



Brown Trout Population Structure & Genetic Stock identification of the Middle Shannon & Lough Ree Catchments

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Inland Fisheries Ireland
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**Population Structure and Genetic Stock Identification of Trout (*Salmo trutta*)
of the Middle Shannon and Lough Ree Catchments**

INTERIM REPORT

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Cover photo: Brown trout in the River Suir at Cahir, Co. Tipperary © Inland Fisheries Ireland



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- Lough Derravaragh Anglers
- Lough Ennell Trout Preservation Association
- Lough O'Flynn Anglers
- Lough Owel Anglers
- Lough Ree Angling Federation
- Lough Sheelin Trout Preservation Association
- Suck Valley Angling Hub

Inland Fisheries Ireland in partnership with Queens University Belfast are co-project leaders for this study.



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1. Introduction

The wild brown trout (*Salmo trutta*) displays a remarkable level of variation in its external appearance, behaviour, ecology, biology and many other aspects of its life-history. The realisation that much of this variation has a genetic basis, has led scientists to also study the genetic make-up of brown trout in the recognition that there is enormous genetic diversity within and among brown trout populations, which is of great importance for both management and conservation of the species.

Since 2006 Inland Fisheries Ireland (IFI) have commissioned a number of genetic based studies of brown trout, in selected catchments across Ireland (e.g. Mask, Corrib, Sheelin, Ennell, Suir, Boyne) to understand more about how genetic diversity is distributed among populations in order to assist in making the correct and most cost effective management decisions (e.g. is a particular tributary stream contributing more fish to a lake or river main channel than any other stream, or is there one genetic strain in a catchment completely different and unique than all others, if so how can IFI manage this) (EREP, 2014; O'Grady and Delanty, 2014; Massa-Gallucci and Mariani, 2011). This ongoing work is providing IFI with valuable information for fisheries management purposes.

In 2014, IFI in collaboration with Queen's University Belfast (QUB) began a three-year research programme to examine the genetic diversity of brown trout in the Middle Shannon and Lough Ree Catchments, in tandem with two other catchments. The Middle Shannon and Lough Ree Catchments include two of the River Shannon's largest sub-catchments' (River Inny and River Suck), one of its three largest lakes (Lough Ree) and three other lakes which are regarded as important brown trout fisheries (Loughs' Owel, Ennell, Derravaragh and Sheelin). Genetic profiling of the trout stocks has already been completed on the Lough Sheelin subcatchments (*in press*) and on Lough Ennell (Massa Gallucci and Mariani, 2011).

The main objectives of the middle Shannon and Lough Ree study were:

- To investigate if there are a number of discrete genetic stocks of brown trout within the Middle Shannon and Lough Ree catchments.



- To understand how important each genetic group is to the fishery.
- Examine the behaviour and other processes occurring within individual populations and between populations over their life span.
- Estimate the percentage contribution of the various sub-catchments to the adult brown trout stocks of Lough Ree and a small number of other brown trout lakes (Loughs' Owel and Derravaragh).
- Investigate if the River Inny and River Suck arterial drainage scheme impacted on the genetic diversity of brown trout within the Middle Shannon and Lough Ree catchment.

Preliminary results from the genetic analysis are presented in this report. A final report will be available mid 2017.

2. Methods

Fish samples

Where possible 50 one year-old trout were captured by electrofishing in each tributary sub catchment from each of the three rivers (Fig. 1). A small sample, comprising of non-destructively collected scales, was retained from each individual fish for genetic analysis. To ensure that samples provided a proper representation of brown trout inhabiting those catchments, sampling was carried out as extensively as possible covering both main channel and associated tributary rivers. This extensive sampling also minimised possible family bias which are known to take place when large number of samples are taken from few locations. Location details of all sample sites were recorded by taking a GPS reading. The number of scale samples taken from each catchment is shown in Table 1. In addition, anglers from various fishing clubs kindly agreed to forward scale samples and relevant location details to IFI as part of this study. Prior to the fish scales being processed, all sampling information was collated and transferred to IFI's electronic database.

Genetics – DNA profiling



DNA was extracted from each fish sample and DNA profiling (genetic testing or DNA fingerprinting) carried out. Genomic DNA was extracted using the Promega Wizard SV 96 genomic DNA purification system and subsequently transferred to 96 well microtitre plates for storage at -20°C and subsequent genetic analysis. Genetic analysis (i.e. DNA profiling) was carried out using a panel consisting of 22 microsatellite marker loci developed at QUB. This DNA fingerprinting based technique has been routinely used for parentage analysis (i.e. identification of individuals to families), identification of population genetic sub structuring and also to identify the source population to particular individuals (e.g. genetic stock identification and/or individual assignment). The data obtained was then analysed using specific computer software for genetic analysis.

Table 1. Number of samples collected.

Middle Shannon & L. Ree Catchment		Number Samples
Number of river samples collected		2,279
Fish Farm samples		150
Lough Ree	393	
Lough Owel	182	
Lough Derravaragh	86	
Lough O' Flynn	23	
Total number of lake samples collected		684
Total number of samples collected		3,113

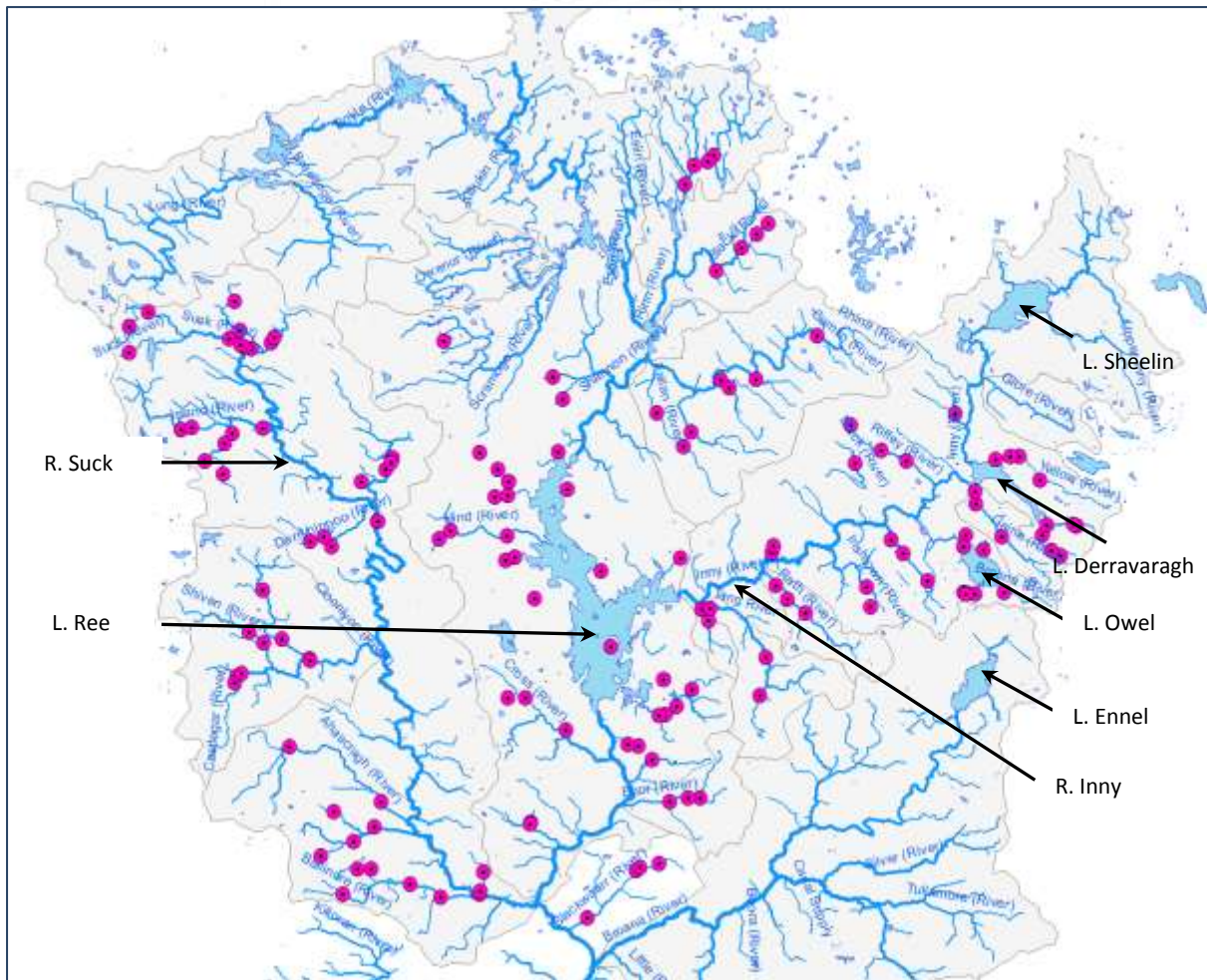


Figure 1. Location of sampling sites mid-Shannon and Lough Ree catchment (not all sites from Loughs' Ree and Owel shown on map)

3. Progress to date and preliminary results

- a. Statistical analysis of genetic data is under way by Queen's University Belfast.
- b. Early difficulty with samples has been overcome; thus additional samples have been collected from relevant tributaries and the main channel where insufficient number of samples and/or sampling sites were identified. Additional scale samples have also been provided from the IFI archival collection of scale samples.

- c. Preliminary STRUCTURE analysis of the genetic data indicates that there are several distinct genetic groups within the Middle Shannon and Lough Ree catchment (Fig. 2).

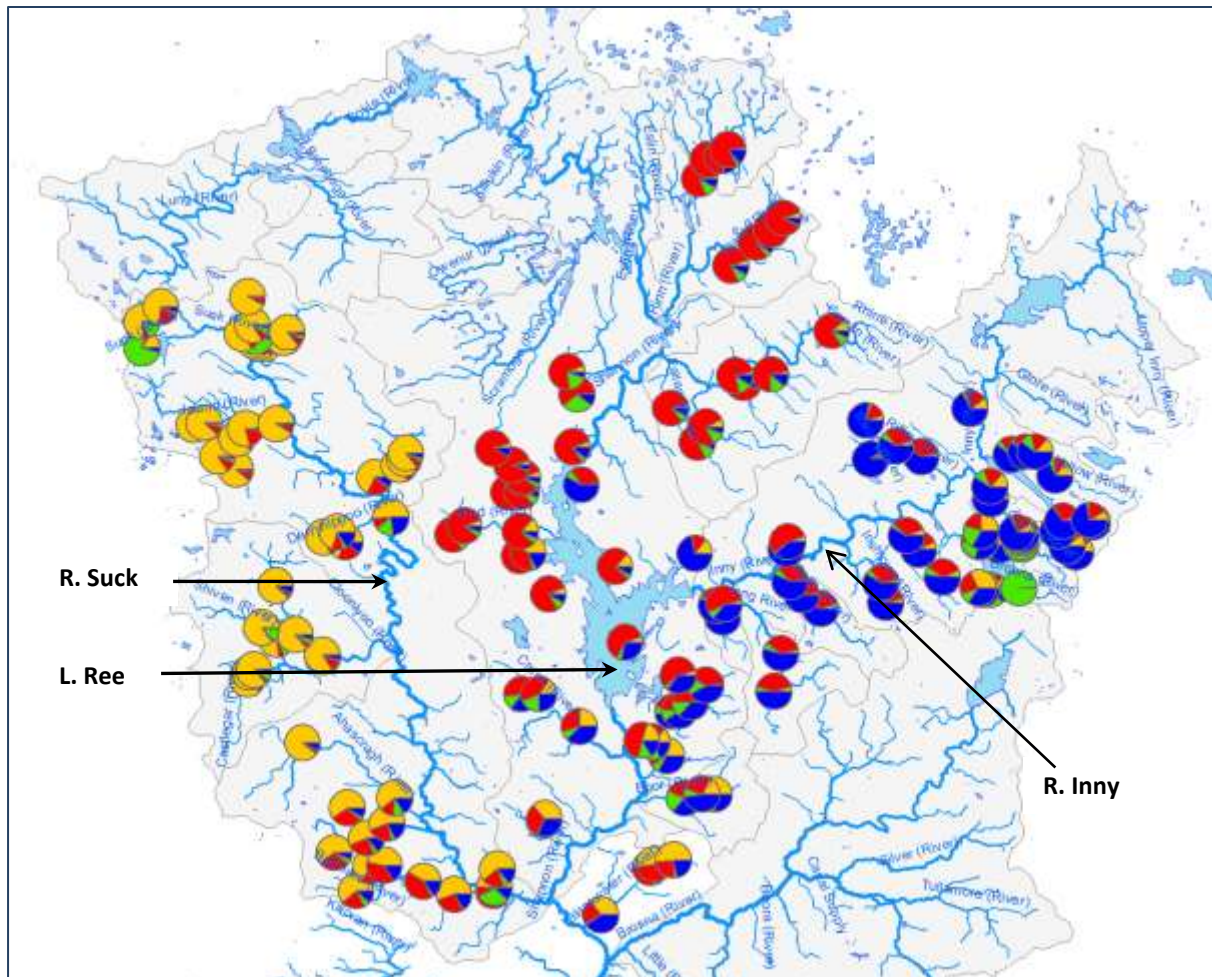


Figure. 2. Hierarchical Genetic Structure Analysis – mid-Shannon and Lough Ree catchment. First Level Genetic Structuring.

4. Next Phase (January 2016 to June 2017)

Additional fish scale samples were collected from a number of sites in 2015, these samples will be sent to QUB for analyses and included in the over-all results. Lake samples that have been processed will now be analysed and the data interpreted. It is expected that all samples will have



been processed and all lab work completed by mid-2016. Statistical analysis of the data along with interpretation of such analysis will be reported in the Final Report expected mid-2017.

5. References

EREP (2014) <http://www.fisheriesireland.ie/EREP/brown-trout-genetics-and-fisheries-management-in-ireland.html>).

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