

Co-occurrence and reproductive synchrony do not ensure hybridization between an alien tunicate and its interfertile native congener

Sarah Bouchemousse, Laurent Lévêque, Guillaume Dubois, Frédérique Viard

▶ To cite this version:

Sarah Bouchemousse, Laurent Lévêque, Guillaume Dubois, Frédérique Viard. Co-occurrence and reproductive synchrony do not ensure hybridization between an alien tunicate and its interfertile native congener. Evolutionary Ecology, 2015, 30 (1), pp.69-87. 10.1007/s10682-015-9788-1. hal-01227971

HAL Id: hal-01227971 https://hal.sorbonne-universite.fr/hal-01227971

Submitted on 12 Nov 2015

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

1	Co-occurrence and reproductive synchrony do not ensure hybridization
2	between an alien tunicate and its interfertile native congener
3	
4	Sarah Bouchemousse ^{1,2,} *, Laurent Lévêque ^{1,3} , Guillaume Dubois ^{1,2} and Frédérique
5	Viard ^{1,2,*}
6	(1) Sorbonne Universités, UPMC Univ Paris 6, UMR 7144, Station Biologique de Roscoff,
7	Place Georges Teissier, 29680 Roscoff, France
8	(2) CNRS, UMR 7144, Equipe Div&Co, Station Biologique de Roscoff, Place Georges
9	Teissier, 29680 Roscoff, France
10	(3) CNRS, FR 2424, Station Biologique de Roscoff, Place Georges Teissier, 29680 Roscoff,
11	France
12	*Correspondence : UMR7144, Equipe Diversité et Connectivité dans le paysage marin Côtier
13	(Div&Co), CNRS-UPMC, Station Biologique de Roscoff, Place Georges Teissier, 29680
14	Roscoff, France
15	Email: sbouchemousse@sb-roscoff.fr, viard@sb-roscoff.fr
16	
17	
18	EVOLUTIONARY ECOLOGY
19	This article is available online (doi: 10.1007/s10682-015-9788-1)
20	Received: 20 March 2015 / Accepted: 5 August 2015 / Published online: 9 August 2015

21

22 Abstract

Biological invasions can promote secondary contacts between related species and thus 23 provide excellent case studies for investigating the joint ecological and evolutionary 24 trajectories of interfertile taxa. Here, we studied two tunicates living in sympatry, and 25 sometimes in syntopy, in the English Channel, *Ciona intestinalis* species A (presumed native 26 to the NW Pacific) and species B (native to the N Atlantic). In addition to monitoring their co-27 existence over time, we examined the level of interspecific gene flow, a process that may 28 increase the invasiveness of the non-native species. The sampling scheme was repeated twice 29 a year for three years (6 distinct generations) to determine the relative abundance of the two 30 species in 11 localities along the coasts of the English Channel and the Iroise Sea (covering 31 1600 km) in Brittany, France. We examined 23,000 individuals, including 5,315 specimens 32 for which reproductive status was determined. Four species-diagnostic molecular markers 33 34 traced interspecific gene flow on a random subset of 3,048 individuals. Regardless of the sampling date, the two species co-occurred in most of the study sites, with species A showing 35 higher frequency in the autumn. The regional pattern of seasonal variation in relative 36 abundance of the two congeners appears to correspond to different thermal growth optima. 37 Abrupt variations in environmental parameters can act synergistically and may favor the non-38 native species locally. Despite syntopy, synchronous gamete production and successful in 39 *vitro* interspecific crosses, only 4.3% individuals showed an admixed genome (i.e. footprint of 40 present-day or past introgression events), most of them with a species A maternal lineage, of 41 which only one was a putative first generation hybrid. Altogether, efficient barriers seem to 42 prevent interspecific crosses between the two interfertile congeners in the wild: present-day 43 hybridization may have less impact than competitive interactions on the fate of the two study 44 species over their sympatric range. 45

46

47 Introduction

Biological introductions (i.e. transport of species away from their native range via 48 human activities) are modifying species ranges at an unprecedented rate and on global scales 49 (e.g. in the marine environment, Molnar et al. 2008). Among the various ecological and 50 evolutionary consequences of species introduction, hybridization between native and non-51 native species can dramatically alter the evolutionary trajectories of both species (Allendorf et 52 al. 2001). Hybridization sensu lato commonly refers to interspecific gene flow, including 53 first-generation hybrids and repeated backcrossing of their offspring with parental species 54 (Harrison 2012). Such interspecific gene flow between formerly allopatric taxa is not rare and 55 can have diverse consequences (Allendorf et al. 2001), including an increased risk of 56 extinction of the native species (Rhymer and Simberloff 1996; Fitzpatrick et al. 2010), 57 increased invasiveness through, for instance, adaptive introgression mechanisms (Currat et al. 58 59 2008; Schierenbeck and Ellstrand 2009) and the emergence of new species (Abbott 1992). Hybridization facilitated by human activities has been studied mainly in plant species (e.g. 60 Schierenbeck and Ellstrand 2009; Guo 2014) and to a lesser extent in animals (e.g. Fitzpatrick 61 et al. 2010; Steeves et al. 2010), with only a few cases reported in marine systems (but see, for 62 instance, Abudefduf vaigiensis and A. abdominalis, Coleman et al. 2014). However, marine 63 species live in a dispersive environment and there is a large number of cryptic, co-existing 64 native and non-native marine species (e.g. in tunicates; Bock et al. 2012; Perez-Portela et al. 65 2013). Furthermore, the increasing rate of marine biological invasions on the global scale 66 facilitates numerous secondary contacts between allopatric taxa (Geller et al. 2010). 67

The recently described *Ciona intestinalis* species complex presents an interesting case to study. The nominal species *C. intestinalis* (Linnaeus, 1767) covers a complex of four cryptic species (Zhan et al. 2010). Two of them, *C. intestinalis* species A and *C. intestinalis* species B (hereafter referred to species A and species B, respectively) are now considered

pseudo-cryptic species since the advent of morphological criteria to distinguish them (Sato et 72 al. 2012). In addition, very recently, Brunetti et al. (2015) showed that species A displays 73 morphological features specific to the formerly described Japanese species Ciona robusta 74 75 Hoshino and Tokioka 1967, later synonymized under C. intestinalis, whereas species B fits with the C. intestinalis description by Millar (1953). These new alpha-taxonomy discoveries 76 have not yet been implemented in the World Register of Marine Species (e.g. C. robusta is 77 still a non-accepted name) and we will use 'species A' and 'species B' in the following text. 78 79 Despite a substantial time elapsed since their divergence (estimated at around 4 Mya; Nydam and Harrison 2011; Roux et al. 2013), the two species are not reproductively isolated: viable 80 81 and fertile F1 hybrids are easily produced under laboratory conditions (Sato et al. 2014). As in many other tunicates (Shenkar and Swalla 2011), the distribution range of these two species 82 has expanded in the last two centuries due to their accidental introduction via human activities 83 84 (Zhan et al. 2010). In particular, species A, has been recently introduced (ca. 15-20 years ago; Nydam and Harrison 2011; J.D.D. Bishop, personal communication) in the native European 85 range of species B. Although the two species are widely distributed around the world, the 86 western English Channel and the South of Brittany in the Northeast Atlantic (hereafter 87 referred to as WEC) constitute the only confirmed region in which both species have been 88 89 reported in sympatry.

Like many other ascidians (Airoldi et al. 2015), the nominal species *C. intestinalis* often forms well-established populations in artificial habitats (e.g. marinas with floating docks, commercial harbors and aquaculture installations). In their area of sympatry — the WEC — species A and species B can also live in syntopy (i.e. in the same locality, Fig. 1). However, because of the cryptic nature of these two species, most published ecological studies do not distinguish between them (Procaccini et al. 2011). Furthermore, *C. intestinalis* spp. is a model organism for evolutionary developmental biology research as well as

phylogenetic studies. Nonetheless, ecological data are still lacking with regard to the recent 97 discovery of the cryptic species. Due to its recent introduction in the WEC, species A 98 experiences numerous, unprecedented biotic interactions and environmental changes that may 99 affect its invasion dynamics (Blackburn et al. 2014). Consequently, there are many issues 100 regarding the history, dynamics and fate of the recent introduction of species A in the native 101 range of species B, including the stability of co-occurrence in species that share the same 102 habitat and localities, the intensity of interspecific competitive interactions, and the 103 104 occurrence of introgression or a hybrid swarm in sympatry.

To address these issues, we surveyed 11 marinas located along the coasts of Brittany for three years, and examine six distinct generations (i.e. the spring and autumn generations of the same year). We carried out genetic analyses to investigate 1) regional and local variation in the relative abundance of species A and species B; 2) their potential to mate; and 3) the rate and direction of interspecific crosses in the wild.

110

111 Materials and Methods

112 Field survey: sampling, morphological species identification and determination of 113 reproductive status

We selected 11 marinas (out of 27) with floating pontoons located along the 1600 km 114 long coastline of Brittany, France. These marinas were representative of a range of 115 characteristics (i.e. open to the sea or closed during low tide (by means of tidal or sill gates)), 116 fully marine or under freshwater (estuarine) influence; see Table S1 for details of each 117 locality). In spring 2012, Ciona spp. populations were sampled in 10 marinas over two weeks 118 (Fig. 2a). The same sampling was repeated five times, with an additional site (no. 11 in Fig. 2) 119 in autumn 2012, spring and autumn 2013, and without sites nos. 10 and 11 (see Fig. 2) in 120 spring and autumn 2014. The six sampling dates correspond to at least six different adult 121

generations in European waters (e.g. Dybern 1965; Caputi et al. 2014). In each locality, ca.
200-300 adult individuals (Table 1 for details) were randomly collected along two pontoons
during SCUBA diving operations over ca. 50 m. Additionally, in most of the studied marinas
(all except nos. 1, 2, 10 and 11, Fig. 2), seawater temperature was recorded using data loggers
(TidbiT[®]v2) located at 1.5 m depth.

Following their collection, individuals were sedated with phenoxy-2-propanol 127 (1:1000) for 20-30 min to facilitate species identification and excision of tissue samples. 128 Species were identified using morphological criteria according to Sato et al. (2012). For each 129 site, a random subset of 87 specimens (SD \pm 12.6; sample size detailed in Table S2) was used 130 examine 131 to the reproductive status (modified from ProtocolJRA1-04.00, http://www.assemblemarine.org/assets/ASSEMBLE-JRA1-Protocol-04.00mk.pdf). Given that 132 both species are simultaneous hermaphrodites, although slighty protandrous, three sequential 133 134 stages of individual development were recorded: immature individuals, presence of sperm only, and presence of sperm and oocytes. A piece of branchial basket was preserved 135 individually in 100% ethanol for further genetic studies. 136

All statistical analyses were performed using R vers. 3.1.1 (R Development Core 137 Team 2005). To investigate temporal and spatial variations in the relative abundance of both 138 species, a linear mixed-effects model with a binomial error distribution was computed using 139 the *lme4* package (glmer function; Bates et al. 2014). Three sites (nos. 6, 10, 11, Fig. 2) with 140 missing data or complete absence of species A were excluded. "Season" (spring and autumn 141 generations) and "Year" (2012, 2013 and 2014) were considered as fixed factors. The factor 142 "Sites" represented pseudo-replicates and was thus categorized as a random factor. In 143 addition, pairwise comparisons among fixed factors were done. Comparisons of the 144 proportion of individuals with sperm, or individuals producing sperm and oocytes, were tested 145 using a Cochran-Mantel-Haenszel (CMH) chi squared test (Mantel 1963) using one 146

147 contingency table per site, at each sampling date. Only localities with more than 10
148 individuals for each species were included in these analyses. For pairwise comparisons and
149 CMH chi squared test, *P*-values were adjusted with a Bonferroni correction.

150

151 Molecular identification of hybrids

F1 hybrids and introgressed individuals (the two categories being referred to "admixed individuals" in the following text) cannot be discriminated morphologically (Sato et al. 2012). To identify them, species-diagnostic molecular markers were used on a random subset of individuals (average of 60 individuals \pm 6.9 (SD) per location and sampling date; Table 2) collected in 2012 and 2013. DNA extraction was performed with Nucleospin® 96 Tissue Kit according to the manufacturer's protocol (Macherey-Nagel, Germany).

Four species-diagnostic markers were used: one mitochondrial marker (mtCOI, 158 cytochrome oxidase I) to identify the maternal lineage, and three nuclear loci, namely 159 vAChTP (vesicular acetylcholine transporter), CesA (cellulose synthase) and Hox5 (intronic 160 nuclear regions of Hox5 gene) to identify the nuclear background. The Hox5 locus was 161 amplified using the primers and PCR protocol described in Caputi et al. (2007). For this locus, 162 species-diagnostic alleles differ in their length and allele size was scored on simple agarose 163 gels (2%). For mtCOI, vAChTP and CesA, amplifications (protocols detailed in Nydam and 164 Harrison, 2007, 2010) were followed by enzymatic digestions as explained in Nydam and 165 Harrison (2011). 166

For each site and sampling date, the proportion of admixed individuals (i.e. displaying at least one alternative species-diagnostic allele) was computed across the four loci. To test for stability of admixture across samples, a Pearson's chi-squared test was used, and *P*-values were calculated using a Monte Carlo simulation with 5000 replicates. To further examine admixture patterns, a hybrid index per maternal lineage was computed for each sampling date using the above-described random subset and additional selected individuals from the field samples to reach a minimum number of 20 individuals per species when possible. The hybrid index was calculated by adding, over the three nuclear loci, the number of alleles specific to species B. It varies from zero to six: zero if each of the three nuclear loci are homozygous for the species A allele and six if the three nuclear loci display only species B alleles.

177

178 *Laboratory crosses*

Although the two species have been previously shown to be interfertile (e.g. Suzuki et 179 al. 2005; Caputi et al. 2007; Sato et al. 2014), we carried out additional fertilization tests to 180 181 ascertain that F1 hybrids could be easily produced with individuals from our study area. A series of bi-parental crosses (47 conspecific, 38 heterospecific and 23 self-crosses) were 182 carried out using individuals sampled in autumn 2013 in the marinas of Aber Wrac'h (species 183 184 B) and Moulin Blanc (species A and species B) (site nos. 6 and 7 in Fig. 2, respectively) following protocols available in Cirino et al. (2002) and Sato et al. (2014). Fertilization 185 success was estimated by computing the proportion of eggs with cellular division after 1 h 186 (i.e. fertilization rate). Following Sato et al. (2014), a linear mixed-effects model and pairwise 187 comparisons were used to investigate differences in fertilization rate according to the type of 188 189 cross (i.e. six categories: two heterospecific (with reverse parental roles for each species), two conspecific and two self-crosses) as a fixed factor. Because the same individuals were used in 190 different crosses, a random effect of male genotype nested by female genotype was added. 191

192

193

Results

194 Significant variation in the relative abundance of the two species across generations

In the first study generation (i.e. spring 2012), species A and species B co-occurred in
8 localities out of the 10 surveyed, although species A was never abundant (Fig. 2). Detailed

values per site and sampling date are given in Table 1. Although abundance varied across
localities, regionally 6.0% of the 2,316 individuals were morphologically identified as species
A in spring 2012. This spatial pattern changed dramatically in autumn 2012 with 32.2% of the
individuals identified as species A out of the 3,678 individuals collected in 11 marinas (Fig.
Similar patterns were observed in 2013 and 2014 with an increase in the relative
abundance of species A in autumn (Table 1, Fig. 2).

203 At the locality level, 7 of the 11 studied marinas showed temporal variation similar to 204 the regional pattern, with some showing particularly strong contrasts between spring and autumn generations (e.g. Perros Guirec; no. 3 in Fig. 2). The remaining four localities showed 205 206 distinct features. Moulin Blanc (no. 7, Fig. 2) showed a different pattern in 2013, with spring abundance of species A (35.8%) being much higher than in autumn (2.2%). In Roscoff (no. 5, 207 Fig. 2), a regular decrease in species A was observed over the course of the survey, starting in 208 209 spring 2012 with 8.8% of species A dropping to 0% during the last four sampling dates. Conversely, the presence of species A was first recorded in St Malo (no. 1, Fig. 2) during the 210 211 last sampling date (autumn 2014; 1.1% of species A). Finally, species A was absent in one 212 site (Aber Wrac'h, no. 6 in Fig. 2) on all sampling dates.

Altogether, a significant interaction was found between season and year (Table 3a) which reflects 1) an increase in the relative abundance of species A in autumn compared with spring of the same year and 2) a higher relative abundance of species A in 2012 compared with the following two years (Fig. 2).

217

218 Synchronous gamete production and successful fertilization between the two species

The reproductive status of individuals at each sampling date for both study species is illustrated with ternary diagrams (Fig. 3): the distribution of the three categories varied among species and localities. When comparing species for the proportion of individuals with sperm

only, there were significant differences in spring and autumn 2013 (P<0.001 and P<0.001, 222 respectively) and in autumn 2014 (P=0.032). The proportion of individuals with both types of 223 gametes showed a similar pattern with no significant difference except for two dates (in 224 autumn 2012 and autumn 2014; P<0.001). Altogether, regardless of the species, a high 225 proportion of individuals produced gametes on all sampling dates. For example, in 226 Trébeurden (no. 4, Fig. 2) in spring 2012, 100% of species A individuals and 84% of species 227 228 B individuals showed both sperm and oocytes. Detailed values per site and sampling date are 229 provided in Table S2.

There were significant differences in fertilization rates when comparing cross type (Fig. 4, Table 3b). In particular, selfing success was very poor. Fertilization rates of heterospecific crosses with oocytes from species B did not differ from those of the two conspecific crosses (ca. 80%, Fig. 4). Fertilization rates dropped to very low values (<6%) when species A was the female parent (Fig. 4).

235

236 *mtDNA-based species identification*

Altogether, 3,048 individuals collected during the four surveys carried out in 2012 and 2013 were genotyped over four loci including one mitochondrial marker for identifying the maternal lineage. Only 33 of them (1.08%) showed discordance between morphological and mitochondrial identification, indicating a close association between maternal type and species assignment based on morphology. During the 2012 and 2013 field surveys, 90 individuals out of 15,463 (0.59%) were morphologically recorded as "unidentified" (Table 1); most (82%) of these showed a species B maternal lineage.

244

245 A unique putative F1 hybrid and little genetic admixture in the wild

Only 131 of the 3,048 individuals (4.3%) showed an admixed genome and all of them displayed very low hybrid index values (Fig. 5). In addition, only one (0.03%) individual was possibly a first-generation hybrid (i.e. heterozygote across the three nuclear loci). This putative F1 hybrid displayed a species B maternal lineage and was found in Perros Guirec (no. 3, Fig. 2) in autumn 2013.

Regardless of maternal type, at the regional level, the proportion of admixture varied 251 from 0.8% (spring 2013) to 6.3% (autumn 2012). A slightly higher rate of admixture was 252 253 found in the autumn generations compared with the spring generations (Table 1). The admixture rate varied slightly across localities (Table 1). In particular, in localities where the 254 two species co-occurred, admixed individuals were frequently found. For instance during the 255 first sampling date 1.6% in St Quay, Trébeurden and Moulin Blanc (nos. 2, 4 and 7, Fig. 2) 256 and 9.7% in Perros Guirec and Roscoff (nos. 3 and 5, Fig. 2). In contrast, no admixed 257 258 individuals were observed in the locality where species A was absent throughout the survey (Aber Wrac'h, no. 6 in Fig. 2). These variations are, however, explained by differences in 259 260 admixture patterns between individuals with different maternal backgrounds (Table 2). Large differences in the admixture proportion were indeed observed between the two groups with 261 82.4% of the 131 of individuals showing an admixed genome characterized by a species A 262 maternal lineage. In addition, the admixture proportion of individuals with a species A 263 maternal lineage was stable across localities and time (all localities and sampling date 264 comparison, P=0.178) and across localities at each sampling date separately (P>0.05 except 265 in autumn 2013: P=0.032). In contrast, the proportion of admixed individuals with a species B 266 maternal lineage was variable across localities and time (all localities and sampling date 267 comparisons, P=0.002) and across localities for each sampling date (P<0.05 except in spring 268 2013: P=0.129). Altogether, these results show that most of the variation in admixture among 269

270 localities or sampling dates (Table 1) is due to variation in the relative abundance of species271 A, which showed the highest admixture rate.

272

273 Discussion

274

The non-native tunicate Ciona intestinalis species A is well established

Based on the morphological examination of 23,000 individuals covering six different 275 generations, we documented the durable establishment of the non-native species (NNS) C. 276 277 intestinalis species A along the coasts of Brittany, ca. 15-20 years after the first reports of its introduction in the WEC. The first detailed study on the co-occurrence of species A and 278 species B in the English Channel (Nydam and Harrison 2011) revealed no samples of species 279 A specimens during a follow-up survey (in 2009, two years after their first survey), 280 interpreted as a possible decline of the NNS in the localities surveyed. This decline was not 281 282 confirmed in our study. Our data, combined with those of Nydam and Harrison (2011), illustrate the importance of temporal monitoring over a substantial time window, particularly 283 during the establishment stage, as well as during different seasons for short-lived species. 284

Despite the sustainable regional establishment of species A, there was local population 285 instability: for instance, the Roscoff marina showed a steady decline leading to complete 286 disappearance. Local population dynamics are likely to be unstable in this short-lived and 287 recently introduced NNS, as observed in other introduced regions (e.g. Saldanha Bay in South 288 Africa, Rius et al. 2011). Such major changes in site occupancy and local abundance in just a 289 few years have already been documented in other NNS discovered in the English Channel 290 (e.g. Bishop et al. 2014). Many environmental and biotic mechanisms influence the successful 291 and durable establishment of NNS (Blackburn et al. 2014), including competitive interactions 292 which may exacerbate invasion dynamics (Simberloff and Stiling 1996; Alpert 2006). This 293

294 mechanism may be particularly important here because the non-native species A co-occurs295 with its congener (Fig. 1).

296

297 Seasonal variation in species abundance: the outcome of competition in a changing 298 environment

Regular field work, sampling and monitoring as well as panels experiments examining 299 settlement dynamics of *Ciona* sp. (S. Bouchemousse, L. Lévêque, F. Viard, unpublished data) 300 showed that spring and autumn generations are two separate generations, for the two study 301 species. This is in agreement with the few data documenting the number of generations per 302 year in the study area (Dybern 1965 in the North Atlantic for species B). By examining these 303 two distinct generations of the same year, during three years, we documented a significant 304 increase in the relative abundance of species A in autumn. Adults sampled in autumn likely 305 306 correspond to juveniles that had settled from spring to early summer, when sea water temperatures increase from ca. 12°C in April to ca. 18°C in August-September in the study 307 308 area (Figure S1). Conversely, adults sampled in spring likely correspond to juveniles that have 309 settled in late summer / early fall, and which survive across the winter season (S. Bouchemousse, L. Lévêque, F. Viard, unpublished data). Seawater temperature greatly 310 influences the development, growth and survival of Ciona intestinalis spp. (Dybern 1965; 311 Marin et al. 1987), with species A and species B reported as warm-water and cold-water 312 species, respectively (Procaccini et al. 2011; Caputi et al. 2014). We observed higher growth 313 rates at 17°C, for species A than species B during laboratory experiments (data not shown), 314 315 confirming previous findings (Petersen et al. 1995) based on the growth rate of the nominal species C. intestinalis in localities where only species A or species B are now reported (e.g. at 316 317 15°C, growth rate varies between 2 and 3% in length per day for Japanese populations (species A) and between 0.7 and 1.1% per day for individuals from Scotland (species B)). In 318

the study area, temperatures above 15°C are only observed from June to October (Figure S1). It is also noteworthy that in the localities with the lowest maximum values of sea water temperatures (i.e. Aber Wrac'h and Roscoff, with a maximum always below 17°C) *C. intestinalis* species A has never been observed or declined up to disappearance. The observed seasonal variations may thus partly result from spatial competition among species A and B. The autumn generation of species A may have a competitive advantage, due to its faster growth rate during the warmer season.

Although temperature is likely the main environmental driver of the seasonal 326 dynamics of the two congeners at a regional scale, other factors can drive local population 327 dynamics. In particular, episodes of low salinity, due to rainfall and river inputs, can decrease 328 survival of C. intestinalis (Lambert and Lambert 1998). Such perturbation events due to 329 abrupt variations in environmental parameters have been recorded in our study area, as 330 331 illustrated in Figure S2 for the marina of Moulin Blanc (no. 7 in Fig. 2), where additional monitoring (independent of our study; L. Lévêque, unpublished data) for C. intestinalis spp. 332 abundance and salinity was carried out in 2013-2014. Salinity declined sharply and 333 subsequently Ciona spp. died off massively during winter months from January to March 334 2014. Synergistic effects between temperature and salinity may explain the very high 335 percentage of species A observed in some localities such as Perros-Guirec (up to 90%; Fig. 336 2): this marina is closed off from the sea at low tide and remains several days without 337 seawater renewal during neap tides such that 1) salinity can rapidly decrease in winter (due to 338 rainfall) and 2) temperature can increase on the surface in summer (Figure S1). After winter 339 die-offs of both species, due both to low temperatures and low salinity episodes, increasing 340 seawater temperature may favor a more rapid colonization of species A over species B, taking 341 into account its faster growth rate, on pontoons from adjacent sources (e.g. pillars, sea-wall), 342 giving locally and at some particular season, a competitive advantage to species A over 343

species B. Conversely, Roscoff is an open, fully marine marina in the coldest part of the Brittany coastline (i.e. 13°C annual average, Gallon et al. 2014). No massive mortality of *Ciona intestinalis* spp. has ever been observed and low temperatures may favor the development of species B, leading to competitive exclusion of species A.

Altogether, our study suggests that, with a few exceptions, environmental conditions in the 348 study sites meet the niche requirements of the NNS species, though local variations in 349 environmental parameters may favor one or the other of the two species, and thus may 350 influence the outcome of competitive interactions among them. In particular, species A, 351 thanks to its faster growth rate, may have a better adaptive potential than species B for 352 (re)colonizing substrates during warmer seasons after disturbances due to variations in 353 environmental factors, like a sharp decline in salinity after rains. Over larger temporal scales, 354 the predicted increase of sea surface temperature (i.e. 0.35°C per decade; Gallon et al. 2014) 355 356 and winter rainfalls (Ouzeau et al. 2014) in Brittany, due to climate change, could promote a substantial increase of the relative abundance of the NNS compared with its native congener 357 358 in its introduced range.

359

360 *Efficient barriers prevent hybridization in the wild*

Sexually mature, gamete-producing individuals occurred simultaneously in the two 361 study species which are interfertile and live in syntopy in most of the study localities. Despite 362 these features that are expected to favor hybridization, the admixture rate was very low 363 (4.3%) and only one putative F1 hybrid was observed in this study on more than 3,000 364 individuals, confirming previous studies (4.2% in localities of the WEC, Nydam and Harrison 365 2011; 6.3% in one British locality, Sato et al. 2014). Ecological and/or genetic barriers thus 366 367 seem to be at play and limit hybridization between the two species in the wild in Brittany. The success of interspecific fertilization in laboratory conditions (Fig. 4) seemingly suggests that 368

post-zygotic isolation mechanisms act in the wild through a reduction in hybrid fitness 369 (Abbott et al. 2013). However, Sato et al. (2014) showed that F1 hybrids are viable and 370 produce functional gametes, suggesting that hybrid depression, if any, is expressed at an 371 372 earlier stage (e.g. larvae or juveniles). However, preliminary findings from a molecular study of juveniles of species A and species B in four marinas of the WEC (nos. 4, 5, 7 and 8; Fig. 2) 373 showed rates of admixture similar to those observed in adults (S. Bouchemousse, L. Lévêque, 374 F. Viard, unpublished data). Pre-zygotic isolation mechanisms can enhance assortative 375 mating; however, given the close contact (see Fig. 1), habitat segregation and behavior cannot 376 be efficient reproductive isolation mechanisms. Differences in the timing of reproductive 377 378 development, as suggested by Sato et al. (2014), are also unlikely because we observed a high proportion of individuals producing gametes in both species and each sampling date. Gamete 379 release occurs over several days or even weeks (Carver et al. 2003), invalidating any 380 381 consideration of slight shifts in the timing of gamete release in light of the short survival time of the gametes in seawater (i.e. 16 h after release for sperm and 30 h for oocytes; Svane and 382 Havenhand 1993). Assortative fertilization, facilitated by species-specific chemical attraction, 383 can be a key mechanism for reproduction in broadcast-spawning marine invertebrates in 384 marine systems (Palumbi 1994). This mechanism has been described already within species 385 complexes, for instance in two tropical sea urchins of the Echinometra species complex 386 (Geyer and Palumbi 2005) and in two mussels of the Mytilus species complex (Bierne et al. 387 2002). Laboratory gamete choice experiments are needed to investigate this mechanism in the 388 C. intestinalis species complex. 389

390

391 The source of admixture: historical or contemporary processes?

In the laboratory, F1 hybrids are easily obtained in one direction only, i.e. with species
B oocytes (Fig. 4). Asymmetrical interspecific fertilization success is common, including in

free-spawning marine invertebrates (e.g. Rawson et al. 2003; Geyer and Palumbi 2005). The 394 direction of this asymmetry was however unexpected based on the observed admixture rates 395 that we computed according to the maternal lineage (82.4% of the 131 admixed individuals 396 397 showed a species A maternal lineage). There are two possible explanations of this discrepancy between laboratory and field data. First, the few offspring produced by the least productive 398 heterospecific crosses (i.e. a species A female crossed with a species B male) may be 399 particularly fertile and vigorous. Similar situations with successful hybrids produced by 400 parental combinations with low fertilization success have already been described, even in 401 marine systems (e.g. Blum et al. 2010). This process may foster adaptive introgression of the 402 NNS (species A) and/or drive hybrids to replace parental species (e.g. Rosenfield et al. 2004; 403 Schierenbeck and Ellstrand 2009). Second, conditions that promote successful crosses in the 404 laboratory may not be the conditions found in the wild (Sato et al. 2014). Monitoring survival 405 406 of hybrid offspring obtained from experimental crosses is one way to test these two hypotheses. It is also interesting to note that the direction of the asymmetry is variable across 407 408 studies: the direction observed here is in agreement with what has been reported by Caputi et 409 al. (2007) but not with Sato et al. (2014), although in both studies some of the crosses involved individuals from the North Atlantic. Factors promoting (preventing) the 410 hybridization success are potentially numerous, and among them the origin and the genetic 411 background, in particular the introgression profiles (see below), may be important factors to 412 consider in future studies. 413

Alternatively, from a conceptually different viewpoint, observed admixture may reflect the footprint of a previous secondary contact between species A and species B (Roux et al. 2013). Roux et al. (2013) compared various speciation models (e.g. divergence models with or without interspecific gene flow) using Approximate Bayesian Computations based on full transcriptomes of species A and species B (10 individuals for each). The best model to

explain the data was a model of divergence with gene flow resulting from a secondary contact 419 between the two species after their primary divergence (4 Mya ago). During this secondary 420 contact, ca. 20% of loci presumably crossed the species barrier in both directions (Roux et al. 421 422 2013). The authors then estimated the age of this secondary contact between 4,300 and 56,800 years ago. Many secondary contacts have been documented in marine systems during this 423 period which corresponds to the end of the Pleistocene (Maggs et al. 2008; Geller et al. 2010). 424 The number of studies showing interspecific gene flow following these secondary contacts 425 also recently increased (Abbott et al. 2013, see Becquet et al 2012 for an example). In this 426 context, past hybridization is very plausible explanation of our results because it can account 427 428 for 1) the discrepancy observed between laboratory and field experiments; 2) the temporal and spatial stability of the proportion of admixed individuals for species A; and 3) the complex 429 evolutionary history of the two study cryptic species (Roux et al. 2013). Although historical 430 431 processes may explain most of the admixture observed, contemporary interspecific gene flow remains possible based on our results in two localities: in St Malo, no admixed individuals 432 433 were observed until autumn 2013 following the colonization of this locality by species A and 434 in Roscoff, admixed individuals were observed in 2012, but none afterwards when species A disappeared. Finally, at Aber Wrac'h, the only locality where no species A specimens were 435 ever observed, did not show any admixed specimens. Furthermore — and interestingly — in 436 St Malo and Aber Wrac'h, all admixed individuals displayed a species B maternal lineage, as 437 did the only putative F1 hybrid found in our study (in Perros Guirec). 438

Altogether, our results suggest that past secondary contacts influenced the introgression rates measured here and rare contemporary hybridizations in the wild account mainly for the admixed individuals with a species B maternal background, in agreement with laboratory assays. The status of the presumed species diagnostic markers used so far (Caputi et al. 2007; Nydam and Harrison 2011; Sato et al. 2014; this study) need to be re-evaluated

because the three loci behave differently: CesA and vAChTP highlight admixture in species B 444 maternal backgrounds whereas Hox5 revealed admixture with species A maternal 445 backgrounds (see Table S3). Although not discernable in our laboratory crosses (or in the 446 447 literature, Caputi et al. 2007), we suggest that Hox5 crossed the species barrier a long time ago, in contrast to the two other loci (similar to the Glu locus which was mistakenly 448 considered as a diagnostic marker of Mytilus species, Borsa et al. 2012). High-throughput 449 genotyping based on SNPs are currently in progress to better investigate the fate of the 450 introgression hot-spots defined by Roux et al. (2013) and the true extent of contemporary 451 hybridization in wild Ciona populations. 452

453

In conclusion, our study highlights the importance of temporal monitoring adapted to 454 the life cycle and the generation time of short-lived NNS. This type of monitoring is critical 455 456 for early-warning and accurate assessments of the durable establishment of introduced species. Our results also illustrate how difficult it is to predict the outcome of human-457 458 mediated introductions, even in supposedly well-known model species: we expected to find a large proportion of hybrids and introgression events between species A and species B, but 459 only rare events (if any) were uncovered despite extensive sampling. Our results pave the way 460 461 for future research on the reproductive isolation mechanisms acting in the wild between these model organisms, as well as on the processes that can sustain long-term co-occurrence of two 462 functionally similar and congeneric species living in syntopy. 463

464

465 Acknowledgments

We are very grateful to the divers of the Marine Operations department (*Service Mer & Observation*) at the Roscoff Biological Station for help in the field and to M. Danielo for assistance in data acquisition. FV thanks M. Nydam for her recommendations regarding

469	molecular protocols. We are thankful for the numerous marina operators who provided access
470	to pontoons and permission to carry out this study. We acknowledge S. Le Cam and T.
471	Broquet for advices regarding statistical analyses, N. Bierne for stimulating discussions about
472	hybridization and introgression processes, and C. Lejeusne and T. Comtet for comments on
473	earlier versions of this manuscript. This work was supported by the Interreg IVa Marinexus
474	program and the ANR project HYSEA (no. ANR-12-BSV7-0011).
475	

477 **References**

- Abbott RJ (1992) Plant invasion, interspecific hybridization and the evolution of new plant
 taxa. Trends Ecol Evol 7:401-405.
- Abbott R, Albach D, Ansell S et al (2013) Hybridization and speciation. J Evol Biol 26:229246.
- Airoldi L, Turon X, Perkol-Finkel S et al (2015) Corridors for aliens but not for natives:
 effects of marine urban sprawl at a regional scale. Divers Distrib doi:
 10.1111/ddi.12301
- Allendorf FW, Leary RF, Spruell P et al (2001) The problems with hybrids: setting
 conservation guidelines. Trends Ecol Evol 16:613-622.
- 487 Alpert P (2006) The advantages and disadvantages of being introduced. Biol Invasions
 488 8:1523-1534.
- Bates D, Maechler M, Bolker B et al (2014) lme4: Linear mixed-effects models using Eigen
 and S4. R package version 1.1-7 http://CRAN.R-project.org/package=lme4.
- Becquet V, Simon-Bouhet B, Pante E et al (2012) Glacial refugium versus range limit:
 Conservation genetics of *Macoma Balthica*, a key species in the Bay of Biscay
 (France). J Exp Mar Biol Ecol 432-433:73-82.
- Bierne N, David P, Boudry P et al (2002) Assortative fertilization and selection at larval stage
 in the mussels *Mytilus edulis* and *M. galloprovincialis*. Evolution 56:292-298.

Bishop JDD, Wood CA, Lévêque L et al (2014) Repeated rapid assessment surveys reveal 496 contrasting trends in occupancy of marinas by non-indigenous species on opposite 497 sides of the western English Channel. Mar Pollut Bull, 498 doi:10.1016/j.marpolbul.2014.11.043. 499

- Blackburn TM, Essl F, Evans T et al (2014) A unified classification of alien species based on
 the magnitude of their environmental impacts. PLoS Biol 12,
 doi:10.1371/journal.pbio.1001850
- Blum MJ, Walters DM, Burkhead NM et al (2010) Reproductive isolation and the expansion
 of an invasive hybrid swarm. Biol Invasions 12:2825-2836.
- Bock DG, MacIsaac HJ, Cristescu ME (2012) Multilocus genetic analyses differentiate
 between widespread and spatially restricted cryptic species in a model ascidian. Proc
 R Soc B 279:2377-2385.
- Borsa P, Rolland V, Daguin C (2012) Genetics and taxonomy of Chilean smooth-shelled
 mussels, *Mytilus* spp. (Bivalvia: Mytilidae). C R Biol 335:51-61.
- Brunetti R, Gissi C, Pennati R et al (2015) Morphological evidence that the molecularly
 determined *Ciona intestinalis* type A and type B are different species: *Ciona robusta*and Ciona intestinalis. J Zoolog Syst Evol Res, doi: 10.1111/jzs.12101
- Caputi L, Andreakis N, Mastrototaro F et al (2007) Cryptic speciation in a model invertebrate
 chordate. Proc Natl Acad Sci USA 104:9364-9369.
- 515 Caputi L, Crocetta F, Toscano F et al (2014) Long-term demographic and reproductive trends
 516 in *Ciona intestinalis* sp. A. Mar Ecol 36:118-128.
- 517 Carver CE, Chisholm A, Mallet AL (2003) Strategies to mitigate the impact of *Ciona* 518 *intestinalis* (L.) biofouling on shellfish production. J Shellfish Res 22:621-631.

519 Cirino P, Toscano F, Caramiello D et al (2002) Laboratory culture of the ascidian *Ciona*520 *intestinalis* (L.): a model system for molecular developmental biology research.
521 Marine Models Electronic Record. Available from

522 http://www.mbl.edu/html/BB/MMER/CIR/CirTit.html

- Coleman RR, Gaither MR, Kimokeo B et al (2014) Large-scale introduction of the Indo Pacific damselfish *Abudefduf vaigiensis* into Hawai'i promotes genetic swamping of
 the endemic congener *A. abdominalis*. Mol Ecol 23:5552-5565.
- 526 Currat M, Ruedi M, Petit RJ et al (2008) The hidden side of invasions: Massive introgression
 527 by local genes. Evolution 62:1908-1920.
- 528 Dybern BI (1965) The life cycle of *Ciona intestinalis* (L.) f. *typica* in relation to the 529 environmental temperature. Oikos 16:109-131.
- Fitzpatrick BM, Johnson JR, Kump DK et al (2010) Rapid spread of invasive genes into a
 threatened native species. Proc Natl Acad Sci USA 107:3606-3610.
- Gallon RK, Robuchon M, Leroy B et (2014) Twenty years of observed and predicted changes
- in subtidal red seaweed assemblages along a biogeographical transition zone: inferring
 potential causes from environmental data. J Biogeogr 41:2293-2306.
- Geller JB, Darling JA, Carlton JT (2010) Genetic perspectives on marine biological invasions.
 Annu Rev Mar Sci 2:367-393.
- Geyer LB, Palumbi SR (2005) Conspecific sperm precedence in two species of tropical sea
 urchins. Evolution 59:97-105.
- Guo Q (2014) Plant hybridization: the role of human disturbance and biological invasion.
 Divers Distrib 20:1345-1354.
- Harrison RG (2012) The language of speciation. Evolution 66:3643-3657.
- Lambert CC, Lambert G (1998) Non-indigenous ascidians in southern California harbors and
 marinas. Mar Biol 130:675-688.
- Maggs CA, Castilho R, Foltz D et al (2008) Evaluating signatures of glacial refugia for North
 Atlantic benthic marine taxa. Ecology 89:S108-S122.
- 546 Mantel N (1963) Chi-square tests with one degree of freedom: Extensions of the Mantel-
- 547 Haenszel Procedure. J Am Statist Assoc 58:690-700.

- Marin MG, Bressan M, Beghi L et al (1987) Thermo-haline tolerance of *Ciona intestinalis*(L., 1767) at different developmental stages. Cah Biol Mar 28:47-57.
- 550 Millar RH (1953) Ciona. In: Colman JS (ed.) L.M.B.C. Memoirs of Typical British Marine
- 551 Plants and Animals, XXV. Liverpool University Press, Liverpool, pp 123.
- 552 Molnar JL, Gamboa RL, Revenga C et al (2008) Assessing the global threat of invasive 553 species to marine biodiversity. Front Ecol Environ 6:485-492.
- Nydam ML, Harrison RG (2007) Genealogical relationships within and among shallow-water
 Ciona species (Ascidiacea). Mar Biol 151:1839-1847
- 556 Nydam ML, Harrison RG (2010) Polymorphism and divergence within the ascidian genus
 557 *Ciona*. Mol Phylogenet Evol 56:718-726.
- Nydam ML, Harrison RG (2011) Introgression despite substantial divergence in a broadcast
 spawning marine invertebrate. Evolution 65:429-442.
- Ouzeau G, Déqué M, Jouini M et al (2014) Scénarios régionalisés édition 2014 pour la métropole et les régions d'outre-mer. In : Jouzel J (ed) Le climat de la France au XXI^e
 siècle. Direction Générale de l'Energie et du Climat 4: 62.
- Palumbi SR (1994) Genetic divergence, Reproductive isolation and marine speciation. Annu
 Rev Ecol Syst 25:547-572.
- Perez-Portela R, Arranz V, Rius M et al (2013) Cryptic speciation or global spread? The case
 of a cosmopolitan marine invertebrate with limited dispersal capabilities. Sci Rep 3,
 doi:10.1038/srep03197.
- Petersen JK, Schou O, Thor P (1995) Growth and energetics in the ascidian *Ciona intestinalis*.
 Mar Ecol Prog Ser 120:175-184.
- Procaccini G, Affinito O, Toscano F et al (2011) A new animal model for merging Ecology
 and Evolution. In: Pontarotti P (ed) Evolutionary Biology: concepts, biodiversity,
 macroevolution and genome evolution. Springer-Verlag, Berlin, pp 91-106

- 573 R Development Core Team (2005) R: A language and environment for statistical computing.
- 574 R Foundation for Statistical, Vienna, Austria. ISBN 3-900051-07-0, URL:
 575 http://www.R-project.org.
- Rawson PD, Slaughter C, Yund, PO (2003) Patterns of gamete incompatibility between the
 blue mussels *Mytilus edulis* and *M. trossulus*. Mar Biol 143:317-325.
- 578 Rhymer JM, Simberloff D (1996) Extinction by hybridization and introgression. Annu Rev
 579 Ecol Syst 27:83-109.
- 580 Rius M, Heasman KG, McQuaid CD (2011) Long-term coexistence of non-indigenous
 581 species in aquaculture facilities. Mar Pollut Bull 62:2395-2403.
- Rosenfield JA, Nolasco S, Lindauer S et al (2004) The role of hybrid vigor in the replacement
- of Pecos pupfish by its hybrids with sheepshead minnow. Conserv Biol, 18 1589-1598.
- Roux C, Tsagkogeorga G, Bierne N et al (2013) Crossing the species barrier: genomic
 hotspots of introgression between two highly divergent *Ciona intestinalis* species. Mol
 Biol Evol 30:1574-1587.
- Sato A, Satoh N, Bishop JDD (2012) Field identification of 'types' A and B of the ascidian
 Ciona intestinalis in a region of sympatry. Mar Biol 159:1611-1619.
- Sato A, Shimeld SM, Bishop JDD (2014) Symmetrical reproductive compatibility of the two
 species in the *Ciona intestinalis* (Acidiacea) species complex, a model for marine
 genomics and developmental biology. Zool Sci 31:369-374.
- Schierenbeck KA, Ellstrand NC (2009) Hybridization and the evolution of invasiveness in
 plants and other organisms. Biol Invasions 11:1093-1105.
- 595 Shenkar N, Swalla BJ (2011) Global diversity of Ascidiacea. PLoS ONE 6,
 596 doi:10.1371/journal.pone.0020657.
- 597 Simberloff D, Stiling P (1996) How risky is biological control? Ecology 77:1965-1974.

- Steeves TE, Maloney RF, Hale ML, Tylianakis JM et al (2010) Genetic analyses reveal
 hybridization but no hybrid swarm in one of the world's rarest birds. Mol Ecol
 19:5090-5100.
- Suzuki MM, Nishikawa T, Bird A (2005) Genomic approaches reveal unexpected genetic
 divergence within *Ciona intestinalis*. J Mol Evol 61:627-635.
- Svane I, Havenhand JN (1993) Spawning and dispersal in *Ciona intestinalis* (L.). Mar Ecol
 14:53-66.
- Zhan A, Macisaac HJ, Cristescu ME (2010) Invasion genetics of the *Ciona intestinalis* species
 complex: from regional endemism to global homogeneity. Mol Ecol 19:4678-4694.

607

Table 1. Sample size (N_{tot}), number of individuals unidentified based on morphological criteria (N_{uni}), and percentage of *Ciona intestinalis* species A specimens (based on morphology; $%_{spA}$), for each study site and sampling date. The overall introgression rate (i.e. proportion of individuals showing an admixed multilocus genotype whatever their maternal lineage; $%_{mix}$) is indicated for the four surveys for which there were molecular data (i.e. all except in 2014).

	26	Sprin April	g 2012 – 10 M	ay	20 20	Autun 6 Oct.	m 2012 – 6 Nov	2 v.		Sprin 15 – 2	g 2013 5 April	l	1	Autun 14 – 2	m 2013 24 Oct.	3	Spring 15 – 2	g 2014 2 May	Autum 24 – 3	n 2014 1 Oct.
Site	N _{tot}	N _{uni}	‰ _{spA}	‰ _{mix}	N _{tot}	N _{uni}	‰ _{spA}	‰ _{mix}	N _{tot}	N _{uni}	‰ _{spA}	‰ _{mix}	N _{tot}	N _{uni}	‰ _{spA}	‰ _{mix}	N _{tot}	‰ _{spA}	N _{tot}	‰ _{spA}
1- St Malo	311	1	0.0	0.0	375	1	0.0	0.0	736	1	0.0	0.0	490	1	0.0	1.6	399	0.0	823	1.10
2- St Quay	178	14	5.6	1.6	335	0	33.1	3.3	269	2	3.0	0.0	341	1	12.6	0.0	157	0.6	763	14.2
3- Perros Guirec	297	6	13.5	9.7	305	0	90.2	10.9	223	3	8.5	0.0	531	8	67.0	3.2	217	14.3	495	96.0
4- Trébeurden	228	4	6.6	1.6	262	0	61.1	12.7	436	0	6.7	0.0	474	4	43.2	8.1	281	6.4	809	16.4
5- Roscoff	160	8	8.8	9.7	203	0	2.5	0.0	329	5	0.0	0.0	626	0	0.0	0.0	311	0.0	508	0.0
6- Aber Wrac'h	171	3	0.0	0.0	236	2	0.0	0.0	290	1	0.0	0.0	523	0	0.0	0.0	36	0.0	315	0.0
7- Moulin Blanc	168	1	18.5	1.6	234	1	42.7	13.8	120	1	35.8	7.8	543	1	2.2	1.7	99	0.3	424	3.3
8- Château	205	0	3.4	0.0	721	6	19.1	8.3	300	0	0.0	2.2	778	0	6.0	7.9	295	0.0	906	8.0
9- Camaret-sur-Mer	260	4	6.5	0.0	306	1	30.4	10.0	214	2	5.1	0.0	543	4	20.3	9.4	236	4.7	463	38.2
10- Concarneau	338	1	1.5	0.0	474	1	60.1	9.7	264	0	0.0	0.0	712	0	27.2	3.2	-	-	-	-
11- Quiberon	-	-	-	-	227	1	8.4	0.0	367	1	0.5	0.0	360	0	3.6	3.2	-	-	-	-
Mean	232	4.2	6.4	2.4	334	1.2	33.9	6.2	323	1.5	5.9	0.9	538	1.7	17.9	3.5	226	2.9	612	19.7
Standard deviation	66	4.3	5.9	3.9	150	1.7	29.6	5.6	160	1.5	10.5	2.4	131	2.6	21.7	3.5	113	4.9	213	31.1
Total	2316	42	6.0	2.0	3678	13	32.2	6.3	3548	16	3.1	0.8	5921	19	16.6	3.5	2031	3.1	5506	22.0

Table 2. Proportion of admixed individuals, i.e. individuals showing a mixture of alleles diagnostic for *Ciona intestinalis* species A and *C. intestinalis* species B, for each maternal lineage separately ($%_{mix spA}$ and $%_{mix spB}$ for individuals diagnosed with species A mitochondria and a species B mitochondria, respectively), for each site and sampling date studied in 2012 and 2013. N_{spA} and N_{spB} are the number of specimens for which admixture was examined.

Spring 2012				Autumn 2012				Spring 2013					Autumn 2013			
Site	N _{spA}	‰ _{mix spA}	N _{spB}	‰ _{mix spB}	N _{spA}	‰ _{mix spA}	N _{spB}	‰ _{mix spB}	N _{spA}	% _{mix spA}	N _{spB}	‰ _{mix spB}	N _{spA}	‰ _{mix spA}	N _{spB}	‰ _{mix spB}
1- St Malo	0	-	56	0.0	0	-	62	0.0	0	-	60	0.0	0	-	64	1.6
2- St Quay	5	20.0	58	0.0	28	7.1	33	0.0	2	0.0	55	0.0	19	0.0	44	0.0
3- Perros Guirec	18	33.3	44	0.0	56	12.5	8	0.0	4	0.0	44	0.0	50	4.0	12	0.0
4- Trébeurden	4	25.0	59	0.0	40	15.0	23	8.7	5	0.0	54	0.0	29	10.3	33	6.1
5- Roscoff	5	40.0	26	3.8	1	0.0	57	0.0	0	-	77	0.0	0	-	60	0.0
6- Aber Wrac'h	0	-	62	0.0	0	-	58	0.0	0	-	63	0.0	0	-	62	0.0
7- Moulin Blanc	11	9.1	51	0.0	33	18.2	25	8.0	19	21.1	32	0.0	3	33.3	56	0.0
8- Château	0	-	64	0.0	23	21.7	37	0.0	0	-	46	2.2	6	16.7	57	7.0
9- Camaret-sur-Mer	8	0.0	56	0.0	28	17.9	32	3.1	3	0.0	46	0.0	17	29.4	47	2.1
10- Concarneau	1	0.0	63	0.0	48	12.5	14	0.0	0	-	60	0.0	20	5.0	42	2.4
11- Quiberon	-	-	-	-	5	0.0	59	0.0	0	-	55	0.0	5	40.0	56	0.0
Mean	5.2	18.2	53.9	0.4	23.8	11.7	37.1	1.8	3.0	4.2	53.8	0.2	13.6	17.3	48.5	1.7
Standard deviation	5.8	15.8	11.5	1.2	20.0	7.8	19.2	3.4	5.6	9.4	11.8	0.7	15.6	15.1	15.4	2.6

Table 3. Results of linear mixed models testing a) the effects of season and sampling year on the relative abundance of *Ciona intestinalis* species A and *C. intestinalis* species B in syntopic localities and b) the effect of cross type on the fertilization rate. Degrees of freedom (d.f.), residual d.f., residual deviation and *P*-value (from Chi-squared test) are given. Significant *P*-values are shown in italics.

Va	riable	Model	d.f.	Residual d.f.	Residual deviation	<i>P</i> -value
a)	Relative species abundance	Null model		46	2968.1	
		Year	2	44	2804.9	<0.01
		Season	1	45	1667.9	<0.001
		Year x Season	5	41	1319.2	< 0.001
b)	Fertilization rate	Null model		105	720.85	
		Cross type	5	100	203.44	<0.001

Figure Legends

Figure 1. Artificial plastic substrates are heavily colonized in the study area, including by *Ciona intestinalis* species A (white form) and *C. intestinalis* species B (with yellow rim around siphons) as shown in this picture, which also illustrates the syntopy between the two study species. Photo credit: Wilfried Thomas, Station Biologique of Roscoff.

Figure 2. Relative abundance of *Ciona intestinalis* species A (in black) and species B (in gray) in the 11 study sites (1: St Malo, 2: St Quay, 3: Perros Guirec, 4: Trébeurden, 5: Roscoff, 6: Aber Wrac'h, 7: Moulin Blanc, 8: Château, 9: Camaret-sur-Mer, 10: Concarneau, 11: Quiberon) from spring 2012 to autumn 2014. Maps with the same letter indicate non-significant differences between sampling dates (pairwise comparisons, P > 0.05).

Figure 3. Ternary diagrams representing the proportion of the three recorded reproductive stages for *Ciona intestinalis* species A (black circles) and for species B (gray circles), for each sampling date. Numbers in the circles refer to site numbers (see Table 1).

Figure 4. Fertilization rate for conspecific crosses (i.e. using female (Fe) and male (Ma) gametes of the same species, gray bars), heterospecific crosses (i.e. using female and male gametes from different species, white bars) and self-crosses (i.e. using gametes from the same individual, black bars). Values with the same letter are not significantly different (pairwise comparisons, P > 0.05).

Figure 5. Hybrid index computed for each sampling date for individuals with a *Ciona intestinalis* species A (black bars) and *C. intestinalis* species B (gray bars) maternal lineage.

Maternal lineage was ascertained with a diagnostic mitochondrial marker (see text). N_{spA} and N_{spB} are the number of specimens examined. The individual (sampled in autumn 2013) indicated by an arrow has a hybrid index of 3 and is the only putative F1 hybrid found of the 3,048 study individuals.

Figure 1.







Figure 3.







Figure 5.



Supplementary Information for online appendix

Table S1. Geographical coordinates and characteristics of each site, i.e. open or closed marinas (by means of tidal or sill gates) at low tide, freshwater (estuarine) or marine influence.



Site	Coordinates	Open/ Closed	Estuarine/Marine
1- St Malo	48.638617; -2.026411	Open	Marine
2- St Quay	48.646136; -2.820925	Open	Marine
3- Perros Guirec	48.804877; -3.441954	Closed	Marine
4- Trébeurden	48.769510; -3.585811	Closed	Marine
5- Roscoff	48.717500; -3.965401	Open	Marine
6- Aber Wrac'h	48.598626; -4.562438	Open	Estuarine
7- Moulin Blanc	48.390365; -4.432140	Open	Estuarine
8- Château	48.379489; -4.489469	Open	Estuarine
9- Camaret-sur-Mer	48.279674; -4.596113	Open	Marine
10- Concarneau	47.870150; -3.914604	Open	Estuarine
11- Quiberon	47.488223; -3.103269	Open	Marine

Table S2. Detailed sampling size used for analyzing the reproductive status and proportions of the observed reproductive stages for *C. intestinalis* species A (N_{spA}) and species B (N_{spB}) at each study site and sampling date. Three categories were recorded: 1) immature individuals (imm), 2) individuals with sperm only (sp) and 3) individuals with both sperm and oocytes (sp+ooc).

A) Spring 2012

		Spe	cies A		Species B					
Site	N _{spA}	%imm	%sp	%sp+ooc	N _{spB}	%imm	%sp	%sp+ooc		
1- St Malo	0	-	-	-	80	5.0	75.0	20.0		
2- St Quay	10	0.0	80.0	20.0	70	7.1	62.9	30.0		
3- Perros Guirec	38	0.0	31.6	68.4	53	7.5	83.0	9.4		
4- Trébeurden	15	0.0	0.0	100.0	74	1.4	14.9	83.8		
5- Roscoff	13	7.7	46.2	46.2	40	15.0	65.0	20.0		
6- Aber Wrac'h	0	-	-	-	77	0.0	14.3	85.7		
7- Moulin Blanc	23	26.1	65.2	8.7	64	64.1	28.1	7.8		
8- Château	7	0.0	71.4	28.6	80	2.5	87.5	10.0		
9- Camaret-sur-Mer	16	12.5	37.5	50.0	73	1.4	58.9	39.7		
10- Concarneau	5	0.0	20.0	80.0	79	10.1	77.2	12.7		
11- Quiberon	-	-	-	-	-	-	-	-		
Mean	12.7	5.8	44.0	50.2	69	11.4	56.7	31.9		
Standard deviation	11.5	9.5	27.3	31.2	13.2	19.1	27.6	29.6		
Total	127	7.1	41.7	51.2	690	10.4	56.2	33.3		

B) Autumn 2012

		Spe	ecies A		Species B					
Site	N _{spA}	%imm	%sp	%sp+ooc	N _{spB}	%imm	%sp	%sp+ooc		
1- St Malo	0	-	-	-	79	16.5	63.3	20.3		
2- St Quay	42	7.1	42.9	50.0	45	28.9	53.3	17.8		
3- Perros Guirec	69	1.4	36.2	62.3	30	23.3	63.3	13.3		
4- Trébeurden	50	14.0	44.0	42.0	42	16.7	45.2	38.1		
5- Roscoff	5	20.0	60.0	20.0	78	23.1	55.1	21.8		
6- Aber Wrac'h	0	-	-	-	80	2.5	88.8	8.8		
7- Moulin Blanc	41	31.7	34.1	34.1	42	45.2	26.2	28.6		
8- Château	40	5.0	40.0	55.0	55	32.7	32.7	34.5		
9- Camaret-sur-Mer	41	7.3	41.5	51.2	46	19.6	71.7	8.7		
10- Concarneau	59	15.3	33.9	50.8	40	37.5	35.0	27.5		
11- Quiberon	19	15.8	31.6	52.6	77	42.9	48.1	9.1		
Mean	33.3	13.1	40.5	46.5	55.8	26.3	53.0	20.8		
Standard deviation	23.8	9.2	8.5	12.7	18.9	12.8	18.4	10.4		
Total	366	11.5	38.5	50.0	614	25.1	55.2	19.7		

C) Spring 2013

		Spe	ecies A		Species B					
Site	N _{spA}	%imm	%sp	%sp+ooc	N _{spB}	%imm	%sp	%sp+ooc		
1- St Malo	0	-	-	-	80	23.8	38.8	37.5		
2- St Quay	6	33.3	16.7	50.0	76	3.9	38.2	57.9		
3- Perros Guirec	16	81.3	0.0	18.8	74	2.7	77.0	20.3		
4- Trébeurden	28	28.6	39.3	32.1	73	2.7	68.5	28.8		
5- Roscoff	0	-	-	-	115	9.6	47.0	43.5		
6- Aber Wrac'h	0	-	-	-	80	20.0	72.5	7.5		
7- Moulin Blanc	26	15.4	34.6	50.0	42	9.5	47.6	42.9		
8- Château	0	-	-	-	80	21.3	56.3	22.5		
9- Camaret-sur-Mer	11	27.3	45.5	27.3	75	6.7	56.0	37.3		
10- Concarneau	0	-	-	-	80	32.5	62.5	5.0		
11- Quiberon	2	0.0	0.0	100.0	80	3.8	63.8	32.5		
Mean	8.1	31.0	22.7	46.4	77.7	12.4	57.1	30.5		
Standard deviation	10.8	27.4	20.0	29.1	16.5	10.3	13.1	15.9		
Total	89	33.7	29.2	37.1	855	12.6	57.0	30.4		

D) Autumn 2013

		Spe	ecies A		Species B					
Site	N _{spA}	%imm	%sp	%sp+ooc	N _{spB}	%imm	%sp	%sp+ooc		
1- St Malo	0	-	-	-	80	7.5	52.5	40.0		
2- St Quay	40	2.5	2.5	95.0	57	3.5	33.3	63.2		
3- Perros Guirec	65	4.6	29.2	66.2	41	4.9	56.1	39.0		
4- Trébeurden	40	5.0	15.0	80.0	43	2.3	25.6	72.1		
5- Roscoff	0	-	-	-	80	11.3	56.3	32.5		
6- Aber Wrac'h	0	-	-	-	80	3.8	58.8	37.5		
7- Moulin Blanc	15	13.3	6.7	80.0	77	0.0	19.5	80.5		
8- Château	43	4.7	11.6	83.7	70	1.4	12.9	85.7		
9- Camaret-sur-Mer	40	5.0	27.5	67.5	60	3.3	36.7	60.0		
10- Concarneau	40	10.0	25.0	65.0	58	1.7	22.4	75.9		
11- Quiberon	13	0.0	53.8	46.2	72	6.9	54.2	38.9		
Mean	26.9	5.0	19.5	75.5	65.3	4.2	38.9	56.8		
Standard deviation	22.1	4.3	16.4	15.9	14.5	3.2	17.2	19.8		
Total	296	5.0	19.0	76.0	718	4.5	39.7	55.8		

E) Spring 2014

		Spe	ecies A		Species B					
Site	N _{spA}	%imm	%sp	%sp+ooc	N _{spB}	%imm	%sp	%sp+ooc		
1- St Malo	0	-	-	-	80	10.0	62.5	27.5		
2- St Quay	4	0.0	25.0	75.0	79	0.0	40.5	59.5		
3- Perros Guirec	31	12.9	51.6	35.5	67	6.0	29.9	64.2		
4- Trébeurden	28	0.0	32.1	67.9	75	4.0	48.0	48.0		
5- Roscoff	0	-	-	-	80	3.8	45.0	51.3		
6- Aber Wrac'h	0	-	-	-	36	0.0	5.6	94.4		
7- Moulin Blanc	0	-	-	-	80	31.3	15.0	53.8		
8- Château	1	0.0	0.0	100.0	80	1.3	26.3	72.5		
9- Camaret-sur-Mer	11	9.1	45.5	45.5	77	1.3	29.9	68.8		
10- Concarneau	-	-	-	-	-	-	-	-		
11- Quiberon	-	-	-	-	-	-	-	-		
Mean	8.3	4.4	30.8	64.8	72.7	6.4	33.6	60.0		
Standard deviation	12.5	6.2	20.2	25.4	14.4	9.9	17.4	18.6		
Total	75	6.7	41.3	52.0	654	6.9	35.5	57.6		

		Spe	ecies A		Species B					
Site	N _{spA}	%imm	%sp	%sp+ooc	N _{spB}	%imm	%sp	%sp+ooc		
1- St Malo	9	11.1	55.6	33.3	76	23.7	57.9	18.4		
2- St Quay	27	0.0	11.1	88.9	65	10.8	40.0	49.2		
3- Perros Guirec	79	6.3	36.7	57.0	27	22.2	55.6	22.2		
4- Trébeurden	31	9.7	19.4	71.0	59	11.9	25.4	62.7		
5- Roscoff	0	-	-	-	80	17.5	51.3	31.3		
6- Aber Wrac'h	0	-	-	-	80	18.8	46.3	35.0		
7- Moulin Blanc	34	5.9	14.7	79.4	76	11.8	21.1	67.1		
8- Château	27	18.5	29.6	51.9	72	44.4	30.6	25.0		
9- Camaret-sur-Mer	40	2.5	5.0	92.5	49	8.2	38.8	53.1		
10- Concarneau	-	-	-	-	-	-	-	-		
11- Quiberon	-	-	-	-	-	-	-	-		
Mean	27.4	7.4	25.3	67.3	64.9	18.8	40.8	40.4		
Standard deviation	24.3	6.0	19.0	22.2	17.6	11.0	13.2	18.1		
Total	247	6.9	25.7	67.4	584	19.2	40.2	40.6		

F) Autumn 2014

Table S3. Proportions of admixture per locus, sampling date and maternal lineage (i.e. identified with one species-diagnostic mitochondrial marker) for the 131 individuals that showed an admixed multilocus genotype with the three nuclear loci scored (i.e. CesA, Hox5 and vAChTP).

0	Maternal Lineage	N .T			
Generation	(mtDNA)	N _{ind}	%CesA	%Hox5	%vAChTP
Spring 2012	sp A	19	5.2	89.5	5.2
	sp B	2	100.0	0.0	0.0
Autumn 2012	sp A	44	2.3	97.7	0.0
	sp B	9	88.8	11.1	11.1
Spring 2013	sp A	10	0.0	100.0	0.0
	sp B	1	100.0	0.0	0.0
Autumn 2013	sp A	35	17.1	82.9	5.7
	sp B	11	100.0	27.3	9.1

Figure S1. Monthly mean of seawater temperature (°C) recorded for this study using data loggers (TidbiT[®]v2) located at 1.5 m depth in most of the studied marinas (all except nos. 1, 2, 10, 11, in Fig. 2 in the main text).



Figure S2. Salinity values and abundance of *C. intestinalis* spp. recorded in Moulin Blanc (no. 7 in Fig. 2 in the main text) between November 2012 and December 2014. Each month, salinity was recorded at two depths (0.25 m and 1.5 m) using a Hach Lange HQ40d multimeter equipped with a CDC 40115 conductivity probe. Every three months, the abundance of *C. intestinalis* spp. was estimated by SCUBA divers using a visual census method along ca. 30 m under one pontoon, according to a semi-quantitative scale (0 = absent, 1 = 0-20%, 2 = 20-40%, 3 = 40-60%, 4 = 60-80% and 5 = 80-100% of coverage).

