THE CHANGE OF POWER COEFFICENT IN 'METABOLISM-MASS' RELATIONSHIP ACROSS LIFE'S TAXONS DURING EVOLUTION: PREDICTION FOR 'MASS-DEPENDENT METABOLIC MODEL'

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ABSTRACT

In this work we have to show that during the increasement of the order in the organisms from Unicellular to Plants, Poikilotherms and Homeotherms, the power coefficient in 'metabolism-mass' relationship $P=aM^k$ changes from taxa to taxa varying between the optimal value of k=0.85-0.90. The organisms with high complexity and differentiation (non-continuously growing organisms) are characterized with values of exponent k lower than 0.85-0.90. The organisms with low complexity, differentiation, and high growing processes (continuously growing organisms) are characterized with value of exponent k higher than 0.85-0.90. The ontogenetic organism has values of k around 0.85-0.90. Here, we presented for first time a new "mass-dependent metabolic model" based on connection between power coefficient k and growing processes.

Key words: metabolism, exponent, poikilotherms, mammals, aves, mass-dependent metabolism.

INTRODUCTION

Bioenergetics is connected with evolution of organisms. Handbooks of bioenergetics show that the basal metabolic rate (P, J/s) of animals is connected with their mass (M, kg) by the equation

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

The coefficient a means a mass-specific metabolic rate for an organism with unit body mass (1g or 1kg). The biological mean of power coefficient (exponent) k is trouble.
Organismal complexity is positively correlated to body size (1, 2). Both size and complexity have increased throughout the evolutionary history of life (3, 4, 5). While these patterns are widely accepted, the mechanisms behind the evolution of organismal complexity are poorly understood (6). However, there is not any standard definition of complexity. McShea (7) 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 increasements in the body size of the organism (1, 2). 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 (5, 8). However, none 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 macroevolution (9, 10). In the contrary, Makarieva et al. (11) have showed that the mean mass-specific metabolic rate is strikingly similar across life's major domains and has an evidence for life's metabolic optimum.

The scaling of basal metabolic rate with body mass (eqn. 1) has long been a controversial

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topic (12). Some investigators (13) have claimed that the slope k in eqn. 1 typically obeys a universal 3/4 – power law resulting from the geometry of resource-transport networks. After surveying numerous data sets, several workers concluded that the body-size scaling of metabolic rate is highly variable and that there is no single universal scaling exponent k. Substantial variation in exponent k has been observed both among taxa (14, 15, 16, 17, 18, 19, 20) and others physiological states. Furthermore, many log-log metabolic scaling relationships are nonlinear and cannot be represented by a single power function (15). In previous work Atanasov and Dimitrov (14) have showed that power coefficient k changes in interval 0.67-1.0 from one to other taxonomic groups along evolution, but mean value of power coefficient for studied main taxonomic groups is 0.807. Nearly the same, higher than 0.75 power coefficient (exponent), has been reached by other authors too. Atanasov and Dimitrov (14) have proposed that power coefficient k might represent the increase of complexity of animal organization between major taxonomic groups and domains (Prokaryotes, Eukaryotes, Poikilotherms, Mammals and Aves). The purpose of this investigation is to study the direct connection between values of power coefficient k and corresponding taxonomic groups as a prediction of 'mass-dependent metabolic model'.

DATA AND METHODS

The data for power coefficient (exponent) k in 'metabolism-mass' relationship $P=aM^k$ was collected from other literature and scientific sources given in Table 1. Most 'metabolism-mass' scaling relations were examined using least-squares regression analyses. All taxonomic groups and their corresponding values of exponent k are given in Table 1. The statistical software 'STATISTICA' was used for all calculations.

RESULTS

On **Table 1** are given data for 236 taxonomic groups and species and their corresponding values of power coefficient ($k \pm 95\%$ confidence limits, C.L.) from eqn.1. The taxonomic groups are ranged following a classification similar toTudge (21).

On **Fig.1** are presented main taxonomic groups and domains (Prokaryotes, Eukaryotes, Plants, Invertebrates Poikilotherms, Vertebrates

Pokilotherms, Ontogenetic species, Species with Minimal and Maximal metabolic rate, Aves and Mammals) and their corresponding interval of k-data from Table 1. The point on every vertical k-data line is geometric middle of k-data interval. It is observed that values for exponent k between 0.85 and 0.9 are common for every group and domains (see horizontal line on Fig.1). The k-values of intervals (and geometric mean-point of intervals) for Prokaryotes, Plants, Poikilotherms(vertebrates) with minimal MR are placed over 0.85. The k-values of intervals (and geometric mean-point of intervals) for Aves, and Mammals are placed under k=0.85. The k-values of intervals (and geometric mean-point of intervals) for Eukaryotes, Poikilotherms (invertebrates), Ontogenetic MR and High MR are placed over and under the line of k=0.85. The dashed S-line on Fig.1 marks the geometric middle of k-values for all taxonomic groups. The diapason of values corresponding to geometric middle-point of all taxonomic groups is between k=0.65(for Mammals) and k=1.35(for prokaryotes) with mean value equal to k=1.0. However, this geometric mean point is far away from k= 0.75 and k=0.67.

On **Table 2** are calculated the mean algebraic values of power coefficient k (mean ± SD) for all taxonomic groups and graphically presented on Fig.2.The groups that are placed on the left of Ontogenetic group present "the continuously growing organisms". Such organisms are Protozoa, Plants and Poikilotherms (invertebrates and vertebrates). The groups that are placed on the right of Ontogenetic group present "the non-continuously growing organisms". Such organisms are Aves and Mammals. The Ontogenetic group (Ontogenetic MR) appears in the middle, between "continuously" and "non-continuously" groups. Exactly, the group with Ontogenetic, Minimal MR and High metabolic rate shows "transitional" groups with short-living periods and after that they are transformed in group with stabile physiological state (Poikilotherms, Mammals and Aves). The 'stressed' organisms (starving Prokaryotes, Mammals and Aves in exercise, running, torpor, hibernating state and others) have power coefficient close to 1.0. These changes of power coefficient have a biological mean of 'adaptation' and have transitional character. However, the mean algebraic values of exponent k are far away from k= 0.75 and k=0.67.

Table 1. *Taxonomic group of organisms and values of k in eqn. P = aM^k*

N TAXONOMIC GROUP	k± 95% C.L.	Reference
(Basal Metabolic rate)		
PLANTS		
1. Field/US tree saplings (24°C)	1.062-1.117	(18, 22)
2. GH/tree seedlings(24°C)	1.012-1.037	(18, 22)
3. GC/tree seedlings(24°C)	1.027-1.058	(18, 22)
4. GH/herb seedlings(24°C)	0.942-0.967	(18, 22)
5. Trees(Japan sample) (24°C)	0.858-0.968	(18, 22)
VASCULAR PLANTS		
6. Green leaves	1.0	(11)
7. Tree saplings	1.0	(11)
8. Seedlings	1.0	(11)
9. Leaves (pooled)	0.92	(18, 22)
10.Broad leaves(photosynthesis)	0.97	(18, 22)
11.Needle leaves(photosynthesis)	1.01	(18, 22)
UNICELLULARS (BACTERIA, PROTOZOA)		
12. Prokaryotes (25°C)	1.79	(23)
13. Prokaryotes	1.0	(24)
14. Prokaryotes (32°C) (growth)	0.91	(25a, b)
15. Prokaryotes (30°C) (endogenous)	0.88	(25a, b)
16. Eukaryotes(20°C)	0.92	(23)
17. Eukaryotes	0.74	(26)
18. Eukaryotes	0.70	(24)
19. Protozoa(20°C) (endogenous)	0.90	(25)
20. Protozoa(20°C)(starved cells)	0.74	(27, 25a, b)
21. All Protozoa	0.99	(23)
22. All Protozoa	0.95	(24)
23. All Protozoa (20°C)	0.74	(28)
24. All Protozoa (20°C)	0.83	(29)
PHOTOAUTOTROPHS		
25. Cyanobacteria	1.0	(11)
26. Eukaryotic microalgae	1.0	(11)
27. Eukaryotic macroalgae	1.0	(11)
POIKILOTHERMS (INVERTEBRATES)		
28. PORIFERA	0.927	(15)
CNIDARIA		
29. Anthozoa (20°C)	0.86	(30)
30. Anthozoa	0.732±0.133	(15)
31. Scyphozoa	0.948±0.048	(15)
32. Hydrozoa	0.951±0.113	(15)
33. **CTENOPHORA**	0.935±0.172	(15)
34. **PLATYHELMINTES**	0.728±0.097	(15)
35. **NEMERTEA**	0.478	(15)
36. **BRYOZOA**	0.982±0.188	(15)
37. **ANTHOZOA(20°C)**	0.86	(29)
38. **BENTHIC ANTHOZOA**	0.732	(15)
39. **ANNELIDA(20°C)**	0.876	(14)
40. ANNELIDA	0.680±0.084	(15)
41. **AMPHIPODA**	0.900	(31)
42. **ISOPODA(*Idotea baltica*)**	1.07-1.20	(32)
43. **NEMATODA(20°)**	0.76	(26)

44. NEMATODA	0.677±0.117	(15)
45. NEMATODA(28°)	0.75	(33)
46. NEMATODA (marine) (15°)	0.73	(34)
47. NEMATODA(20°)	0.9-1.0	(35)
48. Soil-Inhabiting Nematodes(20°C)	0.62-0.72	(36)
Nematoda (0°C-15°C)		
49. *Alaskozetes antarcticus*	0.69-0.72	(37)
50. *Tetranychus cinnabarinus*	1.21	(38)
51. *Phytoselutus persimills*	0.97	(39)
52. **Rotifers(20°C)**	0.52	(26)
53. **Enchytraeids(20°C)**	0.85	(26)
54. **Mytes(20°C)**	0.67	(26)
55. **Polychaetes(20°C)**	0.850±0.106	(39)
56. **Oligochaeta(20°C)**	0.61	(29)
57. **Xipnosura(20°C)**	0.81	(29)
58. **ONYCHOPHORA**	0.932	(15)
59. **GASTROPODS (20°C)**	0.78±0.04	(40)
ARTHROPODA		
60. **Terrestrial arthropods (25°C)**	0.86	(41)
61. **Arachnida(25°C)**	0.854±0.076	(15)
62. Arachnida(20°C)	0.80	(34)
63. Spiders(22°C)	0.781±0.117	(42, 43, 44)
64. **Gastropods (20°C)**	0.78±0.04	(39)
65. **Crustaceans (all) (20°C)**	0.74±0.06	(45)
66. **Crustaceans (all) (20°C)**	0.60-0.79	(46)
67. **Crustaceans(all) (20°C)**	0.81	(29)
68. **Benthic Crustaceans**	0.72	(47)
Branchipoda		
69. Anostraca	0.641±0.306	(15)
70. Conchostraca	0.840	(15)
71. Notostraca	0.803	(15)
72. Cladocera	0.863±0.086	(15)
Maxillopoda		
73. Ostracoda	0.746	(15)
74. **Copepods(15°C)**	0.814	(48)
75. Copepoda	0.845±0.060	(15)
76. Artemia(20°C)	0.77	(34)
77. Uca pugilator(20°C)	0.78	(34)
78. Homarus (20°C)	0.88	(34)
79. Balanus(20°C)	0.794	(34)
80. Cirripedia	0.694±0.114	(15)
Malacostraca (Eucarida)		
81. Euphausiacea	0.859±0167	(15)
82. Decapoda	0.718±0.056	(15)
Malacostraca (Peracarida)		
83. Peracarida	0.686±0.088	(15)
84. Isopoda	0.723±0.027	(15)
85. Amphipoda	0.719±0.085	(15)
86. **Myriapoda**	0.756±1.187	(15)
87. **Insecta**	0.750	(49)
88. Insecta	0.830±0.036	(15)
89. Non-winged insects(25°C)	0.821±0.065	(50)
90. Winged insects(25°C)	0.717±0.048	(50)
91. Winged insects(22°C)	0.662±0.058	(51)
92. Hymenoptera(20°C)	0.92	(34)

93.	Coleoptera(20°C)	0.77	(34)
94.	Collembola	1.0	(34)
95.	Ant (*Atta sexdens*)	0.79	(34)
96.	**ECHINODERMATA**	0.720±0.078	(15)
	CHORDATA		
	Urochordata		
97.	Ascidiacea	0.775±0.210	(15)
98.	Colonial ascidians (20°C)	0.828	(52)
99.	Salpida	1.110±0.233	(15)
	MOLLUSCA		
100.	All Molluscs	0.76	(29)
101.	Bivalves(20°C)	0.781±0.06	(15)
102.	Cephalopoda(20°C)	0.915±0.209	(15)
103.	Gastropoda(20°C)	0.717±0.036	(15)
	Cephalopod families(20°C)		
104.	Loliginidae	0.916±0.010	(46)
105.	Ommastrephidae	0.923±0.015	(46)
106.	Gonatidae	0.98	(46)
107.	Octopodidae	0.73±0.054	(46)
108.	Histioteuthidae	0.76±0.083	(46)
109.	Cranchidae	0.81±0.089	(46)
110.	Bolitaenidae	0.75±0.072	(46)
111.	Vampyroteuthidae	0.77±0.115	(46)
112.	**All Cephalopoda(20°C)**	0.8±0.036	(46)
113.	Anguilliformes (benthic eels)	0.80	(53)
114.	Medusae(jellyfish)	0.78	(53)
115.	Mytilus(20°C)	0.918	(14)
116.	Antarctic scallop(20°C)	0.807	(54)
117.	Littorina(20°C)	0.902	(14)
118.	Nassa(20°C)	0.820	(14)
119.	ACRANIA(20°C)	0.91	(29)
120.	CYCLOSTOMATA(20°C)	0.80	(29)
	POIKILOTHERMS (VERTEBRATES)		
121.	FISHES (38°C)	0.879±0.06	(19)
122.	Teleost fishes(20°C)	0.833±0.007	(55)
123.	Teleost fishes(20°C)	0.793±0.023	(52)
124.	Sea Trout (*Salmo trutta trutta*)	0.86	(56)
125.	**ALL AMPHIBIA(38°C)**	0.844	(19)
126.	Amphibians(20°C)	0.884	(48)
127.	Amphibians(20°C)	0.884±0.05	(19)
128.	Anura(20°C)	0.842±0.103	(15)
129.	Urodela(all spp.)(15°C)	0.807±0.090	(15)
130.	Urodela(excluding spp.>30g)	1.077±0.139	(15)
131.	**All REPTILES(38°C)**	0.769	(19)
132.	All Reptiles(20°C)	0.768-0.800	(29)
133.	Reptiles(38°C)	0.768±0.04	(19)
134.	Reptiles(Field Metabolic Rate)	0.889±0.059	(15)
135.	Squamata (all. spp)(30°C)	0.702±0.038	(15)
136.	Squamata(excluding boids)	0.807±0.040	(15)
137.	Squamata(boids only)	1.179±0.351	(15)
138.	**LIZARDS(20°C)**	0.83	(28)
139.	Lizards(20°C)	0.83	(48)
140.	**SNAKES(20°C)**	0.980	(29)
141.	Snakes(20°C)	0.86	(34)

142. Boidae(20°C)	1.09	(34)
143. Colubridae(20°C)	0.98	(34)
144. Leatherback Sea Turtles (14°C)	0.93	(58)
145. Leatherback Sea Turtles(19°C)	0.86	(58)
146. Leatherback Sea Turtles(24°C)	0.89	(58)
147. Leatherback Sea Turtles(34°C)	0.77	(58)
148. Leatherback Sea Turtles(24°C)	0.88(mean)	(58)
MAMMALS		
149. All Mammals	0.693±0.011	(59)
150. All Mammals	0.75	(60)
151. All Mammals(38°C)	0.676±0.013	(46)
152. All Mammals(Field MR)	0.731-0.750	(12)
153. Small Mammals (2.5g-100g)	0.23	(61)
154. Small Mammals (2.5g-260g)	0.42	(61)
155. All Wild Mammals	0.713±0.009	(59)
156. **Prototheria**	0.379	(58)
157. **Prototheria**	0.572	(59)
158. **Theria**	0.697±0.010	(58)
159. **Metatheria**	0.747±0.013	(58)
160. **Metatheria**	0.698	(59)
161. Polyprotodonts	0.753±0.046	(62)
162. Diprotodonts	0.756±0.018	(62)
163. **Eutheria**	0.696±0.011	(58)
164. **Eutheria**	0.761	(62)
165. **Eutheria**	0.741	(59)
166. Marsupials	0.754	(62)
167. Edentata	0.656±0.052	(58)
168. Chiroptera	0.714±0.055	(58)
169. Insectivora	0.418±0.085	(58)
170. Lagomorpha	0.668±0.085	(58)
171. Rodents	0.751±0.010	(62)
172. Carnivora	0.738±0.010	(58)
173. Perissodactyls	0.793	(62)
174. Artiodactyls	0.811±0.076	(62)
175. Artiodactyls	0.802±0.060	(58)
176. Bats	0.790±0.136	(62)
177. Primates	0.757±0.028	(62)
AVES		
178. All Aves(38°C)	0.644±0.03	(19)
179. All Aves(Field Metabolic Rate)	0.681±0.036	(19)
Nonpasseriformes		
180. Charadriiformes	0.89	(63)
181. Strigiformes	0.77	(63)
182. Anseriformes	0.73	(63)
183. Galliformes	0.71	(63)
184. Falconiformes	0.66	(63)
185. Gruiformes	0.66	(63)
186. Psittaciformes	0.59	(63)
187. All Nonpasseriformes	0.729-0.734	(63)
188. Passeriformes	0.704-0.726	(63)
ECTOTHERMS AND ENDOTHERMS		
High Metabolic Rate		
189. Exercise of Ectothermic animals (Active MR)	0.918	(17)

190. Marsupials (exercise)	0.882	(64)
191. Mammals (running)(AMR)	0.870±0.06	(65)
192. Wild Mammals (MMR)	0.790	(66)
193. Domestic Mammals (MMR)	0.885	(66)
194. Mammals (exercise-indused)	0.87	(20)
195. Mammals (cold-induced)	0.65	(20)
196. Mammals (cold-induced)	0.668±0.060	(67)
197. Marsupials (cold-induced)	0.772	(64)
198. Birds(cold-induced)	0.600±0.033	(68)
199. Flying Insects(AMR)	1.08±0.062	(50)
200. Flying Aves(AMR)	0.87	(12)
201. Swimming fish, reptiles (MMR)	0.87	(28)
Strenuous activity (High MR)		
202. Athletic Mammals	0.942±0.050	(65)
203. Athletic Mammals	0.841±0.045	(69)
204. Nonathletic Mammals	0.849	(65)
205. Athletic Birds	0.837±0.107	(70)
206. Athletic Mammals&Birds	0.879±0.020	(71)
Minimal Metabolic Rate		
207. Immobile Insect pupae(25°C)	0.939-1.0	(12)
208. Diapausing Insect pupae(25°C)	1.013-1.04	(12)
209. Shallowly hibernating mammals(20°C)	0.794±0.064	(72)
210. Deeply hibernating mammals(5°C)	0.941±0.086	(72)
211. Hibernating Mammals (4.3°- 10.1°C)	0.879±0.082	(67)
212. Torpor (Bats)	0.96	(63)
213. Torpor (Mammals)	0.88	(63)
214. Torpor (Birds)	1.028±0.210	(63)
Ontogenetic Metabolic Rate		
215. All Invertebrates	0.7	(74)
216. Pelagic Invertebrates	0.98	(74)
217. Benthic Invertebrates	0.63	(74)
218. Terrestrial Invertebrates	0.78	(74)
219. Pelagic Salpida	1.11	(15)
220. Benthic ascidiacea	0.775	(15)
221. Pelagic crustaceans	0.873	(15)
222. Benthic crustaceans	0.735	(15)
223. Invertebrates species	0.947±0.046	(15)
224. Amphipoda	0.900±0.159	(15)
225. Mytilus(20°C) fast-growing larvae	0.9	(75)
226. Mytilus(20°C) slow-growing adult	0.7	(75)
227. Copepods (nauplii)	0.87-1.09	(76)
228. Snails (*Helix aspersa*)	1.03-0.74	(77)
229. Benthic bivalves	0.774	(15)
230. Pelagic Cephalopods	0.922	(16)
231. Nematoda	0.82	(78)
232. Vertebrates	0.82	(73)
233. Fish (20°C)	0.8	(79)
234. Cod *Gadus morhua*(larvae)	0.88-0.91	(53, 79)
235. Teleosts fish	0.8-0.88	(53, 79)
236. Frog(20°C)	0.97-1.02	(78)

Table 2.*Mean values of exponent k ± SD for other taxonomic groups*

N TAXONOMIC GROUP	Mean k± SD	n-number of species
1. Prokaryotes	1.116 ±0.380	5
2. Eukaryotes	0.864±0.117	11
3. Plants	0.996±0.061	16
4. Poikilotherms(invertebrates)	0.813±0.121	108
5. Poikilotherms(vertebrates)	0.878±0.108	26
6. Poikilotherms (All)	0.825±0.115	134
7. Ontogenetic MR	0.864±0.122	27
8. Minimal MR	0.947±0.078	10
9. High MR	0.837±0.112	18
10. Aves	0.703±0.035	6
11. Mammals	0.712±0.158	5
12. All(without Ontog., Max. MR, Min. MR)	0.831±0.159	170
13. All (without Ontog., Max. MR, Min. MR, Plants)	0.815±0.156	186
14. All	0.873±0.110	232
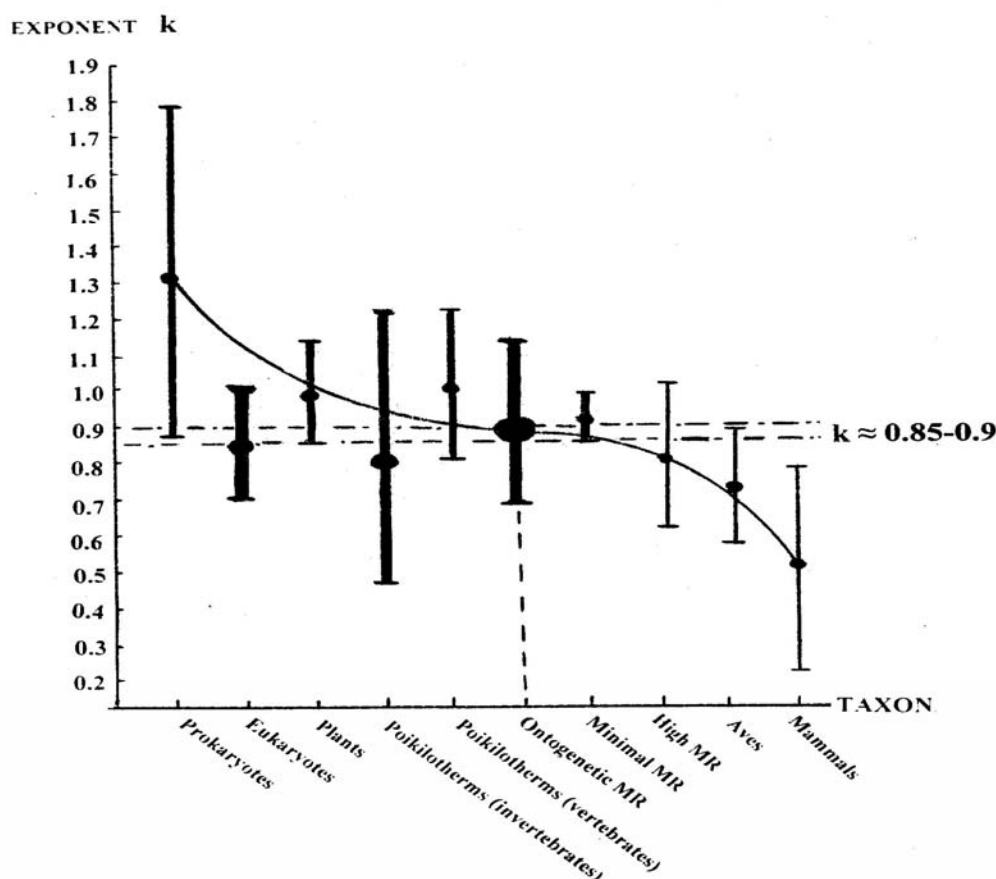
Fig.1. Main taxonomic groups and intervals of theirs corresponding exponent *k* given from Table 1. S-curve marked geometric middle point of *k*-intervals.

MASS-DEPENDENT METABOLIC MODEL

Here, for the first time, we present a new "mass-dependent metabolic model" based on connection between power coefficient *k* and growing processes in living organisms. In evolutionary aspect the most simple Prokaryotic organisms grow continuously and have no differentiation, while the simple

Eukaryotic (Plants and Poikilotherms) grow continuously, have relatively high differentiation (or low number of cell lines) and clearly express regeneration of organs and tissues. The organisms with high organization and complexity (Mammals and Aves) grow non-continuously, have higher differentiation (or high number of cell lines) and particularly express regeneration of some organs and tissue only.
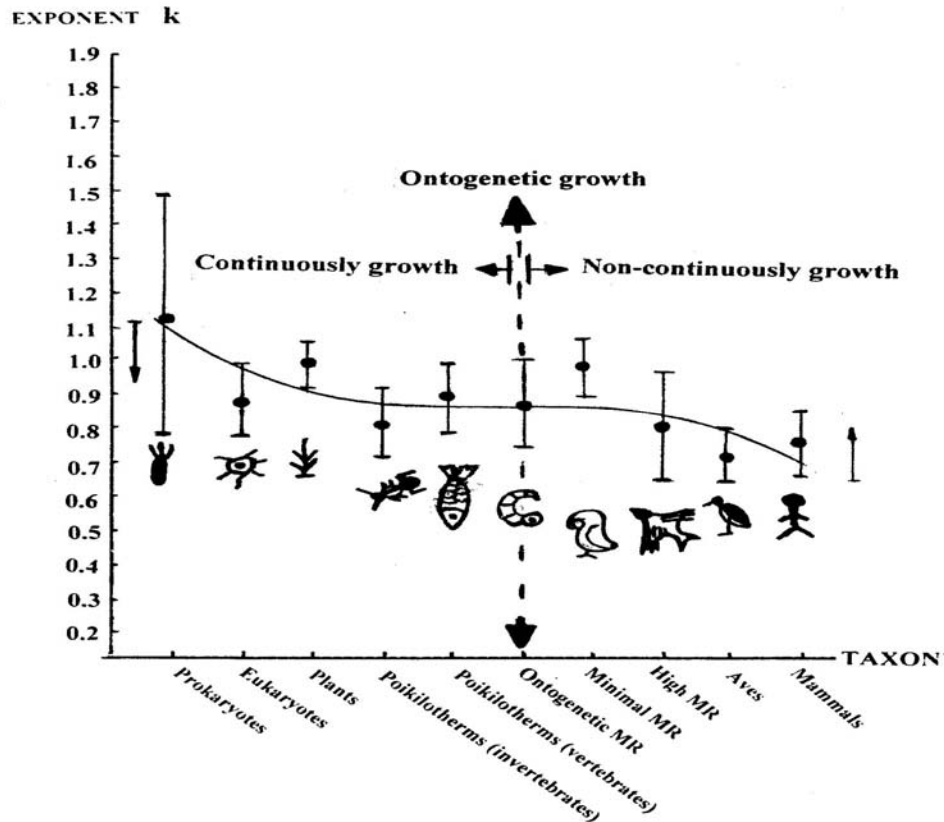

Fig.2. Main taxonomic groups and mean ± SD of their corresponding exponent *k* given from Table 2.

From 'complexity' point of view, we may separate three types of organisms with corresponding mass-specific metabolic rate: a first type organism with 'mass-specific stimulated metabolism' ($k > 1.0$), a second type organism with 'mass-specific independent metabolism' ($k \approx 1.0$), and a third type organism with 'mass-specific inhibited metabolism' ($k < 1.0$). In the first type of organisms (Prokaryotes), the growing of body mass and interaction between part of mass (structure and functional coupling between genes and cells) leads to high non-linear growth of metabolic rate i.e. $P = aM^{k>1.0}$ and growing(stimulation) of mass-specific metabolic rate too. From a thermodynamic point of view this process is irreversible (because of the increasing of the mass-specific metabolic rate for $k > 1.0$) and bacteria growth and divided by binary. They can only build the linear cell aggregates, live separately and have no differentiation of cells in aggregates. In the second type organisms (Eukaryotes, Plants, Poikilotherms and Embryos) the growing of body mass and interaction between part of organism leads to isometric-linear growth of metabolic rate $P = aM^{k \approx 1.0}$ and constantly mass-specific metabolic rate. From thermodynamic point of view this process appears to be reversible (because of constantly mass-specific metabolic rate for $k \approx 1.0$). The living cells build aggregates and form organisms with low differentiation and high-regeneration possibility. In the third type of organisms (Mammals and Aves) growing of body mass and interaction between part of organism (structure and functional coupling between genes, cells, organs, tissues, vascular, hormonal and neuronal systems etc.) leads to a low non-linear growth of metabolic rate

P $= aM^{k<1.0}$ and decreasing (inhibition) of mass-specific metabolic rate. From thermodynamic point of view this process is irreversible (because of decreasing of the mass-specific metabolic rate for $k < 1.0$). The living organisms grow non-continuously and are characterized with high differentiation of cells and low-regeneration possibility. The transition from 'mass-specific inhibited' to 'mass-specific stimulated' metabolism is accompanied by a transition from non-continuously to continuously growing organisms and acceleration of syntheses processes. This one allows us to connect the power coefficient k with complexity of organisms indirectly, trough intensity of growing processes. However, the organisms with negligible and low complexities are characterized with high growing states and negligible differentiation, and the ones with high complexity are characterized with low growing state and high differentiation of organs and tissues. The mass-specific stimulated metabolism, mass-specific independent and mass-specific inhibited metabolism leads to 'mass-dependent metabolic model'. According this model, the metabolic levels (P) depend on mass (M) trough values of exponent k. The values of exponent k correspond with interaction (structure and functional coupling) between parts of organisms (genes, cells, organs, tissues, vascular, hormonal and neuronal systems etc.) in a spatial or temporal scale. In the first type of organisms (Prokaryotes), the growing of body mass and interaction between cells leads to high non-linear growth of metabolic rate i.e. $P = aM^{k>1.0}$. In the second type organisms (Eukaryotes, Plants, Poikilotherms and Embryos) the body metabolism don't depends on body mass and interaction between parts of organisms that leads to isometric-linear growing of metabolic rate i.e. $P = aM^{k\approx1.0}$. In the third type of organisms (Mammals and Aves) growing of body mass and interaction between parts of organisms leads to inhibition of body metabolism i.e. to non-linear growing of metabolic rate $P = aM^{k<1.0}$. However, such model corresponds with definition of McShea (7) for biological complexity. The number of different parts within a hierarchy in organism (genes, cells, organs, vascular system etc.) correspond with coefficient a, while the number of interactions between parts correspond with exponent k. With the approaching of exponent k to 1.0 the

metabolism becomes mass-specific independent. If we present the 'metabolism-mass' equation (1) as 'mass-specific metabolism' form (P*=P/M):

$$P^*=P/M=aM^k/M^{1.0} \qquad (2)$$

We receive equation:

$$P^*/a=M^k/M^{1.0} \qquad (3)$$

In equation (3) the coefficient a corresponds to $M^{1.0}$ i.e. $k=1.0$ (mass-specific independent metabolism), while the 'current' mass-specific metabolic rate P^* corresponds to M^k. This shows that there are at least tree mechanisms for mass-regulation of metabolic level: one- by values of exponent k (i.e. interaction between parts of organism), two- by values of coefficient a (i.e. number of parts of organism) and three- by body mass M. For every given value of exponent k the corresponding coefficient a presents the mass-independent metabolism per unit of body mass. In this sense P^*/a represents the ratio between the 'current mass-specific metabolism' (P*) and the 'mass-specific independent' metabolism (a) and could have values above, equal or under 1.0 (mass-specific stimulated, mass-specific independent or mass-specific inhibited metabolism).

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