

The Tale in a Scale

Dr. Andrew King of Exeter University describes the work taking place to unravel some of the mysteries surrounding trout and their life at sea along the southern coast of Britain.

Let me start by asking you a question. How can we conserve something (in this case trout) if we don't know where they are? At first, this may seem a strange question. Surely we know a lot about where trout are?

Through the work of the Wild Trout Trust, Environment Agency, Rivers Trusts and local fishing associations, for any particular trout river we generally have a fair idea of the size of the population on each tributary/stream, the levels of stocking, the location of spawning grounds and the potential problems (i.e. habitat and water quality, location of barriers to fish movement) and threats (i.e. pollution) to the river that all impact on the overall health of trout populations. The river can then be managed and stocks conserved, taking into account all this information. However, for sea trout rivers there is an extra dimension that has to be considered, one that is not so easily incorporated into management plans and this is the marine environment.

Sea trout spend a significant proportion of their life at sea, but for such an iconic fish many aspects of the marine phase of their life cycle are currently a 'black box'. We know they go to sea, but once in the marine realm they seem to disappear. Here, they face many threats including net fisheries, such as the North East Coast drift nets, the construction of renewable energy projects in sea trout feeding grounds and possible changes in food availability due to climate change. And this makes conserving sea trout stocks all the harder. So, I will ask again (slightly re-worded

this time), how can we conserve sea trout if we don't know where they are at sea?

Of course, efforts have been made to find out where sea trout go when they are at sea. For instance, tagging studies on the Tweed have shown that their fish can end up off the Dutch coast. But such studies are few and far between. Recently, the SALSEA project used a genetic tagging approach to identify the origins of Atlantic salmon post-smolts caught in Arctic waters. At the University of Exeter, we have built on our participation in the Atlantic Salmon Arc Project (ASAP) and SALSEA (both of which focused on salmon) and are using a similar genetic approach to study resident brown trout and migratory sea trout to inform the management of trout stocks in southern Britain. Our ultimate aim is to improve understanding of the marine phase of the sea trout life cycle, to build up a picture of when and where sea trout from southern British rivers are at sea, so that they can be better protected by regional, national and European law.

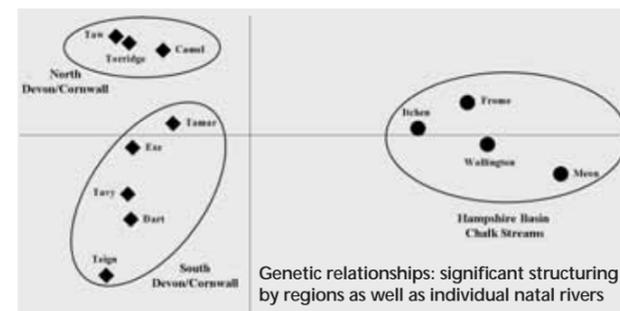
The project is part of the Atlantic Aquatic Resource Conservation (AARC) consortium which is a European Union, Interreg IV-funded programme with partners in Britain, Ireland, France, Spain and Portugal. Projects include conservation genetics of anadromous fish species, evaluation of supportive breeding practices, aquaculture, river restoration, education and communication.

Initially, genetic data must be gathered for resident brown trout populations from potential source rivers of sea-caught sea trout. Samples for this phase of the project have been collected from trout parr and sub-adult fish by the Environment Agency

A scale from an 11lb multiple spawning Tavy sea trout. But where has she been at sea?

and the Westcountry Rivers Trust during electrofishing surveys from major sea trout rivers in southern Britain, from the Severn around to the Thames, including well known sea trout rivers such as the Tamar and Sussex Ouse. The genetic characterisation of these trout stocks is now well under way, but has already thrown up some interesting results. For instance, initial findings indicate significant genetic structuring, with south-eastern chalk stream populations being distinct from populations from more acidic south-western rivers. Each of these two main groups can be further subdivided such that there are several distinct genetic units, usually corresponding to a number of neighbouring rivers. Within some catchments, such as the River Exe, there can be strong genetic differences between major tributaries.

Once we have the genetic information for the resident brown trout, we can then start to look at the sea trout populations within our target rivers. To do this, we have been asking anglers to send us scale samples from rod-caught sea trout. The samples sent to the AARC project are an invaluable resource and will be analysed in two different but



complementary ways that will provide us with important information to help guide future conservation efforts for sea trout.

Firstly, we are able to use scales as a source of DNA to allow genetic characterisation of sea trout samples in the same way as for the resident brown trout. In-river rod-caught sea trout samples can be used as an initial test of our brown trout genetic baseline. For example, we would assume that a sea trout caught in the Tamar is returning to its natal river. If the genetic profile of a sea trout does not accord with that of the river in which it was caught, then this may be interpreted as

It is known that different regions of the sea differ in their chemical signatures and that these differences are transferred up food chains. By analysing the chemical composition of scales, it is therefore possible to tell which region of the sea a fish has spent time feeding in. This approach has successfully been applied to Atlantic salmon. For this part of the study, we are collaborating with the Celtic Sea Trout and Living North Sea projects. Scientists at CEFAS are currently generating a map of carbon and nitrogen isotope levels in the North Sea, English Channel and Irish Sea using scallop shells. The next step is to

“...how can we conserve sea trout if we don't know where they are at sea?”

A sea trout makes its way back up the Sussex Ouse to spawn