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2 Nanofibers: an *in vitro/in vivo* Comparison

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- 17
- 18 Key Words: Carbon nanofibers, Transcriptomics, *in vitro/in vivo* exposure, *Mytilus edulis*19 Hemocytes

20 Abstract

21 Manufactured nanomaterials are an ideal test case of the precautionary principle due to their novelty and potential environmental release. In the context of regulation, it is difficult to 22 implement for manufactured nanomaterials as current testing paradigms identify risk late into the 23 24 production process, slowing down innovation and increasing costs. One proposed concept, namely 25 safe(r)-by-design, is to incorporate risk and hazard assessment into the design process of novel manufactured nanomaterials by identifying risks early. When investigating the manufacturing 26 process for nanomaterials, differences between products will be very similar along key 27 28 physicochemical properties and biological endpoints at the individual level may not be sensitive 29 enough to detect differences whereas lower levels of biological organization may be able to detect 30 these variations. In this sense, the present study used a transcriptomic approach on *Mytilus edulis* hemocytes following an *in vitro* and *in vivo* exposure to three carbon nanofibers created using 31 32 different production methods. Integrative modeling was used to identify if gene expression could 33 be in linked to physicochemical features. The results suggested that gene expression was more strongly associated with the carbon structure of the nanofibers than chemical purity. With respect 34 to the in vitro/in vivo relationship, results suggested an inverse relationship in how the 35 physicochemical impact gene expression. 36

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42 **1. Introduction**

43 The assessment of environmental risk of manufactured nanomaterials (MNMs), or nanomaterials designed for a specific purpose, in the marine environmental is more of a hypothesis 44 than an established risk (Matranga and Corsi, 2012). Ecosystems are also influenced by multiple 45 stressors (e.g. urban and industrial runoff) often from nonpoint sources limiting the ability to prove 46 that MNMs pose significant risks. To assess the potential environmental risk of emerging 47 contaminants, environmental programs, like the European Water Framework Directive (WFD) 48 which follows the precautionary principle, aim to focus on prevention rather than mitigation. In 49 this sense, hazard assessment aims to identify the associated environmental impact with MNMs 50 51 prior to their use and, in some cases, eventual release into the environment (Canesi et al., 2008a). In the context of regulation, it is difficult to implement this approach as current testing paradigms 52 identify risk late into the production process, slowing down innovation and increasing costs. To 53 54 address this, one of the proposed approaches, safe(r)-by-design (SbD), aims to incorporate hazard assessment into the design process of novel MNMs(Schwarz-plaschg et al., 2017). The application 55 of SbD to MNMs was developed in the European FP7 projects NANoREG and Prosafe and is 56 being expanded on in the European Horizon 2020 project NanoReg2. The objectives of an SbD 57 58 approach is to apply the precautionary principle early in the production/innovation process and in this way, hazards and risks can be identified early and strategies to mitigate their effects without 59 placing significant burdens for industry(Kraegeloh et al., 2018). It is important to note however 60 that the aim of SbD is not to completely remove the risk but to find ways to lower the risk without 61 62 hindering the performance of the product.

To adequately implement a SbD approach, rapid and cost-effective techniques need to be 63 developed to quickly screen the potential hazards of products. Testing that focuses on sub-64 individual multi-endpoint responses may provide an ideal starting point for developing a rapid 65 prescreening strategy for MNMs (Moore, 2006). In the context of SbD, MNMs produced by a 66 company are also likely to have minimal differences which may make individual endpoints (e.g. 67 68 growth, mortality...) unsuitable in accurately detecting differences in the potential adverse effects between MNMs. As a result, testing at lower levels (e.g. molecular or biochemical) of biological 69 organization may be more appropriate in discriminating between MNMs that are similar along 70 71 many key physicochemical properties. Due to the rapid rate that new nanomaterials are being produced, as well as legislative and public concerns over the ethics of animal testing promoting 72 the use of the 3 R's (Replacement, Reduction and Refinement), in vitro testing that can be adapted 73 74 to a high throughput screening (HTS) approach can provide a relatively low cost means of screening a large number of chemical in a short amount of time (Barrick et al., 2017). One of the 75 challenges however, is that *in vitro* testing has not been adequately demonstrated to date to be a 76 suitable alternative to *in vivo* testing for marine environmental risk assessment. 77

Transcriptomic tools could be considered as a suitable "HTS approach" for ecotoxicity as it allows for an improved understanding of the molecular mechanisms underlying responses to environmental contaminants and can screen a large number of endpoints in a short amount of time (Snape et al., 2004). However, it is important to note that for marine species there is limited knowledge for genes, limiting the number of available endpoints for testing (Revel et al., 2017). Transcriptomics could also provide knowledge on mode of actions (MoAs) for MNMs and represent a way to predict toxicity before stronger effects occur at higher levels of biological organization (Revel et al., 2017). In the context of integrating ecotoxicological hazards into aSbD
approach, this is could be ideal in discriminating between similar products.

In this sense, the present study implemented a transcriptomic approach through real-time 87 quantitative PCR (qPCR) on a primary cell culture of *M. edulis* hemocytes to measure the 88 89 ecotoxicity of 3 carbon nanofibers (CNFs), GANF, GATam and GANFg, under development by an industrial partner. The objectives of the study were i) to identify the impact of these products 90 on gene expression, ii) identify if the CNFs could be discriminated from one another through gene 91 92 expression, and iii) if *in vitro* testing could be considered a suitable alternative testing strategy. To determine if the *in vitro* exposure could adequately be used as an alternative testing strategy, an *in* 93 94 vivo exposure was also conducted for comparison. The aim was not to have equivalent values between *in vitro* and *in vivo* testing but to determine if both testing strategies developed the same 95 conclusions. After a 24-hour exposure, expression levels of a battery of genes implicated in 96 97 xenobiotic transport/transformation, oxidative stress, metabolic activity, cell transport, cytoskeleton and cell cycle control were investigated. These endpoints were selected have been 98 used previously in to investigate the effects of nanomaterials on gene expression in M. edulis 99 (Châtel et al., 2018). The 24-hour exposure was selected as previous studies have shown this to be 100 101 the optimal duration to maintain *Mytilus* hemocytes in cell culture and previous study have shown hemocytes, in vitro and in vivo, to respond to MNMs during this time period (Barrick et al., 2018; 102 Canesi et al., 2008b; Gagné et al., 2008; Katsumiti et al., 2014). 103

104 2. Material and Methods

105 2.1 Nanomaterials used in the study

106 Three CNFs (GANF, GATam and GANFg) were provided by Grupo Antolin. The 107 CNFsare an industrial grade product for commercial use in automobile parts. Grupo Antolin initially produced GANF through catalytic vapor deposition (CVD) using a natural gas and sulfur 108 109 feed stock at temperatures greater than 1100°C in a floating catalyst reactor (Vera-Agullo et al., 2007; Weisenberger et al., 2009). Deposition of graphene layers is promoted by metallic nickel 110 while catalytically inactive NiS allows for the formation of helical-ribbons with a stacked cup 111 structure. To scale up production, a new method was developed to produce higher volumes of 112 CNFs. This is the process used to create GATam, which has slight differences in physicochemical 113 properties when compared to GANF. GANFg CNFs are created by super heating GANF at 114 2500°C, which decreases the interlayer spacing in the CNF and removes Nickel and Sulfur 115 impurities (Weisenberger et al., 2009). Physicochemical differences measured by Grupo Antolin 116 117 are summarized in table 1.

118 2.2 Preparation and characterization of nanomaterials

Nanomaterial suspensions were prepared following the NANoREG Standard Operating
Procedure (SOP) (Jensen et al., 2011). Briefly, 15.36mg of nanomaterial powder was measured
into a 20mL Scint-Burk glass vial (WHEA989581; Wheaton Industries Inc.) which is prewet with
30µL of absolute ethanol. The volume was adjusted to 6mL with 0.05% Bovine Serum Albumin
(BSA)-water (w/v) to achieve a final concentration of 2.56mg/mL. The suspension was then placed
in an ice-water bath solution and sonicated using a Branson-S450 sonicator at 10% amplitude for
16 minutes. The suspension was left on ice for 10 minutes prior to use.

To characterize the ENM behavior, suspensions were diluted to 25.6mg/L in BSA stock
suspension, cell culture media and in 30 p.s.u. (practical salt units) of artificial sea water (ASW),

Tropic Marine, in 20mL Scint-Burk glass vials and maintained at test conditions. This concentration was selected as it was found to achieve reliable results. Dynamic light scattering (DLS) and zeta potential (Malvern ZS90) was measured at 0, 2, 4, 6 and 24 hours for each suspension to characterize the behavior of the nanomaterials over the duration of the experiment. Due to high ionic strength, zeta potential could not reliably be measured in cell culture media and ASW.

Transmission Electron Microscopy (TEM) was also used for each suspension to 134 characterize the relative particle sizes of the ENMs. TEM (JEOL JEM 1400 plus @120kV, Japan) 135 was used to visualize morphology of CNFs in the stock suspensions, culture media and artificial 136 sea water. Carbon-coated grids were hydrophilized using a glow discharge apparatus (K100X, 137 Emitech, UK). The glow discharge was performed for 180 s at an air pressure of 10⁻¹ mbar and an 138 electric current of 40 mA. This treatment was applied to TEM grids prior to the suspension 139 140 deposition as it prevents most of the artefactual agglomeration phenomenon during the drying of the suspensions on the TEM grids (Dubochet et al., 1982). 141

CNFs suspensions were also analyzed using a Tecan Sunrise spectrometer to measure 142 optical density as an approximation of stability over the duration of the experiment. Each 143 suspension was measured across the visible light wavelength to determine which wavelength 144 yielded the highest value. It was identified that a 340nm wavelength yielded the highest 145 absorbance values for all three CNFS. 60µL of suspension was taken from the surface of the 146 liquids and triplicates were measured using a 96-well plate for all time points. The results were 147 then normalized using a blank for each media suspension and values at each time point were 148 149 adjusted relative to the start of the experiment.

Raman spectroscopy was performed using a confocal Jobin Yvon LABRAM HR800 spectrometer (red laser at 633 nm) using a maximum power of 5 mW with a spot size of*ca*. 1 µm. Ten accumulations of 5s were acquired. Irradiation of the samples started 30s before acquisition to limit the possible interference with fluorescence. 5 spectrums were obtained in 5 different areas of each sample.

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2.3 Hemocyte collection and establishment of primary cell culture

M. edulis individuals of the same size $(4.2 \pm 0.23 \text{ cm})$ were collected from a relatively clean sight, Saint-Cast-le-Guildo $(48^{\circ}37'48''N \ 2^{\circ}15'24''W)$, previously identified as suitable for experimental research (Chevé et al., 2014). Sampling was conducted in late fall to avoid the reproductive period, which would potentially influence results. Mussels were placed in artificial sea water (30 psu, at 15°C with a 12-hour light/day cycle) for a 2-day acclimation period prior to testing.

A primary cell culture on *M. edulis* hemocytes was established following the methodology described in (Barrick et al., 2018). A 23-guage, 2mL syringe containing 0.1mL of Alseve (ALS) buffer (20.8 g.L⁻¹ glucose, 8 g.L⁻¹ sodium citrate, 3.36 g.L⁻¹ EDTA, 22.5 g.L⁻¹NaCl, pH 7.0) was used to extract the hemolymph (Cao et al., 2003). After aspirating hemolymph from 5 organisms, the needle was removed from the syringe and the contents were filtered through a 70 μ m filter into a falcon tube maintained at 4°C. After extracting hemolymph from 40 mussels the total volume was recorded.

170 Cell viability and cell concentration was then recorded through trypan blue exclusion.
171 Hemocyte concentration was diluted to 1x10⁶cells.mL⁻¹ using the ALS solution. 200µL of

hemolymph was then seeded into a 96-well microplate (2x10⁵ cells/well). The plate was then
placed into an incubator at 18°C for 30 minutes, 3.5% CO₂. After 30 minutes, hemolymph was
aspirated and replaced with adjusted Leibovitz L-15 medium (20.2 g.L⁻¹NaCl, 0.54 g.L⁻¹KCl, 0.6
g.L⁻¹ CaCl₂, 1 g.L⁻¹ MgSO₄, 3.9 g.L⁻¹ MgCl₂, 100 units.mL⁻¹ penicillin G, 100µg.mL⁻¹
streptomycin, 1% gentamycin, 10% glucose and 10% Fetal Bovine Serum (FBS), pH 7.0). Cells
were left to adhere overnight prior to exposure.

178 2.4 In vitro exposure

Cell quality and attachment was visually confirmed the next day prior to ENM exposure 179 using an inverted confocal microscope. Cell culture media was then refreshed with cell culture 180 media containing ENMs in suspension (0.01, 0.1 and 1mg.L⁻¹) with three replicates per test 181 concentration. These concentrations were selected as they are within the range of previous test 182 concentrations used with Mytilus hemocytes(Canesi et al., 2008b). The cell culture was then 183 returned to the incubator for 24 hours. After 24 hours, the media was removed and the cells were 184 185 washed twice with PBS (1,100mOSM). 50µL of trypsin was then added for to each well to detach the cells. After 5 minutes, detachment was confirmed using an inverted confocal microscope after 186 gently mixing the solution with a 20μ L pipette. 150μ L of cell culture media containing 10% FBS 187 was then added to arrest trypsin activity. The cells were then collected in an Eppendorf tube and 188 centrifuged at 500g for 5 minutes at 4°C to pellet the cells. Cell culture media was removed and 189 the cells were washed with PBS (1,100mOsm). This step was repeated twice, after which the cell 190 pellet was stored at -80°C prior to analysis. 191

192 2.5 In vivo exposure

193 60 Mussels were placed in four 12L aquariums (1.25 mussels.L⁻¹) and maintained in the same 194 conditions as the acclimation period. ENMs were spiked once into each aquarium at the three test 195 concentrations (0.01, 0.1 and 1mg.L^{-1}) with 15 organisms per test concentration. Organisms were 196 exposed for 24 hours, unfed and oxygenated using a glass Pasteur pipette, after which hemolymph 197 was pooled for each test concentration following the previously described method.

198 **2.6 qPCR** assay

199 2.6.1 RNA extraction

200 RNA extraction was conducted using a previously defined protocol (Châtel et al., 2018). Briefly, the hemocytes were ground in TRIzol Reagent® (Ref: 15596026, Invitrogen TM) 1ml per 201 202 100 mg of cells. Centrifugation (12000g for 10 minutes at 4°C) was then used to suppress cellular debris. 0.2 mL Chloroform per 1mL of TRIzol was added to the supernatant and shaken vigorously 203 204 prior to centrifugation (12000 g for 15 minutes at 4°C) to ensure a phase separation with the clear 205 upper aqueous phase, containing RNA, being collected. 0.5 mL of isopropanol per ml of TRIzol 206 Reagent[®] was then added and the solution was incubated for 10 minutes at room temperature, to 207 precipitate the RNA. Centrifugation (12000g for 10 minutes at 4°C) was then used to the pellet RNA. The pellet was washed with 200µL of absolute ethanol and the RNA was then pellet again 208 through centrifugation (12000g for 5 minutes at 4°C). The ethanol was then evaporated and the 209 210 pellet was allowed to completely dry under a flow hood before adding 10µL of Diethyl pyrocarbonate (DEPC) water. 211

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2.6.2 Determination of total RNA and preparation of cDNA

Determination of total RNA of each extraction was carried out with a Nanodrop using 1µL
of RNA per sample (Thermo Scientific ™ NanoDrop 2000). First strand cDNA synthesis was

215	conducted	using (0.2 μg	of RNA	extractand	was	mixed	with	oligo-dT	primers	following	the
216	SuperScrip	ot TM III	First-S	trand Sy	nthesis Supe	rMix	protoc	ol sup	plied by I	nvitrogei	n TM .	

217 *2.6.3 qRT-PCR analysis*

cDNA amplification was performed using a LightCycler 480 Real Time PCR system
(Biorad) using SYBR Green Power Master Mix (Invitrogen) with specific primer pairs (see
supplemental material). Thermocycling was conducted using polymerase activation at 94°C for 2
minutes with an amplification and quantification cycle repeated for 50 cycles (94°C for 30 seconds,
58°C for 30 seconds, 72°C 30 seconds). The cq (Threshold cycle) values were recorded for analysis
using actin as a housekeeper gene. Each gene was analyzed in triplicate.

224 2.6.4 Statistical analysis and modelling

225 Statistical Analysis was conducted using "R Studio 3.3.1" (R Studio Team, 2015). The 226 measured values were compared among the different groups using nonparametric analysis through 227 Kruskall-Wallis and Dunn's analysis (R package dunn.test) with a P<0.05 indicating statistical 228 significance. P-values were then corrected using false discovery rate (fdr) using the R-package 229 hmisc. To create an integrative analysis, partial least square discriminant analysis (PLS-DA) was 230 used to determine if test conditions could be discriminated from the control(Bertrand et al., 2017; Cho et al., 2008). PLS-DA was selected as it has good performance when dealing with multi-231 collinear data with small samples and many variables (genes). ENMs and test condition (in vitro 232 233 or *in vivo*) were analyzed separately to identify which genes were significantly impacted by the exposure conditions used. Variable Importance on Projection (VIP) was scored to identify which 234 235 genes were most important in group discrimination (Jaumot et al., 2015). For each CNF, both in vitro and in vivo exposures were plotted together. For each test condition, a correlation circle was 236

plotted on the factorial plane combining the first two axes of the PLS-DA model. Vectors of the
correlation circle represent the variables (genes) used to generate the model. Vectors describe the
relationships between the genes and each of the axes.

To identify if production process influenced ecotoxicity, results were analyzed to 240 241 determine if product features could be linked to gene expression. As the CNF products were similar in all aspects except for small differences due to the production process, the focus of the 242 analysis was to determine if these differences could be linked to gene expression results. Two 243 analyses of correlation were conducted to *i*)determine if gene expression could be correlated with 244 the I_D/I_G-band ratio from Raman spectroscopy and *ii*)determine if there is a relationship between 245 the reported purity of the CNFs. To achieve this, foreach test condition (in vitro or in vivo) results 246 were separated based on test concentration (0.01, 0.1 and 1 mg. L^{-1}). Using these groups, Pearson's 247 correlation coefficient was used to define their relationship between I_D/I_G ratio and chemical purity 248 249 with gene expressions. Each gene was analyzed at each test concentration to determine statistical significance using at P < 0.05. 250

251

252 **3.** <u>Results</u>

253 3.1 Physicochemical characterization

TEM results indicated that aggregation/agglomeration occurred in all media but no clear differences between suspensions could be identified (Figures 1a-i). TEM results for ASW media were difficult to analyze due to deposition of salt during the grid preparation. Raman spectroscopy results indicated that the ratio between the Dband and Gband (I_D/I_G) could be used to discriminate between the CNFs. GANF had a higher I_D/I_G -band ratio (1.26) than GATam (1.07) and

GANFg(0.78) indicating that GANF has the highest number of structural defects and GANFg hasthe lowest number of structural defects (Figure 2a-c).

All suspensions could be analyzed through DLS with results being considered good quality 261 (Table 2). Stock suspensions for GANF (489.3 d-nm), GATam (414.3 d-nm) and GANFg (479.8 262 d-nm) were all comparable in the size of agglomerates. When prepared in culture media, GANF 263 (260.1 d-nm), GATam (197.8 d-nm), and GANFg (244.1 d-nm) were still comparable in e but 264 agglomerate sizes were notably smaller than the stock suspensions. This was also observed in 265 ASW where GANF (186.7 d-nm), GATam (223 d-nm) and GANFg (217.4 d-nm) agglomerates 266 were smaller in size when compared to the stock media but were similar in size to the 267 268 measurements obtained in the cell culture media. The size of agglomerates after 24 hours were similar to the start of the experiment for all test media. 269

The optical density measured in the stock suspension suggested that CNFs remaining in suspension were similar between GANF (11.5%) and GATam (17.62%) in the stock suspensions whereas GANFg was higher (47.72%), suggesting more CNFs remained in suspension (Figure 3). Optical density in cell culture media for GANF (47.88%), GATam (86.34%) and GANFg (89.80%) was notably increased when compared to the stock suspension. For suspensions prepared in ASW, GANF (40.67%) and GATam (77.79%) where similar in optical density to the cell culture media. GANFg (40.67%) had lower optical density in ASW.

277 *3.2 Gene expression Analysis*

278 *3.2.1 in vivo*

279	Mussels exposed to the CNFs showed limited statistical significant between the control
280	and the test concentrations for many of the genes suggesting little effects when exposed to the
281	CNFs (Table 3). Histograms associated with the results can be found in the supplemental material.
282	3.2.1.1 Oxidative stress/detoxification
283	SOD mRNA levels were not significantly impacted. Catalase gene was significantly
284	increased when exposed to GANF (0.01 and 1 mg.L ⁻¹) and GATam (0.01mg/L) HSP70 was also
285	not significantly increased when exposed to GANF (0.01 mg.L ⁻¹). GST was significantly increased
286	by GATam (1mg.L ⁻¹). Cytochrome P450 was significantly MT was significantly increased when
287	exposed to GANFg (0.1 and 1mg.L ⁻¹).

288 *3.2.1.2Cytoskeleton, Cell metabolism &Cell Cycle Control*

B-tub was not significantly impacted. MRP was significantly decreased by GATam (0.01 and 1mg.L⁻¹) and GANFg (1mg.L⁻¹). Na/K ATPase was not significantly impacted. P53 was significantly decreased by GANF (0.01 and 1mg.L⁻¹). Lysozyme gene expression was not significantly impacted.

293 *3.2.2in vitro*

Mussels exposed to the CNFs showed statistical significance with the *in vitro* exposure to all three CNFs with more significant effects occurring than with the *in vivo* exposure (Table 4). Histograms associated with the results can be found in the supplemental material.

297 3.2.2.1 Oxidative stress/detoxification

SOD mRNA levels were significantly decreased when mussels were exposed to GANF (1mg.L^{-1}) , GATam (0.01 and 0.1 mg.L⁻¹) and GANFg (0.01 and 0.1 mg.L⁻¹). Catalase gene had no

significant effects. HSP70 was also significantly increase for GANF (0.01 and 1mg.L⁻¹), GATAM (0.1 and 1mg.L⁻¹) and GANFg (0.01 and 1mg.L⁻¹). GST was significantly increased by GANF (0.1 and 1mg.-1L), GATam (0.1mg.L⁻¹) and GANFg (0.01 and 1 mg.L⁻¹). Cytochrome P450 was not statistically significant. MT was significantly increased when exposed to GANF (0.1 and 1mg.L⁻¹), GATAM (1mg.L⁻¹) and GANFg (0.01 and 1mg.L⁻¹).

305 *3.2.2.2 Cytoskeleton, Cell metabolism &Cell Cycle Control*

B-tub was significantly decreased when exposed to GANF (0.1 and 1mg.L⁻¹), GATam (0.01 and 0.1mg.L⁻¹) and GANFg (1mg.L⁻¹). PgP was only significantly affected by GANF (1mg.L⁻¹). MRP was only affected by GATam (0.01mg.L⁻¹). Na/K ATPase was only significantly affected by GANF (0.1 and 1mg.L⁻¹) and GATam (0.1 and 1 mg.L⁻¹). P53 was significantly increased by GATam (0.01mg.L⁻¹). ATP synthase was significantly increased by GATam (1mg.L⁻¹) 1) and significant decreased by GANFg(0.01 and 1 mg.L⁻¹). Lysozyme gene expression was not significantly impacted.

313 *3.3 PLS-DA analysis*

VIP values were identified for all 6 conditions and summarized in the table 5. When analyzing the *in vivo* and *in vitro* exposure conditions most of the genes were identified as important in describing variation between test conditions (>0.8). Of the genes used, consistently high VIP values were found with ATP synthase, P53, metallothionein, lysozyme, catalase and superoxide dismutase indicating these genes were essential in discriminating between test concentrations. The results of the model were then plotted on a factorial plane describing the relationship between genes (Figure 4). This was then used to plot the test conditions of each CNF with their orientation dependent on which genes more effectively described the test condition(Figure 5).

PLS-DA analysis for GANF in vivo showed that 0.01mg.L⁻¹ and 1mg.L⁻¹ test 323 concentrations were be discriminated from the control and showed a high degree of separation 324 (Figure 5A). 0.1 mg.L⁻¹could be discriminated from the control but was similar in gene expression. 325 When analyzing the PLS-DA model for GANF in vitro results showed that all three test 326 concentrations could be discriminated from the control and showed a high degree of separation 327 between concentrations. 0.01 and 0.1 mg.L⁻¹exposure times were similar in response. For both *in* 328 *vivo* and *in vitro* results the 1mg.L⁻¹ test concentration was clearly separated. 329 The PLS-DA model for GATam *in vivo* results also showed discrimination from the control 330 at 0.01, 0.1mg.L⁻¹ and at 1mg.L⁻¹ (Figure 5B). This pattern was observed as well for the *in vitro* 331 test condition but little similarities were observed between the two test conditions. 332 The PLS-DA model GANFg in vivo had a clear separation of the test concentrations from 333

the control (Figure 5C). GANFg *in vitro* showed clear separation from the control for all three test concentrations and 0.01mg.L⁻¹ and 1mg.L⁻¹exposure conditions were similar in response.

336 *3.4 Correlating CNF form with gene expression*

To determine if relationships between gene expression and differences in the CNF production process could be established Pearson's correlation coefficient and CNF structural purity (as measured through Raman spectrometry) was used. Positive correlations would indicate that as the I_D/I_G -band ratio increases, gene expression increases where as a negative correlation would result in an inverse interpretation. Significant positive correlations in the relationship between gene expression and CNF purity would imply that as purity increases, gene expression
increases. A negative correlation would suggest that as purity decreases, gene expression increases.

When test concentrations were controlled for strong correlations between gene expression 344 and I_D/I_G -band ratio could be identified (Table 6). For the *in vivo* exposure there were clear 345 346 differences with test concentration and relationship I_D/I_G-band ratio. At a concentration of 0.01 mg.L⁻¹ HSP70, GST, SOD, ATP synthase and B-tubulin gene expressions had strong positive 347 correlations with the I_D/I_G -band ratio where at a dose of 0.1 mg.L⁻¹ only MRP gene had a significant 348 correlation. For mussels exposed to 1mg.L⁻¹, metallothionein, lysozyme, PgP, ATP synthase, P53 349 350 and MRP gene expression levels had all positive correlations. However, mussels exposed in vitro to 0.01mg.L⁻¹, showed that HSP70, GST, metallothionein and ATP synthase mRNA levels had 351 significant negative correlations with the I_D/I_G-band ratio where Na/K ATPase and MRP genes 352 had significant positive correlations. At a concentration of 0.1 mg.L⁻¹, SOD, lysozyme, PgP and 353 354 cytochromeP450 gene expression levels had negative correlations and GST, Na/K ATPase and P53 genes had positive correlations. At a concentration of 1mg.L⁻¹, SOD, lysozyme, 355 cytochromeP450 and ATP synthase mRNA levels had strong positive correlations. 356

When determining the relationship between gene expression and CNF chemical purity (as 357 reported in Table 1), there were some significant relationships were identified but there were less 358 correlations than when comparing gene expression to the D/G band ratio (Table 7). When looking 359 at the *in vivo* exposure condition, β-tubulin, Na/K ATPase and P53 genes had significant negative 360 correlations with purity of the CNF at 0.01 mg.L⁻¹. At 0.1 mg.L⁻¹ exposure condition, HSP70, 361 GST, SOD, β-tubulin and MRP mRNA expressions depicted significant negative correlations with 362 purity whereas catalase gene had a significant positive relationship. At 1mg.L⁻¹, only MRP showed 363 a significant negative correlation to the purity. For the in vitro exposure condition, PgP, 364

365 cytochromeP450 and Na/K ATPase mRNA levels had negative correlations whereas GST and P53
 366 genes had positive correlations. At 1mg.L⁻¹, HSP70 and Na/K ATPase expressions had significant
 367 negative relationships whereas GST and PgP mRNA levels had significant positive relationships
 368 with purity of CNF.

369

370 **4. Discussion**

The aim of the study was to investigate whether or not differences in the production process of CNFs would alter gene expression profiles as well as to establish an *in vitro/in vivo* comparison. In this sense, the first objective was to establish if the three CNFs have similar physicochemical and to determine differences between *in vitro* and *in vivo* stability and hydrodynamic diameters.

375 *4.1 Physico-chemical characterization*

To maintain a relevant comparison between the 3 CNFs, the physico-chemical properties 376 of the CNFs in suspensions need to be accounted for. In this sense, DLS is a commonly used 377 technique for measuring ENMs in suspension but it is limited in the sense that it assumes a 378 spherical shape for the particles. In the context of CNFs this does not hold true for the single fibers, 379 but agglomerates can be approximated as ovoid and the size of the particles can be approximated 380 (Reinert et al., 2015). The DLS results suggest that particle sizes are comparable between CNFs as 381 well as between *in vitro* and *in vivo* assays. In addition to this, the optical density results suggest 382 383 that the test suspensions are somewhat stable with slight differences between *in vitro* and *in vitro* test media for GATam and GANF. As a result, the CNFs used in the study can be considered to 384 have similar physico-chemical properties between the two testing strategies, facilitating an in 385

vitro/in vivo comparison. It is however important note that differences between the media may
lead to differences in sedimentation and effectively change the dosimetry.

Another interesting observation is that the CNFs displayed poor stability in ultra-pure water whereas in both culture media and ASW the stability was improved. One potential explanation for this observation is that the ionic strength of these suspensions decreased the surface potential of the CNFs, reducing rate at which particles interact with other another (Pavlin and Bregar, 2012). This is interesting as it would imply that the behavior of the CNFs in the ocean will be different than the behavior in fresh water ecosystem, which can lead to distinct differences in toxicity profiles.

Of the methods used to characterize the CNFs in the present study, only Raman 395 396 spectroscopy demonstrated clear differences between the CNFs. The comparison of the Raman spectra of the 3 samples illustrates the influence of the annealing treatment with a clear 397 improvement of the I_D/I_G intensity ratio, decreasing from 1.3 (Fig. 2(a)) to 0.8 (Fig. 2(c)) and 398 399 evidencing a significant improvement of the structure of the carbon network, also visible with the increased intensity of the 2D band (2650 cm-1). Sample GATam (Fig. 2(b)) lies in between with 400 401 an intermediate value of the I_D/I_G intensity ratio of 1.1 but a noisier spectrum, although all data were acquired exactly in the same experimental conditions. All 3 samples exhibited some 402 403 fluorescence leading to an important background signal. For this reason, irradiation of the samples started 30s before acquisition to limit this phenomenon. It is important to note that Raman 404 spectroscopy does not allow a direct measurement of the chemical purity of the samples but more 405 of the level of structural defects (Ivanova et al., 2012). In the context of SbD and the case study 406 407 this is important because the structural quality of the CNFs may impact the performance of the products and GATam may be a more desirable product than GANF as a result. In the context of 408

409 ecotoxicological hazards structural defects can lead to the functionalization of CNFs, providing410 favorable binding sites for ions or molecules, which can lead to differences in hazard profiles.

411 *4.2 Gene expression*

The endpoints used in the present study provides broad spectrum response analysis of 412 413 hemocyte gene expression to CNF exposure, which allows for characterization of mechanisms of 414 action. To the authors' best knowledge, this is the first time that carbon nanofibers have been investigated for ecotoxicological effects on mussels. As a result, there are limited examples that 415 could be considered a suitable comparison. Of the information available mussel hemocytes, 416 exposed *in vitro* and *in vivo* for 24 hours, have been shown to display sublethal responses to carbon 417 black and fullerene (0.01-1mg.L⁻¹) with little to no effects when exposed to a carbon nanotube 418 (0.01-1mg.L⁻¹) (Canesi et al., 2010, 2008b; Moore et al., 2009). Previous studies in human 419 toxicology have shown induction of oxidative stress and inflammation when cells, IL-8, A549 and 420 HaCaT, were exposed to multi-walled carbon nanotubes at 1mg/L and 25mg.L⁻¹ for 24 hours 421 422 (Vitkina et al., 2016; Ye et al., 2009). When analyzing the *in vivo* responses, the gene expression had little significant effects (which may be attributed to the small sample sizes) with all three CNFs 423 424 and little clear pattern is evident with the CNFs. There is a however a notable trend for GATam to have higher fold expressions which could suggest more adverse effects may occur with this CNF. 425

When looking at the *in vitro* exposure however, hemocytes showed more significant effects when compared to the *in vivo* exposure for all CNFs with many of the gene response associated with oxidative and xenobiotic stress. This can be attributed to the simpler exposure scenario for the *in vitro* exposure as the cells are directly exposed to the CNFs. When looking at the results for approximated stability, GANF showed the least stability of the three CNFs in culture media. This

431 observation could suggest that due to the a sedimentation effect the effective dosage for GANF is higher than the other two CNFs (Deloid et al., 2017; Hinderliter et al., 2010). This could also 432 suggest that these CNFs are aggregating at the bottom of the well and not interacting with the cells, 433 which can complicate the comparison between the three CNFs. Looking at the gene expression 434 holistically more significant effects occur with GANFg at 0.01mg.L⁻¹ which could suggest this 435 product is more hazardous. The results of the *in vitro* approach may suggest that all three CNFs 436 could potentially cause oxidative and xenobiotic stress, which is not in agreement with the in vivo 437 approach. It is also important to note that the cell culture is a complex media consisting of a mixture 438 439 of proteins, which can lead to protein corona that does not occur naturally. As a result, further analysis of dosimetry may be necessary when applying an *in vitro* approach for SbD in order to 440 demonstrate it is an accurate predictor of in vivo effects. 441

442 *4.3 PLS-DA analysis*

The integrative analysis through PLS-DA showed some unexpected results in that almost 443 444 all of the genes were important in the discrimination between test concentrations for all the CNFs and for both *in vivo* and *in vitro* test conditions, highlighting its sensitivity in identifying sublethal 445 effects. Of these genes however, ATP synthase, P53, metallothionein, PgP and HSP70 were 446 identified as the most important discriminators for almost all test conditions. This suggests that 447 exposure to the CNFs is influencing a wide array of cellular functions (oxidative stress, 448 detoxification, cytoskeleton, cellular metabolism and cell cycle control) which can alter cell 449 functioning and potentially cascade into higher levels of biological organization. When comparing 450 the VIP values *in vivo* to *in vitro* it became apparent that in general there were some similarities in 451 452 the values between the two testing conditions. However, when analyzing the correlation circles the relationship between genes was not consistent between the *in vitro* and *in vivo* exposures. The *in* 453

454 *vivo/in vitro* relationship is a challenge to many investigators as gene responses are often not
455 consistent between the two testing strategies (Heise et al., 2012).

456 *4.4 Correlation CNF properties to Gene expression*

In the context of applying ecotoxicology to a SbD for MNMs, there needs to be an 457 458 identification of what features of MNMs cause toxicity. The CNFs used in the present study 459 provide an ideal case study for the application of SbD as the products are very similar which allow for an analysis on how the differences in production influence ecotoxicity. In this sense, structural 460 purity, measured through the I_D/I_G-band ratio, and overall purity were identified as potential 461 discriminators between the CNFs. Of these two measurements, the relationship between the I_D/I_G-462 band ratio proved to be more strongly correlated with gene expression than chemical purity of 463 464 CNF. In vivo, all the genes showed a positive correlation with the I_D/I_G -band ratio indicating that gene expression increased with structural impurities. With the *in vitro* results however, the inverse 465 466 is observed in the fact that gene expression was more strongly correlated with a decrease in the 467 I_D/I_G-band ratio. A previous study investigating the physicochemical relationship between toxicity and MWNCT was able to demonstrate that the presence of proteins profoundly affects their 468 469 behavior in media and could alter their toxicity as a result, which may explain the difference in interpretation(Allegri et al., 2016). The relationship between test media properties and CNFs 470 behavior requires further investigation, in particular the role of a protein corona in gene expression. 471 472 This does however provide insight that could be useful in linking ecotoxicity results in a way that can promote SbD strategies. 473

474

475 **5.** Conclusion

476 Transcriptomic is a promising emerging tool to implement ecotoxicology into a SbD approach for MNMs. The results in the present study demonstrate a way in which gene expression 477 can be used to provide information to improve the safety of MNM products. In the context of the 478 479 current study the *in vitro* and *in vivo* tests were not consistent in their interpretation of which CNF was "least safe", suggesting that in vitro and in vivo strategies need to be investigated in parallel 480 to verify that an *in vitro* approach using *M. edulis* hemocytes is a suitable alternative testing 481 strategy. It is however important to note that while in vitro/in vivo extrapolation remains a 482 challenge requiring additional research, the application of ecotoxicology in SbD may require the 483 484 use of *in vitro* testing to adequately screen products produced by industry in a cost effective and timely manner. 485

486

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Measured property	Unit	GANF	GANFg	GATam
Fiber diameter (TEM)	nm	20-80	20-80	20-80
Carbon purity (TGA)	%	>85	>99	>80
Apparent density	g/cc	~0.06	~0.08	~0.08
Specific surface area (BET N ₂)	m²/g	100- 170	70-90	70-140
Graphitization degree (XRD)	%	≈70	≈90	≈60
Electrical resistivity	Ω-*m	1*10 ⁻³	1*10 ⁻⁴	1*10 ⁻³

Table 1: Physico-chemical properties reported by the industrial partner

Start of Experiment											
		Gant	f		Gatar	n	Ganfg				
	Z-average (d-nm)	Pdl	Zeta potential (mV)	Z-average (d-nm)	Pdl	Zeta potential (mV)	Z-average (d-nm)	Pdl	Zeta potential (mV)		
Stock Suspension	489.3	0.128	-10.1	414.3	0.231	-13.8	479.8	0.178	-15.6		
M. edulis Culture Media	260.1	0.359	-	197.8	0.272	-	244.1	0.325	-		
Artificial Sea Water	186.7	0.306	-	223 0.311 -		217.4	0.307	-			
				End of Experimen	t						
		Gant	f		Gatam GANFg						
	Z-average (d-nm)	Pdl	Zeta potential (mV)	Z-average (d-nm)	Pdl	Zeta potential (mV)	Z-average (d-nm)	Pdl	Zeta potential (mV)		
Stock Suspension	527.5	0.123	-15.9	389.4	0.164	-13	441.2	0.285	-14.8		
M. edulis Culture Media	221.4	0.32	-	164.3	0.23	-	237.2	0.226	-		
Artificial Sea Water	278.3	0.418	-	220.5	0.348	-	348.1	0.77	-		

Table 2: DLS results measured in stock suspension, cell culture media and ASW at the start of the experiment and at the end. Zeta potential was only able to measured in the stock suspensions due to the high ionic strengths in the test media.

Statistical Significance in gene expression: in vivo											
		GANF			GATam		GANFg				
	0.01 mg/L	0.1 mg/L	1 mg/L	0.01 mg/L	0.1 mg/L	1 mg/L	0.01 mg/L	0.1 mg/L	1 mg/L		
Cat	0.01	0.09	0.05	0.04	0.37	0.5	0.15	0.15	0.15		
HSP70	0.13	0.13	0.5	0.06	0.15	0.15	0.15	0.15	0.06		
GST	0.29	0.29	0.29	0.19	0.46	0.03	0.06	0.13	0.13		
SOD	0.11	0.11	0.45	0.13	0.15	0.13	0.33	0.23	0.08		
МТ	0.37	0.37	0.06	0.15	0.06	0.15	0.01	0.03	0.1541		
P53	0.15	0.15	0.06	0.15	0.06	0.15	0.01	0.15	0.01		

PgP	0.01	0.33	0.16	0.21	0.05	0.19	0.11	0.41	0.01
CP450	0.05	0.5	0.5	0.37	0.32	0.32	0.29	0.29	0.06
Asyn	0.03	0.15	0.01	0.15	0.06	0.15	0.01	0.07	0.07
Lys	0.33	0.33	0.33	0.15	0.06	0.15	0.16	0.29	0.04
Na.K	0.08	0.25	0.23	0.15	0.06	0.15	0.15	0.15	0.13
MRP	0.43	0.45	0.43	0.04	0.41	0.04	0.41	0.32	0.03
Btub	0.15	0.06	0.02	0.15	0.06	0.015	0.15	0.15	0.06

 Table 3: P-values, measured through Kruskall-Wallis and Dunn, of *M. edulis* hemocytes exposed *in vivo*.

 Stars indicate p-values <0.05 with + indicating a up regulation and – indicating down regulation.</td>

Statistical Significant in gene expression: in vitro										
	GANF				GATam			GANFg		
	0.01 mg/L	0.1 mg/L	1 mg/L	0.01 mg/L	0.1 mg/L	1 mg/L	0.01 mg/L	0.1 mg/L	1 mg/L	
Cat	+0.37	+0.37	+0.37	0.27	0.323	0.17	0.21	0.21	0.21	
HSP70	-0.03*	-0.15	-0.03*	0.15	0.03*	0.01*	0.01*	0.13	0.01*	
GST	-0.15	-0.03	-0.01*	0.15	0.01*	0.10	0.01*	0.15	0.01*	
SOD	-0.09	-0.07	-0.01*	0.01*	0.02*	0.15	0.01*	0.01*	0.15	
MT	-0.15	-0.03*	-0.01*	0.06	0.06	0.01*	0.04*	0.13	0.01*	
Lys	0.06	0.15	0.15	0.16	0.29	0.04	0.15	0.15	0.08	
PgP	+0.33	+0.33	+0.03*	0.21	0.08	0.19	0.06	0.15	0.15	
СР450	-0.33	+0.16	-0.16	0.11	0.11	0.25	0.29	0.19	0.19	
Asyn	+0.13	+0.13	+0.13	0.09	0.21	0.01*	0.01*	0.15	0.03*	
Btub	-0.11	-0.05*	-0.01*	0.01*	0.02*	0.15	0.07	0.07	0.01*	
Na.K	-0.15	-0.03*	-0.01*	0.15	0.02*	0.01*	0.15	0.15	0.08	
P53	+0.13	+0.13	-0.15	0.01	0.07	0.37	0.06	0.15	0.15	

MRP	+0.33	-0.16	+0.16	0.33	0.16	0.16	0.04*	0.16	0.29

Table 4: P-values, measured through Kruskall-Wallis and Dunn, of *M. edulis* hemocytes exposed in vitro.

Stars indicate p-values <0.05 with + indicating a up regulation and – indicating down regulation.

VIP Values									
	GAtam	GAtam	GANFg	GANFg	GANF	GANF			
	(in vivo)	(in vitro)	(in vivo)	(in vitro)	(in vitro)	(in vivo)			
Asyn	1.06	0.97	1.34	0.94	0.95	1.43			
P53	1.05	1.13	1.34	1.14	0.97	1.3			
MT	1.09	1	1.4	1.02	0.89	1.28			
PgP	1.16	1.01	0.93	1.02	0.67	1.06			
HSP70	0.94	1.01	1.08	0.92	0.94	1.03			
B.Tub	0.92	1.17	0.93	0.98	0.96	1.03			
SOD	0.82	1.16	0.84	1.49	0.97	0.98			
Na.K	0.97	1.01	0.84	0.51	0.87	0.98			
Cat	1.39	0.72	0.33	0.82	0.28	0.92			
CP450	0.78	0.88	0.62	1.16	0.61	0.9			
Lys	1.3	0.96	0.82	1.06	1.8	0.6			
GST	0.65	1.07	0.85	1.04	1.21	0.53			
MRP	0.6	0.8	1.04	0.12	0.95	0.4			

Table 5: VIP values of genes expression for each exposure condition to CNFs. VIP values below 0.8 were removed from the analysis.

Correlation with I _D /I _G -band ratio									
	0.01 ı	mg/L	0.1 n	ng/L	1 mg/L				
			initure		initure				
	IN VITRO	IN VIVO	IN VITRO	IN VIVO	IN VITRO	IN VIVO			
Cat	0.52	0.06	-0.16	-0.44	0.56	0.51			
HSP70	-0.93*	0.84*	-0.3	0.26	0.32	0.23			
GST	-0.91*	0.69*	0.7*	0.59	-0.22	0.49			
SOD	-0.55	0.85*	-0.74*	0.55	0.79*	0.57			
MT	-0.88*	0.54	-0.07	0.42	0.48	0.77*			
Lys	-0.07	0.30	-0.92*	0.12	0.83*	0.86*			
PgP	0.69	-0.36	-0.93*	0.32	-0.29	0.94*			
CP450	0.46	-0.39	-0.94*	0.3	0.84*	0.66			
Asyn	-0.97*	0.87*	-0.29	0.29	0.78*	0.89*			
Btub	-0.62	1*	-0.65	0.21	-0.18	0.51			

Nak	0.94*	0.53	0.9*	0.19	0.32	0.39
P53	-0.34	0.15	0.96*	0.26	0.34	0.89*
MRP	0.75*	0.5	0.06	0.82*	0.45	0.97*

Table 6: Table showing the correlation between the D/G-band ratio, measured through Raman spectroscopy, and gene expression. *Indicates statistical significant (P<0.05) with + indicating a positive relationship with purity and – indicating a negative relationship with purity.

Conselections with Descented CNIF Durity										
Correlation with Reported CNF Purity										
	0.01	mg/L	0.1 n	ng/L	1 mg/L					
	in vitro	in vivo	in vitro	in vivo	in vitro	in vivo				
Cat	-0.66	0.28	0.47	0.75*	-0.2	-0.58				
HSP70	0.57	-0.33	-0.35	-0.79*	-0.76*	0.39				
GST	0.74*	-0.23	-0.92*	-0.65	0.70*	0.13				
SOD	-0.02	-0.35	0.23	-0.92*	-0.21	0.02				
MT	0.67	-0.34	-0.12	0.22	0.1	-0.26				
Lys	-0.52	-0.37	0.64	0.5	-0.33	-0.38				
PgP	-0.89*	-0.27	0.58	0.32	0.8*	-0.54				
CP450	-0.73*	-0.03	0.68*	0.16	-0.54	-0.43				
Asyn	0.64	-0.39	-0.30	0.36	-0.3	-0.43				
Btub	0.03	-0.83*	0.06	-0.76*	0.64	0.11				
Nak	-0.85*	-0.93*	-0.84*	-0.74*	-0.69*	0.23				
P53	0.82*	-0.69*	-0.64	0.39	0.05	-0.5				
MRP	-0.84*	-0.11	-0.57	-0.77*	0.04	-0.78*				

Table 7: Table showing the correlation between carbon nanofiber purity and gene expression. *indicate statistical significant (P<0.05) with + indicating a positive relationship with purity and – indicating a negative relationship with purity.



Figure 1a-i: TEM images of GANF (1a), GATam (1b) and GANFg (1c) prepared in stock suspensions compared with GANF (1d), GATam (1e) and GANFg (1f) in culture media and GANF (1g), GATam (1h) and GANFg (1i) prepared in ASW. Black bars indicate 1µm.



Figure 2a-c: Raman spectra of carbon nanofibers are expressed as a function of intensity in relation to the raman shift with peaks representing the D-band and G-band. To measure the structural purity of

GANF (A), GATam (B) and GANFg (C) the ratio of intensity between the D-band and G-band (I_D/I_G) is used.



Figure 3: Optical density (340nm) as an approximation of suspension stability of the CNFs in the stock suspensions, cell culture media and in ASW over 24 hours.



Figure 4: PLS-DA correlation for all test conditions *in vivo* for GANF (A), GATam (B) and GANFg (C) as well as *in vitro* for GANF (D), GATam (E) and GANFg (F) plotted on a factorial plane. Orientation of the vectors describes how strongly each gene describes the axes as well as the relationship between genes.



Figure 5: PLS-DA analysis of *M. edulis* hemocytes exposed *in vitro and in vivo* to GANF (A), GAtam (B) and GANFg (C) at 0.01, 0.1 and 1mg.L⁻¹.