

BY PAUL GASKELL

In Part 1 (page 26) we looked at how material is passed on from parents to offspring and also explained exactly what is meant by "inbreeding" and "outbreeding" depression. It also introduced the idea of the "library" of genes that is a catalogue of all versions of genes that have ever existed in the brown trout. Figure 1 represents certain combinations that could have originated from this wild ancestral "master library". Naturally, this is a dramatically simplified cartoon version of reality but some useful concepts are highlighted.

First of all, the brown trout "master library" consists of the wild populations that survived the last ice age. In contrast, only a small subset of this total genome is represented within the domesticated strains of farmed fish. This is an unavoidable consequence of the domestication process. The readily observable fact that the vast majority of wild fish fare very poorly in captivity (often succumbing to disease) indicates that many of the characteristics present in wild fish are lost during domestication. The resultant selection of the small minority of fish that can cope with fish farm conditions gives rise to the less genetically diverse domesticated strains. Sadly, even by cross-breeding several different strains of farmed trout, it is not possible to regain the full diversity represented in the wild "library" of alleles (you can't recreate bison by cross-breeding domestic cattle). This is not a problem in and of itself – as many of us can enjoy hectic fishing on wholly stocked enclosed stillwater fisheries that contain only domestic stock fish. These fisheries are typically (but not always) based on rainbow trout, rather than our native brown trout and the head of fish is not reliant on natural reproduction. In contrast, interbreeding can become a big problem when both wild and stocked fish of the same species co-exist...

A single example of a range of alleles present in a particular wild fish is given in Figure 1. The total collective character of all genes in this fish has been (arbitrarily) represented by a "yellow" colour code. Clearly, there will be many more than just the highlighted three characteristics







A range of different conditions and colonisation histories over different sites on a hypothetical river system has produced a range of distinct populations. Some (A, B and C) are dominated by a relatively small amount of inter-individual variation. Others, (D) have a wide mix of individuals of different genetic character.

that contribute to this overall condition. Furthermore, there will be many additional populations of fish that account for the remainder of the master library (some arbitrary representations of characteristics in other wild fish are colour coded in burgundy, pink, black and purple in Figure 2).

The localised environments in different areas of an imaginary river system will favour specific combinations of alleles (Fig. 2). Let us imagine that our "yellow" coded fish with their dark spotting camouflage and thick-skinned, acid-resistant eggs (from Fig. 1) find themselves perfectly suited to the peaty, dark and acidic headwaters at site A (Fig.2). Similarly, other headwater populations at sites B and C are also dominated by individuals that are strongly adapted to the specific conditions at each site. The individuals within each headwater population are relatively similar to each other in overall character (in our example). However, when

comparing across the populations at A, B and C (as well as amongst the populations present at D), a large variety of different characteristics is represented. The key to successful establishment and adaptation of these populations is the high overall genetic variation present in wild fish. How, then, could introducing some "fresh blood" in the form of fertile farmed fish possibly reduce rather than increase variation? Figure 3 indicates what would occur during a period that stocked fish bred (and interbred) successfully in the wild. Perhaps this would come about due to a period of uncharacteristic weather or flow conditions in combination with a large number of fish stocked.

STOCKING WITH FERTILE FISH COULD REDUCE WILD POPULATION SIZE

What about where there is heavy stocking and there is no (or very little) evidence of domestic-strain genes in stream-bred fish?



FIGURE 3 -

Successful interbreeding of fertile stock fish with wild fish makes fish at each location more similar to each other (more similar to the stock fish strain). The differences between individual fish at site D are also reduced.

So, simplistically, the apparent paradox of "bringing in new blood" actually reducing genetic diversity is the same process of most modern UK high streets now looking very similar to each other. High street retail premises, on the whole, belong to standardised national chains and unique local businesses have been ousted. Consequently, many cities now look very similar if you judge them on the shops or, more importantly, pubs that they offer.

Total gene pool (i.e. wild) estic stock at site A at site B at site C Fish at site D

Surely, there is no risk to wild fish from fertile stock fish in that case? Unfortunately, in reality this finding could mask a much more sinister and invisible risk. You see, the main reason that it is unpredictable as to how much genetic homogenization will occur is the generally very poor survival and reproduction of those hybrid stocked/native fish. A superb example of this would be studies that observe almost 100% mortality at sea of stock fish/sea trout hybrids. This might, at first viewing, seem like the perfect protection against the invasion of domestic genes into wild populations. However, the fact that any wild fish committing their breeding efforts to stock fish will not vield any surviving offspring is a serious problem (Fig. 4).

WHAT DO WE KNOW AND WHAT IS UNCERTAIN?

Finally, in relation to the concepts outlined above, what do we actually know? One thing that you can be assured of is that there are hundreds of peer-reviewed scientific studies documenting cases of the "homogenising" effect of stocking fertile brown trout. Anybody who says

"there are no studies to suggest that fertile stock fish reduce the genetic variation in wild fish" is a dead giveaway as someone who simply does not know what they are talking about. Sorry to be brutal, but that fallacy just has to be kicked into touch. There are dozens of studies from across Europe (including the UK) and North America where it has been demonstrated. In just one really neat example, studies in Denmark used DNA extracted from museum "glass case" trout specimens and compared it to DNA taken from fish living in the same populations today (1). They found precisely the homogenizing effect and reduction of localized adaptation due to stocking that we represented in Figure 3. What we don't yet know is when the degree of homogenization becomes harmful (i.e. scuppers a population's capacity to adapt). In other words do you have to reach rates of 3%, 10%, 70% or any other percentage invasion of domestic alleles before the wild populations become too poorly adapted to their environment to survive without the help of supplemental stocking? Furthermore, we do not know what would



(W) actually make it back as well. However, it is easy to see that any matings of wild fish with stock fish are wasted. In effect, the number of effectively "breeding" fish is dramatically reduced in heavily stocked systems. If you breed and all your offspring die, it is the same as if you don't breed at all. This reduction in the "effective breeding population size" has implications for populations in terms of the total numbers of wild fish (i.e. it could actively reduce the numbers of wild fish year on year). Additionally, with reduced wild population sizes, random or fluke events have a much increased impact compared to adaptive natural selection. Scientists use the term "genetic drift" to describe when a simple reduction in the overall size of the population makes completely random (rather than usefully adaptive) changes in the gene pool more likely.

happen to any threshold(s) of where harm occurs under the differences caused by climate change (or even whether any threshold would be constant across different populations).

What we do know for sure is that hybrids of domesticated and wild trout have poorer survival and reproduction in the wild, i.e. they become less well adapted (References 2 and 3 are just two of many examples). Examples of the incredibly poor survival (virtually zero) of hybrid fish - and consequent wasted wild breeding effort - in marine migratory populations have also been documented (4). There are too many additional examples to list here of the reduced survival of domesticated fish (through poor disease resistance, poor foraging and predator avoidance for example). More detail is given in the "stocking position statement" that appears on the Wild Trout Trust website www.wildtrout.org.

Overall, the preservation of genetic variation is undoubtedly absolutely crucial to the current and future wellbeing of our wild trout. To achieve this protection, we must provide good quality habitat, plentiful clean water and ensure that fish can move freely between habitats according to their changing needs throughout their lifecycle. We must avoid over-exploitation of wild stocks by promoting catch and release of wild fish. We must avoid causing irreversible losses of genetic material through the homogenising effects of fertile stock fish. So where you have some wild fish and your club absolutely feels it has to stock, just use sterile stockies (marked with a tiny tag under the chin) and keep the stocking densities something like realistic based on the available adult fish habitat – simple!

Dr. Paul Gaskell is an angler and freshwater ecologist with 10 years of academic research experience. He currently works for the WTT conservation team.

REFERENCES:

1 HANSEN, M.M., FRASER, D.J., MEIER, K and MENSBERG, K.D, (2009) "Sixty years of anthropogenic pressure: a spatio-temporal genetic analysis of brown trout populations subject to stocking and population declines" Molecular Ecology 18, 2549–2562

2 POTEAUX C, BEAUDOU D, BERREBI P (1998) "Temporal variations of genetic introgression in

stocked brown trout populations" Journal of Fish Biology 53, 701–713 **3 MILLER, L.M., CLOSE, T. and KAPUSCINSKI**,

A.R. (2004) "Lower fitness of hatchery and hybrid rainbow trout compared to naturalized populations in Lake Superior tributaries" Molecular Ecology 13, 3379–3388

4 HANSEN, M.M., RUZZANTE, D.E., NIELSEN, E.E. and MENSBERG K.D. (2000) "Microsatellite and mitochondrial DNA polymorphism reveals lifehistory dependent interbreeding between hatchery and wild brown trout (Salmo trutta L.)" Molecular Ecology 9, 583–594