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Annual and seasonal variability in leaf traits of *Iris variegata* genotypes growing in contrasting light conditions

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Many organisms vary in their plasticity over their lifetime and the induction of plastic traits is sometimes limited to certain developmental windows of an organism's lifetime. In a mesocosm experiment with tadpoles of the agile frog, *Rana dalmatina*, we varied the timing of introduction of caged dragonfly larvae. The tadpoles were photographed in lateral view at weekly intervals, to study growth as well as shape variation assessed by geometric morphometrics. In the presence of predators, tadpoles reduced growth and developed higher tail fins. These effects on growth rates and body shape were stronger in tadpoles first confronted with predators in the second week, than in those exposed to caged predators from the onset of the experiment (a few days after hatching). Our results indicate that there exist windows of predator-induced plasticity in *Rana dalmatina* tadpoles.

Poster session B - POL 300

Evolutionary medicine and intrinsically vulnerable facultative adaptations (52044)

Randolph Nesse.

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A major focus for evolutionary medicine has been how natural selection shapes mechanisms that regulate facultative responses, especially defensive responses such as vomiting or the fight-flight response. A signal detection analysis reveals that optimal systems give rise to many false alarms, a phenomenon described as the Smoke Detector Principle. However, some systems enter runaway positive feedback loops, such as in panic disorder. This presentation offers mathematical models describing the characteristics of systems that are intrinsically vulnerable because their thresholds adjust adaptively to increased sensitivity on repeated arousal. This phenomenon is likely to provide explanations for vulnerability to anxiety disorders and chronic pain. The tradeoffs involved are likely to constrain selection for mechanisms that adjust thresholds or response intensity as a function of experience in a particular environment.

Poster session B - POL 300

Annual and seasonal variability in leaf traits of *Iris variegata* genotypes growing in contrasting light conditions (52088)

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During their evolution plants developed a set of mechanisms to adapt to the varying environmental conditions, resulting in diversified phenotypes. We were interested in the response of plants towards changing environmental parameters, to light in particular. For this study we selected genotypes of *Iris variegata* that experienced different light

conditions in their habitats: a) genotypes situated along the top and slope of a dune, where it coexisted with annual and perennial herbs and low shrubs; b) genotypes inhabited the woodland understories.

We grew *I. variegata* genotypes in two experimental light treatments (high and low) and tested differences between spring, summer and autumn as well as between two successive years. The plants responses were analysed at different levels of biological information and it was revealed that dissimilar light conditions markedly affected all aspects of plant anatomy and physiology. Repeated measures model ANOVA detected a significant effect of year, habitat and genotype in most analysed traits. Models of changes during growing seasons were treatment- and year-specific.

We also present results from an on-going study which aims to assess occurrence patterns of phenotypic plasticity based on system-level analysis of the same samples that includes metabolic profiling approach combined with robust statistical analysis.

Poster session B - POL 300

Evolutionary and ecological patterns of global DNA cytosine methylation in angiosperm plants (51693)

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DNA cytosine methylation is an ubiquitous epigenetic mechanism involved in many important functions, including regulation of gene expression and maintenance of genomic integrity. In plants, intraspecific variation in cytosine methylation has been related to genetic and ecological factors. Genome-wide cytosine methylation is also known to vary substantially between the few species that have been thoroughly studied, but little is known on interspecific patterns, or the degree to which differences between species in methylation levels are related to evolutionary history, ecological settings and/or biogeography. DNA methylation has been implicated in plant macroevolution through effects on speciation and appearance of evolutionary novelty, although these suggestions still lack compelling empirical support. We will contribute to fill this gap by analyzing global DNA cytosine methylation levels obtained by HPLC in a large sample of phylogenetically diverse angiosperms (ca. 100 families) from a broad range of habitat types on two continents. The following three questions will be addressed: (i) is interspecific variation in DNA methylation levels phylogenetically structured?; (ii) are there discernible regional or ecological patterns in genome methylation levels?; and (iii) what are the relative importances of phylogeny, ecology and biogeography in determining plant community-wide levels of cytosine methylation?

Poster session B - POL 300