1	Growth, female size and sex ratio variability in American Eel (Anguilla rostrata) of
2	different origins in both controlled conditions and the wild: Implications for
3	stocking programs
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21	Running title: Growth variation by sex and origin in American Eel
22	

## 23 ABSTRACT

24 Freshwater eels (Anguilla spp.) are declining worldwide and a major challenge is 25 understanding why these panmictic species show contrasting patterns of intra-specific 26 phenotypic variation and recruitment. Here we present results on American Eel (A. 27 rostrata) to understand and discriminate the effects of origin and plasticity on growth and 28 sex determination. We considered two separate growth and one length-at-age dataset. The 29 first growth dataset originated from a long-term rearing experiment starting from the 30 glass eel life stage for 34 months to test the effects of origin, salinity and density on 31 growth and sex determination. The second growth dataset originated from a shorter 32 rearing experiment of 18 months starting at the yellow eel stage (around 3 years old) and 33 compared transplanted individuals in Lake Ontario (LO) with natural migrants to the LO 34 area. The third dataset compared individuals from electrofishing sampling of transplanted 35 individuals in LO with naturally migrating individuals. Sex ratios were identical for all 36 origins and treatments in the long-term growth experiment (34-35% females). While male 37 size distribution had little variance, certain female groups had large variance in growth 38 and presented fast and slow growing clusters. On the other hand, both cases of natural 39 migrants to the LO area were consistent with only slow growth females. We found that 40 wild individuals rearing in the LO area were nearly exclusively transplanted individuals 41 and that males, as well as fast growing females, were present. Despite the fact that the 42 entire species is panmictic, these results support a role for spatially varying selection in 43 explaining the phenotypic variation observed among regions and among individuals of 44 the same region, which must be considered for any successful management strategies of 45 American Eel.

46 <A>Introduction

47	The economically important American Eel (Anguilla rostrata) poses a substantial
48	puzzle for managers. Although it has been firmly established that the entire species is
49	comprised of a single panmictic population (Côté et al. 2013), there is also extreme
50	phenotypic variation among natural rearing environments in growth rate, sex ratio and
51	size at maturity (Jessop 2010). In particular, eels from the upper St. Lawrence River
52	(USL) and Lake Ontario (LO; together abbreviated by USL_LO) are phenotypically
53	distinct in that they are exclusively female and achieve larger ultimate size due to delayed
54	sexual maturation compared to more coastal rearing areas (Dutil et al. 1985; Tremblay
55	2009). Moreover, recruitment in the USL_LO has declined by 98% over the last 30 years
56	threatening this unique life history variant found only in this portion of the species range.
57	These declines are puzzling given the variable abundance trends that have been observed
58	in Atlantic Canada (COSEWIC 2006; DFO 2010; COSEWIC 2012). Possible causes of
59	the decline include fishing, pollution, habitat loss and alteration, barriers to migration,
60	and hydroelectric turbine mortality (Castonguay et al. 1994). However, despite panmixia,
61	the population dynamics of this unique life history appears to be independent from the
62	rest of the species, complicating the conventional wisdom of management by genetically
63	defined conservation units (Waples et al. 2008). The Committee on the Status of
64	Endangered Wildlife in Canada (COSEWIC) has recommended that American Eel status
65	listing be changed from "Special Concern" (COSEWIC 2006) to "Threatened"
66	(COSEWIC 2012). Ontario has declared it "Endangered" under Ontario's Endangered
67	Species Act (MacGregor et al. 2010), and its status is under review for possible listing
68	under the U.S. Endangered Species Act. 3

69 In order to mitigate the drastic decline in the USL\_LO, glass eels were 70 translocated from Nova Scotia and New Brunswick. Though these individuals did survive 71 and grow, they did not adopt the characteristic life history of that area (slow growing, 72 large maturing females), as they exhibit a strikingly different growth rate compared with 73 eels that previously characterized the region and a significant proportion of translocated 74 eels were early sexually maturing males (Verreault et al. 2009; Verreault et al. 2010; Pratt 75 and Threader 2011). This suggested that environmentally driven plasticity alone is 76 unlikely to explain regional phenotypic variations and that genetically based differences 77 could also be involved. To test this hypothesis, we recently performed a nine-month experiment that revealed differences in growth and reaction norms between glass eels 78 79 from the St. Lawrence Estuary (Québec) and Nova Scotia under controlled conditions 80 (Côté et al. 2009).

81 The main goal of this study was to compare growth in controlled conditions and 82 size variation of wild individuals from different rearing origins to help to determine if 83 these important life history traits differ between geographic locations. To this end, we 84 analyzed three separate datasets. First, a long-term growth experiment was performed 85 representing an additional 25 months of growth (34 months total) as well as sex 86 determination from a previously published experiment that was initiated with individuals 87 at the glass eel stage (Côté et al. 2009). An additional treatment of high density rearing 88 conditions from the above experiment for one of the sampling locations was conducted to 89 test the influence of density on sex ratio. Second, a separate, shorter (18 months) 90 experiment was conducted with yellow eels, which were reared in controlled conditions 91 with samples collected from naturally migrating wild individuals at the fish ladder of the 4

92 Beauharnois Dam (BH, Québec), and electrofished LO individuals that were likely the 93 result of glass eel transplants from the Maritimes (Figure 1). Finally, in the third dataset 94 we extensively sampled wild individuals in the USL\_LO to determine the extent to which 95 transplanted eels compared to naturally migrating eels for the presence of males and 96 growth rate. Based on the general expectations that eel life history is driven by their 97 environmental rearing conditions, we would expect that eels captured from different 98 locations and reared in identical conditions would have similar growth trajectories and 99 sex ratios at the end of our experiment. However, if there is a genetically based difference to observed life history variation, we would expect to see these life history differences 100 101 when reared in a common garden experiment.

102

## 103 <A>Materials and methods

104 Long-term growth experiment.--Non-pigmented glass eels were obtained in 2007 from 105 two sampling locations at river outlets, one in the St. Lawrence Estuary and one in Nova 106 Scotia, just prior to entering freshwater, therefore potentially avoiding time spent in 107 freshwater before experiments. Grande-Rivière-Blanche (GRB) drains into the lower St. 108 Lawrence Estuary, Québec. Mira River (MR) is located in Cape Breton, Nova Scotia and 109 drains into the Atlantic Ocean (Figure 1). The GRB glass eel represents the most upriver 110 location where glass eels are known to occur in the St. Lawrence watershed. Eels bound 111 for the LO USL undertake a protracted upstream migration in the St. Lawrence River; as 112 they transition from pigmented glass eels to yellow eels it takes them at least two to three 113 years to reach the upper St. Lawrence River (Castonguay et al. 1994; Zhu et al. 2013). 5

114	Our intention was to collect glass eels in the St. Lawrence Esturary as close as possible
115	to the St. Lawrence River, and the mouth of GRB is the furthest west in the St Lawrence
116	Estuary where glass eels are known to occur. Earlier experiments compared eels from
117	these two origins after nine months of rearing in contrasting salinity treatments (Côté et
118	al. 2009). In the present experiment, we report the continued long-term growth of these
119	individuals. All controlled rearing was conducted at the Laboratoire de Recherche en
120	Sciences Aquatiques (LARSA) at Université Laval. There were two salinity condition
121	treatments: freshwater (salinity 3 $\pm$ 1 ppt; hereafter FW) and brackish water (salinity 22 $\pm$
122	1 ppt, hereafter BW) and 2 tanks per treatment at an initial density of 100 individuals or
123	45g m <sup>-2</sup> . Standard 20 gallon aquaria were used with interior dimensions of (60.0 cm X
124	30.5 cm 29.2 cm) and height of water was 17.1 cm. With the MR glass eels, we
125	established an additional high density treatment of 3x the density (135 g $m^{-2}$ ) for both FW
126	and BW. After nine months, eels from each of the four low density groups (sample size in
127	Table 1) were distributed by size (to reduce cannibalism and antagonistic behavior) in
128	two half-filled (to avoid escape) 1 $\text{m}^3$ tanks. The high density groups were transferred
129	into one 1 m <sup>3</sup> tank per treatment and all groups were reared for another 25 months for a
130	total of 34 months. Temperature and salinity were 21°C $\pm$ 1 and 2.5 $\pm$ 0.5 ppt,
131	respectively. Physical-chemical parameters, including nitrites (NO $_2 < 0.1 \text{ mg L}^{-1}$ ),
132	nitrates (NO <sub>3</sub> < 200 mg L <sup>-1</sup> ), ammonia (NH <sub>4</sub> < 0.004 mg L <sup>-1</sup> ), and pH (7-7.5 adjusted
133	with $Na_2CO_3$ ) were monitored daily, and oxygen level monitoring was automated (YSI
134	Oxyguard probe Type 3, 90-100% saturation: 8.2 mg $L^{-1}$ at 22°C to 9.1 mg $L^{-1}$ at 20°C).
135	For optimal growth, eels were fed twice a day with a mixture of fish roe, pellets, and
136	capelin to complete their dietary needs (De Silva et al. 2008). Eels were fed ad libitum

137 and feeding was monitored so that if some food did not remain (before daily cleaning), 138 the ration was increased. This resulted in eels consuming 2-5% of body weight per day. 139 In all tanks and treatments, mortality always involved the small subordinate individuals. 140 Eels were provided a heterogeneous environment (pipes in which to hide) that reduced 141 agonistic behaviors (Knights 1987). Total length (TL) and weight (W) were measured on 142 all individuals every four months. In April 2010, all eels were euthanized with an 143 overdose of eugenol. The majority had reached a TL of 30 cm or more, and thus sex 144 could be determined based on visual inspection of the gonads (Beullens et al. 1997) and 145 confirmed using the histological acetocarmine (1% staining solution, S70078, Fisher 146 Scientific) squash method (Guerrero and Shelton 1974). 147 Short-term Growth Experiment.--In our second growth experiment, putative stocked

148 yellow eels (see Results) were obtained by electrofishing in LO (Bay of Quinte; 44°8'N 149  $77^{\circ}8'W$ ). Natural upriver migrants were captured in the act of ascending the BH fish 150 ladder (Figure 1). Both groups were transported to the LARSA and reared only in FW conditions in 1 m<sup>3</sup> tanks as above. The food for this experiment was blood worms and 151 152 brine shrimp ad libitum. Eels were individually PIT tagged and length and mass for each 153 individual were measured every three months. As routinely done in any controlled studies 154 of this type on eels, individuals were redistributed by size to prevent cannibalism and 155 minimize strong dominance hierarchies that can prevent subordinate individuals from 156 eating. At the end of 18 months a final measurement was taken and individuals were 157 sacrificed to determine sex by visual inspection of gonads.

158 Length-at -age in the wild.--In our third dataset, individuals transplanted as glass eels into 159 LO were electrofished from shoreline areas in the upper St. Lawrence River (44°25'N 160 75°52'W) and the Bay of Quinte (44°8'N 77°8'W), Ontario. Eels were sampled in May 161 (2009-2013) and September (2009-2011). Sampling was conducted with boat-162 electrofishing along 100 m shoreline transects at approximately 1 m depth at night (Pratt 163 and Threader 2011). The eels were captured using dip nets, and were euthanized with 164 MS-222 for age and sex determination. When the glass eel transplants occurred, all 165 transplanted individuals received an otolith mark with oxytetracycline hydrochloride 166 (OTC) (Pratt and Threader 2011). Otoliths in this study were evaluated for this mark 167 (except 2013 sample year) and also used to determine age in all sampling years. In a 168 targeted subset of individuals focused below 40 cm (as males rarely attain greater length 169 than 40 cm) gonads were analyzed for sexual differentiation. Gonads were fixed in 170 Bouin's fixative, then dehydrated with 100% EtOH. Tissues were then embedded in wax, 171 cut to 5 µm thickness, stained, and viewed under a microscope. Naturally migrating eels 172 were collected from the eel ladder at the Moses Saunders Generating Station in Cornwall, 173 Ontario, and included specimens ascending from Lac St. François into the upper St. 174 Lawrence River (Figure 1). This provided a comparison group for the LO electrofishing 175 as few naturally recruiting eels remain in USL\_LO.

176 Statistical analysis of growth clustering.--For the two controlled growth experiments, we

177 examined the total length size distribution for the final measurement of each sex

178 separately by creating kernel density plots from the "lattice" R package. Kernel density

179 plots are specifically designed to non-parametrically depict the population distribution

180 from a sample. For each distribution, we used the "mclust" R package which uses AIC to 8 determine the most likely number of clusters represented in the data, i.e. whether the growth best represents one or more clusters. Here, in instances where two clusters were found (see Results), we designated individuals as fast or slow growing based on the break in the distribution by visual inspection of the density plot.

- 185 Statistical analysis of growth and sex.--For the growth experiments, generalized linear
- 186 models were performed with the  $\log_e$  transformed final length as the dependent variable.
- 187 In the case of the long-term growth experiment, the independent variables were
- 188 treatment, sex, origin, and interactions. In the case of the short-term growth experiment,
- 189 only origin was the independent variable as the BH origin contained only females. A
- 190 logistic regression was used to determine if origin or treatment (independent variables)

191 affected sex (dependent variable). Also, to determine if rearing density had an effect on

192 sex, chi-square tests were performed on the high density treatment of MR separately for

- 193 brackish and freshwater initial salinities.
- 194

195 <A>Results

Size-at-age differences between eels from MR and GRB observed during the first
nine months were still observed after the transfer to large tanks and until the end of the
first (34-month) growth experiment (Figure 2). Eels from MR had a greater size at age
(both TL and W) throughout the rearing experiment compared to GRB eels (Table 1).
However, only MR eels retained the positive initial salinity effect on growth and
development. The generalized linear model indicated a significant effect of sex (t=-5.56,

202 P < 0.001) and origin (t=5.50, P < 0.001) and their interaction (t= -3.92, P < 0.001). In 203 the previous step of model simplification, treatment was not significant (t=-0.53 P = 204 0.597) but the origin\*treatment interaction was suggested although it was not significant 205 (t=1.92 P = 0.0698). For the second (short-term) growth experiment (Table 2), only 206 females were present in BH, so only females were compared in this GLM, and origin had 207 a significant effect on length (t=2.25, P = 0.025).

208 At the end of the 34-month growth experiment, the general pattern was that 209 female length exhibited two clusters and males exhibited one cluster (Figs. 3-5). The 210 "mclust" procedure indicated two clusters in five out of six times for females with a large 211 spread between the modes (Table 3). Two clusters were detected in both treatments of 212 males of GRB only, but unlike in the females, the clusters were so close together that the 213 density plot did not exhibit a clear bimodal pattern. The logistic regression revealed no 214 significant effect of origin or salinity treatment (or their interaction) on sex 215 differentiation, since the proportions of females were similar among all origins and 216 treatments (34% female overall; Table 1). The high density treatment had nearly exactly 217 the same sex ratio in both salinities and was not significantly different (BW 35% female, 218 P = 1 FW 35% female, P = 0.343). In all groups of the long-term experiment, males were 219 on average smaller than females at the end of the experiment (Table 1). The mean size 220 and weight was 41.0 cm and 136 g for males compared to 55.0 cm and 442 g for females. 221 Similarly, in the short-term growth experiment, the female length from LO

222 represented two significant clusters, but the females from BH and the males from LO did

not (Table 3, Figure 6 and Figure 7). Sex was skewed toward female in the short-term
growth experiment (BH: 100% female; LO: 76% female).

225 Between 2009 and 2013, 510 individuals were captured via electrofishing and 226 otoliths were extracted and assessed for age and 433 of these (all except 2013) were 227 assessed for the OTC mark. All individuals assessed with the exception of one had the 228 OTC mark. That one non-transplanted individual was an 11 year old female that was 82.0 229 cm long. The rest of the individuals from LO USL ages ranged between 2-7 years old, 230 with age class 7 represented by only a single individual (Table 4). With the 96 individuals 231 sampled at Moses Saunders, ages ranged from 3-9, with a single individual (length 52.3 232 cm) that was age 9. Of the 150 LO USL individuals analyzed for sexual differentiation, 233 65 were female, 14 were male, and the remaining 71 were undifferentiated. Overall, there 234 was a pattern of faster growth and higher variance at LO USL, whereas the natural 235 upriver migrants at MS were slower growing with less variance (Table 4).

236

237 <A>Discussion

In this paper, we combined three different and independent experiments: a longterm (34-month) growth experiment of glass eels from two different origins, a short-term (18-month) growth experiment starting with small yellow eels electro-fished in LO compared with individuals naturally migrating upriver, and finally length-at-age data of translocated individuals at LO and naturally migrating individuals at the MS dam. These data support three conclusions about American eel life history. First, sex was not affected by salinity, origin or density when reared in controlled conditions from the glass eel 11

245	stage. Thus, even the most upriver location of glass eel freshwater dispersal does not
246	exhibit a greater proportion of females. Second, there is high variance in female growth
247	rate that is not present in males, whereby females tend to group into slow- and fast-
248	growing according to kernel density plots and AIC criterion, which are influenced by
249	origin and possibly the salinity environment. Third, results suggest that only individuals
250	of the slow-growing female cluster undertake the long migration to the USL_LO. Below
251	we discuss each of these in turn, and then the management implications of these
252	conclusions.
253	<b>Sex determination not affected by salinity, origin, or density</b>
254	We did not observe any significant difference in sex ratio between origins,
255	treatments or rearing densities of glass eels. Given that sex ratios differ between feeding
256	locations in natural conditions, it has been suggested that sex determination is primarily
257	environmentally determined in American Eel through as yet unknown mechanisms
258	(Holmgren and Mosegaard 1996; Davey and Jellyman 2005). Here, regardless whether
259	the eels were reared in brackish or freshwater for the first nine months, the sex ratios
260	were nearly identical, thus our study adds to the empirical evidence that salinity does not
261	influence sex (Tesch 1977; Davey and Jellyman 2005).
262	The present study found different results from previous studies on the relationship
263	between origin and sex ratio. Vladykov and Liew (1982) reared glass eels from two
264	origins, similar to the present study (GRB and Didgeguash River (DR), in the Maritimes).
265	In a single freshwater pond, they performed each experiment consecutively. Unlike our
266	study, they found extremely different sex ratios between the origins; only 18% female 12

267 from the DR origin and 65% females from GRB. This result was logical as the GRB 268 sampling location is the furthest upriver location of glass eels known, and would 269 seemingly be the most likely to exhibit a female biased sex ratio, but our study did not 270 repeat this result. Vladykov and Liew (1982) collected their samples 4 years apart, thus 271 temporal fluctuations (genetic or plastic) in sex were confounded with origin. This could 272 have affected their results in several ways. First, the different cohorts of glass eels 273 collected could have differed in sex ratio. Second, the environmental conditions for 274 rearing could have differed between the growth periods. Third, since all individuals were 275 in a single pond and not graded as they grew, cannibalism could have affected the sex 276 ratios.

277 Density is thought to be the most important parameter in sex determination due to 278 suppression of growth rate (Davey and Jellyman 2005). Several studies reporting 279 correlations of density and sex in different natural environments provided support for this 280 prediction (Parsons et al. 1977; Krueger and Oliveira 1999; Beentjes and Jellyman 2003; 281 Huertas and Cerda 2006; Melia et al. 2006). These studies provide observation in the 282 natural environment that brackish areas tend to have higher density and a greater 283 proportion of males. However, this observation could also be explained by non-random 284 migration and/or locally varying selection (Edeline 2007; Edeline et al. 2007). Roncarati 285 et al. (1997) performed the only other controlled experiment having three densities at the 286 glass eel stage of European Eel (A. anguilla) from a single origin and they found that the 287 proportion of males increased with density. That study demonstrated a plastic response 288 with density, but since they used only a single origin, they could not assess reaction norm 289 variability by origin. In our side experiment, we found no effect of density on sex ratio of 13

MR eels. This could be because our density treatments were not in the range to influence
sex or it may suggest differences in sex determination plasticity in the American Eel
compared with the European Eel.

293 <B>Two clusters in female growth

294 The overall pattern for the controlled rearing experiments is that females, not 295 captured in the act of an upriver migration, exhibited high variability and two size 296 clusters and males did not. This was the case in females of 5/6 origin treatments in the 297 long-term growth experiment and also in the short-term growth experiment from those 298 individuals electrofished from LO USL. In the full wild capture length-at-age data, 299 USL\_LO had higher variability than MS. The long-term growth experiment also 300 suggested an origin by treatment interaction effect for the MR females as the size 301 distribution in the brackish water treatment was heavily skewed toward the fast growing 302 cluster with the opposite skew in the freshwater treatment. An origin by treatment effect 303 on growth was also suggested by results obtained during the 9-month glass eel/elver 304 growth experiment of Côté et al. (2009). Such origin\*environment interactions 305 determining growth is corroborated by studies in tilapia and other fishes, which reported 306 that by promoting the production of growth hormones, osmoregulation also results in 307 faster growth in individuals that are better adapted to saline environment compared to 308 those better adapted to freshwater (Degani et al. 2003; Sakamoto and McCormick 2006). 309 These differences are most parsimonious with quantitative genetic differences in 310 geographically different groups of glass eels. An alternative hypothesis is that there as of 311 yet unknown environmental effects on female growth variation (but not sex

312 determination) caused by the environment in the St. Lawrence Estuary that are not 313 experienced by the MR individuals. Although this remains to be rigorously investigated, 314 most of these observations suggest that geographic variations in growth result from 315 gene\*environment interactions and could reflect adaptive plasticity for maximizing 316 fitness in the face of variable environmental constraints, not the least of which could be 317 the length of the reproductive migration to the Sargasso Sea. It is also noteworthy that 318 gene\*environment interactions between a subset of eels from the same MR and GRB 319 samples used here in the long-term experiment has also been document at the level of 320 gene expression, including for genes involved in growth metabolism (Côté et al. 2014). 321 The observed patterns in growth over 34 months of common rearing support the 322 hypothesis of a partial genetic basis for the differences in growth and growth reaction 323 norms in eels from these two origins. Another recent experiment that used eels from the 324 same regions starting from the glass eel stage also found differences in growth by origin 325 (Boivin et al. In Review). This is also supported by other indirect evidence. Namely, 326 recent studies on glass eels have revealed contrasting growth rates between translocated 327 eels from Nova Scotia and eels that naturally use Lake Ontario and the upper St. 328 Lawrence River (Verreault et al. 2010; Pratt and Threader 2011). These authors observed 329 a much higher growth rate for translocated eels, which also began to sexually mature at a 330 much younger age than previously observed in this region. This indicates that 331 environmentally driven plasticity alone cannot explain regional phenotypic variations and 332 that genetically based differences could also be involved.

If so, what could be the possible explanations for genetically based differences in
 growth between sites? Given definite evidence for panmixia (Côté et al. 2013), plausible

335 non-mutually exclusive hypotheses could be that genetically based phenotypic 336 differences may reflect either non-random dispersal and/or differential mortality 337 associated with individual genetic variation within a single panmictic population (Rousset 338 2000). For instance, Edeline et al. (2007) proposed that genetic differences among 339 individuals could explain alternative dispersal tactics (Tsukamoto and Arai 2001; Daverat 340 et al. 2006; Daverat and Tomas 2006; Thibault et al. 2007), whereby fast-growing eels 341 would tend to remain in lower reaches and brackish/saltwater while those adopting a 342 slow-growing strategy would be more likely to migrate further inland and may have 343 better survival. Higher mobility has recently been documented for GRB glass eels relative 344 to those from Nova Scotia (Boivin et al. In Review). Moreover, a pronounced clinal 345 genetic variation in allozymes has been interpreted as evidence for a single-generation 346 footprint of spatially varying selection (Williams et al. 1973; Koehn and Williams 1978). 347 This was further supported by a recent study that revealed spatial variations in allele 348 frequencies (based on the analysis of coding SNP markers) at many genes of known 349 functions that covaried with sea surface temperature at sites of capture (Gagnaire et al. 350 2012). Also selection operating within a single generation has recently been demonstrated in European eel also (Pujolar et al. 2014). These studies demonstrate that 351 352 spatially varying selection generates genetic differences between eels from different 353 locations. Along with the recent study of Côté et al. (2014) that revealed regional 354 differences in patterns of gene expression and the results of this study, this strongly 355 suggests that regional variations in growth could result from differential survival 356 associated with variations in individual genetic characteristics related to contrasting 357 coastal conditions when glass eels enter continental waters (Wang and Tzeng 1998). Both

processes could result in regional genetic variations (and perhaps associated phenotypic
variations) among individuals from a same cohort within an otherwise panmictic
population.

361 <B> Fast growing, transplanted individuals dominate USL\_LO but upriver migrants are
 362 slow growing females

363 It is clear that the transplanted individuals have survived and thrived at LO\_USL, 364 but they are not exhibiting the phenotypes and behaviors that characterize the region. 365 Instead, the growth patterns of these transplanted individuals are similar to the controlled 366 experiments, with females exhibiting larger size variance than males, with many 367 individuals exhibiting fast growth. All individuals that were captured at the BH dam were 368 females. In the lab, they grew the slowest of any other group in either growth experiment. 369 The size-at-age data from individuals caught at MS exhibited low length variability 370 within year class, and consistent with being slow growing females, though they were not 371 all sexed. We expect that these individuals would reach the larger size at maturity (but an 372 old age at maturity), which is the characteristic phenotype of the region. It has been 373 hypothesized that reaching a larger size at maturity may allow females to attain ample 374 fatty acid reserves for undertaking and successfully completing the long migration 375 towards the Sargasso Sea and fully developing gametes (Larsson et al. 1990; De Silva et 376 al. 2002; Pierron et al. 2007; Van den Thillart et al. 2007). Such a female phenotype 377 would best correspond to eels generally encountered in the upper reaches of the St. 378 Lawrence River, including Lake Ontario (Tremblay 2009), which have among the longest 379 migration back to the Sargasso across the species range.

380 <B>Relevance for management and conservation; future research avenues

381 Along with previous studies on eel population genetics, the relevance of these 382 findings for the management and conservation of American Eel is two-fold. On the one 383 hand, definite evidence for panmixia (Côté et al. 2013) justifies the need for global 384 coordinated actions towards improved management and conservation of eel. On the other 385 hand, evidence for local and partially genetically based phenotypic differences also 386 justifies the need for local management. In particular, these results suggest that unique 387 phenotypic attributes of eels using the upper parts of the St. Lawrence River basin for 388 rearing habitat may be genetically distinct (from a functional standpoint) from those 389 using the Maritimes region, and as such could be irreplaceable. Management efforts should 390 focus on promoting the natural migration of female eels to the upper St Lawrence, allow them 391 to reach full maturity, and promote the natural migration to the Sargasso Sea. This also means 392 that stocking the upper St. Lawrence River and Lake Ontario with glass eels from the 393 Maritimes will not produce eels with same phenotypic attributes as those naturally 394 migrating to these waters, as already confirmed by the observation that stocked glass 395 eels migrate as young and small silver eels with a high proportion of males, a 396 phenomenon never reported before (Verreault et al. 2010).

While this study improves our knowledge of eel biology, the efficiency of its management is still compromised by an insufficient understanding of the factors affecting its distribution and abundance in the various habitats it occupies. To this end, three future research avenues should be pursued: i) characterize the availability of marine and estuarine habitats to see how important they are relative to those in freshwater, which have been better documented, ii) test the existence of glass eel/elver ecotypes in fresh and 18 403 brackish/marine waters within the theoretical framework of conditional strategies, where 404 coastal (brackish or salt water) and inland (freshwater) may be differentially colonized by 405 such ecotypes, and iii) document the genomic, physiological, and behavioral bases 406 controlling the expression of these ecotypes and their propensity to occupy different 407 habitats. This would represent a major step towards improved management of the species, 408 its sustained exploitation, and conservation. From a more fundamental point of view, this 409 would also contribute to a better understanding of the mechanisms underlying the 410 proximal and ultimate control of continental dispersion of eel and their consequences on 411 eel adaptation to heterogeneous habitats.

412

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583 <A>Figure Captions

584 Figure 1: Map of sampling sites. The sampling sites are Mira River (MR), and Grande-

585 Rivière-Blanche (GRB), Lake Ontario (LO), and Beauharnois Dam (BH), Upper St.

586 Lawrence (USL) and the Moses Saunders Generating Station (MS).

587 Figure 2: Growth in total length observed for eels from Mira River (MR) and Grande-

588 Rivière-Blanche (GRB) initially reared in fresh or brackish water aquaria for 9 months

589 prior to being transferred to freshwater tanks for another 25 months. Mean total length

590 of eels transferred from small aquaria to large tanks were measured from month 11 to

591 month 34, that is from March 2008 to the end of the experiment in April 2010. Symbols

592 correspond to the means of all individuals measured for each group. Symbols:

593 diamonds=Mira River in freshwater; squares=Mira River in brackish water;

594 circles=Grande-Rivière-Blanche in freshwater, and triangles=Grande-Rivière-Blanche in

595 brackish water.

**Figure 3:** Density plots of final length for the females of the long-term (34-month)

597 growth experiment including both origins, Mira River (MR) and Grande Rivière Blanche

598 (GRB) with fresh and brackish water and density treatments. The open circles along the

599 x-axis represent the lengths of each individual. The distributions represent the kernel

600 density estimation from the raw data.

**Figure 4:** Density plots of final length for the males of the long-term (34-month) growth

602 experiment including both origins, Mira River (MR) and Grande Rivière Blanche (GRB)

603 with fresh and brackish water and density treatments. The open circles along the x-axis

represent the lengths of each individual. The distributions represent the kernel densityestimation from the raw data.

**Figure 5:** Distributions of total lengths for each measurement period (approx. 4 month intervals) over the 25 months for the long-term growth experiment for both origins Mira River (MR) and Grande Rivière Blanche (GRB) with fresh (FR) and brackish water (BR) and density treatments. Females are separated into life history (fast growing, dark grey and slow growing, black) based when the data represented two clusters. Males are represented in light grey. Boxes represent the inter-quartile range (IQR) and whiskers extend to 1.5\*IQR.

**Figure 6:** Density plots of final length for the short-term (18-month) growth experiment including two origins, individuals naturally migrating upstream at the Beauharnois dam (BH) and transplanted individuals captured via electrofishing in Lake Ontario (LO). The open circles along the x-axis represent the lengths of each individual. The distributions represent the kernel density estimation from the raw data.

**Figure 7:** Total length for each measurement for the short-term (18-month) growth

619 experiment Females are separated into life history (fast growing, dark grey and slow

620 growing, black) based when the data represented two clusters. Males are represented in

621 light grey. Boxes represent the inter-quartile range (IQR) and whiskers extend to

622 1.5\*IQR.

623 <A>Tables

624	<b>Table 1:</b> Final size for long-term (34-month) growth experiment. Mean total weight and
625	length (mean $\pm$ SD) reached after 34 months of rearing for eels from the Mira River
626	(MR) and Grande-Rivière-Blanche (GRB) initially reared in either fresh water (FW) or
627	brackish water (BW) for 9 months prior to transfer to freshwater for another 25 months.
628	N refers to the number of males (M) and females (F) (and percent) in each group at the
629	end of the experiment.

Origin	Treatment	Sex	N (%)	Length (cm)	Weigh (g)
MR	BW	F	25 (35)	63 ± 15	$658\pm408$
		Μ	47 (65)	$43 \pm 4$	$160\pm56$
	FW	F	32 (36)	$58 \pm 16$	$522\pm503$
		М	57 (64)	$41 \pm 5$	$127\pm47$
GRB	BW	F	40 (35)	48 ± 12	$281\pm288$
	DW	Μ	79 (64)	$42 \pm 5$	$135 \pm 45$
	FW	F	24 (34)	$52 \pm 14$	311 ± 296
		М	44 (66)	$41 \pm 5$	$126\pm43$

632	<b>Table 2:</b> Final sizes for short-term (18-month) growth experiment. Mean total weight
633	and length (mean $\pm$ SD) reached after 18 months of rearing for eels from Lake Ontario
634	(LO) and Beauharnois Dam (BH). N refers to the number of individuals in each group at
635	the end of the experiment. Since some individuals lost their PIT tag, their sex specific
636	starting length weight could not be determined (and thus N for start measurement is
637	lower than finish)

Origin	Sex	Start/Finish	Ν	Length(cm)	Weight(g)
BH	F	Start	140	28.7±3.1	30±10
		Finish	156	29.7±3.5	32±13
LO	F	Start	86	28.8±5.1	36±23
		Finish	91	32.0±7.7	51±55
LO	М	Start	36	28.5±4.8	39±23
		Finish	36	32.4±5.6	57±38

639 **Table 3:** Cluster analysis for final length distributions of controlled rearing experiments.

640 Results of the R package "mclust" indicating the number of clusters, one or two, is more

- 641 likely (bolded) to describe each distribution (by origin\*sex\*treatment) as determined by
- 642 the higher AIC value.

Origin	Treatment	Sex	Clusters	AIC
	Long-term (3	34 months):	low density	
GRB	FR	F	1	-252.5
			2	-249.7
GRB	BR	F	1	-193.1
			2	-196.5
MR	FR	F	1	-191.5
			2	-183.6
MR	BR	F	1	-319.2
			2	-315.2
GRB	FR	М	1	-252.5
			2	-249.7
GRB	BR	М	1	-279.7
			2	-285.3
MR	FR	М	1	-276.4
			2	-274.5
MR	BR	М	1	-477.8
			2	-476.8

Long-term (34 months): high density

MR	FR	F	1	-283.5

			2	-278.8
MR	BR	F	1	-212.3
			2	-210.4
MR	FR	М	1	-283
			2	-284.7
MR	BR	М	1	-227
			2	-228.7
	Shor	t-term (18 mor	nths)	
BH	BR	F	1	-1566.3
			2	-1571.2
LO	BR	F	1	-1057.7
			2	-1043.6
LO	BR	М	1	-398.1
			2	-398.4

650	<b>Table 4:</b> Mean length for each age class of American Eel in the wild experiment.
651	Samples were collected via electrofishing at the Lake Ontario and Upper St. Lawrence
652	and regions (LO_USL) and ascending the eel ladder at the Moses Saunders Generating
653	Station in Cornwall, Ontario (MS) between 2009 and 2013. Age was determined by
654	otoliths. Length and sample sized are in the following format: $(cm\pm SD(n))$ .

<b>Otolith Age</b>	Season	LO_USL	MS
0	Fall	13.3±1.9 (7)	
1	Spring	$12.4 \pm 1.4$ (17)	
I	Spring	13.4±1.4 (17)	
	Fall	$20.0 \pm 2.7$ (42)	
	Fall	20.9±3.7 (43)	
2	Spring	$20.0\pm5.1(70)$	
4	Spring	30.0±3.1 (79)	
	Fall	20 4+6 7 (76)	
	1'a11	29.4±0.7 (70)	
3	Spring	31.0+0.3(112)	$30.1 \pm 4.8(17)$
5	Spring	51.7±7.5 (112)	50.1± <del>4</del> .8 (17)
	Fall	39 7+9 9 (51)	
	I ull	59.729.9 (51)	
4	Spring	43.7±13.4 (75)	33.6+4.5 (27)
	~8		()
	Fall	52.7±9.84 (11)	
5	Spring	54.5±15.5 (33)	37.8±5.7 (21)
	Fall	63.5 (1)	

	6	Spring		40.3±6.7 (17)
		Fall	69.6±19.2 (3)	
	7	Spring		40.1±6.7 (10)
		Fall	28.7 (1)	
	8	Spring		35.6±0.86 (3)
	9	Spring		52.3 (1)
655				

Figure 1:



Figure 2:







## Figure 4:



Figure 5:



life\_history female female (fast growing) male

Figure 6:



Figure 7

