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Genes and environment — Striking the fine balance between sophisticated biomonitoring and true functional environmental genomics

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ABSTRACT

This article provides an overview how the application of the gene profiling (mainly via microarray technology) can be used in different organisms to address issues of environmental importance. Only recently, environmental sciences, including ecotoxicology, and molecular biology have started to mutually fertilize each other. This conceptual blend has enabled the identification of the interaction between molecular events and whole animal and population responses. Likewise, striking the fine balance between biomonitoring and functional environmental genomics will allow legislative and administrative measures to be based on a more robust platform. The application of DNA microarrays to ecotoxicogenomics links ecotoxicological effects of exposure with expression profiles of several thousand genes. The gene expression profiles are altered during toxicity, as either a direct or indirect result of toxicant exposure and the comparison of numerous specific expression profiles facilitates the differentiation between intoxication and true responses to environmental stressors. Furthermore, the application of microarrays provides the means to identify complex pathways and strategies that an exposed organism applies in response to environmental stressors. This review will present evidence that the widespread phenomenon of hormesis has a genetic basis that goes beyond an adaptive response. Some more practical advantages emerge: the toxicological assessment of complex mixtures, such as effluents or sediments, as well as drugs seems feasible, especially when classical ecotoxicological tests have failed. The review of available information demonstrates the advantages of microarray application to environmental issues spanning from bacteria, over algae and spermatophytes, to invertebrates (nematode *Caenorhabditis elegans*, crustacea *Daphnia* spp., earthworms), and various fish species. Microarrays have also highlighted why populations of a given species respond differently to similar contaminations. Furthermore, this review points at inherent limits of microarrays which may not yet have been properly addressed, namely epigenetics, which may explain heritable variation observed in natural population that cannot be explained by differences in the DNA sequence. Finally, the review will address promising future molecular biological developments which may supersede the microarray technique.

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1. Introduction

The '-omics' trend has found its way into environmental sciences which has resulted in a reciprocal fertilization of two highly contrasting disciplines. The disparities derive not only from the intrinsic differences in scale, but also from their paradigmatic backgrounds and practical approaches. On the one hand, the machinery and conceptional approaches of molecular biology become, when merged with ecotoxicology, visible at the individual, community or even population level. One the other hand, the interactions of organisms with their environment can be traced to the molecular level. This paper examines how the application of molecular biological tools, such as microarrays, can be used to study issues of environmental importance, with a strong focus on non-human organisms exposed to chemical stressors. This approach is of critical importance to identify major and minor pathways of toxic action and decipher what drives the interaction between environment and the organism (and vice versa). By doing so, the molecular biological approach will undoubtedly provide a robust platform for legislative and administrative purposes.

Environmentalists traditionally deal with the protection and casual restoration of landscapes, rivers, lakes, and the sea. One may ask if it is necessary to understand the molecular basis of, for instance, an endocrine disrupting chemical, if the adverse effect in the impacted population has already been established. It appears self-evident that these chemicals do not belong in the environment and, *per se*, should be abolished in the first place. Although this so called 'precautionary principle' builds on an ethic, convivialistic rather than a scientific base, several environmental regulations incorporate it. Furthermore, the traditional ecotoxicological approach is more chemical compound, rather than mechanisms orientated and considers organisms in their environment as somewhat sophisticated monitors of chemical burdens and effects. It may be trivial, but it is certainly worth mentioning: The presence of natural endogenic and exogenic chemical stressors have been instrumental for, and in fact have driven, the development of stress defense systems, such as the antioxidant or biotransformation systems, expression of stress proteins or metal-binding proteins. Consequently, anthropogenic chemical stress, though sometimes severe or even lethal, is one of several stressors that impacts on organisms. It therefore may be argued that the use of gene expression experiments in environmental studies is only another fashionable and sophisticated means to identify potentially adverse effect of chemicals in the environment, not unlike a set of highly developed biomarkers.

According to Selye (1936, amended by various authors), a stress response includes three different phases: the bipartite alarm phase, the resistance phase, and the exhaustion phase (Fig. 1). The alarm phase corresponds to modifications of biochemical and genetic parameters in the absence of reduced vital activities and growth. These physiological reactions terminate a primary disturbance and enable restitution. An exposure that is too strong and/or fast will result in acute damage and cell death. The resistance phase is characterized by the activation of defense mechanisms (e.g. antioxidant defense, protein repair, biotransformation) that are concomitant with first signs of reduced vital activity and growth. The exhaustion phase becomes apparent by a collapse of vital cellular functions (e.g. photosynthesis, membrane integrity, reproduction), leading to chronic damage and ultimately death. Especially at the molecular level, the differences between chronic vs. acute effects as well as low- vs. high-concentration exposures are typically neglected. We assume that specific differentially expressed genes can be used to characterize and distinguish between the three phases of stress and possibly the differentiation between natural and anthropogenic stressors (see section 2).

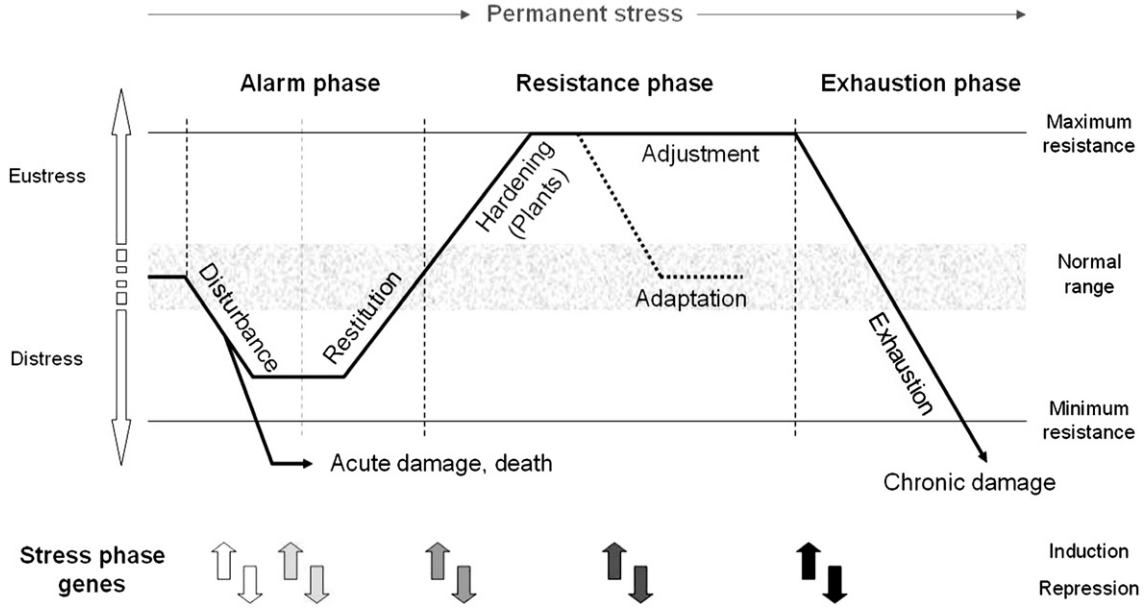

Fig. 1 – Stress phase model based on Selye (1936) and amended by several authors. Shades of grey of arrows represent different genes specifically expressed during the individual stress phases. Note, the gene profiles in the various stress phases are unique, even when exposed to the same stressor at a different intensity (see Section 2).