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ACCEPTED MANUSCRIPT Adaptive response under multiple stress exposure in fish: from the molecular to

2 individual level

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13 Abstract

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Aquatic systems are subjected to various sources of stress due to global changes, such as increasing 14 15 temperature and pollution. A major challenge for the next decade will be to evaluate the combined effects of 16 these multiple stressors on organisms and ecosystems. For organisms submitted to chemical, biological or 17 physical stressors, the capacity to set up an efficient adaptive response is a fundamental prerequisite for their 18 long-term survival and performance. In this study, goldfish (Carassius auratus) were subjected to individual 19 and combined pesticide mixtures and increased temperatures to evaluate their adaptive response in 20 multistress conditions from the molecular to the individual level. Fish were exposed for 16 days to a mixture of 21 pesticides at environmental relevant concentrations (S-metolachlor, isoproturon, linuron, atrazine-desethyl, aclonifen, pendimethalin and tebuconazole) and at two temperatures (22 °C and 32 °C). Three major 22 physiological traits of the stress response were measured: the hormonal response (i.e. plasma cortisol), the 23 24 metabolic balance from molecular to individuals' levels (metabolomics, cellular energy allocation, energy 25 reserves and global condition indexes), and the cellular defense system induction (SOD, CAT and GST). Results 26 show that (1) environmentally relevant concentrations of pesticides lead to significant responses in fish at all biological levels; (2) the metabolic response depends on the nature of stress (thermal vs. chemical); and (3) 27 28 fish may be unable to set up an efficient adaptive response when chemical and thermal stresses were 29 combined, with adverse outcomes at the individuals' level.

Keywords: Pesticides mixtures, Climate Change, Temperature, Metabolomics, Nuclear Magnetic Resonance NMR, Oxidative stress, Goldfish

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1. Introduction

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34 Global changes are increasingly exposing aquatic systems to multiple stressors, but predicting their effects on aquatic organisms at different biological levels remains a challenge. The stress response is a set of 35 36 adaptive physiological responses of organisms submitted to a stimulus (a stressor) perceived as dangerous, that helps maintaining homeostasis (Selye, 1950; Barton, 2002). For this purpose, the activation of the 37 38 sympathetic nervous system and Hypothalamic-Pituitary-Adrenal (HPA) axis initiates a cascade of physiological changes triggered by catecholamines (i.e. adrenaline) and corticosteroid (i.e. cortisol) stress hormones. When 39 40 stress persists, organisms enter in a phase of resistance characterized by the induction of cellular defense 41 systems (Selye, 1946; 1950). The bioenergetic cost of the defense is supported by metabolic trade-offs between maintenance, activity, growth, reproduction and energy storage (Calow, 1991; Handy et al., 1999; 42 43 Marchand et al., 2004). When stress is chronic or exceeds the defense and compensation capacities, adverse effects on survival and fitness of organisms may occur (Selye, 1950; Barton, 2002). 44

45 France is the leading European country in terms of agricultural area (Alim'agri, 2012) and the fourth largest consumer of pesticides in the world (Bonnefoy, 2012). The 15 most frequently detected molecules in 46 47 surface waters are herbicides and fungicides, essentially used to limit weeds production and control pathogen invasion in field crops and viticulture (Butault et al., 2010). While the adverse effects of insecticides on non-48 49 target species are subject to a broad consensus within the scientific community, the toxicity of herbicides at 50 environmentally relevant concentrations for aquatic vertebrates remains largely controversial (Solomon et al., 2008, 2013; Van Der Kraak et al., 2014). Previous studies focused almost exclusively on the effects of a single 51 52 molecule. Studies on the effects of complex and realistic mixtures of pesticides on aquatic vertebrates are extremely rare, which can lead to a dramatic underestimation of the risks for wildlife (Hayes et al., 2006). At 53 the same time, aquatic systems are submitted to environmental changes, such as increasing temperature. 54 55 Interactions between contaminants and water temperature can be particularly deleterious for ectothermic 56 species as the temperature directly affects many biochemical and physiological processes (López-Olmeda, and Sánchez-Vázquez, 2011; Manciocco et al., 2014). Higher temperature leads to increased energy demand. By 57 58 affecting the metabolic level of individuals, the temperature can change the ability of aquatic organisms to effectively respond to chemical contamination, and vice versa (Lemly, 1996; Kennedy and Ross, 2012; 59 Sokolova, 2013). The majority of studies thus shows a synergistic effect of temperature on the toxicity of 60 pollutants, especially in aquatic species (Schiedek et al., 2007; Noyes et al., 2009; Holmstrup et al., 2010; Laetz 61 62 et al., 2014). Inversely, the exposure to pollutants may affect the temperature tolerance in fish species (Manciocco et al., 2014). However, there is a lack of knowledge about combined effects between temperature 63 64 and pesticide mixtures on aquatic vertebrates. In previous studies (Gandar et al., 2015, 2017), we exposed 65 goldfish (Carassius auratus) to higher temperature and a mixture of herbicides and fungicides at realistic 66 concentrations for 96 hours. Results showed significant cross effects between temperature and pesticides on 67 behavioral responses, energy reserves and hepatic proteome profile, suggesting that combined thermal and

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68 chemical stressors impaired the stress response of the goldfish to individual stressors (Gandar et al., 2015, 69 2017). However, the effects of a longer exposure on fish global performance across biological levels remain to 70 be determined.

71 Therefore, the aim of this study was to assess the adaptive response to stress of goldfish submitted to 72 single and combined chemical and thermal stresses, integrating responses from the molecular to the whole 73 organism level. To that end, goldfish were exposed during 16 days to a mixture of six herbicides (S-74 Metolachlor, Isoproturon, Linuron, Aclonifen, Atrazine-desethyl and Pendimethalin) and one fungicide (Tebuconazol) to a total concentration of 42 μ g.L⁻¹ at two temperatures (22 °C and 32 °C). The stress response 75 was investigated at 6 h, 96 h and 16 d of exposure, including plasma cortisol concentration, hepatic induction 76 77 of antioxidant enzymatic defenses (superoxide dismutase SOD, catalase CAT) and enzymatic system of detoxification Glutathion-S-Transferase (GST), hepatic metabolome response by ¹H-NMR metabolomic 78 79 analysis, energy reserves and cellular energy allocation in liver and white muscle, somatic indexes (muscle and 80 hepatic indexes) and global condition of fish (Fulton's condition factor).

2. Materials and methods

82 2.1. Pesticide mixture

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The objective of the study was to characterize fish responses to environmentally relevant pesticide mixtures at different temperatures. The mixture was developed on the basis of the pesticide contamination of the Save River (France), assessed from March 2008 to November 2009 (Polard et al., 2011) as described by Gandar et al. 2017. According to the analysis conducted by Pollard et al. (2011) and Taghavi et al. (2011), we selected six herbicides and one fungicide using three criteria: the frequency of detection, the concentration and the representation of the different families of molecules detected. Selected molecules are S-metolachlor, Isoproturon, Linuron, Tebuconazol, Aclonifen, Atrazine-desethyl and Pendimethalin (Supplementary Table 1).

90 Pesticide concentrations in water were measured after 16 d of exposure. Water samples of 1 mL were spiked 91 with internal standards solution (Simazine D10, Atrazine-desethyl D7, Isoproturon D6, Linuron D6, Metolachlor 92 D6, Pendimethalin D5, Tebuconazole D6) and directly analyzed on an Agilent liquid chromatographic system 93 coupled with a triple quadrupole mass spectrometer (Agilent LC 1290 Infinity / 6460 Triple quadrupole) 94 equipped with an electrospray ionization source used in positive mode (ESI+) (adapted from Gamain et al., 95 2016). Pesticides were quantified using a quantification transition. Analytical method was validated in terms of calibration linearity, specificity, and limits of quantifications (0.005 to 0.5 μ g.L⁻¹). Recoveries of samples of 96 97 fortified mineral water were evaluated for water analysis (from 89 to 116%). Control calibrating standards 98 were also injected every 15 samples and analytical blanks were performed. All solvents for chemicals analysis 99 were at least of analytical grade. The measured concentration of pesticides showing a slight decrease compared to expected values (total concentration of 38.7 µg.L⁻¹, Supplementary Table 1). Pesticide standards 100 101 were obtained from Sigma-Aldrich (St. Louis, MO, USA): S-metolachlor (CAS-No: 87392-12-9,

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Tebuconazol (CAS-No:107534-96-3, PESTANAL®, 99,3% pure). Acetone (CAS: 67-64-1, Fisher Chemical, HPLC
solvent) was purchased from Fisher Scientific (Illkirch, France). Scintillation liquid (Flo-Scint II[™]) was purchased
from Perkin Elmer (Waltham, Massachusetts, USA).

108 2.2. Animal care

Fish were purchased from the fish farming Carpio (Consac, France) in the size range 10-12 cm. They were first acclimatized for two weeks in opaque tanks under controlled conditions (18 °C with a 12:12 h light regime). Water was aerated and dechlorinated prior to fish introduction. Half of the water was renewed every day and fish were fed daily with commercial pellets. No mortality occurred during the acclimation period. Experimental procedures were conducted under French animal handler's certificate n°.31-103, giving authorization to experiment on living vertebrates.

115 2.3. Experimental design

Fish were exposed to a pesticide mixture and/or temperature increased to obtain four conditions: the 116 117 CONTROL group (fish at 22 °C non-exposed to pesticides), the TEMP group (fish at 32 °C non-exposed to 118 pesticides), the PEST group (fish exposed to pesticides at 22 °C) and the PEST*TEMP groups (fish exposed to pesticides at 32 °C) as previously described (Gandar et al., 2017). Goldfish were placed in 60 L opaque aquaria 119 120 in a temperature controlled room (22 °C, 12 fish per aquarium and 2 aquaria per condition*exposure time). Prior to pesticide exposure, the water of the TEMP and PEST*TEMP groups was gradually heated (1 °C/day) to 121 122 reach 32 °C. Fish were then exposed for 6 h, 96 h or 16 d to the mixture of pesticides. Water was renewed by 123 half every day. Temperature, pH, oxygenation and conductivity were assessed 1 h after the water renewal 124 (Supplementary Table 2). Ammonium, nitrites and nitrates concentrations were measured by colorimetry at **1**25 each time of exposure (Supplementary Table 2). Fish were fed daily and no mortality occurred during 126 exposures.

Twelve fish per condition were randomly sampled at 6 h, 96 h and 16 d. Fish were euthanized with an overdose of benzocaine. Blood samples were collected from the caudal vein by puncturing using a heparinized syringe and centrifuged. Plasma samples were kept at -80 °C. Fish were weighted (to the nearest 10 mg) and measured (fork length to the nearest mm). Livers and white muscles were collected, weighted (to the nearest 0.1 mg), frozen in liquid nitrogen and kept at -80 °C.

132 2.4. Plasma cortisol concentration

Plasma cortisol concentration was assessed by radioimmunoassay (RIA) as previously described (Désautés et al., 1997). The plasma cortisol concentration was expressed in ng.mL⁻¹. 135 2.5. Metabolomic analysis

136 2.5.1. Metabolite extraction

Metabolites were extracted from 50 mg tissue samples with a methanol/chloroform/water (2.0:2.0:1.8) solvent mixture using a Twostep protocol adapted from Lin et al. (2007) and Wu et al. (2008) with slight modifications. Briefly, livers of fish were ground and weighted. A 50 mg sample was homogenized using a Fastprep[®] homogenizer with methanol (4 mL.g⁻¹) and Milli-Q water (0.85 mL.g⁻¹) and vortexed for 5 s. Samples were then mixed with chloroform (4 mL.g⁻¹) and Milli-Q water (2 mL.g⁻¹) and vortexed during 5 s, incubated 15 min at 4 °C and then centrifuged at 2800 g for 15 min. The entire upper layer was collected and kept at -20 °C.

144 2.5.2. 1D-¹H NMR spectroscopy and spectral preprocessing

Samples were evaporated using a SpeedVac and resuspended in a phosphate buffer (pH 7.4) prepared 145 146 in a deuterated water (D₂O) and containing 1 mM of sodium 3-trimethylsilyl-2,2,3,3-d₄-propionate (TMSP, 147 internal chemical shift standard). Samples were centrifuged and 600 μ l of supernatant were transferred in 5 mm NMR tubes. NMR Spectra were acquired at 600 MHz with a Bruker Avance spectrometer (Bruker, 148 149 Karlruhe, Germany) with a SampleJet autosampler using a NOESY 1D sequence to remove the water signal. For 150 1D spectra, 256 scans were collected into 64,000 data points with a relaxation delay of 2 s. The free induction decays (FID) were Fourier transformed and spectra were phased, baseline corrected and calibrated (TMSP, δ 0 151 152 ppm) using TOPSPIN v2.1 software (Bruker, Karlsruhe, Germany). A variable size bucketing was used and 102 153 buckets were selected according to resonance signals and multiplicity between 9.4 and 0.5 ppm, excluding 154 residual water signal. The signal intensity in each bucket was integrated using AMIX software (version 3.9.13, Bruker, Karlsruhe, Germany). Data were normalized with respect to the total spectrum intensity using mean-155 centering and Pareto scaling to allow comparison between samples. 156

157 2.5.3. Statistical analysis

Supervised Partial Least Square-Discriminant Analysis (PLS-DA) was used to assess the discrimination 158 between groups. OSC filter was applied prior to the analysis to remove the analytical and biological variations 159 that were not related to group discrimination (Beckwith-Hall et al., 2002). Q² (predictability of the model, 160 threshold of 0.4) and R^2 (total explained variations) values were used to confirm the validity of the models. 161 Permutation tests (200 iterations) were then applied to assess PLS-DA model robustness. The Variable 162 163 Importance in Projection (VIP, weight of variables for each component; value > 1.0 - arbitrary threshold) was used to determine discriminant buckets. Comparisons between conditions were performed using Kruskal-164 165 Wallis tests and post-hoc tests (significance threshold = 0.05).

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SIMCA P and R softwares were used respectively for PLS-DA analysis and Kruskal-Wallis test.

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167 2.5.4. Peak assignments

168 The discriminant metabolites were identified using the literature, home-made and freeware databases 169 such as the Biological Magnetic Resonance Data Bank (<u>www.bmrb.wisc.edu/</u>) (Ulrich et al., 2008) and the 170 Human Metabolome Database (<u>www.hmdb.ca/</u>) (Wishart et al., 2007). To confirm the chemical structure of 171 metabolites of interest, 2D ¹H-¹H COSY (Correlation Spectroscopy) and 2D ¹H-¹³C HSQC 5Heteronuclear Single 172 Quantum Coherence Spectrosocpy) NMR experiments were performed on selected samples. The spectral 173 assignment was based on matching 1D and 2D data to reference spectra.

174 2.6. Energy reserves and cellular energy allocation

Energetic reserves at the molecular and cellular level are essential to sustain the stress responses of 175 176 fish. Total carbohydrate, lipid and protein contents and oxygen consumption rate in the electron transport system (ETS) were measured in liver and white muscle of fish with protocols adapted from De Coen and 177 Janssen (1997). Carbohydrate concentration (μ g.mg⁻¹ of tissue) was quantified using a microplate 178 spectrophotometer at 492 nm against glucose in TCA. Protein concentration (µg.mg⁻¹ of tissue) was quantified 179 by adding Bradford reagent and reading absortion at 595 nm against bovine serum albumin in 0,2 N NaOH **1**80 (Bradford, 1976). Total lipid concentration (µg.mg⁻¹ of tissue) was measured by reading absorption at 525 nm <mark>1</mark>81 against tripalmitin in chloroform. The ETS activity (mJ.mg⁻¹ tissue.h⁻¹), was measured by absorbance reading at 182 490 nm when iodonitrotetrazolium (INT) was added and during 3 min. The molar extinction coefficient of 183 184 15,900 M⁻¹cm⁻¹ was used.

Carbohydrate, protein and lipid concentrations were transformed in their energetic values (mJ. mg⁻¹ of tissue) using their enthalpy of combustion (17, 24 and 39.5 kJ.g⁻¹ respectively). Available energy (AE), energy consumption (EC) and cellular energy allocation (CEA) in liver and white muscle were then calculated according to Verslycke et al. (2004):

AE = carbohydrates + proteins + lipids (mJ.mg⁻¹ tissue)(1)

 $EC = ETS activity (mJ.mg tissue^{-1}.h^{-1})$ (2)

$$CEA = \frac{AE}{EC} (h^{-1})$$
(3)

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193 **2.7.** Antioxidant and detoxification enzymes

The antioxidant system is a central component of the defense system against chemical and thermal stressors. The activities of the SOD, CAT and GST were measured in the liver of fish by spectrophotometry. Protocols were adapted from Feirrera et al. (2015). Briefly, tissue (50 mg) was homogenized at 4 °C using a FastPrep[®] in K-phosphate buffer (1 mL, 0.1 M pH 7.8; 100 mM K-phosphate, 20% (v/v) glycerol and 0.2 mM fluoride phenylmethylsulphonyl). Homogenates were centrifuged at 10,000 *g* for 15 min at 4 °C. Supernatants 199 (post-mitochondrial fraction, PMS) were distributed in 4 volumes of 100 mL and stored at -80 °C for two 200 weeks.

Protein concentrations were determined with the Bradford method. CAT activity was determined at 202 240 nm by measuring the breakdown of H_2O_2 (Babo and Vasseur, 1992). SOD activity was measured at 340 nm 203 for 5 minutes against standard SOD (Paoletti et al., 1986). GST activity was assessed at 340 nm for 5 min by 204 measuring the conjugation between 1-chloro- 2,4-dinitrobenzene and reduced glutathione (Habig et al., 1974). 205 The enzyme activity was expressed in units per mg of proteins (U.mg⁻¹).

206 2.8. Somatic and condition indexes

At the individual level, energetic reserves and condition indexes are an essential component of the physiological state of the fish. Hepatosomatic index (HSI) and white muscle index (MI) reflect the metabolic status of the liver (Chellappa et al., 1995; Zheng et al., 2013) and white muscles (Moon and Johnston, 1980) respectively. They were calculated as follow:

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$$ISI = \frac{\text{liver weight (g)}}{\text{total weight(g) - liver weight (g)}} \times 100$$
(4)

$$MI = \frac{\text{muscle weight (g)}}{\text{total weight(g)}} \times 100$$
(5)

The Fulton's condition factor (FCF) is an index of the "well-being" of fish and reflects their global metabolic status (Smolders et al., 2005). It was calculated from weight and length of fish as follow:

$$FCF = \frac{\text{weight (g)}}{\text{length (cm)}^3}$$
(6)

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217 2.9. Statistical analyses

Except for the metabolomics data, differences between groups were analyzed with ANOVA software and LSD post-hoc tests after validation of the assumption of homogenous variances with Levene test. Canonical analyses were used to integrate data from plasma cortisol concentration, AE and CE in liver and muscle, somatic indexes (HSI and MI) and condition factor (FCF) of fish. The distance between groups was calculated for each time of exposure with the Mahalanobis distance, and the obtained p-value was used to determine significant separation with a threshold of 0.05.

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3. Results

226 3.1. Endocrine, metabolic and physiological responses

The direction and significance of the endocrine, metabolic and physiological responses of fish to individual and combined chemical and thermal stresses are presented in Table 4. The mean values for all parameters are listed in the Supplementary Table 3. Compared to the CONTROL group, PEST exposure significantly increased
plasma cortisol at T6 h, hepatic carbohydrates at T6 h and T16 d, hepatic proteins at T6 h, liver EC at T6 h,
lipids and AE in muscle at T96 h and HSI at T6 h and T16 d. A decrease was found in liver lipids. At T6 h, the
TEMP group showed increases in cortisol, hepatic protein concentration and EC in liver and white muscle. A
decrease was observed in muscle AE and CEA. No effects were found at T96 h and T16 d (Table 4, Table S3).

The PEST*TEMP group showed an increase of plasma cortisol at T6 h compared to CONTROL, but the concentration was similar to that observed in both individual stress groups (Supplementary Table 3). There was no other effect compared to CONTROL at T6h. On the opposite, PEST*TEMP significantly increased muscle lipids, AE and CEA, HSI and MI at T16d. A significant decrease in the FCF was observed at T16d. PEST*TEMP also tended to decrease the plasma cortisol concentration compared to CONTROL group at T16d (p=0.053, LSD post-hoc test).

Plasma cortisol concentration, liver and muscle AE and CE, somatic indexes (HSI and MI) and condition factor 240 **2**41 (FCF) of fish were integrated in canonical analyses associated to Mahalanobis distance computation to **2**42 measure the separation between groups. Canonical representations for each exposure time and Mahalanobis **2**43 distances between CONTROL and stressed groups were shown in the Fig. 1. Results showed a stress-specific <mark>2</mark>44 and time-dependent response of fish with an opposite trend between individual and combined stress effects. **2**45 The canonical analysis and Mahalanobis distances showed a significant separation between the CONTROL **2**46 group and both the TEMP and PEST groups at T6 h (Fig. 1A), but not at T96 h and T16 d (Fig. 1B and C <mark>2</mark>47 respectively). On the opposite, the distance between the PEST*TEMP and the CONTROL groups was non-<mark>2</mark>48 significant after 6 h but increased over time to become significant after 16 d.

249 3.2. ¹H-NMR metabolomic analysis

250 Representative 600 MHz ¹H NMR spectra of control and exposed goldfish obtained from aqueous 251 extracts of liver tissues at time-point 16 days were shown in Supplementary Fig. 1. Primary metabolites have 252 been annotated in the spectra. OSC-PLS-DA score plots obtained for each exposure duration are shown in Fig. 253 2.

At T6 h, a valid and robust model (A=3 latent component, R2=52.7%, Q2=0.37) has been built for the integrated spectra: the score plot of the PLS-DA (Fig. 2A) showed a clear separation between the group of fishes at 22 °C and the group of fishes at 32 °C, regardless pesticides exposure.

257 36 buckets had a VIP value > 1.0 and was statistically different by the Kruskal–Wallis test. These 258 differences corresponded to 12 metabolites, according to 2D NMR spectra annotation. High temperature 259 (TEMP) increased glutamine, reduced glutathione, phosphorylcholine, taurine, and decreased UDP and UTP 260 compared to CONTROL group. The PEST*TEMP and the TEMP groups were not clearly separated on the OSC-261 PLS-DA score plot (Fig. 2A). However, PEST*TEMP exposure significantly decreased proline, UDP and UTP levels 262 compared to control fish, and PEST exposure significantly increased glutamine, reduced glutathione, succinate,
 263 choline, AMP, NAD+ and decreased maltose level compared to control fish (Table 1 and Fig. 2D).

264 At T96 h, the score plot of the PLS-DA showed a clear separation between the 22 °C group and the 32 265 °C group along the first latent component, and between the exposed fish and the non-exposed fish for the 32 °C group (Fig. 2B). This analysis generated a PLS-DA model with three latent components, with R2Y = 54.3% 266 and Q2 = 0.34. Thirty buckets were identified as discriminant in the metabolic profiles, corresponding to 8 267 268 metabolites. Despite close metabolic fingerprints for these two groups, PEST exposure significantly decreased AMP compared to CONTROL. In the TEMP group, significant increase was observed for maltose, while proline, 269 270 malonate, AMP, NAD+, UDP and UTP decreased. PEST*TEMP exposure significantly decreased proline, succinate, AMP, NAD+, UDP and UTP (Table 2 and Fig. 2E). 271

At T16 d, same patterns were observed in the score plot (Fig. 2C) but difference between exposed and non-exposed fishes at 32 °C was more pronounced. 15 metabolites were found significant between at least two groups. As compared to CONTROL, decreases were found in isoleucine, leucine, valine, alanine, proline, lysine, glutamine, creatine, taurine, lactate, AMP, NAD+ and increases were found in maltose for the PEST*TEMP group. TEMP condition increased significantly reduced glutathione and phosphorylcholine, and decreased proline compared to CONTROL. No discriminant metabolites were found for PEST exposure (Table 3 and Fig. 2F).

3.3. Defense system induction

SOD, CAT and GST activities were measured in the liver of fish (Fig. 3). An increase of CAT activity was observed in the PEST group at T6 h. CAT and SOD activity decreased in the PEST*TEMP group at T96 h and then increased at T16 d. GST activity tended to increase in the PEST group at T6 h compared to the CONTROL and was significantly higher than in the PEST*TEMP group. No effects were observed at T96 h and T16 d. The TEMP group showed no response of these enzyme activities.

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4. Discussion

The aim of this study was to assess the adaptive response of goldfish submitted to individual and 287 combined chemical and thermal stress. We first characterized the primary endocrine stress response (plasma 288 cortisol), then secondary responses (hepatic induction of enzymatic defense systems and metabolic responses 289 290 in liver and white muscles) and tertiary responses (global condition of fish). We found stress-specific and timedependent responses of goldfish at all biological levels observed. Multivariate analyses showed two 291 292 contrasting patterns of response (1) Fish exposed to single chemical or thermal stressors had a significant stress response at T6 h followed by a recovery at T96 h and T16 d from the molecular to the individual levels 293 294 (significant stress response and low deleterious effects across biological levels). In contrast, (2) fish exposed to

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 changes at T16 d from the molecular to the individual levels (absence of stress response and high deleterious
 effects across biological levels).

298 4.1 Responses to individual stress (PEST and TEMP groups): an adapted and coordinated early 299 response.

300 4.1.1 Cortisol response to single stressors

301 In fish exposed to single stressors, we found an increase of plasma cortisol concentration at T6h in all 302 stressed groups compared to the CONTROL groups. Several studies have shown an increase in plasma cortisol **3**03 in fish exposed to herbicides (Waring and Moore, 2004; Soso et al., 2007), fungicides (Hashim and Zaki, 2005; 304 Tierney et al., 2006) or temperature increase (Lyytikäinen et al., 2002; Fernandino et al., 2013). Our results 305 show that both pesticide mixture and temperature increase triggers an endocrine stress response, showing 306 that fish have initiated a general stress response. It was associated to the induction of a number of antioxidant defense systems, depending on the nature of the stress. For instance we observed an increase in CAT and GST 307 308 activities, glutathione, and glutamine - on which glutathione synthesis depends - and taurine.

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4.1.2 Antioxydant response to single stressors

310 CAT and SOD catalyze the reduction of ROS, participating to their detoxification (Regoli et al., 2011; 311 Regoli and Giuliani, 2014). In another hand, GST intervenes in the detoxification of both ROS and lipophilic 312 chemicals, such as pesticides, by catalyzing their conjugation with glutathione. Induction of CAT, SOD and/or GST are consistent with results of previous studies in fish exposed to herbicides (Jin et al., 2010; Guilherme et 313 314 al., 2012; Stara et al., 2012; Xing et al., 2012; Blahová et al., 2013; Nwani et al., 2013; Sinhorin et al., 2014) and 315 high temperature (Gorbi et al., 2005; Madeira et al., 2013; Yin et al., 2013). We observed a transient increase 316 activity of CAT and GST in the PEST group at T6 h, suggesting an increase in ROS production under the pesticide exposure, although SOD activity remained at the control level. GST activity increased also suggesting an 317 318 induction of the hepatic detoxification process. In contrast, no responses of CAT, SOD and GST activity were 319 observed in the TEMP group, despite the fact that temperature increase is a well-known pro-oxidant factor in 320 ectothermic species (Cui et al, 2014).

Glutathione is a well-known ROS scavenger and was used as a biomarker of oxidative stress in many studies (Regoli et al., 2011). Glutathione synthesis depends on the cellular concentration of glutamate and glutamine (DeBerardinis and Cheng, 2010). NMR analysis showed an increase of these molecules at T6 h in both the PEST and TEMP groups. Considering their extensive variety of critical roles in cell function and antioxidant defenses, the increase of glutamine in the liver of fish can be considered as an important response to both chemical and thermal stressors.

Thermal stressor also increased hepatic taurine levels at T6 h and decreased malonate at T96 h. Taurine is a sulfur-amino acid which counteracts oxidative stress, although specific mechanisms are poorly

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understood (Kumar et al., 2009; Rosemberg et al., 2010). On the opposite, malonate induces mitochondrial
 potential collapse and ROS production, leading to cell death (Fernandez-Gomez et al., 2005). Consequently,
 increased taurine level and decreased malonate may act in the same way to prevent ROS induced damages in
 thermal exposed fish.

An increase in phospholipid precursor concentrations (choline and derivative) in both groups may also be a response to lipid peroxidation caused by oxidative stress and requiring the synthesis of novel phospholipids (Li et al., 2014; Xu et al., 2015).

336 4.1.3 Metabolic response to single stressors

337 At the same time, an increase in energy consumption is observed in the liver - increased liver energy 338 consumption (EC) at T6 h in both the PEST and TEMP groups - and, for the TEMP group, in the muscle. The 339 increase in basal metabolism is classic in fish subjected to stress and corresponds to the bioenergetic cost of 340 the induction of systems of protection, detoxification and repair of damage. Increased ETS activity was shown in ectotherm species in response to chemical exposure and temperature increase (Gagné et al., 2006, 2007; 341 342 Sappal et al., 2015; Schmidlin et al., 2015), which is consistent with our results. ETS activity reflects the production of ATP by mitochondria which depends directly on the cellular energy demand (Gagné et al., 2007; 343 Smith et al., 2012). The induction of defense systems, including detoxification, protection and reparation 344 processes, is a costly process which increases the cellular energy demand and requires metabolic 345 346 compensations (Sherwood et al., 2000; Trudel et al., 2010; Sokolova et al., 2012). Proteins are the most costly 347 energy molecules to synthesize (Jorgensen, 1988; Smith et al., 2001). Increased hepatic protein concentrations were observed at T6 h in both the PEST and TEMP exposed fish. These increases may reflect the induction of 348 349 defense systems, including antioxidant enzymes or heat shock proteins (Viant et al., 2003). Increased bioenergetic cost due to defense protein induction was shown in fish exposed to heat shock (Viant et al., 2003) 350 351 or pollutants (Smith et al., 2001). We can also note that protein concentrations increased at T6 h but not at T96 h or T16 d, which is consistent with the induction of antioxidant defenses and the increased energy 352 consumed. In PEST exposed fish, the co-occurring increases observed at T6 h in liver EC, AMP and succinate, an 353 354 intermediary product of the TCA cycle, showed a metabolic compensation to the increased energy 355 requirement. In a consistent way, hepatic glucose and lipids, which are important substrates for the energy 356 production pathways, showed important decreases at T6 h. However, we found an increase in total 357 carbohydrate concentration in liver at T6 h and T16 d. Glycogen is the common form of storage of 358 carbohydrates in cells and increased glycogen deposition is a classic metabolic response to cortisol (Mommsen 359 et al., 1999). Maltose was also significantly decreased in livers after 6 h of pesticides exposure. Maltose as a 360 disaccharide could yield two monosaccharides of glucose upon hydrolysis. Maltose degradation could serve as 361 an energy supplement to replenish pesticides induced energy demand (Li et al., 2017). In the TEMP group, energy consumption increased at T6 h both in liver and white muscle, associated with significant decreases in 362 363 muscular AE and CEA. In the tolerance range, a higher temperature affects biochemical kinetics and enzyme

CCEPTED MANUSCRIP activity leading to basal and active metabolism increased (Cech et al., 1985; López-Olmeda and Sánchez-364 365 Vázquez, 2011; Manciocco et al., 2014). The increased energy consumption observed in liver and muscle at T6 <mark>3</mark>66 h, and the decreased available energy in muscle are consistent with systemic metabolic acceleration under higher temperature. The drop observed at T6 h in the muscle CEA reflected a decreased metabolic status. <mark>3</mark>67 <mark>3</mark>68 Inversely, the hepatic CEA remained constant despite the increased energy consumption. A similar dichotomy 369 between muscular and hepatic metabolic responses to heat shock was observed in Oncorhynchus mykiss 370 (Viant et al., 2003). Under stress, lipid and protein reserves in white muscles are released into the blood 371 system, carried to the liver and used as substrates for gluconeogenesis and protein synthesis (Mommsen et al., 372 1999). These results show that higher temperature induce an increased energy demand and metabolic <mark>3</mark>73 compensation through the whole organism. The vast majority of metabolic responses to higher temperature <mark>3</mark>74 disappeared at T96 h and T16 d, suggesting that thermal exposed fish reached an adapted physiological status. So, with increased temperatures, the increase in metabolism is also directly related to the effect of <mark>3</mark>75 temperature on the enzymatic activity and kinetics of biochemical reactions. This energy cost is supported by 376 an increase in ATP production by ETS as well as glycolysis, Krebs cycle and gluconeogenesis from liver and / or 377 378 muscle proteins or lipids.

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4.1.4 Physiological response to single stressors

Finally, the lack of effect on the general condition of the fish and the disappearance of most of these 380 381 responses at the end of the experiment suggest that the fish have an effective response to achieve a more <mark>3</mark>82 appropriate physiological state. However, some effects persist at T16 d in the liver of the PEST group, 383 especially for the HSI that increase at T6 h and T16 d. HSI increase was shown in fish exposed to pesticides 384 (Arnold et al., 1995; Biagianti-Risbourg and Bastide, 1995; Bacchetta et al., 2014). HSI is correlated to the 385 metabolic status of the liver, and may reflect increased glycogen storage (Chellappa et al., 1995; Zheng et al., 2013). But a swollen HSI may also be due to sequestration of lipophilic pollutants in lipid droplets (Biagianti-386 387 Risbourg and Bastide, 1995), increased detoxification capacities (Arnold et al., 1995; Bacchetta et al., 2014) or <mark>3</mark>88 degenerative changes in the liver tissue (Arnold et al., 1995; Guardiola et al., 2014). Histopathological analyzes 389 could determine whether this effect is indicative of histological damage caused by pesticides, increased liver 390 detoxification capacities or pesticide trapping in lipid vacuoles. We can therefore conclude that pesticide **3**91 exposure induced an increased energy demand in the liver of the goldfish, probably due to defense system induction, and metabolic compensations. While other responses shut down, the increased HSI, MI and hepatic <mark>3</mark>92 <mark>3</mark>93 carbohydrate concentration observed at T16 d indicated persisting metabolic and/or histological perturbations <mark>3</mark>94 in goldfish exposed to the pesticide mixture. However, compared to fish exposed to combined stressors, fish exposed to single stressors had lower deleterious effects of treatments at the individual level. <mark>3</mark>95

To summarize, fish exposed to single stressors displayed a significant cortisol response with coordinated effects on the metabolism and energetic reserves and low deleterious effects at different time scales. These results are consistent with a metabolic compensation strategy, i.e. the set-up of a coordinated stress responses and metabolic responses with a depletion of energetic reserves to maintain homeostasis and
 limit the deleterious effects of single stressors (Sokolova et al., 2013). However, it is not clear yet whether fish
 can implement such coordinated stress response when exposed to a combination of stressors that may have
 synergistic or antagonistic effects.

403 4.2 Responses to combined stressors (PEST * TEMP group): an inhibited early response and significant 404 effects from the molecular to the individual scale at T16 d.

405 4.2.1 Cortisol response to combined stressors

406 Cortisol level in fish subjected to both an increase in temperature, and pesticides mixture increased at 407 T6 h. Surprisingly, combined stressors did not lead to an additional increase in cortisol secretion. This result 408 shows that fish under thermal stress does not respond to pesticide exposure by an increase in cortisol 409 secretion. First, a possible explanation is that pesticide mixture toxicity decreases with the increase in 410 temperature. However, the vast majority of studies on aquatic vertebrates showed an opposite effect (Gluth and Hanke, 1984; Ferrando et al., 1987; Osterauer and Köhler, 2008; Rohr and Palmer, 2013). Second, the 411 412 exposure to a first stressor may affect the normal function of the HPI axis and prevent the induction of a stress response to a subsequent stressor (Romero, 2004; Auperin and Geslin, 2008). In this last case, the 413 hyporesponsive HPI axis to a consecutive stressor could shut down the fish ability to perform an appropriate 414 415 stress response (Romero, 2004, 2010).

416 It is also interesting to note that cortisol concentration tended to decrease in the PEST*TEMP group 417 compared to controls after 16 days of pesticide exposure (p=0.053, LSD post-hoc test). A lower level of cortisol is generally observed in organisms submitted to an extreme stress (Romero, 2004, 2010). This decrease could 418 419 be due to pesticide induced endocrine perturbation of the HPI axis function. Studies have shown that fish 420 exposed to chronic chemical stressors such as pesticides display a decreased corticosteroid response to a second (Cericato et al., 2008, 2009; Bisson and Hontela, 2002; Nascimento et al., 2012; Koakoski et al., 2014). 421 422 This inhibition could be linked to a toxic effect of pesticides, including tebuconazole, on interrenal cells or a regulation of the activity of the HPI axis at the level of the hypothalamus or pituitary (Koakoski et al., 2014; 423 Zhang et al. 2015). Endocrine disruption of the synthesis of steroid hormones, i.e. cortisol and/or sex 424 hormones can have important consequences on the fitness and survival of fish, affecting physiological traits 425 426 and behaviors associated with stress adaptation and reproduction (Ankley et al., 2002).

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4.2.2 Antioxydant responses to combined stressors

Surprisingly, all defense systems and metabolic responses observed in response to individual stresses were inhibited in fish exposed to multiple stressors at early time. The PEST*TEMP exposed fish showed no response of CAT, GST, glutathione, glutamine, taurine, choline and phosphorylcholine at T6 h. Moreover, CAT and SOD activities were reduced compared to control fish at T96 h. Similar patterns of reciprocal inactivation of defense systems were shown in *Pimephales promelas* exposed to copper and heat shock (Lapointe et al.,

2011). Moreover, it is well established that ROS (e.g. superoxide) oxidizes non enzymatic antioxidant defenses 433 **4**34 and inactivates several enzymes including CAT (see a review in Valavanidis et al., 2006). Inhibition of the stress **4**35 defenses may indicate an overproduction of ROS under combined chemical and thermal stresses which exceeded the antioxidant capacity of the cells. Inhibition of defense system reflects an antagonistic effect of 436 **4**37 thermal and chemical stressors on the overall stress response. Interestingly, CAT and SOD activity increased 438 significantly at T16 d while other responses were still shut down. This delayed response emphasizes the 439 adverse effect of chemical and thermal induced oxidative stress on cellular components, with increased risk of 440 cell and tissue injuries.

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4.2.3 Metabolic responses to combined stressors

At the molecular level, a decrease in the concentration of a large number of metabolites indicates a <mark>4</mark>42 443 significant disturbance of amino acid metabolism, energy production and defense against oxidative stress. In **4**44 the PEST*TEMP group, the metabolic responses to individual stressors measured at T6 h disappeared, including the responses observed at the molecular, cellular and tissue levels. In particular, the ETS activity in 445 446 both liver and muscle decreased compared to the PEST and TEMP groups. The decreased ETS activity under 447 combined stressors could result from (1) perturbations in the normal function of the ETS or (2) a decreased mitochondrial densities in cells (Lannig et al., 2006; Sokolova and Lannig, 2008; Lavergne et al., 2015). In **4**48 **4**49 ectothermic species, mitochondrial plasticity plays a critical role in the metabolic response to environmental **4**50 stressors (Strobel et al., 2013). The incapacity of fish to maintain an elevated energy production under multiple **4**51 stress exposures could explain the absence of induction of the defense system observed at T6 h. 452 Consequently, it could potentiate oxidative damages on cellular components, including proteins. The creatine phosphocreatine system plays a critical role in cellular energy metabolism (Sun et al., 2012; Wang et al., 2017). 453 **4**54 Thus, the decreased creatine, found under combined exposure stressors at T16 d strengthens the perturbation of energy metabolism which is consistent with the above conclusion. 455

PEST*TEMP exposed fish showed significant decreases in amino-acids levels as soon as T6 h, with reduced levels of proline and lysine. At T16 d, reduced concentrations were found for isoleucine, leucine, valine, alanine, proline, lysine, glutamate, glutamine, creatine and taurine, indicating an important perturbation of amino-acid metabolism and/or oxidative damages on proteins.

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4.2.4 Physiological responses to combined stressors

At the tissue level, the increase in HSI and the deposition of lipids in the muscles also indicate disturbances in energy metabolism, sequestration of pesticides in lipid vacuoles and / or tissue damage. Finally, a significant decrease in the overall condition of the fish (FCF) is visible at T16 d. When fish are subjected to both combined stressors, the general stress response is inhibited, at least initially, with significant individual-level effects on overall fish health. Given that the stress response is fundamental in enabling organisms to acclimate to changes in their environment, its inhibition under multiple stressors seems to have 467 important consequences on fitness and fish performance affecting physiological traits and behavioral 468 responses related to stress adaptation and reproduction (Pankhurst and Van Der Kraak, 2011).

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470 5. Conclusion

471 Taken together, these results indicate that (1) single thermal and chemical stressors lead to a general 472 stress response and a metabolic compensation strategy, i.e. the set-up of a coordinated stress response and depletion of energetic reserves limiting adverse effects at higher biological levels. The lack of effect on the 473 474 general condition of the fish (i.e. tertiary response) suggests that the stress response set up is adapted and effective. However, (2) the patterns of metabolic response and defensive systems strongly depended on the 475 476 nature of the stress (thermal vs. chemical). Finally, (3) fish were unable to establish an effective stress 477 response when chemical and thermal stressors were combined, with deleterious effects at the individual level. 478 Exposure to combined chemical and thermal stressors disrupts the stress response and results in a decrease in the overall condition of the fish, indicating a synergistic effect of temperature and pesticide mixture on 479 480 goldfish. These results also outline the central role of metabolism in these stress responses. The decrease in 481 cellular energy metabolism when the two stresses are combined is consistent with the shift from a 482 compensation strategy to a metabolic conservation strategy (Sokolova et al., 2013). In other words, exposure 483 to a combination of stressors might exceed the metabolic capacity of the fish, leading to an early inhibition of 484 the stress response (lower level of cortisol, antioxydant defenses, and lower depletion of energy reserves) with 485 potential high deleterious effects at the individual level.

486 To our knowledge this study is the first to evaluate the combined effects on the fish stress response of 487 temperature warming and water contamination by pesticide mixtures with an integrated molecule- individual scale. The combined analysis of omic approaches, here metabolomics, and more conventional biochemical 488 489 approaches seems to be a powerful way to evaluate the response of organisms undergoing multiple stresses. 490 Future studies should now consider different combinations of stressors and evaluate their effects on individuals across biological levels, from the molecules to the whole individual, while taking into account the 491 492 inter-individual variability of sensitivity. Because global changes are exposing organisms to a combination of 493 stressors at the same time, this will help understanding and predicting the responses of natural populations to 494 actual and future stresses.

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 (Zn) exposure on hepatic lipid deposition and metabolism in yellow catfish *Pelteobagrus fulvidraco*. Aquat.
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Comment citer ce document : Gandar, A., Laffaille, P., Canlet, C., Tremblay-Franco, M., Gautier, R., Perrault, A., Gress, L., Mormède, P., Tapie, N., Budzinski, Jean, S. (2017). Adaptive response under multiple stress exposure in fish : From the molecular to individual level. Chemosphere, 188, 60-72. DOI : 10.1016/i.chemosphere.2017.08.089 Fig. 1. PLS-DA scores (top) and loadings plot (bottom) plots of integrated ¹H-NMR spectra of liver extracts for each time point independently.

For scores plots, each dot represents an observation (fish), projected onto first (horizontal axis) and second/third (vertical axis) PLS-DA variables. Temperature is shown in different colors: 22 °C (CONTROL) in black, 32 °C in blue; exposition to pesticides is shown in different symbols: box for non-exposed fish, four-point star for exposed fish. The black ellipse determines the 95% confidence interval, which is drawn using Hotelling's T2 statistic. For loading plot, the horizontal axis corresponds to the value of the loading in the discrimination model. The positive part of the loadings plot represents metabolites higher for group(s) in the left section of the scores plot whereas the negative part of the loadings plot represents metabolites that are higher for group(s) in the right section of the score plot. Corresponding loading plots color coded according to the correlation coefficients from blue to red. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of the article.)

A. T6h liver extracts (A=3, R²=52.7%, Q²=0.368). B. T96h liver extracts (A=3, R²=54.3%, Q²=0.343). C. T16d liver extracts (A=2, R²=55.4%, Q²=0.507). D. T6h liver extracts. E. T96h liver extracts. T16d liver extracts.

Fig. 2. Canonical representations of endocrine, physiological and metabolic responses of goldfish to individual and combined chemical and thermal stresses.

Fish were exposed for 6 h, 96 h or 16 d to a mixture of pesticides (PEST), temperature increased (TEMP) or a combination of pesticide mixture and temperature increased (PEST*TEMP). Integration of endocrine, metabolic and physiological responses was realized using canonical analysis and Mahalanobis distance calculs. Blue diamonds: position of variables on the first canonical plan. Red squares: mean positions of groups. Blue boxes: Mahalanobis distances between exposed groups and control group. Asterisks: significant Mahalanobis distances with *: p-value<0.05, **: p-value<0.01. Abbreviations: AE: available energy; EC: energy consumed; HSI: hepaosomatic index; MI: muscle index; FCF: Fulton's condition factor.

Fig. 3. Defense system induction in goldfish exposed to individual and combined chemical and thermal stresses.

The activity of CAT, SOD and GST were measured in the liver of goldfish exposed to pesticide mixture (PEST), temperature increased (TEMPS) or a combination of both stresses (PEST*TEMP). Boxplots at 6 h, 96 h and 16 d are presented. N=12.

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Table 1. Fold-change of discriminant metabolites identified by ¹H NMR metabolomics approach in aqueous liver extracts of *Carassius auratus* exposed to pesticide mixture (PEST), temperature increased (TEMP) or both (PEST*TEMP) compared to CONTROL group at T6 h.

	Metabolites	Chemical shift ^a δ^{1} H (ppm)	FC ^b PEST	P°	FC TEMP	Р	FC PEST*TEMP	Р
Amino-acids	Glutamine	2.14 (m), 2.45(m), 3.78(t)	1.43	**	1.32	**	1.32	
	Proline	2.00(m), 2.04(m), 2.35(m),3.34(m), 3.41(m),4.14(dd)	1.15		0.72		0.65	*
Organic acids	Glutathione (reduced)	2.17(q), 2.55(m), 2.98(ddd), 3.80(m), 4.57(m)	1.29	**	1.27	**	1.14	
	Succinate	2.40(s)	1.29	**	1.00		0.97	
	Taurine	3.27(t), 3.43(t)	1.15		1.18	**	1.09	
Sugars	Maltose	3.29(dd), 3.43(t), 3.56-4.00, 4.66(d),5.24(d), 5.42(d)	0.91	**	0.99		0.98	
Phosphagens	Choline	3.20(s), 3.53(m), 4.07(m)	1.49	***	1.15		1.08	
	Phosphoryl- choline	3.22(s), 3.60(m),4.17(m)	1.31		1.78	*	1.54	
Nucleotides	AMP	4.03(m), 4.38(m),4.52(dd),6.15(d),8.24(s),8.5 6(s)	1.40	***	1.14		1.00	
	NAD+	4.24(m), 4.35-4.44,4.47- 4.56,6.03(d), 6.10(d),8.14(s),8.20(dd),8.41(s), 8.84(d),9.15(d)	1.40	***	1.20		1.08	
	UDP/UTP	4.22-4.30, 4.38-4.47,5.98(m), 7.99(d)	1.28		0.79	***	0.74	*

^aMultiplicity : s, singlet; d, doublet; t, triplet; q, quartets; m, multiplet. ^bFC, Fold Change = exposed samples/control samples.^cP values were calculated using a nonparametric Kruskal-Wallis test.*P<0.05, **P<0.01, ***P<0.001.

Table 2. Fold-change of discriminant metabolites identified by ¹H NMR metabolomics approach in aqueous liver extracts of *Carassius auratus* exposed to pesticide mixture (PEST), temperature increased (TEMP) or both (PEST*TEMP) compared to CONTROL group at T96 h.

	Metabolites	Chemical shift ^a δ^{1} H (ppm)	FC ^b PEST	P°	FC TEMP	Р	FC PEST*TEMP	Р	
Amino-acids	Proline	2.00(m), 2.04(m), 2.35(m),3.34(m), 3.41(m),4.14(dd)	1.11		0.69	***	0.85	***	
Organic acids	Malonate	3.14(s)	0.87		0.75	*	0.77		
	Succinate	2.40(s)	1.02		0.92		0.74	**	
Sugars	Maltose	3.29(dd), 3.43(t), 3.56-4.00, 4.66(d),5.24(d), 5.42(d)	1.03	1.03 1.24 *** 1.04		1.04			
Nucleotides	AMP	4.03(m), 4.38(m),4.52(dd),6.15(d),8.24(s),8.56(s)	0.85	***	0.83	***	0.68	***	
	NAD+	4.24(m), 4.35-4.44,4.47-4.56,6.03(d), 6.10(d),8.14(s),8.20(dd),8.41(s),8.84(d), 9.15(d)	0.95		0.82	***	0.73	***	
	UDP/UTP	4.22-4.30, 4.38-4.47,5.98(m), 7.99(d)	0.94		0.72	***	0.57	***	
Non identified	,	1.09(d)	1.00		0.68	***	1.50	***	
		3.09(m)	0.97		0.72	**	0.91	**	

^aMultiplicity : s, singlet; d, doublet; t, triplet; q, quartets; m, multiplet. ^bFC, Fold Change = exposed samples/control samples. ^cP values were calculated using a nonparametric Kruskal-Wallis test. *P<0.05, **P<0.01, ***P<0.001.

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Table 3. Fold-change of discriminant metabolites identified by ¹H NMR metabolomics approach in aqueous liver extracts of *Carassius auratus* exposed to pesticide mixture (PEST), temperature increased (TEMP) or both (PEST*TEMP) compared to CONTROL group at T16 d.

	Metabolites	Chemical shift ^a δ^{1} H (ppm)	FC ^b PEST	P°	FC TEMP	Р	FC PEST*TEMP	Р
Amino-acids	Alanine	1.48 (d), 3.77 (q)	1.01		1.05		0.82	**
	Glutamine	2.14 (m), 2.45(m), 3.78(t)	0.97		1.27		0.71	***
	Isoleucine	0.94 (t), 1.01 (d), 1.26 (m), 1.46 (m), 1.98(m), 3.68(d)	1.00		0.81		0.57	***
	Leucine	0.96(d), 0.97(d), 1.70(m), 3.73 (t)	0.96		0.84		0.55	**
	Lysine	1.44(m), 1.50(m), 1.73(m), 1.90(m), 3.02(t), 3.77(t)	1.04		1.04		0.68	**
	Proline	2.00(m), 2.04(m), 2.35(m),3.34(m), 3.41(m),4.14(dd)	0.93		0.83	**	0.64	**
	Valine	0.99(d), 1.04(d),2.28(m), 3.62(d)	0.98		0.92		0.62	***
Organic acids	Creatine	3.04(s), 3.93(s)	0.94		0.76		0.55	***
	Glutathione (reduced)	2.17(q), 2.55(m), 2.98(ddd), 3.80(m), 4.57(m)	0.94		1.65	***	0.99	
	Lactate	1.33(d), 4.10(q)	1.05		0.99		0.83	*
	Taurine	3.27(t), 3.43(t)	1.02		0.96		0.86	***
Sugars	Maltose	3.29(dd), 3.43(t), 3.56-4.00, 4.66(d),5.24(d), 5.42(d)	0.88		0.99		1.08	***
Phosphagens	Phosphoryl- choline	3.22(s), 3.60(m),4.17(m)	1.04		1.68	*	1.18	
Nucleotides	AMP	4.03(m), 4.38(m),4.52(dd),6.15(d),8.24(s),8.56(s)	1.03		1.08		0.83	**
	NAD+	4.24(m), 4.35-4.44,4.47-4.56,6.03(d), 6.10(d),8.14(s),8.20(dd),8.41(s),8.84(d),9.15(d)	1.06		1.12		0.69	***
Non identified		3.09(m)	1.12		0.97		0.67	**

^aMultiplicity : s, singlet; d, doublet; t, triplet; q, quartets; m, multiplet. ^bFC, Fold Change = exposed samples/control samples. ^cP values were calculated using a nonparametric Kruskal-Wallis test. *P<0.05, **P<0.01, ***P<0.001.

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Table 4. Endocrine, metabolic and physiological responses in CRIPT goldfish exposed to individual and combined chemical and thermal stresses.

	T6h			T96h			T16d		
Variables	PEST	TEMP	PEST*TEMP	PEST	TEMP	PEST*TEMP	PEST	TEMP	PEST*TEMP
Cortisol	↑ *	↑ *	1 *	-	-	-	-	-	↓°
Liver									
carbohydrates	个 *	-	<mark>۲</mark> °	-	-	-	^ *	-	-
proteins	↑ *	个 **	-	-	-	-	-	-	-
lipids	↓ *	-	-	-	-	-	-	-	-
AE	-	-	-	-	-	-	-	-	-
EC	个 *	个 **	-	-	-	-	-	-	-
CEA	↓ °	-	-	-	-	-	-	-	-
White Muscle									
carbohydrates	-	-	-	-	-	-	-	-	-
proteins	-	-	-	-	-	-	-	-	-
lipids	-	↓ °	-	↑ *	-	-	-	-	↑ *
AE	-	↓ *	-	↑ *	-	-	-	-	1 *
EC	-	↑ *	-	-	-	-	-	-	-
EA	-	↓ ***	-	-	-	-	-	-	↑ *
HSI	个 **	-	-	-	-	-	^ *	-	1 **
МІ	-	-	-	-	-	-	^ *	-	个 **
FCF	-	-	-	-	-	-	-	-	↓**

Fish were exposed for 6 hours, 96 hours or 16 days to a mixture of pesticides (PEST), temperature increased (TEMP) or a combination of both (PEST*TEMP). At each time, ANOVA analyses followed by LSD post-hoc tests were performed. Red arrows indicate increased values compared to CONTROL group while green arrows correspond to decreased values. Asterisks: significance of the differences compared to CONTROL group with: °: p<0.1, *: p<0.05, **: p<0.01, ***: p<0.001. *Abbreviations:* AE: available energy; EC: energy consumed; CEA: cellular energy allocation; HSI: hepatosomatic index; MI: muscle index; FCF: Fulton's condition factor.

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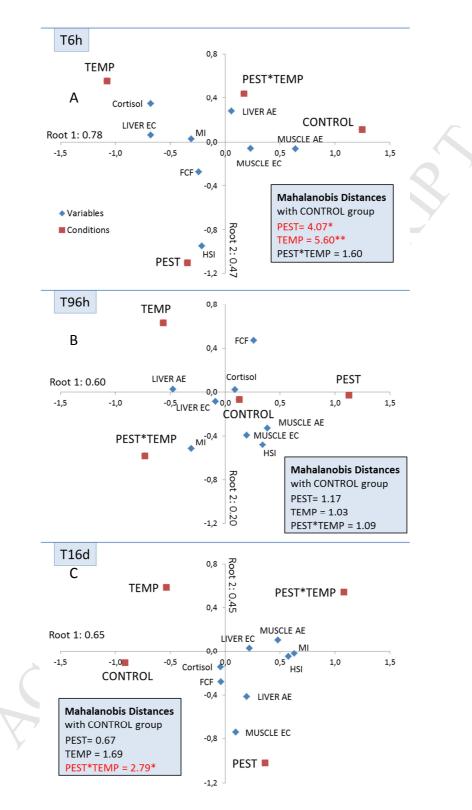


Fig. 1. Canonical representations of endocrine, physiological and metabolic responses of goldfish to individual and combined chemical and thermal stresses.

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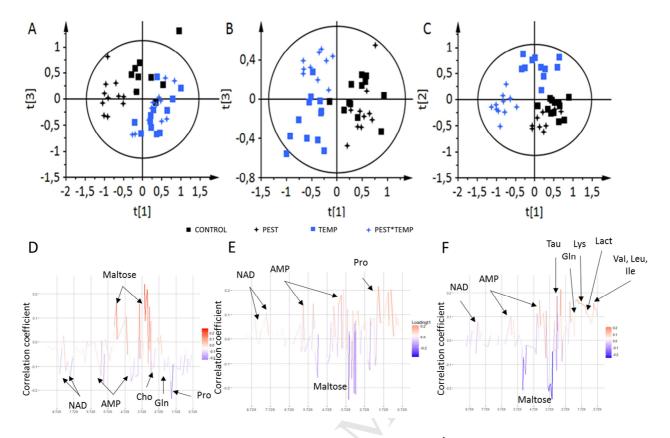


Fig. 2. PLS-DA scores (top) and loadings plot (bottom) plots of integrated ¹H-NMR spectra of liver extracts for each time point independently.

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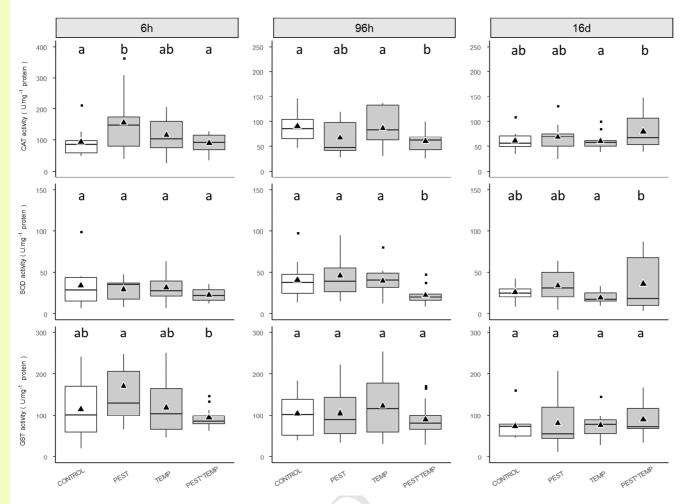


Fig. 3. Defense system induction in goldfish exposed to individual and combined chemical and thermal stresses.

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Highlights

- Goldfish were exposed to a pesticide mixture and elevated temperatures for 16 days
- Metabolomics and biochemical approaches were conducted
- Adapted and coordinated early responses to individual stressors were observed
- Multistress reduced earlier endocrine response, antioxidant defense and metabolic compensation

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