Physics International

Original Research Paper

Metabolic Potential Versus Genome Size

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Article history
Received: 02-03-2022
Revised: 15-04-2022
Accepted: 21-04-2022

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Abstract: In this study, we have shown that there is a connection between the metabolic potential (the coefficient 'a' in metabolic-mass relationship $P = aMk$, where P- basal metabolic rate, M-body mass, k-power coefficient) and the corresponding genome size (C-value diapason) of the given organismal taxon. With the increase of the metabolic potential of living organisms in evolution, the C-value diapason of a given taxon decreases. The study shows the metabolic and genomic characteristics of the simplest bacterial cells that represent the natural scale. The metabolic and genomic characteristics of all more complex organisms that emerge after them are adjusted with this natural scale. This finding may provide an answer to the genome-size enigma.

Keywords: Metabolic Potential, Genome Size, Taxon, Enigma, Epigenetics

Introduction

The first living organisms are believed to have arisen more than 3.85 billion years ago (Holland, 1999). Presumably, the metabolic capability and genetic systems of the earliest cellular entities are two basic organismal systems. Genome size has been traditionally measured as the mass of DNA within the nucleus. The haploid genome size or C-value has been given as mass in a picogram (p.g.,) of DNA per haploid nucleus (Mirsky and Ris, 1951). The haploid genome size of eukaryotes varies by a factor of more than 200 000. This variation is not correlated with organismal complexity or the number of coding genes- an observation formerly known as the 'C-value paradox' or 'C-value enigma (Gregory, 2001a). For instance, unicellular eukaryotes include taxa with a genome that exceeds all studied genomes of multicellular animals. Theories to explain the observed pattern of genome size fall mainly into two categories: Those in which natural selection is viewed as the primary mechanism controlling genome size and those in which variation in genome size is thought to be essentially neutral to natural selection, with genome size instead dependent on stochastic processes and historical accident (Brainerd *et al*., 2001; Cavaller-Smith, 1985; Tiersch and Wachtel, 1993; Petrov, 2001). However, in the scientific literature, there are many strong relationships between genome size and the energetic characteristics of large groups of animals.

The idea that the general energy for vital activity of living organisms increased in the course of progressive evolution was assumed by Sewertzoff (2010). Handbooks of bioenergetics show that the basal metabolic rate (P, J/s) of animals is connected with their mass (*M*, kg) by the Equation:

$$P = aM^k \quad (1)$$

where the linear coefficient ‘a’ is considered as ‘metabolic potential’ given in mW/g or in W/kg and ‘*k*’ is a non-dimensional power coefficient.

Other scientists (Hemmingsen, 1960; Ivlev, 1963) proposed to use the linear coefficient ‘a’ from Eq. (1) as a measure of standard metabolism in different species of animals. This implies that there is a comparison between hypothetical animals of 1 g or 1 kg body mass that do not necessarily exist in nature. This coefficient can be regarded as 'metabolic potential' because of the dimension given in mw per 1 g or W in 1 kg body mass. Zotin and Lamprecht 1996; Zotin and Konoplev, 1984) are showed that the metabolic potential of organismal taxa increases in evolution and there is a connection between the 'metabolic potential' and the time of organismal appearance (Zotin *et al*., 2001), as well as and body temperature of organisms (Swenson and Turvey, 1991).

Some scientists have shown that the two organismal characteristics (body size and complexity) have increased throughout the evolutionary history of life and organismal complexity is positively correlated to size (Bonner, 1968, 1988; Valentine *et al*., 1994; Bell and Mooers, 1997; Vermeij, 1999). While this approach is widely accepted, the mechanisms behind the evolution of organismal complexity are poorly understood (McCarthy and Enquist, 2005). However, there is not a standard definition of complexity. McShea (1996) provides several definitions for biological complexity. These include The number of different parts within a hierarchy (genes, cells, organs, etc.), the number of interactions between parts in

this hierarchy, the number of parts for a particular spatial or temporal scale and the number of interactions between parts in a spatial or temporal scale. Some conceptual models have linked the evolution of organismal complexity, measured by the number of cell types, with increases in organismal body size (Bonner, 1968; 1988). Other conceptual models have connected the evolution of metabolic intensity, the mass-specific rate of energetic processing for a given body mass, with body size (Zotin and Lamprecht, 1996; Vermeij, 1999). However, non of these approaches have considered the mechanistic linkage between the number of cell types, body size and metabolic intensity. Interestingly, body size, complexity and metabolic intensity have all increased throughout macroevolutionary time (Carroll, 2001; Witting, 2003).

In the scientific literature, there are many strong relationships between genome size and energetic characteristics of large groups and taxa of animals**.**

On the cellular level, there is a strong positive correlation between red blood cell size (mean diameter, dry cell area and cell volume) and genome size in vertebrates (Gregory, 2001b). A positive correlation between genome size and cell volume within and across amphibians exists also (Olmo and Morescalchi, 1975). Genome size is correlated with both nuclear and cell volume in red blood cells, taken from a variety of organisms (Olmo, 1983). Recently, Kozlowski *et al*. (2003; 2005) have developed a model, in which cell size appears a link between noncoding DNA and metabolic rate scaling.

In combined poikilotherms (pisces, reptilia, amphibians) with homeotherms (mammals and aves) the genome size is positively correlated to the total life potential (total metabolic energy per lifespan per 1 kg body mass) with a correlation coefficient of 0.495 (Atanasov and Petrova-Tacheva, 2009).

On the level of whole organisms, in mammals, the body-mass corrected basal metabolic rate is inversely related to genome size with a high correlation coefficient (0.73) (Vinogradov, 1995) and in passerine birds, the body-mass independent resting metabolic rate is inversely related to their genome size with correlation coefficient 0.80 too (Vinogradov, 1997).

In Homeotherms (mammals, order Rodentia) and in poikilotherms (amphibians) the development rate is strongly linked to genome size (Gregory, 2002a, b). In this study, we investigate the possible statistical connection between the values of coefficient 'a' in a metabolism-mass relationship (named by us as metabolic potential a, W/kg) and the corresponding C-value diapason of a given organismal taxon.

In birds exists a relationship between regression residuals of C-value versus body mass and resting metabolic rate versus body mass with a correlation coefficient of 0.39 (Gregory, 2002a).

For all organismal taxa, the genome size correlates to the radioresistance of living organisms (Atanasov and Ignatova, 2021).

Data and Methods

C-Value Data

Animals groups are arranged accordingly to their organismal complexity. The range of the eukaryotes and prokaryotes taxa along with increasing their organismal complexity in evolution were given from data analyses by Hedges *et al*. (2004), Raff and Kaufman (1983), Oliver *et al*. (2007), Bonner (1968; 1988), Markov *et al*. (2010), Valentine *et al*. (1994), Tudge (2000), Hedges and Kumar (2003).

Organismal taxa, C-value and Data sours: Prokaryotes: 1. Archea (2×10^{-3}-6×10^{-3} p.g.,); 2. Eubacteria (8×10^{-4}-2×10^{-2} p.g.,) Gregory (2001a); Grimaldi *et al*. (2005); Matsunada *et al*. (2004); Eukaryotes: 3. Protozoa (5×10^{-3} - 8×10^{2} p.g.,); 4. Algae (9×10^{-2} p.g.,) 5. Fungi (1×10^{-2} -20 p.g.,); 6. Sponges (7×10^{-2} -20pg) Gregory (2001b); Markov *et al*. (2010); 7. Cnidarians (4×10^{-1}-20 p.g.,); 8.Nematodes (9×10^{-2}–20 p.g.,) Grimaldi *et al*. (2005); 9. Bryophytes (2×10^{-1} -5 p.g.,) Matsunada *et al*. (2004); 10. Pteridophytes (7×10^{-2}- 80 p.g.,) Scott *et al*. (1985), Dunlop (1997); 11. Gymnosperms (3-50 p.g.,) Matsunada *et al*. (2004); Scott *et al*. (1985);12. Angiosperms (6×10^{-2} - 2×10^{2} p.g.,) Scott *et al*. (1985), Dunlop (1997); 13. Rotifers (5×10^{-1}- 1 p.g.,) Gregory (2002a, b); 14. Flatworms (7×10^{-2} -30 p.g.,) Gregory (2002a, b); 15. Tardigrades (9×10^{-2}- 1 p.g.,) Gregory (2002a, b), Fortey *et al*. (1997); 16. Echinoderms (5×10^{-1} - 4.4 p.g.,) Wray and Love (2000); 17. Annelids (6×10^{-2}-7.6 p.g.,) Gregory (2001a; 2002a, b; 2005); 18. Molluscs (4×10^{-1}- 5.9 p.g.,) Gregory (2001b; 2002a, b; 2005); 19. Myriapods (4×10^{-1}- 3.0 p.g.,) Gregory (2001a; 2002a, b; 2005); 20. Arachnids (8×10^{-2}- 5.7 p.g.,) King (2004), Stanley (1075); 21. Insects (1×10^{-1}- 16.9 p.g.,) Tudge (2000), Martin (2001), Tiersch and Wachtel (1991); 22. Crustaceans (0.16- 38 p.g.,) Martin (2001), Tiersch and Wachtel (1991);23. Non-vertebrate chordates (9×10^{-2}-7×10^{-1} p.g.,) Gregory (2005); 24. Agnathans (1-4.0 p.g.,) Gregory (2005), Tudge (2000); 25. Chondrichthytes (4-30 p.g.,) Andrews *et al*. (2009); 26. Teleosts (4×10^{-1}- 4.4 p.g.,) Gregory (2001b, 2005); 27. Lungfishes (50-133 p.g.,) Gregory (2001b, 2005); 28. Salamanders (20-130 p.g.,) Olmo and Morescalchi (1975); 29. Frogs (Amphibians) (0.9-10 p.g.,) Gregory (2001a, 2005); 30. Reptiles (Amphibians) (1.1-5.4 p.g.,) Gregory (2001b, 2005); 31. Birds (1-2.2 p.g.,) Vinogradov (1997); Mei (1087), Prosser (1986); 32. Mammals (1.7-8.4 p.g.,) Gregory (2005), Tudge (2000).

Metabolic Potential Data

The data for the values of the linear coefficient 'a' in a metabolism-mass relationship, named 'metabolic potential' in 'W/kg' were summarized the given

temperatures correspond to the conditions under which the 'metabolic potential is determined.

Organismal taxa, Metabolic potential and Data sours: 1. Prokaryotes (Archea, Bacteria) (20°C), 0.08 W/kg (endogenous) Makarieva *et al*. (2005; 2008), DeLong *et al*. (2009); 2. Protozoa (20°C) All Protozoa (0.098 W/kg), Apicomlexa (0.046 W/kg), Sarcomastigophora (0.081 W/kg), Ciliophora (0.313 W/kg) Zotin and Lamprecht (1996); 3. Sponges (20°C) (0.140 W/kg) Zotin and Lamprecht (1996), (0.025 W/kg) McCarthy and Enquist (2005); 4. Cnidarians (20°C), (0.192 W/kg) Zotin and Lamprecht (1996),(0.297 W/kg) Dolnik (1968); 5 Echinoderms (20°C) Echinodermata (0.356 W/kg), Echinodea (0.249 W/kg), Asteroidea (0.310 W/kg) Dolnik (1968); 6. Plants(24°C) Field/US tree saplings (0.0222 W/kg) Reich *et al*. (2001), GH/tree seedlings (0.150 W/kg) Glazier (2009), GC/tree seedlings (0.195 W/kg) Makarieva *et al*. (2008), GH/tree seedlings (0.178 W/kg), Trees (Japan sample) (0.028 W/kg)Glazier (2009), Makarieva *et al*. (2008); Vascular Plants (24°C) Green leaves (0.31 W/kg) Reich *et al*. (2001) Tree saplings (0.19 W/kg), Seedlings (1.6 W/kg) Glazier (2009); 7. Myriapods (20°C) (0.405 W/kg) Dolnik (1968); 8. Flatworms (20°C) (0.582 W/kg) Dolnik (1968); 9. Arachnids(20°C), (0.530 W/kg) Dolnik (1968), (0.767 W/kg) Prosser (1986); Glazier (2009); 10. Algae (20°C) Microalgae (1.3 W/kg), Macroalgae (0.19 W/kg) Makarieva *et al*. (2008); 11. Arthropods (20°C) (0.881 W/kg) Dolnik (1968); 12. Molluscs (20°C) (0.895 W/kg) Ivlev (1963), (1.060 W/kg) Dolnik (1968); 13. Crustaceans (20°C), (1.208W/kg) Dolnik (1968), (0.95 W/kg) Glazier (2009); 14. Annelids (20°C) (0.2-2.2 W/kg) Zotin and Lamprecht (1996); 15. Nematodes (20°C) (1.4 W/kg) Klekowski *et al*. (1972); 16. Amphibians (20°C) (all) (1.86 W/kg) White *et al*. (2006); Frogs (1.45 W/kg) Zotin and Lamprecht (1996), Salamanders (0.415 W/kg) Zotin (2018); 17. Teleosts (20°C) Teleost Fishes (1.816 W/kg) Dolnik (1968), All fishes (1.245 W/kg) White *et al*. (2006), All fishes (1.66-3.2 W/kg) Glazier (2009); 18. Insects (20°C) (all) (1.792-3.15 W/kg) Dolnik (1968); 19. Reptiles (20°C) (all) (3.11 W/kg) White *et al*. (2006), (2.46 W/kg) Zotin and Lamprecht (1996), (2.246 W/kg) Glazier (2009, 2010), (4.60 W/kg) Dolnik (1968); 20. Rotifers (20°C) (17 W/kg) Banse (1982); 21. Mammals (38°C) All (22 W/kg) Makarieva *et al*. (2008), (24 W/kg) Hayssen and Lacy (1985), (26 W/kg) White *et al*. (2006), (28.36 W/kg) Glazier (2010); 22. Aves (38°C) All (29.80 W/kg) Glazier (2010), (32.64 W/kg) Dolnik (1968), (34.15 W/kg) White *et al*. (2006), (37 W/kg) Makarieva *et al*. (2008). Software Package 'STATISTICA' was used in all calculations.

Results

In Fig. 1 are presented the C-values of the animal's group and taxa in the order of increase of their organismal complexity (numbered in C-value Data**)**. The C-values-diapason (marked vertical area from 1 p.g., to 3 p.g.,) appears common geometric mean for all taxa. Since Aves are the latest branch of the evolution, the common diapason (1÷3 p.g.,) coincides with the diapason of birds' C-values. Because the geometric mean diapason of genome sizes in all taxa don't differ more than one order of magnitude this allows us to make the hypothesis that during increasing of the organismal complexity, the genome size varies around this optimal diapason of C-values, which is common for Bacteria, Protozoa, Plants, Poikilotherms, Mammals and Aves. During increasing organismal complexity, the C-value diapasons approximately close to this optimal diapason. In Table 1 are selected the combined data for mean values of metabolic potential **'**a**'** and the C-value diapasons for studied taxa, using data given in C-value Data and Metabolic Potential Data.

The mean value of 'metabolic potential' for each taxon was calculated using all values of 'metabolic potential'. The organismal taxa are arranged according to the magnitude of their 'metabolic potential'.

The selected data in Table 1 are graphically presented in log-log plots in Fig. 2. The data for the 'metabolic potential' (W/kg) are placed on the ordinate, while the C-values data (p.g.,) are placed on the abscissa. All data in Fig. 2 are well approximated by a bell-shaped curve. In all further calculations, instead of the tabular values of the C-value, we will use the corresponding values (C*v-values) approximated horizontally on the approximation curve- (Fig. 3).

One of the tasks of our research is to find out the allometric relationship between the metabolic potential (a, W/kg) and the C*-value diapasons (in kg) i.e., $C^*_{v(min)}$ diapason and $C^*_{v(max)}$ diapason (Fig. 3).

The graphic relationships between the 'metabolic potential' and $C_{v(min)}$ and $C_{v(max)}$ diapasons are presented in Fig. 4 and 5.

The mathematic relationships in Fig. 4 and 5 can be presented as.

For Log a-Log $C^*_{v(min)}$: Y = 0.7607x + 12.428 (R = 0.926); After transformation: $A = 10^{12.428} C_{v(min)}{}^{0.7607}$ with p<0.00001 for n = 22 points and Student t-criteria t =11.1.

For Log a - Log $C^*_{\mathbf{v(max)}}$: Y = -0.8143x – 10.551 (R = 0.935) After transformation: $A = 10^{-10.551} C_{v(max)}{}^{-0.8143}$ with p<0.00001 for n = 22 points and Student t-criteria t = 11.1.

The very high correlation coefficients (r = 0.93-0.92) and low p-level show, that the relationships between the metabolic potential 'a' and C*v data are not random.

From a dimension point of view, we can present the C-values in SI metrical system (in kg). The metabolic potential 'a appears organismal characteristics, while C-value appears cellular characteristics. The two characteristics changes about 2 orders of magnitude. For example, the a_{max}/a_{min} ratio is equal to 417 folds from 33.4 W/kg in Aves to 0.08 W/kg in Prokaryotes. The $C_{v(max)}/C_{v(min)}$ ratio is equal to 364 folds from 8×10^2 p.g., in Protozoa to 2 p.g., in Aves. This is an indication that between two quantities can exist direct or indirect statistical connection.

In this direction, we analyzed the product: $A \times C^*_v$, where the C^*_v values lie on the approximate bell-shaped curve, parallel to the horizontal lines presented given C-values diapason.

The analysis of the product between the maximum approximate values and 'metabolic potential' shows that this product ($a\times C^*_{v(max)}$) has a dimension of metabolic rate in Joule per second. In Table 2 are given the calculated values of the product ($a\times C^*_{v(max)}$). The values of the genome size are given in 'kg' and the product ($a\times C^*_{v(max)}$) is given in 'J/s'.

From Table 2 it can see that the product ($a\times C^*_{v(max)}$) changes from 0.617×10^{-13} J/s in Arthropods to 6.40×10^{-13} J/s in Prokaryotes i.e., about 10 times. The basal metabolic rate in the order of 10^{-12} J/s-10^{-14} J/s is typical for the growth metabolism of Bacteria (Atanasov, 2005; Makarieva *et al*., 2005**)**.

The data analysis for the product ($a\times C^*_{v\,(max)}$) shows that this product appears nearly constant parameter with a Mean value ± SD (Eq. 4):

$$a\times C^*_{v(max)} = 1.5\times10^{-13} \pm 1.678\times10^{-13}\, J/s \quad (4)$$

In the same fashion, we analyze the product between $C^*_{v(min)}$ values and the values of the 'metabolic potential'(Table 2).

From the Table**,** it can see that the values of the product ($a\times C^*_{v(min)}$ change from 4.8×10^{-20}J/s in Prokaryotes to 2.67×10^{-14} J/s in Aves i.e., about 6 orders of magnitude. The data analysis for Mean value ± SD shows:

$$a\times C^*_{v(min)} = 2.15\times10^{-15} \pm 6.62\times10^{-15}\, J/s \quad (5)$$

The basal metabolic rate in the order of ~10^{-15} J/s is typical for Bacteria with minimum metabolism (Makarieva *et al*., 2005**)**. In principle, the basal metabolic rate lower ~10^{-15} J/s is typical for bacterial spores. Because the diapason of the product ($a\times C^*_{v(min)}$) changes 6 orders of magnitude, this product van is regarded as a parameter, but not as constant.

In the calculation of Eq. 4 and 5 are used the extremely low and extremely high values of the $C^*_{v(max)}$ and $C^*_{v(min)}$.

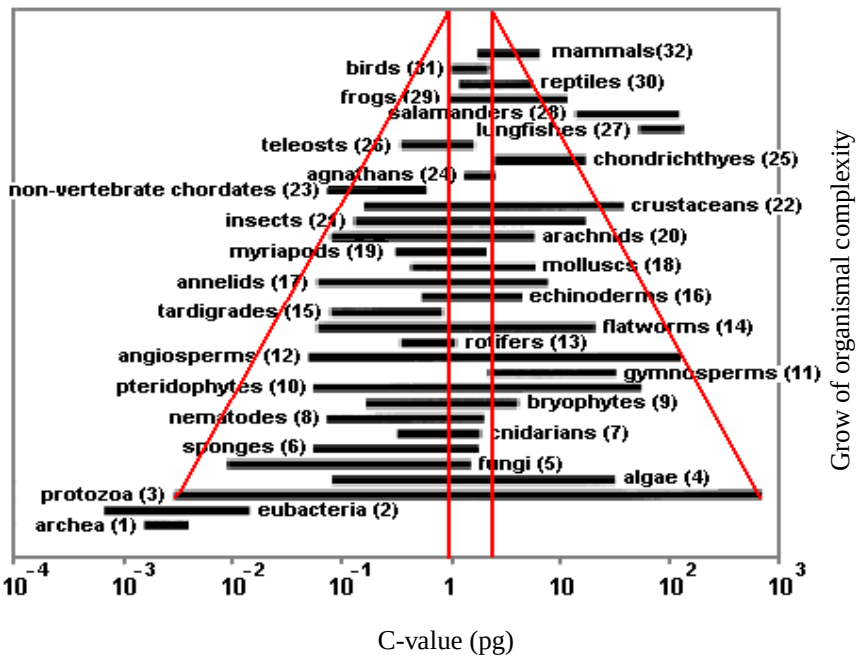

Fig. 1: The organismal taxa arranged to their organismal complexity. The C-values diapason (the marked area from 1 p.g., to 3 p.g.,) appears common for taxa. The Figure is taken from Gregory (2005**)** and is modified by the authors

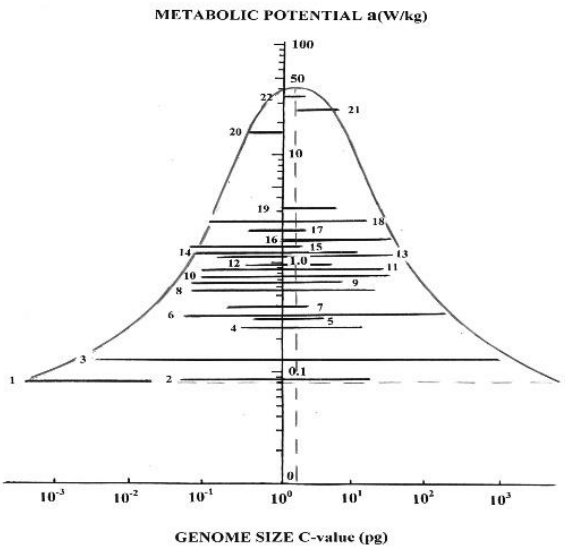

Fig. 2: Distribution of metabolic potential 'a' and C-values in living organisms. The maximum of 'metabolic potential' ~34 W/kg in Aves corresponds to C-value ~1-3p.g. The minimum 'metabolic potential' ~0.08 W/kg in Prokaryotes correspond to C-value diapason from 10^{-3} p.g., to 10^{3} p.g.

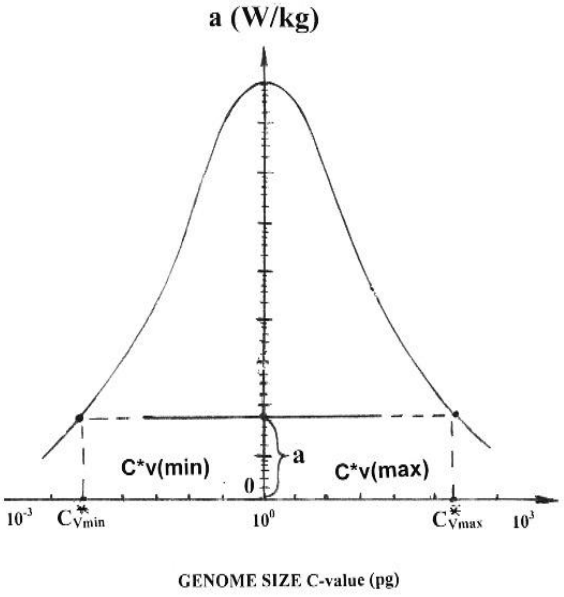

Fig. 3: We look for the relationship between the values of the metabolic potential 'a' and $C^*_{v(max)}$ diapason (from Cgeometric mean ~ 1 to 10^3 p.g.,) i.e., the right part of the bell-shaped curve, as well as the relationship between the values of the metabolic potential 'a' and $C^*_{v(min)}$ diapason (form Cgeometric mean ~ 1 to 10^{-3} p.g.,) i.e., the left part of the bell-shaped curve

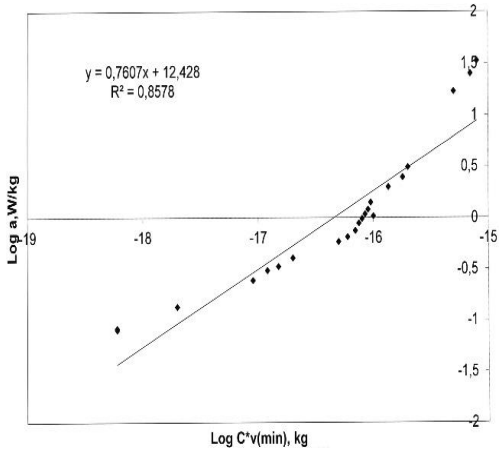

Fig. 4: Relationship between the values of 'metabolic potential' and corresponding values of C*v(min) for minimal genome size

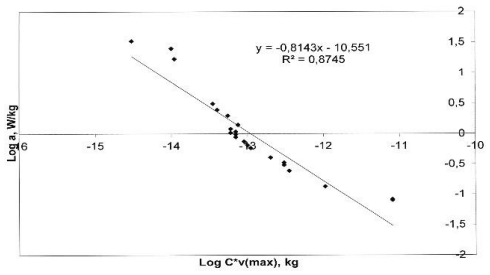

Fig. 5: Relationship between the values of 'metabolic potential' and corresponding values of C*v(max) for maximum genome size

From Fig. 1 and 2, it can see that the genome size varies around an optimal interval of C-values, which is common for all taxa (Bacteria, Protozoa, Plants, Poikilotherms, Mammals, Aves). This common diapason of 1-3 p.g., appears 'geometric mean' ($C^*_{v(gm)}$ of hole C_v- diapason from 10^{-3} p.g., to 10^3 p.g., In Table 2 the values of the product ($a \times C^*_{v(gm)}$) are calculated for $C^*_{v(gm)}$ =1 p.g. From Table 2 it can see that the values of the product ($a \times C^*_{v(gm)}$ change from 0.8×10^{-16} J/s in Prokaryotes to 3.339×10^{-14}J/s in Aves i.e., 417 folds. The data analysis for Mean value ± SD shows that:

$$a \times C^*_{v(gm)} = 4.25\times10^{-15} \pm 8.91\times10^{-15}\ J/s \qquad (6)$$

The basal metabolic rate in the order of ~10^{-16} - 10^{-14} J/s is typical for Bacterial growth and endogenous metabolism of the big bacteria (Atanasov, 2005; Makarieva *et al*., 2005). In this case, the product $a\times C^*_{v(gm)}$ changes about 2.5 orders of magnitude, but the mean of Eq. 6 has the same order of magnitude as the mean of Eq. 5. In this case, the product $a\times C^*_{v(gm)}$ can regard rather as a parameter than as a constant.

Table 1: Organismal taxa, C-values and mean metabolic potentials ([a]mean ± SE (W/kg))

N Taxa	C-value (Cv, p.g.,)	[a]mean ± SE (W/kg)
1. Prokaryotes		
Archea	2×10^{-3}- 6×10^{-3}	0.08
Bacteria	8×10^{-4}- 2×10^{-2}	
2.Sponges	7×10^{-2}- 20	0.0825±0.05750
3.Protozoa	5×10^{-3}- 8×10^{2}	0.1345±0.06047
4.Cnidarians	4×10^{-1}- 20	0.2445±0.05250
5.Echinoderms	5×10^{-1}- 4.4	0.305±0.030900
6. Plants	7×10^{-2}- 2×10^{2}	0.334±0.183000
7. Myriapods	4×10^{-1}- 3.0	0.405000000000
8. Flatworms	7×10^{-2}- 30	0.582000000000
9. Arachnids	8×10^{-2}- 5.7	0.648±0.118000
10.Algae	9×10^{-2}- 50	0.745±0.555000
11. Arthropods	1×10^{-1}- 50	0.881000000000
12. Molluscs	4×10^{-1}- 5.9	0.977±0.082500
13. Crustaceans	0.16-38	1.079±0.129000
14. Annelids	6×10^{-2}- 7.6	1.2±1.00000000
15. Nematodes	9×10^{-2}- 20	1.4.0000000000
16. Amphibians		1.035 all amphibians (mean)
Frogs	0.95-12	1.655±0.205000
Salamanders	13-120	0.415±0.032000
17. Teleosts	4×10^{-1}- 4.4	1.98±0.2990000
18. Insects	1×10^{-1}- 16.9	2.471±0.679000
19. Reptiles	1.1-5.4	3.104±0.376000
20. Rotifers	5×10^{-1}- 1.0	17.000000000000
21. Mammals	1.7-8.4	25.09±0.9630000
22. Aves	1.0-2.2	33.39±1.0610000

Table 2: Calculated values of the product $a\times C^*_{v(min)}$, $C^*_{v(max)}$ and $C^*_{v(gm)}$

Taxona	(W/kg)	$C^*_{v(max)}$ (kg)	$a\times C^*_{v(max)}$ (J/s)	$C^*_{v(min)}$ (kg)	$a\times C^*_{v(min)}$ (J/s)	$C^*_{v(gm)}$ (kg)	$a\times C^*_{v(gm)}$ (J/s)
1. Prokaryotes	0.0800	8×10^{-12}	6.4×10^{-13}	6×10^{-19}	0.480×10^{-19}	1×10^{-15}	0.08×10^{-15}
2. Sponges	0.0825	8×10^{-12}	6.6×10^{-13}	6×10^{-19}	0.495×10^{-19}	1×10^{-15}	0.0825×10^{-15}
3. Protozoa	0.1345	10.5×10^{-13}	1.41×10^{-13}	2×10^{-18}	0.269×10^{-18}	1×10^{-15}	0.1345×10^{-15}
4.Cnidarians	0.2445	3.5×10^{-13}	0.855×10^{-13}	9×10^{-18}	2.2×10^{-18}	1×10^{-15}	0.2445×10^{-15}
5. Echinoderms	0.3050	3.0×10^{-13}	0.915×10^{-13}	1.2×10^{-17}	3.66×10^{-18}	1×10^{-15}	0.305×10^{-15}
6. Plants	0.3340	3.0×10^{-13}	1.002×10^{-13}	1.5×10^{-17}	0.516×10^{-17}	1×10^{-15}	0.334×10^{-15}
7. Myriapods	0.4050	2.0×10^{-13}	0.810×10^{-13}	2.0×10^{-17}	0.810×10^{-17}	1×10^{-15}	0.405×10^{-15}
8. Flatworms	0.5820	1.1×10^{-13}	0.640×10^{-13}	5.0×10^{-17}	2.91×10^{-17}	1×10^{-15}	0.582×10^{-15}
9. Arachnids	0.6480	1.0×10^{-13}	0.648×10^{-13}	6.0×10^{-17}	0.3888×10^{-17}	1×10^{-15}	0.648×10^{-15}
10. Algae	0.7450	9.0×10^{-14}	0.670×10^{-13}	7.0×10^{-17}	0.5215×10^{-16}	1×10^{-15}	0.745×10^{-15}
11. Arthropods	0.8810	7.0×10^{-14}	0.617×10^{-13}	7.5×10^{-17}	0.6607×10^{-16}	1×10^{-15}	0.881×10^{-15}
12. Molluscs	0.9770	7.0×10^{-14}	0.684×10^{-13}	8.0×10^{-17}	0.7816×10^{-16}	1×10^{-15}	0.977×10^{-15}
13. Crustaceans	1.0790	7.0×10^{-14}	0.755×10^{-13}	8.5×10^{-17}	0.9171×10^{-16}	1×10^{-1}	1.079×10^{-15}
14. Annelids	1.2000	6.0×10^{-14}	0.720×10^{-13}	9.0×10^{-17}	1.08×10^{-16}	1×10^{-15}	1.2×10^{-15}
15. Nematodes	1.4000	7.5×10^{-14}	1.05×10^{-13}	9.5×10^{-17}	1.33×10^{-16}	1×10^{-15}	1.4×10^{-15}
16. Amphibians	1.0350	6.0×10^{-14}	0.621×10^{-13}	1.0×10^{-16}	1.35×10^{-16}	1×10^{-15}	1.035×10^{-15}
17. Teleosts	1.9800	5.5×10^{-14}	1.089×10^{-13}	1.5×10^{-16}	2.97×10^{-16}	1×10^{-15}	1.98×10^{-15}
18. Insects	2.4710	4.0×10^{-14}	1.096×10^{-13}	1.8×10^{-16}	0.445×10^{-15}	1×10^{-15}	2.71×10^{-15}
19. Reptiles	3.1040	3.5×10^{-14}	1.086×10^{-13}	2.0×10^{-16}	0.621×10^{-15}	1×10^{-15}	3.104×10^{-15}
20. Rotifers	17.0000	10×10^{-15}	1.70×10^{-13}	5.0×10^{-16}	0.850×10^{-14}	1×10^{-15}	17×10^{-15}
21. Mammals	25.0900	8.0×10^{-15}	2.0×10^{-13}	7.0×10^{-16}	1.756×10^{-14}	1×10^{-15}	25.09×10^{-15}
22. Aves	33.3900	3.0×10^{-15}	1.002×10^{-13}	8.0×10^{-16}	2.670×10^{-14}	1×10^{-15}	33.39×10^{-15}

Discussion

In this study, we have to show that during the increase of the order of the organismal complexity in evolution, expressed by the metabolic potential a (W/kg), the C-value diapason decrease. The organisms with negligible and low complexity characterized with low values of coefficient *a* have high values of C-value diapason. The organisms with high complexity are characterized by a high value of the 'metabolic potential' and a low value of the C-value

diapason. In some theoretical approaches to the pattern of metabolic potential during evolution, some researchers such as Sewertzoff (2010) accept the hypothesis that the general energy for vital activities of animals increased in the course of evolution. The later concrete definition of this theory by Ivlev (1963) has stimulated Dolnik (1968) to the idea that the evolution of the animals is connected with a steady increase in the rate of standard metabolism i.e., of mass-specific consumption rate of oxygen in a state of low activity at 20°C for poikilotherms and the thermoneutral zone for homeotherms.

Zotin (1990) explained the change of 'metabolic potential' with the connection between upper limits for the increase of metabolic potential and body temperature of poikilotherms and homeotherms. The other author Swenson and Turvey (1991) explained this fact with thermodynamic reasons for perception-action cycles. From our point of view, the increase of metabolic potential and decrease in genome size can be explained by the increase in sensors, nervous systems and the brain of the organisms during evolution. This leads to arise of sensor information for orientation and adaptation of organisms, which is connected to an increase in organismal complexity and metabolic potential. The very simplest organisms can be adapted to the environment preferably by the genetic path of biochemical processes. On the contrary, the more complex organisms can move to a better environment (good perception-action cycle). In this sense, we can consider the values of metabolic potential as qualitative indicators of the evolution of sensory systems of organisms. The obtained result shows that the metabolic and genomic characteristics of the simplest bacterial organisms represent the natural scale against which the metabolic and genomic characteristics of all the more complex organisms that emerged after them are adjusted. The data analysis for the product ($a \times C^*_v$) shows that this product appears nearly constant parameter, representing the given standard metabolic rate of the bacterial cells in the range of $\times 10^{-15}$-$\times 10^{-13}$ joule per second (Eq. 7-9):

$$a \times C^*_{v(max)} = 1.5 \times 10^{-13} \pm 1.678 \times 10^{-13} \quad (7)$$

$$a \times C^*_{v(min)} = 2.15 \times 10^{-15} \pm 6.62 \times 10^{-15} \quad (8)$$

$$a \times C^*_{v(gm)} = 4.25 \times 10^{-15} \pm 8.91 \times 10^{-15} \quad (9)$$

Indeed, in his previous research, Atanasov (2016a, b) has shown that the mass, size, doubling time, and density of bacterial cells have remained constant for billions of years, as they are determined by the fundamental physical constants. (Gravitational constant and Planck constant). Through bacteria, these two fundamental physical constants have built a natural scale for other living organisms. In this sense the relationship (4): $A \times C^*_{v(max)} = 1.5 \times 10^{-13}$J/s can regard as a universal statistical connection and compare with the universal metabolism-mass relationship ($P = aM^k$). In the future, it can analyze a new statistical connection between P/M^k and $P_{bacteria}/ C^*_{v(max)}$ ratio, for the basic taxonomic groups, giving in the mind that $P_{bacteria} = 1.5 \times 10^{-13}$ J/s = const.). The ratio $P/P_{bacteria} \sim M^k/ C^*_{v(max)}$ can present some new universal connection between metabolism, mass, and genome size of the living organisms. The big scientific interest is the idea of whether a given combination of parameters (a, $C^*_{v(max)}$, k, M) cannot be related to the place of animal orders in the evolutionary tree. In some previous studies by Atanasov and Dimitrov (2002) and Atanasov (2005), the authors have shown that in the process of evolution the values of power coefficient '*k* 'range from 1.0 to 0.67 and form several evolutionary groups. This idea can be subject to further study due to the possibility of classifying organism groups according to several evolutionary parameters.

As a direct proof of the possibility the metabolic and cellular parameters of bacterial cells represent a natural scale for more complex organisms, we can give a new interpretation of the biological meaning of metabolic potential. Other scientists proposed to use the linear coefficient 'a' from Eq. (1) as a measure of standard metabolism in different species of animals. This implies that there is a comparison between hypothetical animals of 1 g or 1 kg body mass that do not necessarily exist in nature. However, this factor can be given another, real biological meaning. If we bring the values of the coefficient (from 0.1 to 34 W/kg) to the average bacterial mass (about 10-15 kg) we will get a metabolic rate in the bacterial range. Indeed for Bacteria, if we reduce the value of a = 0.08 W/kg not to 1 kg, but to the average bacterial mass (10-15 kg) we will get a = 0.08 × 10-15 Watts per 10-15 kg or 8.10-17 J/s per 1 bacterial cell. The same calculation at the value of the metabolic potential for birds: A = 34×10-15 W per 10-15 kg gives a metabolic rate of 0.34.10-13 J/s per 1 bacterial cell. Considered in this way, the biological meaning of metabolic potential 'a' acquires a real biological meaning. The metabolic potential values thus obtained are bacterial metabolism values taken as a benchmark for comparing the metabolism of higher organisms.

Conclusion

In this study, we have shown that there is a connection between the metabolic potential (the coefficient 'a' in metabolic-mass relationship $P = aM^k$, where P-basal metabolic rate, M-body mass, k-power coefficient) and the corresponding genome size (C-value diapason) of the

given organismal taxon. With the increase of the metabolic potential of living organisms in evolution, the C-value diapason of a given taxon decreases. This finding can explain the genome-size enigma.

Acknowledgment

'I would like to thank the Medical Faculty, Thracian University for supporting this study'

Author's Contributions

Atanas Todorov Atanasov: Designed the research plan and organized the study. Coordinated the data-analysis and wrote of the manuscript. Summarizing and interpreting the results.

Dimitar Todorov Valev: Done the statistical calculations and estimations. Drawing of Fig. 4 and 5.

Ethics

This article is original and contains unpublished materials. The corresponding author confirms that all of the other authors have read and approved the manuscript and no ethical issues are involved.

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