

## Publication

Abiotic and past climatic conditions drive protein abundance variation among natural populations of the caddisfly *Crunoecia irrorata***JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 4604336**Author(s)** Ebner, Joshua Niklas; Ritz, Danilo; von Fumetti, Stefanie**Author(s) at UniBasel** [von Fumetti, Stefanie](#) ; [Ritz, Danilo](#) ; [Ebner, Joshua Niklas](#) ;**Year** 2020**Title** Abiotic and past climatic conditions drive protein abundance variation among natural populations of the caddisfly *Crunoecia irrorata***Journal** Scientific Reports**Volume** 10**Number** 1**Pages / Article-Number** 15538

Deducing impacts of environmental change on species and the populations they form in nature is an important goal in contemporary ecology. Achieving this goal is hampered by our limited understanding of the influence of naturally occurring environmental variation on the molecular systems of ecologically relevant species, as the pathways underlying fitness-affecting plastic responses have primarily been studied in model organisms and under controlled laboratory conditions. Here, to test the hypothesis that proteome variation systematically relates to variation in abiotic conditions, we establish such relationships by profiling the proteomes of 24 natural populations of the spring-dwelling caddisfly *Crunoecia irrorata*. We identified protein networks whose abundances correlated with environmental (abiotic) gradients such as in situ pH, oxygen- and nitrate concentrations but also climatic data such as past thermal minima and temperature seasonality. Our analyses suggest that variations in abiotic conditions induce discrete proteome responses such as the differential abundance of proteins associated with cytoskeletal function, heat-shock proteins and proteins related to post-translational modification. Identifying these drivers of proteome divergence characterizes molecular "noise", and positions it as a background against which molecular signatures of species' adaptive responses to stressful conditions can be identified.

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