A genetic perspective on global change

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Heat stress events associated with global climate change may indirectly alter the interactions among marine species, for example among parasites and their fish hosts. At the same time, rapid frequency changes of immune genes, driven by parsite selection, may determine which indiviudals survive, providing an example of "evolution-in-action".

Global environmental change is altering the selection regime for all animal and plant species. The key selective factors are increases in mean temperature and its variability, as well as increase in atmospheric and oceanic CO_2 concentration.

Most studies on the biological effects of global change have thus far focussed on ecology, i.e. the immediate responses or organisms and communities to above changes. Aside from the analysis of the resulting range expansions due to shifting climate zones, there is a growing interest in the genetic basis of critical traits that would allow genotypes or populations to either persist or even evolve under climate change. As one major effect hitting coastal systems, prolonged periods of heat waves impose increasing stress on organisms in these ecosystems, already now leading to severe damage, for example in coral reefs or seagrass based systems. Heat stress may directly interfere with basic physiological processes at the individual level (Pörtner and Knust, 2007), or alter the equilibrium in other 'natural' biotic interactions.

Host-parasite interactions are one of the most important biological interactions, given that all free-living organisms are exposed to multiple parasite species. Hence, one focus of our research is the role of immune defence genes in fish hosts under global warming. We ask whether the fish hosts or the parasites will benefit from global warming. One first goal is to predict the survival of coastal fish as a function of their genotype at those genes that are responsible for recognition and defence against macroparasites such as trematodes, cestodes, protozoans and other metazoan parasites. Therefore controlled enclosure experiments were conducted in which three-spined sticklebacks (*Gasterosteus aculeatus*) were exposed, as a proof-of-principle, to the natural parasite fauna in a lake (Wegner et al., 2008). All experimental fish were descendants from a wild parental generation that gave rise to a first filial (F1) generation. This was necessary to ensure that all experimental animals were parasite free sibships. Subsequently, all fish were genotyped at genes encoding major histocompatibility complex molecules (MHC class II) prior to exposure. MHC class II genes come in several different variants (alleles) within individuals and populations. Their striking diversity is responsible for recognizing a diverse array of up to 25 parasite species present in the system. Interestingly, the immune defence is best when an individual fish carries between 5 and 6 of those variants. Previous data thus allowed us to formulate a prediction, namely that a strong

Sampling on a sea grass meadow in the Baltic Sea. Photo: T. Reusch, IFM-GEOMAR.

selection event, a heat wave, in combination with the natural parasite pressure in, would led to enhanced survival in those individuals that display an intermediate diversity at MHC genes.

This prediction was confirmed in a large exposure experiment across in a among 200 fish coming from 10 different crossings. Those individuals, corrected for sibship differences, that would have around 6 variants per individual had the highest likelihood of surviving a natural heat wave with water temperatures >25°C (Fig. 1). Moreover, it could be shown that possibly, increased parasite pressure, mediated by physiological stress and enhanced vulnerability of individual fish, was the selective agent.

But not only diversity at specific genes determines which genotypes will survive best. In another suite of experiments, the general standing genetic diversity of a habitat

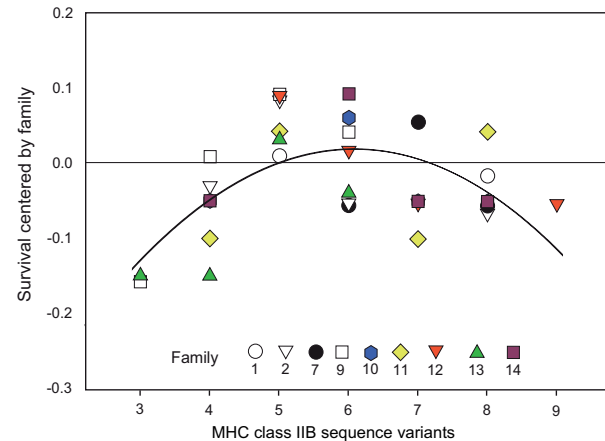*Seagrass Zostera marina. Photo: T. Reusch, IFM-GEOMAR.*

*Fig. 1 . Results of a 14-week exposure experiment of three-spined sticklebacks to their natural parasite fauna during summer heat wave (water temperature >25°C). Survival of three-spined stickebacks as a function of the individual MHC gene variants they carry. The y-axis depicts the residual mortality rate that is corrected for the differences among sibships. The quadratic polynomial (survival = - 0.5595 + 0.1899 * $N_{sequence\ variants}$ – 0.0156 * $N_{sequence\ variants}^2$, $R^2 = 0.364$, $F_{2,30} = 8.601$, $P = 0.001$) shows that within segregating families fish with approximately six MHC class IIB sequence variants survived best. Source: Wegner et al., 2008.*

forming plant, the seagrass *Zostera marina* was manipulated by combining previously genotyped clones using a genetic fingerprint technique. Using scuba diving, experiental patches composed of one, three and six different genotypes were assembled in situ. Following these patches through the 2003-European heat wave revealed that units composed of multiple seagrass genotypes recovered faster than genetic monocultures. Next, we wanted to verify this in mesocosm experiments that involved control temperature conditions and a parallel heat stress treatment simulating the 2003-European heat wave. The results confirmed that the heat wave was responsible for increased mortality under a global warming scenario, and that genotype diversity enhances the resilience of seagrass populations (Ehlers et al., 2008).

In summary, these data provide a glimpse into the complex evolutionary processes that have been triggered by global environmental change. Such studies should complement ecological assessments of the biological effects (Reusch and Wood, 2007). Given that genomic tools are expanding exponentially, rapid progress in the identification of responsible genes for surviving or evolving global change can be expected. One family of these genes, the so-called heat-shock genes are currently being analyzed in mesocosm experiments in coastal fish and the habitat forming seagrass, in order to develop a predictive framework to assess which populations are most vulnerable to global warming.

Argulus spec, a member of a species rich family of crustaceans that are entirely parasitic and live attached to fish, sucking their blood. Photo: M. Kalbe.

References

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