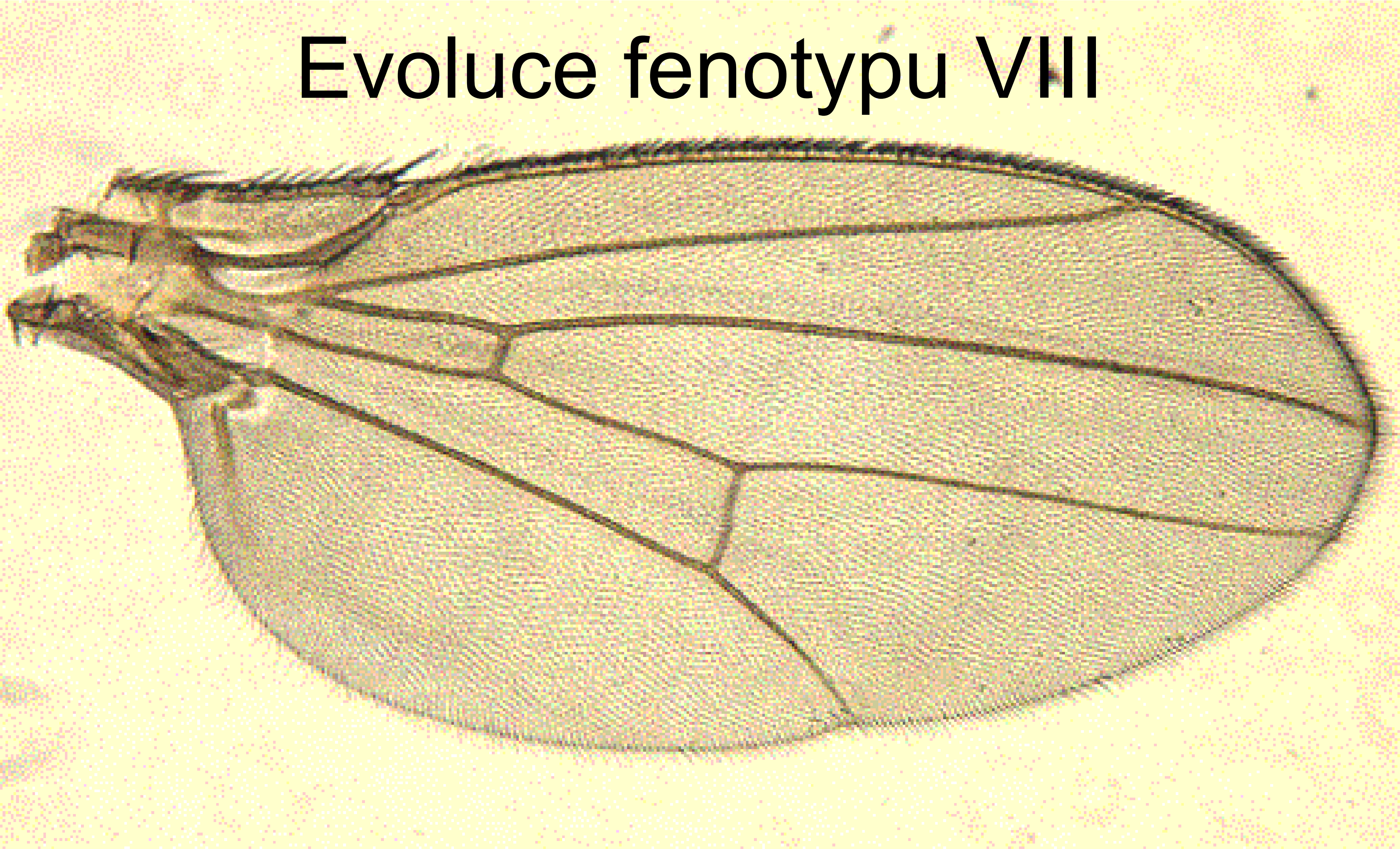
Evoluce fenotypu VIII



http://www.mheresearchfoundation.org

Vztah ontogenetické, statické a evoluční alometrie

Size and shape: the developmental regulation of static allometry in insects

Alexander W. Shingleton,[1]* W. Anthony Frankino,[2] Thomas Flatt,[3]
H. Frederik Nijhout,[4] and Douglas. J. Emlen[5]

BioEssays 29:536–548, © 2007

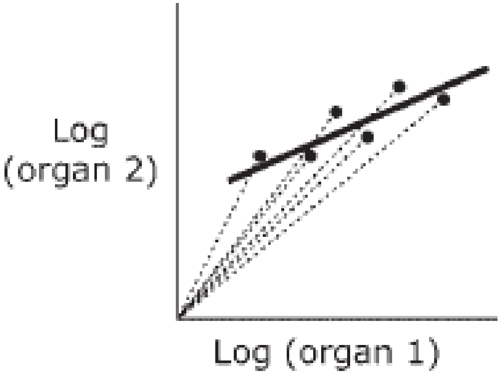


Figure 2. The relationship between evolutionary, static and ontogenetic allometries. If each point represents the organ sizes of a different species at the same developmental stage, then the solid line is an evolutionary allometry. If each point represents the organ sizes of a different individual within a species at the same developmental stage, then the solid line is a static allometry. In both cases, the allometry arises due to variation in the relative growth trajectories, or ontogenetic allometry, of the two organs (broken lines).

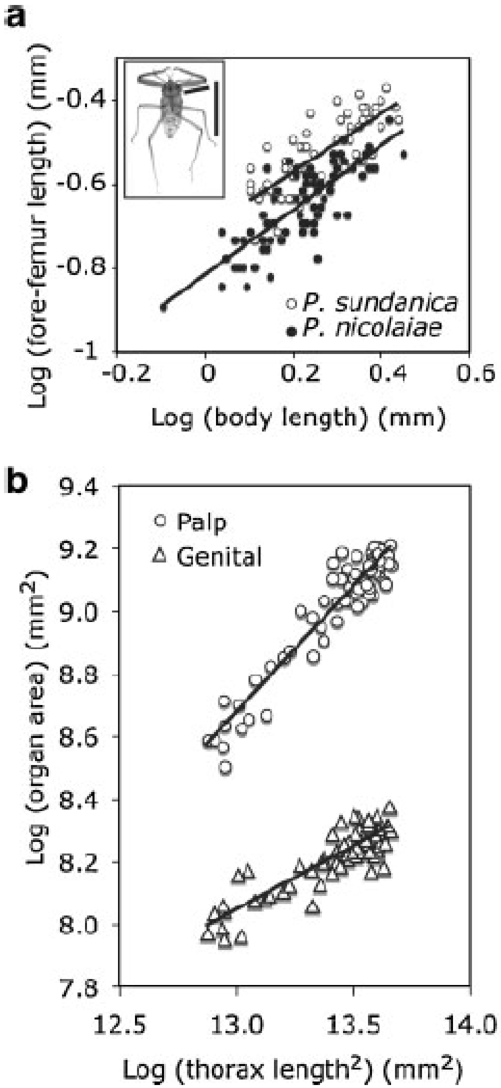


Figure 1. Static allometries can vary for the same organ between species and between different organs within a species. **a:** The static allometry of fore-femur length against body length for two soldier-aphid species, *Pseudoregma sundanica* (open circles) and *P. nicolaiae* (closed circles). Inset shows measurements on *P. sundanica*.[84] **b:** The static allometry of maxillary palp area and genital arch area for male OreR *D. melanogaster*. The palps are almost isometric to body size, while the genitals have a flatter allometry, such that larger flies have proportionally smaller genitals.

Statická alometrie může vzniknout složením norem reakce pro jednotlivé znaky

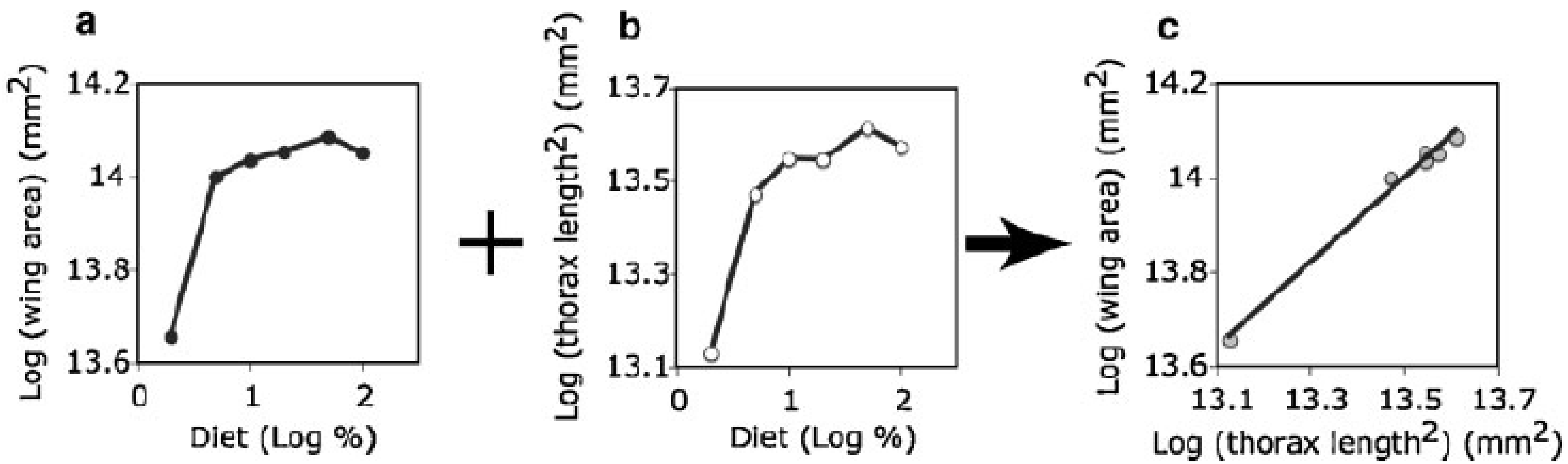


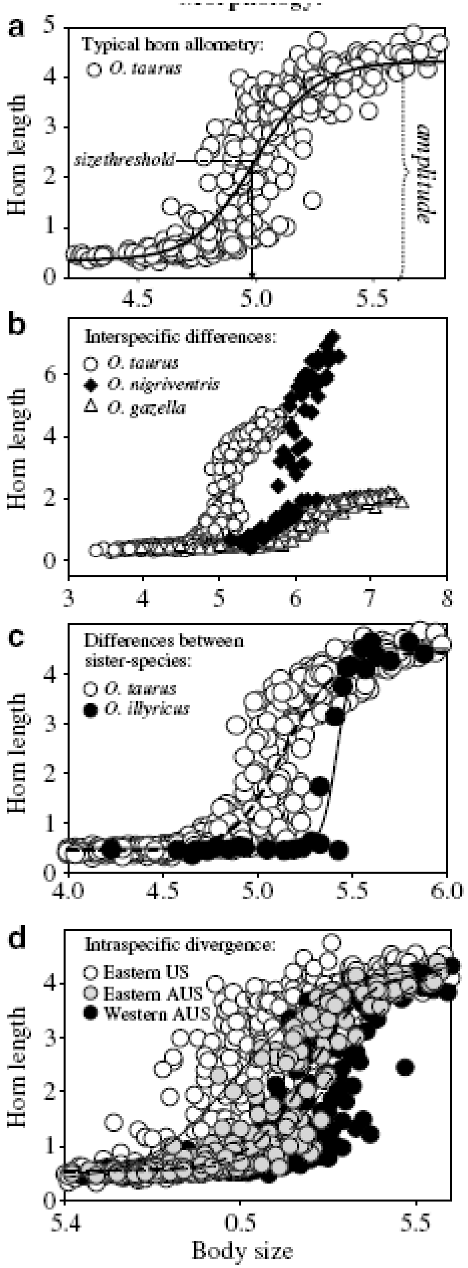
Figure 3. The relationship between reaction norms and allometries. The relationship between larval nutrition and **a** wing area and **b** thorax length in *Drosophila*. **c:** The two reaction norms can be re-plotted to reveal the nutritional static allometry between wing area and thorax length. All the flies were wild-type reared on a corn flour and molasses medium, diluted by 2% agar in water.

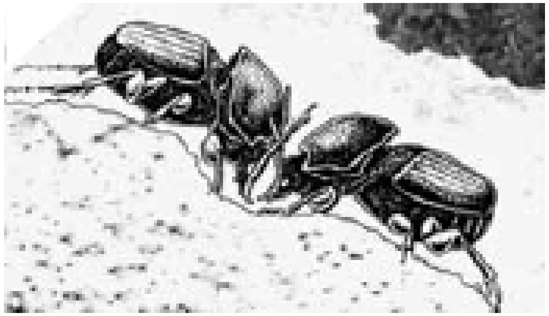
Složitější alometrie a jejich interpretace

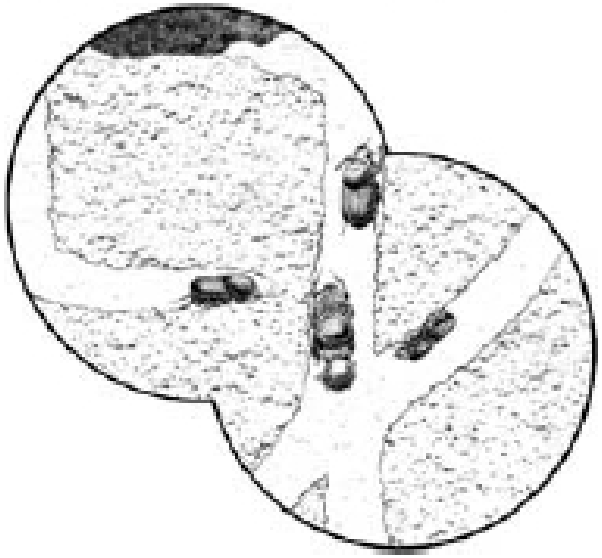
Integrating micro- and macroevolution of development through the study of horned beetles

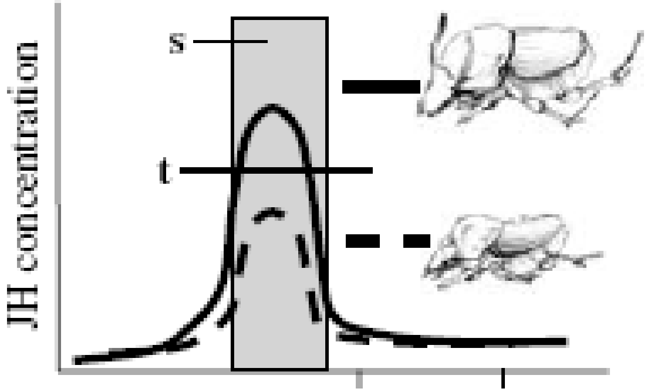
AP Moczek
Department of Biology, Indiana University, 915 E. Third Street, Myers Hall 150, Bloominton, IN 47405-7107, USA

Heredity (2006) 97, 168–178







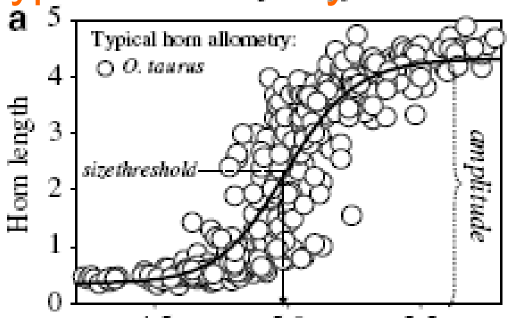


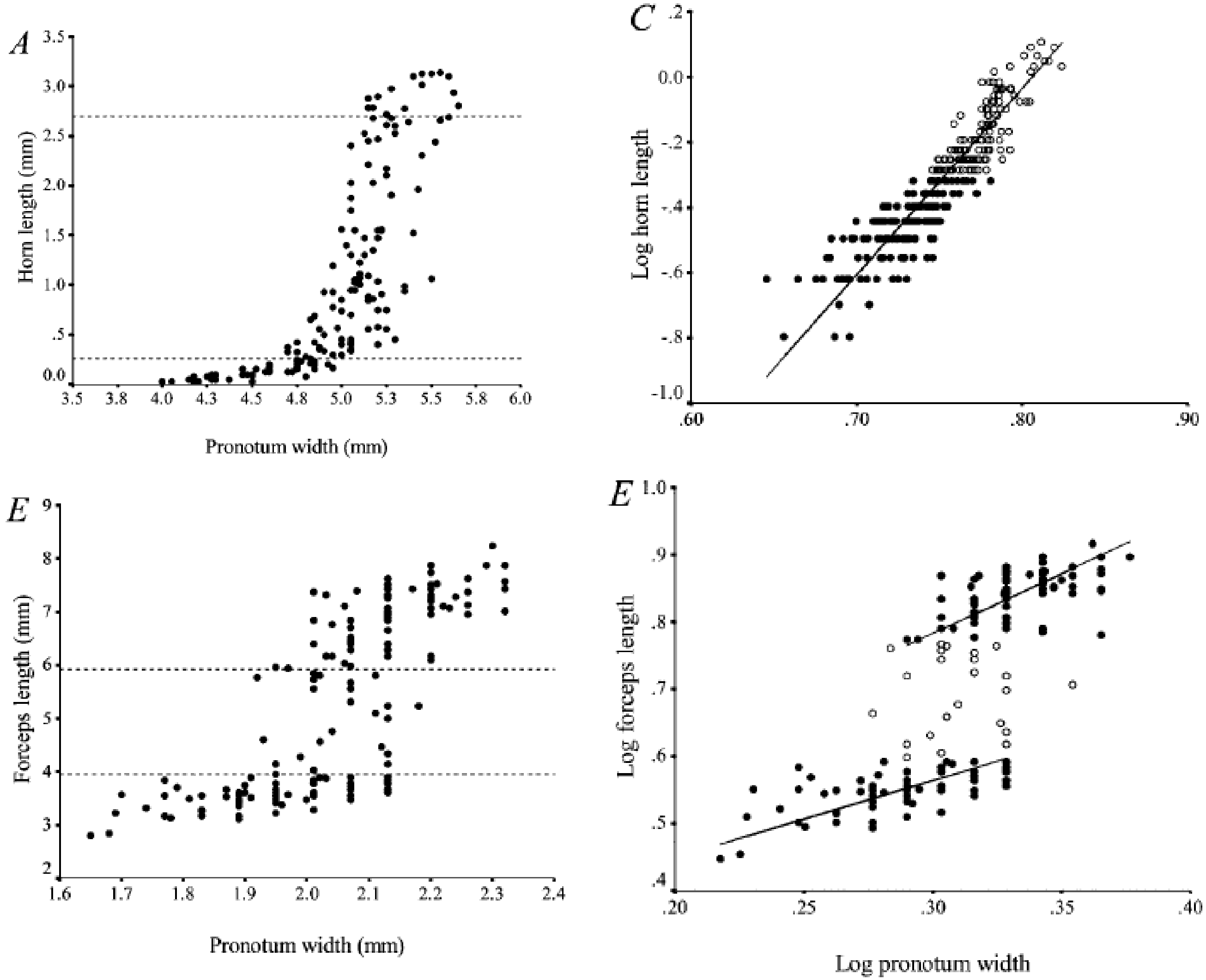
Interpretace mění pohled na proximátní mechanismus fenotypové variability.

Matters of Scale: Positive Allometry and the Evolution of Male Dimorphisms

VOL. 165, NO. 3 THE AMERICAN NATURALIST MARCH 2005

Joseph L. Tomkins,[1,*] Janne S. Kotiaho,[2,†] and Natasha R. LeBas[1,‡]





Proximátní mechanismy změny ve velikosti

- změna v množství mezibuněčné hmoty

Vol. 113, No. 1 The American Naturalist January 1979

SCALING OF SKELETAL MASS TO BODY MASS IN BIRDS AND MAMMALS

HENRY D. PRANGE, JOHN F. ANDERSON, AND HERMANN RAHN

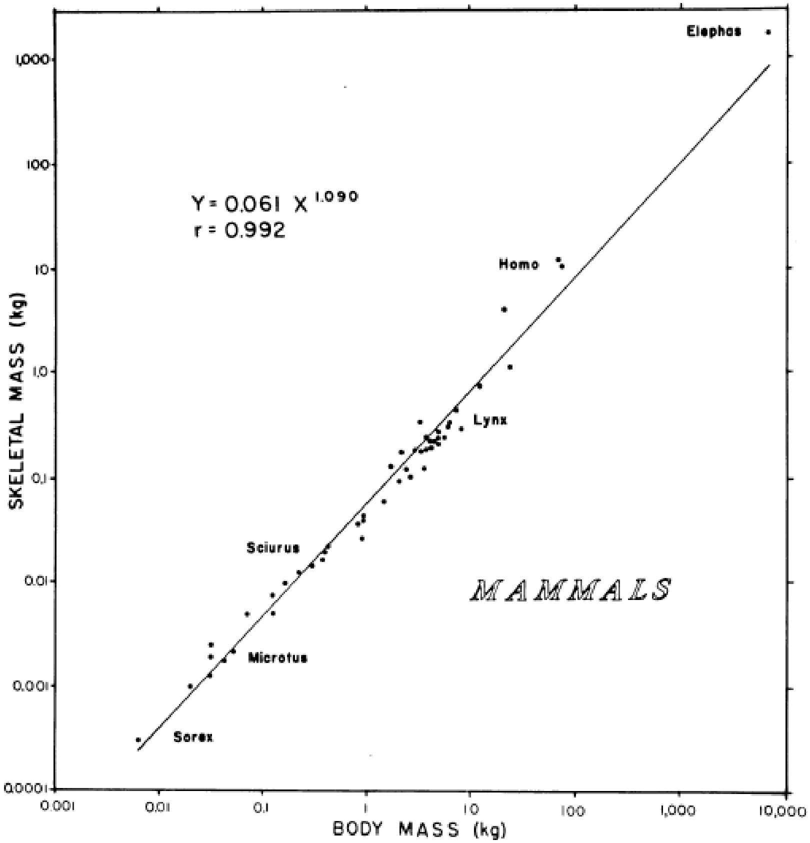


FIG. 1.—Relationship between skeletal mass (y) and body mass (x) for mammals. The sample for the logarithmic regression consisted of 49 data; the standard error of estimate for y on x was 0.154; the range of body mass values included in the sample was 0.006–6,600 kg. Examples of representative animals are listed with their genus name on a line intersecting their skeletal mass.

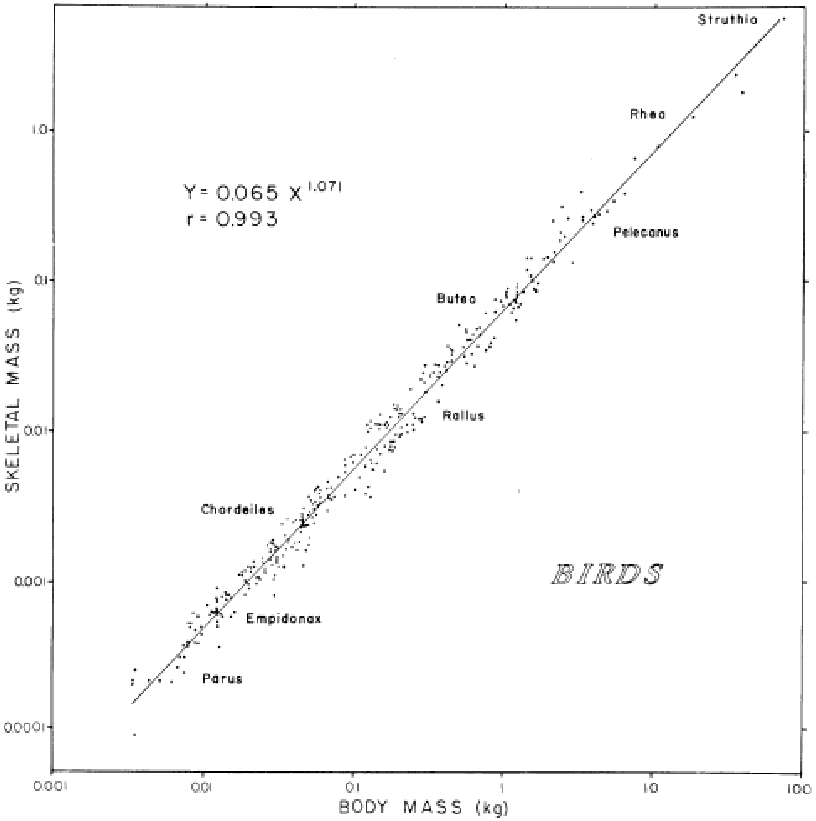


FIG. 2.—Relationship between skeletal mass (y) and body mass (x) for birds. The sample for the logarithmic regression consisted of 311 data; the standard error of estimate for y on x was 0.102; the range of body mass values included in the sample was 0.0031–80.920 kg. Examples of representative animals are listed with their genus name on a line intersecting their skeletal mass.

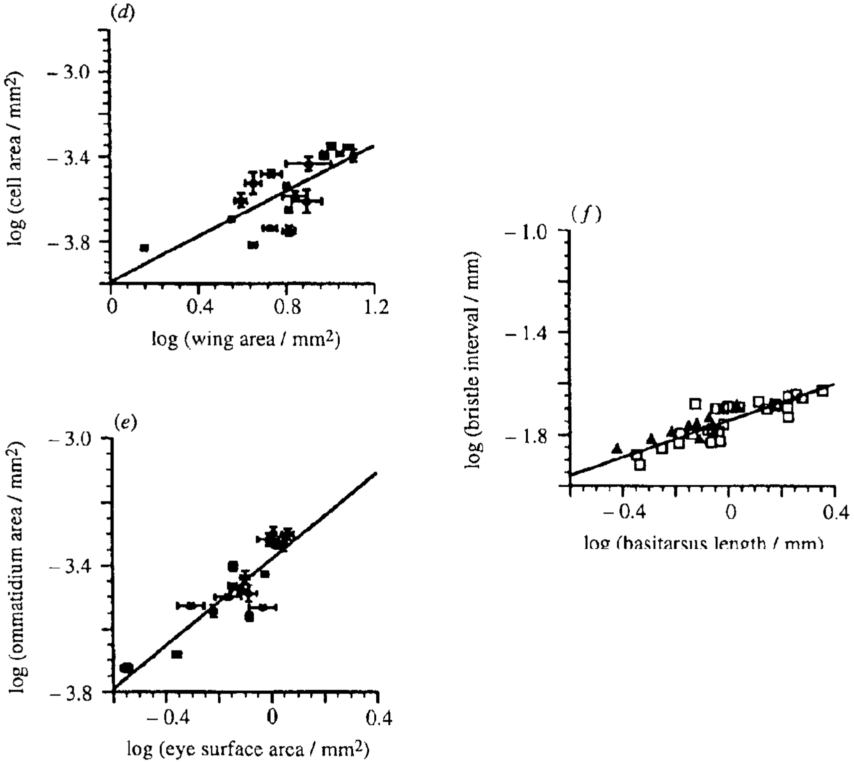
Proximátní mechanismy změny ve velikosti

- změna v množství mezibuněčné hmoty
- změna v počtu buněk (hyperplázie/hypoplázie)
- změna ve velikosti buněk (hypertrofie/hypotrofie)

Organ and cell allometry in Hawaiian *Drosophila*: how to make a big fly

R. D. STEVENSON[1], MARK F. HILL[1] AND PETER J. BRYANT[2]

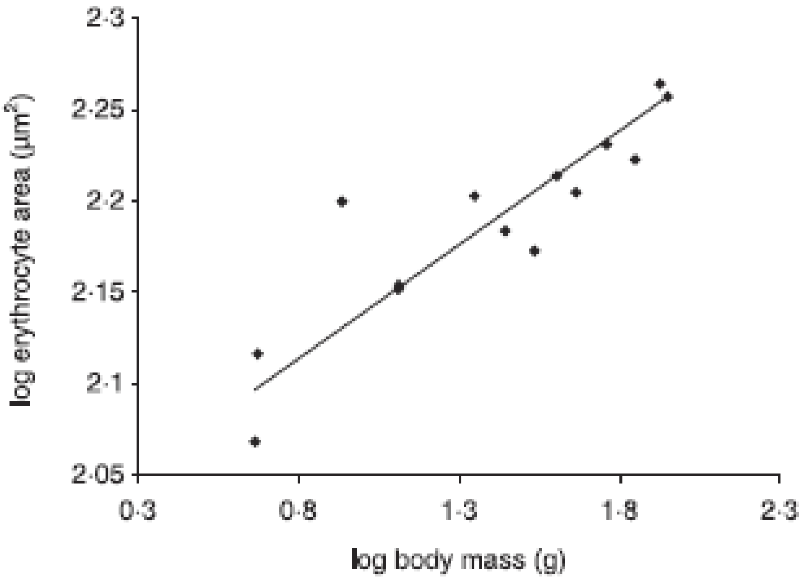
Proc. R. Soc. Lond. B (1995) **259**, 105–110



Dwarf and giant geckos from the cellular perspective: the bigger the animal, the bigger its erythrocytes?

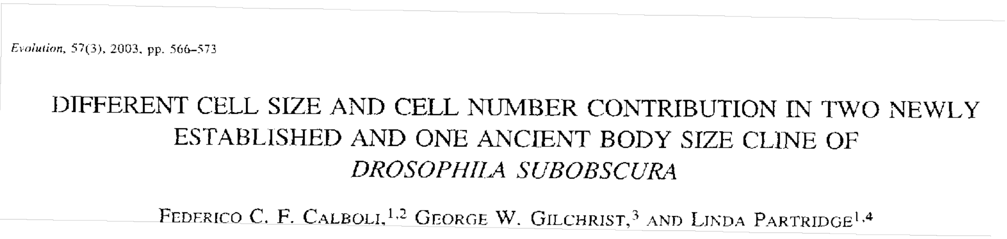
ZUZANA STAROSTOVÁ, LUKÁŠ KRATOCHVÍL* and DANIEL FRYNTA

Functional Ecology 2005 **19**, 744–749



Proximátní mechanismy změny ve velikosti

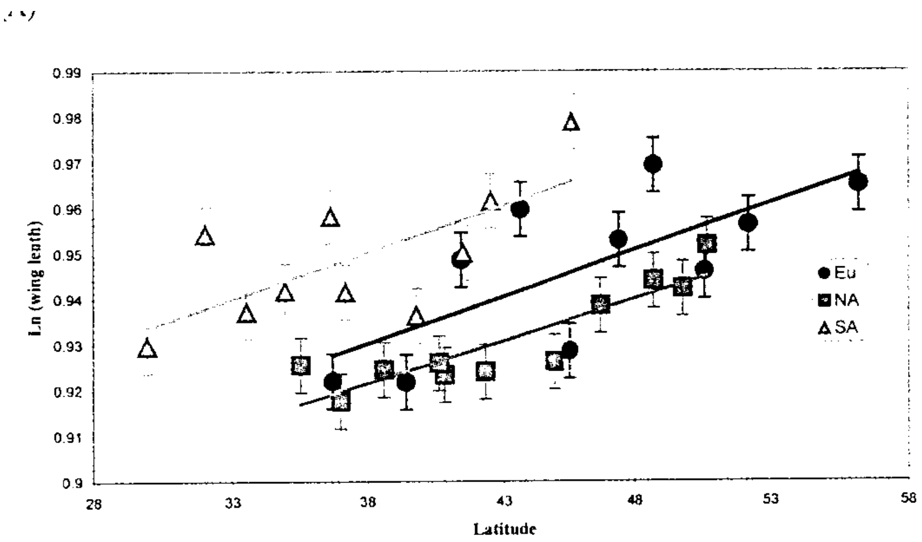
- změna v množství mezibuněčné hmoty
- změna v počtu buněk (hyperplázie/hypoplázie)
- změna ve velikosti buněk (hypertrofie/hypotrofie)



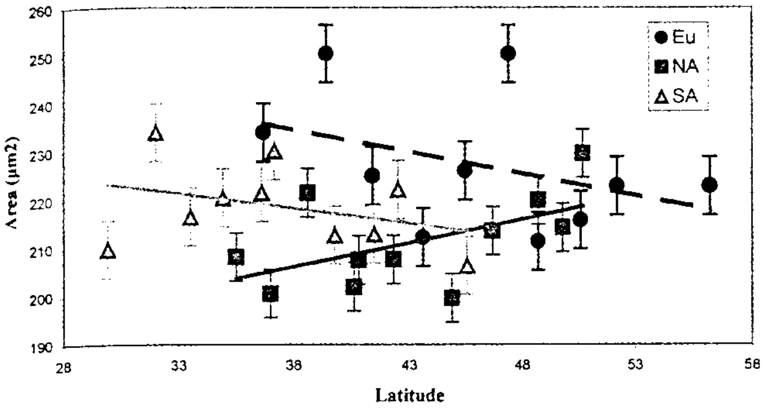
Evolution, 57(3), 2003, pp. 566–573

DIFFERENT CELL SIZE AND CELL NUMBER CONTRIBUTION IN TWO NEWLY ESTABLISHED AND ONE ANCIENT BODY SIZE CLINE OF *DROSOPHILA SUBOBSCURA*

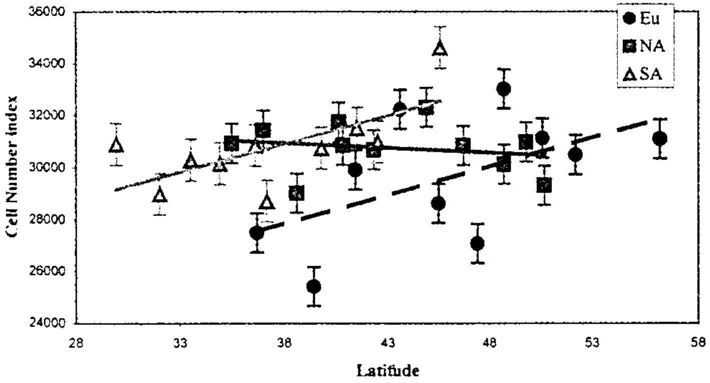
FEDERICO C. F. CALBOLI,[1,2] GEORGE W. GILCHRIST,[3] AND LINDA PARTRIDGE[1,4]



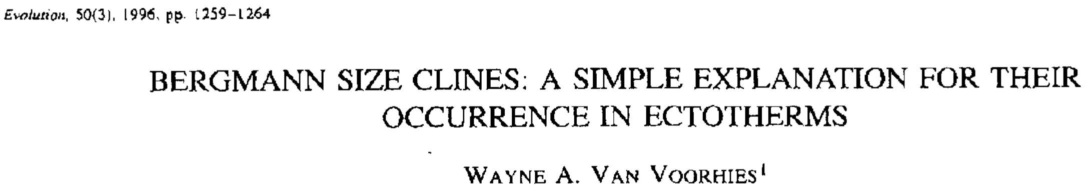
(A)



(A)



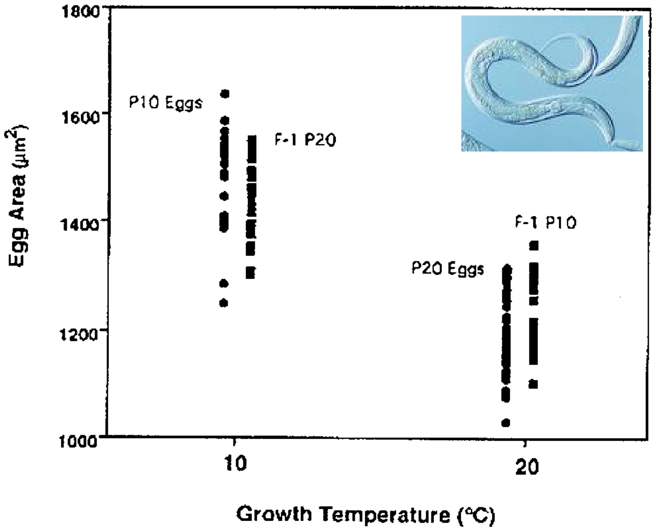
Proximátní mechanismy změny ve velikosti

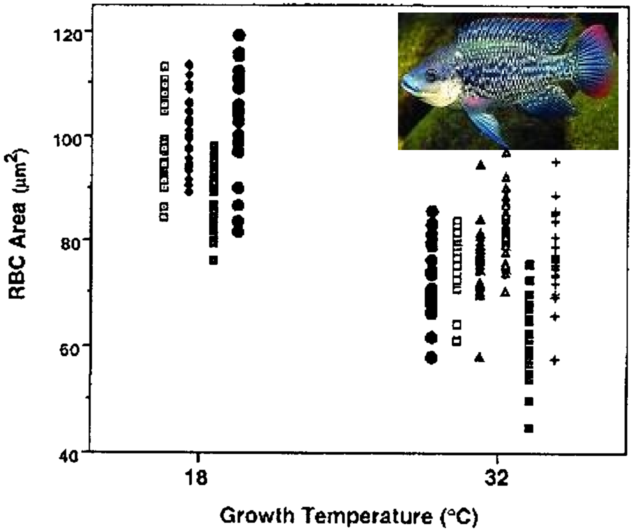


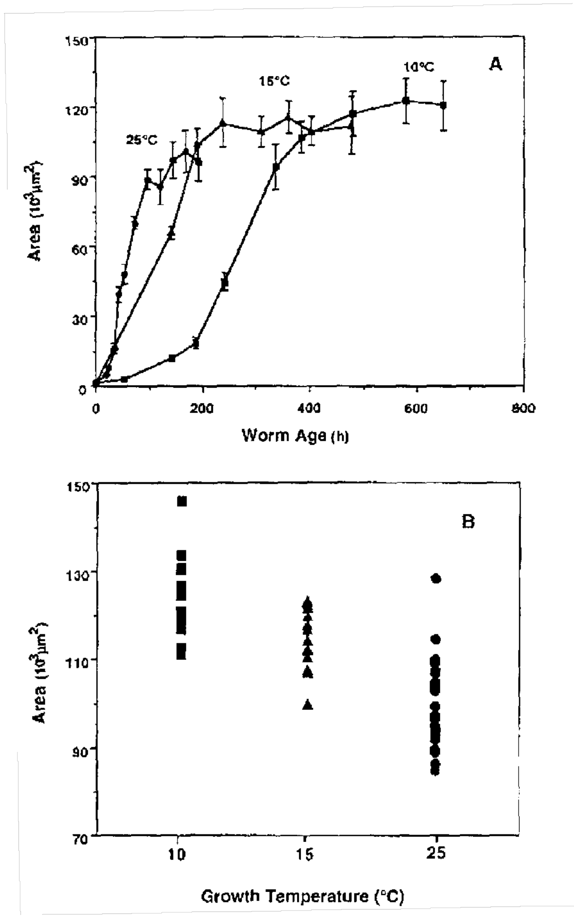
Evolution, 50(3), 1996, pp. 1259–1264

BERGMANN SIZE CLINES: A SIMPLE EXPLANATION FOR THEIR OCCURRENCE IN ECTOTHERMS

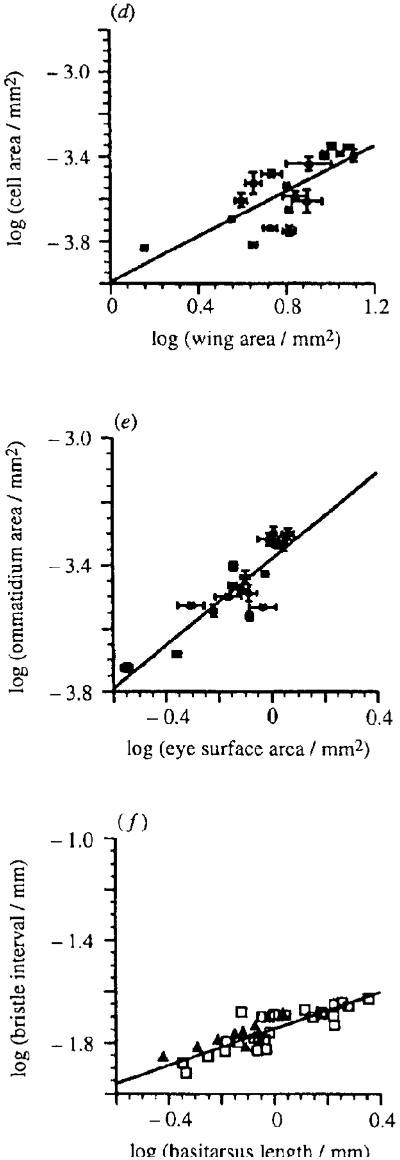
WAYNE A. VAN VOORHIES[1]

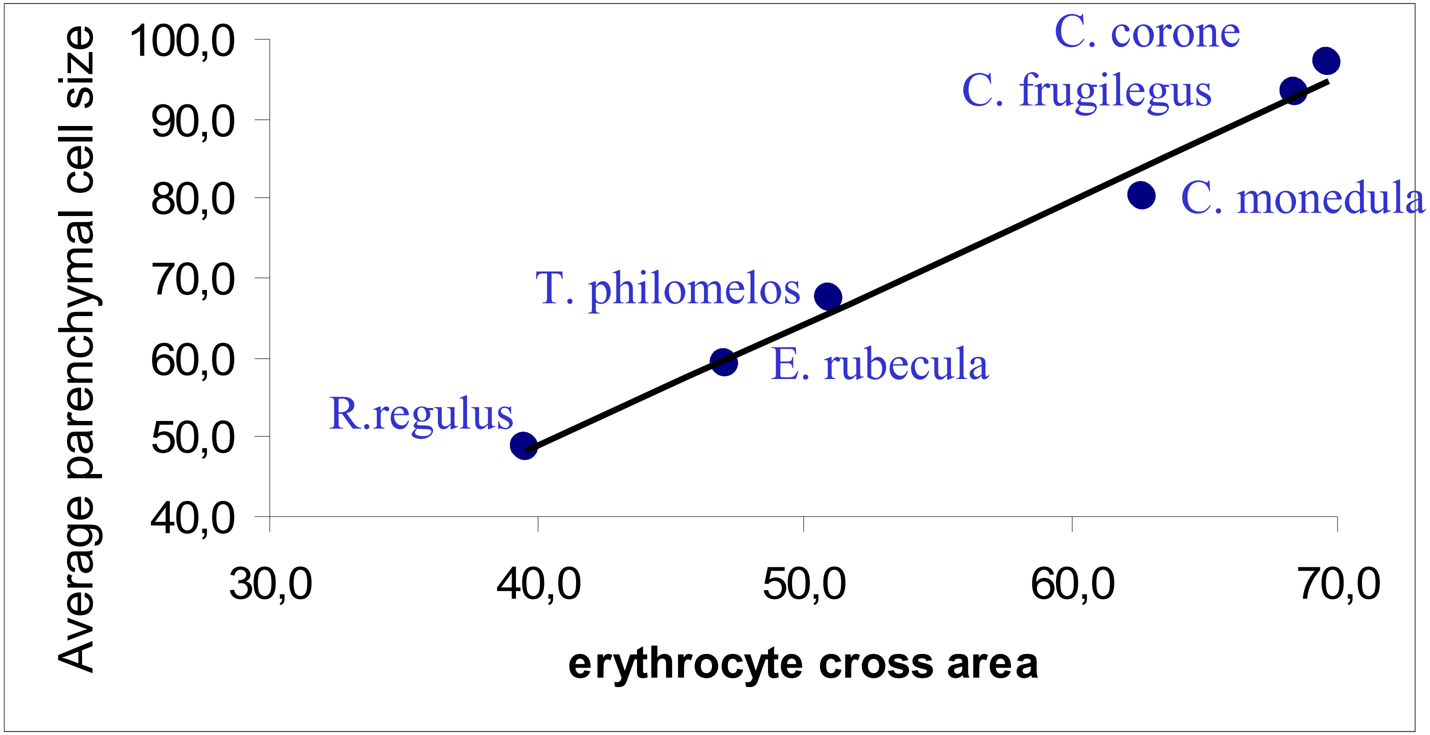






Korelují spolu velikosti buněk v různých tkáních?





Nitecki, unpubl.

Vztah velikosti buněk a intenzity metabolismu

Scaling of insect metabolic rate is inconsistent with the nutrient supply network model

S. L. CHOWN,*† E. MARAIS,* J. S. TERBLANCHE,* C. J. KLOK,
J. R. B. LIGHTON‡§ and T. M. BLACKBURN¶

Functional Ecology 2007
21, 282–290

The intraspecific scaling exponents varied from 0·67 to 1·0. Moreover, in the species where metabolic rate scaled as mass$^{1\cdot 0}$, cell size did not contribute significantly to models of body size variation, only cell number was significant. Where the scaling exponent was < 1·0, cell size played an increasingly important role in accounting for size variation.

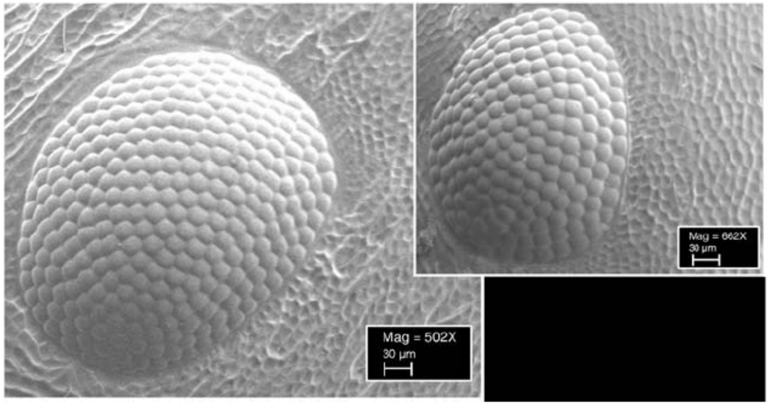
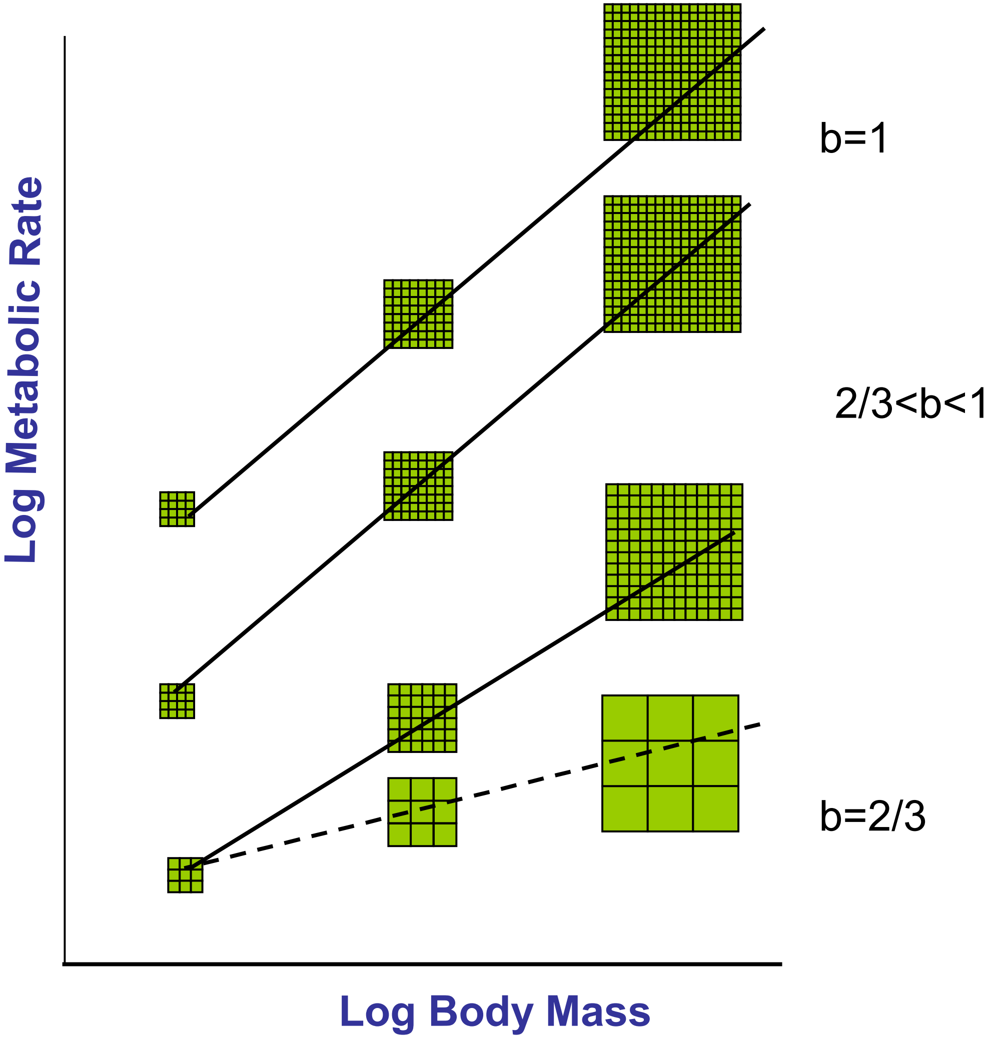


Fig. 1. Scanning electron micrographs of the compound eye of a large individual (9·8 mg, 7·56 mm) (left), and small individual (3·1 mg, 5·30 mm) (right) of *Messor capensis*. Note the similarity in cell size, but difference in cell number.

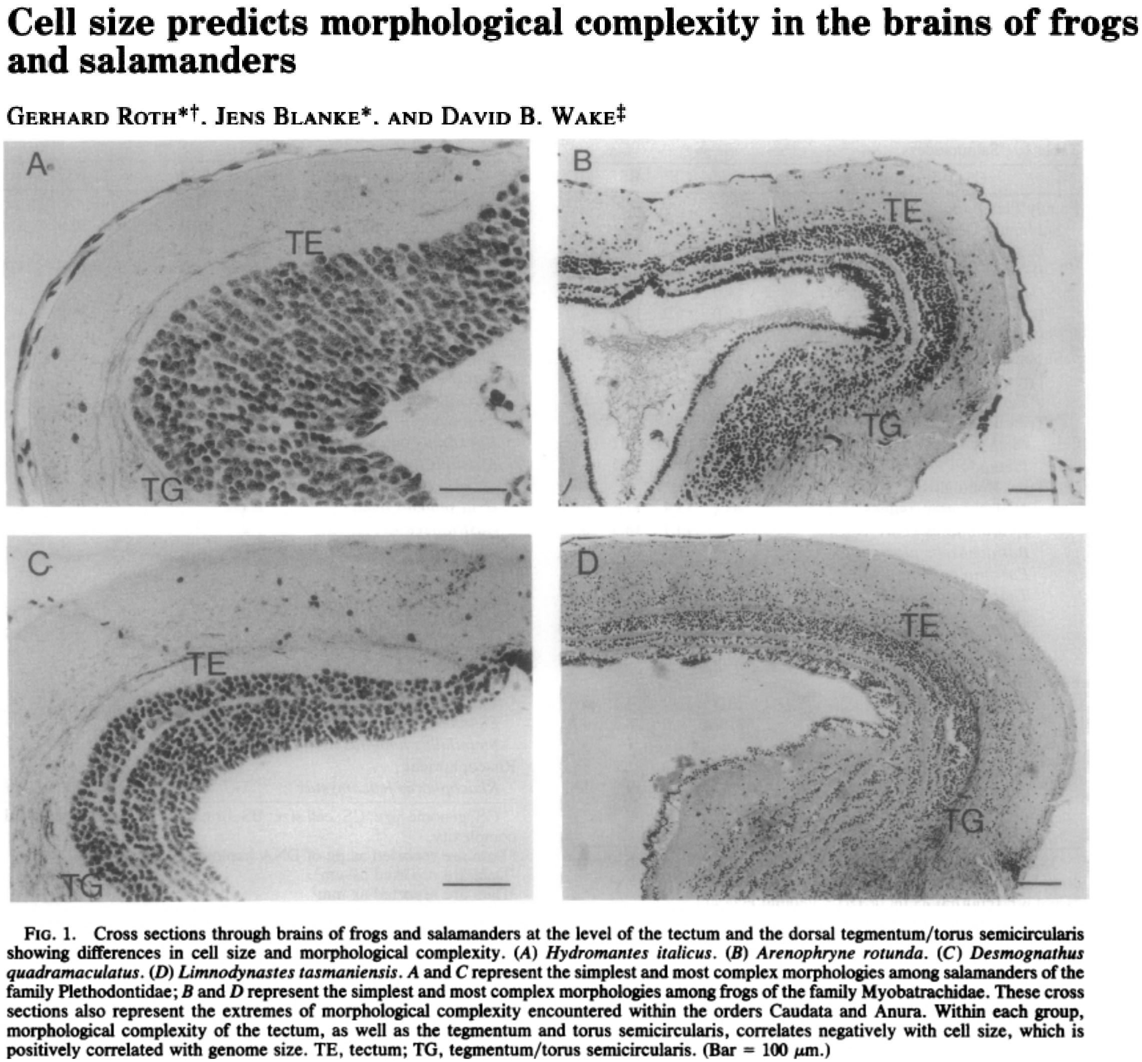


Kozłowski, Konarzewski, Gawełczyk, PNAS 2003

Vztah velikosti buněk a komplexity

Loricifera

Minelli 2003



Cell size predicts morphological complexity in the brains of frogs and salamanders

Gerhard Roth*†, Jens Blanke*, and David B. Wake‡

Fig. 1. Cross sections through brains of frogs and salamanders at the level of the tectum and the dorsal tegmentum/torus semicircularis showing differences in cell size and morphological complexity. (*A*) *Hydromantes italicus*. (*B*) *Arenophryne rotunda*. (*C*) *Desmognathus quadramaculatus*. (*D*) *Limnodynastes tasmaniensis*. *A* and *C* represent the simplest and most complex morphologies among salamanders of the family Plethodontidae; *B* and *D* represent the simplest and most complex morphologies among frogs of the family Myobatrachidae. These cross sections also represent the extremes of morphological complexity encountered within the orders Caudata and Anura. Within each group, morphological complexity of the tectum, as well as the tegmentum and torus semicircularis, correlates negatively with cell size, which is positively correlated with genome size. TE, tectum; TG, tegmentum/torus semicircularis. (Bar = 100 μm.)

Roth, G., K.C. Nishikawa & D.B. Wake, 1997. Genome size, secondary simplification, and the evolution of the brain in salamanders. *Brain Behav. Evol*. 50: 50–59.

Velikost genomu a její fenotypové koreláty

Chromosome evolution in eukaryotes: a multi-kingdom perspective

Avril Coghlan[1,2,*], Evan E. Eichler[3,*], Stephen G. Oliver[4,*], Andrew H. Paterson[5,*]
and Lincoln Stein[6,*]

TRENDS in Genetics Vol.21 No.12 December 2005

C-value paradox

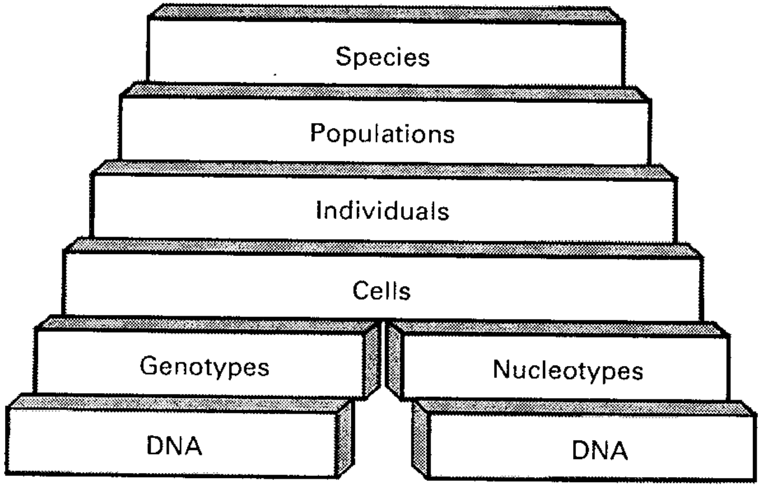


Fig. 7. The revised biological hierarchy, which acknowledges the dual role of DNA – both in terms of protein-coding and bulk DNA effects – in generating phenotypic variation at the cellular level and above. Note that there is interaction between genotypes and nucleotypes, as well as among the different levels of the hierarchy. Adapted from Gregory & Hebert (1999).

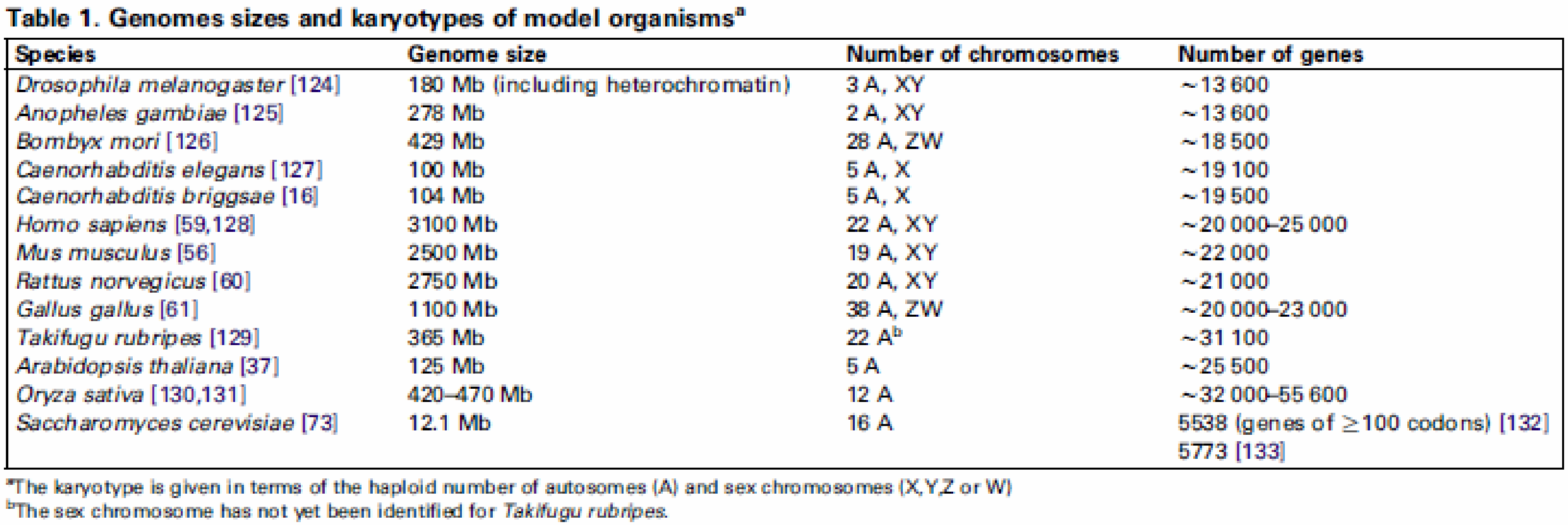
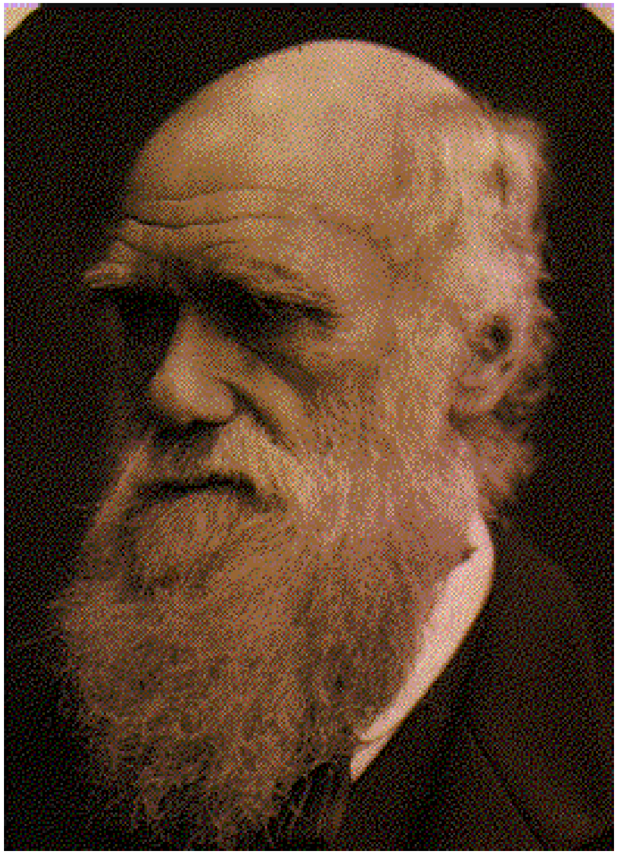


Table 1. Genomes sizes and karyotypes of model organisms[a]

Species	Genome size	Number of chromosomes	Number of genes
Drosophila melanogaster [124]	180 Mb (including heterochromatin)	3 A, XY	~13 600
Anopheles gambiae [125]	278 Mb	2 A, XY	~13 600
Bombyx mori [126]	429 Mb	28 A, ZW	~18 500
Caenorhabditis elegans [127]	100 Mb	5 A, X	~19 100
Caenorhabditis briggsae [16]	104 Mb	5 A, X	~19 500
Homo sapiens [59,128]	3100 Mb	22 A, XY	~20 000–25 000
Mus musculus [56]	2500 Mb	19 A, XY	~22 000
Rattus norvegicus [60]	2750 Mb	20 A, XY	~21 000
Gallus gallus [61]	1100 Mb	38 A, ZW	~20 000–23 000
Takifugu rubripes [129]	365 Mb	22 A[b]	~31 100
Arabidopsis thaliana [37]	125 Mb	5 A	~25 500
Oryza sativa [130,131]	420–470 Mb	12 A	~32 000–55 600
Saccharomyces cerevisiae [73]	12.1 Mb	16 A	5538 (genes of ≥100 codons) [132] 5773 [133]

[a] The karyotype is given in terms of the haploid number of autosomes (A) and sex chromosomes (X,Y,Z or W)
[b] The sex chromosome has not yet been identified for *Takifugu rubripes*.

$C_{ameba} = 200 \times C_{Darwin}$

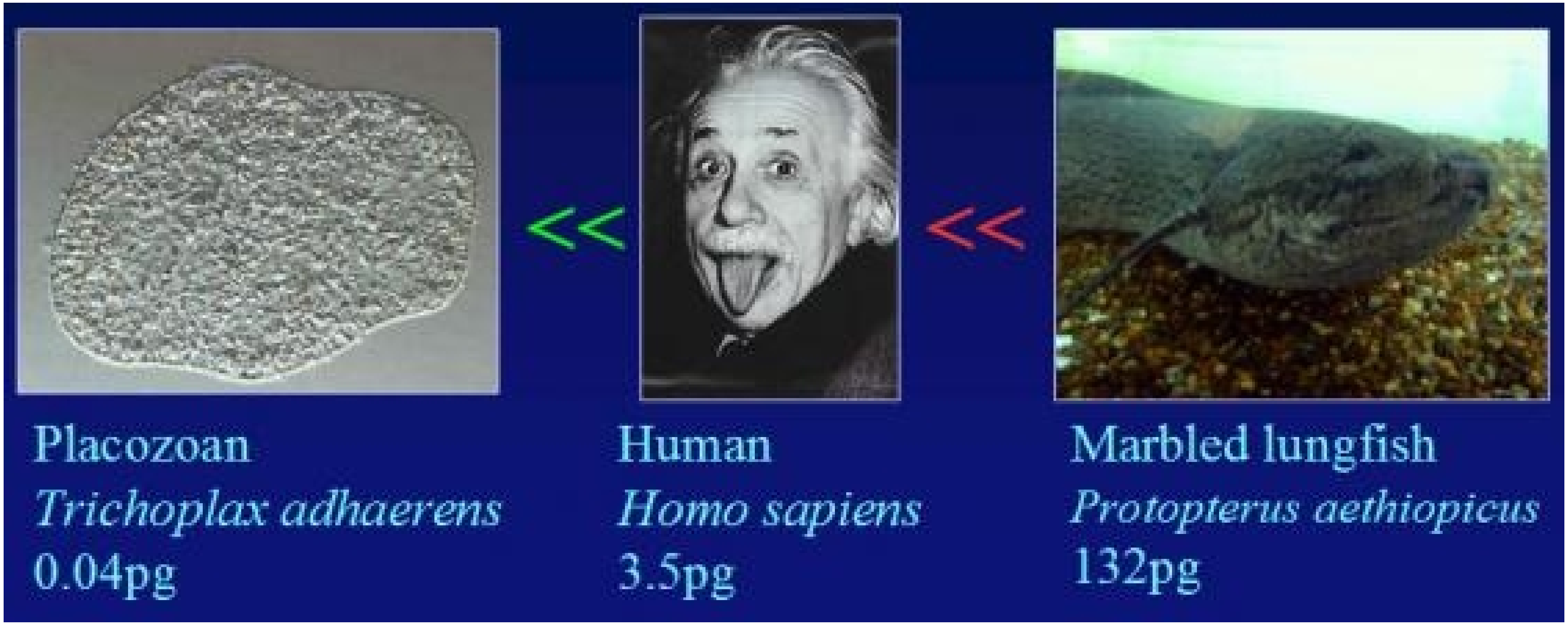


$<<$

C-value=3.5 pg

C-value=700 pg

Konarzewski



Placozoan
Trichoplax adhaerens
0.04pg

<<

Human
Homo sapiens
3.5pg

<<

Marbled lungfish
Protopterus aethiopicus
132pg

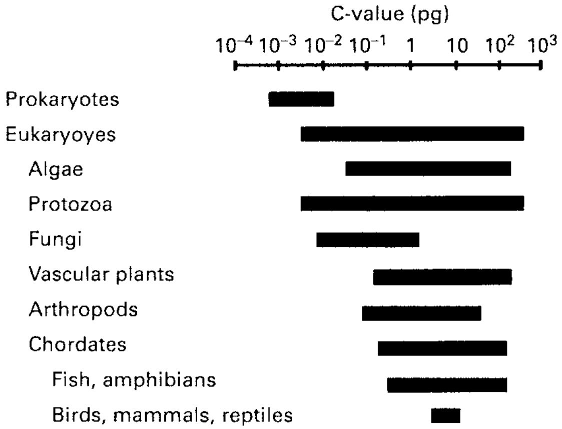
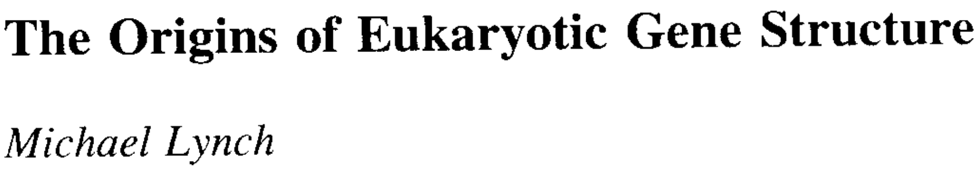


Fig. 1. A generalized overview of genome size variation among major groups of organisms. Clearly, no relationship exists between genome size and either number of coding genes or organismal complexity. Note also the tight constraints on genome size among prokaryotes and amniote vertebrates. Adapted from Cavalier-Smith (1982).

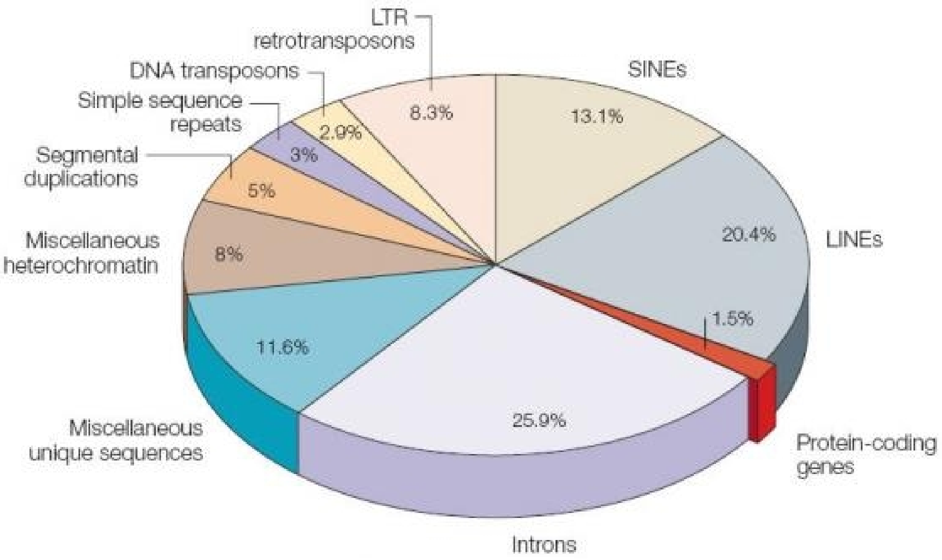
Gregory

Velikost genomu určuje především nekódující DNA



The Origins of Eukaryotic Gene Structure

Michael Lynch



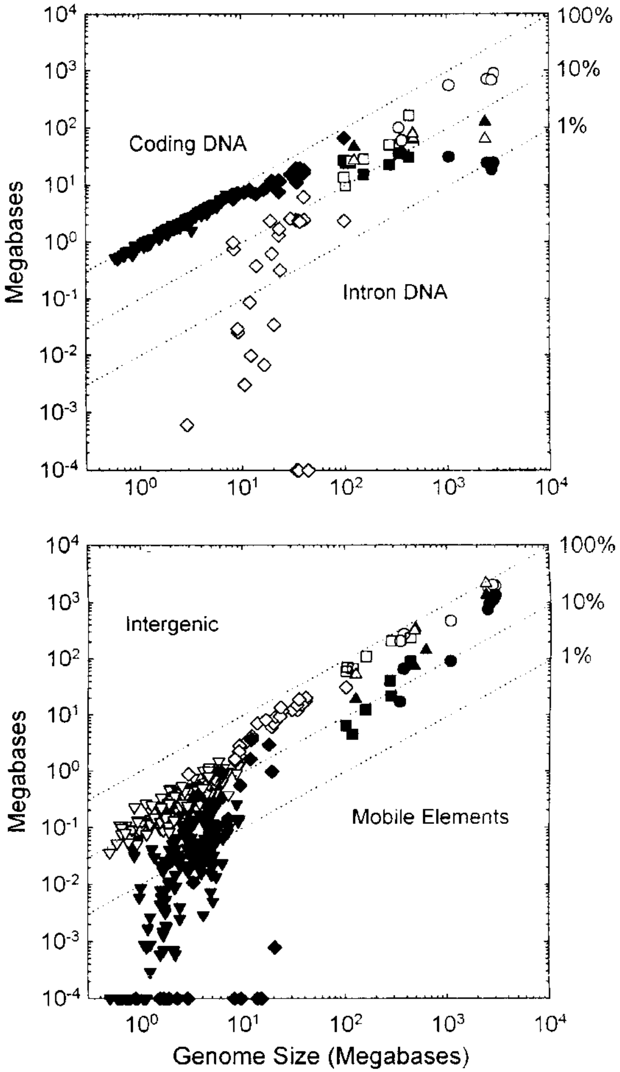
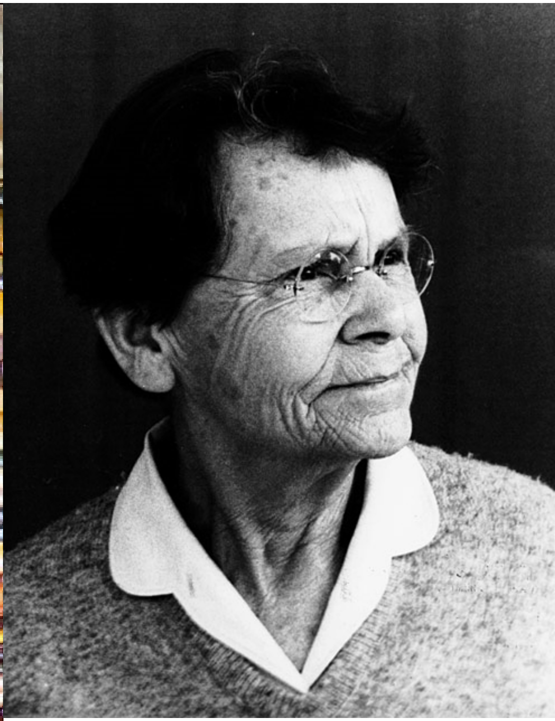


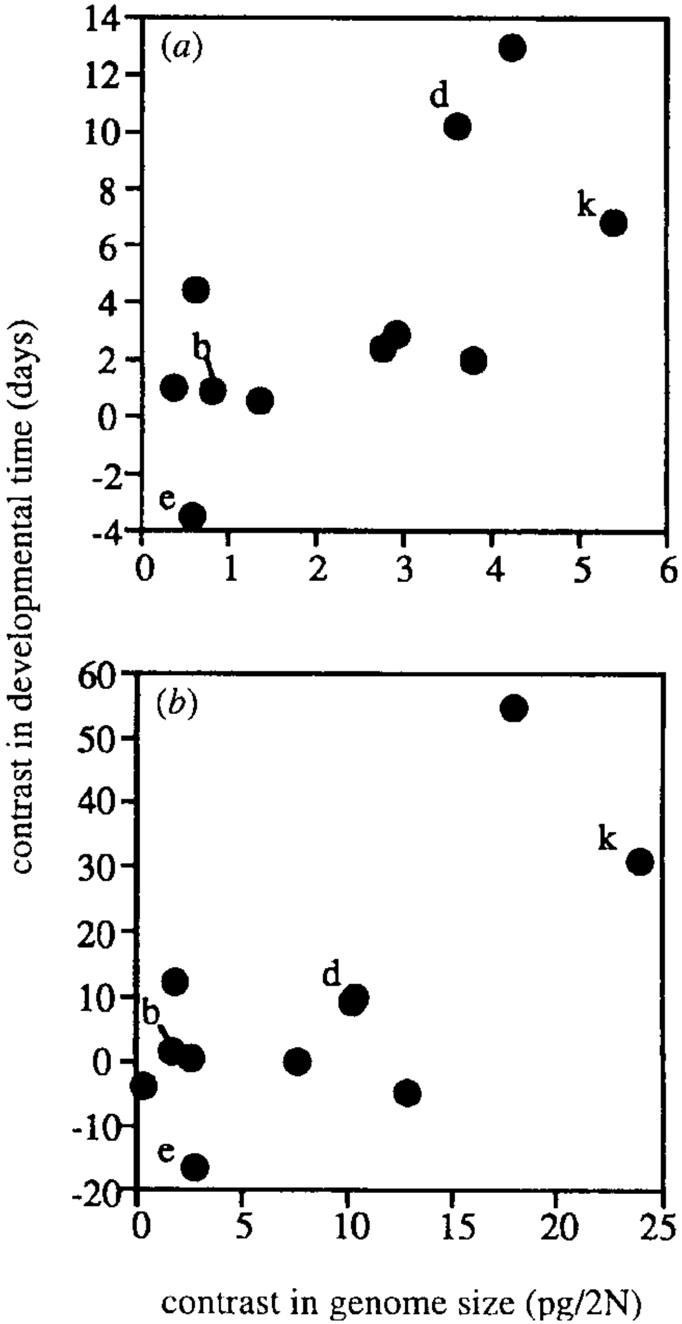
FIG. 5.—Scaling of genome content with genome size in prokaryotes (inverted triangles) and various eukaryotic groupings: unicellular and oligocellular species (diamonds), invertebrates (squares), vertebrates (circles), and land plants (triangles). Diagonal dashed lines denote points of equal proportional contributions to total genome content. Note that mobile-element associated DNA (which includes retrotransposons and DNA-based transposons) may be found in introns as well as intergenic regions and that the intronic DNA depicted here does not include introns in noncoding exons (UTRs). The data were obtained from the various whole-genome sequencing projects.



Barbara McClintock

Velikost genomu a její fenotypové koreláty

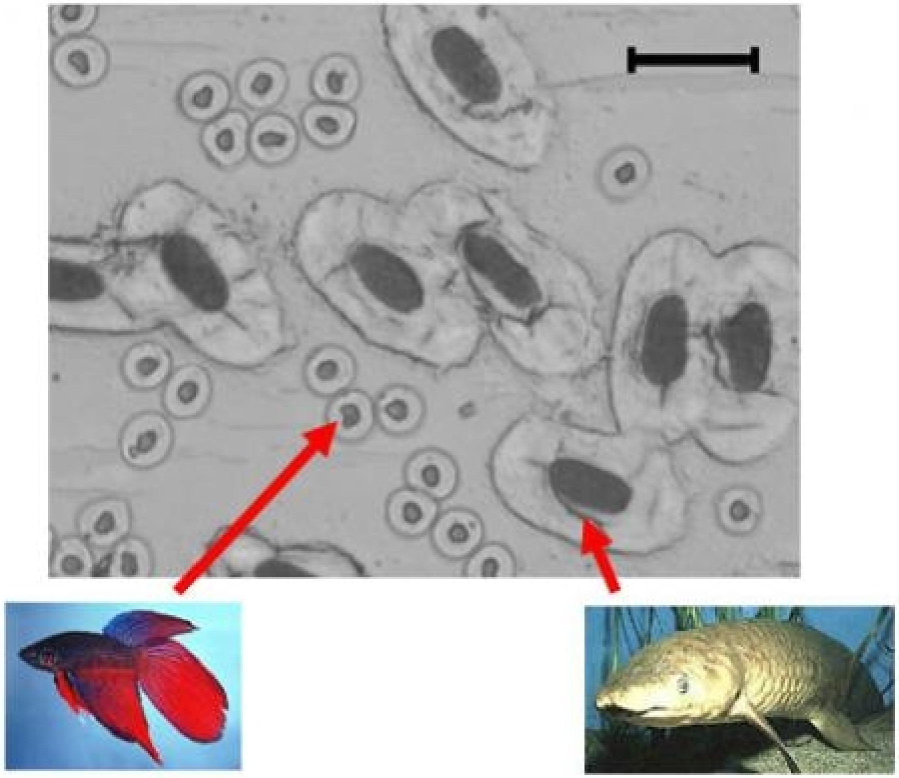
- velikost jádra
- velikost buněk
- rychlost buněčného dělení
- rychlost vývoje a jeho komplexita
- minimální generační doba u rostlin
- velikost těla
- rychlost metabolismu
- komplexita těla (mločíci)



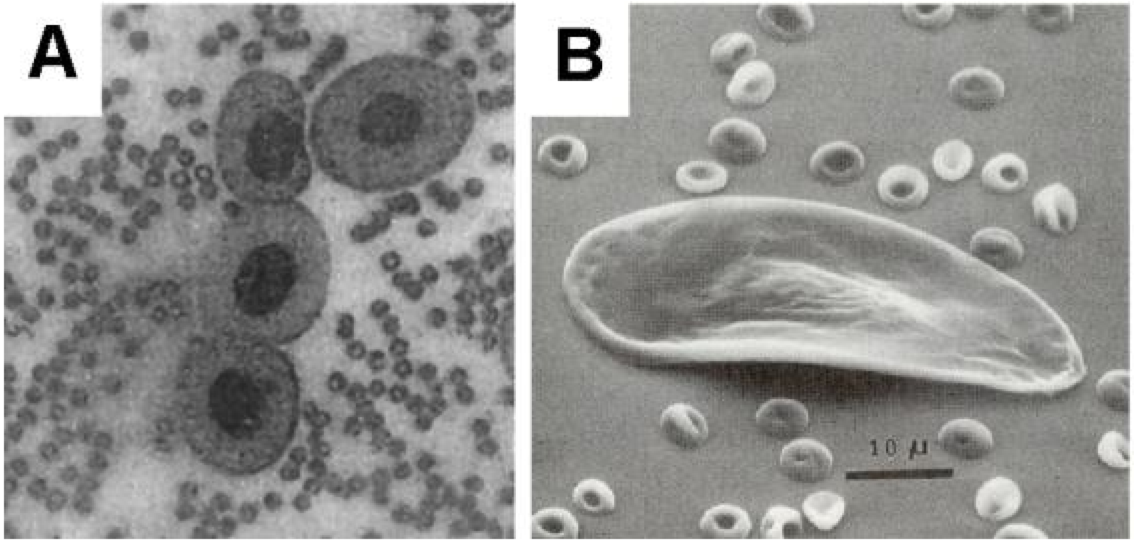
An evolutionary correlate of genome size change in plethodontid salamanders

ELIZABETH L. JOCKUSCH*

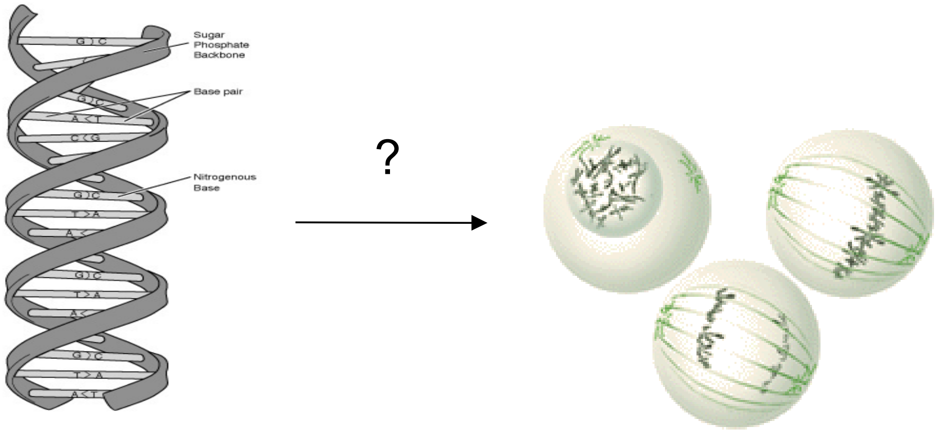
Proc. R. Soc. Lond. B (1997) **264**, 597–604



The extraordinary variation in red blood cell sizes among vertebrates. In both images, the large elliptical cells in the centre are those of the aquatic salamander *Amphiuma means* (2C = 165pg) and the small discs surrounding them are those of humans (2C = 7.0pg). Note that mature mammalian red blood cells can achieve a particularly tiny size despite a relatively large genome because they do not contain nuclei. (A) taken using light microscopy by Wintrobe (1933); (B) taken using scanning electron microscopy by Lewis (1996). As reprinted in Gregory (2005a).



Velikost genomu a její fenotypové koreláty – „optimal DNA theories“



Genome Size Variation

Cell Size Variation

Coincidence, coevolution, or causation? DNA content, cell size, and the C-value enigma

T. RYAN GREGORY

Biol. Rev. (2001), **76**, *pp*. 65

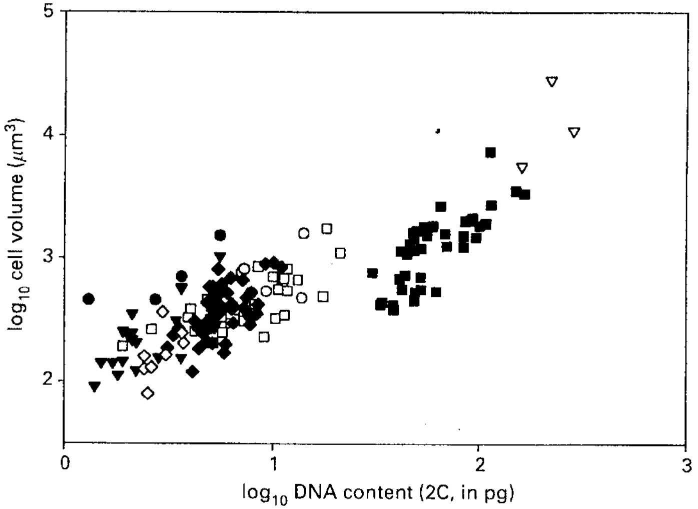


Fig. 2. An illustrative example of the relationship between cellular DNA content (2C in pg) and erythrocyte volume (in μm^3) among 159 species of vertebrates. Different symbols represent different groups of vertebrates: jawless fishes (●), cartilaginous fishes (○), teleost fishes (excluding lungfish) (▼), lungfishes (▽), urodele amphibians (■), anuran amphibians (□), reptiles (◆), birds (◇). Mammals, which have enucleate erythrocytes, were not included in this dataset, although the relationship does extend to these organisms as well (Gregory, 2000). Note that urodeles and lungfish generally have smaller cells per unit DNA content than other vertebrates, but *within* these groups the relationship is positively allometric. Data from Olmo (1983).

Velikost genomu a její fenotypové koreláty – „optimal DNA theories“

Kritika:

- velká variabilita kolem vztahu (kondenzace chromatinu)
- plasticita ve velikosti buněk
- geny ovlivňující velikost buněk
- velikost buněk u polyploidů

Control of body size by SMA-5, a homolog of MAP kinase BMK1/ERK5, in *C. elegans*

Naoharu Watanabe[1], Yasuko Nagamatsu[1], Keiko Gengyo-Ando[2], Shohei Mitani[2] and Yasumi Ohshima[1,*,†]

Development 132 (14)

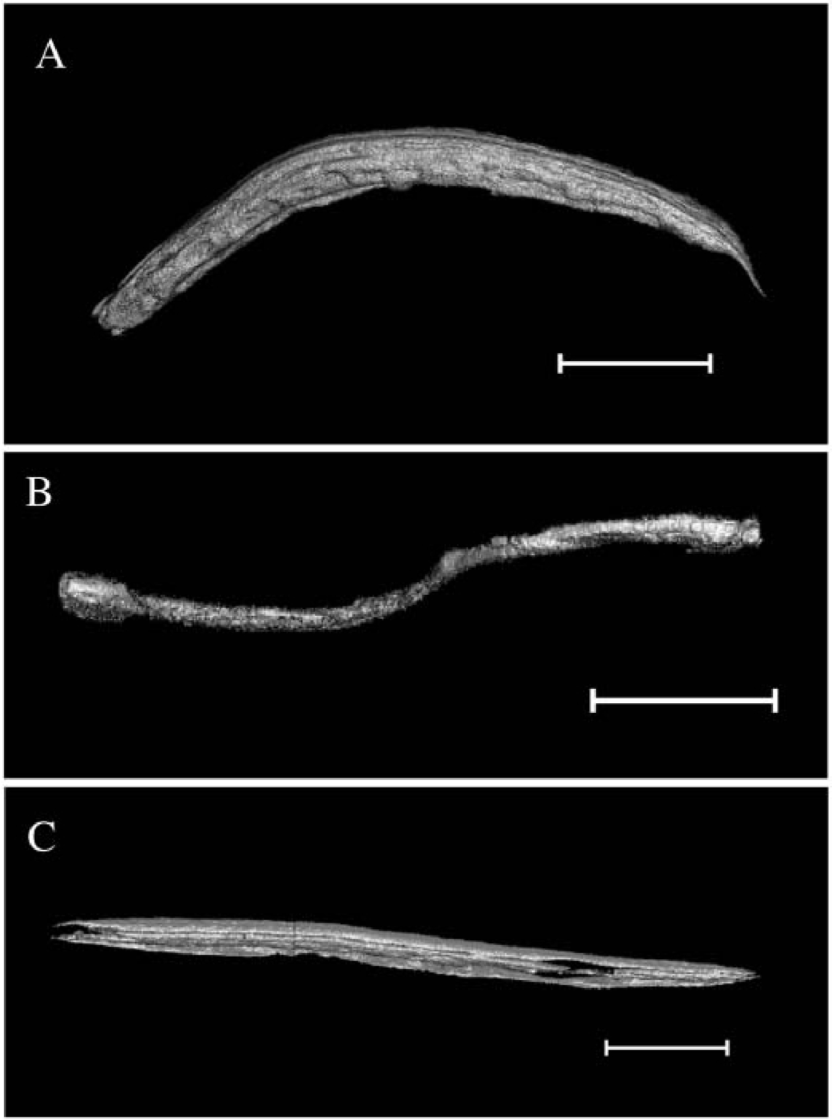


Fig. 6. Three-dimensional reconstructed images of hypodermis (A), intestine (B) and muscles (C) in the *sma-5(n678)* background. Scale bar: 200 µm.

Velikost genomu a její fenotypové koreláty – „mutation-selection balance“ Lynch 2004

- původně Ohno (1972)

Genome size is negatively correlated with effective population size in ray-finned fish

Soojin Yi and J. Todd Streelman

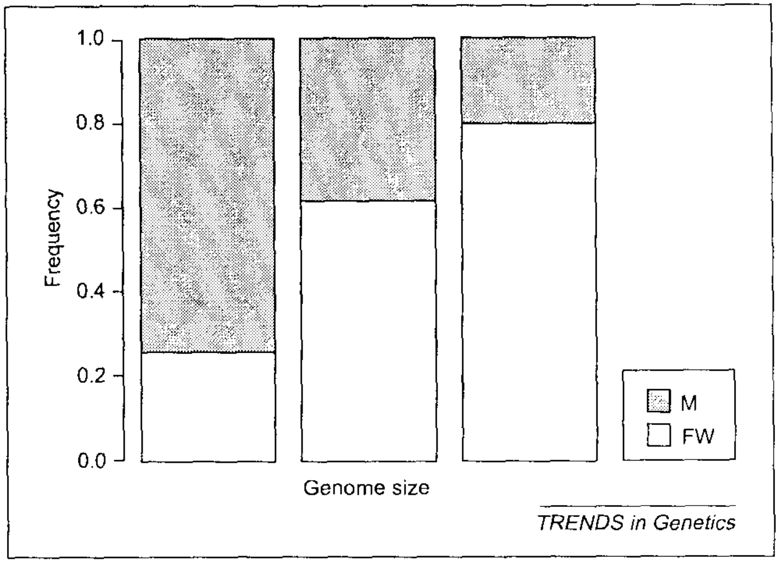
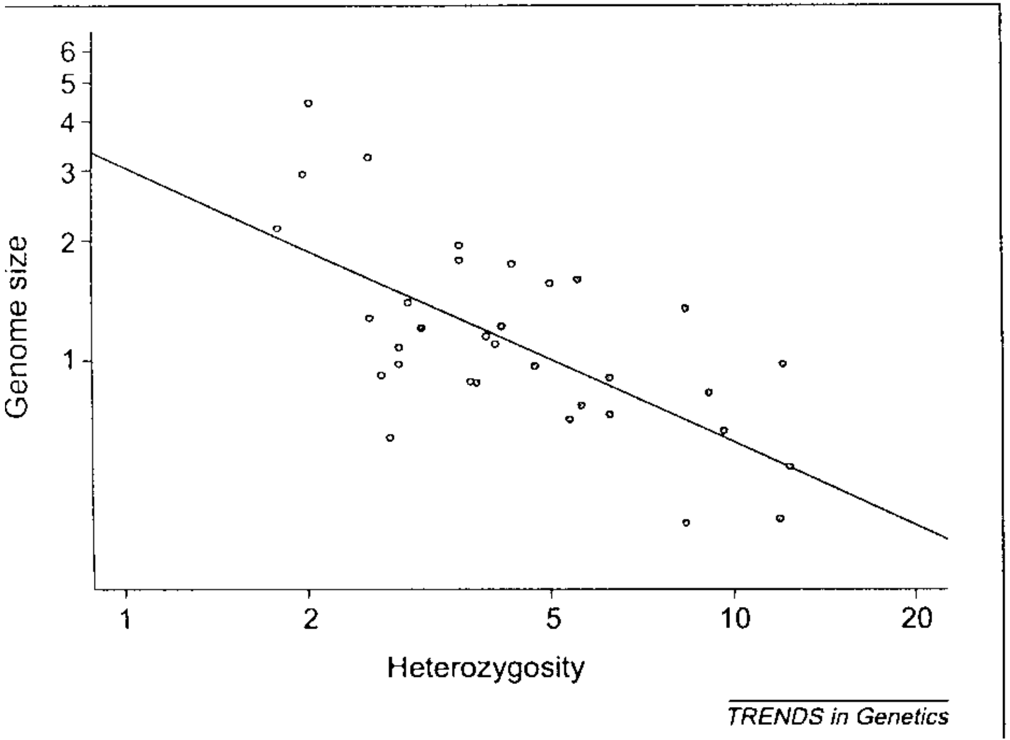
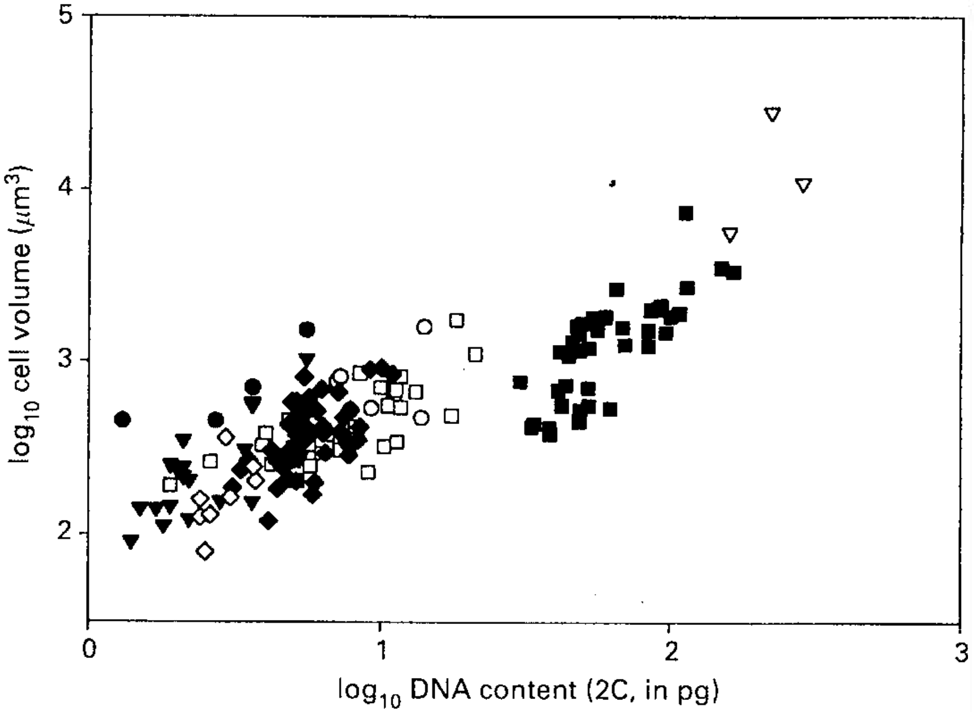
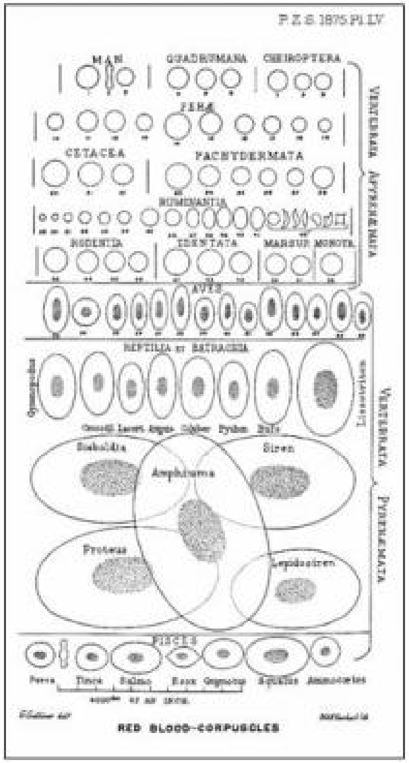


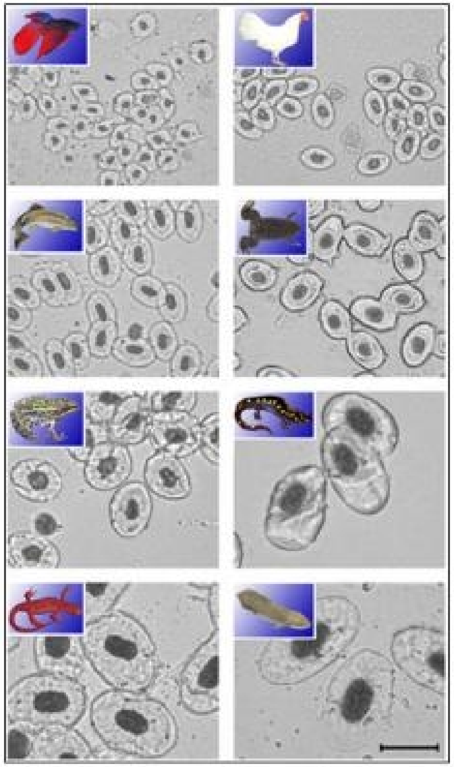
Figure 1. Marine species (M) have smaller genomes than freshwater species (FW). We divided 1043 taxa into three approximately equal bins, according to the distribution of genome sizes. Bins correspond to C-value$\leq$0.92 (353 species), 0.92$<$C-value$\leq$1.26 (339 species) and 1.26$<$C-value$<$6.58 (351 species). Within each bin, the relative frequencies of M (blue) versus FW (white) species are shown



Může „mutation-selection balance“ vysvětlit korelaci mezi velikostí buněk a genomu?







Cell size does not always correspond to genome size: Phylogenetic analysis in geckos questions optimal DNA theories of genome size evolution

Zuzana Starostová[a], Lukáš Kratochvíl[b,*], Martin Flajšhans[c,d]

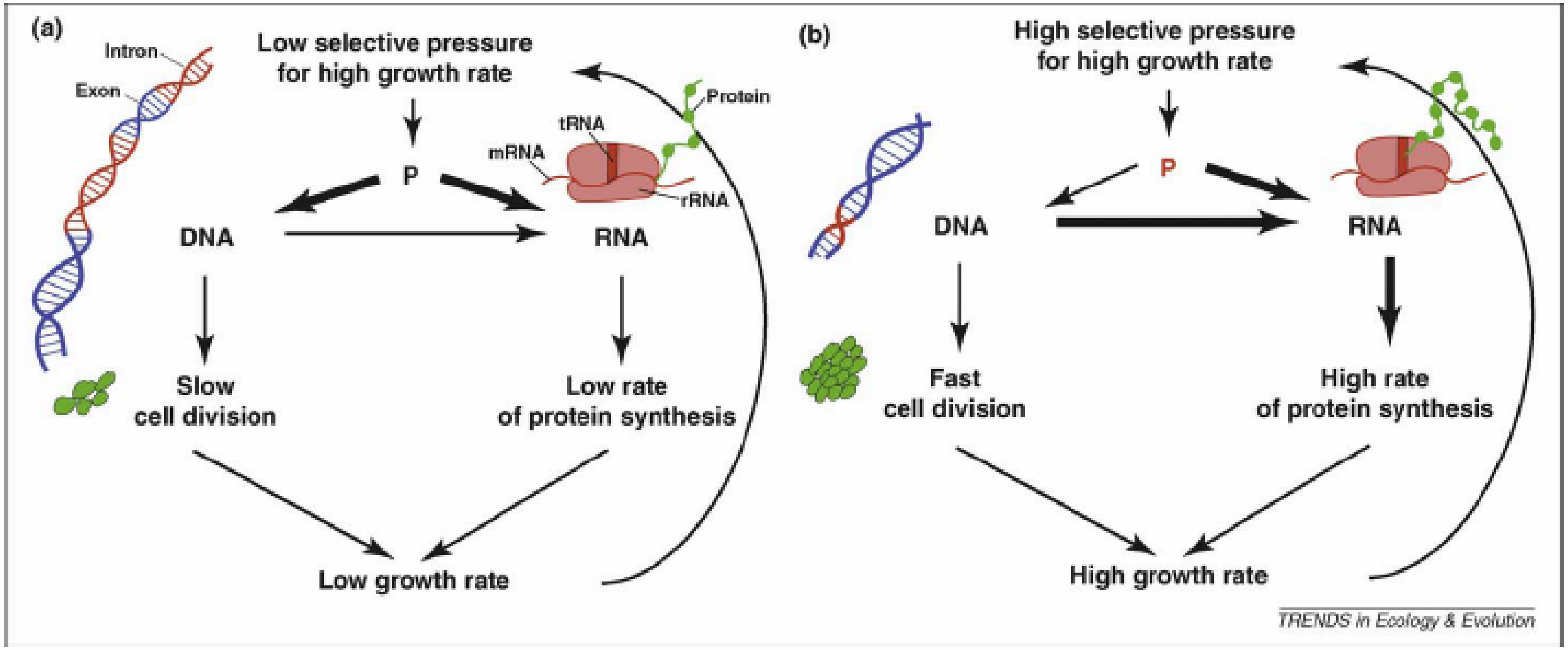
Zoology 111 (2008) 377–384

Selekčním tlakem na zmenšování velikosti genomu může být kompetice mezi DNA a RNA o zdroj fosforu

Genome streamlining and the elemental costs of growth

Dag O. Hessen[1], Punidan D. Jeyasingh[2], Maurine Neiman[3] and Lawrence J. Weider[4]

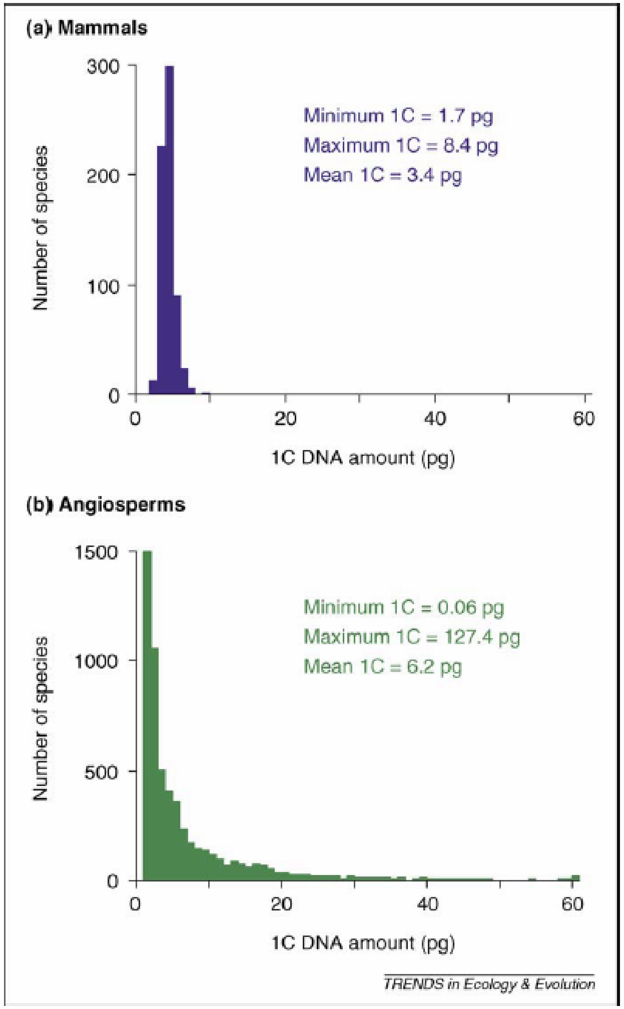
Trends in Ecology and Evolution Vol.25 No.2 *2009*



TRENDS in Ecology & Evolution

Figure 1. Two scenarios illustrating the effects of different evolutionary allocations of P to DNA or RNA. **(a)** Under low selective pressure for high growth rate, a significant share of P is allocated to DNA (and implicit large genome size) potentially causing slow growth rate and low rate of protein synthesis. **(b)** Under strong selection for high growth rate, there will be selective pressure for reallocating P from non-coding DNA to RNA that promotes high growth rate. Selection favoring 'r-selected' life-history traits under nutrient scarcity might generate evolutionary pressure for this sequence of events. Thickness of arrows indicates relative importance of P allocation or causality. Scenario (a) indicates large genome, high intron:exon ratio, slow rate of protein synthesis and slow cell division as opposed to scenario (b).

Za rozdíly ve velikosti genomu a její variabilitě může být zodpovědná dynamika genomu



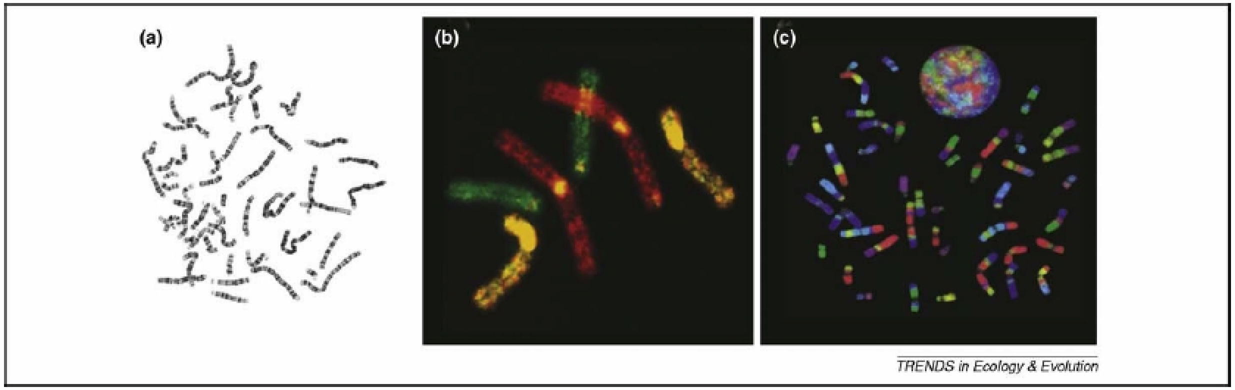
TRENDS in Ecology & Evolution

Figure 2. Histograms showing the distribution of genome sizes in mammals and angiosperms. (a) Data for mammals (data for ca. 400 species (656 estimates) taken from the Animal Genome Size database [85]) and (b) angiosperms (data for 5770 species from the Plant DNA C-values database [13] plus additional data not yet incorporated into the database; values for 19 species which are >1C = 60 pg have been binned at 60 pg).

Contrasting evolutionary dynamics between angiosperm and mammalian genomes

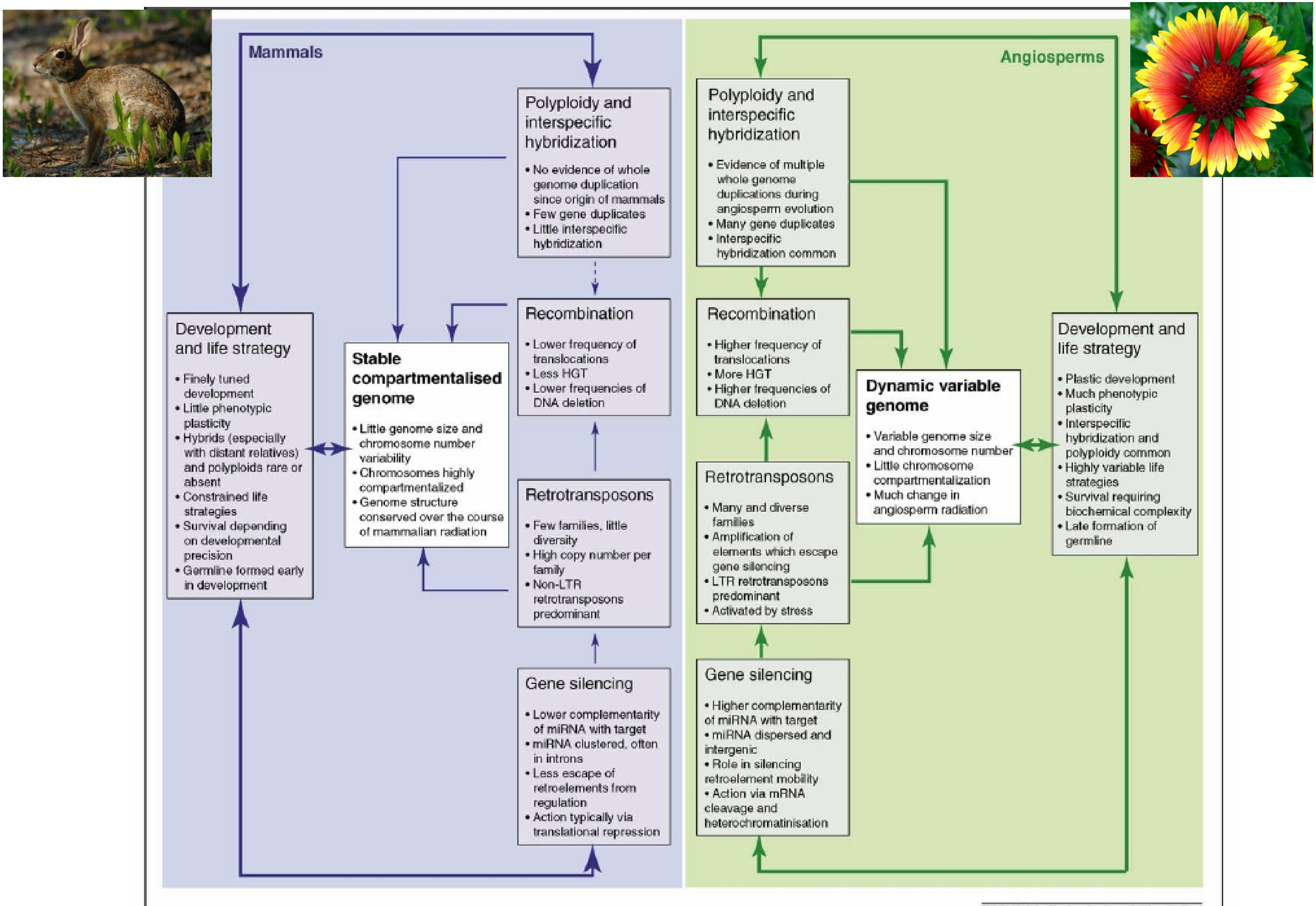
Eduard Kejnovsky[1], Ilia J. Leitch[2] and Andrew R. Leitch[3]

Trends in Ecology and Evolution Vol.24 No.10



TRENDS in Ecology & Evolution

Figure 1. Cytogenetic banding and chromosome painting. (a) Human metaphase showing G-bands enabling the identification of individual chromosomes (used with permission from Mr R. Palmer). (b) Chromosome painting using whole chromosome paints derived from Indian muntjac to metaphases of the same species (reprinted with permission from Oxford University Press (Human Molecular Genetics) [84], copyright 1998) (c) Human metaphase probed with gibbon chromosome paints (reprinted with permission from Macmillan Publishers Ltd (Nature Reviews Genetics) [8], copyright 2007).



TRENDS in Endocrinology & Metabolism

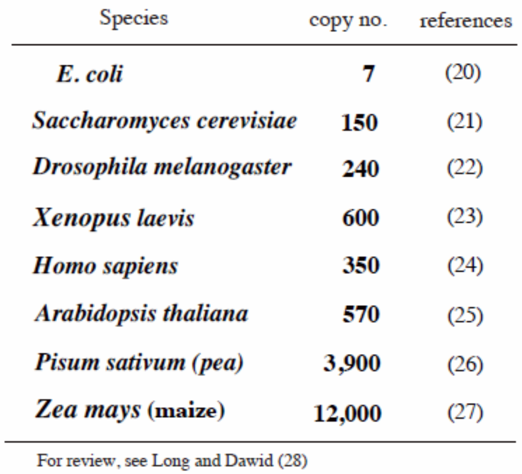
Figure 3. Different interrelationships and their relative strengths, represented by the direction and thickness of the arrows, between mechanisms generating genomic change and the life strategy options and developmental constraints in mammals and angiosperms. HGT refers to Horizontal Gene Transfer, the integration of DNA from sources outside of the nucleus.

Míra transkripce může ovlivňovat integritu genomu

Abundance of Ribosomal RNA Gene Copies Maintains Genome Integrity

Satoru Ide,[1] Takaaki Miyazaki,[1,2] Hisaji Maki,[3] Takehiko Kobayashi[1,2]*

5 FEBRUARY 2010 VOL 327 **SCIENCE**



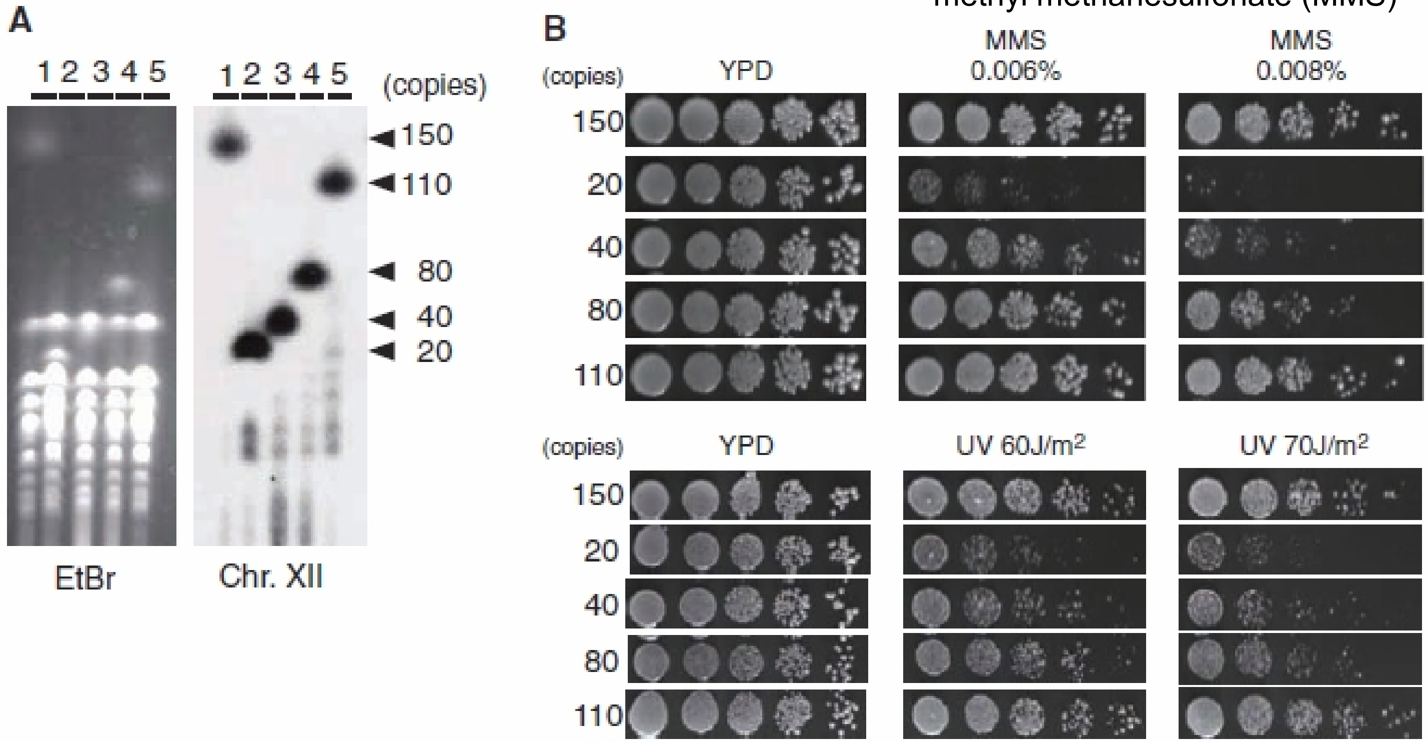
Species	copy no.	references
E. coli	**7**	(20)
Saccharomyces cerevisiae	**150**	(21)
Drosophila melanogaster	**240**	(22)
Xenopus laevis	**600**	(23)
Homo sapiens	**350**	(24)
Arabidopsis thaliana	**570**	(25)
***Pisum sativum* (pea)**	**3,900**	(26)
***Zea mays* (maize)**	**12,000**	(27)

For review, see Long and Dawid (28)

Fig.S1 rDNA copy numbers in various organisms (haploid)

Fig. 1. Low-rDNA-copy strains are sensitive to DNA damage by MMS and UV. (**A**) Detection of the length of chr XII in different rDNA copy number strains by CHEF. The left panel shows the ethidium bromide (EtBr)–stained chromosome profile, and the right panel is hybridization with chr XII probe. Positions of chr XII and approximate rDNA copy numbers are indicated. (**B**) Spot test for DNA damage sensitivity of yeast cells with different rDNA copy numbers. YPD, yeast extract, peptone, and dextrose.

methyl methanesulfonate (MMS)



Shrnutí

- změny ve velikosti těla se dějí změnou v množství mezibuněčné hmoty, změnou v počtu buněk (hyperplázie/hypoplázie) nebo změnou ve velikosti buněk (hypertrofie/hypotrofie)

- jednotlivý mechanismus má různé důsledky pro fenotyp (rychlost metalismu, komplexita těla)

- velikost genomu koreluje s nejrůznějšími fenotypovými projevy, většinou ale není jasná kauzalita

- dynamika genomu je odlišná mezi taxonomickými skupinami a patrně odráží jejich strategie ontogenetického vývinu