Modelling metabolism to test alternative hypotheses on intraspecific life-history variation

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Physiology is the integrator through which genes and environmental conditions produce an individual's phenotype and life history traits. Physiological processes are however rarely explicit in evolutionary and species distribution models. These models rather rely on empirical functions linking environmental conditions to life history traits. Such functions might not hold under a larger range of conditions and are often unable to predict potential non-linear responses to environmental changes. Extrapolating organisms' responses beyond current conditions is however crucial to conservation and management. Mechanistic theories linking physiology and life-history traits have been around for decades but mostly focussed on interspecific variation. We here propose to apply these approaches to the study of intraspecific variation in a species with striking discrete variation in life-history strategies, the Atlantic salmon *Salmo salar*. Using a model based on the Dynamic Energy Budget theory, we predicted growth, maturation and seaward migration decision in salmon parrs (pre-migratory freshwater stage) as a function of environmental parameters (food availability and temperature) in a small coastal river (Scorff, Brittany). We also compared the effects of early-environment to permanent individual differences of genetic or epigenetic origin in driving individual life history strategies. Although parameters estimation used data from other populations and strains, the model accurately predicted traits values and within-year relationships between traits in this population. Between-years dynamics were however inconsistent with observations in the Scorff river. We will discuss explanations for this discrepancy and perspectives for testing them within this framework. Other potential applications will also be presented with examples in salmonids.

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