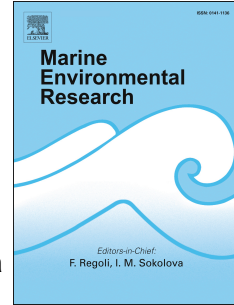


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Adverse Effects of Plastic Ingestion on the Mediterranean Small-Spotted Catshark (*Scyliorhinus canicula*).

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Author contributions

AM, AC and LP originally formulated the idea. AM, GB and LP conceived and designed the experiments; AM, TC, GB and MLG developed and constructed experimental setup; AM, TC, GB and MLG conducted fieldwork and performed the experiments; AM, CV and LP performed statistical analyses; AM wrote the manuscript. All the authors contributed with the interpretation of results and provided editorial advice.

1 **Adverse Effects of Plastic Ingestion on the Mediterranean Small-Spotted Catshark**
2 **(*Scyliorhinus canicula*).**

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13

14 **Keywords**

15 Microplastics, macroplastics, μ -Raman spectroscopy, small-spotted catshark, immunity

16

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19

20 Abstract

21

22 Plastics are widely diffused in the oceans and their ingestion by marine organisms is raising concern for
23 potentially adverse effects. The risk of harmful interactions with marine plastic pollution depends on
24 the biology of the species as well as the distribution and abundance of the different plastic types.

25 The aim of this study was to assess the occurrence of plastic ingestion by the small-spotted catshark
26 (*Scyliorhinus canicula*), one of the most abundant elasmobranchs in the Mediterranean Sea. The
27 expression levels of genes indicative of total immune system function were analyzed to gather
28 preliminary data for further investigation of any potential correlations between plastic presence and
29 immune activation.

30 One hundred catsharks were collected during the Spring 2018 in two geographic locations in the
31 southern region of the central Mediterranean Sea: 1) near Mazara del Vallo, SW Sicily and 2) near
32 Lampedusa island, Italy's southernmost. Standard measurements were recorded for each specimen and
33 its organs and sex was determined. The gastrointestinal tract (GIT) was preserved for plastic detection
34 and identification. Where present, plastics (macro- and micro-) were characterized in terms of size,
35 shape and polymer typology through microscopy and μ -Raman spectroscopy. Spleen from a subset of
36 thirty samples was preserved for RNA extraction, then used to quantify by real time PCR the
37 transcripts of T cell receptor beta (TCRB), T cell receptor delta (TCRD) and IgM genes.

38 The results indicated that ingestion of plastic is widespread, with microplastics (MP, from 1 μ m to <1
39 mm) abundantly present in nearly all samples and macroplasticplastic (MaP, > 1 cm) in approximately
40 18% of the specimens collected. A significant increase in the expression of TCRB, TCRD and IgM was
41 observed in the spleen of MaP+ specimens from Mazara del Vallo waters, in parallel with 67% increase
42 in liver weight.

43 While the presence of MP alone is not enough to induce a strong activation of the immunity, some type
44 of plastics falling into the MaP category may be more toxic than others and crucial in the activation of
45 the immune response.

46 The results of this study represent a first evidence that plastic pollution represents an emerging threat to
47 *S. canicula*, the Mediterranean food web and human consumers.

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49 **1. Introduction.**

50 The abundance of plastic debris floating in Mediterranean waters was first reported in 1980 (Morris RJ
51 1980). Later studies confirmed the distribution, abundance and characteristics of plastic debris in the
52 basin thanks to visual counts supported by surface nets tows allowing detection and quantification of
53 microplastics, (MP, from 1 μm to <1 mm) (Aliani et al., 2003; Suaria et al., 2014; Faure et al., 2015;
54 Ruiz-Orejón et al., 2016; Zeri et al., 2018). Plastic particles are in fact typically grouped into categories
55 from macro (MaP >1 cm) to nano (from 1 to <1000 nm) depending on their size (as measured by their
56 diameter or by considering the larger dimension as classifier for irregular or fiber debris) according to
57 the classification proposed by Hartmann et al., 2019.

58 In the Mediterranean Sea, MP concentrations is ranging from tens to hundreds of thousands of items
59 per square kilometer; this abundant presence of buoyant plastic debris is likely related to the high
60 human pressure and the hydrodynamics of this semi-enclosed basin (Eriksen et al., 2014; Cozar et al.,
61 2015) which is also one of world's busiest shipping routes, receiving waters from densely populated
62 river shorelines (e.g., Nile, Ebro, Rhone and Po) while being connected to the Atlantic Ocean only by
63 the Strait of Gibraltar. For its characteristics, the Mediterranean basin has a water residence time as
64 long as a century (Lacombe et al., 1981) and its shores house 10% of the global coastal population (ca.
65 100 million people within the 10-km coastal strip (CIESIN, 2012)).

66 MP are divided in two types: 1) primary, found in most commonly utilized products (e.g. cosmetic and
67 personal care products, insect repellents, sunscreens, products for children), and 2) secondary,
68 originating from the fragmentation of larger plastic debris through biological degradation, photo-
69 degradation, chemical deposition and physical fragmentation (Auta et al., 2017). Both primary and
70 secondary MP are present in sea water where the most represented synthetic polymers
71 are polypropylene (PP), polyethylene (PE), polystyrene (PS), polyvinylchloride (PVC) and polyethylene
72 terephthalate (PET) (Rocha-Santos and Duarte, 2015).

73 MP in the marine environment are dispersed via oceanic currents and wind patterns throughout the
74 water column (Lebreton et al., 2012), in a variety of colors, shapes, sizes and densities (Reisser et al.,
75 2014). Their persistence, availability and the biomagnification of the associated harmful chemicals,
76 represent a potential hazard to marine life throughout the food web also if there is very few studies in
77 field (Lusher et al., 2017; Romeo et al., 2015). MP interaction with marine organisms has been
78 described for zooplankton (Botterell et al., 2019), invertebrates (Avio et al., 2015; Digka et al., 2018),
79 fish (Digka et al., 2018; Compa et al., 2018; Renzi et al., 2019), turtles (Domenech et al., 2019), birds
80 (Wilcox et al., 2015) and mammals (Fossi et al., 2016), including endangered species (Deudero and
81 Alomar, 2016).

82 Fish may accidentally ingest particulate while they are feeding on their prey or ingest plastic debris
83 because of their resemblance to prey: the first report of MP ingestion in fish was in 1972 (Carpenter et
84 al., 1972). Depending on plastic size and species, particles may be expelled or accumulate in the
85 gastrointestinal tract (GIT), where could cause physical damage (e.g. block of feeding appendages or
86 filters, and obstruction of GIT), and in some cases inflammation leading to death (Li et al., 2016;
87 Werner et al., 2016).

88 In the last few years, the presence of plastics debris in fish has been described in species captured in the
89 oceans, seas and freshwater raising concerns on their potential negative effects (e.g Ory et al., 2018;
90 Bessa et al., 2018; Pellini et al., 2018; Silva-Cavalcanti et al., 2017). In addition, several authors have
91 studied in controlled conditions the effects of virgin MP intake or as vehicles of other toxic
92 compounds. Potential damage is related to the physical properties, regarding the interaction of the
93 particles with the organism tissues and to the chemical properties, concerning the transfer of
94 contaminants or leaching of plastic additives (Rochman et al., 2013; Pedà et al., 2016; Limonta et al., in
95 review). Indeed, plastics, due to their lipophilic nature, have the potential to adsorb many hydrophobic
96 persistent organic pollutants which may increase their harmful effect on biota. Up to now, it has not

97 been completely elucidated the contribution of chemicals to plastic toxicity. Recent studies suggest that
98 the two main routes of uptake in fish are represented by the ingestion and inhalation, since MP were
99 found to accumulate and cause tissue damage in GIT and gills (Li et al., 2016, Pedà et al., 2016).
100 Histological observations on exposed fish confirmed that MP were able to induce a strong
101 inflammatory response in the target tissues (Limonta et al., 2019). The transcriptomic profiling of
102 zebrafish larvae exposed to PS also suggested the activation of immune response, with the up-
103 regulation of genes related to the complement system (Veneman et al., 2017; Pitt et al., 2018). Lu et al.
104 (2016) reported how the accumulation of PE in gills, gut and liver of zebrafish causes oxidative stress,
105 inflammation in fish liver and a disturbed lipid and energy metabolism (Lu et al., 2016).

106 Besides inflammation and metabolic disorders, MP absorption and distribution in different tissues and
107 cells can result in several types of effects, such as behavior alterations, predatory performance
108 reduction, neurotoxicity, decreased growth (Rochman et al., 2013; Rochman et al., 2014; Ferreira et al.,
109 2016; Pedà et al., 2016; Barboza et al., 2018a; Barboza et al., 2018b). Moreover, given the chemical
110 properties, the MP uptake by aquatic organisms with other contaminants is a route to harmful
111 chemicals including styrene, metals, phthalates, bisphenol A, polycyclic aromatic hydrocarbons
112 (PAHs), polychlorinated biphenyls (PCBs) or polybrominated diphenyl ethers (PBDEs) (Koelmans et
113 al., 2014; Barboza et al., 2018c). For example, the japanese medaka (*Oryzias latipes*), exposed for
114 short-time to both virgin and marine PE fragments, showed bioaccumulation of PAHs, PCBs and
115 PBDEs, with signs of liver stress and early tumor formation (Rochman et al., 2013; Rochman et al.,
116 2014).

117 The small-spotted catshark (*Scyliorhinus canicula*, Linnaeus, 1758, SC) is a species of the family
118 Scyliorhinidae. It is one of the most abundant cartilaginous fish in the central Mediterranean Sea
119 (Ragonese et al., 2013) and inhabits the continental shelves of off the coasts of Norway and the British
120 Isles up to Senegal. It is a small, shallow-water shark inhabiting waters of depths ranging from a few

121 meters (mt) down to 400 mt (Geraci et al., 2017; Rodriguez-Cabello et al. 2007). SC feeds
122 opportunistically on a wide range of macrobenthic fauna, with Crustacea, Mollusca, Annelida, and
123 Echinodermata as preferred prey. Feeding preference may depend on SC age and feeding intensity is
124 highest during the summer due to the higher availability of living preys (Rodriguez-Cabello et al.
125 2007).

126 Given their low commercial value and abundance in the Mediterranean Sea (this species is currently
127 listed as "Least Concern" on the IUCN Red List of Threatened Species), SC has been chosen as model
128 in this study, as representative sample of the potential hazard fish in the southern waters of Italy are
129 subject.

130 Here we present the description and analysis of effects of plastics (MP and MaP) in SC from two
131 different geographic locations in the southern region of the central Mediterranean Sea, near: 1) Mazara
132 del Vallo (MDV), SW Sicily and 2) Lampedusa (LMP), Italy's southernmost island. Plastics have been
133 isolated from the GIT of SC, quantified and analyzed with Raman spectroscopy to identify the polymer
134 category. *S. canicula* was further investigated through the analysis of spleen transcripts of key genes
135 involved in adaptive and innate immunity to evaluate the potential of future research hypothesis linking
136 plastic presence to health status.

137

138

139 **2. Materials and Methods.**

140 **2.1 Samples collection.**

141 One hundred specimens of SC were collected on March 16, 2018 near Mazara del Vallo (N=48, N=25
142 females, F, and N=23 males, M), SW Sicily, Italy and on May 7th, 2018, near Lampedusa island (N=52,
143 N=14 females, F, and N=38 males, M), Italy's southernmost island, in the FAO General Fisheries
144 Commission for the Mediterranean (GFCM) areas marked as Geographical Sub-Area (GSA) 16 and
145 GSA13 in Figure 1, respectively (Figure 1; Supplementary Table 1).

146

147 **2.2 Morphometric indices.**

148 Fish total length (TL), body weight (BW), spleen weight (SPL W), liver weight (LIV W) and GIT
149 weight (GIT W), gender and maturity stage were recorded. Visceral weight (VW) was calculated
150 subtracting the carcass weight (CW) to the BW. Fish were weighed after sampling, then spleen, liver
151 and GIT were removed by dissection and weighted after evisceration. All the weights were measured
152 using Sartorius balance (model: MSEE6202P-000-D0) to an accuracy of 0.01 grams.

153 Sexual maturity was defined by 6 stages of gonadic development according to the Medits (International
154 Bottom Trawl Survey in the Mediterranean) scale (Anon., 2016).

155 Condition factor (CF) was calculated as follows: $(BW*100)/TL^3$. The hepato-somatic index (HSI),
156 the spleno-somatic index (SSI) and the GIT somatic index (GSI) were calculated as follows: $HSI =$
157 $liver\ weight\ (g) \times 100/body\ weight\ (g)$, $SSI = spleen\ weight\ (g) \times 100/body\ weight\ (g)$, $GSI = GIT$
158 $weight\ (g) \times 100/body\ weight\ (g)$ (Supplementary Table 1).

159

160 **2.3 Chemistry: plastic isolation and identification in the GIT.**

161 After sampling, fish were quickly frozen and stored at -20°C. Successively, they were processed in the
162 laboratory, where they were washed with MilliQ water, sectioned and the entire GIT (esophagus to

163 vent), liver and spleen were removed. Liver and spleen were fixed in RNAlater® and stored in
164 separated closed container at -20°C for subsequent isolation of RNA, whereas GIT was wrapped in
165 aluminum foil and then frozen at -20°C in a closed container.

166 GIT samples were digested at 60°C for 24 h in 10% KOH (Merck) in MilliQ® water, filtered with 0.45
167 µm nitrocellulose filter before use, according to the protocol published by Dehaut A et al. (2016).

168 Following digestion, samples were filtered on 8 µm cellulose nitrate filters (Whatman). In the case of
169 the presence of debris in the digestate, a density-based separation step using a ipersaline solution of

170 NaCl (Sigma Aldrich) was performed. The solution was added to the digestate (2:1, v/v) and stirred for
171 10 min before being left to settle for 1 h. The supernatant, containing the floating plastic particles was

172 collected and filtered, as previously described. Plastic debris of big size that could not be digested nor
173 filtered were isolated and analyzed as undigested MaP. The filters that by visual inspection contained

174 plastic debris contaminated with undigested organic residues or minerals were subject to an additional
175 basic digestion step according to the procedure reported in Roch et al. (2017) and washed by a dilute

176 acid aqueous solution (HCl 0.1M); it was observed that even after this treatment plastic debris were not
177 broken into smaller fragments. Blank samples were prepared and analyzed in parallel as controls to

178 account for MP contamination from the digestion and filtering processes (i.e., 'digestion control'). In
179 detail, digestion solutions were placed into a clean beaker, heated at 60 °C for 24 h, and vacuum

180 filtered onto a nitrocellulose filter 0.45 µm, (the procedure was repeated ten times; n = 10). MP was
181 quantified and characterized for fish samples (see below). The blank samples contamination (mean No.

182 filter-1) consisted only of fibers with average values of 4.2 (± 0.5).

183 Measure to avoid contamination were adopted during all the extraction procedure, cotton lab coat and
184 nitrile gloves were used and glassware equipment were thoroughly washed and rinsed with MilliQ

185 water before use, all materials were covered between use with aluminum foils, and filters were stored
186 in glass petri dishes.

187 Filters were first examined and sorted by visual inspection with a stereo microscope following protocol
188 (Dehaut A et al., 2016). Microscopic analysis of the filters was performed with a Nikon SMZ745T
189 stereomicroscope, equipped with a Nikon Digital Sight DS-F12 camera.

190 All the MaP, fragments and filaments, were analyzed with Raman spectroscopy. The size of the
191 analyzed subset should insure a representative view of the particle size distribution and chemical nature
192 as suggested by Kedzierski M et al. 2019. Spectra were generated with a LabRam HR800 micro-
193 Raman instrument from Horiba Scientific equipped with an air-cooled CCD detector at -70°C , an
194 Olympus BXFM microscope, a 600 groove/mm grating and a $50\times$ objective were used to collect the
195 Raman scattering signals. The excitation source was a He-Ne laser (632.8 nm line) with a maximum
196 laser power of 20 mW. A minimal spectral accumulation of 10 times 1 s was used; if a high
197 background was recorded the accumulations were increased to a maximum of 100 times 1 s to improve
198 the signal-to-noise ratio.

199

200 **2.4 Gene expression analysis.**

201 *RNA Extraction.* Total RNA from spleen samples of thirty selected samples (Table 1) was extracted
202 using RNeasy Plus Mini Kit (Qiagen, Hilden, Germany) following the manufacturer's instructions.
203 Tissue (about 30 mg) lysis and homogenization was performed with T 10 basic ULTRA-TURRAX®
204 (IKA, Staufen, Germany). Genomic DNA was removed through an in-column DNase I digestion
205 (Qiagen). The RNA concentration and the quality of the extractions were assessed with a BioSpec-nano
206 UV-Vis spectrophotometer (Shimadzu Italia S.r.l., Milan, Italy). The RNA samples that did not meet
207 the absorbance ratio cutoff (1-8-2.0 for the 280/260; 2.0-2.2 for the 260/230) were extracted more than
208 once.

209 *Quantitative real time PCR (q-PCR)*. A panel of immunity genes [*T cell receptor beta (TCRB)*, *T cell*
210 *receptor delta (TCRD)* and *immunoglobulin M (IgM)*], and housekeeping genes [*ribosomal protein 13*
211 (*RPL13*), *actin beta 1 (ACTb)* and *ribosomal protein L29 (RPL29)*] was selected from the literature.

212 Primers for the selected genes were obtained from literature or designed with Primer 3 on different
213 exons to exclude any genomic DNA co-amplification: ncbi accession numbers of the sequences used
214 were KY434203 (TCRB); KY434205 (TCRD); JX555996 (μ heavy chain IgM) (Crouch et al., 2013; Li
215 et al., 2015; Pettinello et al., 2017) (Table 2). Reverse transcription was performed using iScript™
216 cDNA synthesis kit (Bio-Rad, California, USA) according to the manufacturer's instructions using 1 μ g
217 total RNA. The qPCR reaction was performed in triplicates in 96 wells plates, using the EvaGreen Dye
218 Master mix (Bio-Rad) on CFX Connect Real-Time Detection system (Bio-Rad). qPCR efficiencies
219 were calculated using the equation from Dhar et al. (2009). The amplification efficiency of each primer
220 couple was checked through the creation of a five points standard curve with serially diluted 1:5 cDNA
221 from 5 samples (MDV: SC7, SC9, SC11 and LMP: SC56, SC57) (Table 2). cDNA was reverse
222 transcribed from 1 μ g of total RNA using SsoFast™ EvaGreen® Supermix (Bio-Rad) in a total
223 volume of 10 μ l of a reaction mix containing 10 ng cDNA, 0.3 μ M of each primer, 2 \times Evagreen
224 enzyme and DNase-free sterile water. qPCR reactions were run as follows: 1 cycle of 98 °C for 30 min,
225 49 cycles of 95 °C for 5 s, 60 °C for 10 s; melting curve 65 °C–95 °C: increment 0.5 °C every 5 min.

226 Each reaction was run in triplicate, together with a tri- plicate of no-template controls. The average Ct
227 values were normalized to the values of the housekeeping genes RPL13. RPL13 was the most stable
228 house-keeping gene amongst those tested (e.g RPL13, ACTb, RPL29). Comparative Ct method of
229 analysis ($2^{-\Delta\Delta Ct}$) was used to determined changes of expression between control and treated samples
230 on CFX connect manager software 3.1 (Bio-Rad). Fold differences were calculated accounting for
231 differences in primer efficiencies using the Pfaffl method (Pfaffl, 2001).

232

233 **2.5 Statistical analysis.**

234 Data were analyzed within and between locations. Morphometric data were analyzed within MDV and
235 LMP, related to gender (male and females) and/or presence or absence of ~~MP~~ and MaP in the GIT.
236 Student t-test and ANOVA were used in comparison to detect significant differences between groups
237 compared, for morphometric data and for gene expression analysis.

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239 **3. Results and Discussion.**

240 **3.1 Morphometric data analysis.**

241 All the morphometric data for the 100 samples were analyzed to examine if significant differences exist
242 between the samples from the two locations studied. Variation in TL and BW did not account for a
243 difference in CF between MDV and LMP while the gonadal maturity and liver size had interesting
244 dissimilarities (Table 3, Supplementary Table 2).

245 In detail: MDV, both females and males SC have smaller ($< 34\%$) index of gonadal maturity when
246 compared to samples from LMP. Moreover, MDV males have bigger liver ($HSI > 20\%$), while females
247 have smaller liver ($HSI < 24\%$) compared to LMP specimens.

248 The smaller gonadal maturity in MDV specimens may be linked to the great difference in the existing
249 anthropogenic activities in the two locations of sampling. MDV sampling site is close to a port with the
250 largest fishing fleet in Italy, while LMP sampling site is in a pristine area, near Lampedusa, the Italian
251 southernmost island inhabited by only 6.000 people in an area of 20.2 square kilometers. The
252 difference in human activity, contamination and consequently greater stress conditions in MDV, may
253 have an effect on the appropriate development of the MDV fish and may correlate to the overall
254 differences we observed amongst the two shark's populations. The translation of stress to the
255 organismal/population level and higher is not straightforward. In teleosts, acute and chronic stressors
256 can stimulate physiological changes at the organismal level, impacting growth rate, reproductive output
257 or investments, and disease resistance (Davis, 2002; Iwama et al., 2006; Ramsay et al., 2009). In
258 contrast, very little is known about the physiological changes linked to stress in elasmobranchs. Indeed,
259 the extent to which elasmobranchs are affected by pervasive anthropogenic threats, such as habitat
260 degradation, climate change and pollution and its transient or prolonged impacts on health and fitness
261 (e.g., somatic growth and reproduction) remains poorly understood (Skomal and Mandelman, 2012).

262 We could assume that they respond to threats in a similar way teleosts do, but the nature and magnitude
263 of the response could be highly species-specific and related to ecological factors and the type and
264 duration of the stressors. Plastic contamination and the ingestion by aquatic organisms, including
265 species of commercial importance for fisheries, are well documented in the Mediterranean Sea (Lusher
266 et al., 2017) and we can reasonably assume that it will continue to increase in the foreseeable future;
267 filling the knowledge gaps on the occurrence and adverse effects caused by (of the) polymers actually
268 present in the environment is necessary to assess / understand the impact of these contaminants on biota
269 (degree of the biological impact).

270

271 **3.2 Effects and composition of plastics in the GIT of *S. canicula*.**

272 The GIT of 50 selected specimens was analyzed for plastic presence, quantity and type. Plastic were
273 either grouped as fibers, MP fragments or MaP (Figure 2 and Figure 3) following the classification
274 proposed by Hartmann et al., 2019. The occurrence of plastic was considered by the number of
275 ingested plastics as well as the frequency of ingestion (Avio et al., 2020).

276 We found debris in the shape of fibers (filaments and lines) and fragments in about 80% of the samples
277 analyzed (86.3 % of the MDV samples, and 75.7 % from LMP samples), both colored and clear (Figure
278 3; Table 4). Artificially dyed debris and filaments ~~and debris~~ identified by Raman spectroscopy were
279 referred as plastic particles. Fibers in most cases were characterized by a not regular diameter along the
280 particle, with diameter values lower than 10 μm . A total number of 138 particles were counted by
281 visual inspection: 115 fibers shape (83.3%; which were classified based on the diameter size in 68
282 fibers and 59 filaments) and fragments (16.7%). According to size classes, the plastic debris were
283 divided up as follows: 17 were in the range 1-10 μm , 72 were in the range 20 μm e 100 μm , 38 the
284 range 20 μm e 100 μm and 11 were in the range 1cm – 5cm (MaP). Considering the color, 88 debris
285 were dark colored (63.8%), 30 were light colored (21.7%) and 20 were transparent (14.5%).

286 All fragments and filaments were analyzed by Raman microspectroscopy: fibers identification resulted
287 in many cases problematic possibly due to additive/pigments contained in the fibers or to adhesion of
288 organic residues. The uncertainty in identification of fibers constituents and therefore the bias induced
289 by a partial identification of the samples, combined with the fact that fibers can also derive from
290 contamination during the sample preparation procedure suggest us to limit the data only to MaP,
291 fragments and filaments.

292 In addition, in the present work we aimed to investigate possible correlation of MaP presence and
293 variation of immune-related gene expression in *S. canicula*.

294 MP filaments and fragments accounted for a similar number in the two location with an ingested
295 average by individual of 1.32 items in MDV vs 1.04 items in LMP and a frequency of ingestion of 71%
296 in MDV vs 62% in LMP (Table 4).

297 Differently, MaP were detected in 18% of the samples analyzed. Specifically, in 20% of the MDV
298 samples, and 16% from LMP samples (Table 4). All specimens with MaP from MDV were females,
299 while those with MaP from LMP were 50% males and 50% females (Supplementary Table 3).

300 MaP were composed of the polymers polypropylene, polyethylene and polyethylenterephthalate whereas
301 MP were mainly identified as polyester, acrylic and nylon 6, ~~and colorant~~ (Figure 4). Average values of
302 MP composition were not significantly different in the two sites.

303 The analysis of morphological data associated to the presence of MaP in samples from both locations
304 showed no correlation to CF and VW. However, a significant increase in liver weight (49%, $p<0.05$),
305 and HIS (26%, $p<0.01$) was observed (Supplementary Table 4A). In the correlation to MaP, MDV
306 specimens showed an increase in the weight of all organs, although only the liver and HSI returned a
307 significant increase of 67% and 34%, respectively of the total weight ($p<0.005$) (Figure 5,
308 Supplementary Table 4B). In LMP, the MaP specimens showed an increase of VW but the variation

309 was non-significant; nevertheless, the liver was still subject to the highest increase (Figure 5,
310 Supplementary Table 4C).

311 In general, females from both location have higher VW probably due to higher structural and functional
312 demands linked to vitellogenesis and maternal immunity (LIV W is 25% and 44% higher in females
313 than males in MDV and LMP, respectively) (Supplementary Table 4D and 4E).

314 The analysis of morphometric data of specimens sampled at MDV and LMP related to both MaP
315 detection and gender, resulted in non-significant differences although it is evident that MDV females
316 have an increase of BW that is only in part related to the increase in VW (Supplementary Table 5A). In
317 LMP the increase of VW is more evident in females than males (Supplementary Table 5B). The
318 females have VW that is 31% ($p < 0.05$) than males (Supplementary Table 5C). BW and VW were
319 higher in samples with MaP females and lower in males (Supplementary Table 5D and 5E). The
320 correlation analysis is clearly showing that females in MDV have smaller liver activity than those in
321 LMP, while the males in MDV have higher liver activity, almost as the males in MDV are stimulated to
322 invest more in liver functions, which is usually a female feature (e.g. vitellogenesis) rather than in male
323 characters (in males the body weight should be higher because is correlated to bones and muscles, for
324 examples). The feminization-like evidence and the smaller gonadal maturity overall observed could
325 severely impact the reproduction rate and fitness of the SC population in MDV. It has been previously
326 observed that the exposure to endocrine disrupting chemicals (additives of plastics) can strongly
327 influence the course of sex differentiation and unbalance the sex ratio in zebrafish populations; in other
328 freshwater species vitellogenin concentration in male fish have been described in correlation to the
329 exposure to estrogenic contaminants (Von Hippel et al., 2017; Santos et al., 2017). Decreased growth
330 rate, decreased fecundity and negative impacts on subsequent generations have also been linked to
331 plastic exposure in both marine and terrestrial species (Huerta-Lwanga et al., 2016; Sussarellu et al.,
332 2016).

333

334 **3.3 Gene Expression.**

335 In order to move beyond simply studying the presence and type of plastics, the effects on the
336 underlying physiological and biochemical mechanisms should be investigated. The effects can be many
337 and diverse, and may involve a stress response implicating several systems, such as the immune, the
338 endocrine or reproductive one. A first step to identify changes that may be associated to the presence of
339 plastic described was to evaluate changes in the expression of genes known linked to the immune
340 system. There are two main layers of immune responses: innate immune responses and adaptive
341 immune responses. The innate immune system creates a fast, non-specific reaction to the pathogen
342 infecting the host organism. If the pathogen persists despite innate defenses, then the adaptive immune
343 system will engage the microbe with specificity and memory. The adaptive (or acquired) immune
344 system mounts to a discriminating long lasting immune response directed by two types of lymphocytes,
345 T cells (cell-mediated immunity) and B cells producing immunoglobulins (Ig) (humoral immune
346 response) (Rauta et al., 2012). Cartilaginous fish and elasmobranchs (sharks, skates and rays), in
347 particular, are the first jawed vertebrate group to emerge in evolution and are the oldest group relative
348 to mammals having an immune system grounded upon Ig, T cell receptors (TCR), the major
349 histocompatibility complex (MHC), as well as RAG-mediated rearrangement, somatic hypermutation
350 and the presence of primary and secondary lymphoid tissues (Flajnik MF, 2002). Immunoglobulins
351 (IgM) were discovered in sharks almost 40 years ago and while some features of the immune system
352 are simple and primordial, other features, including the Ig system, can be quite complex (e.g. the
353 presence of two non-IgM isotypes, IgW and IgNAR) (Dooley and Flajnk, 2006; Flajnik MF, 2002). It
354 is highly probable that each of these isotypes evolved to mediate a particular type of defense
355 mechanism, although there are no functional data as yet for the non-IgM isotypes. The genes that were

356 analyzed in this study were those related to canonical immune response pathways, *IgM*, *TCRB* and
357 *TCRD* (Pettinello et al., 2017; Crouch et al., 2017).

358 RNA extraction from spleen of the 30 specimens was successful and all samples were retrotranscribed
359 and used as template in the real time qPCR of *TCRB* and *IgM*, specifically related to adaptive immunity
360 activity and *TCRD*, linked to innate immunity activity. Samples analyzed within location group (MDV
361 and LMP separately), considering the presence (MaP +) or absence (MaP -) of plastics, showed
362 differences in the expression of the genes (immune-related) tested.

363 In MDV (5 MaP + and 8 MaP -) specimens, MaP + spleens showed a significant increase in the
364 expression of all immune-related genes: fold increases were: 1.2 for *TCRB* ($p < 0.02$), 2.1 for *TCRD*
365 ($p < 0.01$) and 3.1 for *IgM* ($p < 0.01$) (Figure 6). When the analysis was restricted to only females (5 MaP
366 + and MaP -), fold increases were: 3.5 for *TCRB* (not significant), 6.3 for *TCRD* ($p < 0.02$), and 16.4 for
367 *IgM* ($p < 0.02$) (Figure 6).

368 In LMP specimens (4 MaP + and 11 MaP -), MaP + spleens showed minimal and not significant
369 variations of immune-related gene transcripts: fold increases were 0.13 (*TCRB*), 0.23 (*TCRD*) and 0.18
370 (*IgM*). Data analyzed separating males and females gave the same outcome (data not shown).

371 Results from spleen gene expression were somewhat correlated with what we observed in the previous
372 analyses. The changes observed in the expression of the three immune-related genes in spleen were
373 greater in MDV samples than in LMP samples, consistent with the hypothesis that the adverse effects
374 observed may be correlated to the highest degree of MDV anthropogenic pollution, in which MaP, co-
375 present with MP (detected in on nearly all samples) are most likely additive for chemical co-
376 contaminants.

377

378 **4. Conclusion.**

379 The present study reports high frequencies of microplastic consumption as well as the presence of
380 macroplastic ingestion in the small spotted shark, *S. canicula*, sampled in two different locations of the
381 Mediterranean Sea. From a first examination, it may be hypothesized that sharks could be less
382 susceptible to microplastic ingestion than macroplastics, given the potential correlation of macroplastic
383 presence to changes in expression of immune-related genes. But the link between plastics and the
384 unavoidable absorbed chemicals, differently distributed in the locations examined, needs to be
385 specifically addressed, given the estrogenic effects hereby reported on maturity and gender
386 development that could be caused, for example, by endocrine disruptors present in the most
387 contaminated site. Correspondingly, immunology data describing the full functionality of T- and B-
388 cells needs to be specifically gathered and integrated.

389 To our knowledge, this is the first study to explore the influence that plastic ingestion by a shark
390 species in the Mediterranean Sea. The occurrence and high frequency of ingested plastic debris hereby
391 reported highlights the ubiquitous nature of this pollutant throughout the Mediterranean Sea and the
392 importance of targeting plastics and their co-contaminants in future pollution control efforts.

393

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397

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693

694 **Figure legends.**

695 ***Figure 1. Sampling sites, located within FAO GFCM GSAs.***

696 Dots represent the 2 locations of sampling, south of Mazara del Vallo, GSA 16 and south of
 697 Lampedusa, GSA 13. Lampedusa samples were collected in deep water. GFCM, General Fisheries
 698 Commission for the Mediterranean; GSA, Geographical Sub-Area.

699
 700 ***Figure 2. Images of undigested plastics MaP from 3 different samples.***

701 **A**, Digested GIT tissue with undigested plastic; same specimen is shown in **B**. **C- D** MaP found in the
 702 GIT of two other specimens. MaP were identified by Raman spectroscopy: **B** (polypropylene), **C**
 703 (Polyethylene terephthalate), **D** (polyethylene).

704
 705 ***Figure 3. Microscope images of MP debris found on filters in 2 different samples.***

706 **A, B**. Filters after digestion of SC6 and SC7. **C, D**. Microscope image of plastic debris on filters.

707
 708 ***Figure 4. Plastic debris composition.***

709 **A, B**. MaP and MP composition: PE polyethylene, PP polypropylene, PET Polyethylene terephthalate,
 710 PA Polyamide, PAC Polyacrylate, PAN Polyacrylonitrile. The numbers refer to percentage values.

711
 712 ***Figure 5. Morphometric changes correlated to the presence of MaP in GIT samples from both***
 713 ***locations.***

714 **A**, Condition factor, CF. **B**, Viscera weight. **C**, liver weight, LIV W. **D**, Hepato-somatic index, HSI.
 715 (+), MaP isolated; (-), no MaP detected. * $p < 0.05$, ** $p < 0.01$. 30. Samples/individuals: MDV, N =
 716 15; LMP, N = 15. MDV: N = 10 MaP (+), N = 5 MaP (-); LMP: N = 4 MaP (+), N = 11 MaP (-).

717

718 **Figure 6. Expression of immune-related genes in *S. canicula* spleen samples from MDV.**
719 **A, D, TCRB; B, E, TCRD; C, F, IgM.** Normalized fold expression relative to HK gene (RPL13) in
720 spleen of specimens with macroplastic MaP (+) vs specimens without MaP (-) in the digested GIT of
721 all MDV samples (A-C) or only female MDV samples (D-F). Statistically different comparisons are
722 represented by asterisks: *, $p < 0.02$; **, $p < 0.01$. MDV, 1, Mazara del Vallo.

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Table 1. Sample subset of *S. canicula* used in the chemistry and gene expression analyses.

Sample ID	Gender	MAT	TL	BW	CW	VW	CF	SPL W	SSI	LIV W	HSI	GIT W	GSI (g)	Date 2018	LS
SC1	M	1	42,00	245,10	200,62	44,48	0,33	0,66	0,27	17,17	7,01	16,78	6,85	16-mar	MDV
SC2	M	2	39,00	186,11	157,77	28,34	0,31	0,75	0,40	10,34	5,56	11,01	5,92	16-mar	MDV
SC3	F	4	45,00	294,11	230,23	63,88	0,32	0,79	0,27	14,39	4,89	20,60	7,00	16-mar	MDV
SC4	F	5	43,00	254,05	198,29	55,76	0,32	0,98	0,39	26,66	10,49	19,43	7,65	16-mar	MDV
SC5	M	2	39,50	182,92	155,00	27,92	0,30	0,66	0,36	10,58	5,78	10,50	5,74	16-mar	MDV
SC6	M	1	33,50	104,68	91,01	13,67	0,28	0,37	0,35	4,76	4,55	7,72	7,37	16-mar	MDV
SC7	F	3	40,50	245,02	187,62	57,40	0,37	0,88	0,36	24,58	10,03	14,43	5,89	16-mar	MDV
SC8	F	2	33,50	118,53	99,08	19,45	0,32	0,78	0,66	6,08	5,13	11,09	9,36	16-mar	MDV
SC9	M	4	45,00	303,99	248,30	55,69	0,33	0,67	0,22	14,10	4,64	13,57	4,46	16-mar	MDV
SC10	M	1	39,50	209,30	166,67	42,63	0,34	0,79	0,38	13,16	6,29	15,38	7,35	16-mar	MDV
SC11	F	3	41,00	260,30	205,87	54,43	0,38	0,78	0,30	21,25	8,16	17,17	6,60	16-mar	MDV
SC12	F	1	34,50	127,30	110,60	16,70	0,31	0,51	0,40	6,03	4,74	8,87	6,97	16-mar	MDV
SC13	F	1	35,50	137,50	118,32	19,18	0,31	0,57	0,41	10,01	7,28	8,23	5,99	16-mar	MDV
SC14	M	4	40,50	197,58	159,56	38,02	0,30	0,60	0,30	10,95	5,54	10,36	5,24	16-mar	MDV
SC15	F	4	41,00	267,70	186,99	80,71	0,39	0,43	0,16	14,07	5,26	24,32	9,08	16-mar	MDV
SC49	M	4	36,50	151,80	127,41	24,39	0,31	0,36	0,24	5,14	3,39	7,97	5,25	7-mag	LMP
SC50	F	3	35,00	151,82	118,48	33,34	0,35	0,54	0,36	15,59	10,27	10,66	7,02	7-mag	LMP
SC51	F	2	32,00	121,80	98,75	23,05	0,37	0,45	0,37	10,85	8,91	8,87	7,28	7-mag	LMP
SC52	M	2	36,00	155,08	130,58	24,50	0,33	0,68	0,44	7,03	4,53	9,13	5,89	7-mag	LMP
SC53	F	2	37,00	157,90	131,39	26,51	0,31	0,67	0,42	10,87	6,88	11,62	7,36	7-mag	LMP
SC54	M	2	38,00	173,59	138,99	34,60	0,32	0,51	0,29	9,66	5,56	11,92	6,87	7-mag	LMP
SC55	M	4	35,50	129,70	105,39	24,31	0,29	0,29	0,22	6,76	5,21	9,87	7,61	7-mag	LMP
SC56	M	2	36,00	144,72	115,63	29,09	0,31	0,57	0,39	9,42	6,51	13,71	9,47	7-mag	LMP
SC57	F	4	36,50	161,30	122,43	38,87	0,33	0,56	0,35	13,03	8,08	8,64	5,36	7-mag	LMP
SC58	M	2	35,50	147,88	126,27	21,61	0,33	0,40	0,27	7,39	5,00	6,83	4,62	7-mag	LMP
SC59	M	5	38,50	206,30	167,04	39,26	0,36	0,62	0,30	10,38	5,03	12,78	6,19	7-mag	LMP
SC60	F	5	35,50	155,94	123,01	32,93	0,35	0,63	0,40	15,95	10,23	10,13	6,50	7-mag	LMP
SC61	F	3	36,50	174,00	131,86	42,14	0,36	0,53	0,30	20,13	11,57	8,77	5,04	7-mag	LMP
SC62	M	2	35,50	120,46	102,45	18,01	0,27	0,62	0,51	6,21	5,16	6,62	5,50	7-mag	LMP
SC63	M	4	38,50	171,80	145,30	26,50	0,30	0,55	0,32	10,25	5,97	6,59	3,84	7-mag	LMP

SC, *S. canicula*. Gender: M, male sample, F, female sample. MAT, stage of gonadal maturity (1-5). L, total length; W, total weight. CW, carcass weight. VW, viscera weight. SPL W, spleen weight. LIV W, liver weight. GIT W, gastro-intestinal tract weight. SSI, spleno-somatic index. HIS, hepato-somatic index. GSI, GIT somatic index. Length is measured in centimeters (cm); weight is measured in grams (g). LS, location of sampling. MDV, Mazara del Vallo; LMP, Lampedusa.

Table 2. Sequences and amplification efficiency of primers used in q-PCR analysis.

Label	Gene Description	Sequence (5' -> 3')	Acc. n.	Slope	R ²	Eff	Amp
RPL13	Large Ribosomal Subunit Protein 13	F: GCTCCAAGTTAATCATCTTCCCA R: GCCTTGAAATTCTTCTCATCCTC	AY130423	-3,2	0,91	104	2,0
ACTb	Actin beta	F: CGAGACCTTCAATACCCCTGC R: CATAACCTTCGTAGATGGGCACAG	AJ312004	-3,1	0,95	110	2,1
RPS29	Large Ribosomal Subunit Protein 29	F: CATCAGCAGCTTACTGGTCTCATC R: GAAGCCGATGTCTTTAGCGTATTG	n/a	-3,0	0,95	114	2,1
TCRB	T cell receptor beta, B (TCRbB)	F: CGTCAATGGCGAAGAAATGC R: TGTCATGTTGCGTGCTCTTGG	KY434203	-3,1	0,9	110	2,1
IgM	Immunoglobulin M heavy chain	F: CGATGGACTACTCCCCAGAA R: CACAGCTGATTTTGCTGCAT	JX555996	-3,1	0,97	110	2,1
TCRD	T cell receptor delta (TCRD)	F: TGCTTGGCATCAGACTTCTACCC R: TTACCCAGGTGAGATTTTCGG	KY434205	-3,2	0,98	100	2,0

Slopes (-3.1, -3.6), R², efficiencies (Eff, 90-110) and amplification (Amp) for each primer couple was checked through the creation of a five points standard curve with serially diluted 1:5 cDNA from 5 samples (MDV: SC7, SC9, SC11 and LMP: SC56, SC57). Amplification and efficiency were calculated using the equation from Dhar et al. (2009).

Table 3. Percentage of change in MDV samples compared to LMP samples.

	Md	MAT	CF	HSI
Diff				
F		- 34%	0%	- 24%
M		- 34%	- 3%	+ 20%

Md, Morphometric data. Diff, % of change in MDV vs LMP. F, females; M, males. MAT, gonadal maturity. CF, condition factor. HIS, hepato-somatic index.

Table 4. Microplastic (MP) and Macroplastic (MaP) total number, particles, fibers, average ingested by individual fish and frequency of ingestion.

Catch area	N. specimens	Total number MP	Filaments	Fragments	Average / fish	Frequency of ingestion
GSA 16 MDV	25	33	24	9	1.32	71%
GSA 13 LMP	25	26	19	7	1.04	62%
Catch area	N. specimens	Total number MaP	Filaments	Fragments	Average / fish	Frequency of ingestion
GSA 16 MDV	25	6	-	6	0.24	20%
GSA 13 LMP	25	5	-	5	0.2	16%

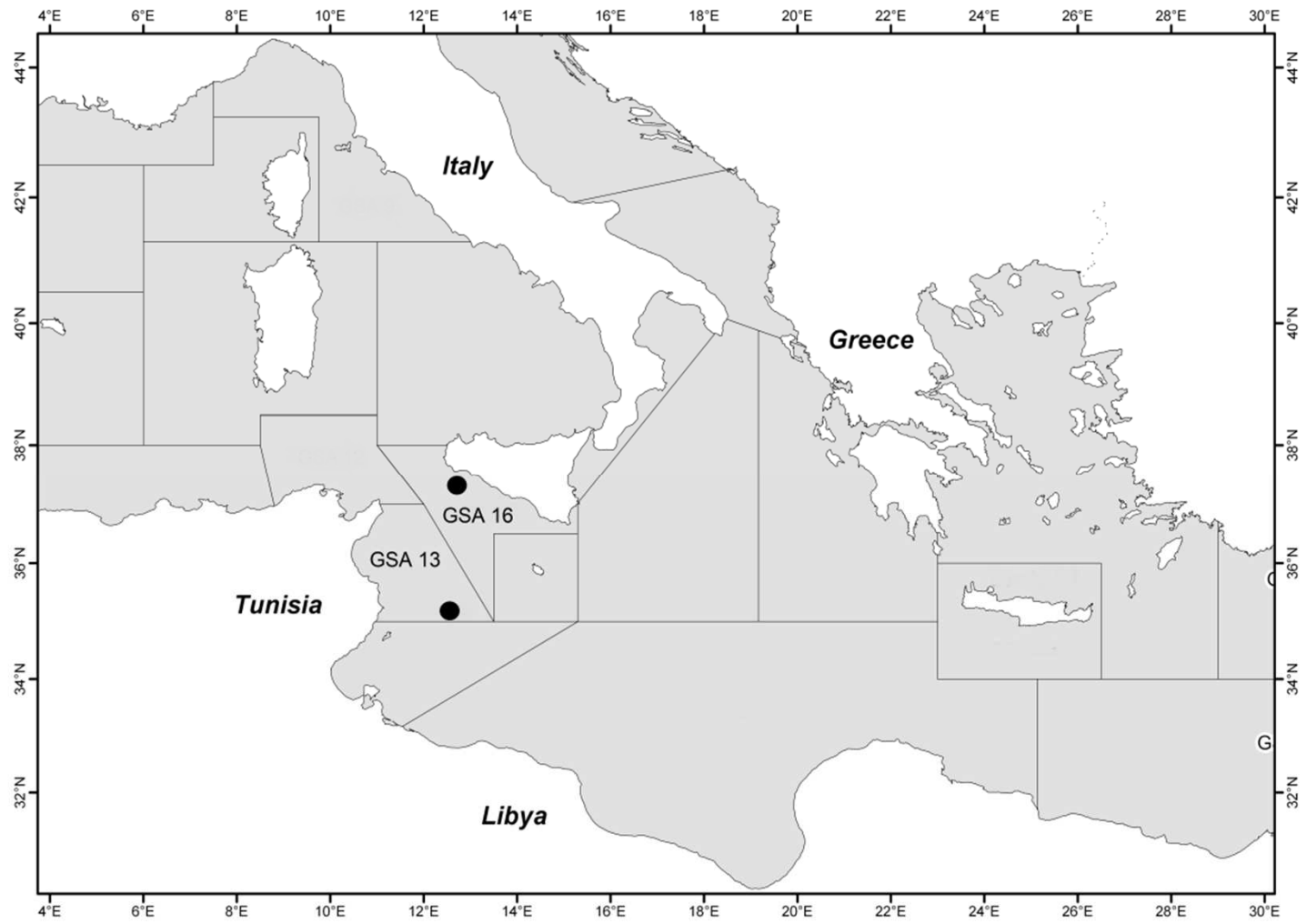


Figure 1.

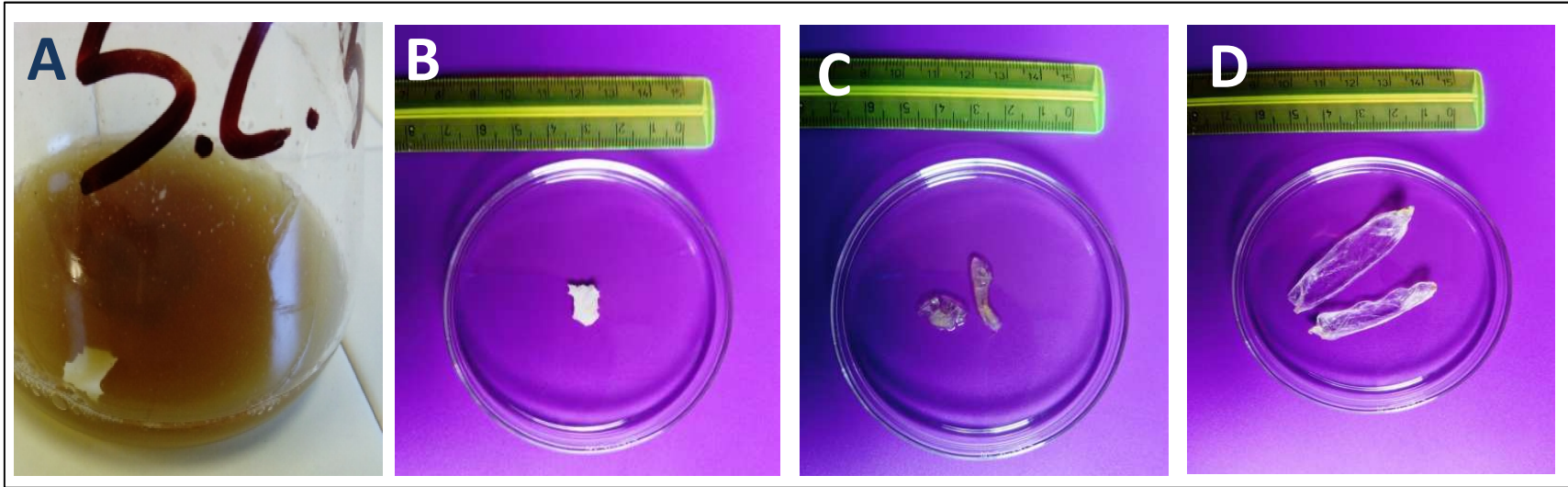


Figure 2.

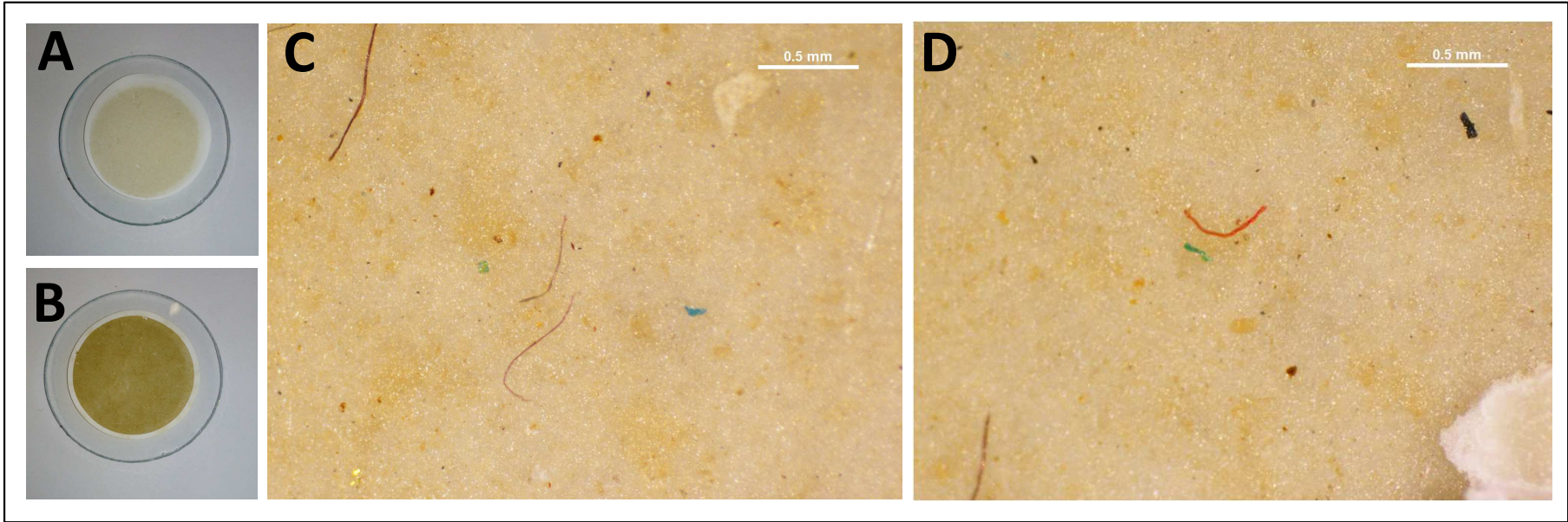


Figure 3.

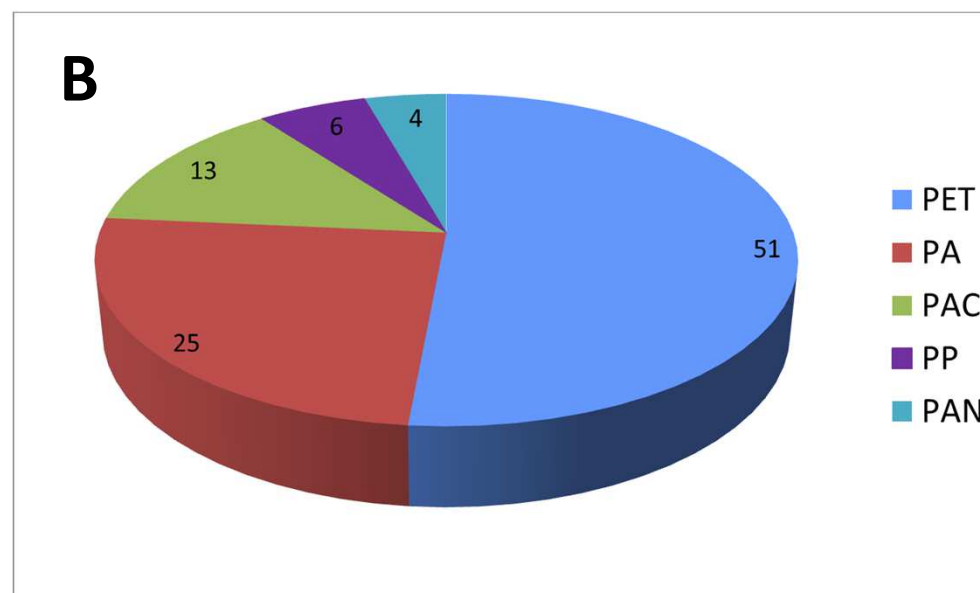
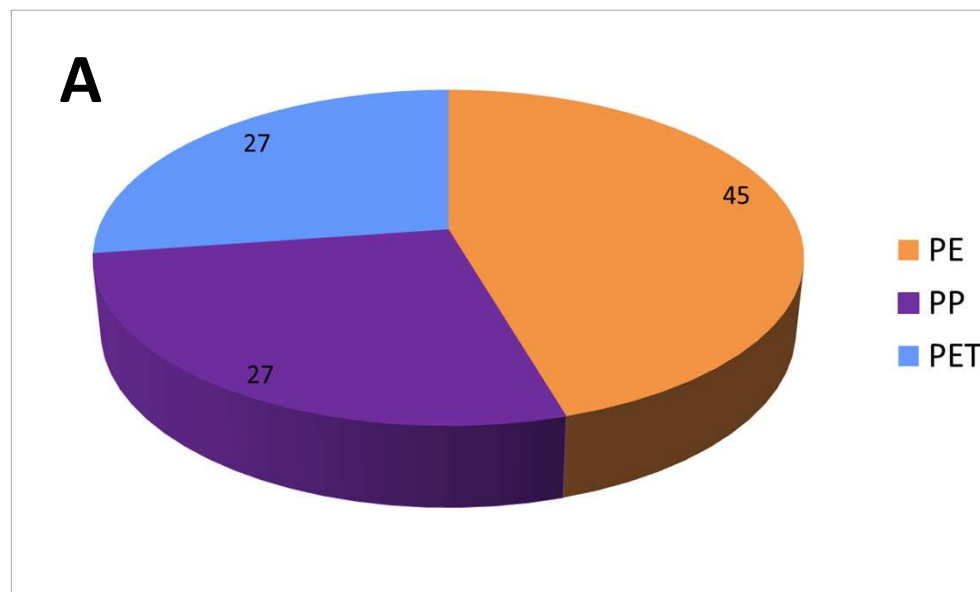


Figure 4.

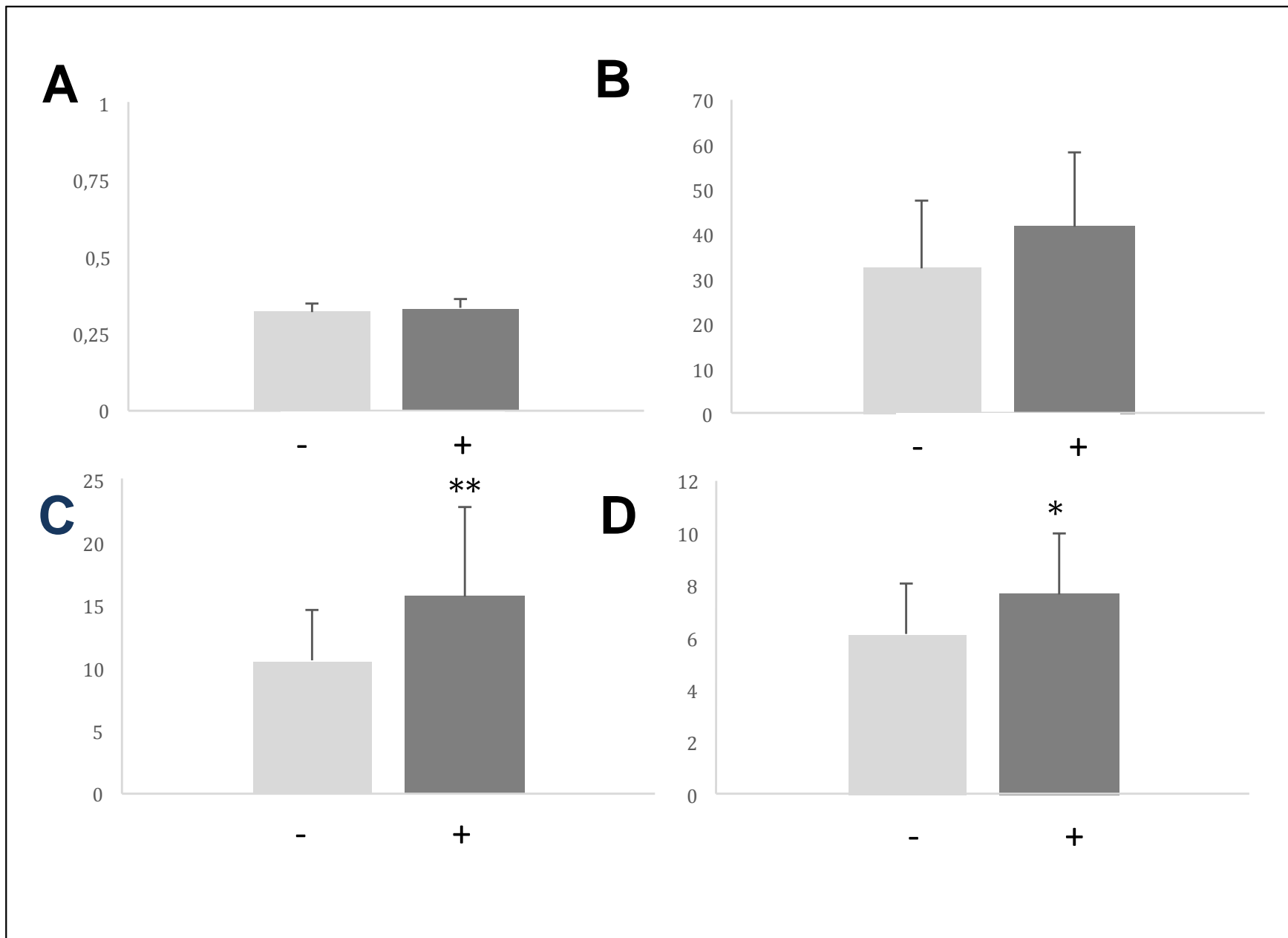


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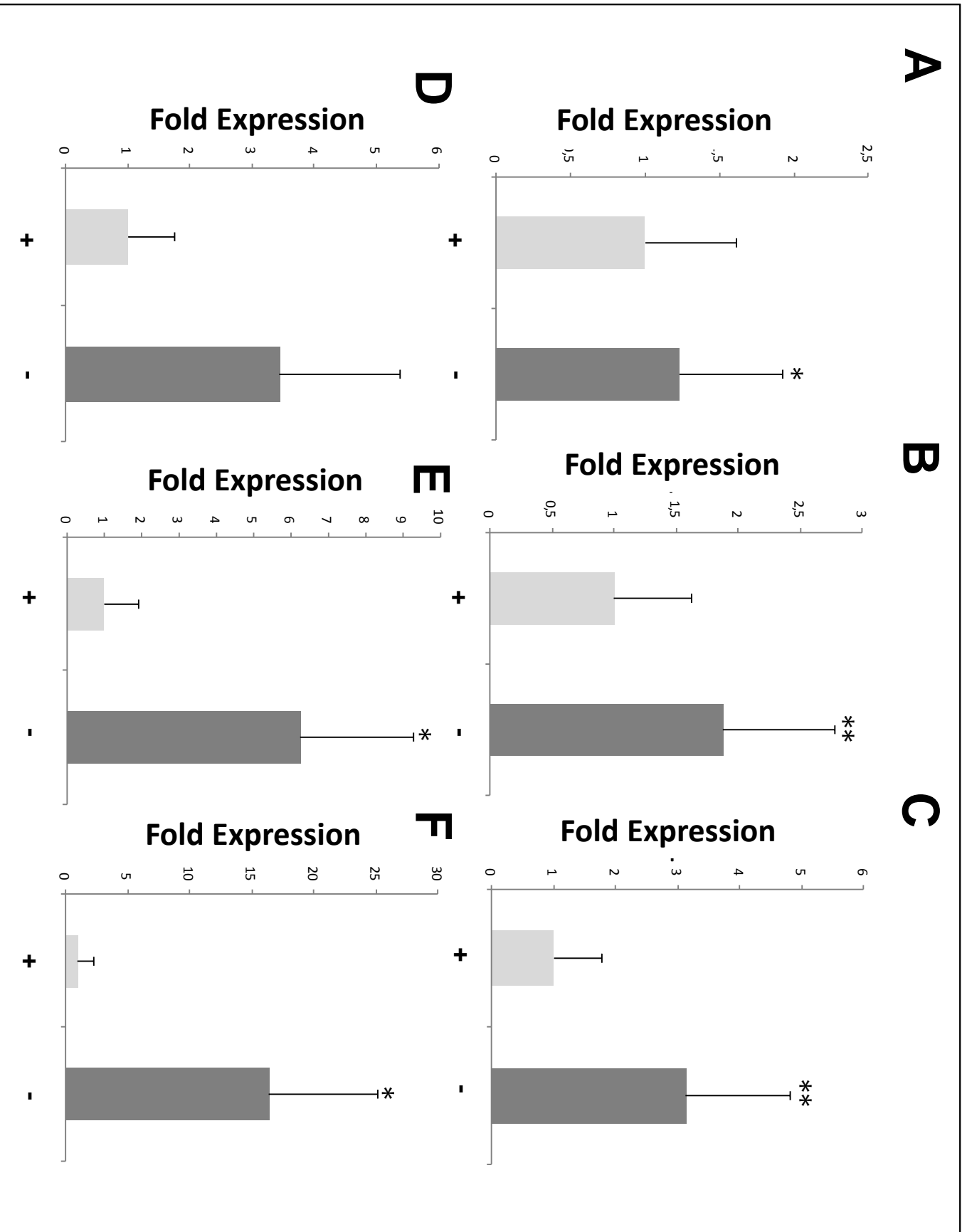


Figure 6.

- We describe microplastics and macroplastics in small spotted sharks (*S. canicula*) sampled in two geographic locations in the southern region of the central Mediterranean Sea;
- We characterized the plastics in the shark's gastrointestinal tract (GIT) using microscopy and μ -Raman spectroscopy;
- We analyzed morphometric data in correlation of geographical location and plastic load;
- We measured the expression of immune-related genes for potential correlation to location and plastic detection.

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