Forum

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The mechanistic basis of the metabolic theory of ecology

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We welcome the opportunity to respond to O'Connor et al. (2007). We hope that this exchange will help to clarify some of the strengths and weaknesses of the Metabolic theory of ecology (MTE), and will point towards fruitful areas for future research.

The MTE has been formulated based on the premise that the structure and dynamics of ecological communities are inextricably linked to individual metabolism. The individual metabolic rate is the rate at which an organism takes up energetic and material resources from the environment, transforms them into useable forms, and allocates them to the fitness-enhancing processes of survival, growth, and reproduction. Interactions between organisms and their environment (including other organisms) are therefore constrained by metabolic rate. Physiologists have long known that there are three primary factors that control metabolic rate: body size, body temperature, and resource availability. MTE builds on this earlier work by providing a quantitative framework to better understand how these three variables combine to affect metabolic rate, and how metabolic rate, in turn, influences the ecology and evolution of populations, communities, and ecosystems (Brown et al. 2004).

Gillooly et al. (2001) developed a model for the scaling of metabolic rate that combines the effects of body size and temperature (West et al. 1997, Gillooly et al. 2002, Charnov and Gillooly 2003, Brown et al. 2004). The model leads to a single equation for individual metabolic rate:

$$B = b_o M^{3/4} e^{-E/kT} \quad (1)$$

where b_o is a normalization constant, M is body mass, and T is absolute temperature in degrees Kelvin. The size-dependence, $M^{3/4}$, is attributed to geometric constraints on the delivery of energy and materials to cells through biological distribution networks (West et al. 1997). The Boltzmann-Arrhenius term, $e^{-E/kT}$, characterizes the exponential effect of temperature, where E is the average activation energy of the respiratory complex ($\sim$0.65 eV), and k is Boltzmann's constant (8.62×10^{-5} eV K^{-1}) (Gillooly et al. 2006). This simple analytical expression yields quantitative predictions on metabolic rate that are supported by empirical data for a broad assortment of taxonomic groups (Gillooly et al. 2001).

Points of contention

O'Connor et al. (2007) raise issues with the MTE that deserve attention and/or clarification. These issues can be divided into two major points of contention: (1) they argue that the proposed mechanisms underlying the size- and temperature-dependencies of individual metabolic rate in Eq. 1 are invalid; and (2) that attempts to link individual metabolic rate to higher levels of biological organization (populations, communities, ecosystems) using MTE are overly simplistic and should therefore be abandoned. Here we respond to these criticisms, and then conclude by discussing the philosophical issues that underlie them.

1. Individual-level mechanisms

Is the derivation of the body-size term in Eq. 1 mechanistic?

O'Connor et al. (2007) take issue with the West et al. (1997) (WBE) network model as a mechanistic

explanation for the 3/4-power scaling of metabolic rate. Yet, according to their criteria, the WBE model is indeed mechanistic because: (1) it invokes a few simplifying assumptions (discussed below) that allow causal linkages to be made; (2) it yields quantitative predictions (including the size-dependence for metabolic rate in Eq. 1) by explicitly linking organism structure to function based on these assumptions; and (3) it can be extended (below) to predict how deviations from assumptions affect model predictions.

In addition to the WBE model for animal metabolism (West et al. 1997), West et al. (1999a, 1999b) proposed two other models for plant and unicellular metabolism. These three models represent particular manifestations of the same general principles. The principles entail simultaneously maximizing the numbers of metabolic units where metabolism occurs (e.g. respiratory complexes), while minimizing the transport distances to those metabolic units (West et al. 1999a). Since these more general principles are geometric, they do not invoke specific dynamical mechanisms. They do, however, assume that natural selection will lead to evolutionary optimization of network geometry subject to physical, evolutionary, and physiological constraints. Given this evolutionary-optimization assumption, quarter-power scaling of metabolic rate is predicted to apply at multiple levels of biological organization, from respiratory complexes and mitochondria, to unicells and multicellular eukaryotes, in agreement with empirical data (West et al. 2002).

O'Connor et al. (2007) do not agree with the general hypothesis that natural selection results in the optimization of network geometry in organisms. For example, they argue that the fraction of metabolic energy allocated to cardiac work in a mammal is too small to affect individual fitness (8% at rest according to their calculations). However, this 8% value, even if it is close to a minimum, represents a substantial fraction of an organism's total energy budget. Given that positive selection coefficients, s (Kimura 1983), measured in the wild are often $<10^{-3}$ (Rockman et al. 2005), decreasing the energetic costs of transport by even 1% could significantly improve fitness if this additional energy could be allocated to the production of progeny. Thus, the minimization of transport costs is a tenable criterion for evolutionary optimization, although it is clearly not the only factor upon which selection operates.

Is there empirical evidence to support the WBE model assumptions and predictions?

Considerable evidence has been presented in support of model predictions with respect to both the structure and function of organisms. First, with respect to function, there is broad support for the predicted 3/4-power scaling of individual metabolic rate for unicells, plants, and a variety of animal taxa (Niklas and Enquist 2001, Savage et al. 2004a, Farrell-Gray and Gotelli 2005). There is also support for the prediction that the metabolic rates of cells in vivo should scale as the $-1/4$ of body size, whereas the metabolic rates of cells grown in vitro should be about the same, irrespective of the size of the organism from which the cells originated. In other words, the metabolic rate of cells from a mouse and a horse should not scale with body size when they are placed in culture and freed from the constraints of the network. This prediction is supported by empirical data compiled by proponents of MTE (West et al. 2002) and others (Brown et al. in press).

Moreover, there is also considerable support for network model predictions regarding the structure of organisms related to metabolism. First, for example, it has been shown that the densities of metabolic organelles at the whole-organism level, such as ribosomes and mitochondria show the predicted ¼ scaling (Gillooly et al. 2005). Second, for plants, it has been shown that xylem conduits taper from the roots to the leaves in order to minimize the cost of water transport (Anfodillo et al. 2006). Note that an observation such as this cannot be explained by the other, more restrictive hypotheses for the scaling of metabolic rate listed in Table 1 of O'Connor et al. (2007).

That said, this is a work in progress and much remains to be done to further test both assumptions and predictions of the MTE. Not all data are supportive of model predictions, and deviations from predictions are important to understand. For example, statistically significant deviations from 3/4-power scaling of metabolic rate have been observed for some datasets, including some analyzed by Gillooly et al. (2001). These deviations are often partially attributable to statistical issues (Farrell-Gray and Gotelli 2005). As such, when results of multiple studies are summarized, the scaling exponents are often centered around $\frac{3}{4}$, indicating that Eq. 1 is predicting the central tendency (Savage et al. 2004). However, biological mechanisms may also lead to deviations from 3/4-power scaling. In some cases, these deviations have been predicted by MTE in multicellular plants (West et al. 1999b, Enquist et al. 2007) and animals (West et al. 1997). For example, with respect to mammals, Gillooly and Allen (2007) recently showed that the steeper size-dependence of maximum metabolic rate is attributable to greater increases in muscle temperature for large mammals (e.g. $>6^{\circ}$C for a horse) than for small mammals (e.g. $<1^{\circ}$C for a rat) during exercise. In other cases, deviations from $\frac{3}{4}$ power scaling are expected, but have not yet been integrated into the theory. For example, most of the variation from 3/4-power scaling of metabolic rate in deep-sea squid can be

explained by differences in body-water content (B. A. Siebel, pers. comm.).

Is the derivation of the temperature term in Eq. 1 mechanistic?

O'Connor et al. (2007) take issue with our use of the Boltzmann–Arrhenius term on the grounds that it fails to capture all of the complexities of intermediary metabolism. They claim, for example, that organisms can completely compensate for differences in environmental temperature by acclimation, and that MTE does not account for such evolutionary adaptations.

The Boltzmann–Arrhenius term is based firmly in statistical thermodynamics (Gillooly et al. 2006). It incorporates both the general theory of chemical reaction kinetics (Boltzmann 1870), and the empirically determined activation energies of respiratory reactions, which have been known since at least the time of Crozier (1924). Contrary to the claims of O'Connor et al. (2007), the Boltzmann–Arrhenius relationship is not fundamentally different than the "exponential" relationship or the Q10 relationship (i.e. the fractional increase in rate per 10°C increase in temperature). The latter expression is by definition an approximation of the Boltzmann–Arrhenius relationship, which characterizes the exponential the effects of temperature on biochemical reaction rates.

For heterotrophic organisms, the model of Gillooly et al. (2001) predicts that the temperature dependence of metabolic rate reflects the temperature dependence of respiration for individual mitochondria, as has since been shown (Gillooly et al. 2006). The average activation energy of respiration is predicted to fall between 0.6 and 0.7 eV (and not 0.2–1.2 eV, as sometimes suggested). For plants, this same temperature dependence is expected to hold over the short term (Allen et al. 2005), as shown by Gillooly et al. (2001). However, over the long term, the temperature dependence of plant respiration is predicted to be weaker. This is because plant respiration is ultimately controlled by photosynthesis (Dewar et al. 1999), and the "effective" activation energy of C_3 photosynthesis is lower ($\sim$0.32 eV, Allen et al. 2005) because carbon fixation by Rubisco becomes increasingly inefficient at higher temperatures due to photorespiration (Farquhar et al. 1980).

The temperature dependence for heterotrophic respiration predicted by Eq. 1 is consistent with the classic work of Krogh (1916), among others, and is supported by a large body of literature showing that Q10 values for respiration often fall between 2.2–2.6 over the biologically relevant temperature range of 0 to 40°C. Recent work by others has confirmed the predicted temperature dependence of Eq. 1 for diverse taxa of insects (Frazier et al. 2006) and marine larvae (O'Connor, M. I et al. 2007). These studies are consistent with the findings of Addo-Bediako et al. (2002), which demonstrate that acclimation accounts for only a minor fraction ($<4\%$) of the variation in metabolic rate for a global compilation of insect data (Gillooly et al. 2006). Thus, a large and growing body of work speaks to the commonality of the temperature response rather than the ability of individual species to overcome the physical constraints of temperature.

Is the normalization constant, b_o, predicted in Eq. 1?

We cannot yet predict the normalization constants, but we have made it clear that variation among taxonomic groups in these constants reflects important phylogenetic, physiological, and ecological factors (Brown et al. 2004). We agree with the statement of O'Connor et al. (2007) that "variation in normalization constants suggests that factors unrelated to allometric constraints can affect a taxon's mass, metabolic rate, or both." We have shown, for example, that the normalization constant for zooplankton growth is correlated with the whole-body phosphorus concentration (Gillooly et al. 2002).

2. Linking individual metabolism to ecology and evolution

O'Connor et al. (2007) argue that attempts to link metabolism to the structure and function of higher levels of biological organization are not useful or valid, that MTE only describes "pre-existing patterns", and that these patterns are dissociated from underlying mechanisms. These claims are false, and reflect a poor understanding of MTE.

The vast majority of MTE studies have been motivated by new questions that have resulted in the generation of new hypotheses, models, and empirical relationships. To name just a few examples, recent MTE studies have directly linked individual metabolic rate, and thus body size and temperature, to rates of molecular evolution in genomes (Gillooly et al. 2005b, Allen et al. 2006), the amounts of RNA and phosphorus maintained in individuals (Gillooly et al. 2005a), the dynamics of growth in populations (Savage et al. 2004b), and the cycling of nutrients in ecosystems (Allen et al. 2005). In each of these studies, new, patterns were described, and directly linked to individual metabolic rate. For example, in the RNA study, the slope and intercept of the relationship between the concentration of phosphorus-rich ribosomes and body size was predicted for a broad assortment of organisms

based on the biochemical kinetics of ATP synthesis and protein synthesis (Gillooly et al. 2005a). Understanding this relationship is important for quantifying the dynamics of phosphorus cycling in ecosystems.

Concluding remarks

It is important to recognize that many of the criticisms of MTE by O'Connor et al. (2007) are not based on data, but on deep-seated philosophical beliefs. O'Connor et al. (2007) repeatedly describe the predictions and assumptions of MTE as "highly unlikely", "improbable", etc. based on their belief that metabolism at the individual level, and ecology at higher levels, are too inherently complex to be modeled without a "plethora of assumptions". In doing so, they look past a large body of data in support of MTE that tells a very different story. For example, O'Connor et al. (2007) argue that the Boltzmann–Arrhenius relationship in Eq. 1 cannot possibly describe variation in natural systems because of the complexities of intermediary metabolism. MTE studies have shown, however, that the temperature dependence of respiration is essentially identical (i.e. $E \approx 0.65$ eV in Eq. 1) for isolated mitochondria (Gillooly et al. 2006), individual organisms (Gillooly et al. 2006), soil microbial communities (Allen et al. 2005), and entire ecosystems (Enquist et al. 2003). These studies derive predictions at different levels of biological organization using very few simplifying assumptions.

More generally, O'Connor et al. (2007) seem to operate under the belief that unifying principles do not exist in biology, and that all species are unique. In particular, they argue that the optimization of physiological traits is "difficult, if not impossible" in natural environments, that symmorphosis is rare or nonexistent, and thus that all aspects of natural selection are inherently idiosyncratic and therefore unpredictable. This perspective leaves little or no room for the development of general predictive theories. It suggests that, at best, ecologists can only hope to provide retrospective descriptions of natural phenomena in the face of dramatic environmental change.

The approach taken in developing the MTE stands in stark contrast to this perspective. We believe that ecology is well-served by the development of general, quantitative theories that yield testable predictions, including how organisms will respond to environmental change. MTE is formulated based on the premise that organisms spanning the diversity of life share many common attributes, particularly with respect to metabolism. It assumes that there are general principles governing the process of evolution, and that these are inextricably linked to individual energetics. Indeed, a rich body of literature has shown that MTE is consistent with life history theory and the evolutionary principles underlying it (Charnov 1993). So, MTE does not reject the principles of symmorphosis and evolutionary optimization, but rather embraces them. In fact, the ubiquity of ¼-power scaling in organisms, from rates of neural firing to rates of red-blood-cell turnover and biomass production, provides perhaps the best evidence for symmorphosis.

Still, we recognize our efforts to uncover and explain general relationships in biology must be tempered by the acknowledgment that biological systems are inherently complex. Consequently, general theories such as MTE will never be capable of explaining all of the variation in biological phenomena, as exemplified by Fig. 1 of O'Connor et al. (2007). This was never the intention of MTE. And again, we recognize that much remains to be done in developing the MTE. In particular, further tests are needed of the assumptions and predictions of the West et al. models for plants, animals, and especially unicells. This may help to further integrate proximate and ultimate mechanisms of allometric scaling. Nevertheless, MTE has succeeded in explaining a wide range of natural phenomena at various levels of biological organization. As we move forward, MTE holds promise for not only linking species to ecosystems and genes to phenotypes, but ultimately, for linking ecology to evolution.

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