Supplementary Information for :

**Predicting predator search rates from metabolic rates: a bottom-up modelling approach.**

Flavio Affinito1, Miguel Matias2, Samraat Pawar1 and Rebecca L. Kordas1

*1. Department of Life Sciences, Imperial College London, Silwood Park Buckhurst Road, SL5 7PY, Ascot UK*

*2. Museo Nacional de Ciencias Naturales (CSIC), Madrid, 28006, Spain*

**Corresponding author.** *E-mail: flavio.affinito@gmail.com*

LENGTH-WEIGHT REGRESSION

Between 50 and 100 individuals of all three tax “types”, *Odonata*, *Ephemeroptera* and *Chironomidae*, were used in each length-weight regression experiments. Each individual was measured under the microscope and placed in an individual foil cup. All cups were labelled and left in an oven at 80°C for 16 to 18 hours. Dry-weight measurements were then done for each individual in turn. The obtained length and biomass measurements were then fitted to two different linear models, one with dry-weight logged and not the other. The best-fit model (highest *R2*) was kept. Only *Odonata* and *Ephemeroptera* linear models yielded satisfactory fit (*R2* > 0.6) and were thus kept. The length-weight regression for *Chironomidae* was taken from (Benke *et al.*, 1999). The equations for *Odonata* and *Ephemeroptera* and corresponding *R2* values can be found in table S2.

RESPIROMETRY PROTOCOL

All individuals selected for respirometry experiments were initially stored in filtered pond water kept at ambient temperature. These were then placed in a water bath, previously heated at the experimental temperature, for 15min to allow them an acclimation time from their ambient temperature storage to the new temperature. After acclimation, individuals were placed in glass chambers, filled with fully oxygenated filtered pond water, of 4, 2 or 0.75 ml depending on the size of the organism. These chambers were then placed in the respirometry apparatus inside the water bath. A total of eight chambers were used per experimental trial, one control -empty- chamber and seven treatment -organism- chambers. A Unisense O2 optical measuring probe was used to measure oxygen consumption over time in the chambers, three readings were recorded for each chamber in order to measure the slope of O2 consumption. This value was corrected for individual chamber volumes and the value of the control was subtracted from the treatment slopes to account for any respiration occurring in the chambers due to microorganisms. This slope value was then used as the value for oxygen consumption of the organism at the corresponding experimental temperature in all subsequent analysis.

RESPIRATION MODEL CHOICE

A simplified version ignoring low temperature inactivation of the mechanistic model for respiration designed by Sharpe & Schoolfield (Schoolfield *et al.*, 1981) was used to fit the respirometry data. Three variants of this model were tested for each species at each site. The model is as follows:

Where *B* is oxygen consumption rate, *B0* is the normalisation constant at 15*°C*, *Ea* is the enzyme’s activation energy, *Ed* is its deactivation energy, *k* is Boltzmann’s constant, *T* is temperature and *Tpk* is the temperature at which *B* is maximised.

The normalisation constant scales with mass as follows:

Where *m* is mass, *β* is the scaling exponent and *b0* is the normalisation constant of the Arrhenius model.

Thus, three Sharpe-Sharpe-Schoolfield models were run with different scalings for *b0*. One model where mass scaling was ignored (*B0* = *b0*), one where *B0* scaled with mass according to the metabolic theory of ecology (*β* = 0.75, (Brown et al., 2004)) and one where mass scaling was left free and β was estimated from the data along with all other parameters of the model. For each species at each site, 10,000 models of each type were run, the best fit model was selected based on the overall mean fit (*R2*), AIC and BIC values of all runs (Table S3).