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1 **Marine transmissible cancer navigates urbanised waters, threatening to spillover**

2

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13

14 **Abstract**

15 Inter-individual transmission of cancer cells represents a unique form of microparasites
16 increasingly reported in marine bivalves. In this study, we sought to understand the ecology of
17 the propagation of *Mytilus trossulus* Bivalve Transmissible Neoplasia 2 (MtrBTN2), a
18 transmissible cancer affecting four *Mytilus* mussel species worldwide. We investigated the
19 prevalence of MtrBTN2 in the mosaic hybrid zone of *M. edulis* and *M. galloprovincialis* along
20 the French Atlantic coast, sampling contrasting natural and anthropogenic habitats. We observed
21 a similar prevalence in both species, likely due to the spatial proximity of the two species in this
22 region. Our results showed that ports had higher prevalence of MtrBTN2, with a possible hotspot
23 observed at a shuttle landing dock. No cancer was found in natural beds except for two sites
24 close to the hotspot, suggesting spillover. Ports may provide favourable conditions for the
25 transmission of MtrBTN2, such as high mussel density, stressful conditions, sheltered and

26 confined shores, or buffered temperatures. Ships may also spread the disease through biofouling.
27 Our results suggest ports may serve as epidemiological hubs, with maritime routes providing
28 artificial gateways for MtrBTN2 propagation. This highlights the importance of preventing
29 biofouling on docks and ship hulls to limit the spread of marine pathogens hosted by fouling
30 species.

31

32 **Keywords:** Transmissible cancer, Bivalve Transmissible Neoplasia, epidemiology, biofouling,
33 spillover, *Mytilus* mussels.

34

35 1. Introduction

36

37 Transmissible cancers are caused by malignant cell lineages that have acquired the ability
38 to infect new hosts through the transmission of living cancer cells. Fourteen transmissible cancer
39 lineages have been described to date: one in dogs (canine transmissible venereal tumour, CTVT
40 [1, 2]), two in Tasmanian devils (devil facial tumour, DFT1 and DFT2 [3, 4]), and eleven in
41 different marine bivalve species (bivalve transmissible neoplasia, BTNs [5–10]). While direct
42 contact is necessary for CTVT and DFTs transmission, via coitus for the former and biting for
43 the latter, the transmission of BTNs between shellfish is assumed to occur through the seawater
44 column [11, 12]. *Mytilus* spp. mussels are affected by two BTN lineages known as MtrBTN1 and
45 MtrBTN2 that originate from two different *M. trossulus* founder hosts. MtrBTN2 is distributed
46 worldwide and has crossed the species barrier several times to infect four *Mytilus* species: *M.*
47 *trossulus* in East Asia and Northern Europe [13–15], *M. chilensis* in South America [9], and *M.*
48 *edulis* and *M. galloprovincialis* in Europe [9, 16]. Cancerous process in mussels was firstly
49 described fifty years ago as disseminated neoplasia (DN, [17]) but the demonstration that some
50 DNs are transmissible is recent [6, 7]. As non-transmissible neoplasia also occurs in mussels [9,
51 16], a genetic diagnosis is required to ensure the identification of MtrBTNs. The oldest known
52 genetically validated MtrBTN2 was sampled in 2009 [9]. Genetic data suggest that it could be at
53 least one or two orders of magnitude more ancient, although dating is difficult due to an apparent
54 acceleration of the mitochondrial clock [15, 16].

55

56 The global distribution of the MtrBTN2 lineage remains enigmatic [9, 14]. The other known
57 transmissible cancer with such a worldwide distribution is CTVT in dogs. CTVT emerged 4,000
58 to 8,000 years ago, probably in Eastern Asia, and has expanded rapidly worldwide over the past
59 500 years, probably facilitated by the development of maritime transportation [18]. Transmission
60 of MtrBTN2 within mussel populations occurs presumably through filter-feeding (discussed in
61 [11, 19]). MtrBTN2 cells can survive for several days in seawater [11], which greatly increases
62 their chances of infecting new hosts. However, it is unlikely that transport of cancer cells by
63 marine currents alone explains such a global distribution. Indeed, the dilution of cancer cells in
64 the marine environment may strongly limit the success of transmission over long distances.
65 Shipping traffic has been proposed as the most likely explanation for the global distribution of
66 MtrBTN2 -i.e., the transport of disease-carrying mussels on ship hulls [9, 14, 15]. To our
67 knowledge, these claims have remained speculative and no formal evidence of the effect of
68 shipping traffic and port habitat on the epidemiology of BTN has been provided to date.

69
70 European mussels are affected by MtrBTN2, with a much higher prevalence in *M. edulis* (of the
71 order of 1/100) than in *M. galloprovincialis* (of the order of 1/1000) [16]. These two host species
72 are parapatric in Europe and can coexist in contact zones where hybridisation is taking place
73 [20–22]. Associations between genetic backgrounds and environmental variables indicate that
74 the environment partly influences the structure and maintenance of the hybrid zones: in the study
75 area, *M. edulis* genotypes are more frequent in sheltered habitats under freshwater influence,
76 while *M. galloprovincialis* genotypes are more frequent in habitats exposed to wave action and
77 ocean salinities [23, 24]. In this context, the distribution and propagation of MtrBTN2 is likely to
78 be influenced by host genetic background and population composition [16], as well as by other
79 environmental factors such as population density, reduced hydrodynamics, and stressful
80 environmental factors (e.g., heat, salinity or pollution stresses). MtrBTN2 global distribution
81 indicates its resilience across a broad range of temperature with varying seasonal patterns [14],
82 reflecting host species distribution range. Prior to evidence of horizontal transmission, pollutants
83 have been suggested as a potential cause of DN; however, the association with disease
84 prevalence remained inconclusive [25–27], and as we now know that some neoplasias are
85 transmissible, it is no longer the initial carcinogenesis but the transmission that needs to be
86 explained. Seasonal influence on DN prevalence was observed at a local scale (higher during

87 winter in *M. trossulus*, [28, 29], and *M. edulis*, [30]), whereas no significant influence of
88 seasonality was noted at the European scale [31]. Unfortunately, in the absence of genetic
89 diagnostics, we cannot know how many of these DNAs were indeed BTNs (i.e. transmissible) or
90 not, and rigorous evaluation of MtrBTN2 prevalence seasonality is still lacking. In brief, little is
91 known about the ecology of MtrBTN2 in relation to its host and the possible environmental
92 factors influencing the epidemiology of this transmissible cancer.

93
94 In the present study, we investigated the occurrence of MtrBTN2 in a survey area in Southern
95 Brittany (France) which has contrasting natural and anthropogenic habitats and a mosaic
96 distribution of *M. edulis* and *M. galloprovincialis*. We sampled 40 natural populations as well as
97 9 mussel farms, 7 floating buoys, and 20 ports. To detect MtrBTN2-infected mussels, we used
98 digital PCR and real-time PCR, amplifying one nuclear and two mitochondrial genes with
99 published and newly designed primers targeting specific variants. We found a low prevalence of
100 MtrBTN2 (23/1516), equally affecting the two coexisting *Mytilus* species. Interestingly, most
101 affected sites (7/9) were ports, suggesting that ports could be favourable habitats for MtrBTN2
102 transmission and/or that maritime transport could play a role as a vector for the spread of the
103 disease. This highlights the possible role of ports as epidemiological hubs for MtrBTN2
104 propagation.

105

106 **2. Material and methods**

107

108 **2.1. Sampling**

109 We collected 1516 *Mytilus* spp. mussels from 76 sites of the French Atlantic coast, from the Bay
110 of Quiberon to Pornic, between January and March 2020. Approximately 20 mussels were
111 sampled at each site (Table S1), allowing us to have a large number of closely located sites. We
112 collected hemolymph from adductor muscle (with a 1 ml syringe, 26G needle) and a piece of
113 mantle; both samples were fixed with 96% ethanol as described in [16]. DNA extraction was
114 performed with the NucleoMag 96 Tissue kit (Macherey-Nagel) using a Kingfisher Flex
115 extraction robot (serial number 711-920, ThermoFisher Scientific). We followed the kit protocol
116 with a modified lysis time of 1 hour at 56°C and modified the volumes of some reagents: beads
117 were diluted twice in water, 200 µl of MB3 and MB4, 300 µl of MB5 and 100 µl of MB6. DNA

118 concentration (ng/ μ l) was quantified using the Nanodrop 8000 spectrophotometer (ThermoFisher
119 Scientific). DNA from hemolymph was used for MtrBTN2 detection and DNA from mantle was
120 used for mussel genotyping (Figure S1).

121

122 **2.2. MtrBTN2 detection**

123 As the prevalence of MtrBTN2 is expected to be low [16, 32] and the number of samples is high
124 ($n = 1516$), we chose to pre-screen by pooling 12 samples (pooled screening step; Figure S1) and
125 then demultiplexing positive pools to specifically target cancerous samples (simplex screening
126 step; Figure S1). Prior to pooling, DNA concentrations were adjusted to 10 ng/ μ l to obtain an
127 unbiased representation of each sample in the pool. This allowed us to considerably reduce the
128 cost and time of detection, but we acknowledge that this protocol could result in some very early
129 stages of the disease being missed. To partly circumvent this problem, MtrBTN2 detection in
130 pools was performed by digital PCR (ddPCR) targeting one nuclear (Elongation Factor, EF) and
131 one mitochondrial (Control region, described in [9]) marker (Table S2). ddPCR is a sensitive
132 method, based on the Taqman method which requires two primers and one probe, and which
133 directly estimates the copy number of the targeted sequence. In addition, the use of a
134 mitochondrial marker should provide a more sensitive detection as the mitochondrial genome has
135 more copies than the nuclear genome. ddPCR primers design and analysis was subcontracted to
136 the company IAGE using the QIAcuity™ system (QIAGEN). Positive pools were then
137 demultiplexed (simplex screening step; Figure S1) and MtrBTN2 detection was performed by
138 real-time PCR targeting one nuclear (Elongation Factor, EF1 α -i3, described in [11]) and one
139 mitochondrial (cytochrome c oxidase I, mtCOI-sub) marker (Table S2). To design the mtCOI-
140 sub primers, we used sequences of *M. edulis*, *M. galloprovincialis*, *M. trossulus*, and MtrBTN2
141 available from the National Center for Biotechnology Information (NCBI). Please note that
142 mtCOI-sub primers were initially designed to amplify a polymorphism that discriminates
143 between two MtrBTN2 sub-lineages “a” and “b” [16]. However, attempts to identify sub-
144 lineages based on melting temperature (T_m) did not yield conclusive results, most likely due to
145 additional polymorphism. Amplification of EF1 α -i3 and mtCOI-sub markers was performed
146 using a three-step cycling protocol (95°C for 10 s, 58°C for 20 s, 72°C for 25 s) for 40 cycles.
147 We carried out real-time PCRs using the SensiFAST™ SYBR No-ROX Kit (Bioline) and the
148 LightCycler 480 Real-Time PCR System (Roche Diagnostics). We also confirmed the positive

149 samples diagnosed by real-time PCR using ddPCR (simplex screening step; Figure S1). The
150 specificity of both methods and markers was tested using various control samples of *M. edulis*,
151 *M. galloprovincialis*, *M. trossulus*, and MtrBTN2 samples of early, moderate, or late stages
152 (based on cytological observations, following [32], Tableau S3). To test the sensitivity, we used
153 positive controls with MtrBTN2 DNA diluted 10-fold (x10) and 100-fold (x100) in *M. edulis*
154 DNA.

155
156 Real-time PCR results were analysed using the LightCycler480 software. Two parameters were
157 extracted: threshold cycle (CT), obtained by Absolute Quantification analysis using the Second
158 Derivative Maximum method, and T_m, obtained by T_m calling analysis. Positive samples were
159 defined as those with a CT of less than 35 cycles and a T_m between 77.46 to 78.71 (based on T_m
160 values of the positive control samples; see result, Figure S2). ddPCR results were analysed with
161 the QuantaSoft™ Analysis Pro software (Bio-Rad), which provides the copy number for each
162 sample. Samples were considered positive when there were more than two positive droplets.

163

164 **2.3. Mussel genotyping**

165 We used 10 biallelic SNPs known to discriminate between *M. edulis* and *M. galloprovincialis*
166 mussel species (Table S4). These markers were identified as being ancestry-informative (fixed
167 for alternative alleles in *M. edulis* and *M. galloprovincialis*) in the [33] dataset and were
168 subsequently confirmed as near diagnostic by analysis of larger datasets [22, 34]. Genotyping
169 was performed using the Kompetitive Allele Specific PCR (KASP) method [35]. As we wanted
170 to know the mean ancestry of each sample (G ancestry) and reduce the cost of genotyping, we
171 developed a multiSNPs marker by multiplexing the 10 SNPs. Rapidly, 1µL of assay mix (KASP-
172 TF V4.0 2X Master Mix, 1X target concentration; primers, 1µM target concentration;
173 HyClone™ HyPure water) and 0.5 µL of DNA at 10 ng/µL were mixed in qPCR 384-well plates
174 using Labcyte Echo525 (BECKMAN COULTER). KASP analysis was performed on the
175 LightCycler 480 Instrument (Roche Diagnostics) with the following thermal cycling conditions:
176 initialisation 15 min at 95°C, first amplification 20 s at 94°C and 1 min at 61°C to 55°C with
177 steps of 0.6°C for 10 cycles, second amplification 20 s 94°C and 1 min at 55°C for 29 cycles,
178 read 1 min at 37°C and 1 s at 37°C.

179 KASP results are a combination of two fluorescence values, one for allele X, and another for
180 allele Y. Here, we oriented all SNPs so that allele X corresponds to *M. edulis* and allele Y to *M.*
181 *galloprovincialis*. Following [36], we transformed the data to obtain a single measure of the
182 relative fluorescence of the two alleles, using the following formula: $y_{i,j} = Y_{i,j}/(X_{i,j} + Y_{i,j})$;
183 where $X_{i,j}$ and $Y_{i,j}$ are the fluorescence values of allele X and allele Y, respectively for, i^{th} SNP of
184 the j^{th} sample. To scale $y_{i,j}$ value from 0 when *M. edulis* allele fluorescence dominates at the 10
185 SNPs to 1 when *M. galloprovincialis* allele fluorescence dominates, we used the following
186 formula: $y'_{i,j} = (y_{i,j} - \min(y_i))/(\max(y_i) - \min(y_i))$; where $y_{i,j}$ is the relative fluorescence
187 value for the i^{th} SNP of the j^{th} sample. In the results section and figures, $y'_{i,j}$ corresponds to “G
188 ancestry”.

189

190 **2.4. Environmental data**

191 ***Source of environmental data***

192 The 76 sampling sites were selected to cover four different habitats (ports, natural beds, farms
193 and floating buoys) presenting contrasted environments and genetic backgrounds (*M. edulis*, *M.*
194 *galloprovincialis* and hybrids). The description of environmental data considered in this study is
195 reported in Table S5 and all site information is available in Table S1. Note that natural beds are
196 intertidal sites, while the other habitats are subtidal. During sampling, we collected two habitat
197 discrete descriptive variables: population density (1: isolated, 2: patchy beds, 3: continuous beds)
198 and wave action (1: exposed, 2: sheltered). We used the E.U. Copernicus Marine Service
199 Information (doi: [10.48670/moi-00027](https://doi.org/10.48670/moi-00027)) to access temperature (°C), salinity (PSU 1e-3) and
200 surface current velocity (m.s-1) data for each site (monthly recorded from 2021, resolution of
201 0.028°x0.028°). The velocity variable was formed by combining its Northward (N) and Eastward
202 (E) components, as follow: $\sqrt{E^2 + N^2}$. We also used EMODnet Human Activities (source:
203 EMSA Route Density Map) to retrieve the maritime traffic density of fishing, passenger, and
204 recreational boats in the study area (seasonal record from 2018, 2019 and 2020, resolution 1x1
205 km).

206

207 ***Preparation of environmental data***

208 Among the 76 sampled sites, 13 fell outside the coverage scope of the Copernicus model (i.e.
209 situated beyond the model’s pixel boundaries). Consequently, for these sites (see Table S1), we

210 were unable to extract temperature, salinity, or velocity data. Certain sites recorded a velocity of
211 0 for all month (Table S1), raising concerns about the model resolution for this variable. To
212 validate the accuracy of Copernicus data, we computed the mean values of neighbouring pixels
213 (MNP, within a 0.05° buffer zone) and compared them to the pixel values at the respective sites
214 of interest (SP, referred to as the 'central' pixel, Table S6). We note that, due to the proximity of
215 our sampled sites to the coastline, the number of neighbouring pixels varied within a certain
216 range (Table S6). Notably, there was no correlation between these variations and the absolute
217 difference between SP and MNP values (Figure S3C). The comparison between SP and MNP
218 values was carried out for all sites, encompassing temperature, salinity, and surface current
219 velocity, and the results are presented in Figure S3. We observed a robust positive correlation for
220 temperature and salinity variables, providing confidence in the reliability of the extracted data for
221 our small-scale analysis. However, as expected, the inconclusive correlation for surface current
222 velocity led us to exclude this environmental variable from the analyses.

223 In the statistical analysis (see section 2.5) we used the annual average of salinity and boat
224 density (maritime traffic). For temperature, we used the annual variance as we identified strong
225 seasonal variations in temperature that would be misinterpreted if only the annual average
226 temperature were used (Figure S4).

227

228 **2.5. Statistical analysis: relationship between MtrBTN2 prevalence, host genotype and** 229 **environmental variables**

230

231 To ascertain whether cancer prevalence varied among the four habitats sampled (ports, natural
232 beds, buoys and farms), we performed Fisher's exact test on the contingency table (*fisher.test()*
233 function of the *stats* package *v4.1.3* [37]). Subsequently, we aimed to determine whether specific
234 environmental variables could provide a more comprehensive explanation of MtrBTN2
235 prevalence across these habitats. To do so, we pursued the following steps: an exploratory
236 analysis with a Principal Component Analysis (PCA), an examination of data dependencies
237 (Spearman correlation test and Moran's I test), and lastly, a regression model adapted to our
238 dataset (spatial logistic regression model). All statistical analyses were performed in R *v4.1.3*
239 [37].

240

241 ***Principal component analysis***

242 As an exploratory analysis, we firstly performed a PCA to investigate the relationship between
243 the quantitative environmental variables. Missing values were estimated using *imputePCA()*
244 (*missMDA* package v1.18 [38]), prior to performing the PCA using *PCA()* (*FactoMineR* package
245 v2.6 [39]).

246

247 ***Spearman correlation test***

248 To test for correlation between environmental variables, we performed a non-parametric test of
249 Spearman using *rcorr()* function from *Hmisc* package [40], that automatically excludes missing
250 data.

251

252 ***Moran I test for spatial autocorrelation***

253 Given the proximity of the sampled sites, which constitutes a fine spatial matrix, we used the
254 Moran's I statistic to test for spatial autocorrelation among the environmental variables. After
255 converting longitude and latitude data into UTM coordinates (*spTransform()* function of *rgdal*
256 package v1.6-7 [41]), this analysis was performed using the *moran.test()* function (*spdep*
257 package version 1.2-8 [42]) with the k-nearest neighbour classification.

258

259 ***Spatial logistic regression model***

260 The association of MtrBTN2 prevalence and environmental variables was tested at the site level
261 using a multivariate spatial logistic regression (*fitme()* function, *spaMM* package v4.3.0 [43]).
262 Spatial autocorrelation was accounted for by including a Matern covariance function as a random
263 effect (i.e. *Matern(1 | Longitude +Latitude)*). MtrBTN2 prevalence was represented as a binary
264 matrix ($N, N_{site}-N$) with N and N_{site} indicating site-specific MtrBTN2 case counts and total
265 number of sampled mussels, respectively. The following explanatory variables were included
266 into the full model: temperature variance, salinity mean, population abundance, wave action,
267 average *M. galloprovincialis* ancestry of the mussel host population (G ancestry), maritime
268 traffic (as described above, section 2.4). We also included a binary variable "port" into the
269 model, where 1 denotes port habitat and 0 represents other habitats. Model suitability was
270 evaluated using the residual diagnostics tool implemented in the "DHARMA" package [44]. To
271 assess the significance of fixed effects (environmental variables), we performed Bartlett-

272 corrected likelihood ratio tests (LR tests) by comparing the full model with a model that
273 excluded the variable of interest (*fixedLRT()* function of *spaMM* package v4.3.0 [45]). To
274 account for bias associated with rare events and collinearity of environmental variables (see
275 results), LR tests were performed using 999 bootstraps.

276

277 **3. Results**

278 **3.1. Validation of the screening method**

279 In order to detect MtrBTN2 in thousands of individuals, we developed dedicated ddPCR and
280 qPCR screening tools. The design of real-time PCR and ddPCR primers and probes allowed us to
281 amplify nuclear and mitochondrial markers specific to *M. trossulus* mussels and MtrBTN2
282 (Figure S5, TableS7). However, for the mtCOI-sub locus, the melting temperature (T_m) range of
283 MtrBTN2 was different from *M. trossulus* controls and allowed us to specifically detect
284 MtrBTN2 based on T_m values (Figure S2). With ddPCR, all MtrBTN2 control samples were
285 detected, regardless of marker or dilution, except for one MtrBTN2 sample diluted at x100 which
286 was negative for the EF locus (Figure S5). Copy numbers appeared higher for the mtCR marker,
287 showing a higher sensitivity for this mitochondrial marker. The same pattern was observed for
288 EF1 α -i3 and mtCOI-sub in real-time PCR, with a higher sensitivity of the mitochondrial marker
289 based on the lower CT values observed (Figure S5). However, two MtrBTN2 samples diluted at
290 x100 were negative for mtCOI-sub and positive for EF1 α -i3. Even though the mitochondrial
291 marker appears to be more sensitive in both methods, we chose to screen for MtrBTN2 using
292 both markers in order to have comparisons and additional validation.

293

294 **3.2. MtrBTN2 screening reveals a low prevalence**

295 We amplified nuclear and mitochondrial markers using ddPCR (EF, mtCR) and real-time PCR
296 (EF1 α -i3, mtCOI-sub) to detect the presence of MtrBTN2 in the 1516 mussels sampled from the
297 76 sites of the study area (Figure S1). All results of the pooled and simplex screening are
298 presented in TableS8.

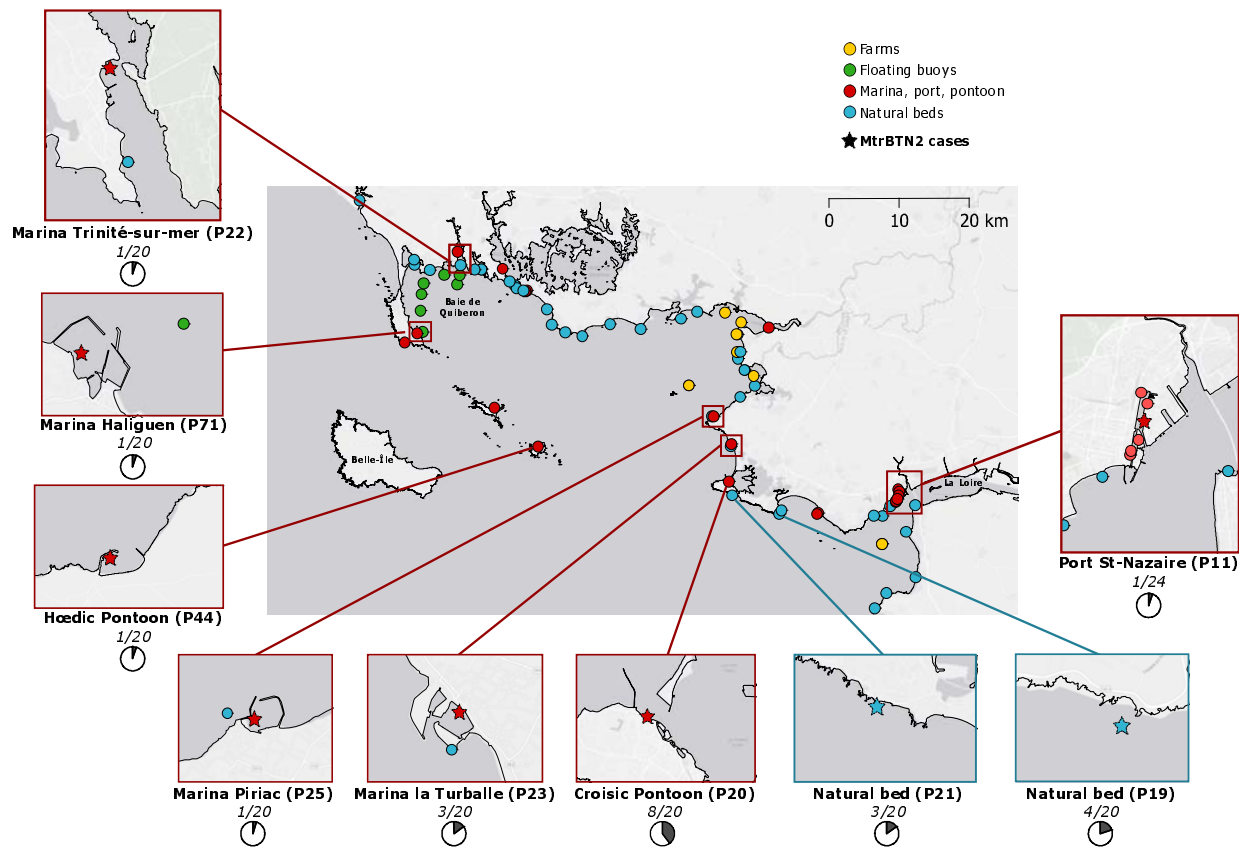
299 The pooled screening step using ddPCR revealed 25/127 positive pools: 9/127 with EF, 14/127
300 with mtCR, and 2/127 were positive for both markers (Figure S5). As the 14 mtCR-positive
301 pools showed low copy numbers (median = 7.59), we assume that EF did not amplify because of
302 a detection threshold. Although the 9 EF-positive pools were not expected, they were included

303 for further investigation by simplex screening (see below). For pools positive for both markers,
304 the EF copy numbers appear relatively low compared to mtCR copy numbers. This is due to the
305 high mitochondrial fluorescence masking the nuclear fluorescence and underestimating EF copy
306 numbers. To eliminate this bias in the simplex ddPCR step (Figure S1), we amplified the two
307 markers separately. In order to maximise cancer detection in the simplex screening step, we
308 chose to keep the pools positive for at least one gene, corresponding to 25 positive pools of 12
309 samples ($n = 300$).

310 We performed the simplex screening step using real-time PCR and then confirmed positive
311 samples with ddPCR (Figure S1). In total, 44/300 samples were positive for at least one real-time
312 PCR marker: 16 with EF1 α -i3 only, 23 with mtCOI-sub only, and 5 with both markers (Figure
313 S5, Table S9). Pooled and simplex screening results are mostly consistent, as 20 of the 25
314 positive pools had at least one individual detected by real-time PCR amplification (Table S10).
315 The 5 pools without positive samples had low ddPCR copy numbers (less than 3.37 for EF and
316 less than 6.65 for mtCR). These false positives were to be expected as we intentionally applied
317 low threshold values in the pooled screening step. Two samples from mtCR-positive pools were
318 found to be positive for both markers at the simplex level, which was expected as the
319 mitochondrial marker is likely to be more sensitive than the nuclear marker. On the contrary, we
320 did not expect to observe samples positive for EF1 α -i3/EF and negative for mtCOI-sub/mtCR.
321 However, all but one of the individuals from the EF-positive pools were positive only for the
322 EF1 α -i3 marker (Table S10). The absence of mitochondrial genes in these samples does not
323 seem to be related to a detection threshold issue, especially as ddPCR and real-time PCR target
324 two different genes (mtCR and mtCOI-sub). We suspect that some host alleles that were present
325 at low frequencies in the ‘dock mussels’ populations (the hybrid lineage found in the port of
326 Saint-Nazaire [34]) may sometimes be amplified with EF1 α -i3. This could be explained by
327 shared polymorphism between host species rather than the presence of MtrBTN2. Therefore, the
328 16 samples positive only for EF1 α -i3 were conservatively considered as false positives (note
329 they were mostly sampled in the port of Saint-Nazaire, which does not affect our main result).
330 For the remaining 28 samples, we performed ddPCR with both markers to confirm the real-time
331 mitochondrial PCR diagnosis (Figure S1, TableS9). For 23/28 samples, mtCR ddPCR confirmed
332 the mtCOI-sub real-time PCR diagnosis. For 10/23 samples positive only for mtCOI-sub, ddPCR
333 revealed few EF copies. Finally, we considered all samples positive for mitochondrial markers

334 with both methods to be cancerous samples. We found 23/1516 positive samples from 9/76 sites
335 in which the number of cases varied from 1 to 8 (Figure 1). The highest proportion of cancerous
336 mussels was found at site P20 (Croisic Pontoon), and the next highest in the vicinity of this site
337 (P19, P21, and P23; Figure 1).

338



339

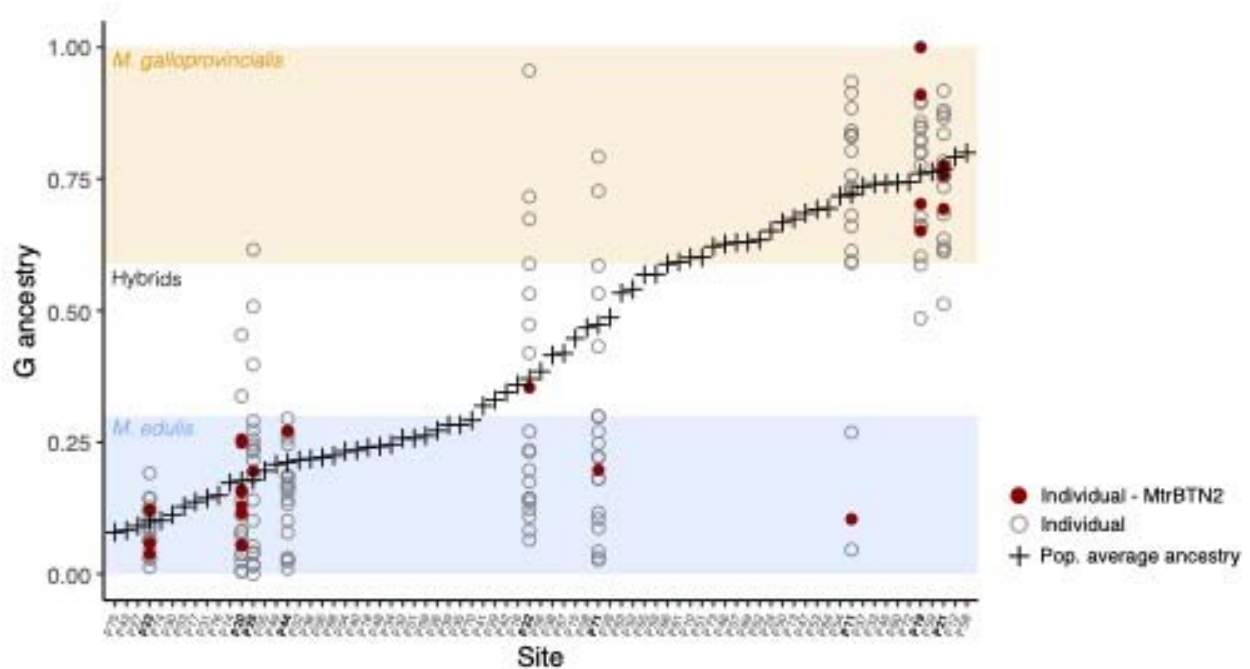
340 **Figure 1: Location of sampling sites.** Zoomed-in sites correspond to sites where mussels are
341 affected by MtrBTN2. Pie graphs and numbers in italics correspond to the proportion of
342 cancerous samples in each site. Coloured points represent the type of site, as indicated in the
343 figure's legend. Map origin: Ersi gray (light).

344

345

346 **3.3. *M. edulis* and *M. galloprovincialis* are equally affected by MtrBTN2**

347 To determine whether host genetic background or population composition influences cancer
348 prevalence and distribution, mussels were genotyped using 10 SNPs known to be diagnostic
349 between *M. edulis* and *M. galloprovincialis* (the two species coexisting in the studied area).
350 To reduce the cost of genotyping, we developed a multiplex assay, mixing 10 SNPs that directly
351 give the average ancestry of the sample (G ancestry, Figure S1). This approach was validated by
352 comparing the multiplex fluorescence and average simplex fluorescence of SNPs from a set of
353 samples (Figure S6a). We genotyped each individual from the 9 sites affected by MtrBTN2 (180
354 mussels) and estimated the average ancestry of each site by genotyping pools of individuals (76
355 pools). The positive correlation between the average individual fluorescence of a site and the
356 fluorescence of the corresponding pool validated our approach (Figure S6b). Mussels with G
357 ancestry values below 0.3 were assigned to *M. edulis*, those with values above 0.59 to *M.*
358 *galloprovincialis*, and those in between were assigned as hybrids (Figure 2, FigureS7). Of the
359 mussels affected by MtrBTN2, 15/23 were assigned to *M. edulis*, 7/23 to *M. galloprovincialis*
360 and 1/23 was a hybrid (Table S11). Considering the sites affected by MtrBTN2, MtrBTN2
361 prevalence did not appear to be significantly different between species with 15/105 (14%) in *M.*
362 *edulis*, 7/60 (11%) in *M. galloprovincialis* and 1/15 (6%) in hybrids (Fisher's exact test, p-value
363 = 0.83). Most *M. edulis* mussels affected by MtrBTN2 were found in populations with a majority
364 of *M. edulis* (P44, P23, P20), only two were found in populations with some hybrids and *M.*
365 *galloprovincialis* mussels (P25, P71) and only one in a population with a majority of *M.*
366 *galloprovincialis* (P11, Figure 2, Figure S7). Interestingly, all *M. galloprovincialis* mussels
367 affected by MtrBTN2 were found in *M. galloprovincialis* populations (P19, P21, Figure 2,
368 FigureS7), which are close to the site with the highest prevalence (Croisic pontoon, Figure 1).
369 Finally, the hybrid individual affected by MtrBTN2 was found in a population where the two
370 species coexist (P22, Figure 2, FigureS7).
371



372

373 **Figure 2: Individual and population ancestry.** G ancestry of healthy (empty grey circle) and
374 MtrBTN2 affected (dark red) hosts is shown for the 9 sites with cancer (bold labels). Population
375 average ancestry for all sampled sites is represented by black crosses. Blue, white and orange
376 rectangles correspond to the G ancestry range of *M. edulis*, hybrids and *M. galloprovincialis*
377 respectively.

378

379 **3.4. *MtrBTN2* infected mussels are mostly found in ports**

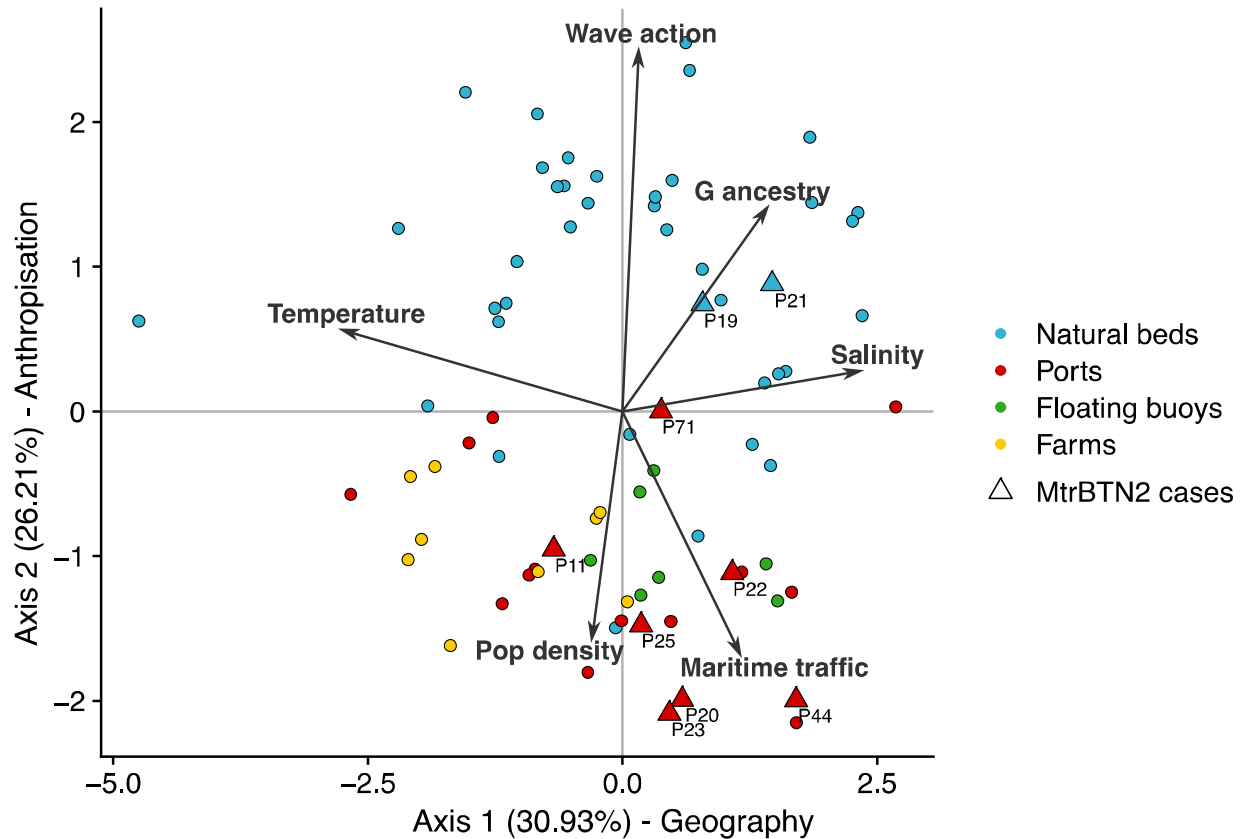
380 After the MtrBTN2 detection step, which revealed 23/1516 individuals infected with this
381 transmissible cancer, we investigated associations with habitat types. Cancerous samples were
382 found in 7 ports (16/23 infected mussels) and 2 natural beds (7/23) near the Croisic pontoon
383 (P20, Figure 1). MtrBTN2 was not detected in the 180 individuals from the 9 mussel farms or in
384 the 140 individuals from the 7 floating buoys. Mussels affected by MtrBTN2 were significantly
385 more frequent in ports than in other habitats (Fisher's exact test, p-value = 0.0001, Table S12). In
386 addition, the sampled ports are not significantly spatially autocorrelated (Moran I test, p-value =
387 0.25, Table S13).

388

389 **3.5. Exploring the effect of some environmental variables, none other than the port habitat**
390 **explains *MtrBTN2* prevalence after accounting for spatial autocorrelation**

391 Given that MtrBTN2 was mostly found in ports, we aimed to gain a deeper understanding of
392 whether environmental variables (including population ancestry) could explain this pattern.
393 Univariate correlation between MtrBTN2 prevalence and all environmental variables across
394 habitats are presented in Figure S8. The two best correlations are found with population density
395 and maritime traffic, but we also have strong multicollinearity among variables that needs to be
396 accounted for (see Table S14). The PCA reveals an association between environmental variables
397 and habitat types rather than the presence of cancer itself (Figure 3). Indeed, anthropogenic
398 habitats (ports, floating buoys and farms) with high population density and sheltered from wave
399 action are well separated from natural beds on the second axis of the PCA. Interestingly,
400 maritime traffic (i.e., annual mean of passenger, fishing, and recreational boat density) explains a
401 direction of variation towards human-altered habitats, but also towards sites affected by
402 MtrBTN2. MtrBTN2 seems to be found in sites with buffered temperature (low annual variance)
403 and higher mean annual salinity, environmental variables that are associated with ports in our
404 study. Water temperature indeed tends to be buffered in ports, being warmer in winter and cooler
405 in summer (Figure S4). However, these variables are difficult to interpret as they also explain
406 well the inertia of axis 1 of the PCA which differentiates the sites located near estuaries (La
407 Loire or La Vilaine) from the others. To investigate more rigorously whether some
408 environmental variables could explain prevalence of MtrBTN2, we used a spatial logistic
409 regression model.

410



411

412 **Figure 3: Principal Component Analysis on environmental variables.** Axis 1 mainly
413 captures the variance associated with annual temperature variance and annual salinity mean and
414 Axis 2 mainly captures the variance associated with wave action, population density and
415 maritime traffic.

416

417 As MtrBTN2 was mostly found in ports (see section 3.4), we included an environmental variable
418 “port” (1 for port habitat, 0 for others) in the regression model analysis. To test for spatial
419 structure, we conducted Moran’s I tests on all environmental variables. The results indicate
420 significant spatial autocorrelation in most environmental variables (Table S13), which was
421 expected as we selected this area due to its mosaic of contrasted environments. However,
422 “population density” and “port” variables were found randomly distributed in space (Table S13).
423 To overcome spatial autocorrelation bias we performed a logistic regression model that corrects
424 for spatial effect (*spaMM* package, [43]) and assessed environmental variables significance via
425 bootstrapped Likelihood Ratio (LR) tests. Bootstrapped LRTs are expected to handle the
426 problem of variables multicollinearity. MtrBTN2 prevalence is significantly explained by the

427 port habitat variable (LR test: $\chi^2 = 7.21$, $df = 1$, $p\text{-value} = 0.0072$; Table S15), and none of
428 the other environmental variables significantly explain MtrBTN2 prevalence after accounting for
429 spatial effects (Table S15). Despite the residuals following the distributional assumptions of the
430 model (Figure S9) and the significance of the ‘Port’ variable (also supported by the Fisher’s
431 exact test, see 3.4), we acknowledge that quantifying the magnitude of this trend remains
432 challenging and requires further investigations.

433

434 **4. Discussion**

435

436 Our results show that MtrBTN2 is present at low prevalence along the French Atlantic coast
437 (23/1516 = 1.5%). Strikingly, it is mostly found in ports and is equally distributed in *M. edulis*
438 and *M. galloprovincialis*. Our analysis shows that ports are likely epidemiological hubs for
439 MtrBTN2 propagation. However, the precise environmental factors influencing MtrBTN2
440 epidemiology have yet to be fully characterised. In this context, we discuss various
441 environmental variables and assess their relevance to the port environment and marine parasite
442 epidemiology.

443

444 Most MtrBTN2-infected mussels were found in ports and a prevalence hotspot was found around
445 the Croisic pontoon. Given the low prevalence of MtrBTN2 previously described [16, 32] and
446 confirmed in this study, we acknowledge that our sample sizes per site may be too small ($n = 20$)
447 to assess MtrBTN2 prevalence with confidence at a site level. However, this was not the scale of
448 resolution we were interested in. Instead, our overall sampling design, capturing replications of
449 habitat features, was chosen to evaluate the effect of habitats and genetic composition of host
450 populations. This allowed us to reveal similar MtrBTN2 prevalence in both species of the mosaic
451 hybrid zone, and a higher prevalence in ports.

452

453 The highest prevalence of MtrBTN2 in ports could be explained by two non-exclusive
454 hypotheses. Firstly, ports could offer a favourable environment as it is conducive to disease
455 development and propagation. Indeed, ports are often polluted, confined and permanently
456 immersed habitats (without tidal constraints) with high density of mussels. It is important to note
457 here that our objective is not to explain the emergence of a transmissible cancer, i.e. the initial

458 carcinogenesis in the founder host, but its maintenance and spread. The emergence probably took
459 place long before the industrial period and, despite studying a cancer, the mutagenic effect of
460 pollutants does not have to be put forward to explain our results, but rather their effect on host
461 resistance to infection by transmissible cancer cells. Secondly, there is increased connectivity
462 between ports due to maritime traffic and ports are connected to other sites (other ports or wild
463 sites) through biofouling from vessels.

464

465 Ports are often confined areas with longer particle residence times which could increase the
466 contact time between parasites and hosts [46, 47], thereby increasing the probability of
467 transmission and favouring the persistence of a passively dispersing parasite. However, the
468 possible hotspot on Croisic Pontoon, which is affected by strong tidal currents, provides
469 evidence against this hypothesis given that it is not a confined area.

470

471 Host population density is an important epidemiological parameter, as high density is known to
472 favour parasite persistence in host populations [48, 49]. Our results suggest that ports are prone
473 to harbouring high population density (Figure 3). However, we found no evidence of MtrBTN2
474 cases in mussel farms or floating buoys despite high mussel population density in these sites as
475 well. Although population density could favour MtrBTN2 persistence in an affected population,
476 this parameter alone cannot explain the higher prevalence of MtrBTN2 in ports.

477

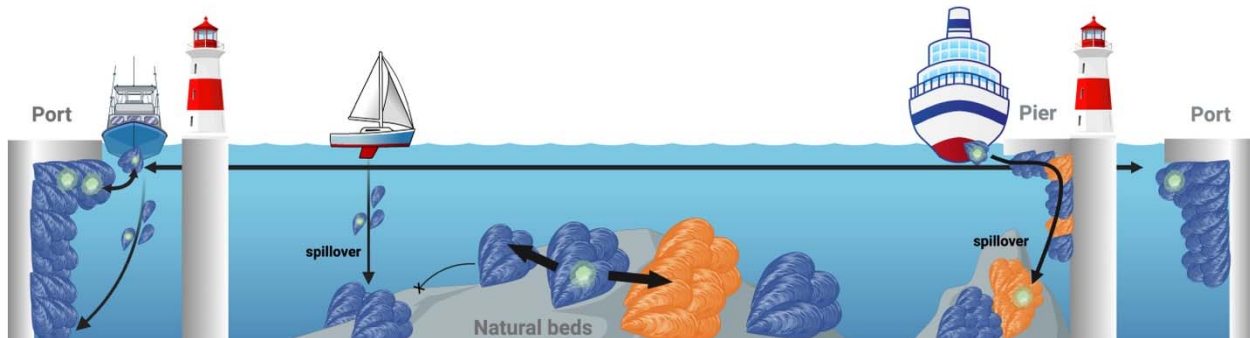
478 Port-based shipping activities are major contributors to water pollution, including issues such as
479 oil spills, plastic contamination, wastewater discharge, and the use of antifouling paint [50, 51].
480 Pollution is a major environmental stressor that could affect host physiology and increase
481 susceptibility to parasites, particularly by altering its immune response (reviewed in [52]). As
482 filter-feeders, species of bivalve molluscs are particularly concerned [53–55]. However, in our
483 study, most of the affected individuals (15/23) were found in three open sea sites known to be
484 healthy and protected ecosystems with abundant resources (Croisic Pontoon, Natural beds 19 and
485 21 part of Natura 2000 area; Figure 1), suggesting that pollution alone cannot explain the higher
486 prevalence of MtrBTN2 cancers in ports. Conversely, it can be hypothesised that a healthy, less
487 stressful environment may increase the host permissiveness and allow MtrBTN2 (and possibly
488 other BTN) to persist at a higher detectable prevalence. Host nutrition can affect disease

489 outcome by driving host immunity and parasite resource availability [56–58]. In invertebrates,
490 increased host nutrition can lead to increased parasite load [59] and improved immunity against
491 parasites [57, 58]. This balance could apply to mussel-MtrBTN2 interaction, and a healthy
492 environment with abundant resources could increase host carrying capacity and/or slow down
493 disease progression. A polluted environment could also affect the survival of MtrBTN2 cells in
494 seawater and reduce their chances of infecting a new host. However, the impact of pollution on
495 mussel hosts and cancer cells needs to be further investigated to clearly establish its influence on
496 the transmission and persistence of such transmissible cancers.

497

498 Connectivity through maritime traffic appears to be the main common feature between affected
499 ports, although this explanatory variable does not withstand spatial logistic regression analysis
500 any better than others. Vessels could facilitate MtrBTN2 propagation through transport of
501 affected mussels fixed on the hull. Maritime traffic has been identified as a vector of marine
502 mollusk pathogens (for review see [60]), microorganisms [61] and non-indigenous species [62,
503 63], through ballast water and/or hull biofouling. As such, ports are considered hotspots of
504 marine non-indigenous species introductions [62, 64, 65] and of marine parasites [66]. *Mytilus*
505 mussels are commonly reported as principal taxa composing hull biofouling (fixed adult mussels;
506 [67–69]). If a port is affected by a local outbreak, it could become a source of contamination to
507 other ports through biofouling of vessels, while natural beds will probably remain isolated by
508 density troughs that could halt the propagation (Figure 4). It is also conceivable that prevalence
509 hotspots exist at other unsampled locations along the coast, either due to environmental factors
510 that have yet to be characterised, or simply due to stochastic local outbreaks. These local
511 outbreaks can be the source of contamination to the anthropogenic connectivity network
512 providing the disease reaches a port. While this does not disqualify the factors discussed above –
513 e.g., pollution, population density and confinement- as drivers of contamination within ports, our
514 study suggests that maritime routes between ports could be anthropogenic gateways to MtrBTN2
515 propagation. Furthermore, despite a high density of maritime traffic around the floating buoys
516 sampled, these sites remained free of MtrBTN2. Long mooring times in ports increase the
517 probability of hull surface colonisation [69–71] as well as the risk of pathogen transmission [60].
518 This suggests that, in addition to cruising, ships may have to dock for the spread of MtrBTN2 to
519 be effective, either through transmission of cancer cells or detachment of infected mussels

520 (Figure 4). This could provide an explanation as to why maritime traffic is not a sufficient
521 explanatory variable for MtrBTN2 prevalence. Further investigations would be necessary to
522 ascertain the requisite propagule density (comprising both numerical and time-scale components)
523 for effective transmission, as well as to evaluate possible disruption of byssus quality in affected
524 hosts.
525



526
527 **Figure 4: Diagram illustrating the discussion on the propagation of MtrBTN2 across**
528 ***Mytilus* sp. populations.** Arrows' widths correspond to the probability of MtrBTN2 propagation.
529 Blue and orange mussels correspond to *M. edulis* and *M. galloprovincialis*, respectively.
530 Diagram created with BioRender.

531
532 A possible hotspot of MtrBTN2 prevalence was found in the area around the Croisic pontoon.
533 Even though this possible hotspot will need to be confirmed, this site could represent a source for
534 other ports and surrounding natural beds. Indeed, this pontoon is frequently used by maritime
535 shuttles, as well as by recreational and fishing boats, and is connected by maritime traffic to
536 many ports in the studied area. In particular, this pontoon is the departure site of boats travelling
537 to Hoedic (site P44 in Figure 1), an isolated island for which the presence of cancer is most
538 likely explained by anthropogenic transport given the distance from the mainland. MtrBTN2 is
539 also found in foreshores near Croisic. This reveals a possible spillover from ports to adjacent
540 wild populations (Figure 4). Maritime traffic has been identified as a vector for non-indigenous
541 species from commercial ports to natural populations via marinas [72, 73]. In our study, when
542 sites outside standard enclosed ports (e.g., enclosed marinas) were sampled, MtrBTN2 was never
543 detected, suggesting that contagion often remains confined to the port area. Spillover may
544 therefore depend on the degree of confinement of a port.

545

546 *Mytilus galloprovincialis* was thought to be more resistant to MtrBTN2 because of lower
547 prevalence in this species [16], and population patches of *M. galloprovincialis* could also have
548 acted as barriers to disease propagation between patches of *M. edulis*. However, our results
549 suggest that *M. galloprovincialis* population patches close to *M. edulis* populations may also
550 show enhanced prevalence. This does not contradict the idea that *M. galloprovincialis* population
551 patches could impose a slightly higher resistance to MtrBTN2 propagation. Under the hypothesis
552 that natural propagation is hindered by density troughs between population patches, or by
553 population patches of a more resistant species, ports and ship traffic would create anthropogenic
554 gateways that favour connections between patches of host populations (Figure 4). This
555 hypothesis could also suggest that BTN2 spread naturally and progressively from one host to
556 another by close contact rather than drifting with the currents, making enhanced R0 by
557 anthropogenic dispersal a threat to host populations.

558

559 Our results represent a significant advance in our understanding of MtrBTN2 epidemiology, both
560 by proposing ports as epidemiological hubs and by suggesting that the natural propagation of this
561 transmissible cancer could be naturally halted by density troughs in the distribution of host
562 mussel populations. Detection of MtrBTN2 presence on boat biofouling would provide more
563 direct evidence of its role as a vector. It would also be interesting to investigate whether
564 prevalence hotspots are more commonly located in areas with particular environmental
565 conditions, or whether they are stochastic local outbreaks. Sampling vessel biofouling in
566 international ports linking known MtrBTN2 sites (East and North Europe, North West and South
567 Pacific) and nearby marinas, along with genetic comparison of cancer cells, would provide a
568 better understanding of the global and local transmission routes of this transmissible cancer since
569 its emergence. While MtrBTN2 is not associated with extensive mortality events [30], other
570 pathogens could be translocated and affect wild and farmed mussel populations. Various
571 measures are employed to mitigate biofouling, including antifouling painting, dry docking, in-
572 water cleaning with capture, and ballast water filtration (as discussed in [60]). While biofouling
573 management for international vessel exchanges is established [74–76], regulations for biofouling
574 control in local recreational boats remain to be improved [67, 77]. This is a significant concern,
575 as the involvement of recreational boats in the spread of invasive species and possible associated

576 pathogens is increasingly documented [78–80]. Prioritising the survey of vessels that stay in port
577 for long periods [81] or identifying nodes of busy maritime route [72] could contribute
578 considerably to local and international biofouling management.

579

580 **5. Conclusion**

581

582 Our study reveals that the prevalence of MtrBTN2 along the South Brittany French coast is low,
583 but that the most affected sites are ports (marinas, commercial ports, and docks). This result
584 suggests that ports are epidemiological hubs and that maritime routes are anthropogenic
585 gateways for the propagation of MtrBTN2. Investigations into the presence of other BTNs in
586 boat biofouling would provide more direct evidence of its role as vector, although mussels are
587 the most common species of bivalve mollusc in biofouling. The spread of marine
588 (micro)parasites and pathogens through vessel biofouling is a legitimate concern, and results
589 such as ours -i.e., on a smaller scale than translocations identified in the literature on marine
590 bioinvasion or by [9]- highlight the critical need for policy regulation to limit the effects of
591 biofouling, both on ship hulls and port docks, in addition to ballast water control.

592

593 **Data accessibility**

594 All data used in this study are available in the supplementary material.

595 **Author's contribution**

596 M.H., Conceptualization, Data curation, Formal analysis, Investigation, Methodology,
597 Supervision, Visualization, Writing – original draft, Writing – review and editing. F.To.,
598 Investigation, Data curation, Writing – review and editing. E.A.V.B., Formal analysis,
599 Investigation, Writing – review and editing. L.P., Data curation, Investigation, Writing – review
600 and editing. F.C., Investigation, Writing – review and editing. E.G., Investigation, Writing –
601 review and editing. I.B., Resources, Writing – review and editing. H.C., Resources, Writing –
602 review and editing. A.S., Formal analysis, Writing – review and editing. F.Th.,
603 Conceptualization, Funding acquisition, Writing – review and editing. D.D-G.,
604 Conceptualization, Funding acquisition, Writing – review and editing. G.M.C.,
605 Conceptualization, Project administration, Funding acquisition, Writing – review and editing.

606 N.B., Conceptualization, Funding acquisition, Formal analysis, Investigation, Methodology,
607 Project administration, Supervision, Writing – original draft, Writing – review and editing.

608

609 **Conflict of interest declaration**

610 We declare we have no competing interests.

611

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619

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626

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628

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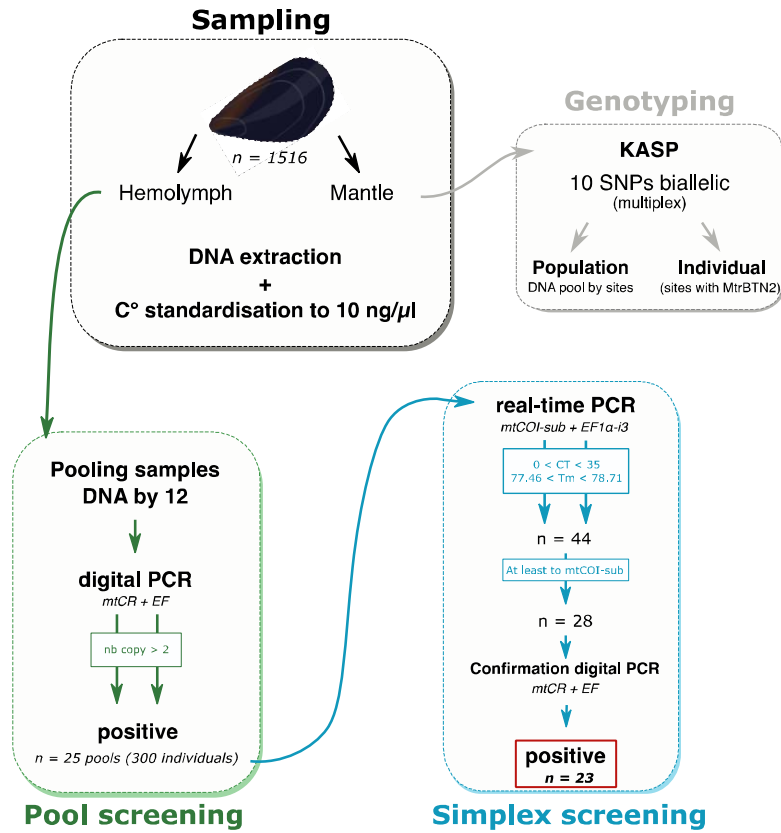
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833

834 Supplementary material

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836

837 **Figure S1: Diagram of screening and genotyping experimental steps.**

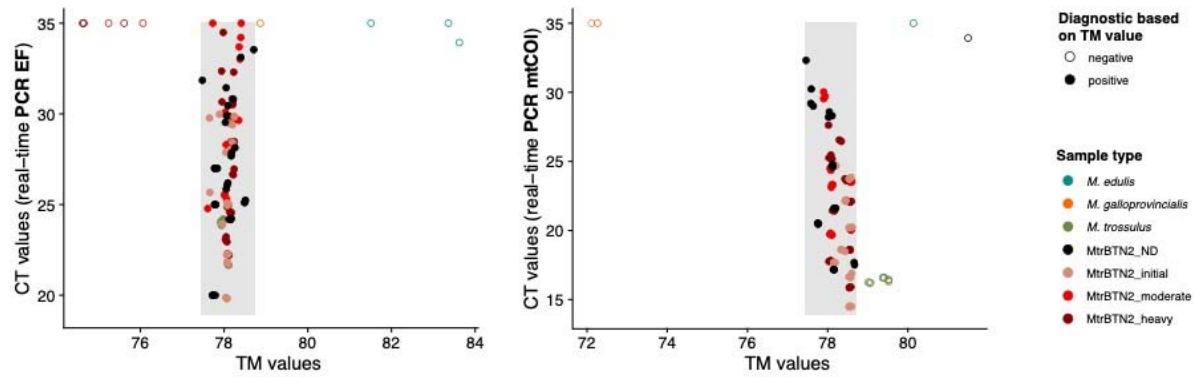
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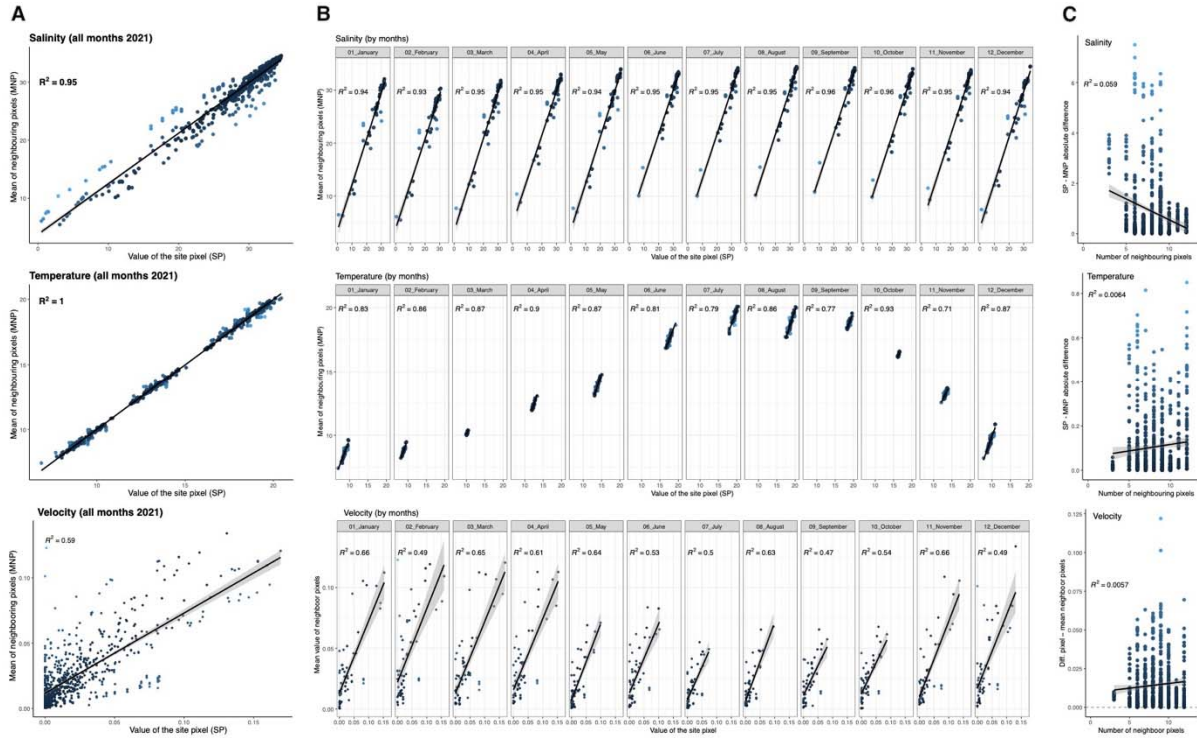


843
844 **Figure S2: TM threshold determination for EF1 α -i3 (left) and mtCOI-sub (right) real-time**
845 **PCR markers.** Grey rectangles correspond to TM threshold based on MtrBTN2 positive control
846 samples (77.46<TM<78.71). Sample type colour and diagnostic based on TM values are
847 indicated in the legend. *M. edulis* and *M. galloprovincialis* correspond to negative controls, *M.*
848 *trossulus* are *M. trossulus* controls, and MtrBTN2 samples are positive controls (ND: cancer
849 stage not defined, initial: early stage, moderate: moderate stage, heavy: late stage, see TableS3)

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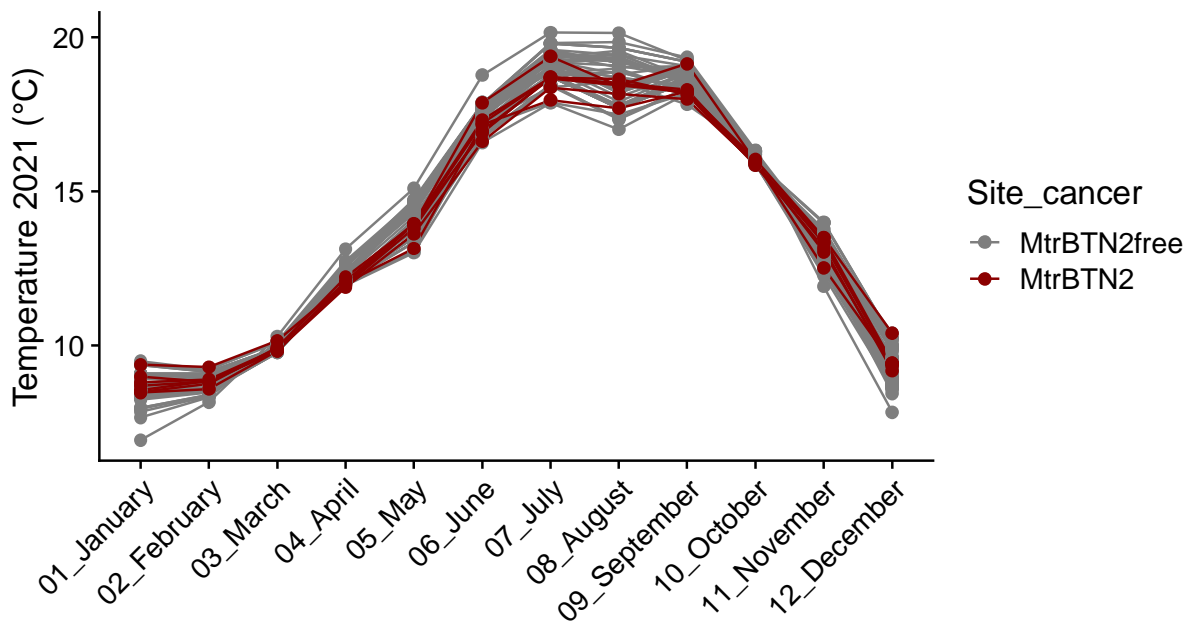
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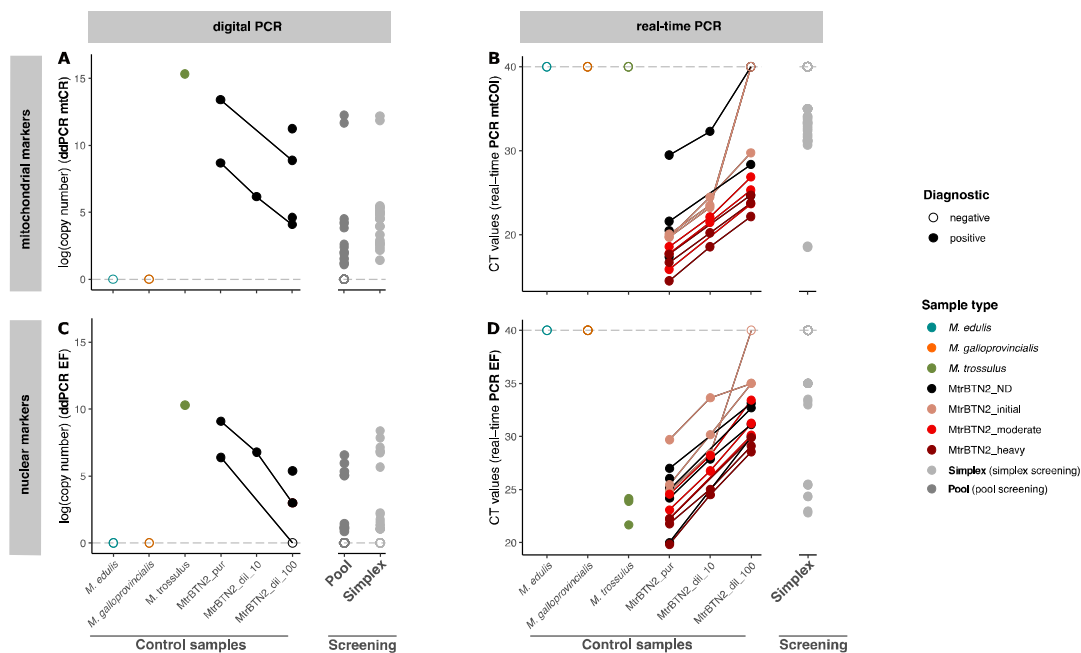
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854 **Figure S3: Evaluation of Copernicus model resolution for salinity, temperature and**
 855 **velocity data.** Correlation between the value of the site pixel (SP) and the mean value of
 856 neighbouring pixels (MNP) for each variable. **(A)** Correlation including all months of year 2021
 857 and **(B)** each month separately. No correlation observed between the absolute difference of SP
 858 and MNP values and the number of neighbouring pixels **(C)**.



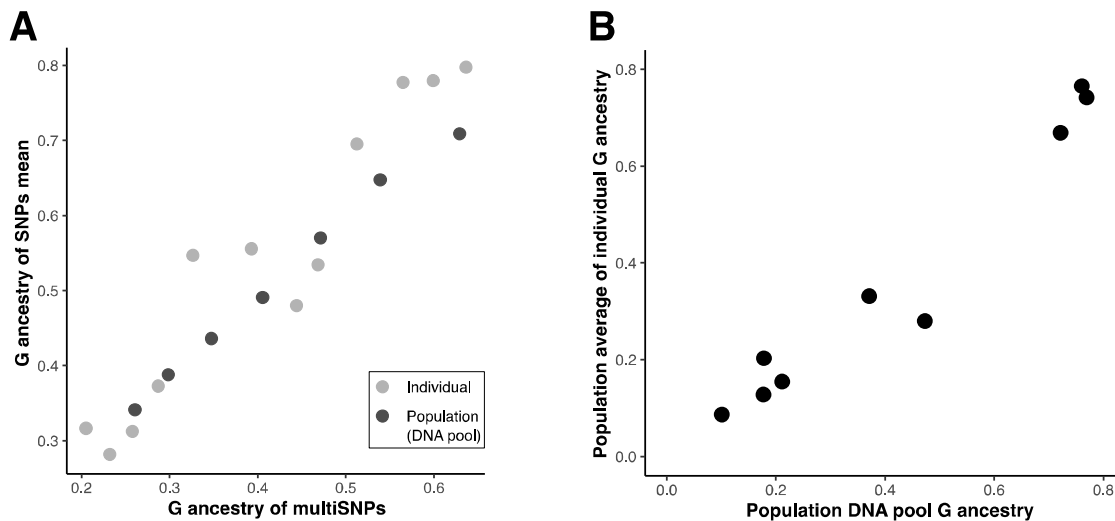
859
 860 **Figure S4: Sampled sites temperature, recorded monthly in 2021.** Points correspond to a
 861 temperature measurement, solid lines refer to MtrBTN2-free sites (grey) and MtrBTN2 affected
 862 sites (darkred).

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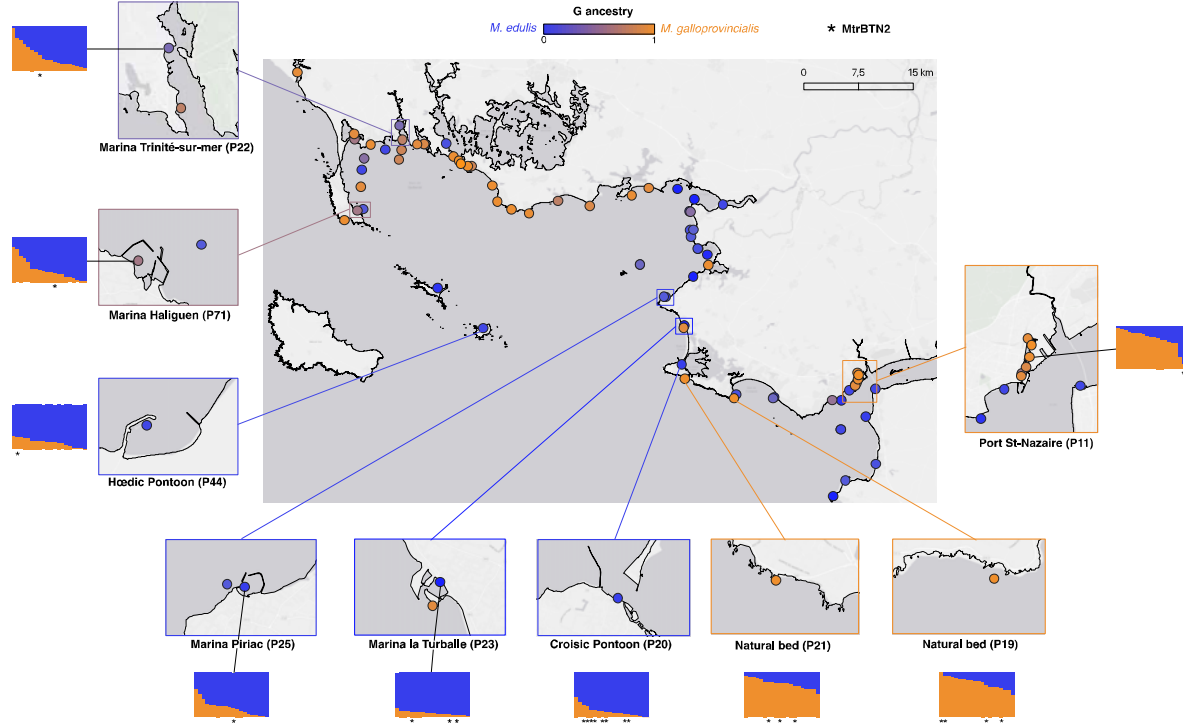
866

867 **Figure S5: Real-time PCR and digital PCR results.** (A) and (C) represent ddPCR results of EF
868 and mtCR, and (B) and (D) represent real-time PCR results of EF1 α -i3 and mtCOI-sub,
869 respectively. Dotted lines correspond to the negative thresholds, 0 for no DNA copy detected by
870 ddPCR and 40 for no amplification in real-time PCR. Solid lines in each graph refer to the same
871 sample diluted to different concentrations (pure, x10, x100). *M. edulis* and *M. galloprovincialis*
872 correspond to negative controls, *M. trossulus* are *M. trossulus* controls, and MtrBTN2 samples
873 are positive controls (ND: cancer stage not defined, Initial: early stage, moderate: moderate
874 stage, heavy: late stage, see TableS2). Screening results using both method and markers are
875 shown for Pool and Simplex. Sample type colours and diagnostic status are indicated in the
876 figure legend.
877



878
879 **Figure S6: Genotyping method validation.** (A) Positive correlation between multiSNPs G
880 ancestry and the mean of the 10 single SNPs from a subset of Individual and Pool samples. (B)
881 Positive correlation between population DNA pool G ancestry and the mean individual G
882 ancestry of individuals from the same population.

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887 **Figure S7: Population and individual ancestry composition across the sampled area.**

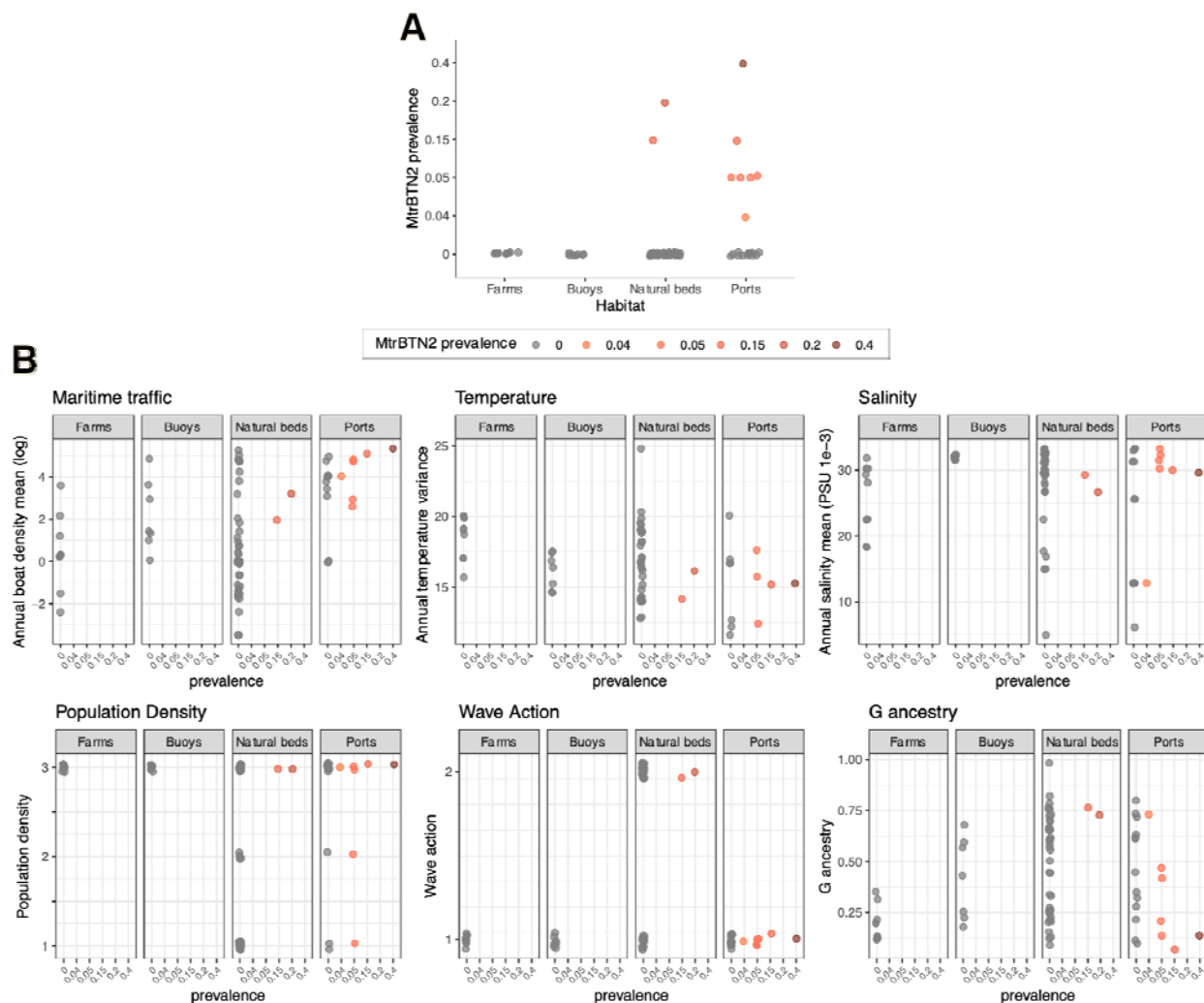
888 Zoomed-in sites correspond to sites with mussels affected by MtrBTN2. Barplots represent the

889 estimated ancestry of individuals based on the 10SNPs multiplex tool. MtrBTN2 individuals are

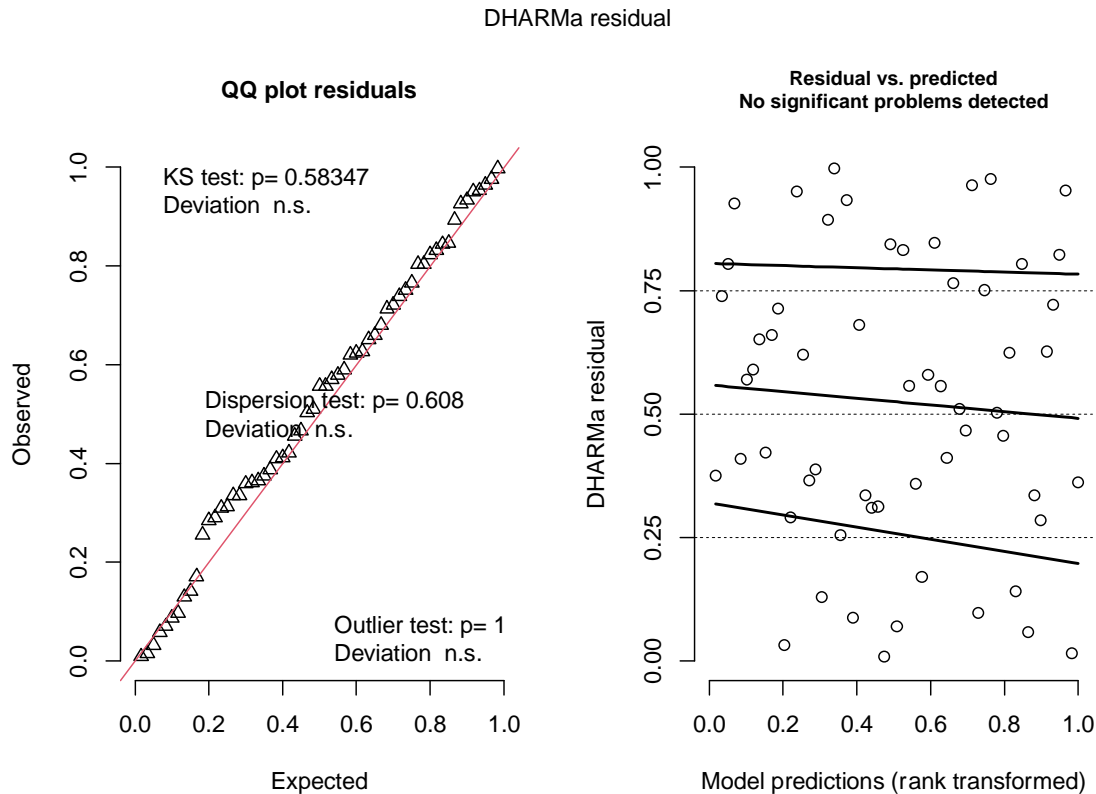
890 indicated by stars under each barplot. Coloured points represent the population average ancestry,

891 as indicated in the figure's legend. Map origin: Ersi gray (light).

892



893
894 **Figure S8: Univariate correlations between the prevalence of MtrBTN2 and environmental**
895 **variables.** (A) MtrBTN2 prevalence among habitats. (B) Correlations for the six environmental
896 variables studied. Coloured points correspond to the prevalence of MtrBTN2 as indicated in the
897 legend.
898



899

900 **Figure S9: Residual diagnostics of the logistic regression model accounting for spatial**
901 **autocorrelation.** Model results are presented in Table S15. Plot generated using
902 *simulateResiduals()* function of DHARMA package in R.

903

904

905 **Supplementary Tables (→ [See excel TableS1-15](#))**

906

907 **TableS1 : Description of sampled sites.** Sources of environmental variables are provided in
908 TableS5. Site: site name; N: number of sampled mussels; MtrBTN2 prevalence: number of
909 MtrBTN2 affected mussels; Temperature: annual variance; Salinity: annual mean; Maritime
910 traffic: annual mean in log; temp: temperature; sal: salinity; vel_E and vel_N: Eastward and
911 Northward current velocity, respectively; [fish-pass-other][19-21]_[1-4] fish: fishing boat
912 density, pass: passenger boat density, other: recreational boat density, 19 to 21 correspond to the
913 year of record, and 1 to 4 correspond to spring, summer, autumn, winter, respectively.

914 Temperature and Salinity missing data (blank) correspond to sites outside of Copernicus model
915 pixels (n = 13).

916

917 **Table S2: Primer and probe sequences used in real-time PCR and digital PCR.**

918

919 **Table S3: Control samples used to validate real-time PCR and ddPCR screening tools.** All
920 samples are from our laboratory sample collection. *M. edulis* and *M. galloprovincialis*
921 correspond to negative controls, *M. trossulus* are *M. trossulus* controls, and MtrBTN2 samples
922 are positive controls. MtrBTN2 stages were defined by cytology of the hemolymph, according to
923 the following classification: early (<15% cancer cells), moderate (15-75% cancer cells), late
924 (>75% cancer cells), ND when cancer stage was not defined.

925

926 **Table S4: Bi-allelic nuclear SNPs used for the multiSNPs genotyping.**

927

928 **TableS5: Source and description of environmental variables collected for each habitat**
929 **(ports, natural beds, farms, buoys).**

930

931 **TableS6: Data for the evaluation of Copernicus model resolution.** Sources of environmental
932 variables are provided in TableS5. Site: site name; N_pixels: number of neighbouring pixels
933 within a buffer zone of 0.05°; SP: value of the site pixel; MNP: mean value of the neighbouring
934 pixels; SP_MNP: absolute difference between SP and MNP values; .s, .t and .v refer to salinity,
935 temperature and velocity values, respectively. Velocity correspond to the combination of squared
936 Northward and Eastward velocity values. Missing data (blank) correspond to sites outside of
937 Copernicus model pixels (n = 13).

938

939 **Table S7: Control sample results validate real-time PCR and ddPCR screening tools.**
940 EF_CopyNb: copy number for EF ddPCR marker; mtCR_CopyNb: copy number for mtCR
941 ddPCR marker; CT: threshold cycle, TM: melting temperature for EF1 α -i3 and mtCOI-sub real-
942 time PCR markers. NP: not performed.

943

944 **TableS8: Pooled and simplex screening results.** Pool_CopyNb_EF: copy number for EF
945 ddPCR marker (pooled screening); Pool_CopyNb_mtCR: copy number for mtCR ddPCR marker
946 (pooled screening); CT: threshold cycle, TM: melting temperature for EF1 α -i3 and mtCOI-sub
947 real-time PCR markers; Simplex_CopyNb_EF: copy number for EF ddPCR marker (simplex
948 screening); Simplex_CopyNb_mtCR: copy number for mtCR ddPCR marker (simplex
949 screening). NP: not performed.

950

951 **TableS9: Simplex screening results for positive samples.** CT: threshold cycle, TM: melting
952 temperature for EF1 α -i3 and mtCOI-sub real-time PCR markers; PCR_result: marker name
953 positive in real-time PCR; EF_CopyNb: copy number for EF ddPCR marker; mtCR_CopyNb:
954 copy number for mtCR ddPCR marker; ddPCR_result: marker name positive in ddPCR;
955 MtrBTN2: final diagnostic status. NP: not performed.

956

957 **Table S10: Correspondence between pool and simplex screening.** Pool_CopyNb_EF : copy
958 number for EF ddPCR marker (pooled screening); Pool_CopyNb_mtCR : copy number for
959 mtCR ddPCR marker (pooled screening); Pool_ddPCR_result: marker name positive in ddPCR
960 (pool); Nb_ind_positive: number of individuals in the pool found positive for one or two marker
961 in simplex screening; Simplex_PCR_result: marker name of the positive individual in real-time
962 PCR; Simplex_ddPCR_result: marker name of the positive individual in ddPCR, negative if the
963 sample did not amplify. NP: not performed.

964

965 **Table S11: MultiSNPs genotyping results.** G ancestry: fluorescence value; Ancestry: ancestry
966 defined based on G ancestry values.

967

968 **Table S12: Contingency table used for the Fisher exact test.**

969

970 **Table S13: Moran I test on environmental variables.** Results were obtained using moran.test()
971 function in R.

972

973 **Table S14: Correlation coefficient and Spearman correlation test results for each**
974 **environmental data pairs.**

975

976 **Table S15: Spatial logistic regression model testing the effect of environmental variables on**

977 **MtrBTN2 prevalence.** Model results were obtained using `fitme()` from `spaMM` package in R.

978 Matern covariance function was included to account for spatial autocorrelation (i.e. `Matern(1 |`

979 `Longitude + Latitude)`. Effects of environmental variables were tested using Likelihood ratio

980 (LR) tests using `fixedLRT()` function from the same package. Temperature: annual variance;

981 Salinity: annual mean; Maritime traffic: annual mean.

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