How can evolutionary ecology support environmental management?

Is a seasonal moratorium sufficient to protect threatened fish populations? What are the impacts of size-selective fishing? Why are disease control efforts involving mass drug administration not always successful? Knowledge of evolutionary processes can make a valuable contribution to decision-making in environmental management. *Text: Kirstin Kopp*

Vario Images

Man-made evolution: as a result of intensive fishing, commercially exploited fish species are maturing ever-earlier.

Evolution is still often considered to be a prolonged process which only becomes visible on a geological timescale and is thus not perceptible to human observers. But we now know that evolutionary changes can be manifested over the same periods of time as ecological processes, i.e. within a few generations. Many of these "rapid" evolutionary changes are a response to environmental changes which act as stressors, exerting selection pressures on individuals and populations. In the case of aquatic ecosystems, stressors which may lead to rapid evolution include overexploitation, water pollution, habitat degradation, climate change and species invasion (Fig. 1). The question of how these evolutionary processes are manifested – and their relevance to environmental management – was discussed at a symposium organized by Eawag.

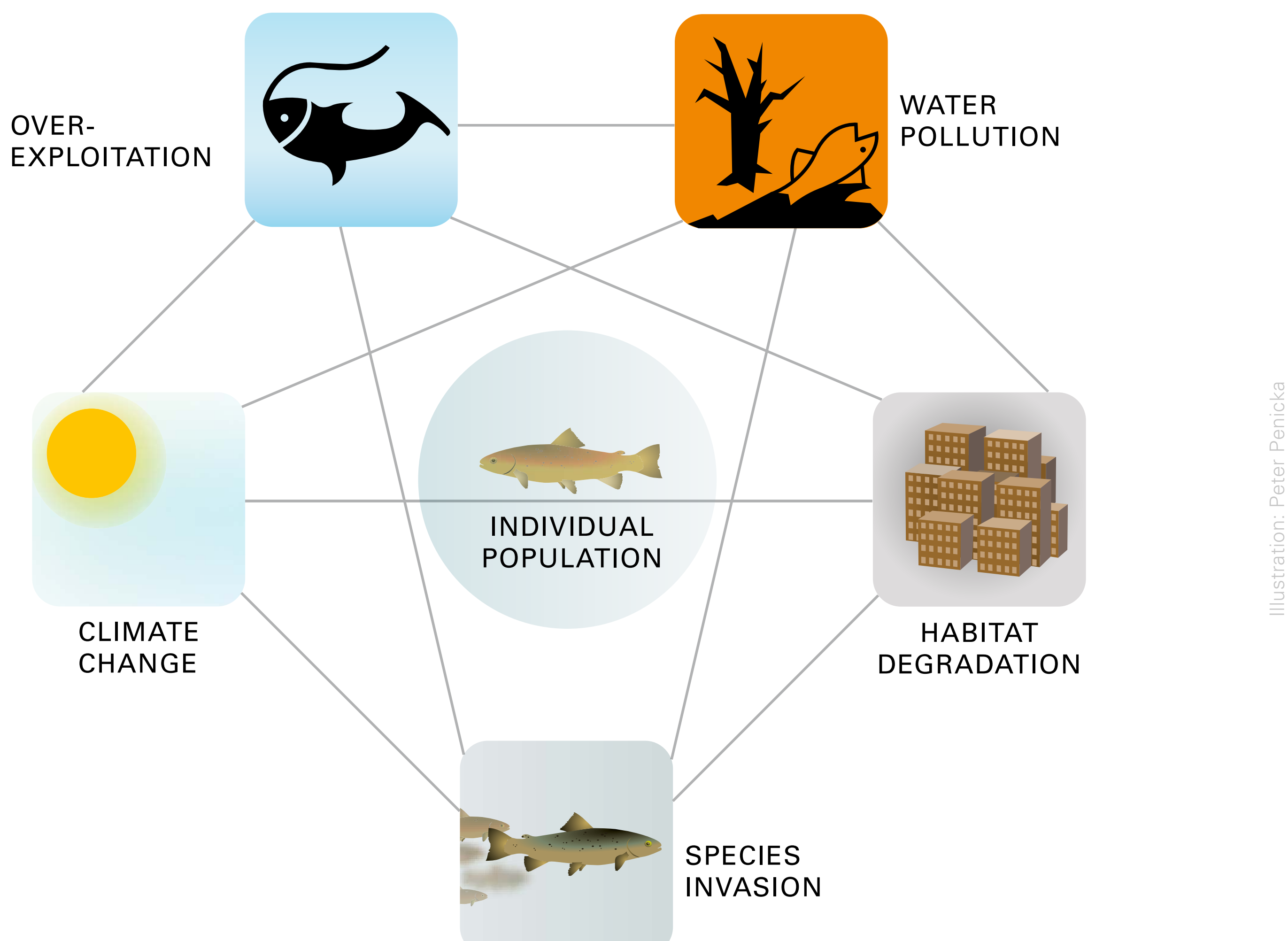

Fig. 1: A wide variety of selection pressures operate in aquatic ecosystems: stressors – and their interactions – affect individuals and populations, driving evolutionary processes.

Acclimation to chronic exposure to pollutants

Surface waters are contaminated not only as a result of major chemical spills (e.g. the incident which occurred at the Schweizerhalle industrial site near Basel in 1986) but also through continuous inputs of small amounts of heavy metals or biocides – even though the effects of such inputs are not visible in the short term. In aquatic organisms, chronic exposure to low levels of pollutants does not always cause poisoning, but may lead to acclimation, a process whereby organisms develop increased tolerance to pollutant concentrations which would originally have had lethal effects. For example, in experiments conducted by Frédéric Silvestre of the University of Namur (Belgium), it was shown that, after only a week, killifish constantly exposed to copper concentrations of 0.15 milligrams per litre had a higher likelihood of surviving exposure to a (generally lethal) concentration of 1 milligram per litre [1].

Acclimation is a physiological response of an individual, emerging from a range of possible responses to stressors (phenotypic plasticity). This increased stress tolerance can be passed on to the next generation via epigenetic mechanisms. Transgenerational phenotypic plasticity thus lies at the interface between individual and population, and between physiology and evolution. Stressors always act on all levels of an ecosystem – from cells through individuals to populations – and drive physiological, evolutionary and ecological processes (Fig. 2). For the purposes of ecological risk assessment, it is therefore desirable to understand as precisely as possible which processes affect which levels and how they are interrelated, since all levels are required for the maintenance of ecosystem functions.

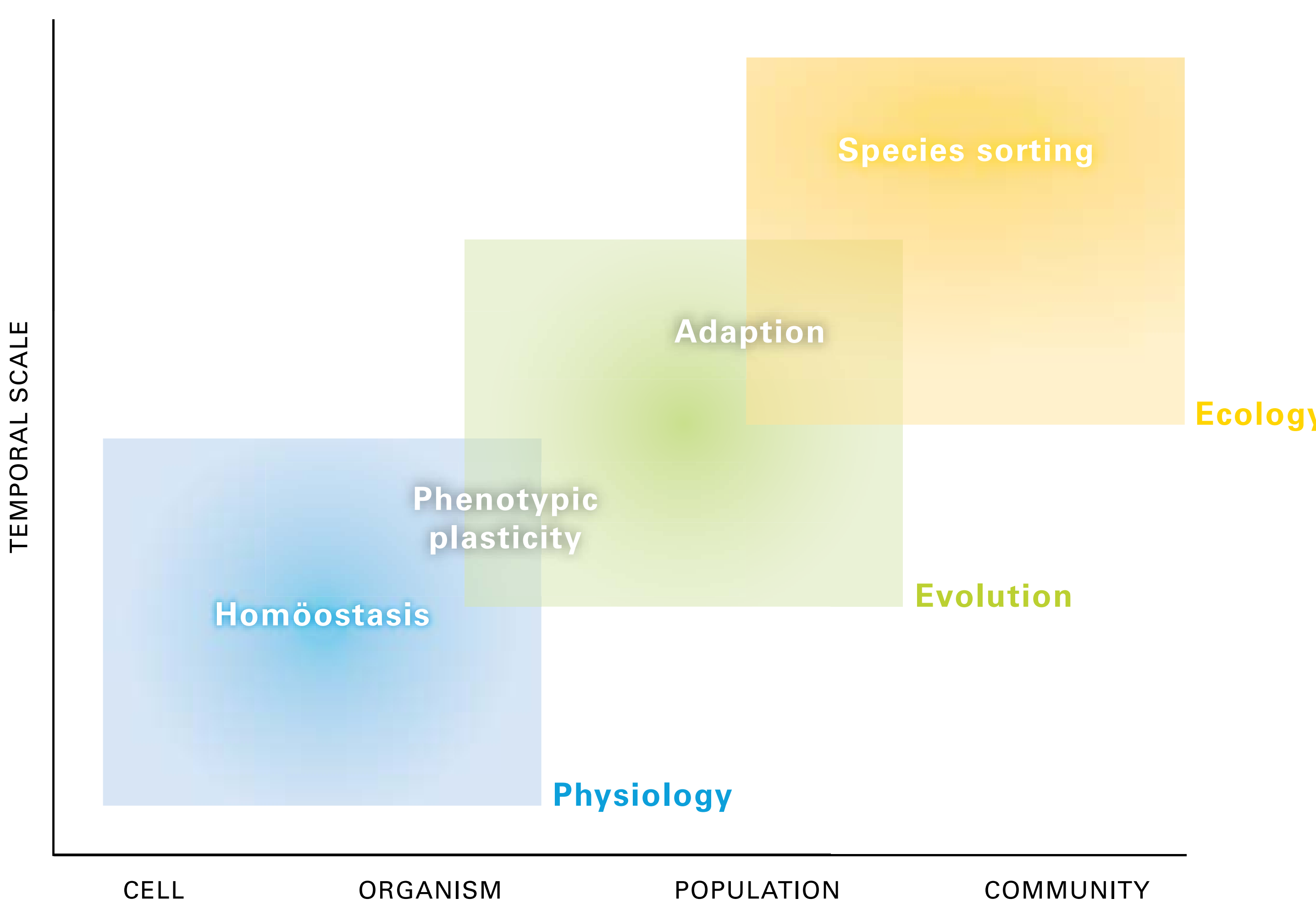

Fig. 2: Environmental influences (stressors) act at all levels of an ecosystem – on cells, organisms, populations and entire communities – driving physiological, evolutionary and ecological processes. The term "homeostasis" refers to the maintenance of a dynamic equilibrium, ensuring physiological stability. Local environmental conditions determine the composition of a community (species sorting).

Here, research can make a contribution. For example, Eawag scientist Francesco Pomati and co-workers investigated the extent to which physiological, evolutionary or ecological processes occur when phytoplankton communities are exposed to triclosan, a biocide detectable in natural waters [2]. Using a mathematical method (the Price equation approach), they demonstrated that the triclosan-induced phenotypic changes observed after two generations are attributable to evolutionary processes and acclimation – in other words, that adaptation occurs.

Improved protection of salmon thanks to genetic analyses

In Finland, the Atlantic salmon *(Salmo salar)* is threatened by the destruction of natural habitats and by overfishing. In 23 of 25 historical salmon rivers, this species is no longer found, mostly because the upstream migration of fish to their spawning grounds is impeded by dams. A fifth of all the salmon caught in Europe come from the (Finnish) River Teno. Until recently, efforts were made to protect salmon stocks in the Teno and its tributaries by permitting fishing only between May and August (from Tuesday to Sunday). However, the fact that tributaries could harbour different genetic variants was not taken into account. If stocks are to be effectively conserved, only large and genetically similar populations should be fished. The conservation strategy also failed to consider whether populations reproduce at different times, which would affect the timing of their migration from the sea to the spawning grounds.

With the aid of genetic analyses, researchers identified 14 genetically distinct salmon populations in the Teno, with the populations in the tributaries showing lower genetic diversity and greater genetic differentiation than those in the main stem of the river [3]. The researchers were then able to assign up migrating salmon to a specific population on the basis of the genetic fingerprint. The first individuals returning upstream were found to come from the more vulnerable tributary populations [4]. These findings were extremely valuable for conservation efforts: as recreational fishing is now banned at the beginning of the salmon migration season and restricted to main stem populations thereafter, the 14 salmon populations of the Teno now have a good chance of surviving over the long term.

Shrinking fish sizes

Harvesting the majority of a fish population has direct numerical and genetic consequences. Over the long term, it can lead to a loss of phenotypic variation in body size, for example, as is the case for numerous commercially exploited fish species. If one compares contemporary trophy photographs with those taken over 100 years ago, it becomes apparent that fish were considerably larger in earlier times. Many of these fish species initially invest their energy in growth, since larger fish have fewer natural predators and a higher likelihood of survival. This means that it is an advantageous strategy to delay the investment of energy in reproduction until a certain body size has been reached. The fishing industry, however, mainly exploits the larger size categories, thus preventing their reproduction. Species that mature early, investing their resources in reproduction rather than growth, will therefore produce more offspring. Both modelling and empirical data indicate that commercially exploited fish species mature at an ever-earlier age. Various studies suggest that this is the result of an evolutionary process, with fish adapting to the selection pressure of fishing. Evolutionary adaptation of this kind cannot be rapidly reversed and will also have economic implications for the fishing industry. When it comes to defining measures for the future management of natural fishery resources, it is essential to take into account the findings of evolutionary research [5].

In many natural waters, stocking measures are used to boost fish populations. But often the juveniles do not derive from local populations. Stocking with non-native fish can lead to the dilution and loss of indigenous genetic diversity. In an Eawag study, for example, Irene Keller and co-workers showed that the genetic diversity of Alpine trout in the drainage systems of the Rhône, Rhine, and Po has declined markedly as a result of intensive stocking with non-native fish in the past [6]. With modern genetic methods, the selection of appropriate broodstock is now relatively simple. But, as shown by studies carried out by Hitoshi Araki and fellow researchers at Eawag, caution is required even in the case of wild fish reared in hatcheries for stocking measures. In the course of their development, hatchery-reared wild trout were found to become morphologically more similar to captive trout [7].

Parasites switching to different hosts

The fact that removal of a large proportion of a population can alter the course of evolution needs to be borne in mind not only in relation to overfishing but also in disease control efforts. Bilharzia – a neglected tropical disease transmitted to humans by contact with infested water – is caused by blood flukes of the genus *Schistosoma.* This group of parasitic flatworms, comprising numerous different species, requires a mammalian definitive host and uses freshwater snails as intermediate hosts. In addition to the three main species which infect humans – *Schistosoma japonicum, S. mansoni* and *S. haematobium* – a number of other species parasitize other mammals. In 2011, over 200 million people were affected by bilharzia worldwide. Efforts to control the disease involve mass drug administration programmes. But these also represent a selection pressure for the parasites. For example, in certain regions of China where mass drug administration has been implemented for several decades, *S. japonicum* now parasitizes new definitive hosts – such as cattle and rodents – as well as humans [8]. This makes it very difficult to eradicate the disease since wildlife represents an almost inexhaustible reservoir for reinfection. In addition, the parasites cannot be readily controlled in animal hosts.

In recent decades, environmental conditions for these parasites have also undergone substantial changes as a result of the construction of dams, new agricultural practices and a warming climate. In Africa, dam construction has created new aquatic habitats which have been colonized by various Schistosoma species. In these regions, too, disease control efforts have been less successful than expected. Researchers have found that, in areas resistant to control measures, the human-parasitic species *S. haematobium* hybridizes with *S. bovis,* which uses exclusively cattle as a definitive host. The hybrid schistosomes can now infect both humans and cattle. In the course of their evolution, Schistosoma species became specialized to different definitive hosts, but in some cases they are closely related to each other. This means that, in the face of strong control pressure, they can easily switch to new hosts or hybridize with other species, leading in either case to widening of the host spectrum. In developing control strategies, it is therefore also important to take into account the evolutionary history of the pathogens concerned.

More flexible environmental management required for complex systems

The intensity and speed of alterations to global ecosystems over the past century have been unprecedented. Accordingly, there have been calls for measures to reverse these changes or at least to mitigate their impacts. What is often forgotten, however, is that an ecosystem is a complex network and that a single change triggers a cascade of reactions throughout the system. Cascade effects and rapid evolution are being documented by increasing numbers of studies on anthropogenic changes. In many cases, it is possible to adapt guidelines in accordance with scientific findings concerning evolutionary processes, as shown by the example of salmon in the Teno. However, the measures adopted do not always produce the desired results and the effects are not always predictable. This poses difficulties for policymakers, as society expects the right decisions to be taken on environmental management. A sustainable strategy for the future would involve an approach to environmental management which is informed by flexibility and a capacity for learning, with policymakers, stakeholders and scientists jointly seeking solutions that leave room for subsequent adjustments.

>>Eawag-Symposium

Kirstin Kopp
Aquatic Ecology department
kirstin.kopp@eawag.ch

[1] Silvestre F., Gillardin V., Dorts J. (2012): Proteomics to assess the role of phenotypic plasticity in aquatic organisms exposed to pollution and global warming. Integr Comp Biol. 52(5), 681–694
[2] Pomati F., Nizzetto L. (2013): Assessing triclosan-induced ecological and trans-generational effects in natural phytoplankton communities: a trait-based field method. Ecotoxicology 22 (5), 779–794
[3] Vähä J.-P., Erkinaro J., Niemelä E., Primmer C. R. (2007): Life-history and habitat features influence the within-river genetic structure of Atlantic salmon. Molecular Ecology 16 (13), 2638–2654
[4] Vähä J.-P., Erkinaro J., Niemelä E., Primmer C. R. (2008): Temporally stable genetic structure and low migration in an Atlantic salmon population complex: implications for conservation and management. Evolutionary Applications 1 (1), 137–154
[5] Ane T Laugen et al. (2012): Evolutionary impact assessment: accounting for evolutionary consequences of fishing in an ecosystem approach to fisheries management. Fish and Fisher ies. doi: 10.1111/faf.12007
[6] Keller I., Schuler J., Bezault E., Seehausen O. (2012): Parallel di vergent adaptation along replicated altitudinal gradients in Alpine trout. BMC Evolutionary Biology 12 (210), doi:10.1186/1471-2148-12-210
[7] Tine Huyse et al. (2009): Bidirectional Introgressive Hybridization between a Cattle and Human Schistosome Species. PLoS Pathogens 5 (9), e1000571
[8] Santamaría L., Méndez P. F. (2012): Evolution in biodiversity policy – current gaps and future needs. Evolutionary Applications 5 (2), 202–218