Salmon assessment in England: time to take stock?

The role of genetics in salmon stock assessment

Jamie Stevens
University of Exeter

Telford, 14th July 2016
Possible roles for genetic methodologies in salmon stock assessment

1. Assessment of reproductive contribution – genetic parentage analysis
2. Sexing of smolts and returning adults
3. Estimation of straying rates
4. Calculation of effective population size (Ne) using genetic methods: problems, and comparison with census-based methods
1. Assessment of reproductive contribution – genetic parentage analysis
A small number of anadromous females drive reproduction in a brown trout (Salmo trutta) population in an English chalk stream

JILL C. A. GOODWIN*, R. ANDREW KING*, J. IWAN JONES†, ANTON IBBOTSON†† AND JAMIE R. STEVENS*
*Department of Biosciences, College of Life and Environmental Sciences, University of Exeter, Exeter, Devon, U.K.
†Centre for Ecology and Hydrology Dorset, Winfrith Technology Centre, Dorchester, Dorset, U.K.
‡The School of Biological and Chemical Sciences, Queen Mary University of London, London, U.K.

SUMMARY

1. Brown trout, Salmo trutta, exhibit one of the most highly variable and polytypic life-history strategies of all salmonids. Populations may be wholly freshwater-resident or almost exclusively migratory (anadromous), or fish of a single population may exhibit varying proportions of the two life-history strategies. Both anadromous and freshwater-resident trout freely interbreed to produce fertile offspring.

2. We quantify maternal reproductive provisioning by anadromous and freshwater-resident brown trout to their offspring and assess relative parental fitness (in terms of number, size and time of emergence of offspring). Newly emerged juvenile trout (fry) were sampled (n = 119) over the emergence period in March–April 2007 in a lowland English chalk stream; samples of adult trout [anadromous (6F : 12M) and freshwater-resident (22F : 56M)], river-resident trout parr and macroinvertebrate prey were also collected.

3. Using a novel combination of stable isotope analysis and microsatellite genotyping we demonstrate the overwhelming contribution of anadromous parents (both female and male) to fry production, despite the obvious presence and numerical dominance of resident adults. We unambiguously identify the maternal origins of 78% of juveniles sampled and show that maternal reproductive contribution to juvenile production in the river was higher for anadromous females (76%) than freshwater-resident fish (2.5%). Offspring of anadromous females emerged earlier and at a larger body size than offspring of resident females. Similarly, while the relative contribution of resident males (37%) was higher than that of resident females, anadromous males sired considerably more offspring (63%) than resident males. This is the first study of its kind to accurately assess the reproductive contribution of anadromous male trout.

4. Overall, this study suggests that anadromous maternal traits provide offspring with an adaptive advantage and greater fitness in early ontogeny, and that a small number of anadromous females (six of 96 adults sampled) are the main drivers of reproduction in this system.

Keywords: microsatellite, parental investment, Salmo trutta, sea trout, stable isotope analysis
Assessment of reproductive contribution – genetic parentage analysis in *salmon*

- Salmon (all go to sea, except precocious parr)
- Application of SIA arguably of less value
- But, still need to understand relationships of parent fish
- Pedigree analysis: use highly variable genetic markers – microsatellites still of value– and relevant pedigree software, e.g. COLONY
- Aim to sample all potential parent fish (*not always achievable!!!*)

*See schema (next slide)*
Fry-parental schema, derived from microsatellite genotyping and analysis of allele frequencies using the COLONY software.
2.
Sexing of smolts and returning adults
The sexually dimorphic on the Y-chromosome gene \(\text{sd}Y\) is a conserved male-specific Y-chromosome sequence in many salmonids

Ayaka Yano,1 Barbara Nicol,1,2 Elodie Jouanno,1 Edwige Quillet,2 Alexis Fostier,1 René Guyomard2 and Yann Guiguen1

Keywords
\(\text{sd}Y\), salmonids, sex-determining gene, sex-determination locus, molecular sexing

Correspondence
Yann Guiguen,
INRA, UR1037, LPGP, Fish Physiology and Genomics, Rennes, France.
Tel.: (33) 2 28 46 58 09;
Fax: (33) 2 28 46 58 20;
E-mail: yann.guiguen@rennes.inra.fr

Abstract
All salmonid species investigated to date have been characterized with a male heterogametic sex-determination system. However, as these species do not share any Y-chromosome conserved synteny, there remains a debate on whether they share a common master sex-determining gene. In this study, we investigated the extent of conservation and evolution of the rainbow trout (Oncorhynchus mykiss) master sex-determining gene, \(\text{sd}Y\) (sexually dimorphic on the Y-chromosome), in 15 different species of salmonids. We found that the \(\text{sd}Y\) sequence is highly conserved in all salmonids and that \(\text{sd}Y\) is a male-specific Y-chromosome gene in the majority of these species. These findings demonstrate that most salmonids share a conserved sex-determining locus and also strongly suggest that \(\text{sd}Y\) may be this conserved master sex-determining gene. However, in two whitefish species (subfamily Coregoninae), \(\text{sd}Y\) was found both in males and females, suggesting that alternative sex-determination systems may have also evolved in this family. Based on the wide conservation of \(\text{sd}Y\) as a male-specific Y-chromosome gene, efficient and easy molecular sexing techniques can now be developed that will be of great interest for studying these economically and environmentally important species.

Introduction
Master sex-determining genes are the main genetic switches controlling the gonadal sex differentiation cascade leading to the development of ovaries or testes. In mammals, which harbor an XX/XY system, the \(S\) (sex-determining region of the Y chromosome) gene was identified in the early 1990s (Sinclair et al. 1990) as the first vertebrate master sex-determining gene. In chickens, which have a female heterogametic (ZZ/ZW) sex-determination system, the Z-linked \(\text{Dmrt1}\) (doublesex and mab-3 related transcription factor 1) gene is a strong candidate for the chicken sex-determining gene (Smith et al. 2009), and this gene triggers gonad masculinization by a double dosage mechanism in males compared with females. Interestingly, \(\text{Dmrt1}\) has also been shown to be conserved on the Z chromosome in the majority of bird species (Stiglec et al. 2007) including in the ancient ratite emu species (Shetty et al. 2002), suggesting a conservation of this gene as the master sex-determining gene in all bird species.

• Application to current stocks

• Can be used with historical material e.g. scale collections

Can look at changing trends over time
3. Estimation of straying rates
Investigating patterns of straying and mixed stock exploitation of sea trout, *Salmo trutta*, in rivers sharing an estuary in south-west England

R. A. KING
Department of Biosciences, College of Life and Environmental Sciences, University of Exeter, Exeter, UK

R. HILLMAN
Environment Agency, Bodmin, Cornwall, UK

P. ELSMERE
Environment Agency, Launceston, Cornwall, UK

B. STOCKLEY
Westcountry Rivers Trust, Callington, Cornwall, UK

J. R. STEVENS
Department of Biosciences, College of Life and Environmental Sciences, University of Exeter, Exeter, UK
Assemble genetic baseline of local populations

Reporting Groups
- Taw/Torridge
- Camel
- Land’s End Complex
- Carrick Roads
- South Cornwall
- Tamar Estuary
- Tamar
- South Hams
- Dart/Teign
- East Devon
Estimating straying rates: river Tamar

A. Tamar tidal limit (EA weir trap)
B. Lower Tamar rod fishery
C. Upper Tamar rod fishery
D. Lynher rod fishery
E. Tavy rod fishery
4. Calculation of effective population size (Ne) using genetic methods

...the most difficult!!!
Calculation of effective population size (Ne) using genetic methods

Need to consider...

• The accuracy of estimating Ne from genetic data

• What does Ne mean?
  – Ne of a catchment
  – Ne of a population
  – Ne of the fish within a trib.? 

• Calibration of genetic estimates of Ne with census data? Initially run in parallel?
Defining Ne – need knowledge of population structure

Ne?

How many populations?
Defining Ne – need knowledge of population structure

Scenario 1

Scenario 2

Scenario 3

Ne

Ne1

Ne2

Ne3

Ne4
Other factors...

• Reliability of current markers (microsatellites) to discriminate within (parentage) and between populations and, thereby, to allow accurate identification of river of origin.

• Other potential marker systems (SNPs) with potentially higher levels of resolution = improved levels of inter-population discrimination?; such factors are essential for calculation of – for example– straying rates.
Thanks to...

- Atlantic Salmon Trust
- Environment Agency
- Game & Wildlife Conservation Trust
- Westcountry Rivers Trust

...for funding and boots in the river