Evaluation of the thermal time hypothesis in insects: a molecular approach to explain the evolution of temperature responses

Ectothermic animals depend on external heat sources to maintain their body temperature, which therefore follows more or less the ambient temperature. As a consequence, all biochemical processes in an ectotherm's body are speeded up by high temperature and retarded by low temperature. The non-diapause temperature response of insects is usually described by two parameters, the lower threshold temperature and thermal constant. The latter parameter measures the steepness of the response to temperature and determines the rapidity of thermal time relative to physical time.

In insects, there is a large degree of inter-species and intra-species variation in the thermal constant. When different species are compared there is also a very strong negative (hyperbolic) relationship between the thermal constant and the threshold temperature. Many authors have noted these patterns and have provided ultimate (evolutionary) explanations, usually related to the timing of the life history in a seasonal environment. A mechanistic (proximate) explanation has not been given, however.

In this study we want to test a novel hypothesis, which holds that the energy equivalent of a temperature change is not only used to fuel the kinetic energy of physiological reactants, but also to induce energy-requiring conformational changes in the cell. It is further assumed that different genotypes of an animal partition the energetic equivalent of a temperature change in different ways over conformational change and kinetic energy. In this study we want to test this hypothesis by performing experimental selection studies using the springtail model species *Orchesella cincta*.

Strong directional selection for a low thermal constant is expected to increase the threshold temperature and at the same time to increase the allocation to energy-requiring conformational change. Genes differentially expressed at different temperatures by two different selection lines will be analyzed to develop a molecular explanation for the difference in partitioning behaviour. Given the universal nature of the thermal time hypothesis, this model has a very wide applicability.

**Duration:**

Three years (September 2002-September 2005)

**Participants:**

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