Received: 7 September 2017 | Accepted: 28 September 2018
DOI: 10.1111/jfb.13826
JOURNAL OF FISH BIOLOGY

REGULAR PAPER

Catch-related and genetic outcome of adult northern pike *Esox lucius* stocking in a large river system

Nicolas Guillerault[1,2] | Géraldine Loot[3] | Simon Blanchet[2] | Frederic Santoul[1]

[1]EcoLab, Université de Toulouse, CNRS, INPT, UPS, Toulouse, France
[2]Station d'Ecologie Expérimentale et Théorique (SETE), CNRS, UPS, UMR 5321, Moulis, France
[3]Laboratoire Évolution et Diversité Biologique (EDB), CNRS, UPS, ENFA, UMR 5174, Toulouse, France

Correspondence
Frederic Santoul, EcoLab, Université de Toulouse, CNRS, INPT, UPS, 31062 Toulouse, France.
Email: frederic.santoul@univ-tlse3.fr

Funding information
Fédération Départementale pour la Pêche et la Protection des Milieux Aquatiques du Lot, FDPPMA 46; Region Midi-Pyrénées ; The agency for water resource management of Adour-Garonne watershed (Agence de l'Eau Adour-Garonne)

Genetic introgression from stocked adult northern pike *Esox lucius* to a wild self-recruiting population was detected in a large river system and some stocked *E. lucius* survived up to two spawning seasons and dispersed over several kilometres in the river. Moreover, the catch rate of stocked *E. lucius* by anglers was low (9.6%), hence suggesting that the efficiency of stocking activity is questionable.

KEYWORDS
captive breeding, conservation, enhancement, genetic diversity, microsatellite, recreational fisheries

Stocking is a common management practice used to enhance wild populations or increase catch opportunities (Cowx, 1994; Lorenzen, 2014; Welcomme & Bartley, 1998). In contrast to the expected economic and conservation benefits from this activity (Leber *et al*., 1995; Uki, 2006), stocking fish into self-recruiting populations has the potential to induce deleterious effects on the wild component of the targeted stocks (Allendorf & Waples, 1996; Lorenzen *et al*., 2012). Among these risks, the effects of genetic introgression from stocked fish to natural populations are of critical importance (Allendorf *et al*., 2001). These effects may vary from barely appreciable to strong alterations of the genetic integrity of wild populations, eventually leading to fitness depression and population replacement (Araki *et al*., 2007; Ryman & Laikre, 1991). The degree of genetic introgression between stocked and wild fish depends on many variables, such as the survival of stocked individuals and their ability to reproduce with their wild counterparts. These variables in turn depend on many other variables such as the body size of stocked fish, their degree of domestication, their genetic relatedness to wild fish and the census size of the wild population (Lorenzen *et al*., 2012). As such, the long-term genetic risks induced by stocking are difficult to predict and documenting the genetic outcomes of stocking is critical to appreciate the relevance of stocking for sustainable fisheries management (*e.g*., maintenance of local genetic characteristics and population fitness).

Species of the genus *Esox* L. 1758 are of major importance for fisheries in the northern hemisphere (Crane *et al*., 2015; Gandolfi *et al*., 2016). In rivers, studies investigating the genetic diversity of northern pike *Esox lucius* L. 1758, aquitanian pike *Esox* aquitanicus Denys, Dettai, Persat, Hautecœur & Keith 2014 (Denys *et al*., 2014), southern pike *Esox cisalpinus* Bianco & Delmastro 2011 (Bianco & Delmastro, 2011) suggested that stocking might be a major source of contemporary change in their genetic diversity (Denys *et al*., 2014; Gandolfi *et al*., 2017; Launey *et al*., 2006; Lucentini *et al*., 2011). *Esox lucius* stocking mainly involves early life stages (larvae, fry and fingerlings) reared in hatcheries, a strategy that has been demonstrated to be poorly efficient for increasing the abundance of the targeted cohort (Jansen *et al*., 2013; Vuorinen *et al*., 1998). Despite possible replacement of a wild fish component by their stocked conspecifics of the same cohort (Hühn *et al*., 2014), Larsen *et al*. (2005) found a low rate of genetic introgression from stocked *E. lucius* fry to a wild brackish population in the Baltic Sea, suggesting little effect of fry stocking on long-term genetic introgression. *Esox lucius* stocking is also carried out with adult individuals (Pierce, 2012). Larger fish suffer density-dependent growth rather than density-dependent mortality (as generally observed for juveniles) and their natural mortality is inversely related to body size (Lorenzen, 2005). Therefore, stocked adult *E. lucius* have the potential to survive in the recipient population (Snow, 1974) and hence to participate in reproduction with their wild conspecifics (Guillerault *et al*., 2018). However, outcomes of this management practice and its genetic effects on wild populations remain poorly documented and understood.

The present study aimed at testing whether stocking of adult *E. lucius* in a self-recruiting river population affects the genetic integrity of the wild *E. lucius* population through estimation of: the propensity of stocked fish to establish and spread in the recipient waterbody using a mark-recapture approach; the propensity of stocked fish to transfer their genes to the gene pool of the wild population using microsatellite genetic markers.

The study focused on an *E. lucius* population from the Lot River in south-western France (44°26′ N, 1°26′ E). The study site was located in a 130 km reach of the river that has been receiving *c.* 1 t of *E. lucius* annually to enhance recreational angling. The *E. lucius* (30–70 cm, total lngth L_T) originated from a single fish farm (Dombes étangs SARL, Saint-Remy, France; located about 450 km away from the Lot River) for almost two decades. All fish sampling and tagging was carried out by the local angling association between 2007 and 2011. While at the time there was no requirement for official permits, the work was carried while taking guidelines for animal welfare into consideration.

For the first aim, survival of stocked *E. lucius* over time as well as the spatial spread of the stocked fish along the river stretch were estimated. To do so, 1839 *E. lucius* were stocked from 2007 to 2011 in November of each year (mean ± SD annual number = 368 fish ±33 year^{-1}, L_T range = 28–82 cm) in four successive stretches of the river (mean ± SD length = 2.9 ± 0.9, 12.8 km long in total) bounded by weirs (*c.* 2.5 m height). Stocked fish were evenly spread along the study area. This represented on average 3.5 fish ha^{-1} years^{-1} stocked fish (as usually done by local fisheries managers), whereas the average density of wild *E. lucius* of the same length class was estimated at *c.* 6 fish ha^{-1} years^{-1} (Guillerault, unpublished data). Other characteristics of stocking, such as time of stocking, body size at stocking, fish origin and rearing conditions respected the usual stocking procedure (Cowx 1994). Before release, each *E. lucius* was marked with a T-bar tag on the anterior part of the dorsal fin to allow anglers to identify them and report the date and the location of their catches. Each year, *c.* 20% of the stocked fish were double tagged to estimate tag-shedding (30% of double tagged fish have lost one tag). The probability of losing a tag was used to correct the number of captures reported by anglers at different periods of time (see below) using a pooled approach (Seber & Felton, 1981) and to calculate a corrected catch rate, which was used as a proxy of minimum fish survival rate. Since *E. lucius* can reproduce from 19 cm for male and 30 cm for female (Raat, 1988), stocked *E. lucius* were considered mature. The stocked fish were divided in two categories based on the mandatory minimum harvest length limit (L_T = 50 cm), *i.e.*, fish protected versus those exposed to fishing mortality. Catch rate was estimated by analysing data directly reported by local anglers. Data to be reported by anglers (date, location, number of *E. lucius* caught with L_T, number of tagged caught) were explained in a document provided with the fishing licence, informative panels placed along the banks of the river and a web document available on the website of the local angling association. A total of 89 anglers have reported information (most anglers reported their catches). A quasibinomial generalized linear model was used to test whether capture rate varied significantly among years and body-size classes at stocking (Table 1) and the significance of the resulting two-way interaction term was tested using the R 3.1.2 (www.r-project.org).

Moreover, results showed that 40.5% of the captures were recorded before the spawning season (*i.e.*, within the 3 months after stocking), 50% of the captures were recorded after one spawning season and 9.5% were recorded after two spawning seasons (Figure 1). As a result, at least (±SD) 27 ± 30 fish year^{-1} had the opportunity to reproduce once and *c.* 5 ± 5 fish year^{-1} could reproduce twice (Figure 1(b)). Most *E. lucius* were captured near their stocking site (median distance = 0.9 km, mean distance ± SD = 0.65 ± 2.9 km). In most cases, captures were recorded in the river stretch where fish were released (63%) or in the next river stretch (33%; Figure 1(c)). However, captures at long distances from the stocking site, *i.e.* up to 14.1 km downstream and 13.4 km upstream (Figure 1(c)) were still recorded, meaning that some *E. lucius* were able to cross respectively four and three weirs. The proportion of *E. lucius* caught upstream and downstream of the stocking point was identical (46% up or downstream and 8% at the stocking site).

For the second aim of this study, the level of genetic introgression from stocked to wild *E. lucius* was assessed. In November 2013, pelvic fin clips from a sample of the stocked fish source population were collected (*n* = 100, size range: 38.5–75 cm L_T) to genetically characterize the stocked population. From 2013 to 2016, pelvic fin clips of each *E. lucius* captured and reported by anglers were collected (*n* = 51, size range: 31–109 cm L_T) to determine the level of genetic introgression. Genetic analyses were carried out on 151 fish samples. Genomic DNA was extracted using a salt-extraction protocol (Aljanabi & Martinez, 1997). PCR amplifications, genotyping and allele scoring were carried out following the protocol described in Paz-Vinaz *et al.* (2013). Seventeen microsatellite loci: Elu-252 (Miller & Kapuscinski, 1997) El-02, El-03, El-05, El-09, El-17, El-20, El-21, El-22, El-23, El-27, El-28

TABLE 1 Results of the generalized linear model aimed at testing the effect of the year (year) and of size (size) at stocking on the reported capture rate (Cr) of *Esox lucius* in the lot river

Parameter	Variable	Deviance	Residual deviance	df	*P*
C_r	Year	68.190	1,009.41	41,834	< 0.01
	Size	74.802	934.41	11,833	< 0.01
	Size × year	20.890	913.72	41,829	< 0.01

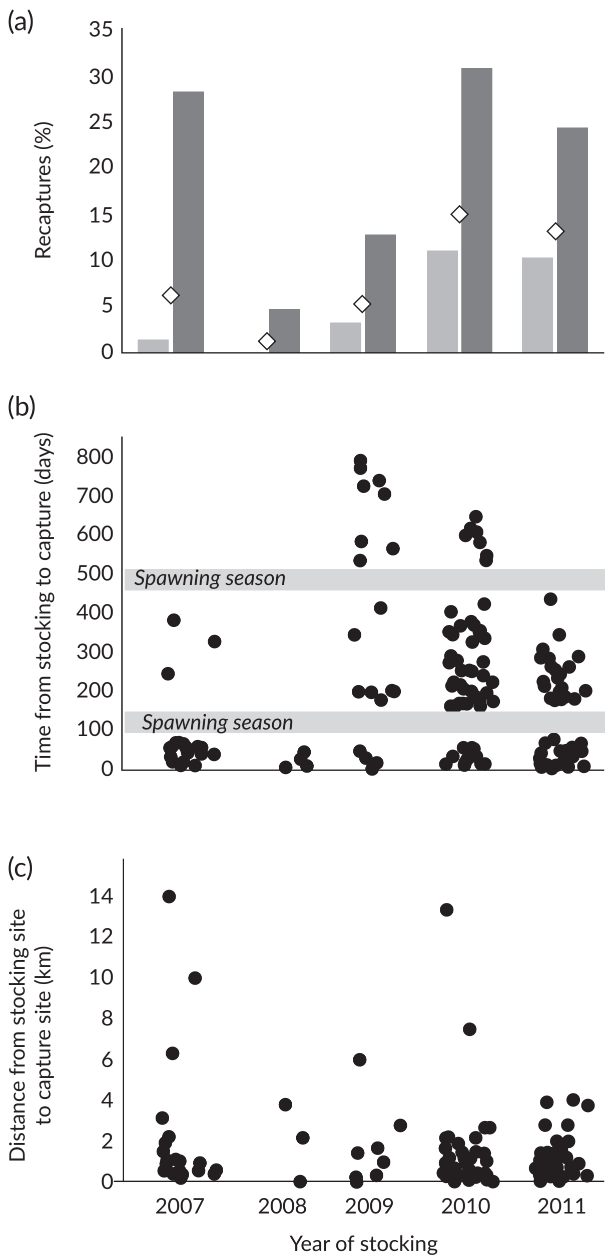

FIGURE 1 Main outcomes of the mark–capture experiment on stocked adult *Esox lucius* in the lot River. (a) Reported annual per cent recaptures of *E. lucius* stocked in the Lot River from 2007 to 2011. ◇, Total annual capture rate; ■, capture rate of fish with L_T < 50 cm at stocking; ■, capture rate of fish with L_T ≥ 50 cm at stocking. (b) Jitter plot of time between stocking and capture of *E. lucius* (1 point = 1 individual). (c) Jitter plot of distance from *E. lucius* stocking site to capture site

(Ouellet-Cauchon *et al.* 2014), Eluc-033, Eluc-040 (Wang *et al.* 2011), EluBe-INRA, EluB-38INRA, EluC-113INRA (Launey *et al.* 2003), were amplified using three multiplexed PCRs. The presence of null alleles was tested from the 100 *E. lucius* stocked using MICRO-CHECKER 2.2.3 (van Oosterhout *et al.*, 2004) after checking for Hardy-Weinberg equilibrium using Fstat 2.9.3.2 (Goudet, 1995). The loci with evidence of null-alleles were dropped from the analyses (El-22, El-23 and El-28), which led to a final set of 14 loci (Supporting Information Table S1).

The identity of fish was examined (allowing 1 mismatch) using CERVUS (Kalinowski *et al.*, 2007) to avoid double counting of fish (from catch and release, or from the capture of fish stocked in 2013). A Bayesian clustering approach was used to infer the likelihood of *K* = 1–4 populations (independent genetic groups) using Structure 2.3 (Falush *et al.*, 2003; Pritchard *et al.*, 2000). Markov chain Monte Carlo (MCMC) iterations were set to 500,000 (burn-in period was set to 100,000) with 15 replicates per *K*. The optimal value of *K* was 2 (ΔK = 333.3; Evanno *et al.*, 2005; Supporting Information Figure S1). One of the two clusters included all 100 fish used to characterize genetically the stocked population and was therefore called $C_{stocked}$. The minimum assignment rate of these 100 fish to $C_{stocked}$ (*i.e.*, 0.91) was hereafter use as a minimum threshold values to assign *E. lucius* to one genetic cluster. The other cluster was hypothesized to characterize wild fish and was called C_{wild}. The optimal alignment of the replicates was determined using CLUMPP (Jakobsson & Rosenberg, 2007), which provides us with estimates of admixture proportions for each individual between the two clusters.

The 51 captures reported by anglers corresponded to 50 *E. lucius* (*i.e.*, one recapture according to the identity analysis). Among those 50 *E. lucius*, 21 *E. lucius* belonged to the cluster $C_{stocked}$ (mean ± SD affiliation to $C_{stocked}$ = 0.98 ± 0.01, range = 0.94–0.99; Figure 2(a)). According to the identity analysis, 17 of those *E. lucius* originated from the stocking carried out in November 2013, whereas the other four *E. lucius* may originate from stocking having occurred at another location or at another timing. They could also be the descendants of a past breeding event between two fish stocked. Twenty-four *E. lucius* were strongly assigned to the cluster C_{wild} (mean ± SD affiliation to C_{wild} = 0.98 ± 0.02, range = 0.94–0.99; Figure 2(a)). Five fish had mixed assignment rates (mean ± SD affiliation to $C_{stocked}$ = 0.59 ± 0.09, range = 0.49–0.67), which suggests that these fish come from interbreeding between wild and stocked fish or hybrids.

In addition, CERVUS was used to calculate the observed heterozygosity (H_O) and expected heterozygosity (H_E) for each group of fish separately (*i.e.*, stocked *E. lucius* and wild *E. lucius*; Supporting Information Table S2). The allelic richness (A_R) and fixation index (I_{FS}) values for each group were estimated using Fstat 2.9.3.2 (Goudet, 1995; Supporting Information Table S2). A_R was significantly lower in stocked than in wild *E. lucius* (Wilcoxon test, $P < 0.01$), probably because of population bottlenecking during broodstock practices (*e.g.*, low A_R in the stocking founder population or small broodstock size). I_{FS} was significantly higher in wild than in stocked *E. lucius* (Wilcoxon test, $P < 0.05$), suggesting non-random mating in the wild population. H_O and H_E tended to be lower in the stocked *E. lucius* than in wild *E. Lucius*, although not significantly (Wilcoxon tests, $P > 0.05$).

Stocking of adult *E. lucius* likely resulted in reproduction between stocked and wild *E. lucius*. At least, 4.6% (mean ± SD = 4.4% ± 4.6 year) of the stocked fish survived until the subsequent spawning seasons. Stocked *E. lucius* also moved over several km despite the presence of weirs; Snow (1974) had similar findings in lakes. Recurrent stocking events in this population induced genetic introgression between wild and stocked *E. lucius* since five fish were considered as introgressed (15–17% of *E. lucius* from the Lot River were hybrids, depending if the four *E. lucius* from $C_{stocked}$ which do not come from stocking of 2013 are considered as having been stocked or hatched in

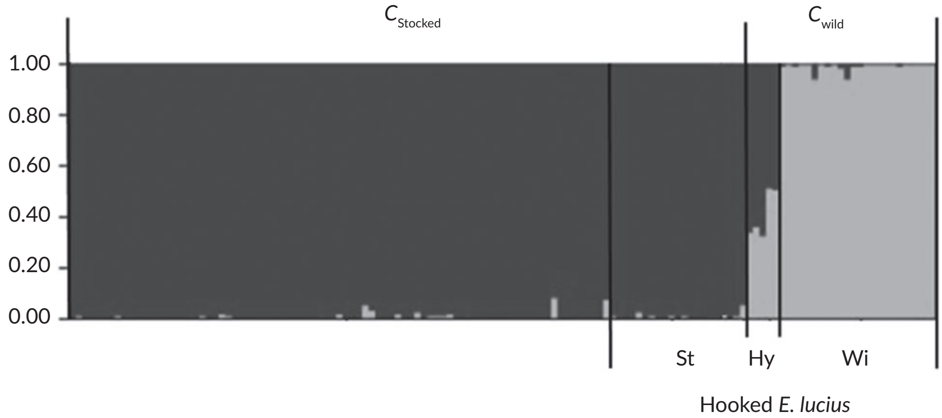

FIGURE 2 Genetic discrimination of *Esox. lucius* stocked (*n*: 100) and caught by anglers (Hooked *E Lucius*; *n*: 50) in the Lot River from November 2013 to August 2016 based on 14 microsatellites. $C_{stocked}$, The genetic cluster of *E. lucius* of hatchery origin (■); *i.e.*, 100 individuals stocked in November 2013 including 17 pikes caught by anglers (St) and four additional individuals (event of stocking unknown) caught by anglers (St). C_{wild}, The genetic cluster of *E. lucius* of wild origin (■); *i.e.*, 24 individuals of strictly wild origin (Wi) and five individuals were hybrids (Hy)

the river (see above). The reproductive success of stocked *E. lucius* in this river, may exceed that for salmonids in which reduced competitive ability in the wild, reproductive isolation or lower survival of the offspring of stocked fish are expected to lower reproductive success compared with their wild conspecifics (Araki *et al.*, 2009; Fleming & Petersson, 2001; Hansen & Mensberg, 2009). Moreover, genetic risks associated with stocking may still increase if a high stocking pressure (*i.e.*, high frequency and quantity) is maintained (Fraser, 2008; Lorenzen *et al.*, 2012) or with other stocking sources potentially more prone to introgression. Indeed, the stocked fish came from a distant fish farm so both domestication and natural genetic differentiation could reduce their performance in the Lot River. Larsen *et al.* (2005) had similar findings with the stocking of freshwater pike in a brackish population.

Despite the lack of data about fishing pressure, the 9.6% catch rate of stocked fish was unexpectedly low. Consequently, in such recreational fisheries, it could be questionable to stock large *E. lucius* intended to be harvested as commonly applied for rainbow trout *Oncorhynchus mykiss* (Walbaum 1792) (Stanković *et al.*, 2015). At best, *E. lucius* may also be stocked after the spawning period to increase their probability of being caught before the spawning season. Yet, stocking of large *E. lucius* may decrease the abundance of smaller fish through competition and cannibalism (Grimm, 1981, 1994; Haugen *et al.*, 2007). In addition, it is uncertain if pond-reared pikes adapt to running water, especially in early winter before or when discharge is rising. Interestingly, the lowest C_r was observed after the stocking in 2008, which was followed by a quick and high increase of river discharge. Further studies should focus on the effect of stocking on *E. lucius* population genetics over time using historical genetic samples. More generally, further studies should balance the costs and benefits of stocking in comparison to alternative fisheries enhancement strategies.

ACKNOWLEDGEMENTS

The authors thank volunteer anglers who participated in samples collection and K. Saint-Pé and anonymous reviewers for useful comments on the manuscript. This study was founded by the local Institute for Fisheries Management and Protection of Aquatic Ecosystems (Fédération Départementale pour la Pêche et la Protection des Milieux Aquatiques du Lot, FDPPMA 46), Region Midi-Pyrénées and the agency for water resource management of Adour-Garonne watershed (Agence de l'Eau Adour-Garonne).

ORCID

Frederic Santoul https://orcid.org/0000-0002-2932-2172

REFERENCES

Aljanabi, S. M., & Martinez, I. (1997). Universal and rapid salt-extraction of high quality genomic DNA for PCR-based techniques. *Nucleic Acids Research*, *25*, 4692–4693. https://doi.org/10.1093/nar/25.22.4692

Allendorf, F. W., Leary, R. F., Spruell, P., & Wenburg, J. K. (2001). The problems with hybrids: Setting conservation guidelines. *Trends in Ecology and Evolution*, *16*, 613–622. https://doi.org/10.1016/S0169-5347(01)02290-X

Allendorf, F. W., & Waples, R. S. (1996). Conservation and genetics of salmonid fishes. In J. C. Avise & J. L. Hamrick (Eds.), *Conservation genetics: Case histories from nature* (pp. 238–280). New York, NY: Chapman & Hall.

Araki, H., Cooper, B., & Blouin, M. S. (2007). Genetic effects of captive breeding cause a rapid, cumulative fitness decline in the wild. *Science*, *318*, 100–103. https://doi.org/10.1126/science.1145621

Araki, H., Cooper, B., & Blouin, M. S. (2009). Carry-over effect of captive breeding reduces reproductive fitness of wild-born descendants in the wild. *Biology Letters*, *5*, 621–624. https://doi.org/10.1098/rsbl.2009.0315

Bianco, P. G., & Delmastro, G. B. (2011). Recenti novità tassonomiche riguardanti i pesci d'acqua dolce autoctoni in Italia e descrizione di una nuova specie di luccio. *Researches Wildlife Conservation*, *2*, 1–14.

Cowx, I. G. (1994). Stocking strategies. *Fisheries Management and Ecology*, *1*, 15–30. https://doi.org/10.1111/j.1365-2400.1970.tb00003.x

Crane, D. P., Miller, L. M., Diana, J. S., Casselman, J. M., Farrell, J. M., Kapuscinski, K. L., & Nohner, J. K. (2015). Muskellunge and northern pike ecology and management: Important issues and research needs. *Fisheries*, *40*, 258–267.

Denys, G. P. J., Dettai, A., Persat, H., Hautecœur, M., & Keith, P. (2014). Morphological and molecular evidence of three species of pikes *Esox* spp. (Actinopterygii, Esocidae) in France, including the description of a new species. *Comptes Rendus Biologies*, *337*, 521–534. https://doi.org/10.1016/j.crvi.2014.07.002

Evanno, G., Regnaut, S., & Goudet, J. (2005). Detecting the number of clusters of individuals using the software STRUCTURE: A simulation study. *Molecular Ecology*, *14*, 2611–2620. https://doi.org/10.1111/j.1365-294X.2005.02553.x

Falush, D., Stephens, M., & Pritchard, J. K. (2003). Inference of population structure using multilocus genotype data: Linked loci and correlated allele frequencies. *Genetics*, *164*, 1567–1587. https://doi.org/10.1111/j.1471-8286.2007.01758.x

Fleming, I. A., & Petersson, E. (2001). The ability of released, hatchery salmonids to breed and contribute to the natural productivity of wild populations. *Nordic Journal of Freshwater Research*, *75*, 71–98.

Fraser, D. J. (2008). How well can captive breeding programs conserve biodiversity? A review of salmonids. *Evolutionary Applications*, *1*, 535–586. https://doi.org/10.1111/j.1752-4571.2008.00036.x

Gandolfi, A., Ferrari, C., Crestanello, B., Girardi, M., Lucentini, L., & Meraner, A. (2017). Population genetics of pike, genus *Esox* (Actinopterygii, Esocidae), in northern Italy: Evidence for mosaic distribution of native, exotic and introgressed populations. *Hydrobiologia*, *794*(1): 73–92. https://doi.org/10.1007/s10750-016-3083-1

Gandolfi, A., Fontaneto, D., Natali, M., & Lucentini, L. (2016). Mitochondrial genome of *Esox flaviae* (southern pike): Announcement and comparison with other Esocidae. *Mitochondrial DNA. Part A DNA Mapping. Sequencing and Analysis*, *27*, 3037–3038. https://doi.org/10.3109/19401736.2015.1063123

Goudet, J. (1995). FSTAT (version 1.2): A computer program to calculate F-statistics. *Journal of Heredity*, *86*, 485–486.

Grimm, M. P. (1981). Intraspecific predation as a principal factor controlling the biomass of northern pike (*Esox lucius* L.). *Aquaculture Research*, *12*, 77–79.

Grimm, M. P. (1994). The influence of aquatic vegetation and population biomass on recruitment of 0+ and 1+ northern pike (*Esox lucius* L.). In I. G. Cowx (Ed.), *Rehabilitation of freshwater fisheries* (pp. 226–234). Oxford, England: Fishing News Bools.

Guillerault, N., Hühn, D., Cucherousset, J., Arlinghaus, R., & Skov, C. (2018). Stocking for pike population enhancement. In C. Skov & P. Anders Nilsson (Eds.), *Biology and ecology of pike* (1st ed., pp. 215–247). Boca Raton: CRC Press.

Hansen, M. M., & Mensberg, K.-L. D. (2009). Admixture analysis of stocked brown trout populations using mapped microsatellite DNA markers: Indigenous trout persist in introgressed populations. *Biology Letters*, *5*, 656–659. https://doi.org/10.1098/rsbl.2009.0214

Haugen, T. O., Winfield, I. J., Vøllestad, L. A., Fletcher, J. M., James, J. B., & Stenseth, N. C. (2007). Density dependence and density independence in the demography and dispersal of pike over four decades. *Ecological Monographs*, *77*, 483–502. https://doi.org/10.1890/06-0163.1

Hühn, D., Lübke, K., Skov, C., & Arlinghaus, R. (2014). Natural recruitment, density-dependent juvenile survival and the potential for additive effects of stock enhancement: An experimental evaluation of stocking northern pike (*Esox lucius*) fry. *Canadian Journalof Fisheries and Aquatic Sciences*, *71*, 1508–1519. https://doi.org/10.1139/cjfas-2013-0636

Jakobsson, M., & Rosenberg, N. A. (2007). CLUMPP: A cluster matching and permutation program for dealing with label switching and multimodality in analysis of population structure. *Bioinformatics*, *23*, 1801–1806. https://doi.org/10.1093/bioinformatics/btm233

Jansen, T., Arlinghaus, R., Als, T. D., & Skov, C. (2013). Voluntary angler logbooks reveal long-term changes in a lentic pike, *Esox lucius*, population. *Fisheries Management and Ecology*, *20*, 125–136. https://doi.org/10.1111/j.1365-2400.2012.00866.x

Kalinowski, S. T., Taper, M. L., & Marshall, T. C. (2007). Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. *Molecular Ecology*, *16*, 1099–1106. https://doi.org/10.1111/j.1365-294X.2007.03089.x

Larsen, P. F., Hansen, M. M., Nielsen, E. E., Jensen, L. F., & Loeschcke, V. (2005). Stocking impact and temporal stability of genetic composition in a brackish northern pike population (*Esox lucius* L.), assessed using microsatellite DNA analysis of historical and contemporary samples. *Heredity*, *95*, 136–143. https://doi.org/10.1038/sj.hdy.6800671

Launey, S., Krieg, F., Morin, J., & Laroche, J. (2003). Five new microsatellite markers for northern pike (*Esox lucius*). *Molecular Ecology Notes*, *3*, 366–368. https://doi.org/10.1046/j.1471-8286.2003.00452.x

Launey, S., Morin, J., Minery, S., & Laroche, J. (2006). Microsatellite genetic variation reveals extensive introgression between wild and introduced stocks and a new evolutionary unit in French pike *Esox lucius* L. *Journal of Fish Biology*, *68*, 193–216. https://doi.org/10.1111/j.0022-1112.2006.001059.x

Leber, K. M., Brennan, N. P., & Arce, S. M. (1995). Marine enhancement with striped mullet: Are hatchery releases replenishing or displacing wild stocks? In H. L. Schramm & R. G. Piper (Eds.), *Uses and effects of cultured fishes in aquatic ecosystems* (pp. 376–387). Bethesda, MD: American Fisheries Society.

Lorenzen, K. (2005). Population dynamics and potential of fisheries stock enhancement: Practical theory for assessment and policy analysis. *Philosophical Transactions of the Royal Society B*, *360*, 171–189. https://doi.org/10.1098/rstb.2004.1570

Lorenzen, K. (2014). Understanding and managing enhancements: Why fisheries scientists should care. *Journal of Fish Biology*, *85*, 1807–1829. https://doi.org/10.1111/jfb.12573

Lorenzen, K., Beveridge, M. C. M., & Mangel, M. (2012). Cultured fish: Integrative biology and management of domestication and interactions with wild fish. *Biological Reviews*, *87*, 639–660. https://doi.org/10.1111/j.1469-185X.2011.00215.x

Lucentini, L., Puletti, M. E., Ricciolini, C., Gigliarelli, L., Fontaneto, D., Lanfaloni, L., … Panara, F. (2011). Molecular and phenotypic evidence of a new species of genus *Esox* (Esocidae, Esociformes, Actinopterygii): The southern pike, *Esox flaviae*. *PLoS One*, *6*(12), e25218. https://doi.org/10.1371/journal.pone.0025218

Miller, L. M., & Kapuscinski, A. R. (1997). Historical analysis of genetic variation reveals low effective population size in a northern pike (*Esox lucius*). *Population Genetics*, *147*, 1249–1258.

Ouellet-Cauchon, G., Normandeau, E., Mingelbier, M., & Bernatchez, L. (2014). EST-based microsatellites for northern pike (*Esox lucius*) and cross-amplification across all Esox species. *Conservation Genetics Resources*, *6*, 451–454. https://doi.org/10.1007/s12686-013-0123-2

Paz-Vinas, I., Comte, L., Chevalier, M., Dubut, V., Veyssiere, C., Grenouilliet, G., … Blanchet, S. (2013). Combining genetic and demographic data for prioritizing conservation actions: Insights from a threatened fish species. *Ecology and Evolution*, *3*, 2696–2710. https://doi.org/10.1002/ece3.645

Pierce, R. B. (2012). *Northern pike: Ecology, conservation and management history*. Minneapolis, MN: Minnesota University Press.

Pritchard, J. K., Stephens, M., & Donnelly, P. (2000). Inference of population structure using multilocus genotype data. *Genetics*, *155*, 945–959. https://doi.org/10.1111/j.1471-8286.2007.01758.x

Raat, A. (1988). *Synopsis of biological data on the northern pike Esox lucius Linnaeus 1758*. FAO Fish. Rome: Synopsis No. 30 Rev. 2.

Ryman, N., & Laikre, L. (1991). Effects of supportive breeding on genetically effective population size. *Conservation Biology*, *5*, 325–329. https://doi.org/10.1111/j.1523-1739.1991.tb00144.x

Seber, G. A. F., & Felton, R. (1981). Tag loss and the Petersen mark–recapture experiment. *Biometrika*, *68*, 211–219. https://doi.org/10.1093/biomet/68.1.211

Snow, H. E. (1974). *Effects of stocking northern pike in murphy flowage. Technical Bulletin 79*. Madison, WI: Wisconsin Department of Natural Resources. Retrieved from https://dnr.wi.gov/files/PDF/pubs/ss/SS0079.pdf.

Stanković, D., Crivelli, A. J., & Snoj, A. (2015). Rainbow trout in Europe: Introduction, naturalization and impacts. *Reviews in Fisheries Science & Aquaculture*, *23*, 39–71. https://doi.org/10.1080/23308249.2015.1024825

Uki, N. (2006). Stock enhancement of the Japanese scallop *Patinopecten yessoensis* in Hokkaido. *Fisheries Research*, *80*, 62–66. https://doi.org/10.1016/j.fishres.2006.03.013

van Oosterhout, C., Hutchinson, W. F., Wills, D. P. M., & Shipley, P. (2004). Micro-checker: Software for identifying and correcting genotyping errors in microsatellite data. *Molecular Ecology Ressources*, *4*, 535–538. https://doi.org/10.1111/j.1471-8286.2004.00684.x

Vuorinen, P. J., Nyberg, K., & Lehtonen, H. (1998). Radioactive strontium (85Sr) in marking newly hatched pike and success of stocking. *Journal of Fish Biology*, *52*, 268–280. https://doi.org/10.1111/j.1095-8649.1998.tb00798.x

Wang, J., Wang, C., Qian, L., Ma, Y., Yang, X., Jeney, Z., & Li, S. (2011). Genetic characterization of 18 novel microsatellite loci in northern pike (*Esox lucius* L.). *Genetics and Molecular Biology*, *34*, 169–172. https://doi.org/10.1590/S1415-47572010005000114

Welcomme, R. L., & Bartley, D. M. (1998). Current approach to the enhancement of fisheries. *Fisheries Management and Ecology*, *5*, 351–382. https://doi.org/10.1046/j.1365-2400.1998.550351.x

SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of the article.

How to cite this article: Guillerault N, Loot G, Blanchet S, Santoul F. Catch-related and genetic outcome of adult northern pike *Esox lucius* stocking in a large river system. *J Fish Biol*. 2018;93:1107–1112. https://doi.org/10.1111/jfb.13826