


# Cytotoxicity and alterations at transcriptional level caused by metals on fish erythrocytes in vitro

Patricia Morcillo<sup>1</sup> · Diego Romero<sup>2</sup> · José Meseguer<sup>1</sup> · M. Ángeles Esteban<sup>1</sup> · Alberto Cuesta<sup>1</sup> 

Received: 19 December 2015 / Accepted: 8 March 2016 / Published online: 15 March 2016  
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**Abstract** The in vitro use of fish erythrocytes to test the toxicity of aquatic pollutants could be a valuable alternative to fish bioassays but has received little attention. In this study, erythrocytes from marine gilthead sea bream (*Sparus aurata* L.) and European sea bass (*Dicentrarchus labrax* L.) specimens were exposed for 24 h to Cd, Hg, Pb and As and the resulting cytotoxicity was evaluated. Exposure to metals produced a dose-dependent reduction in the viability, and mercury showed the highest toxicity followed by MeHg, Cd, As and Pb. Moreover, fish erythrocytes incubated with each one of the metals exhibited alteration in gene expression profile of metallothionein, superoxide dismutase, catalase, peroxiredoxin, glutathione reductase, heat shock proteins 70 and 90, Bcl2-associated X protein and calpain1 indicating cellular protection, stress and apoptosis death as well as oxidative stress. This study points to the benefits for evaluating the toxicological mechanisms of marine pollution using fish erythrocytes in vitro.

**Keywords** Erythrocytes · Metals · Teleost fish · Flow cytometry · Oxidative stress · Cell death

## Introduction

Anthropogenic actions have resulted in an increased flux of metallic substances into the aquatic environment (Yang and Rose 2003), a fact that has led to the investigation of the effect of metals and metalloids on the biological functions of marine organism such as fish. Among the adverse effects, metals can produce mortality or alterations in blood, metabolism, nutrition, reproduction, development and immunity (Bols et al. 2001; Di Giulio and Hinton 2008; Sweet and Zelikoff 2001). Some studies have shown that aquatic pollutants including metals alter fish haematological indices (haematocrit, red blood cell count per unit blood volume and haemoglobin (Hb) concentration), as well as blood/plasma ions, hormones, metabolites, proteins or enzymes (Schlenk et al. 2008). However, there are not many papers dealing with the toxicological effects on fish blood cells, namely erythrocytes.

In vitro toxicological tests are gaining traction as alternatives to in vivo tests because they are more cost- and time-effective and have fewer ethical issues. The fact that fish erythrocytes are nucleated and contain organelles that exhibit good resistance in primary cultures and are easily handled constitutes a very interesting cellular model for toxicological studies in vitro (Bogé and Roche 1996). Furthermore, experimental fish are not killed which turns them into a valuable alternative to fish bioassays and contributes to the three R's. In addition, erythrocytes are targets for metals and used to distribute them along the body. Owing to the high oxygen and iron concentrations in the cytoplasm, erythrocytes can continuously produce reactive oxygen species (ROS) as a result of haemoglobin oxidation to methaemoglobin (Çimen 2008;

Responsible editor: Cinta Porte

**Electronic supplementary material** The online version of this article (doi:10.1007/s11356-016-6445-3) contains supplementary material, which is available to authorized users.

✉ Alberto Cuesta  
alcuesta@um.es

<sup>1</sup> Fish Innate Immune System Group, Department of Cell Biology and Histology, Faculty of Biology, Campus Regional de Excelencia Internacional “Campus Mare Nostrum”, University of Murcia, 30100 Murcia, Spain

<sup>2</sup> Department of Toxicology, Faculty of Veterinary, Campus Regional de Excelencia Internacional “Campus Mare Nostrum”, University of Murcia, 30100 Murcia, Spain

Giulivi and Davies 2001) and therefore are exposed to potential oxidative stress. To maintain the ROS balance, as in mammals, fish erythrocytes are well protected by radical scavengers, including enzymatic and non-enzymatic systems. The enzymatic systems in erythrocytes consist of mitochondrial and cytosolic superoxide dismutase (SOD), catalase (CAT) and glutathione peroxidase (GPx) and peroxiredoxins (Çimen 2008; Scott et al. 1989).

In vivo toxicological studies in fish erythrocytes have reported the effects of various chemicals in the morphology, haemolysis, nuclear deformation, amitosis (Bogé and Roche 1996; Witeska 2013) and genotoxic damage (Bagdonas and Vosylienė 2006; Monteiro et al. 2011). However, fewer studies have evaluated the toxicological role of metals on fish erythrocytes in vitro, which could provide basic information on the nature of the tested agents and/or the cellular response (Binelli et al. 2009). Thus, rainbow trout (*Oncorhynchus mykiss*) naïve erythrocytes exposed in vitro to copper showed little effect on ROS production (Fedeli et al. 2010) whilst exposure to titanium dioxide nanoparticles produced cytotoxicity and DNA damage but not ROS production (Sekar and Falcioni 2014). In the case of a neotropical freshwater fish (*Prochilodus lineatus*), erythrocyte exposure to lead also confirmed genotoxic and cytotoxic effects (Monteiro et al. 2011). Nevertheless, very few papers have evaluated the specific cellular responses of marine fish erythrocytes against pollutants at protein or messenger RNA (mRNA) levels (Roche and Bogé 1993). To our knowledge, only one study (Fulladosa et al. 2006) has evaluated the metallothionein (MT) expression in vitro in fish erythrocytes, showing a similar trend to that recorded in different fish species and models (Carbonell et al. 1998; Morcillo et al. 2015a, b, 2016). MTs, together with heat shock proteins (HSPs), are important proteins involved in cellular protection and concretely in the protection against metals (Bourdineaud et al. 2006; Morimoto 2011). ROS induction by metals provokes DNA damage and apoptosis, but no studies have been found in the literature about the cell death mechanism after metal exposure in fish erythrocytes. In humans, it has been described a particular erythrocyte cell death mechanism called eryptosis that resembles to apoptosis of nucleated cells (Lang et al. 2006). Some differences between eryptosis and apoptosis reside in the fact that mammalian erythrocytes lack nuclei and mitochondria and that the molecular signalling pathways are not identical (Lang et al. 2012). Eryptosis occurs under natural conditions in erythrocytes, and eryptotic cells are engulfed and degraded by macrophages contributing to the animal haemostasis although it also occurs under pathophysiological situations. Among these situations, eryptosis has been demonstrated on human erythrocytes exposed to Cd, Hg, Pb, or As (Eisele et al. 2006; Kempe et al. 2005; Mahmud et al. 2009; Sopjani et al. 2008). In addition, a report has demonstrated the role of B cell lymphoma-2 (Bcl2) and Bcl-2 homologous antagonist killer

(Bak) proteins in the human erythrocyte survival in vitro (Walsh et al. 2002), but no studies were found in fish erythrocytes.

Taking into consideration that pollutants affect fish haematological parameters and the scarce studies evaluating their effects on fish erythrocytes at molecular level, we aimed to evaluate the cytotoxicity of metals (Cd, Hg, Pb) and a metalloid (As) as well as the transcription pattern of genes related to cellular oxidative stress, protection and death after 24-h exposure in two teleost fish species: gilthead sea bream (*Sparus aurata* L.) and European sea bass (*Dicentrarchus labrax* L.), the most important Mediterranean cultured fish species.

## Material and methods

### Animals

Thirty specimens of 80–100-g body weight of the seawater teleost gilthead sea bream (*Sparus aurata* L.) and European sea bass (*D. labrax* L.) obtained from local fish farms were kept in seawater aquaria (250 l) in the Marine Fish Facilities at the University of Murcia (Spain). The water was maintained at  $20 \pm 2$  °C, with a flow rate of 900 l/h, and 28‰ salinity. The photoperiod was 12-h light/12-h dark, and fish were fed with a commercial pellet diet (Skretting) at a rate of 2 % body weight/day. Fish were allowed to acclimatize for 15 days before the start of the experimental trial. All experimental protocols were approved by the Ethical Committee of the University of Murcia.

### Erythrocyte isolation

Fish were taken from the aquaria and 200 µl of blood was immediately withdrawn into a heparinized syringe from the caudal vein and placed into 4 ml of phosphate-buffered saline (PBS, containing 0.35 % sodium chloride, to adjust the medium's osmolarity) with 10 mM glucose, and the fish were returned to the aquaria. Blood was layered over a 51 % Percoll density gradient (Pharmacia) and centrifuged ( $400 \times g$  for 30 min, 4 °C) to separate leucocytes and erythrocytes, which were located in the pellets, collected, washed twice with PBS, counted and adjusted to  $5 \times 10^8$  cells/ml in PBS with 10 mM glucose.

### Metal exposure

Different salts of the tested metals (Sigma-Aldrich) were used: cadmium chloride ( $\text{CdCl}_2$ ), methylmercury (II) chloride [ $\text{CH}_3\text{HgCl}$  (MeHg)], mercury (II) chloride ( $\text{HgCl}_2$ ), lead (II) nitrate ( $\text{Pb}(\text{NO}_3)_2$ ) and trioxide arsenic ( $\text{As}_2\text{O}_3$ ). Each salt was initially dissolved in PBS with 10 mM glucose, and dilutions for each concentration were daily prepared. Prior to carrying

out the assays, the osmolarity of these solutions was measured in an osmometer (Wescor) to avoid effects due to this parameter.

For each individual fish, 100 µl of blood erythrocytes was placed into separate 1.5 ml Eppendorf tubes in triplicate and exposed with 1 ml of PBS with 10 mM glucose (controls) or metal solutions, to make final concentrations of 10–100 µM for Cd, 5–75 µM for MeHg, 1–10 µM for Hg, 0.1–3 mM for Pb and 10–500 µM for As. Samples were gently shaken in an orbital agitator (24 h at 24 °C). Erythrocytes from six different and independent fish were used for cytotoxicity curves and from four for gene expression studies.

## Cytotoxicity assays

### *Propidium iodide uptake*

In order to determinate the viability of the sea bream and sea bass erythrocytes, we assessed the abundance of dead erythrocytes using a flow cytometry technique (Ormerod 1990). Following 24 h of metal exposure, 10 µl of each sample was transferred to 5-ml tubes (Becton Dickinson) containing 400 µl of PBS and 100 µl of propidium iodide (PI; 400 µg/ml; Sigma-Aldrich). All samples were analysed in a flow cytometer (Becton Dickinson) with an argon-ion laser adjusted to 488 nm. Analyses were performed on 10,000 cells, which were acquired at a rate of 300 cells/s. Data were collected in the form of two-parameter side scatter (SSC, granularity) and forward scatter (FSC, size), and green fluorescence (FL1) and red fluorescence (FL2) dot plots or histograms were constructed on a computerized system. With this method, dead (PI<sup>+</sup>) and viable (PI<sup>-</sup>) cells were discriminated and analysed.

### *Oxyhaemoglobin release*

Erythrocyte exposure to metals results in cell death and liberation of their content being haemoglobin, in either oxyhaemoglobin (HbO<sub>2</sub>) or deoxyhaemoglobin forms, the

most abundant protein. Thus, the viability of the cells was determined by the haemolysis of erythrocytes and consequent liberation of the oxyhaemoglobin to the medium (De Kretser and Waldron 1963; Jan and Frantisek 2000; Martínez-López et al. 2005). After 24 h of exposure, the samples were centrifuged (10,000×g, 1 min) and 100 µl of the supernatant transferred to 96-flat-bottomed-well plates (Nunc) and the absorbance at 542 nm (the maximum absorbance for oxyhaemoglobin) analysed in a plate reader (BMG, Fluoro Star Galaxy). Positive (maximum haemolysis and absorbance) or negative (minimum haemolysis and absorbance) controls consisted on 100 µl of erythrocytes in 1 ml of sterile distilled water or in 1 ml PBS with 10 mM glucose, respectively.

### *Data analysis*

For each method, cell viability data and the metal concentrations were represented and fitted with an exponential decay three-parameter curve [ $f=y_0 + a \times \exp(-bx)$ ]. Fitted curves always showed  $r^2$  values higher than 0.96 which are therefore the only ones presented in the cytotoxicity curves. The concentration producing 50 % cell death (EC<sub>50</sub>) was determined for all metals and assays (Table 1) using SigmaPlot software. According to the PI method, EC<sub>0</sub> (the minimum concentrations used and that failed to be cytotoxic) and EC<sub>50</sub> were used in this study as the concentrations to measure gene expression.

## Gene expression analysis by real-time PCR

After 24 h of erythrocyte exposure to the EC<sub>0</sub> or EC<sub>50</sub> of the metals (see Table 1), samples were centrifuged, the supernatants were aspirated and TRIzol Reagent (Life Technologies) was added to the wells in order to extract the total RNA as indicated by the manufacturer. It was then quantified and the purity assessed by spectrophotometry; the 260:280 ratios were 1.8–2.0. The RNA was then treated with DNase I (Promega) to remove any genomic DNA contamination. Complementary DNA (cDNA) was synthesized from 1 µg of total RNA using

**Table 1** Comparing the cytotoxicity of metals to fish erythrocytes from two species by two methods

Metal	Gilthead sea bream erythrocytes		European sea bass erythrocytes	
	PI uptake	Oxyhaemoglobin release	PI uptake	Oxyhaemoglobin release
Cd	22 ± 3.62 <sup>aA</sup>	23 ± 4.5 <sup>aA</sup>	80 ± 12.7 <sup>aB</sup>	71 ± 9.27 <sup>aB</sup>
MeHg	21 ± 1.06 <sup>aA</sup>	20 ± 0.71 <sup>aA</sup>	28 ± 0.76 <sup>bAB</sup>	29 ± 0.5 <sup>bB</sup>
Hg	2.4 ± 0.22 <sup>bA</sup>	2.7 ± 0.45 <sup>bB</sup>	3.6 ± 0.01 <sup>cC</sup>	5.5 ± 0.3 <sup>cD</sup>
Pb	523 ± 103 <sup>cA</sup>	374 ± 64 <sup>cB</sup>	1,100 ± 129 <sup>dC</sup>	1,000 ± 201 <sup>dC</sup>
As	134 ± 0.28 <sup>dA</sup>	129 ± 0.14 <sup>dB</sup>	190 ± 51 <sup>aC</sup>	189 ± 3 <sup>cC</sup>

Values of EC<sub>50</sub> (µM; mean ± SEM;  $n = 6$  independent fish) of fish erythrocytes after exposure to metals for 24 h.  $r^2$  values of the fitted curves were higher than 0.96 in all cases. Statistically significant differences (ANOVA;  $P \leq 0.05$ ) within each column (differences among metals) or row (differences between fish species and method for each metal) are denoted by different lowercase or capital letters, respectively

the SuperScript III reverse transcriptase (Life Technologies) with an oligo-dT18 primer.

The expression of genes involved in cellular oxidative stress [superoxide dismutase (*sod*), catalase (*cat*), glutathione reductase (*gr*) and peroxiredoxin 1 (*prx1*)], cellular protection [metallothionein-A (*mta*) and heat shock proteins 70 (*hsp70*) and 90 (*hsp90*)], cellular apoptosis [pro-apoptotic Bcl2-associated X gene (*bax*)] and eryptosis [calpain1 (*calp1*)] was evaluated by real-time PCR with an ABI PRISM 7500 instrument (Applied Biosystems) using SYBR Green PCR Core Reagents (Applied Biosystems). Reaction mixtures (containing 10  $\mu$ l of 2 $\times$  SYBR Green supermix, 5  $\mu$ l of primers (0.6 mM each) and 5  $\mu$ l of cDNA template) were incubated (10 min, 95  $^{\circ}$ C), followed by 40 cycles of 15 s at 95  $^{\circ}$ C, 1 min at 60  $^{\circ}$ C, and finally 15 s at 95  $^{\circ}$ C, 1 min at 60  $^{\circ}$ C and 15 s at 95  $^{\circ}$ C. For each mRNA, gene expression was corrected by the elongation factor 1 $\alpha$  (*ef1a*) RNA content in each sample and calculated using the  $2^{-\Delta\Delta Ct}$  method (Livak and Schmittgen 2001). Negative controls had no amplification product, and control templates showed no primer–dimer formations. Gene names follow the accepted nomenclature for zebrafish (<https://wiki.zfin.org/>). The primers used in the present study are shown in Table 2. In all cases, each PCR was performed with triplicate samples from four specimens.

### Statistical analysis

Data of the cytotoxic effects are presented for each metal and method using the fitted curves. Gene expression is expressed as fold change with respect to the control samples where values higher than 1 indicate up-regulation and lower than 1 down-regulation of each gene.  $EC_{50}$  values for each fish species and method were analysed by one-way analysis of variance (ANOVA;  $P \leq 0.05$ ) to determine differences among metals, followed by a Student–Newman–Keuls (SNK) comparison mean test. Gene expression data were statistically analysed by two-way ANOVA ( $P \leq 0.05$ ) to determine differences between control and metals and between the two fish species. Normality of the data was previously assessed using a Shapiro–Wilk test, and homogeneity of variance was also verified using the Levene test. A non-parametric Kruskal–Wallis test was used when data did not meet parametric assumptions. Statistical analyses were conducted using SPSS 20.0 software (SPSS).

## Results

### Cytotoxicity assays

After 24-h exposure to metals, the viability of gilthead sea bream and European sea bass erythrocytes declined in a dose-dependent manner compared to controls (Fig. 1). The data were

used to fit curves in order to identify the  $EC_{50}$  (Fig. 1 and Table 1). According to the PI method,  $EC_{50}$  values for sea bream erythrocytes were of 22, 21, 2.4, 523 and 134  $\mu$ M, and for sea bass 80, 28, 3.6, 1,100 and 190  $\mu$ M for Cd, MeHg, Hg, Pb and As, respectively (Table 1). Hg was the most toxic metal for erythrocytes in both species followed by MeHg, Cd, As and Pb (Table 1). Cytotoxicity curves followed different shapes between fish species when the erythrocytes were exposed to Cd or MeHg. Thus, sea bream erythrocytes are more resistant to Cd, Pb and As whilst the susceptibility to MeHg and Hg was roughly the same. PI uptake and oxyhaemoglobin release techniques revealed almost identical cytotoxicity curves except for Hg-exposed sea bass erythrocytes (Fig. 1), which is also evidenced for the  $EC_{50}$  values (Table 1).

### Metals generate oxidative stress in erythrocytes

Exposure of erythrocytes to the  $EC_{50}$  of the metals for 24 h provoked oxidative stress (Fig. 2 and Supplementary data Fig. S1). First, all the metals, except Cd in sea bass, significantly up-regulated the *sod* transcription in erythrocytes, but no differences were observed between species. Surprisingly, *cat* and *gr* gene expression was always down-regulated after  $EC_{50}$  metal exposure of sea bream erythrocytes, but statistically significant for Cd, MeHg and As. By contrast, they were always up-regulated in sea bass erythrocytes being only significant the *cat* gene for  $EC_{50}$  of As and *gr* for  $EC_{50}$  of MeHg, Hg and As. Significant effects between the two fish species were also observed. The *prx1* gene expression was significantly enhanced by  $EC_{50}$  of Cd, MeHg, Hg and Pb in sea bream erythrocytes while only Cd and As exposure induced its transcription, and Hg down-regulated, in sea bass erythrocytes (Fig. 2). As consequence, Hg and Pb effects were significantly different in the two fish species. Interestingly, exposure of erythrocytes to  $EC_0$  provoked roughly the same profile at transcriptional level than the  $EC_{50}$  (Supplementary Fig. S1).

### Cellular protection is differently altered in sea bream and sea bass erythrocytes

We evaluated the cellular protection to metals by the expression of the metallothionein-A gene, *mta* and heat shock proteins 70 and 90 (Fig. 3 and Supplementary Fig. S1). As expected,  $EC_{50}$  of Cd or MeHg exposure of erythrocytes from sea bream and Hg exposure of erythrocytes from both fish species significantly up-regulated *mta* transcription (Fig. 3). Surprisingly, exposure to  $EC_{50}$  of Pb or As did not alter *mta* mRNA abundance in the sea bream and sea bass erythrocytes. All the metals increased *hsp70* gene expression in sea bream erythrocytes; however, Hg and Pb significantly down-regulated it in sea bass erythrocytes although As up-regulated it. Thus, exposure to MeHg, Hg and Pb provoked significant differences between gene expression in

**Table 2** Primers used for analysis of gene expression by real-time PCR

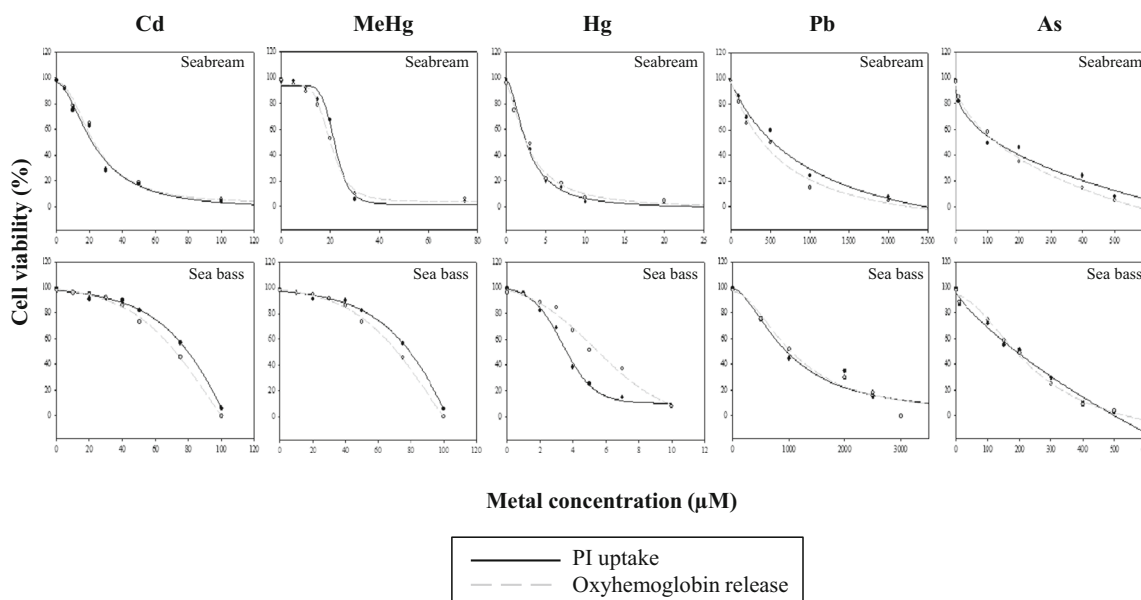
Gene name	Gene abbreviation	Fish specie	Acc. numbers	Sequence (5'-3')
<i>Elongation factor 1-alpha</i>	<i>ef1a</i>	Sea bream	AF184170	CTGTCAAGGAAATCCGTCGT TGACCTGAGCGTTGAAGTTG
		Sea bass	AJ866727	CGTTGGCTTCAACATCAAGA GAAGTTGTCTGCTCCCTTGG
Cu/Zn superoxide dismutase	<i>sod</i>	Sea bream	AJ937872	CCATGGTAAGAATCATGGCGG CGTGGATCACCATGGTTCTG
		Sea bass	FJ860004	TGTTGGAGACCTGGGAGATG ATGGGCCTGTGAGAGTGAG
Catalase	<i>cat</i>	Sea bream	FG264808	TCCCCGTCCTTCATTCACTC CTCCAGAAGTCCCACACCAT
		Sea bass	FJ860003	GAGGTTTGCTGATGGCTAC TGCAGTAGAAAACGCTCACA
Glutathione reductase	<i>gr</i>	Sea bream	AJ937873	CAAAGCGCAGTGTGATTGTGG CCACTCCGGAGTTTTGCATTTT
		Sea bass	FM020412	TGCACCAAAGAACTGCAGAA ACGAGTGTCACTCCAGTCC
Peroxiredoxin 1	<i>prx1</i>	Sea bream	GQ252679	CTCCAAGCAATAATAAGCCCAAAG TCACTCTACAGACAACAGAACAC
		Sea bass	AM987213	CTGCCGAAGATTTTCAGGAAGA CGCCGTGTGTCAGATACCAG
Metallothionein-A	<i>mta</i>	Sea bream	X97276	ACAAACTGCTCCTGCACCTC CAGCTAGTGTGCGACGTCTT
		Sea bass	AF199014	GCACCACCTGCAAGAAGACT AGCTGGTGTGCGACGTCT
Heat shock protein 70	<i>hsp70</i>	Sea bream	EU805481	AATGTTCTGCGCATCATCAA GCCTCCACCAAGATCAAAGA
		Sea bass	AY423555	CTGCTAAGAATGGCCTGGAG CTCGTTGCACTTGTCCAGAA
Heat shock protein 90	<i>hsp90</i>	Sea bream	DQ524994	GGAGCTGAACAAGACCAAGC AGGTGATCCTCCCAGTCGTT
		Sea bass	AY395632	CTCAGGGACAACCTCCACCAT CTTTGTCGTTCTTGTGACGA
Bcl-2 associated X protein	<i>bax</i>	Sea bream	AM963390	CAACAAGATGGCATCACACC TGAACCCGCTCGTATATGAAA
		Sea bass	FM011848	TGTCGACTCGTCATCAAAGC CACATGTTCCCGGAGGTAGT
Calpain1	<i>calp1</i>	Sea bream	KF444899	GTGGAGCTCCTCGCTGTATC GCTTGAAC TGAGGGTTGAGC
		Sea bass	FJ821591	TGCAGAGGGGACTGAGTTCT CCGCCTGTAAAGTCCTCAAA

erythrocytes for the two fish tested species. In contrast, most of the metals down-regulated the transcription of *hsp90* but only Pb and As did to a significant extent in sea bream and sea bass erythrocytes, respectively (Fig. 3).

As above, exposure of sea bream or sea bass erythrocytes to EC<sub>0</sub> of metals induced a very similar transcriptomic profile as the EC<sub>50</sub> (Supplementary Fig. S1).

### Metals induce apoptosis and eryptosis cell death

The expression of typical markers for apoptosis (pro-apoptotic Bcl2-associated X gene, *bax*) and eryptosis ( $\mu$ -calpain, *calp1*) was assayed in fish erythrocytes (Fig. 4 and Supplementary Fig. S1). Sea bream and sea bass erythrocytes exposed to EC<sub>50</sub> of Hg, Pb and



**Fig. 1** Cytotoxicity curves of gilthead sea bream or European sea bass erythrocytes exposed to different metals for 24 h. Lines represent the fitted curve for each method: propidium iodide (PI) and oxyhaemoglobin release

As induced an up-regulation of *bax* transcripts, demonstrating the apoptosis cell death process. On the other hand, EC<sub>50</sub> of Cd and MeHg did not alter it to a significant level. Surprisingly, *calp1* gene expression was greatly impaired by all EC<sub>50</sub> of metals, except MeHg in sea bream erythrocytes; however, exposure to MeHg or Hg produced a general induction of *calp1* mRNA transcription in sea bass erythrocytes (Fig. 4), which could be related to the eryptosis process (Fig. 5) (Lang et al. 2006).

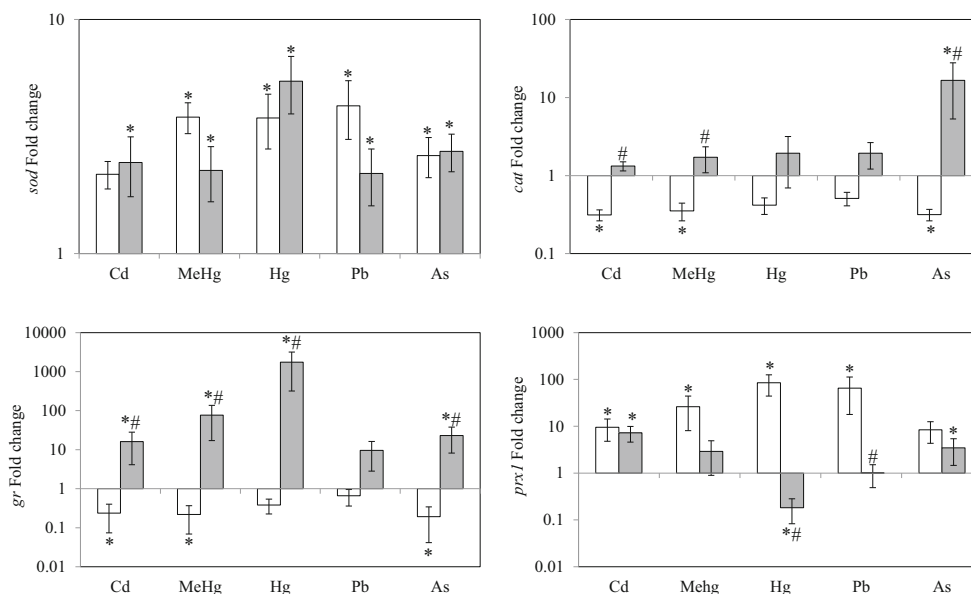
Finally, the effects provoked in fish erythrocytes at gene expression level by EC<sub>0</sub> and EC<sub>50</sub> metals were comparable (Supplementary Fig. S1).

**Discussion**

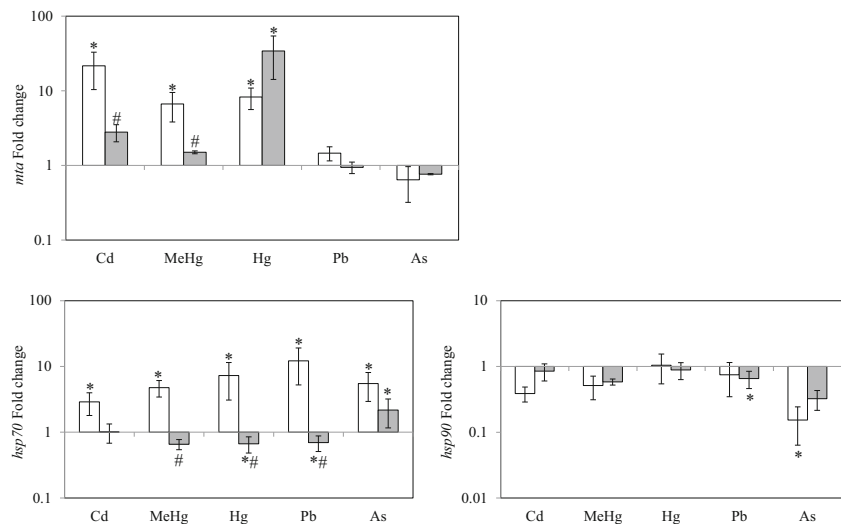
Fish erythrocytes could be useful for toxicological studies of aquatic pollutants because they remain viable in primary cultures and are easy to obtain and manipulate. However, very few papers have evaluated the toxicological effects on fish erythrocytes and those available include morphological changes (Bogé and Roche 1996; Monteiro et al. 2011; Witeska 2004), genotoxic damage (Bagdonas and Vosyliene 2006; Mitchelmore and Chipman 1998) and metallothionein expression (Fulladosa et al. 2006).

Among the cytotoxicity tests used in vitro, flow cytometry and spectrophotometry methods were used to evaluate the cell

**Fig. 2** Expression of genes related to oxidative stress (*sod*, *cat*, *gr* and *prx1*) in gilthead sea bream (white bars) or European sea bass (grey bars) erythrocytes exposed to the EC<sub>50</sub> of each metal for 24 h. Data are expressed as fold change with respect to the control erythrocytes. Bars represent the mean ± SEM from four independent fish. Statistically significant differences ( $P \leq 0.05$ ) between control and metal-exposed (\*) and between the two species (#) are denoted



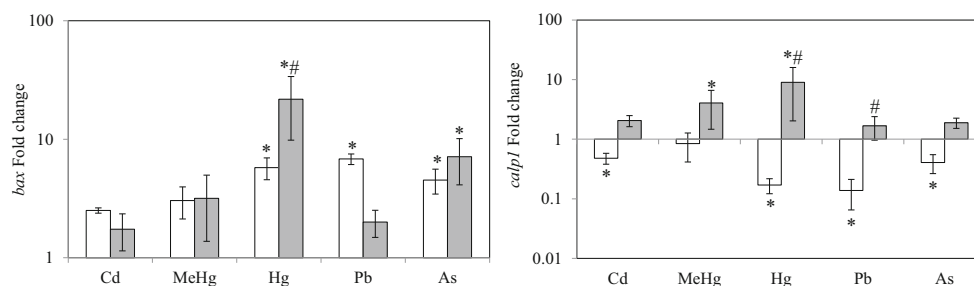
**Fig. 3** Expression of gene related to cell protection (*mta*, *hsp70* and *hsp90*) in gilthead sea bream erythrocytes (white bars) or European sea bass (grey bars) erythrocytes after exposure to the  $EC_{50}$  of each metal for 24 h. Data are expressed as fold change with respect to the control erythrocytes. Bars represent the mean  $\pm$  SEM from four independent fish. Statistically significant differences ( $P \leq 0.05$ ) between control and metal-exposed (\*) and between the two species (#) are denoted



death of fish erythrocytes. The cytotoxicity assays used revealed comparable profiles, showing a dose-dependent curve after 24-h exposure to the metals in erythrocytes from gilthead sea bream and European sea bass. The  $EC_{50}$  values showed that toxicity after 24-h exposure to metals was  $Hg > MeHg > Cd > As > Pb$  for erythrocytes from both species. However, sea bream erythrocytes were more sensitive to the metals than sea bass erythrocytes, showing lower  $EC_{50}$ . Moreover, we have shown for the first time that the oxyhaemoglobin release method could be used in fish ecotoxicological testing and is more sensible than the PI uptake. In addition, it has the advantage of using unsophisticated and affordable equipment and no need for reagents such as PI, which is carcinogenic. This method has been satisfactorily used in toxicological studies conducted in humans, rats and birds (De Kretser and Waldron 1963; Jan and Frantisek 2000; Martínez-López et al. 2005) and should be further explored in fish.

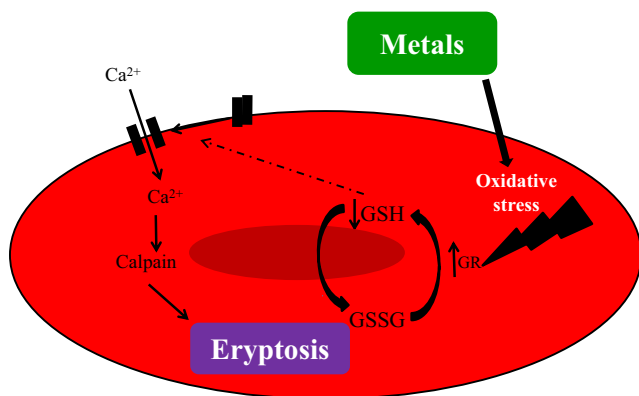
Cytotoxic effects of metals observed on fish erythrocytes were compared to the few studies available in the literature. For instance, sea bream erythrocytes exposed to 100  $\mu$ M Hg for 1 h showed a 6.1 % of haemolysis (Gwozdziński et al. 1992) while this dose for 24 h showed 100 % haemolysis, which could be attributed to a rapid and adverse effect of Hg

upon membrane integrity. Human erythrocytes exposed to 10 mM As (III) for 5 h exhibited 0.7 % haemolysis (Shannon and Winski 1998). Thus, As seems to show a slower and lower toxicity mechanism than Hg, which is also observed in our results. Studies using bird erythrocytes reported a lower  $EC_{50}$  for Cd (0.027 mM) than for lead (1.84 mM) (Hernández-García et al. 2014), which also agrees with our data. Other studies in the RTG-2 fish cell line confirmed the highest toxicity of Hg compared to other metals (Maracine and Segner 1998), whilst in the case of the grass carp (*Ctenopharyngodon idella*) ZC-7901 cell line, the order was  $Cd^{2+} > Hg^{2+} > Pb^{2+} > Cu^{2+} > Cr^{6+} > As^{5+}$  (Xiang et al. 2001). Moreover, in the rainbow trout RTL-W1 (derived from the liver)  $EC_{50}$  values for Cd are quite similar to our data (Dayeh et al. 2005). Differences in the fish environment (fresh or marine water), as well as the metal form, solubility, exposure time, interactions with culture medium components, etc., could be responsible for some of the differences found with those mentioned in the literature. In fact, it is known that culture medium composition or percentage of serum supplementation affects the metal cytotoxicity (Borenfreund and Puerner 1985; Segner 1998; Dayeh et al. 2005). For example, differences between culture medium could be behind the low



**Fig. 4** Expression of genes related to cell death (*bax* and *calp1*) in gilthead sea bream (white bars) or European sea bass (grey bars) erythrocytes exposed to the  $EC_{50}$  of each metal for 24 h. Data are expressed as fold change with respect to the control erythrocytes. Bars

represent the mean  $\pm$  SEM from four independent fish. Statistically significant differences ( $P \leq 0.05$ ) between control and metal-exposed (\*) and between the two species (#) are denoted



**Fig. 5** Synopsis of the mechanisms and the signalling pathways involved in eryptosis. Modified from Lang et al. (2006). *GR*, glutathione reductase; *GSH*, glutathione; *GSSG*, glutathione disulfide

EC<sub>50</sub> values observed in this study (PBS with 10 mM glucose) and the higher values observed in the SAF-1 cell line (derived from fins of gilthead sea bream and exposed in L-15 with 10 % serum) (Morcillo et al. 2016) that would be further investigated.

Very few studies concerned with the erythrocyte toxicology of metals at the gene level are found in the literature. Thus, we have evaluated the transcription of some important genes involved in oxidative stress, cell protection and death after 24 h of exposure to the EC<sub>0</sub> or EC<sub>50</sub> of each metal. With respect to oxidative stress, we found that all the metals induced a significant up-regulation of *sod* gene expression in sea bream and sea bass erythrocytes. In sea bass, erythrocytes exposed to 10–100 μM Hg for 1 h the SOD enzyme activity increased in all doses (Gwozdziński et al. 1992), which agrees with our results. However, the decrease in SOD activity of sea bass erythrocytes by Cu<sup>2+</sup> and Zn<sup>2+</sup> was unexpected (Roche and Bogé 1993), since these metallic ions are potent ROS activators. In vivo experiments with goldfish (*Carassius gibelio*) erythrocytes evaluating SOD activity showed a significant decrease after the first day of Cd exposure or an increase after 7 or 15 days (Zikić et al. 2001). This increased gene and protein SOD could be involved, as demonstrated in human erythrocytes, in the prevention of methaemoglobin formation (Dumaswala et al. 1999). In sea bream erythrocytes, both *cat* and *gr* transcriptions were significantly down-regulated, but in the case of sea bass, *cat* was up-regulated by As and *gr* by most metals. In sea bass, erythrocyte exposure to Cr or Zn increased CAT activity while GR activity was decreased by Cr, Cu and Zn exposure (Roche and Bogé 1993). These opposite effects between sea bream and sea bass erythrocytes were not observed in freshly isolated head-kidney leucocytes (Morcillo et al. 2015a, b). Contradictory results were also found in the literature. For example, CAT activity was increased or decreased after Cd exposure of fish erythrocytes (Firat and Kargin 2010; Kumar et al. 2009) and GR activity was reduced after Pb exposure in human erythrocytes in vitro

or in vivo (Hunaiti et al. 1995; Hunaiti and Soud 2000). In rat erythrocytes exposed to As, the CAT activity remained unchanged (Dwivedi and Flora 2015). It was previously reported that reduced nicotinamide adenine dinucleotide-hydrogen (NADH) plays an important role in the activation of CAT from its inactivated form (Das et al. 2010) and insufficient supply of NADH during arsenic metabolism might decrease the activity of CAT (Kirkman et al. 1987). Special attention should be focussed on the increase (>1000-fold) of the *gr* transcription after Hg exposure in sea bass erythrocytes. Similarly, European sea bass erythrocytes exposed to low HgCl<sub>2</sub> concentrations for 1 h resulted in increased SOD, CAT, peroxidase and glutathione peroxidase activities, but not in the case of human red blood cells, suggesting the presence of ROS and its partial elimination (Gwozdziński et al. 1992). Similarly, in vivo exposure to sublethal dosages of Hg resulted in increased metabolism of glutathione and its associated enzymes in an effort to control the ROS production (Elia et al. 2003). In contrast, inorganic mercury nitrate added in vitro to stroma-free rat erythrocyte haemolysates resulted in a clear inhibition of GR activity (Mykkanen and Ganther 1974). Thus, our data suggest that the overexpression of *gr* could imply that glutathione is in reduced (GSH) state and is ready to be oxidized by glutathione peroxidase and scavenge more ROS. The scavenging of H<sub>2</sub>O<sub>2</sub> and peroxinitrites by Prx1 and Prx2 has been also demonstrated in erythrocytes (Dubuisson et al. 2004; Lee et al. 2003; Low et al. 2008; Neumann et al. 2003). In our study, *prx1* gene expression was intensely up-regulated by metals in sea bream erythrocytes; however, only Cd and As exposure induced *prx1* transcription in sea bass erythrocytes while Hg exposure down-regulated it. In another study, Cd, Hg forms and Pb exposure elicited the increase of *prx1* gene expression in the sea bream SAF-1 cell line but As decreased it (Morcillo et al. 2016). The antioxidant mechanisms (*cat* and *gr* gene expression) in sea bream erythrocytes were more inhibited than in sea bass erythrocytes, and this could explain higher sensitivity of sea bream erythrocytes to metal exposure.

As in mammals, metallothioneins and heat shock proteins are relevant in the cellular protection of fish erythrocytes (Currie and Tufts 1997; Ferencz and Hermes 2015). Present results show an increase of the *mta* gene expression after Cd and Hg forms while Pb or As exposure did not alter it in sea bream or sea bass erythrocytes. The finding that Cd and Hg are transported in the blood bound to MTA cysteine residues (Goyer and Clarkson 1996; Zalups 2000) could partly explain our observations. In contrast, after 1- or 2-h exposure to sublethal concentrations of Cd and Pb in silver sea bream (*Sparus sarba*) in vitro, no overexpression of MTA was evidenced likely due to the short time exposure (Fulladosa et al. 2006). In common carp specimens exposed to Cd, the *mt* transcription was related with low adverse effects in the blood compared to those observed in skin (Ferencz and Hermes 2015). In the case of *hsp* gene expression, mRNA coding for stress



proteins is actively produced in red blood cells of the brook trout (*Salvelinus fontinalis*) submitted to a heat shock (Lund et al. 2003) while we found differences in the gene expression and fish species. This result suggests a possible influence of the metal concentration and exposure time in the stress protein expression. Fulladosa et al. (2006) found that the maximal overexpression of HSP70 occurred after 3-h exposure to 20  $\mu\text{M}$  Cd but also that prolonged exposure reduced it. In addition, they showed that increasing concentrations of Cd failed to further increase the HSP70 overexpression, while in the case of Cr and Pb, this was reduced. Therefore, the relation between ROS production and the oxidative stress mechanisms and cell protection deserves further investigation in fish erythrocytes.

Finally, it is widely accepted that overproduction of ROS induced by metals provokes apoptotic cell death (Rana 2008). In the case of human erythrocytes, these ROS provoke a suicidal erythrocyte death named eryptosis (a type of apoptosis that takes place in erythrocytes) (Föller et al. 2008; Kempe et al. 2005; Lang and Lang 2015; Shin et al. 2007) that may involve stimulation of two proteases that play an essential role in apoptosis (caspases and calpain), with subsequent degradation of the cytoskeleton, but how erythrocyte cell death is regulated is still under debate. Walsh et al. (2002) have demonstrated the role of BAK and BCL2 proteins in the human erythrocyte survival in vitro, but no studies are found in fish erythrocytes in this respect. Fish erythrocytes possess nuclei and mitochondria, both absent in mature mammalian erythrocytes, and the last one are major players in the apoptosis cell death (Moyes et al. 2002). Thus, pro-apoptotic *bax* and  $\mu$ -calpain (*calp1*) gene expression was assessed in sea bream and sea bass erythrocytes. As expected, a significant up-regulation of *bax* transcription after exposure to Hg, Pb and As in erythrocytes from both species suggested that these metals induced apoptosis cell death, which resulted positive to PI uptake and haemoglobin release after 24 h. However, no differences were observed after Cd or MeHg exposure in *bax* mRNA levels, so that this metals could not trigger apoptosis, or alter other genes involved in the regulation of apoptosis in erythrocytes from both species. For example, Cd and MeHg can provoke necrosis or necroptosis cell death in fish cell lines or leucocytes (Kim and Sharma 2004; Krumschnabel et al. 2005; Morcillo et al. 2015a; b; Rana 2008; Selvaraj et al. 2013). In fact, excessive oxidative stress can induce necrosis (Çimen 2008; Hong et al. 2009) and the conversion of apoptosis to necrosis in cultured cells (Higuchi and Yoshimoto 2002). Transcription of *calp1* was strongly down-regulated after metal exposure in sea bream erythrocytes in contrast to sea bass erythrocytes. A possible reason could be the fact that as a result of an oxidative stress situation, reduced glutathione (GSH) is depleted, which triggers activation of  $\text{Ca}^{2+}$ -permeable cation channels, provoking  $\text{Ca}^{2+}$  influx and activation of  $\mu$ -calpain (Lang et al. 2006; Quintanar-Escorza et al. 2010).

Some of the main molecules involved in the eryptosis process demonstrated in the present study are summarized in Fig. 5. In the case of sea bream erythrocytes, *gr* is down-regulated after metal exposure; thus, no GHS depletion and  $\text{Ca}^{2+}$  entry occurs, triggering an inactivation of  $\mu$ -calpain, which is in accordance with the down-regulation of *calp1* in our study. Alternatively, an up-regulation of *gr* in sea bass erythrocytes could deplete GHS leading to the activation of *calp1*, at least at the gene level, which is in agreement with our results.

To conclude, the results of this study show that gilthead sea bream and European sea bass erythrocytes exposed in vitro for 24 h to Cd, MeHg, Hg, Pb and As suffered important toxicological effects. The cytotoxicity was in the order  $\text{Hg} > \text{MeHg} > \text{Cd} > \text{As} > \text{Pb}$ . In general, erythrocytes from both species exposed to either  $\text{EC}_0$  or  $\text{EC}_{50}$  metals modulated oxidative mechanisms and cell protection and died by apoptosis. Furthermore, it is verified that the use of fish erythrocytes appears to be a useful tool to evaluate the toxicological impact of aquatic pollutants and should be further explored, as well as to study of the mechanisms affected by different contaminants.

**Acknowledgments** Financial support by grants AGL2011-30381-C03-01 and AGL2013-43588-P (Ministerio de Economía y Competitividad and FEDER) and 04538/GERM/06 (Fundación Séneca de la Región de Murcia, Spain) is gratefully acknowledged.

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