Body Temperature, Rate of Biosynthesis, and Evolution of Genome Size

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An optimality model relating the rate of biosynthesis to body temperature and gene duplication is presented to account for several observed patterns of genome size variation. The model predicts (1) that poikilotherms living in a warm climate should have a smaller genome than poikilotherms living in a cold climate, (2) that homeotherms should have a small genome as well as a small variation in genome size relative to their poikilothermic ancestors, (3) that cold geological periods should favor the evolution of poikilotherms with a large genome and that warm geological periods should do the opposite, and (4) that poikilotherms with a small genome should be more sensitive to changes in temperature than poikilotherms with a large genome. The model also offers two explanations for the empirically documented trend that organisms with a large cell volume have larger genomes than those with a small cell volume. Relevant empirical evidence is summarized to support these predictions.

Introduction

Genome size varies greatly among living organisms. From *Saccharomyces* to *Amoeba,* the range of genome size is 80,000 fold (Cavalier-Smith 1985*a*). It is not clear why a unicellular organism such as *Amoeba dubia* should have almost 200 times as much DNA as a human being. Although genome size is correlated with the number of genes in viruses and bacteria, such a correlation does not exist in eukaryotes (Cavalier-Smith 1985*a;* Li and Graur 1991). The inability of science to explain the great variation in genome size among different organisms in terms of known functions has been known as the C value paradox (Thomas 1971).

A related puzzle is the variation in genome size within taxonomic groups. The range of genome size in amphibians is 91 fold, whereas the range of genome size is only two- to fourfold within mammals or birds (Cavalier-Smith 1985*a*). This dramatic contrast indicates that body temperature might be involved in the evolution of genome size because the body temperature of amphibians varies greatly in their distributional range whereas the body temperature of birds and mammals is relatively constant. However, no plausible mechanism has been proposed to relate body temperature to genome size, and it is not immediately obvious why the two should be related at all.

Here I present an optimality model relating the rate of biosynthesis to body temperature and gene duplication, the latter being one of the major factors contributing to genome size variation. The model is the first attempt to explain genome size variation in terms of biochemical processes. It leads to a number of predictions that are consistent with observed patterns of genome size variation.

The Rate of Biosynthesis

There is selection pressure for a unicellular organism to replicate itself faster than others and for a multicellular organism to grow faster than others. The replication in unicellular organisms and the growth in multicellular organisms are similar in that both processes involve the accumulation of structural materials through biosynthesis and the division of the accumulated materials into more cells. Here I assume that the time spent in a complete cell cycle (T_c) consists of a period of biosynthesis (T_s) and a period spent in cell division (T_d), so that $T_c = T_s + T_d$. Clearly, there is an evolutionary advantage for an organism to minimize T_c or to minimize one of its two components.

I will focus on the minimization of T_s only. I assume that T_s is made of a period of protein synthesis (T_p), followed by a period of DNA duplication (T_{DNA}), that is,

$$T_s = T_p + T_{DNA}. \quad (1)$$

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Let P be the amount of protein needed for a new cell and r_{ps} be the rate of protein synthesis. Now

$$T_p = \frac{P}{r_{ps}}. \tag{2}$$

Let T_g be the time spent in synthesizing DNA for a single gene during DNA duplication prior to cell division and let N_g be the number of genes in the genome. Now $T_{DNA} = T_g \times N_g$. Letting N_u be the number of unique genes in the genome and N_c be the average number of copies per gene, we have $N_g = N_u \times N_c$ and

$$T_{DNA} = T_g N_u N_c. \tag{3}$$

The supposition above that T_{DNA} should increase with N_g is empirically justified. The DNA with many gene duplications takes longer time to replicate than the DNA with no gene duplication (Hinegardner 1976; Cavalier-Smith 1985*a*). Populations of plasmids often lose their recombinant foreign DNA because those that have done so enjoy an advantage in replication (Watson et al. 1983). Similarly, yeasts containing plasmids grow slower than yeasts without plasmids (Futcher and Cox 1983; Mead et al. 1986; Futcher et al. 1988).

Substitute T_p and T_{DNA} into equation (1), and we have

$$T_s = \frac{P}{r_{ps}} + T_g N_u N_c. \tag{4}$$

Note that the inverse of T_s is a measure of the rate of biosynthesis. Maximizing the rate of biosynthesis is equivalent to minimizing T_s. Equation (4) therefore relates the rate of biosynthesis to r_{ps} and N_c. Below I examine r_{ps} further to introduce the effect of body temperature on T_s.

The Rate of Protein Synthesis: r_{ps}

Protein synthesis depends on the availability of ribosomes, mRNA, tRNA, amino acids, and many other biochemical factors. Here I will focus on the effect of mRNA concentration and body temperature on the rate of protein synthesis. I will assume that enough tRNAs are present in the cell for protein synthesis (i.e., they are not limiting). The process being modeled is one with protein being continuously synthesized and accumulated, not one with protein synthesis being balanced by protein degradation.

Let $r_{m\text{-}r}$ be the rate of mRNA encountering ribosomes and forming mRNA-ribosome complexes and be measured by the number of mRNA-ribosome complexes formed per unit time. Let T_{tln} be the time spent during the actual translation of a protein molecule after the formation of an mRNA-ribosome complex. To synthesize N protein molecules, the total time required is then

$$T_N = \frac{N}{r_{m\text{-}r}} + NT_{tln}, \tag{5}$$

which leads to the rate of protein synthesis (r_{ps}):

$$r_{ps} = \frac{N}{T_N} = \frac{r_{m\text{-}r}}{1 + r_{m\text{-}r}T_{tln}}. \tag{6}$$

The variables $r_{m\text{-}r}$ and T_{tln} in equations (5) and (6) can be found as follows. Let c_m, c_{rib}, and $c_{m\text{-}r}$ be the concentration of free mRNA, free ribosomal subunits, and ribosome-bound mRNA, respectively. Free mRNA ($mRNA_{free}$) and free ribosomal subunits (rib_{free}) combine to form mRNA-ribosome complex (mRNA-ribosome):

$$mRNA_{free} + rib_{free} \xrightarrow{v_1} \text{mRNA-ribosome}. \tag{7}$$

The symbol v_1 in the above reaction is Arrhenius velocity of temperature-dependent chemical reaction and equals

$$v_1 = S_1 e^{-\Delta E_1/RT}, \tag{8}$$

where S_1 is a constant, ΔE_1 is the energy of activation, R is the universal gas constant equal to 1.98, and T is the body temperature in K (White et al. 1954). Note that v_1 is an increasing function of T. Although the rate of most enzyme-catalized reactions increases with temperature only to a certain limit and would eventually level off and crash as enzymes become denatured, I assume that this "crash" phase does not occur often in nature and it is therefore not modeled by equation (8). Now $r_{m\text{-}r}$ can be written as

$$\begin{aligned} r_{m\text{-}r} &= \frac{d(c_{m\text{-}r})}{dt} = v_1 c_m c_{rib} \\ &= S_1 e^{-\Delta E_1/RT} c_m c_{rib}. \end{aligned} \tag{9}$$

At mRNA-ribosome complex, amino acids are assembled into protein:

$$AA \xrightarrow[tRNA]{v_2} \text{Protein}, \tag{10}$$

where v_2 is Arrhenius velocity of chemical reaction with parameters S_2 and ΔE_2. Thus, the number of protein molecules ($N_{protein}$) increases at the sites of mRNA-ribosome complex at the rate

$$\frac{d(N_{\text{protein}})}{dt} = v_2 c_{AA}, \tag{11}$$

where c_{AA} is the concentration of amino acids. Consequently, T_{tln} in equation (1) can be written as

$$T_{tln} = \frac{dt}{d(N_{\text{protein}})} = \frac{1}{v_2 c_{AA}} = \frac{e^{\Delta E_2/RT}}{S_2 c_{AA}}. \tag{12}$$

By substituting $r_{m\text{-}r}$ and T_{tln} into equation (6) and rearranging the equation, we obtain the rate of protein synthesis:

$$\begin{aligned} r_{ps} &= \frac{v_1 c_m c_{rib}}{1 + v_1 c_m c_{rib} \dfrac{1}{v_2 c_{AA}}} \\ &= \frac{S_1 S_2 c_m c_{rib} c_{AA}}{S_2 c_{AA} e^{\Delta E_1/RT} + S_1 c_m c_{rib} e^{\Delta E_2/RT}}. \end{aligned} \tag{13}$$

When mRNA is superabundant in the cell, r_{ps} reaches its maximum limited by

$$\lim_{c_m \to \infty} (r_{ps}) = S_2 e^{-\Delta E_2/RT} c_{AA} = \frac{1}{T_{tln}}, \tag{14}$$

which means that, with superabundant mRNA, the rate of protein synthesis is limited by the time spent in the actual translation. Similarly, when amino acids are superabundant, the protein synthesis becomes limited by the concentration of mRNA (c_m) in the form of

$$\lim_{c_{AA} \to \infty} (r_{ps}) = S_1 e^{-\Delta E_1/RT} c_m c_{rib} = r_{m\text{-}r}. \tag{15}$$

Dependence of c_m on N_c

Recall that N_c is the number of copies of the gene in the genome. Letting r be the rate of transcription and D be the rate of mRNA degradation, we have

$$\frac{d(c_m)}{dt} = rN_c - Dc_m, \tag{16}$$

which has a general solution of

$$c_m = \frac{rN_c}{D} + Ae^{-Dt} \tag{17}$$

with equilibrium value of

$$c_m = \frac{rN_c}{D} \tag{18}$$

when t becomes large. Substituting this value into equation (13), we obtain the rate of protein synthesis in relation to N_c and T:

$$r_{ps} = \frac{S_1 S_2 \dfrac{rN_c}{D} c_{rib} c_{AA}}{S_2 c_{AA} e^{\Delta E_1/RT} + S_1 \dfrac{rN_c}{D} c_{rib} e^{\Delta E_2/RT}}. \tag{19}$$

The Final Model and the Condition for Minimizing T_s

Substituting equation (19) into equation (4), and after some manipulation, we obtain the final model relating T_s to the two key variables, N_c and T:

$$T_s = \frac{PDe^{\Delta E_1/RT}}{S_1 rN_c c_{rib}} + \frac{Pe^{\Delta E_2/RT}}{S_2 c_{AA}} + T_g N_u N_c. \tag{20}$$

To obtain the condition of N_c for minimizing T_s, we take derivative of T_s with respect to N_c, set the derivative to zero, and solve for N_c. This results in

$$N_c = \sqrt{\frac{PDe^{\Delta E_1/RT}}{T_g N_u S_1 r c_{rib}}} = Ce^{\Delta E_1/2RT}, \tag{21}$$

where

$$C = \sqrt{\frac{PD}{T_g N_u S_1 r c_{rib}}}, \tag{22}$$

which is always positive. Evidently, N_c in equation (21) decreases with increasing T. In other words, if there is a selective advantage in minimizing T_s (i.e., maximizing the rate of biosynthesis), then N_c is expected to decrease with increasing T.

To see how much change in N_c is expected with a certain change in body temperature, we can obtain the ratio of N_c at temperature T, denoted by $N_c(T)$, over N_c at temperature $(T+\Delta T)$, denoted by $N_c(T+\Delta T)$, and plot this ratio against T. Figure 1 shows that a 10° increase in temperature is expected to result in a 1.6–1.9-fold decrease in N_c and that a 20° increase in temperature is expected to result in a reduction in genome size about twice as much. It is obvious that the variation in body temperature alone is insufficient to explain the 80,000-fold difference in genome size observed among eukaryotes. Much of this genome size variation is now known to be attributable to accumulation of repetitive DNA

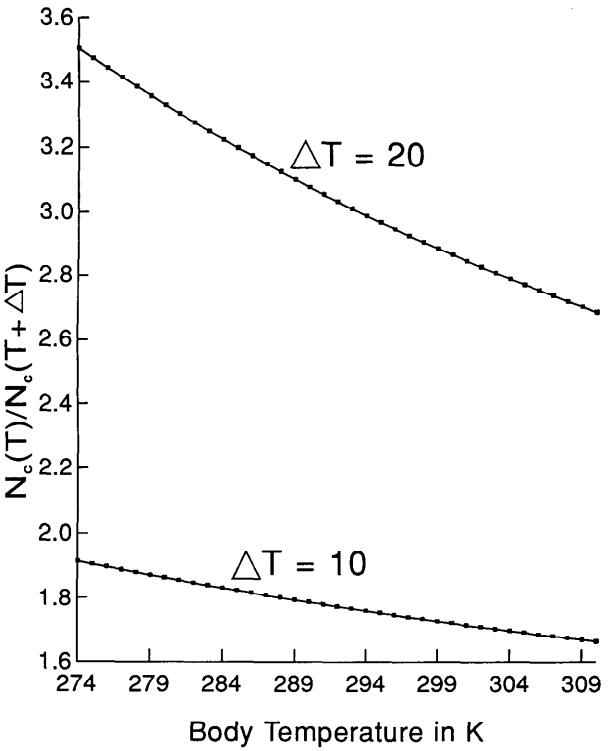

FIG. 1.—A quantitative illustration of the effect of an increase in body temperature (T) on the reduction in genome size (N_c), $N_c(T)$ is the optimal N_c at temperature T, and $N_c(T+\Delta T)$ is the optimal N_c at temperature $(T+\Delta T)$. The X-axis represents values for T in K.

(Charlesworth et al. 1994) and is therefore beyond the domain of the current model, which deals only with the functional components of the genome such as protein-coding sequences.

One may argue that T_g in equations (20) and (21) should also be temperature-dependent. For example, it would seem more reasonable to express T_g in the following form:

$$T_g = \frac{e^{\Delta E/RT}}{Sc_{\mathrm{dNTP}}}, \tag{23}$$

where R and S are constants, ΔE is the energy of activation, and c_{dNTP} is the concentration of dATP, dGTP, dCTP, and dTTP.

There are two reasons (one involving the substrate and the other involving the machinery of biosynthesis) that a complication involving temperature dependence in T_g is unnecessary. First, the four nucleotides are already the activated precursors and ΔE is therefore zero. Second, increasing temperature is expected to aid the initiation of protein synthesis more than it does to the initiation of DNA replication, for the following reason. The DNA polymerases (Pol I, II, and III) are relatively small molecules, with molecular weights of 110,000, 120,000, and 180,000, respectively, in eukaryotes (Aktipis 1986), whereas the 40S and 60S ribosomal subunits are giant molecular complexes with molecular weights of 1,500,000 and 3,000,000, respectively (Muench 1986). DNA replication requires the DNA polymerases to find the DNA template. For protein synthesis, the 40S and mRNA need to find each other to form a complex and then this complex and 60S ribosomal subunit need to find each other to begin translation. A numerical illustration will show differential temperature dependence of these processes.

Assume that both the DNA polymerases and ribosomal subunits are spherical molecules of density, say, 1.35 g/cm^3 (proteins and protein-nucleic acid complexes are heavier than water). The diffusion coefficient D of a rigid spherical molecule is given by

$$D = \frac{kT}{6\pi\eta r}, \tag{24}$$

where η is the viscosity of the solvent, r is the radius of the sphere, k is the Boltzman constant, and T is the absolute temperature (Stryer 1981, p. 231). If the viscosity of cytoplasm is similar to that of water, then $\eta = 1.005$ at 20°C (Sears and Zemansky 1955, p. 246). So D for DNA Pol III can be calculated to be 6.094×10^{-15}, and D for the 60S ribosomal subunit is 2.386×10^{-15}. Thus, even if cells had some mechanism to force the molecules to travel in two dimensions rather than three, it would still take an average of 10.1 minutes for DNA Pol III and 17.1 minutes for 60S ribosomal subunit, to cover the distance of 1 μm. Note that traveling 1 μm may be much more than sufficient for DNA Pol III to find nuclear DNA, which is a very large and permanent target in the confined space of the nucleus. But the 60S ribosomal subunit may need to travel a longer distance in the large volume of cytoplasm to find a 40S-mRNA complex, which is a relatively small and transient target. In addition, the 40S ribosomal subunit should also have difficulty finding mRNA, which is infinitesimal compared to the nuclear DNA. Thus, the initiation process for protein synthesis is expected to be much more temperature-dependent than that for DNA synthesis.

Predictions and Discussion

Equations (20) and (21) lead to four predictions below. Comparative data related to these predictions are not yet sufficient for carrying out a study similar to that of Sessions and Larson (1987) and Pagel and Johnstone (1992), in which comparisons are made between sister taxa. Because genome size may be subject to many modifying evolutionary factors, one is prone to compare

apples and oranges. However, relevant empirical evidence will be summarized here in relation to the predictions to serve as a beginning point for future comparative studies.

Prediction 1.—Poikilotherms living in a warm climate should exhibit less gene duplication (a smaller N_c) than poikilotherms living in a cold climate. Because N_c is a good indicator of genome size in eukaryotes (Nei 1987; Li and Graur 1991), we can make the prediction more testable by stating that poikilotherms living in a warm climate should have a smaller genome than poikilotherms living in a cold climate. I will first present comparative data from salamanders supporting the prediction, then summarize relevant evidence from other taxa.

MacGregor (1982) has speculated on the significance of genome size evolution in speciation of Plethodontid salamanders. There is little morphological variation among plethodontid salamanders, but genome size varies much among species (MacGregor 1982). Because plethodontid salamanders now inhabit a diverse array of habitats with very different ambient temperature, they make an excellent taxonomic group for testing the relationship between genome size and body temperature.

Measurement of body temperature (Brattstrom 1963) and genome size (Sessions and Larson 1987) are available for some plethodontid salamander species. Because body temperature changes seasonally or even daily, all measurements of body temperature included in this article are in fact preferred, and presumably optimal, temperature (Brattstrom 1963). I take the phylogenetic tree, as well as genome size measurements, of salamanders from Sessions and Larson (1987) as a basis to examine whether sister taxa with different body temperatures exhibit genome size differences in the direction expected by the model. Data are presented in table 1.

One problem I encountered during data selection is that some salamander species have wide geographic distribution, with different populations living in regions of quite different ambient temperatures and potentially having different body temperatures. However, usually only one body temperature is given for a species, and it is not clear whether the recorded body temperature is representative of populations in the warm climate or populations in the cold climate. All such cases involving salamander species with a wide geographic distribution were simply eliminated from the data set. This leaves only 10 species with distribution either confined within one state or bordering two states according to Bishop (1967). Of these, *Plethodon jordani* and *P. yonahlossee* do not have recorded body temperature measurements and were excluded from the data set.

The phylogenetic relationship among these eight species is shown in figure 2. Changes in genome size and body temperature partitioned along the branches separately and in such a way as to minimize the total change in body temperature and in genome size. The original paper of Sessions and Larson (1987, and literature cited therein) should be consulted for justification of the phylogenetic relationships.

Table 1
Genome Size (average *C* value) and Body Temperature of Seven Salamander Species

Species	Body Temperature	*C* Value
Desmognathus wrighti	17.1	13.7
Plethodon welleri	16.1	22.6
P. elongatus	?[a]	30.6
P. dunni	10.0	37.9
P. vehiculum	10.5	39.3
Aneides flavipunctatus	?[b]	45.4
A. lugubris	8.1	49.6
Hydromantes platycephalus	5.7	50.0

NOTE.—All body temperatures were from table 2 of Brattstrom (1963). Note the general trend of increasing genome size with decreasing body temperature.

[a] *Plethodon elongatus, P. dunni,* and *P. vehiculum* inhabit the western coast of the United States, with *P. elongatus* found in the southern end (Northern California) and *P. vehiculum* found in the northern end (British Columbia). Thus, the climate for *P. elongatus* is expected to be warmer than that for the other two species.

[b] The climate for *A. flavipunctatus* is likely warmer than that for *A. lugubris.* Mean body temperature of *A. flavipunctatus* recorded by Lynch (1974) in March and April is 14°C.

Figure 2 shows that genome size is small for *Desmognathus wrighti,* which has high body temperature. *Hydromantes platycephlus, Aneides flavipunctatus,* and *A. lugubris* live in the cold alpine environment up the Rockies, and all have large genome size (table 1 and fig. 2). Of the three *Plethodon* species that inhabit the western coast of the United States, *P. elongatus* inhabits northwestern California and southwestern Oregon and has a genome size of 30.6 (table 1), the smallest among the three western *Plethodon* species. *Plethodon dunni* (inhabiting northwestern Oregon) and *P. vehiculum* (inhabiting northwestern Washington and southwestern British Columbia) have genome sizes of 37.9 and 39.3, respectively (table 1). It is evident from figure 2 that the genome size increased almost whenever body temperature decreased, and vice versa. This inverse relationship, depicted in figure 3, is expected from equation (21). Note that there are several equally parsimonious partitions of the changes of body temperature and genome size along the branches, but the general trend of increasing body temperature with decreasing genome size is maintained in these equally parsimonious partitions.

Empirical support for prediction 1 also comes from other organisms, such as plants and fishes. Plants are mostly poikilotherms. Therefore, plants living in a warm

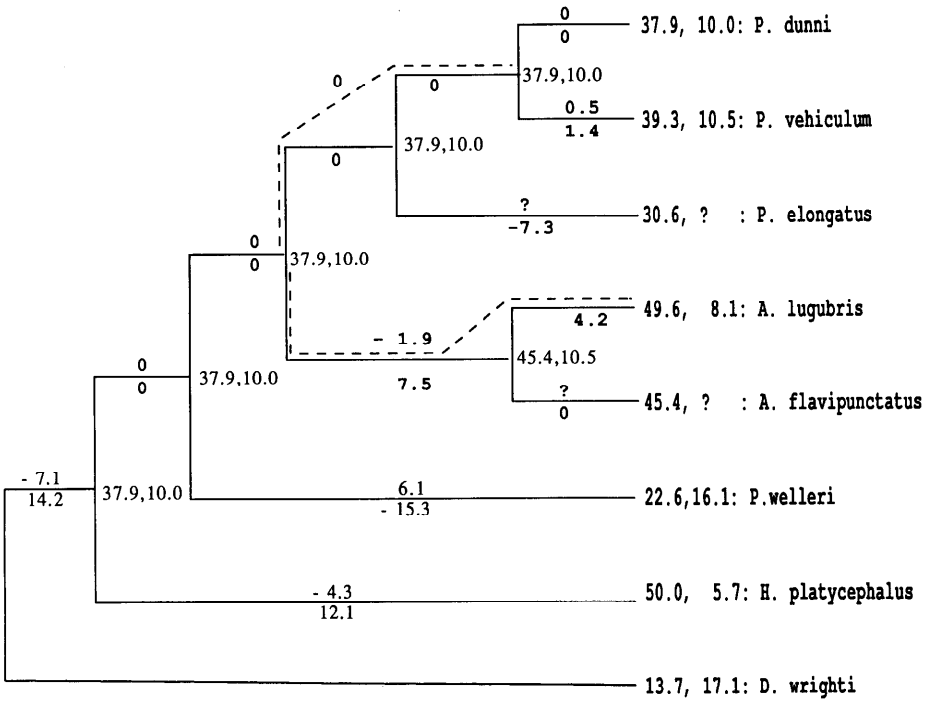

FIG. 2.—Phylogenetic relationship among eight salamander species illustrating the inferred changes of body temperature (the number above each branch) and concurrent changes in genome size (the number below each branch). The paired numbers (genome size, body temperature) at each internal node represent inferred ancestral states. The branching pattern was taken from Sessions and Larson (1987). The changes in genome size and body temperature along the branches were partitioned separately. Note that the changes in body temperature are partitioned along the branches with only six species, excluding *P. elongatus* and *A. flavipunctatus* (which have no record of body temperature in Brattstrom [1963]). The dashed lines designate branches for partitioning changes in body temperature along the branches.

climate are expected to have less gene duplication (hence a smaller genome size) than plants living in a cold climate. DNA contents of several cultivated grasses and legumes fit this prediction well (Bennett 1976). Levin and Funderburg (1979) surveyed the genome size of 332 tropical and 524 temperate angiosperm species in 218 genera. They found that the genome size (measured as total chromosomal length) is significantly smaller ($P<0.001$) in tropical monocotyledons than in temperate monocotyledons. Similarly, the genome size in tropical dicotyledons is also significantly smaller ($P<0.001$) than that in temperate dicotyledons. The total chromosomal length of species in the temperate region is about twice that of the species in the tropical region, which would be expected from equation (21) if the difference in body temperature is slightly more than 10°C between the temperate and tropical species (fig. 1). Levin and Funderburg (1979) also compared the genome size of 335 temperate and 67 tropical species, based on data of DNA content tabulated by Bennett and Smith (1976). The mean 4C DNA content for temperate species is 27.06 pg versus only 12.13 pg for tropical species ($P<0.001$).

One may argue that temperate plants do not grow much at cold temperatures and that most of their growth is in midsummer months when the average daily temperature may not be much different from that in tropics. The second part of this argument is a misconception. For example, there is a roughly linear decrease of about 12°C in mean midsummer air surface temperature from 30°N to 60°N (Davenport 1992).

The number of mitochondria in a cell is equivalent to N_c in equation (21) and is therefore expected to change with body temperature. Empirical evidence reviewed by Johnson and Altringham (1991) supports this expectation. For example, slow muscles in fish species living at −1°C in antarctic waters contain almost 60% mitochondria by volume, which is higher than the corresponding value for temperate species, which in turn is higher than the value for tropical species (Johnston et al. 1988). A similar proliferation of mitochondria occurs with seasonal temperature acclimation in teleosts. In the red fibers of striped bass (*Morone saxatilis*) the fraction of cell volume occupied by mitochondria increases from 0.29 to 0.45 when temperature decreases from 25°C to 5°C, and a similar trend is observed in the white fibers (Egginton and Siddel 1989). Note that the increase in the fraction of cell volume occupied by mitochondria was due to the increase in the number of mitochondria because the size of mitochondria did not

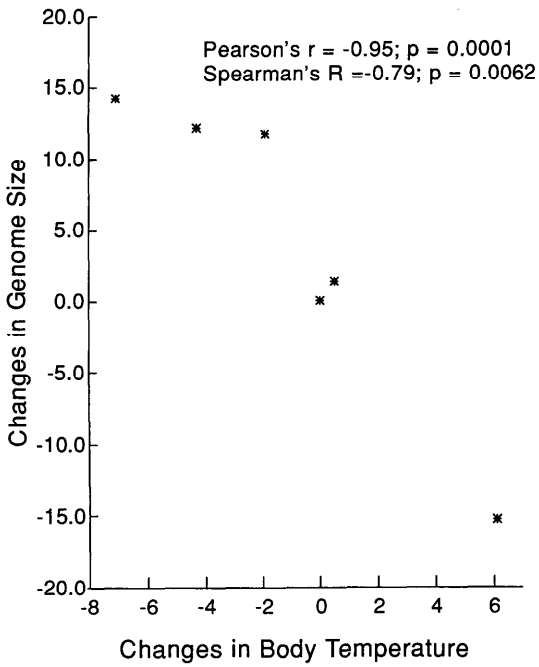

FIG. 3.—An increase in body temperature is associated with a decrease in genome size. Data are from fig. 2 (i.e., those data pairs above and below each branch). Note that there are several equally parsimonious partitions of the changes of body temperature and genome size along the branches, but the general trend of increasing body temperature with decreasing genome size is maintained in these equally parsimonious partitions.

increase (Egginton and Siddel 1989). I regard this proliferation of mitochondria as a special case of gene duplication in response to temperature change.

Prediction 2.—The optimal N_c depends on T, according to equation (21). If T varies greatly among different species in a taxon, which is typical of poikilotherms such as amphibians living in different climatic environments, then optimal N_c should also varies greatly among different species in that taxon. If T varies little, as is the case for birds and mammals, then optimal N_c should also vary little.

The range of genome size is 91-fold in amphibians, but only fourfold in mammals and less than twofold in birds (Li and Graur 1991; Tiersch and Wachtel 1991). Such a contrast is particularly striking when we consider the fact that mammals and birds consist of more species and have much wider geographical distributions than amphibians. One should, however, remember that there is a perfect alternative explanation for the greater variation in genome size in amphibians than in birds and in mammals. If genome size changes according to the model of Brownian motion described in Felsenstein (1985, 1988), then the variance of genome size is expected to increase linearly with evolutionary time. Amphibians apparently have evolved a longer period and therefore are expected to have a greater variance in genome size than either birds or mammals.

Prediction 3.—Cold geological periods should favor the evolution of poikilotherms with a large N_c (and a large genome), and warm geological periods should do the opposite. This should be reflected in relict species of ancient taxa if subsequent evolution has not been too rapid to erase the footprints of the past. This prediction is difficult to test, as is true for almost any prediction concerning the remote past.

Prediction 4.—Poikilotherms with a small genome are more sensitive to temperature change than poikilotherms with a large genome. This is directly derivable from equation (20). For a given temperature change ΔT, a corresponding change in T_s (time spent in biosynthesis during one cell cycle) is

$$\Delta T_s = T_s(T) - T_s(T+\Delta T) = \frac{A_1 A_2}{N_c} + A_3 A_4, \quad (25)$$

where

$$A_1 = \frac{PD}{S_1 r}, \quad (26)$$

$$A_2 = e^{\Delta E_1/RT} - e^{\Delta E_1/R(T+\Delta T)}, \quad (27)$$

$$A_3 = \frac{P}{S_2 c_{AA}}, \quad (28)$$

and

$$A_4 = e^{\Delta E_2/RT} - e^{\Delta E_2/R(T+\Delta T)}. \quad (29)$$

According to equation (25), a given change in T should lead to a smaller change in T_s (and the rate of biosynthesis) in species with a large N_c than in species with a small N_c. A large genome with many gene duplications therefore serves as a buffer against climatic changes in poikilotherms. This implies that the variance of body temperature can affect genome size in such a way that greater variation in body temperature requires a larger genome. Thus, both mean and variance of body temperature can affect genome size.

In addition to the four predictions that relate genome size to body temperature, the model also predicted a positive relationship between genome size and cell volume. It is empirically well documented that organisms with a large cell volume have larger genome sizes than those with a small cell volume, and equation (21) offers two explanations for this trend. First, the larger cell volume may result from an increased protein content per cell, that is, an increased P in equation (21). In this case,

equation (21) predicts that N_c should increase with P and consequently should increase with cell volume as well. Second, an increased cell volume may be caused simply by an increased water content, with no change in protein content or any other cellular component per cell. This dilution of cellular component by water will result in a decrease in the concentration of ribosomal subunits (c_{rib}). Equation (21) predicts that N_c should increase with a decrease in c_{rib}. Hence the increase of genome size with increasing cell volume.

The specific prediction from equation (21) concerning genome size and cell volume is that N_c should not increase linearly with increasing P or with decreasing c_{rib} but should increase linearly with the square root of increasing P or of decreasing c_{rib}. I regard this as the main advantage of modeling because a verbal account of a hypothesis relating genome size and P, such as that done by Cavalier-Smith (1985*b*), will never reach a prediction with such a degree of specificity.

Now I must admit that the model presented in the article is weak in many aspects, especially for its many simplifying assumptions. However, just as art is a lie that helps us to see the truth, a model is a lie that helps us approximate reality (Segel 1984). To this end, the model is well justified.

In summary, environmental temperature, through its effect on body temperature, may be a dominant factor shaping the evolution of genome size. The global temperature has fluctuated widely during geological time, but its effect on organic evolution has been hardly explored. It would be surprising that such wide fluctuations in global temperature during geological time would turn out to be of little evolutionary consequence.

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