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molecular biomarkers, oxidative stress

Abstract

 Continuous anthropogenic inputs of carbon dioxide in the atmosphere are driving ocean warming 23 and acidification. The potential threat represented by these changes for marine species could be amplified in coastal areas, characterized by higher levels of chemical pollutants. In addition, organisms living in temperate areas may exhibit a different seasonal tolerance to stressors influenced by fluctuations of environmental factors and physiological characteristics. In this study, mRNA levels of selected genes related to metal-induced stress response were investigated in the Mediterranean mussel *Mytilus galloprovincialis* collected both in summer and in winter and exposed to combinations 29 of two temperatures (SST, seasonal surface temperature and SST+5 \degree C), two levels of pH (8.20 and 30 7.40) and two doses of cadmium (0 and 20 μ g/L). Selected genes included metal detoxification pathway (metallothionein *mt-20*), cellular stress response (heat-shock protein *hsp70*), and antioxidants network (superoxide dismutase *Cu/Zn-sod*, catalase *cat*, glutathione peroxidase *gpx1* and glutathione S-transferase *gst-pi*). To further elucidate possible differences in responsiveness of various tissues related to metabolic function and physiological characteristics, such analyses were carried out in digestive gland and in gills of exposed mussels. Seasonal- and tissue-specific differences were observed for metallothioneins gene induction after Cd-exposure, while *hsp70* up- regulation was caused by acidification, both alone or in combination with other stressors. A complex array of interactions affected antioxidant genes, with strong differences as a function of analyzed tissue and experimental season and without a clear role of specific stressors and investigated pathways. The overall results highlighted the importance of considering seasonality and responsiveness of different tissues to predict the effects of sudden changes in environmental parameters on responsiveness and toxicity of chemicals to marine coastal organisms.

1.Introduction

 As a consequence of increased anthropogenic carbon dioxide emissions, oceans are threatened by warming and acidification (IPCC, 2013). Since the beginning of the industrial era, ocean has 46 warmed by almost 1 °C because of the greenhouse effect and captured about 30% of anthropogenic CO2, resulting in a pH drop of 0.1 units (Hansen *et al.*, 2016). By the end of the century, temperature 48 is projected to increase by additional 2° C, while ocean mean pH will further decrease by $0.3 - 0.5$ units (IPCC, 2013). These changes could be even more pronounced in coastal areas, where large fluctuations and sudden peaks of temperature and pH naturally occur (Wallace *et al.*, 2014). In addition, these ecosystems are characterized by a higher anthropogenic footprint compared to open ocean and synergistic effects can be expected between a wide range of stressors and climate change (Hewitt *et al.*, 2016).

 Ocean warming and acidification have been described as potential factors affecting trace metals speciation and bioavailability but also their biological effects and toxicity. Such interactions were demonstrated on impaired mitochondrial functioning, energy metabolism, oxidative unbalance, accumulation of lipid peroxidation products, damages to lysosomes, DNA and immune function, as well as to impair larval development (Regoli et al., 2002; Roberts *et al.*, 2013; Rodríguez-Romero *et al.*, 2014; Götze *et al.*, 2014; Izagirre *et al.*, 2014; Múgica *et al.*, 2015; Moreira *et al*., 2018; Cao *et al*., 2019).

 One of the main pathway of trace metals toxicity is exerted through oxidative insult: these elements enhance intracellular production of reactive oxygen species (ROS) affecting electron transport chains and catalyzing Fenton-like and Haber-Weiss reactions, but they can also reduce the amount or efficiency of antioxidant defenses (Regoli et al., 1997, 1998; Regoli and Giuliani, 2014). Oxidative unbalance has been demonstrated to be promoted also by thermal stress and reduced pH- hypercapnic condition in several species, both vertebrates and invertebrates (Tomanek *et al.*, 2011; Wang *et al.*, 2016; Freitas *et al.*, 2017; Andrade *et al.*, 2019; Liao *et al.*, 2019).

 To reduce metal toxicity, the accumulation of these elements is associated with the induction of metallothioneins (MTs), low-molecular weight metal-binding proteins the transcription of which is up-regulated, through the metal transcription factor I (MTF-I) (Kimura *et al.*, 2009). The induction of MT can be affected also by other factors, such as ROS, temperature, nutritional status, salinity, and hypoxia (Le *et al.*, 2016). Similarly, environmental stressors including heat stress, metals, hypoxia and hypercapnia activate the heat shock factor (HSF) transcription factor leading to enhanced formation of heat shock protein (Hsp) families (Wang *et al.*, 2013). Among these, Hsp70s represents one of the most conserved families with chaperone activity, involved in folding and unfolding of damaged proteins and stress response (Wang *et al.*, 2013).

 Previously published researches of our group (Nardi *et al.*, 2017, 2018b), demonstrated oxidative effects of cadmium in association with temperature and pH stress at biochemical and cellular level in *M. galloprovincialis*. Since the use of molecular biomarkers might represent a sensitive tool to identify early biological responsiveness to environmental stressors, this study aimed to characterize the key transcriptional effects in long-term studies to previously tested multiple stressors such as cadmium (Cd), temperature and acidification. The Mediterranean mussel *Mytilus galloprovincialis*, was chosen as a widely used bioindicator organism (Fattorini *et al.*, 2008; Regoli *et al.*, 2014), while selected target genes reflect pathways of metal-detoxification (the Cd-inducible isoform of metallothioneins, *mt-20*), cellular stress (the heat shock protein 70, *hsp70*) and antioxidants network (cytosolic superoxide dismutase, catalase, Se-dependent glutathione peroxidase and the pi isoform of glutathione S-transferase, *Cu/Zn-sod*, *cat*, *gpx1*, *gst-pi*). Gene expression was analyzed both in digestive gland and gills of exposed mussels due to their different ability to concentrate pollutants and tolerate environmental stressors; further, experiments were performed in summer and in winter to elucidate the potential tissue-dependent and seasonal modulation of observed effects of the investigated parameters. The overall results were expected to provide novel insights on mechanisms underlying the onset of biological and interactions of climate change with other environmental stressors.

2.Materials and Methods

2.1 Animal collection and experimental design

 Mussels, *M. galloprovincialis* (6.0 ± 0.5 cm shell length), were obtained from a shellfish farm in an unpolluted area of Central Adriatic Sea (Regoli *et al.*, 2014) in summer (June 2014) and winter (January 2015). For each season, mussels were acclimatized in aerated artificial seawater (ASW; Instant Ocean®) for 7 days at pH 8.20 and salinity 37 (practical salinity unit). Different acclimation 100 temperatures were used for summer (20 °C) and winter (10 °C), representative of the mean seasonal surface temperature (SST) at the sampling site and time of collection. Water was changed every other day and mussels fed 12 hours prior the water change with a commercial mixture of zooplankton (50- $300 \mu m$) for filter-feeding organisms.

 Experimental conditions are those already described in Nardi *et al*., 2017 and 2018b. After the acclimation, mussels (36 individuals in 20 liters) were randomly assigned to one of eight 106 combinations of a multifactorial experimental design with two temperatures (SST and SST+5 $^{\circ}$ C), 107 two pH/pCO₂ (8.20/ \sim 400 µatm and 7.40/ \sim 3000 µatm) and two doses of added cadmium (0 and 20 µg/L). The resulting experimental treatments were: 1) control condition (CTRL), with seasonal mean 109 surface temperature (SST) and normocapnia ($pH=8.20/ pCO₂=~400 \mu atm$); 2) cadmium exposure (Cd), SST, normocapnia and 20 µg/L Cd; 3) acidification (A), SST, hypercapnia (pH=7.40/ 111 *p*CO₂=~3000 µatm); 4) warming (W), 5° C temperature increase in respect to the SST (SST+5^oC) and 112 normocapnia; 5) acidification + Cd (A-Cd), SST, hypercapnia and 20 μ g/L Cd; 6) warming + Cd (W-113 Cd), SST+5°C, normocapnia and 20 µg/L Cd; 7) acidification + warming (A-W), SST+5°C and 114 hypercapnia; 8) acidification + warming + Cd (A-W-Cd), $SST+5\degree C$, hypercapnia and 20 µg/L Cd. Exposure cadmium concentration is representative of a polluted but environmentally realistic scenario in Mediterranean coastal waters (Neff, 2002), while selected pH and temperature were adapted from scenario RCP 8.5 and IPCC WGII AR5 (IPCC, 2013), predicting more pronounced variations in coastal areas than in open ocean. The hypercapnic condition was obtained mixing ASW 119 (pH=8.2) with small amounts of CO_2 -saturated ASW, resulting of bubbling pure CO_2 in ASW for at

 least 24h (Nardi *et al*., 2017). For each experimental condition temperature, pH and salinity were measured daily, while total alkalinity (AT) was measured twice per week. Seawater carbonate 122 parameters (pCO_2 , and saturation state (Ω) for calcite and aragonite) were calculated in CO2SYS (Pierrot *et al.*, 2006), using barometric pressure values, as well as AT, pH, temperature and salinity values for the respective samples (see Nardi *et al.*, 2017, 2018b for details on calculation). Full seawater chemistry, along with Cd bioaccumulation in digestive gland and gills of exposed mussels (previously published in Nardi *et al*., 2017 and 2018b) are provided in Table 1. During the experimental phase, water renewal and feeding regime were the same as in the acclimation phase, 128 and Cd dosed after every water change.

 After four weeks, animals were sampled from each tank, digestive gland and gills rapidly excised, pooled in 12 samples each constituted by tissues of 3 individuals, frozen in liquid nitrogen and 131 maintained at -80°C until molecular analyses.

2.2 RNA isolation and cDNA synthesis

 Total RNA was purified from digestive glands and gills, using the Hybrid-RTM kit (GeneAll Biotechnology) according to the manufacturer's protocol. Total RNA concentrations and purity were measured using Nano-Drop ND-1000 UV-Visible Spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA). RNA quality was verified on an agarose-formaldehyde gel. Total cDNA was generated by RT-PCR (Reverse Transcription-Polymerase Chain Reaction) from 1 µg of total RNA for each sample using combined oligo(dT) and random hexamer primers (iScript cDNA Synthesis Kit, Bio-Rad).

2.3 Quantitative real-time PCR

 Absolute quantitative real-time PCR with gene-specific primer pairs (Table 2) was performed for evaluating the mRNA levels of individual target genes, using SYBR green method in StepOnePlus® Real-Time PCR System (Applied Biosystems). Each 15 µL DNA amplification reaction contained

 7.5 µL of SYBR Select Master Mix (Life Technologies), 5 µL of total cDNA (synthesized as described above and diluted 1:5) and 200 nM of each forward and reverse primers. The real-time 148 PCR program included an enzyme activation step at 95 \degree C (2 min) and 40 cycles composed by 15 s at 95 °C and 1 min at the annealing temperature (Table 2). The specificity of target cDNA amplification was checked by including controls lacking cDNA template and by a melting analysis (95 °C for 1 min, 65 °C for 10 s and fluorescence detection at increasing temperature between 65 and 152 95 °C). For quantification, serial dilutions of known amounts of plasmid containing the amplicon of interest were used as standards to build a standard plot of Ct versus log copy number (for each target gene). Samples and standards were run in duplicate in the same run. Cycle threshold (Ct) values of unknown samples were converted into mRNA copy number interpolating the standard plot. The 156 values were expressed as log₂ of fold change (FC: exposed samples relative to control samples).

2.4 Statistical analyses

 Non-parametric one-way analysis of variance (Kruskal-Wallis test) was used to evaluate the effect of the different treatments. Level of significance was set to *p* < 0.05; *post-hoc* Dunn's test, allowed to compare differences between groups of means. Non-metric multidimensional scaling (NMDS) was applied to each tissue dataset. Statistical analyses were performed using RStudio (version 0.99.491).

3. Results

3.1 Digestive gland

 A significant increase of *mt-20* mRNA was observed in the digestive gland of organisms exposed to all experimental combinations containing Cd (Cd, A-Cd, W-Cd and A-W-Cd), with a lower level of induction in summer compared to winter (Fig. 1a and 2a). Acidification increased significantly *hsp70* mRNA levels independently of additional stressors in summer, while in winter no significant variation occurred despite a slight up-regulation due to acidification alone (Fig. 1b, 2b). Changes in

 Cu/Zn-sod expression were not statistically significant in mussels exposed to various treatments in summer (Fig. 1c), while in winter a significant up-regulation was caused by Cd and acidification, alone or in combination with higher temperature (Fig. 2c). Similarly to *hsp70*, *cat* mRNA was higher in organisms exposed to A, A-Cd and A-W during the summer (Fig.1d), while in winter acidification alone caused a significant induction (Fig. 2d). Levels of *gpx1* mRNA were significantly down- regulated in summer by the exposure to Cd, W, A-Cd and A-W (Fig. 1e), while in winter this effect was observed in organisms exposed to higher temperature with Cd and/or reduced pH (Fig. 2e). The *gst-pi* mRNA was significantly increased in summer by acidification, alone or when organisms were co-exposed to Cd and warming (A and A-W-Cd, Fig.1f), while in winter *gsti-pi* induction occurred in organisms exposed to Cd, acidification and acidification at higher temperature (Cd, A and A-W, Fig. 2e).

3.2 Gills

 Expression of *mt-20* in summer was upregulated in gills of the organisms treated with Cd, but this increase was statistically significant only in those exposed at control temperature with or without acidification (Cd and A-Cd, Fig. 3a); in winter mussels exhibited the induction of *mt-20* when exposed to Cd at control temperature, while increased mRNA levels observed after W-Cd and A-W- Cd treatments did not reach the statistical significance (Fig. 4a) and a statistically significant downregulation of *mt-20* mRNA occurred in organisms exposed to acidification or higher temperature alone (A and W, Fig. 4a). Expression of *hsp70* was downregulated in organisms co- exposed in summer to Cd and reduced pH (A-Cd, Fig. 3b), while in winter a significant upregulation of this gene occurred in organisms exposed to acidification at control and higher temperature (A and A-W, Fig. 4b). No significant variations of *Cu/Zn*-*sod* and *cat* expression (Fig.3c and 3d) were found in summer treatments, while in winter both genes were affected: *Cu/Zn-sod* was upregulated in gills of mussels co-exposed to Cd, acidification and warming (A-W-Cd, Fig. 4c), while *cat* was significantly downregulated in organisms exposed to Cd and acidification, both alone or in

3.3 Non-metric multidimensional scaling (NMDS)

 Non-metric multidimensional scaling provided clear separation between summer and winter experiments in both tissues (Fig. 5a,b), mostly due to *mt20*, *Cu/Zn-sod* and *gpx* in digestive gland, and to *mt20*, *gpx1*, *Cu/Zn-sod* and *gst-pi* in gills. In each tissue, separation between Cd-exposed and non-exposed mussels was also explicitly driven by *mt20*.

4. Discussion

 The present study showed that both acidification and warming can synergistically affect the transcription of genes associated to metal exposure, with the sensitivity of these diverging in different seasons and tissues.

4.1 Digestive gland

 Different isoforms of metallothioneins genes have been described in *M. galloprovincialis*, among which *mt-20* has been shown to be induced by cadmium and oxidative stress (Dondero *et al.*, 2005). Here, *mt-20* gene in the digestive gland showed to be responsive to Cd, independently of temperature and pH, in both summer and winter experiments. However, *mt-20* upregulation was not always proportional to Cd uptake (previously published in Nardi *et al.*, 2017; 2018b): in fact, while exposure at higher temperature always increased Cd accumulation, a parallel modulation of *mt20* induction was observed only in summer for the digestive gland. From these data, a lower responsiveness of metallothionein gene may be hypothesized in a potential scenario of increased temperature in winter. Scientific literature on the role of temperature and pH on *mt-20* transcription in mussels is scarce, and the few available data described an up-regulating effect of temperature on *mt-20* gene expression in

 embryos and larvae of *M. galloprovincialis* exposed to copper (Boukadida *et al.*, 2017; Mlouka *et al.*, 2019).

 Hsp70s are usually associated to folding or degradation of damaged and unrepairable proteins (Mayer and Bukau, 2005) and their induction is a marker of thermal or cellular stress (Wang *et al.*, 2013). In our study, the absence of *hsp70* upregulation after 28 days of exposure to increased temperature alone, confirms that the response to heat-shock is typical of acute stress (Franzellitti and Fabbri, 2005), supporting a physiological adaptation of mussels to long-term warming. Acidification was instead the main driver of *hsp70* induction in mussels digestive gland after 28 days exposure in summer, particularly evident when acidification was combined with other stressors. Similar results would indicate that mechanisms of protein damage are enhanced by changes in the intracellular mileau due to hypercapnic condition (Wang *et al.*, 2016). Acute effects of lowered pH on hsp70s were already demonstrated in several marine species after hours to days of exposure (Hernroth *et al.*, 2011; Moya *et al.*, 2015; Feidantsis *et al.*, 2015), but the induction after longer periods of reduced pH exposure has been documented only in the Antarctic bivalve *Laternula elliptica* (21 days, Cummings *et al.*, 2011) and the cold-water coral *Desmophyllum dianthus* (8 months exposure, Carreiro-Silva *et al.*, 2014). On the other hand, in mussels exposed during the winter the trend toward an induction of *hsp70* expression by lower pH was abolished when also warming and/or Cd were combined as multiple stressors: the different physiological state of mussels in winter period would then reflect a lower sensitivity to cellular impairment compared to summer organisms.

 The battery of antioxidant genes indicated a certain disturbance of the oxidative balance toward investigated stressors, confirming a generally higher responsiveness during the summer. Acidification, alone or in combination with other stressors, was the main factor promoting the up- regulation of *cat* and *gst-pi* both, suggesting a CO2-mediated increase of oxidative challenge as already hypothesized by other authors (Tomanek *et al.*, 2011). Interestingly, heat shock proteins were previously suggested to act as redox sensors activating some antioxidant genes (Madeira *et al.*, 2017 and ref. therein): this hypothesis seems to be confirmed by our observations with similar responses

 to acidification for *cat*, *gst-pi* and *hsp70*. The expression of *gpx1* exhibited a generalized downregulation, with major effects due to Cd-exposure in summer, and by various combinations of temperature with other stressors in winter. Inhibitory effects of Cd on *gpx1* expression have been reported in *Danio rerio* (Banni *et al.*, 2011) and in *Oncorhynchus kisutch* (Wang *et al.*, 2012), while increased temperature was shown to upregulate *gpx1* in the gastropod *Haliotis discus discus* (De Zoysa *et al.*, 2009). The downregulation of *gpx1* is mainly due to degradation through the so-called "nonsense mediated decay" mechanism, which may occur e.g. when intracellular Se concentration are limiting (Sun *et al*., 2000). Although few evidences are available for bivalves, both Cd exposure and changes in pH have been shown to modulate uptake and intracellular levels of Se (Dorey *et al.*, 2018).

4.2 Gills

 In the gills, interactive effects of warming and acidification showed to interfere with Cd-induced *mt-20* transcription in both seasons. Although Cd was bioaccumulated in all treatments with this element (Tab. 1), responsiveness to *mt20* seems more variable in organisms co-exposed to higher temperature in summer and weakened by lowered pH in winter, corroborating the hypothesis of differential sensitivity of mussels to environmental factors in different seasons, and a compromised capacity of gills to counteract Cd contamination in case of prolonged temperature and/or pH stress.

 Similarly to the digestive tissues, *hsp70* was not induced by warming alone in gills, and acidification was confirmed to provoke a certain up-regulation, although less intense and limited to winter mussels. On the other hand, a marked downregulation of *hsp70* was observed in organisms co-exposed to Cd and acidification during the summer: downregulation of *hsp70* mRNA was observed in the haemocytes of clam *Mercenaria mercenaria* exposed to Cd and hypercapnia (Ivanina *et al.*, 2014), in the haemocytes of oyster *Saccostrea glomerate,* and in the digestive gland of *M. galloprovincialis* due to Cd exposure (Thompson *et al.*, 2012; Izagirre *et al.*, 2014); lowered levels of heat shock proteins were also observed in the oysters *Crassostrea virginica*, *Pinctada fucata* and

 Crassostrea gigas exposed to acidification (Liu *et al*. 2012; Ivanina *et al.*, 2014; Dineshram *et al.*, 277 2016). The downregulation of this cellular response has been described as a mechanism of energy allocation trade-off (Goncalves *et al.*, 2017), allowing to hypothesize a decreased adaptability to new environmental scenarios, since the capacity to activate gene expression influence the tolerance of marine species to climate changes (Somero 2010, Logan and Somero, 2011).

 Weak sensitivity of antioxidant responses was generally observed in gills of exposed mussels exposed during both seasons. Most of the observed variations were not statistically significant; only *gpx1* and *cat* were downregulated by single or combined stressors with unclear causative stressor- effect relationships, confirming a lower involvement of gills compared to digestive tissues in counteracting oxidative insult deriving from environmental stressors (Regoli, 1998). Also for the gills, non-metric multidimensional scaling analysis (Fig. 5b) confirms seasonal differences between summer and winter organisms.

4.3 Transcriptional vs. functional investigations

 Responses analyzed in this study at gene expression level were previously characterized in terms of functional effects measuring protein levels of MTs and enzymatic activities of CAT, GST and Se- GPX in mussels exposed to the same experimental conditions as those presented here (Nardi *et al.*, 2017, 2018b).

 These overall results highlight some discrepancies between transcriptional responses and protein or enzymatic activities, as already observed in the European eel *Anguilla anguilla* and in *M. galloprovincialis* exposed to polluted sediments (Regoli *et al.*, 2011; Giuliani *et al.*, 2013), and in the Pacific oyster *C. gigas* exposed to ibuprofen (Serrano *et al.*, 2015). In particular, the magnitude of *mt20* mRNA induction was not always paralleled by a comparable increase of MTs protein levels in Cd-exposed organisms, suggesting a potential steady state in protein synthesis capability, independently on the rate of gene induction.

 Differences between mRNA levels and enzymatic activities are also observed for antioxidants. The mRNA upregulations often observed in the digestive gland were not reflected in a similar increase of the corresponding enzymatic activities. Such evidence may imply that under stressful conditions a higher mRNA transcription is needed to maintain the physiological catalytic level, since mRNA, proteins and enzymatic activities could be target of post-transcriptional and/or post- translational toxicity (*e.g*. reduced mRNA stability, slower protein synthesis, incorrect folding, cofactor depletion). As a consequence, despite the attempt of the cell to counteract the stressors at transcriptional level, the reduced functional response might limit the capacity to adapt to environmental changes.

 In conclusion, this study provided clear evidences that future ocean temperature and pH can interactively modulate transcriptional responses associated both directly and indirectly to metal- exposure; the observed effects are highly tissue- and season-specific, thus depending on tissue metabolic function and physiological characteristics influenced by seasonal life cycle. Nevertheless, our findings further contribute to the growing awareness on discrepancies between biological responses measured at transcriptional and catalytic level, suggesting a complementary use of these approaches, and confirming that mechanisms underlying the effects of future ocean changes are still to be fully elucidated.

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511 **Table 1 -** Summary of water chemistry parameters and Cd burdens (slightly adapted from Nardi *et al*., 2017,2018b) during experimental exposures

512 in summer and winter. S (salinity), T (temperature), pH_{NBS} (pH calibrated with National Bureau of Standard scale), A_T (total alkalinity), *p*CO₂ (partial

513 pressure of CO₂), Ωc and Ωa (saturation state of respectively calcite and aragonite). Data are presented as means \pm standard deviations.

515
516 516 **Table 2 -** Primer pair sequences, amplicon size, annealing temperatures and accession numbers of

517 genes investigated in quantitative PCR.

522 gland of mussels exposed in summer. Data are given as log₂ of the fold change relative to CTRL treatment (red 523 reference line) \pm SEM (n=6). Asterisks indicate significant differences compared to CTRL treatment, *: *p*<0.05; **: 524 *p*<0.01; ***: *p*<0.001. Cd= Cadmium; A= acidification; W= warming; A-Cd= acidification + Cd; W-Cd= warming 525 + Cd; A-W= acidification + warming; A-W-Cd= acidification + warming + Cd.

530 **Figure 2 -** mRNA levels of *mt-20* (a), *hsp-70* (b), *Cu/Zn-sod* (c), *cat* (d), *gpx1* (e) and *gst-pi* (f) in the digestive gland 531 of mussels exposed in winter. Data are given as log₂ of the fold change relative to CTRL treatment (red reference 532 line) ± SEM (n=6). Asterisks indicate significant differences compared to CTRL treatment, *: *p*<0.05; **: *p*<0.01; 533 *******: p <0.001. Cd= Cadmium; A= acidification; W= warming; A-Cd= acidification + Cd; W Cd= warming + Cd; 534 A-W= acidification + warming; A-W-Cd= acidification + warming + Cd.

538 **Figure 3** – mRNA levels of *mt-20* (a), *hsp-70* (b), *Cu/Zn-sod* (c), *cat* (d), *gpx1* (e) and *gst-pi* (f) in the gills of mussels 539 exposed in summer. Data are given as log_2 of the fold change relative to CTRL treatment (red reference line) \pm SEM 540 (n=6). Asterisks indicate significant differences compared to CTRL treatment, *: *p*<0.05; **: *p*<0.01; ***: *p*<0.001. 541 Cd= Cadmium; A= acidification; W= warming; A-Cd= acidification + Cd; W-Cd= warming + Cd; A-W= 542 acidification + warming; A-W-Cd= acidification + warming + Cd.

546 **Figure 4 -** mRNA levels of *mt-20* (a), *hsp-70* (b), *Cu/Zn-sod* (c), *cat* (d), *gpx1* (e) and *gst-pi* (f) in the gills of 547 mussels exposed in winter. Data are given as log₂ of the fold change relative to CTRL treatment (red reference 548 line) ± SEM (n=6). Asterisks indicate significant differences compared to CTRL treatment, *: *p*<0.05; **: *p*<0.01; 549 ***: p <0.001. Cd= Cadmium; A= acidification; W= warming; A-Cd= acidification + Cd; W-Cd= warming + Cd; 550 A-W= acidification + warming; A-W-Cd= acidification + warming + Cd.

553 Fig. 5 – Non-metric multidimensional scaling (NMDS) for digestive gland (a) and gills (b) of exposed mussels.