Aquaculture 434 (2014) 254–263

Contents lists available at ScienceDirect

Aquaculture

journal homepage: www.elsevier.com/locate/aqua-online

A tale of two hatcheries: Assessing bias in the hatchery process for Atlantic salmon (*Salmo salar* L.)

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ARTICLE INFO

Article history:
Received 30 January 2014
Received in revised form 29 July 2014
Accepted 31 July 2014
Available online 12 August 2014

Keywords:
Salmo salar
Supportive-breeding
Genetic diversity
Broodstock
Parental bias

ABSTRACT

Stock enhancement of Atlantic salmon (*Salmo salar* L.), a fish of considerable economic and social importance, is commonplace. Supportive-breeding is a well-recognised method of enhancement which, when compared with traditional hatchery practices, is thought to reduce the severity of selection pressures on broodstock fish. Critically, in supportive-breeding programmes, the eggs and sperm used in the breeding process are taken from wild adult fish originating from the same catchment that resulting juvenile fish are subsequently stocked into, thereby avoiding problems associated with a lack of local adaptation in the stocked fish. Previous studies have indicated that sex bias during the hatchery process may result in reduced genetic diversity of the offspring. Utilising 16 microsatellite loci and two expressed sequence tag (EST) loci, we examined progeny from two hatcheries located on the rivers Exe and Tamar in southwest England, assessing the genetic diversity and parental contribution at each. Two strains were assessed within each hatchery. Genetic diversity was found to be reduced in offspring compared with that of the parent fish. This is likely the result of utilising a small number of broodstock in combination with parental bias. In the four hatchery strains studied (Bar, LEx, Lyd and TXL), parental contribution ranged between 2.1 and 29.2%, 12.2–51.0%, 2.0–70.0% and 4.0–40.0%, respectively. If this practice is to be continued, efforts should be made to improve adherence to national rearing guidelines by increasing the number of broodstock fish utilised and ensuring a more balanced contribution of all adults during the crossing process. Ultimately, we suggest a need to review the suitability of current national Atlantic salmon hatchery guidelines, particularly with regard to their use and relevance in small European rearing systems.

1. Introduction

Atlantic salmon (*Salmo salar* L.) have declined in number across their range due to a variety of factors both in river and at sea (Parrish et al., 1998). In southwest England, potential causes include pollution (Ellis et al., 2011; Hendry et al., 2007), historic exogenous stocking (Ellis et al., 2011 and references therein; Finnegan and Stevens, 2008; D. Solomon, *pers. comm.*), exploitation in river and at sea (Aprahamian et al., 2010; Consuegra et al., 2005; Klemetsen et al., 2003; Roberts, 2007) and disease (e.g. ulcerated dermal necrosis, UDN) (Roberts, 1993).

Due to the socio-economic importance of sport fish such as Atlantic salmon, stock enhancement activities, including exogenous stocking, captive and supportive-breeding, have long been commonplace (Horreo et al., 2011a; Kitada et al., 2009; Solomon et al., 2003). However, an increasing number of studies show exogenous stocking to have been largely ineffective in improving numbers of returning adult fish (Ciborowski et al., 2007; Griffiths et al., 2011; Young, 2013), whilst others have indicated natural re-colonisation from nearby catchments to be the dominant process in salmon population recovery in locations where the cause of decline has been removed (e.g. pollution, fishing pressure) (Griffiths et al., 2011; Ikediashi et al., 2012; Perrier et al., 2010). In some cases the genetic signature of stocked fish can persist in a new environment (e.g. Finnegan and Stevens, 2008; McGinnity et al., 2009), however, it is now deemed more appropriate to stock with 'local' fish that are genetically compatible and locally adapted (Solomon et al., 2003). For this reason, supportive-breeding using eggs and sperm stripped from native adult fish is a more logical option than utilising exogenous or captive-bred fish which are at an adaptive, reproductive and genetic disadvantage (Araki et al., 2007). In some hatcheries these broodstock are collected on one occasion and maintained for generations (e.g. Koljonen et al., 2002), whereas in other situations the broodstock are taken annually from the wild, so that the offspring to be released are all first generation hatchery stock (e.g. Horreo et al., 2008).

Hatchery-reared fish are known to undergo selection to optimise survival in a hatchery environment, not survival in the wild (Blanchet et al., 2008; Christie et al., 2012a); thus, hatchery offspring often suffer reduced genetic diversity (Araki and Schmid, 2010; Horreo et al., 2008; Koljonen et al., 2002; Stahl, 1983; Verspoor, 1988), reduced Ne (Christie et al., 2012b; Ryman and Laikre, 1991; Verspoor, 1988) and reduced fitness (Ford, 2002; Fraser, 2008), though this is not always

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http://dx.doi.org/10.1016/j.aquaculture.2014.07.031
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the case (Araki and Schmid, 2010). In some cases, little impact of hatchery processes has been found. For example, Tessier et al. (1997) found a supportively-bred stock of landlocked *S. salar* to have decreased allele frequencies, however, heterozygosity was not altered. Similarly, Eldridge and Killebrew (2008) found that the genetic diversity of a Chinook salmon (*Oncorhynchus tshawutscha*) supportive-breeding stock did not contribute to a loss of genetic diversity in the captive offspring produced, nor the wild stocks that they were supplementing. Finally, Jeong et al. (2007) found no morphological difference (weight, length) between supportively-bred Black sea bream (*Sponyliosoma cantharus*) and their wild conspecifics, despite 69.3% of the offspring being assigned to one breeding pair of the 51 available broodstock. These examples illustrate that the matter is not clear-cut and that there may be ways to optimise practices and minimise negative effects.

Populations with reduced genetic diversity are known to be more vulnerable to stochastic changes and less able to adapt and survive (Koljonen et al., 2002). Supportive-breeding is known to minimise the effects of traditional hatchery practices on adaptation and selection (Araki, 2008), but this by no means eliminates the problems entirely (Blanchet et al., 2008; Christie et al., 2012a). There is clearly a trade-off between supplementation and the genetic integrity of supplemented stocks (Fraser, 2008).

As evidenced above, a number of empirical and theoretical studies have been completed over the last 50 years to assess the impact of hatchery processes on both the F1 generation and wild fish from genetic and ecological viewpoints. Typically, however, these studies have focused on the Pacific Northwest (Waples, 1991) and/or at a global scale (Araki and Schmid, 2010; Fraser, 2008). These studies demonstrate an inconsistency in the effects on the F1 generation. The majority illustrate a negative effect on the fitness and genetic integrity of the stocks being produced and supported; however, with careful management these effects can be minimised. In England and Wales the Environment Agency (EA) have provided guidelines to minimise these effects (Environment Agency, 2011). These guidelines focus on the number of broodstock, sex ratios, mating strategies and maintaining environmental conditions similar to that in the wild. These strategies will later be discussed in terms of the results of this study.

Considering the inconsistent results, in addition to the calls for further empirical studies to clarify the effects of supportive-breeding practices (Fraser, 2008) and the uncertainties in associated theoretical analyses (Kalinowski et al., 2012), it would seem prudent to explore the impacts of supportive-breeding practice at an approved hatchery following Environment Agency guidelines for the management of Atlantic salmon, to assess whether current UK guidelines are sufficient to preserve the genetic integrity of the F1 stock.

As such, in this study, the effectiveness of two hatcheries operating supportive-breeding programmes in southwest England were compared, with a view to informing management decisions on Atlantic salmon hatchery practice in future years. Using microsatellite-based genetic analysis we examined (i) the effectiveness of the hatchery at preserving genetic diversity, and (ii) the effectiveness of mating strategies in balancing parental contribution and maintaining effective population size. These results have been used to refine hatchery practices and will guide further fish-related management decisions within the catchments, whilst also highlighting potential issues and points of good practice for supportive-breeding programmes in general.

2. Methodology

2.1. Hatchery operations

This study analysed salmon from two hatcheries in Devon and Somerset, England, one at Endsleigh on the river Tamar, the other at Exebridge at the confluence of the Rivers Barle and Exe (Fig. 1). Supportive-breeding comprises the stripping of eggs and sperm from wild, sexually mature adult fish at a hatchery; typically, the adult fish are then returned to their native river. Whilst the stage at which juveniles are released can vary from ova to smolts (Aprahamian et al., 2003; McGinnity et al., 2004; Saltveit, 2006), both the hatcheries studied (Exe and Tamar, Fig. 1) release the majority of their juveniles as 0+ parr; however, in the past some 1+ parr and smolts have also been released.

A small number of broodstock (≤15) were used at each hatchery. It should be noted that throughout this study broodstock collection and mating design followed standard hatchery protocols and guidance from the Environment Agency. Whilst this may not constitute optimal experimental design, we opted to follow standard protocols to allow assessment of the success of current hatchery practices.

2.1.1. Exe catchment

Two separate strains are reared annually at the Exe hatchery. In 2010/2011, 13 adult fish were reported as having been collected by rod and line from two regions of the river Exe: (i) the main river, near the confluence with the Barle tributary (5 male, 4 female); (ii) the Little Exe (2 male, 2 female). In the subsequent analysis, 100 0+ parr were sampled and analysed: 50 were of Barle heritage, and 50 were of Little Exe heritage (Table 1). Barle fish were sampled across three raceways whilst Little Exe fish were sampled from two raceways. The mating design at the hatchery was such that each raceway sampled contained the offspring from two females that had each been paired with two males. In some cases a third male was utilised by hatchery staff as a

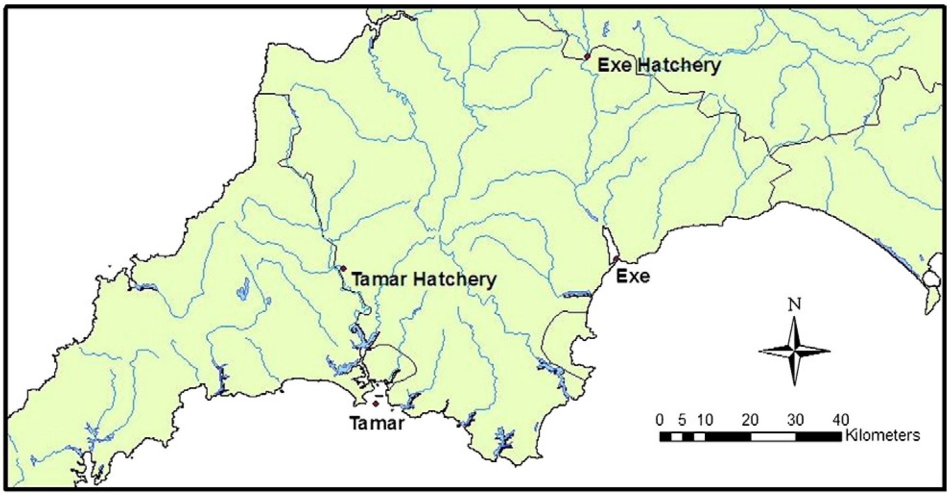

Fig. 1. Map showing the locations of the Exe and Tamar hatcheries. Catchment names are marked at their respective river mouths.