

Why use modelling?

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Genetic interactions between cultured and wild stocks: the problems

Recent years have seen significant increases in the European aquaculture production of fish and shellfish species such as: Atlantic cod, Atlantic halibut, Atlantic salmon, common carp, European sea bass, gilthead sea bream, turbot, European lobster, scallops, mussels, and oysters. Concurrent with these increases comes concerns as to the potential genetic impact on wild populations of escapes and of cultured individuals (1).

Cultured individuals typically represent genetically exogenous populations, and in addition, the genetic constitution of culture populations has frequently been altered through inbreeding, selective breeding, or domestication. These differences become more pronounced the longer a species has been in mariculture production, particularly when closed life-cycle production is used (i.e. using cultured stock as broodstock), but can become apparent even in the first year of production (2). Interbreeding of escaped cultured stocks with wild populations can have serious consequences for the fitness and long-term persistence of the wild population. Introgression of non-native genotypes into wild populations can result in the break-up of local adaptation, resulting in, sometimes dramatic, reductions in fitness of these stocks (3) (Fig.1).

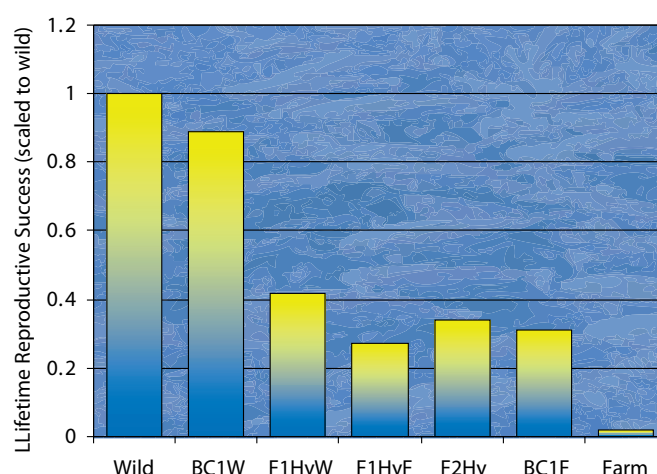


Fig. 1. Example of fitness differences between wild, farmed and hybrid fish: lifetime reproductive success of Atlantic salmon (3). Cross types refer to: BC1W F1 hybrid x wild; F1HyW wild female x farm male; F1HyF farm female x wild male; F2Hy F1 hybrid x F1 hybrid; BC1F F1 hybrid x farm.

Genetic introgression and fitness: the evidence

The whole range of outcomes, from no detectable effect to complete introgression or displacement has been observed after interactions of escaped cultured stocks and wild populations. Where they have been measured, such interactions always appear to have negative effects on the wild population (4) (Fig.2). These findings are in agreement with theoretical models which predict the breakdown of local adaptation during introgression of non-native genotypes.

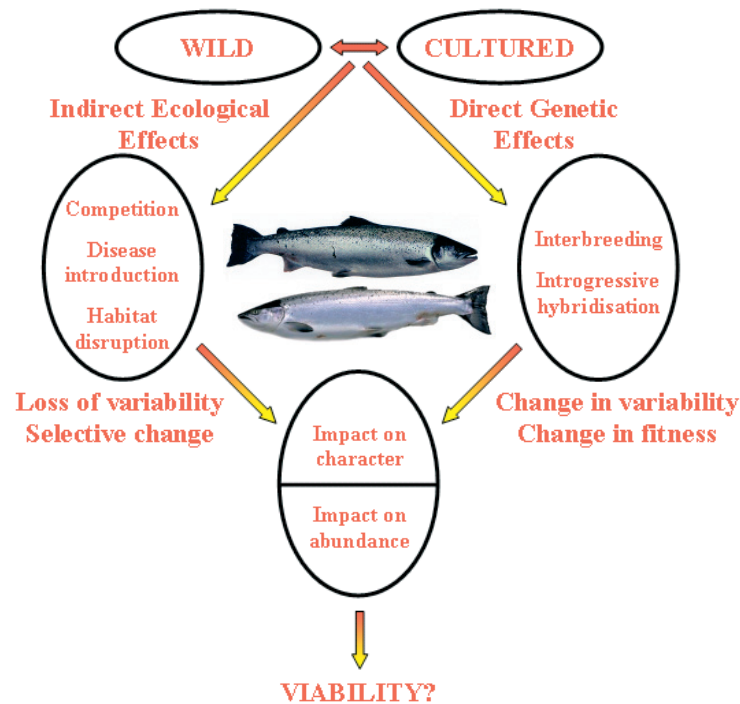
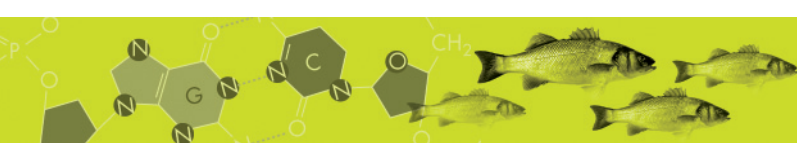


Fig. 2. Genetic and ecological effects of interactions between escaped cultured fish and wild stocks

Effects recorded include decreases in survival at various life-history stages, changes in growth rates and development, a reduction in fecundity, and ultimately, significant decreases in lifetime reproductive success. All these influences interact to reduce the fitness both of individuals and the population as a whole (5). 'Common garden' life-cycle experiments studying farmed and wild salmon, and their crosses, in natural environments have been carried out in Ireland and Norway and well illustrate the potential scale of the problem (3, 6). These studies have found that farmed fish may exhibit a lifetime success of ~2% compared to the wild. Further, the lifetime success of various types of hybrids between these two stock types ranged from 27 to 89% of the wild (Fig. 1). It has been suggested that interactions of this type can result in lowered fitness in the population as a whole, with repeated escapes having the potential to cause cumulative fitness depression and potentially an extinction vortex in vulnerable populations (5).

Why use a modelling approach to study these problems?

The difficulty of predicting the effects of influxes of exogenous stocks on local populations has been shown to be consistent with population genetics theory (7).



Reliable predictions would require that all population parameters are known; but this never occurs in real situations; even basic parameters such as life-cycle descriptions and effective population sizes are often poorly understood. Further, the genetic basis for variation in most fitness traits, such as growth, development, maturation and fecundity, are also largely unknown. Thus there is often little knowledge of the extent to which most genes are subject to selective pressures, fitness differences and/or genetic drift.

The only available solution to this problem is to use the results of empirical studies to develop computer based simulation models. Empirical studies comparing the fitness of wild and escaped cultured stocks, whilst essential for providing baseline measurements of individual and population level fitness, are very expensive and time consuming to perform; this is particularly the case given the many native species now cultured in Europe. It is also difficult to extrapolate from the limited experimental studies to different mixing and local scenarios. For example, the common garden experiment carried out in Ireland on farmed and wild salmon, and hybrids, under natural conditions, although it resulted in invaluable data collection (3), took 10 years to complete yet only studied impacts over two generations of introgression for a single species and a single site.

In contrast, computer-based models of population mixing can easily be used to simulate ecological and genetical interactions between cultured and wild stocks for a complete range of conditions. Thus in principal, at least, modeling can provide a comprehensive insight into the potential consequences for population character and abundance. However, for the modeling to be informative, it needs to contain a realistic representation of both demographic and genetic processes and parameters (Fig.3).

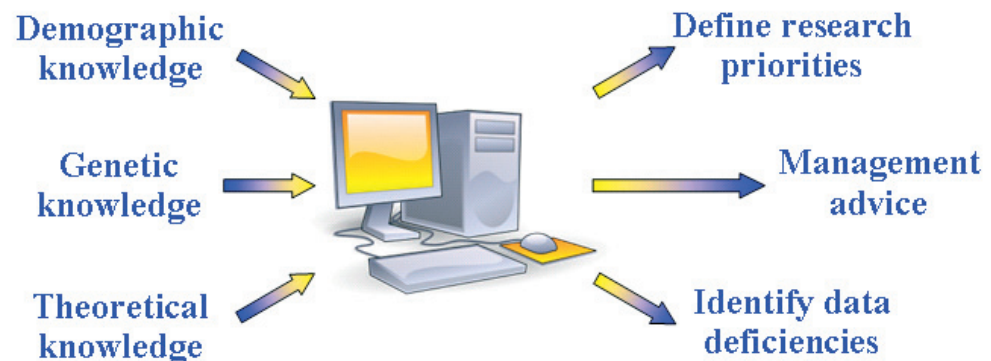


Fig. 3. *Modelling rationale*

A combined modelling approach allows different interaction scenarios to be evaluated for wild populations which will often differ in their demographic and genetic character. In doing so, both a broad-scale overview of expected interaction outcomes can be obtained as well as location-specific population impact predictions.

Just as importantly, modelling is invaluable in helping to identify where genetic or demographic processes are poorly understood or data is lacking. These deficiencies often already become apparent at start of building of such a model. This involves a detailed analysis of the scientific literature relating to species life-cycles, demographic and genetic processes and, in particular, the genetic basis of fitness related traits in

the species under investigation. Knowledge gaps also become apparent during model development and corroboration of the model using empirical data.

Thus combined modeling of cultured-wild interactions, which encompasses both demographic and genetic processes, provides:

- the best way of identifying the impacts from which might be expected both generally, and specifically in any given situation.
- an invaluable tool for identifying research needs and priorities.

References

- (1) Epifanio J. and Philipp D. (2001). Simulating the extinction of parental lineages from introgressive hybridization: the effects of fitness, initial populations of parental taxa, and mate choice. *Reviews in Fish Biology and Fisheries*, 10: 339-354.
- (2) Verspoor E. (1988). Reduced genetic variability in first-generation hatchery populations of Atlantic salmon (*Salmo salar*). *Canadian Journal of Fisheries and Aquatic Sciences*, 45: 1686-1690.
- (3) McGinnity P., Prödhon P. A., Ferguson A., Hynes R., Maoileidigh N. O., Baker N., Cotter D., O’Hea B., Cooke D., Rogan G., Taggart J. and Cross T. (2003). Fitness reduction and potential extinction of wild populations of Atlantic salmon, *Salmo salar*, as a result of interactions with escaped farm salmon. *Proceedings of the Royal Society, London. B.*, 270: 2443-2450.
- (4) Naylor R., Hindar K., Fleming I. A., Glodburg R., Williams S., Volpe J., Whoriskey F., Eagle J., Kelso D. and Mangel M. (2005). Fugitive salmon: assessing the risks of escaped fish from net-pen aquaculture. *Bioscience* 55: 427-437.
- (5) Hindar K., Fleming I. A., McGinnity P. and Diserud O. (2006). Genetic and ecological effects of salmon farming on wild salmon: modelling from experimental results. *ICES Journal of Marine Science*, 63: 1234-1247.
- (6) Fleming I. A., Hindar K., Mjølnerød I. B., Jonsson B., Balstad T. and Lamberg A. (2000). Lifetime success and interactions of farm salmon invading a native population. *Proceedings of the Royal Society, London. B.*, 267: 1517-1523.
- (7) Crow J. F. and Kimura M. (1970). *An Introduction to Population Genetics Theory*. Harper and Row, New York.

