embryos. Further, Jamil et al. (2015) reported that at 100 µg/L of 2,4-D there is an
268 induction of *gpx* gene in 72 hpf zebrafish larvae, indicating its affinity for oxidative stress.

269 In this study, the expression of the *gsr* was up-regulated after 96 h exposure. The observed
270 increase in the transcription of the *gsr* gene suggests its implication in antioxidative defense
271 and its contribution to protect larvae from oxidative stress damage induced by herbicide
272 exposure. Also, it is well known that the signaling pathways of oxidative stress enzyme may
273 be activated by redox-sensitive proteins (Den Hertog et al., 2005) and this may explain the
274 increase of *gsr* level. The results reported by Velki et al. (2017), assessing the effect of diuron
275 in zebrafish embryos, are similar to our findings.

276 In addition to the gene expression analysis, phase I and phase II detoxification
277 enzymes, oxidative stress enzymes as well as lipid peroxidation level were also assessed in
278 zebrafish larvae.

279 Xenobiotic metabolism enzymes, including cytochrome P450 (CYP), play a central role in the
280 biotransformation of foreign compounds (Gueguen et al., 2006). In our work the EROD
281 activity was increased and this effect may be considerate as a toxicity mechanism in exposed
282 larvae. Being a xenobiotic, 2,4-D is metabolized by organisms and 2,4-D or its metabolites
283 may affect normal detoxification processes (Atamaniuk et al., 2013). In this study, the *cyp1a*
284 mRNA abundance and the EROD enzyme showed a disparity and the induction was markedly
285 observed at the transcriptomic level than at the biochemical level.

286 Glutathione S-transferases (GST) are among the primary antioxidant enzymes and the first-
287 line indicators of the antioxidant state (Yang and Lee, 2015). In fact, in phase II of
288 biotransformation, the GST plays a central role through the detoxification of xenobiotic such
289 as herbicides (Higgins and Hayes, 2011) and endogenic compounds that conjugate with
290 glutathione (Domingues et al., 2010). In this study the oxidative stress enzyme GST were
291 inhibited at concentrations equal and higher than 0.128 mg/L. This inhibition could be due to
292 an impairment of the GST pathway in response to a substantial stress increase as previously
293 reported by Oliveira et al. (2013). Similar results were found in *D.rerio* embryos after 96 h

294 exposure to rotenone and potassium dichromate (Melo et al., 2015; Domingues et al., 2010).
295 Further, it was observed that the mRNA level of *gstp1* correlate well with the GST enzyme
296 activity suggesting that this enzyme was controlled at least by transcription regulation rather
297 than at the protein level (Jiang et al., 2016).

298 The ROS detoxification mechanisms are associated with a combination of multiple enzymes
299 such as CAT, and GPx. Hence, CAT and GPx can be considered as the first line of defense
300 against the deleterious effect provoked by excessive production of ROS in response to
301 chemical exposure (Shukla et al., 2017). Regarding, CAT activity our result shows a
302 significant induction at the highest level of 2,4-D (0.8 mg/L). The induction of CAT enzyme
303 can be explained by its catalytic activity to convert hydrogen peroxide (H₂O₂) into water
304 (H₂O) and oxygen (O₂) (Pi et al., 2010). Our results are similar to the findings of Jiang et al.
305 (2016) in which pretilachlor exposure lead to a significant CAT activity in *D. rerio* larvae.
306 Others studies with adult fish showed that 2,4-D exposure increased CAT activity in the
307 kidney of *Cyprinus carpio* and in the gills of goldfish, *Carassius auratus* (Oruc et al., 2004;
308 Atamaniuk et al., 2013). We have noticed that the gene expression level of *cat* showed
309 opposite trend to the activity of corresponding enzyme at 0.8 mg/L. This can be explained by
310 the high CAT activity which may cause a decrease of *cat* mRNA level by the negative
311 feedback mechanism (Xia et al., 2017). Conversely, to CAT enzyme activity, a bell shaped
312 curve response of GPx enzyme was observed in this study. This finding could be an indication
313 that the rate of production of H₂O₂ in exposed larvae surpassed the scavenging ability of GPx,
314 and consequently resulting in oxidative stress. In terms of comparison between Gr activity
315 and *gsr* mRNA expression, the up regulation of this gene was not translated into higher
316 activity of GR enzyme. We can suggest that the transcriptional up-regulation of *gsr* genes
317 may be initiated to compensate the low levels of enzymes (Gagnaire et al., 2015).

318 Lipid peroxidation (LPO) is an oxidative stress marker, indicating that ROS production
319 exceeded antioxidant defenses (Ahmad et al., 2008; Oliveira et al., 2009). MDA is the end
320 product of LPO and considered as an indicator of oxidative stress, which results from the free
321 radical damage to membrane components of cells (Kuder and Philip, 2017). In the present
322 study, the MDA content in zebrafish larvae was increased following exposure to 2,4-D which
323 indicated that the zebrafish larvae suffered from oxidative damage. Previous investigations
324 have also reported that 25 mg/L of 2,4-D induce malondialdehyde (MDA) accumulation in
325 72 hpf zebrafish embryos (Li et al., 2017).

326 **5. Conclusions**

327 In summary, it can be concluded that sublethal exposure to 2,4-D herbicide contribute to
328 oxidative stress in 96 hpf zebrafish larvae. The changes in detoxifying and oxidative stress-
329 genes as well as related enzyme activities could be an adaptive and protective response of
330 larvae from 2,4-D toxicity. However, the mRNA induction patterns were not in conformity
331 with the changes in levels of antioxidant enzymes in most cases, suggesting that certain
332 antioxidant enzymes are controlled by enzyme activity and not by transcriptional regulation.
333 The discrepancy between antioxidant enzymes level and the gene expression level must be
334 taken into consideration when evaluating the oxidative stress in organisms. Thus, a combined
335 stress biomarker pattern at different biological levels provides a reliable prediction of adverse
336 effects of herbicide and emerging pollutants to aquatic organisms.

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340 Department of Biology, University of Aveiro Portugal.

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Figures captions

Fig.1. Relative mRNA expressions of phase I and phase II detoxification enzymes: *cyp1a* (A) and *gstp1* (B) measured in zebrafish larvae exposed to sublethal concentrations of 2,4-D for 96 h. The results of mRNA expression levels are expressed in relation to normalized gene expression average which is set to 1. Values are means \pm standard deviation of 4 replicates. Asterisks indicate statistically significant difference from the control ($P < 0.05$), threshold cycle random reallocation test according to Pfaffl et al. (2002). Red colors indicate up-regulated gene and green color indicate down-regulated gene.

Fig.2. Relative mRNA expressions of oxidative stress enzymes *cat* (A), *gpx1a* (B), *gsr* (C) measured in zebrafish larvae exposed to sublethal concentrations of 2,4-D for 96 h. The results of mRNA expression levels are expressed in relation to normalized gene expression which is set to 1. Values are means \pm standard deviation of 4 replicates. Asterisks indicate statistically significant difference from the control ($P < 0.05$), threshold cycle random reallocation test according to Pfaffl et al. (2002). Red colors indicate up-regulated gene

Fig.3. Detoxification enzymes (mean values \pm standard deviation, $n = 5$) measured in zebrafish embryos after 96 h of exposure to 2,4-D. EROD activity (A) was expressed on pmol/well/larvae. Data, expressed as nmol/min/mg protein for GST (B). Asterisks mean significantly different from the respective control ($p < 0.05$) after one-way ANOVA using Tukey's test.

Fig.4. Biomarkers of oxidative stress (mean values \pm standard deviation, $n = 5$) measured on zebrafish embryos after 96 h of exposure to 2,4-D. Data, expressed as nmol/min/mg protein for CAT (A), GR (B), GPx (C) and LDH (D). Asterisks mean significantly different from the respective control ($p < 0.05$) after one-way ANOVA using Tukey's test.

Fig.5. Lipid peroxidation levels (LPO) expressed on nmol/mg protein. Mean values \pm standard deviation, $n=5$ and asterisks mean significantly different from the respective control ($p < 0.05$) after one-way ANOVA using Tukey's test.

Figure 1

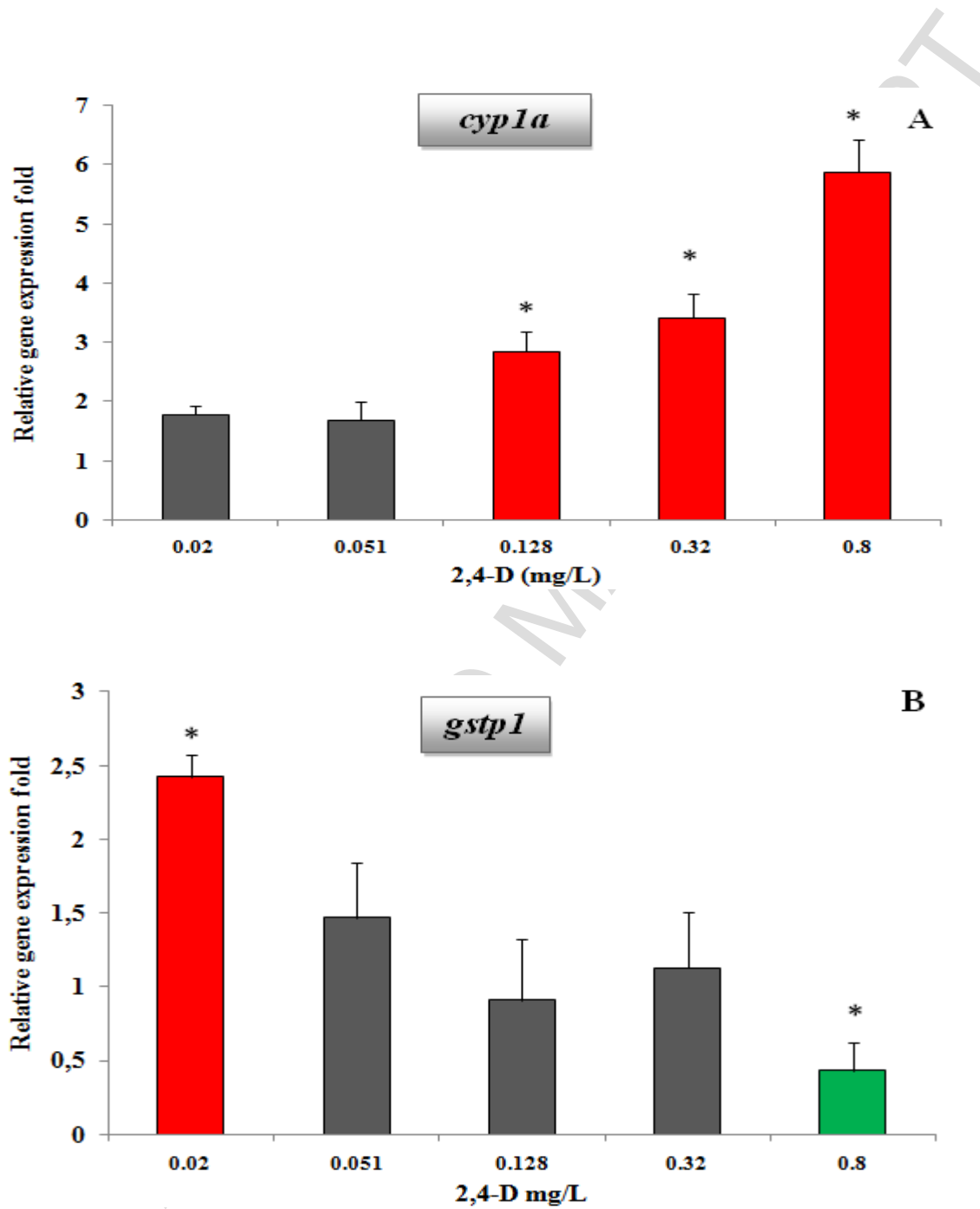


Figure 2

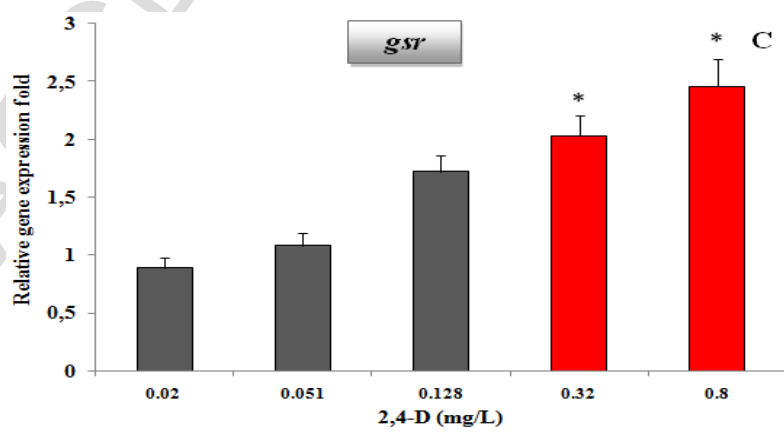
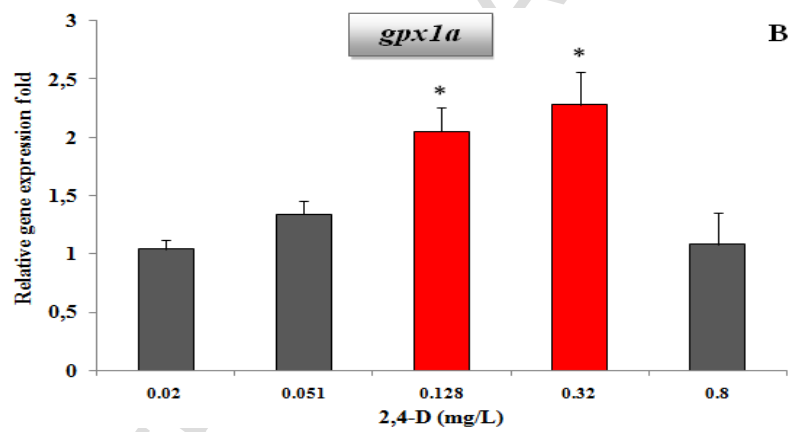
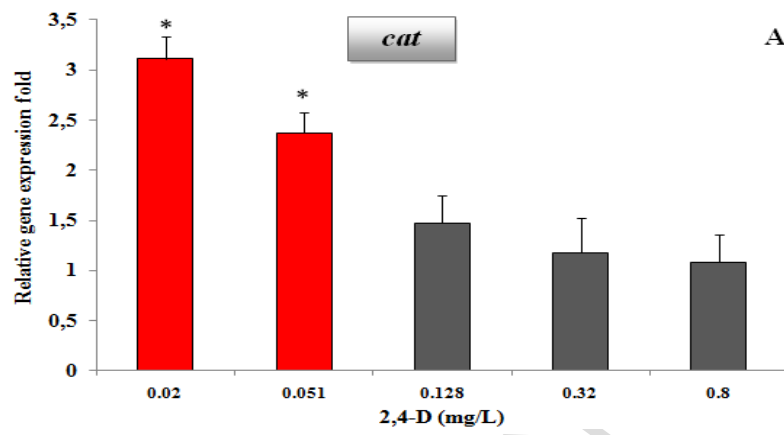


Figure 3

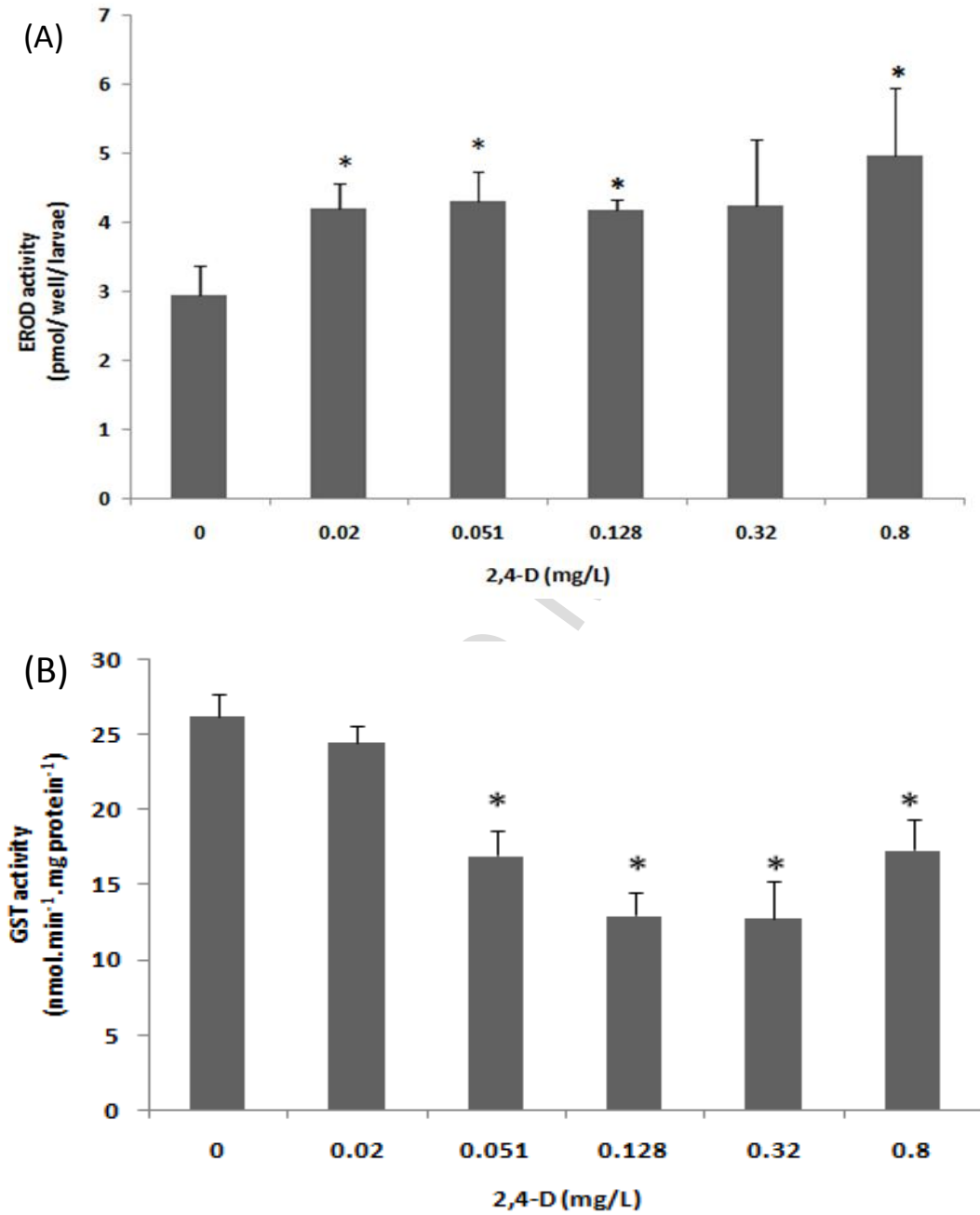


Figure 4

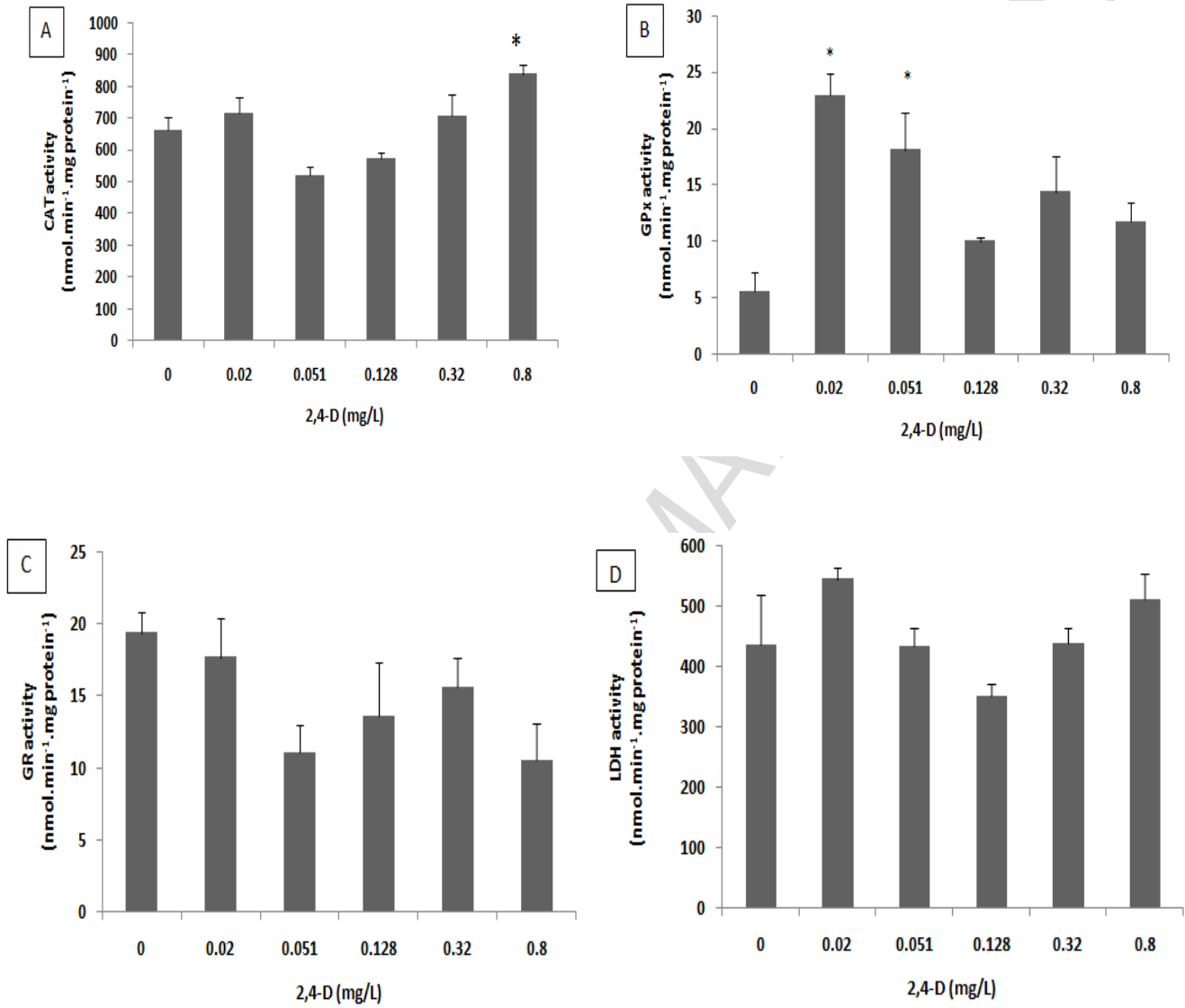
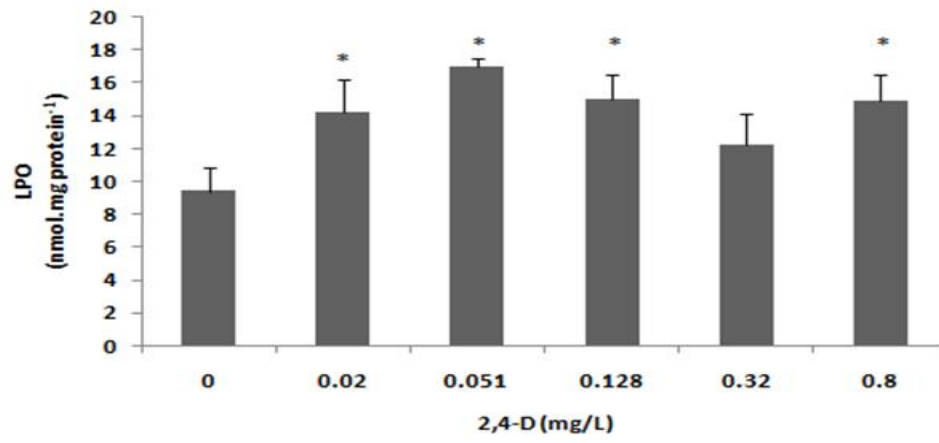


Figure 5



Highlights

- Sublethal exposure to 2,4-D herbicide contribute to oxidative stress in zebrafish larvae.
- 2,4-D alters gene expression of detoxification and oxidative stress enzyme in zebrafish larvae.
- 2,4-D modulate detoxification and oxidative stress enzyme activities in zebrafish larvae.
- 2,4-D enhances MDA level in 96 hpf zebrafish larvae.

Table1. Primer sequences, accession numbers, amplicon sizes, and annealing temperatures used in qPCR reaction.

Target genes	Accession numbers	Primer sequence (5' - 3')	Amplicon sizes
<i>gstp1</i>	NM_131734.3	F: TGGTGCTGTTTCAGTCCAAG R: AGCCTCACTGTCGTTTTTGC	80
<i>cat</i>	NM_130912.1	F: TTTCTCCTACCCAGACACACA R: CACCTGGGTCACGTTGTCAT	169
<i>gpx1a</i>	NM_001007281.2	F: GAGGCACAACAGTCAGGGATT R: CTTCACTTCTGCAGTTCTCCTGGT	126
<i>gsr</i>	NM_001020554.1	F: CGGCCTCAACCTCAGTCAAA R: TGCTTCATCAGGTGTCAGAAG	142
<i>cyp1a</i>	NM_131879.2	F: AAAGACACCTGCGTGTTTGTA R: GAGGGATCCTTCCACAGTTCT	68
<i>eef1a112</i>	NM_001039985.1	F: GTGGTAATGTGGCTGGAGAC R: TGTGAGCAGTGTGGCAATC	138
<i>β-actin</i>	AF025305	F: CGAGCTGTCTTCCCATCCA R: TCACCAACCTAGCTGTCTTTCTG	100
<i>gapdh</i>	BC083506	F: GTGGAGTCTACTGGTGTCTTC R: GTGCAGGAGGCATTGCTTACA	173

Target genes abbreviations: *gstp1* (glutathione S-transferase pi 1); *cat* (catalase); *gpx* (glutathione peroxidase); *gsr* (glutathione reductase); *cyp1a* (cytochrome P450, family 1, subfamily A).

References genes abbreviations: *eef1a112* (eukaryotic translation elongation); *gapdh* (Glyceraldehyde-3-phosphate dehydrogenase); *β -actin* (Beta-actin).

Table2. Data of chemical analysis of 2,4-D in working solutions and in 96 hpf zebrafish larvae. Data of 2,4-D content in larvae are expressed as ng/mg dry weight (n=3); asterisks mean significantly different from the respective control (p<0.05) after one-way ANOVA using Tukey's test.

Nominal concentration of 2,4-D in water (mg/L)	Measured Concentration of 2,4-D in water (mg/L)	% Recovery	2,4-D accumulation in larvae (ng/mg dry weight)
0	0	0	0
0.02	0.022	110	1.42 ± 0.12*
0.051	0.055	107.84	3.58 ± 0.42*
0.128	0.125	97.66	8.47 ± 0.91*
0.32	0.311	97.19	20.38 ± 2.34*
0.8	0.761	95.13	54.44 ± 4.78*