Escola de Astrobiologia

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Rio de Janeiro, 26 outubro 2024

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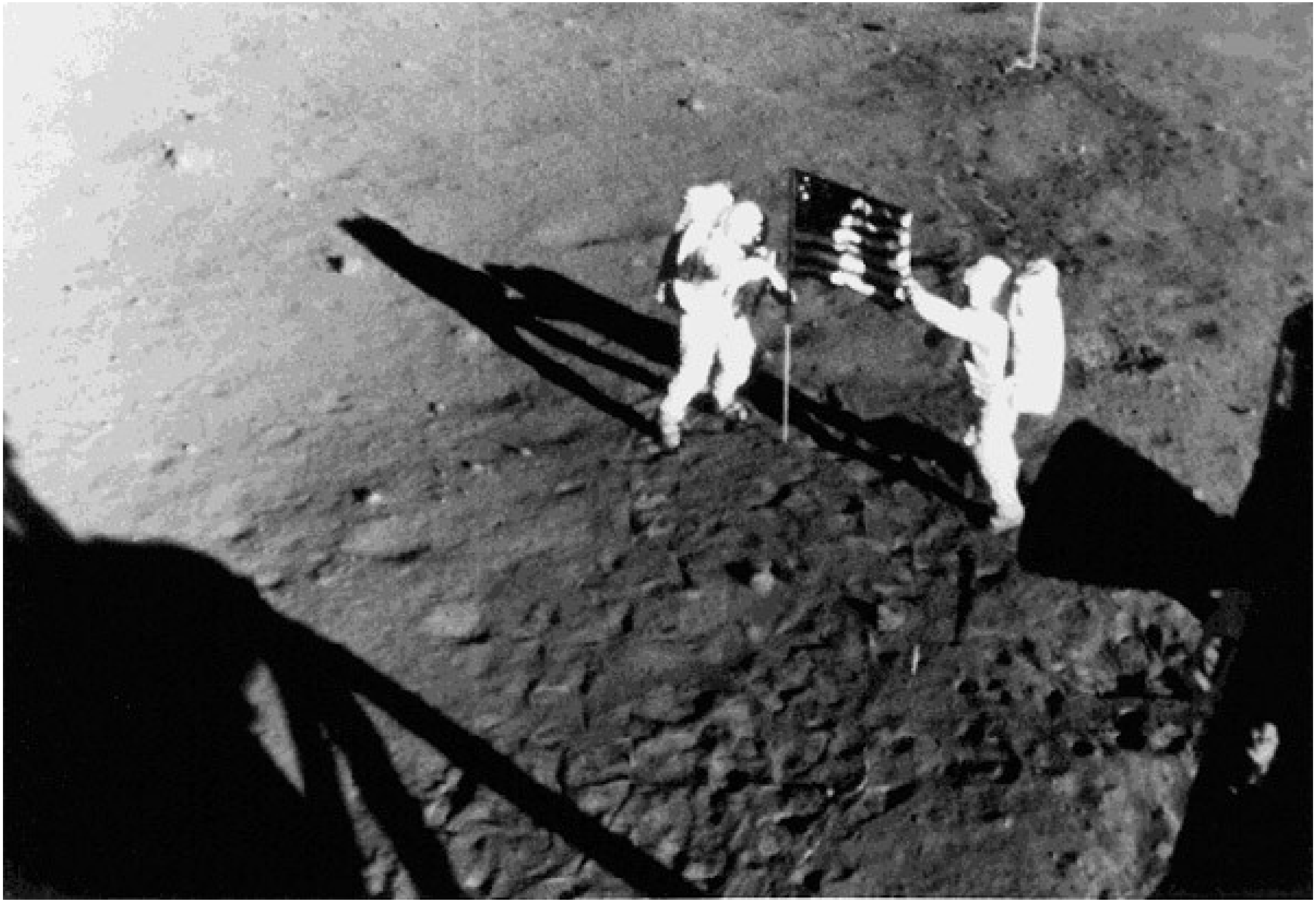
EDEVO
DARWIN



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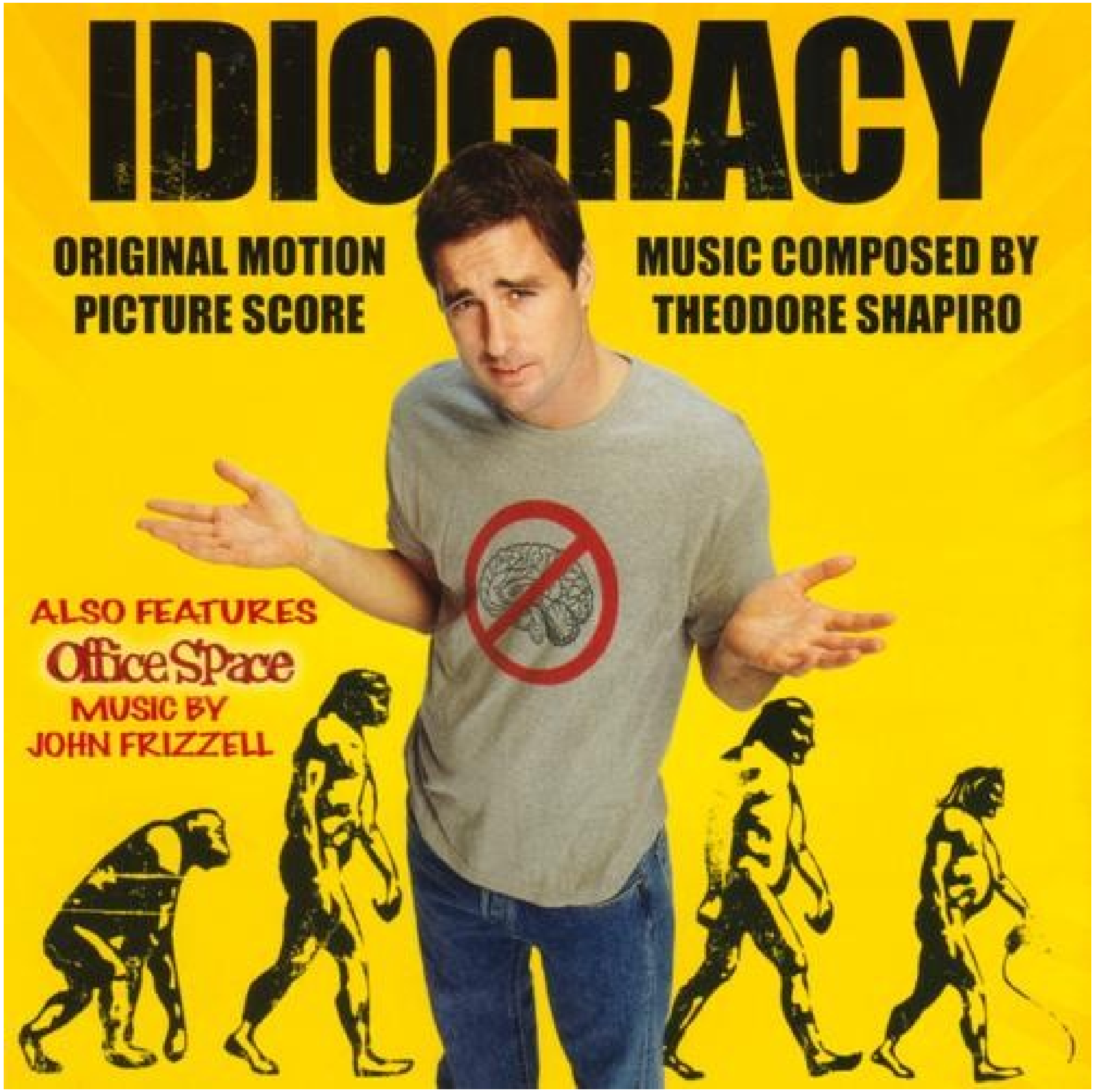
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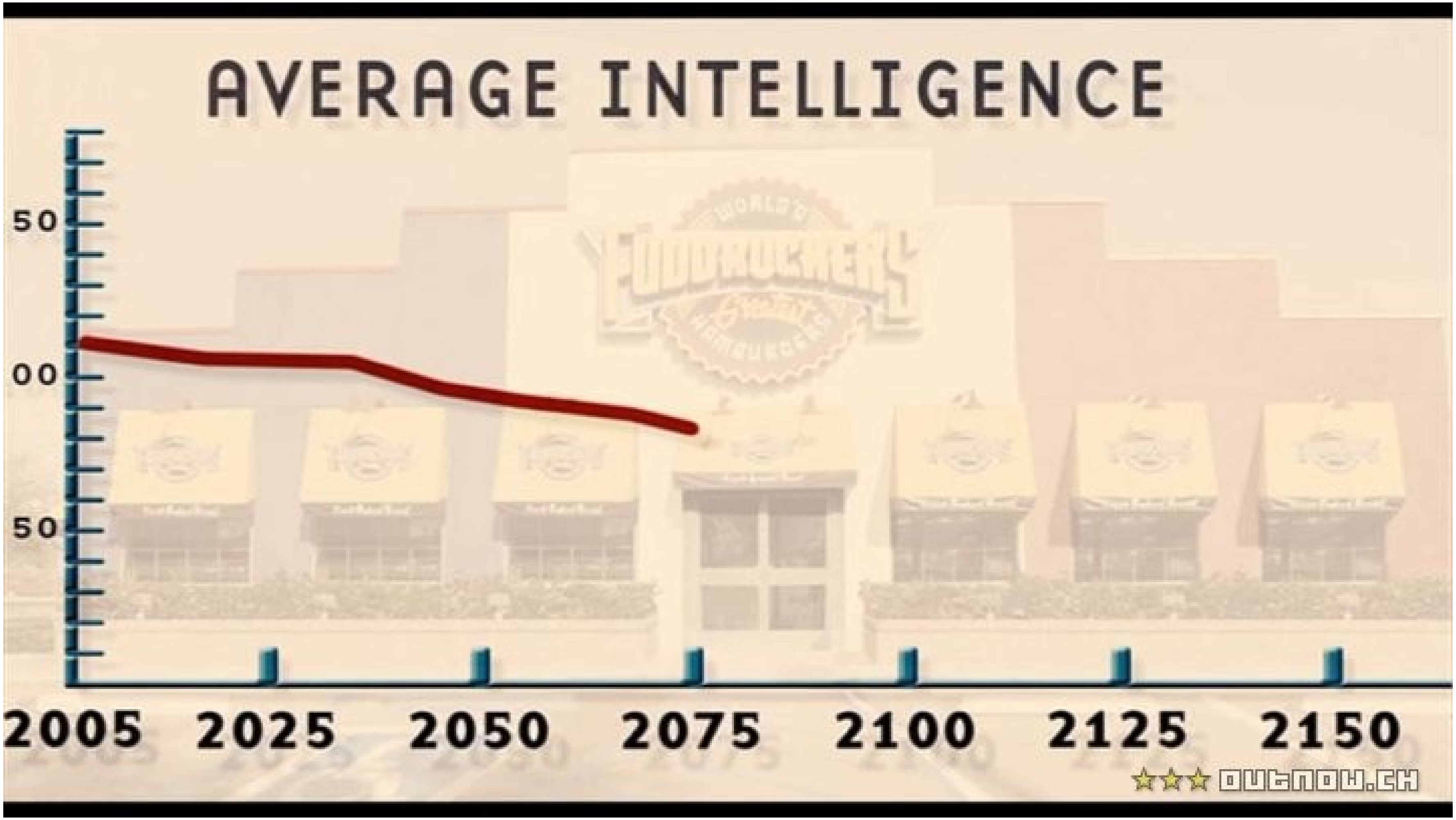
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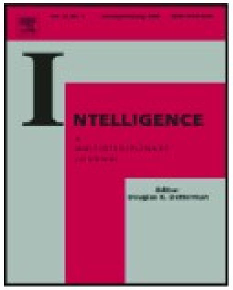

Were the Victorians cleverer than us? The decline in general intelligence estimated from a meta-analysis of the slowing of simple reaction time

Michael A. Woodley [a,b,*,1,2], Jan te Nijenhuis [c,2,3], Raegan Murphy [d,4]

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[b] *Center Leo Apostel for Interdisciplinary Studies, Vrije Universiteit Brussel, Belgium*
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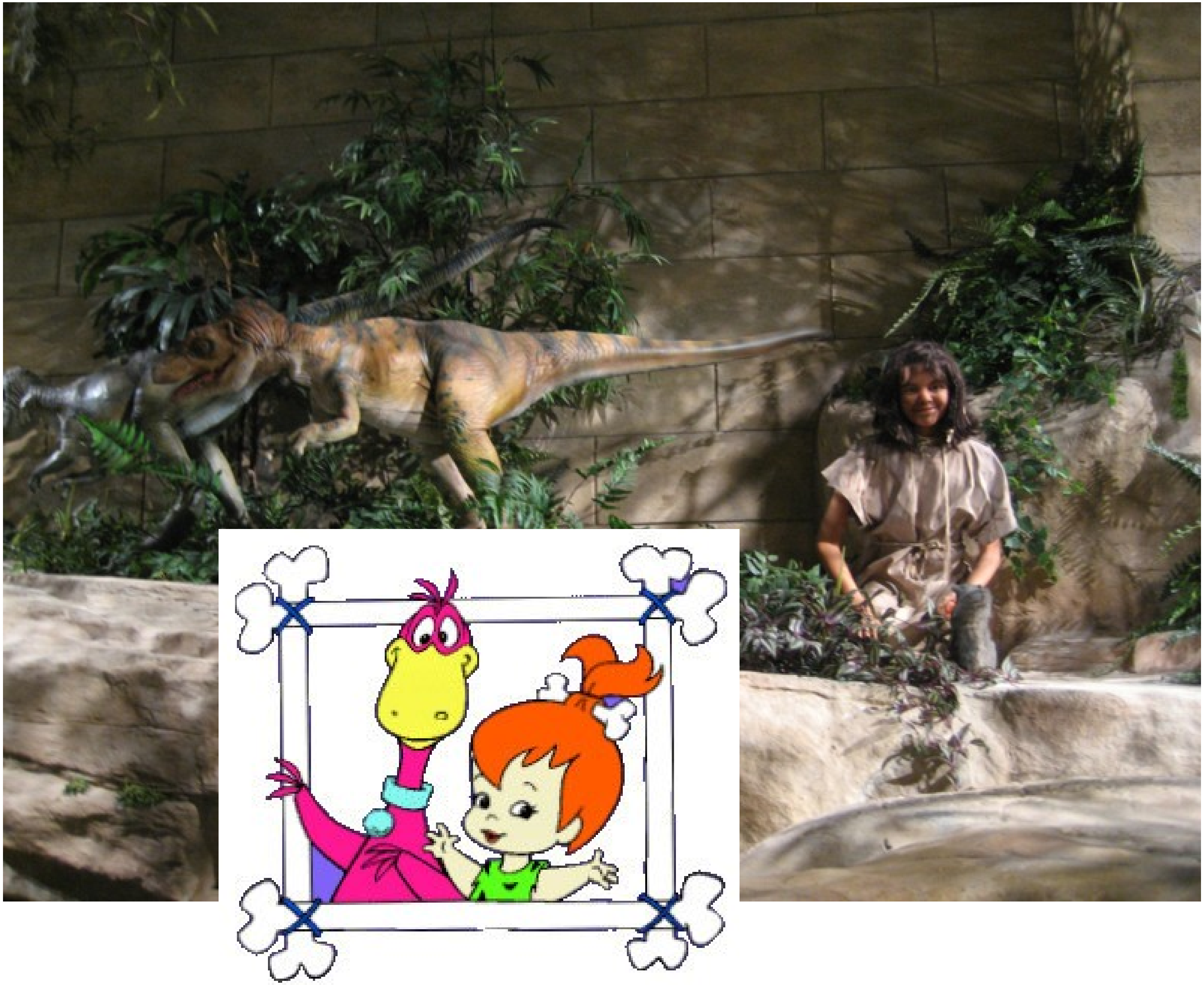
ABSTRACT

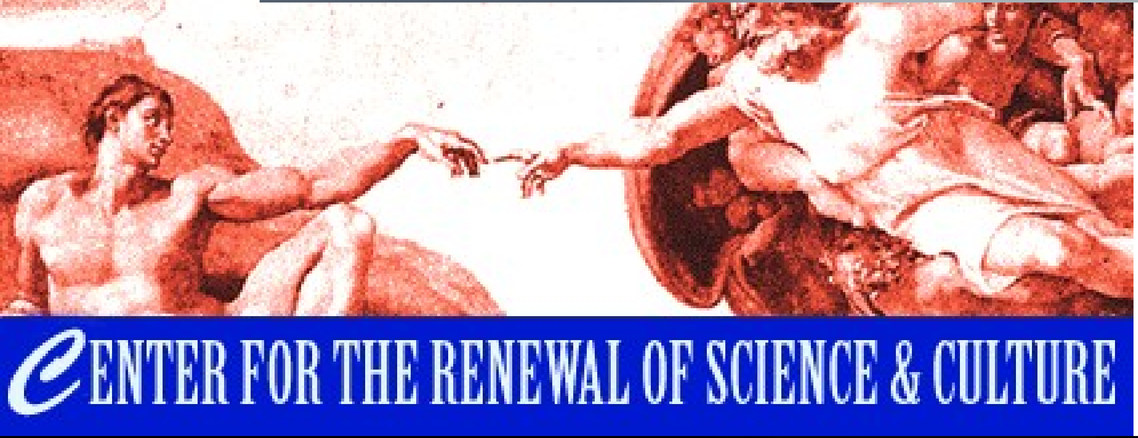
The Victorian era was marked by an explosion of innovation and genius, per capita rates of which appear to have declined subsequently. The presence of dysgenic fertility for IQ amongst Western nations, starting in the 19th century, suggests that these trends might be related to declining IQ. This is because high-IQ people are more productive and more creative. We tested the hypothesis that the Victorians were cleverer than modern populations, using high-quality instruments, namely measures of simple visual reaction time in a meta-analytic study. Simple reaction time measures correlate substantially with measures of general intelligence (*g*) and are considered elementary measures of cognition. In this study we used the data on the secular slowing of simple reaction time described in a meta-analysis of 14 age-matched studies from Western countries conducted between 1884 and 2004 to estimate the decline in g that may have resulted from the presence of dysgenic fertility. Using psychometric meta-analysis we

Albert Parr

Image: Craig Chesek / American Museum of Natural History

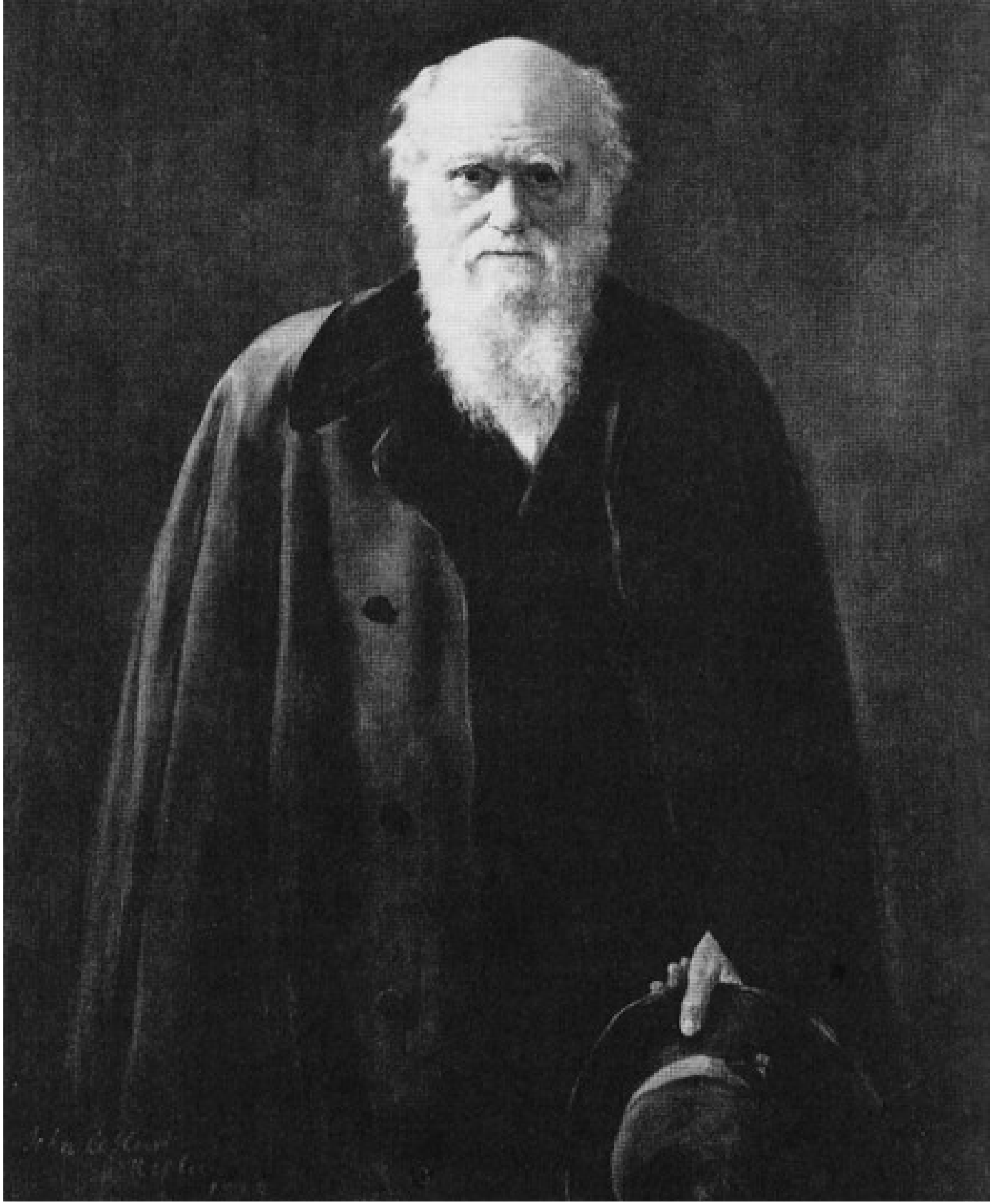

MUSEUM of CREATION and EARTH HISTORY

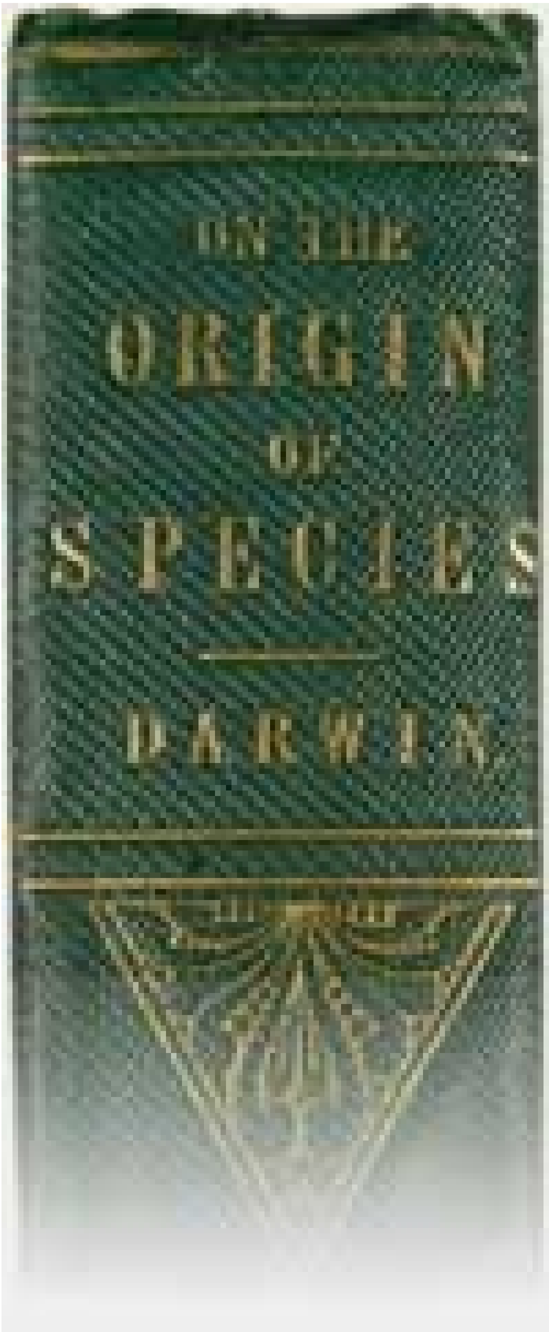




1996-1999

1999-2001




ON THE
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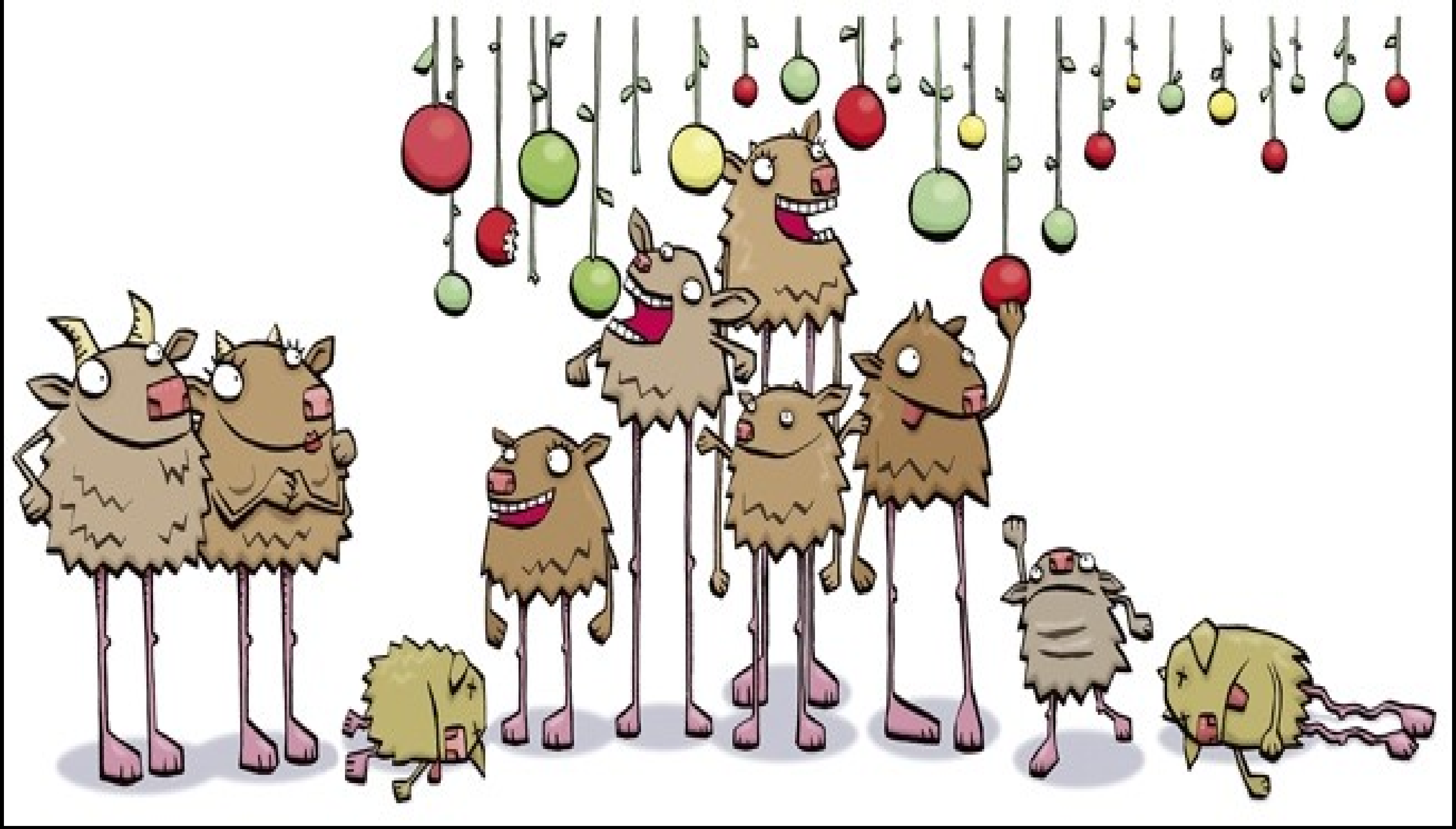


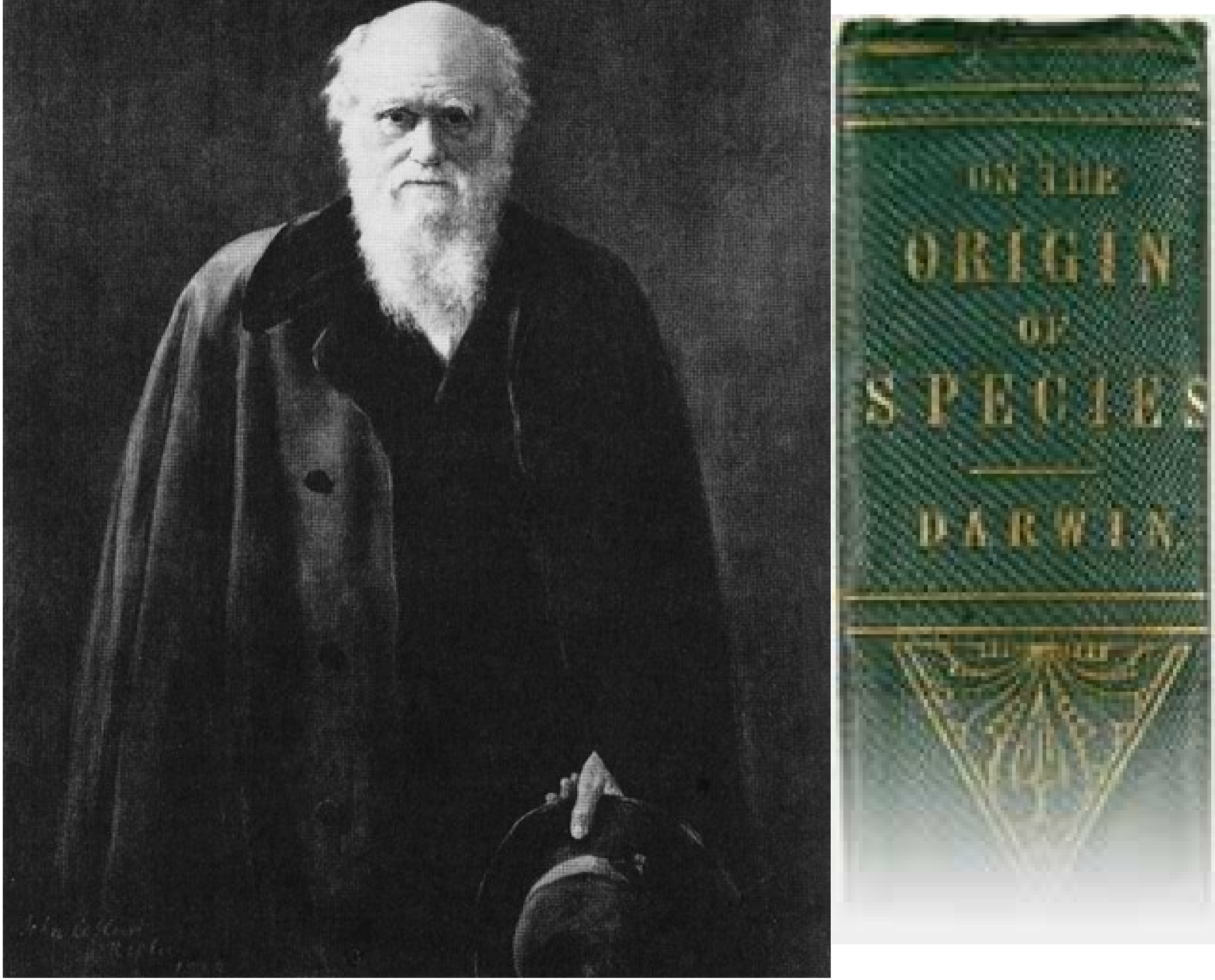
Natural Selection

1. Individuals in natural populations display variation.

2. Certain individual variations are inheritable.

3. Certain heritable variations result in differential reproductive success.

4. Differences in reproductive success due to heritable variation cause changes in the relative representation of such variations in the population.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SPECIES
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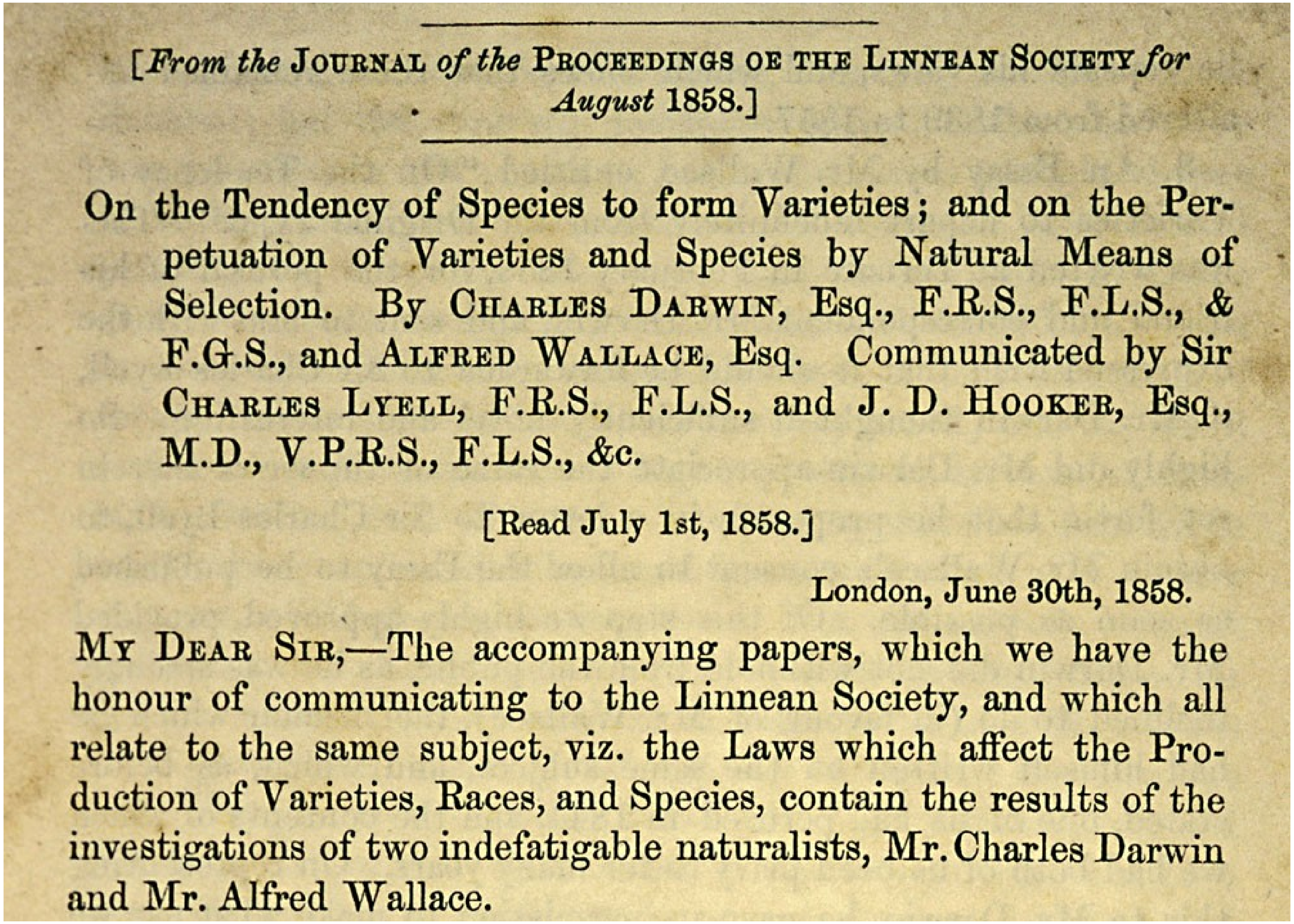


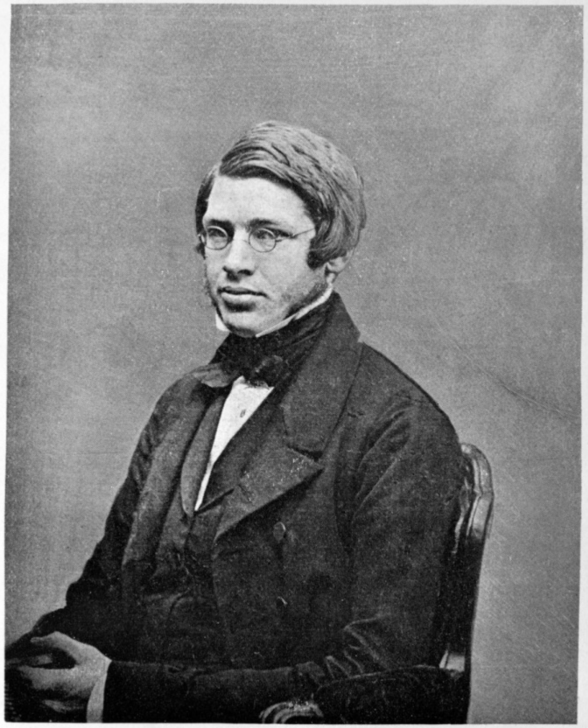
[*From the* JOURNAL *of the* PROCEEDINGS OF THE LINNEAN SOCIETY *for August* 1858.]

On the Tendency of Species to form Varieties; and on the Perpetuation of Varieties and Species by Natural Means of Selection. By CHARLES DARWIN, Esq., F.R.S., F.L.S., & F.G.S., and ALFRED WALLACE, Esq. Communicated by Sir CHARLES LYELL, F.R.S., F.L.S., and J. D. HOOKER, Esq., M.D., V.P.R.S., F.L.S., &c.

[Read July 1st, 1858.]

London, June 30th, 1858.

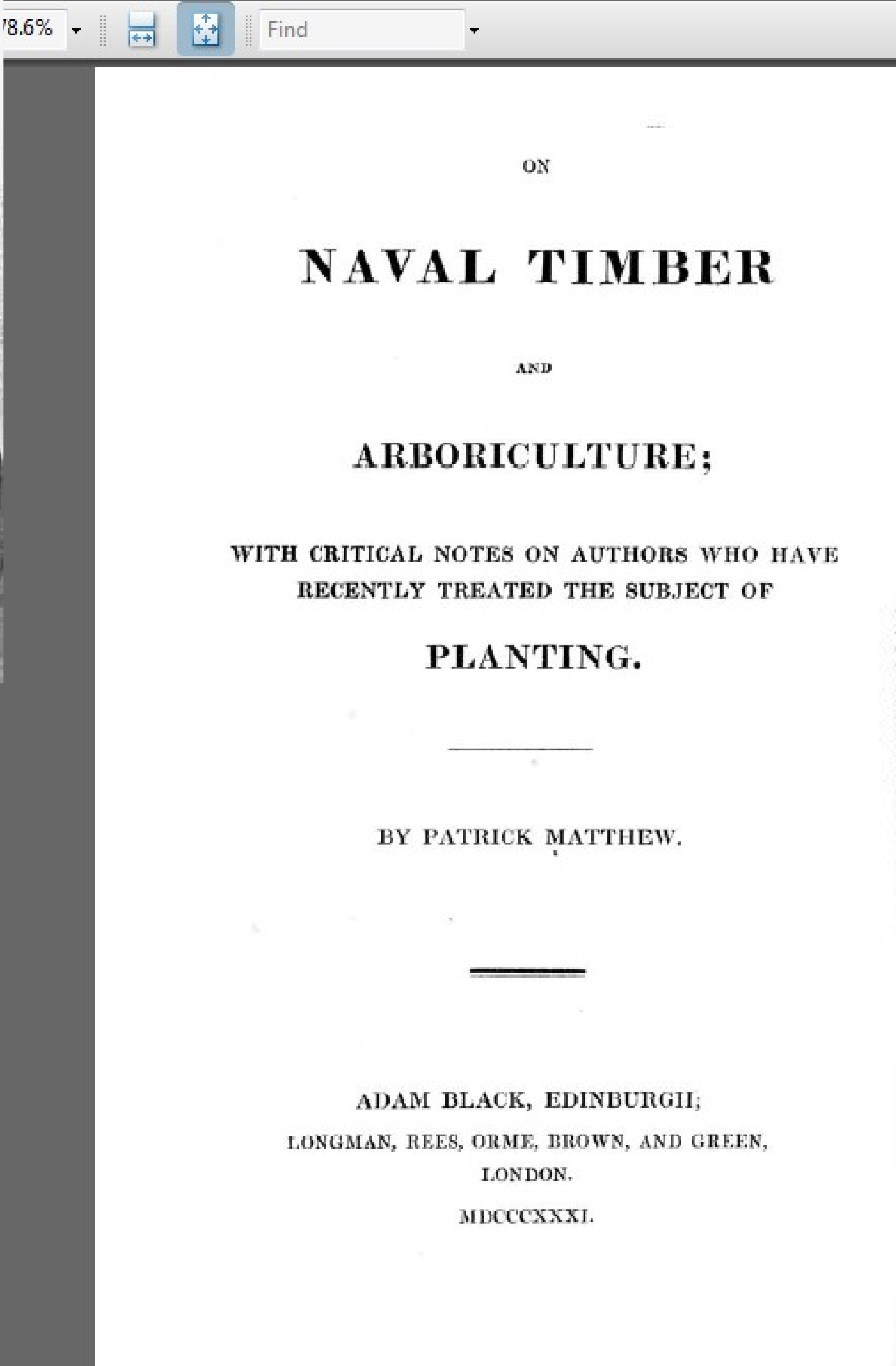
MY DEAR SIR,—The accompanying papers, which we have the honour of communicating to the Linnean Society, and which all relate to the same subject, viz. the Laws which affect the Production of Varieties, Races, and Species, contain the results of the investigations of two indefatigable naturalists, Mr. Charles Darwin and Mr. Alfred Wallace.



ALFRED R. WALLACE. 1848.

(*From a daguerrotype.*)

Patrick Matthew
(1790-1874)



ON

NAVAL TIMBER

AND

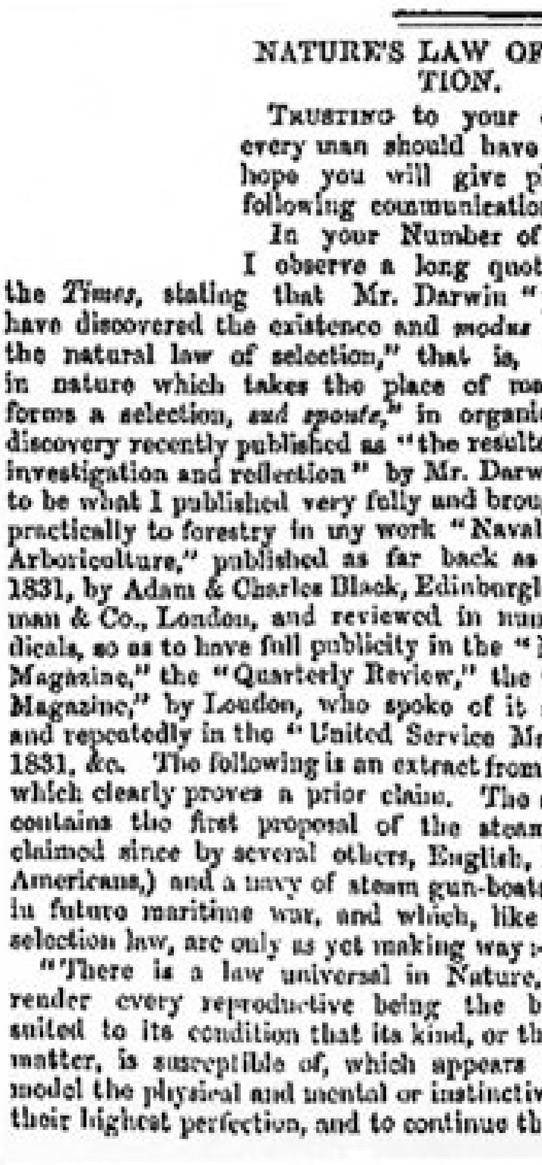
ARBORICULTURE;

WITH CRITICAL NOTES ON AUTHORS WHO HAVE
RECENTLY TREATED THE SUBJECT OF

PLANTING.

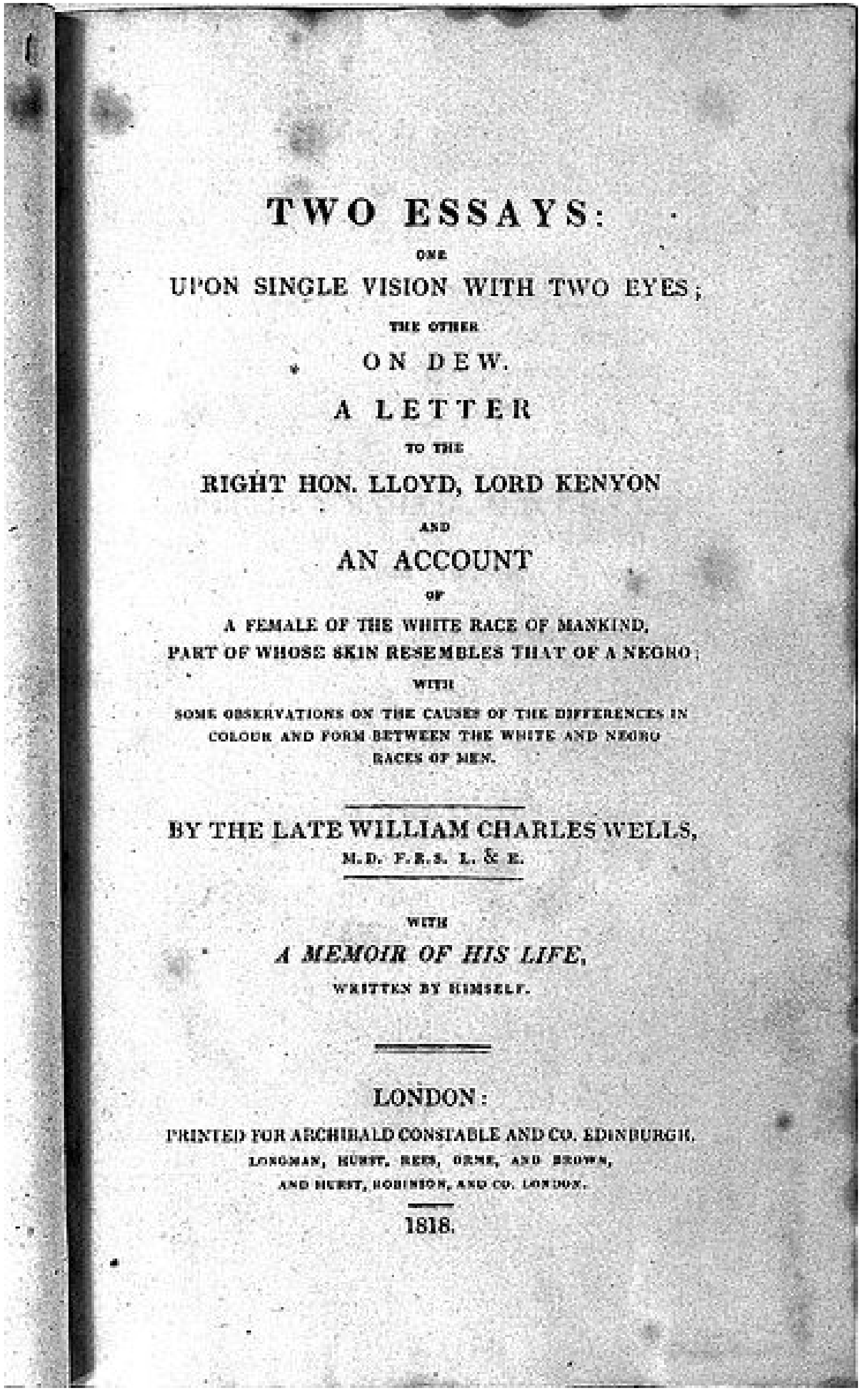
BY PATRICK MATTHEW.

ADAM BLACK, EDINBURGH;
LONGMAN, REES, ORME, BROWN, AND GREEN,
LONDON.
MDCCCXXXI.



NATURE'S LAW OF
TION.

Trusting to your
every man should have
hope you will give p
following communicatio
In your Number of
I observe a long quot
the *Times*, stating that Mr. Darwin "
have discovered the existence and *modus*
the natural law of selection," that is,
in nature which takes the place of ma
forms a selection, *sud sponte*," in organic
discovery recently published as "the result
investigation and reflection" by Mr. Darw
to be what I published very fully and brou
practically to forestry in my work "Naval
Arboriculture," published as far back as
1831, by Adam & Charles Black, Edinburgh
man & Co., London, and reviewed in num
dicals, so as to have full publicity in the "
Magazine," the "Quarterly Review," the
Magazine," by Loudon, who spoke of it
and repeatedly in the "United Service Ma
1831, &c. The following is an extract from
which clearly proves a prior claim. The
contains the first proposal of the steam
claimed since by several others, English,
Americans,) and a navy of steam gun-boat
in future maritime war, and which, like
selection law, are only as yet making way
"There is a law universal in Nature,
render every reproductive being the b
suited to its condition that its kind, or th
matter, is susceptible of, which appears
model the physical and mental or instincti
their highest perfection, and to continue th



TWO ESSAYS:
ONE
UPON SINGLE VISION WITH TWO EYES;
THE OTHER
ON DEW.
A LETTER
TO THE
RIGHT HON. LLOYD, LORD KENYON
AND
AN ACCOUNT
OF
A FEMALE OF THE WHITE RACE OF MANKIND,
PART OF WHOSE SKIN RESEMBLES THAT OF A NEGRO;
WITH
SOME OBSERVATIONS ON THE CAUSES OF THE DIFFERENCES IN
COLOUR AND FORM BETWEEN THE WHITE AND NEGRO
RACES OF MEN.

BY THE LATE WILLIAM CHARLES WELLS,
M.D. F.R.S. L. & E.

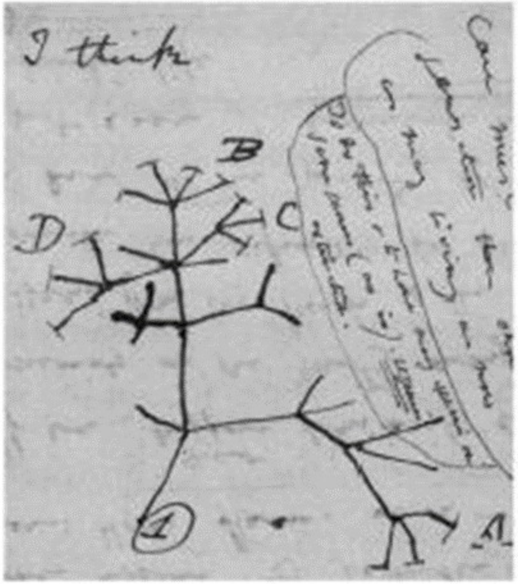
WITH
A MEMOIR OF HIS LIFE,
WRITTEN BY HIMSELF.

LONDON:
PRINTED FOR ARCHIBALD CONSTABLE AND CO. EDINBURGH.
LONGMAN, HURST, REES, ORME, AND BROWN,
AND HURST, ROBINSON, AND CO. LONDON.
1818.

"[What was done for animals artificially] seems to be done with equal efficiency, though more slowly, by nature, in the formation of varieties of mankind, fitted for the country which they inhabit. Of the accidental varieties of man, which would occur among the first scattered inhabitants, some one would be better fitted than the others to bear the diseases of the country. This race would multiply while the others would decrease, and as the darkest would be the best fitted for the [African] climate, at length [they would] become the most prevalent, if not the only race."

Jean-Baptiste Lamarck (1744-1829)

A



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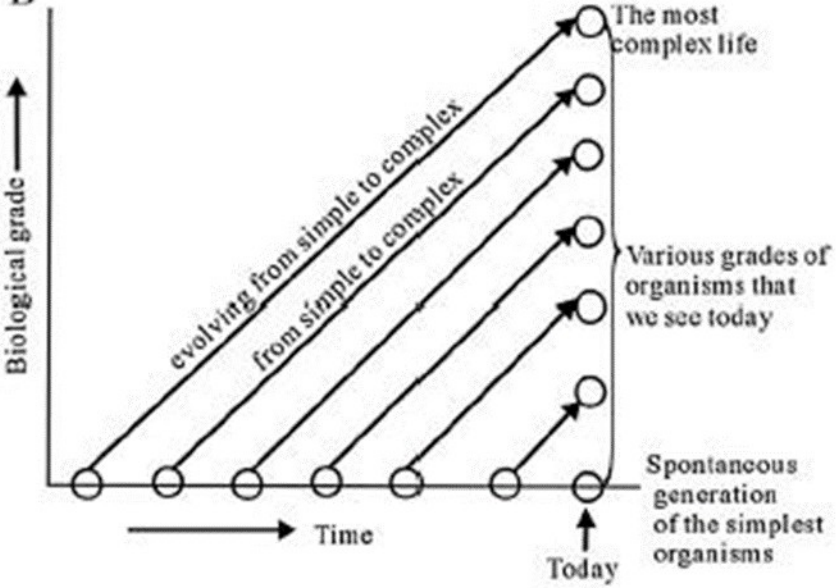
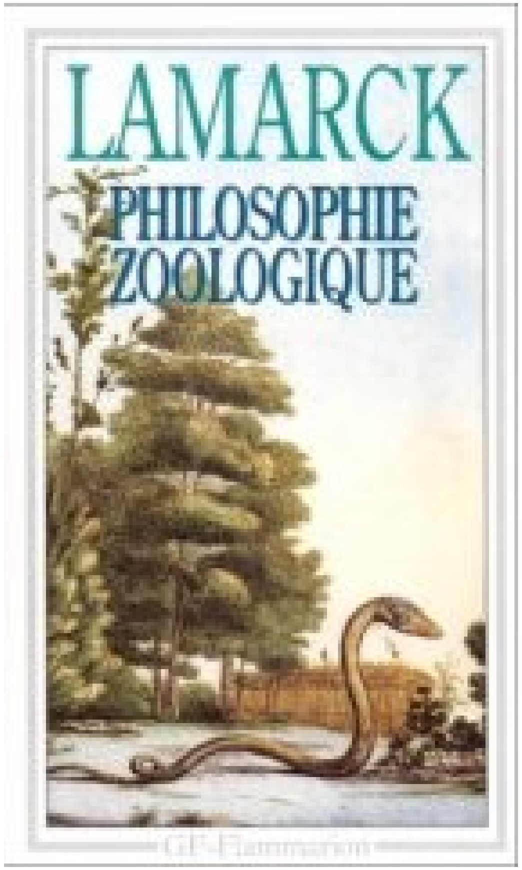
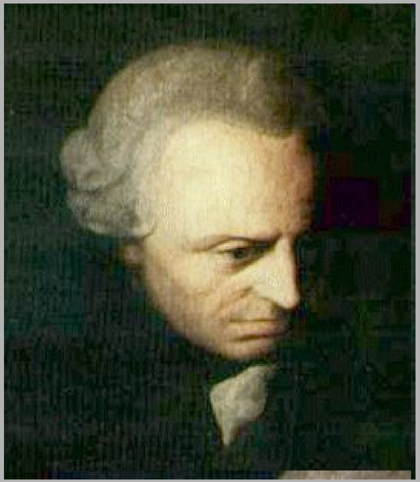




“This analogy of forms supports the supposition that there is among them a real blood relationship, due to the derivation from a common progenitor; a supposition reached by the observation of the gradual approximation of one class of animals to another"

Kant (1790)



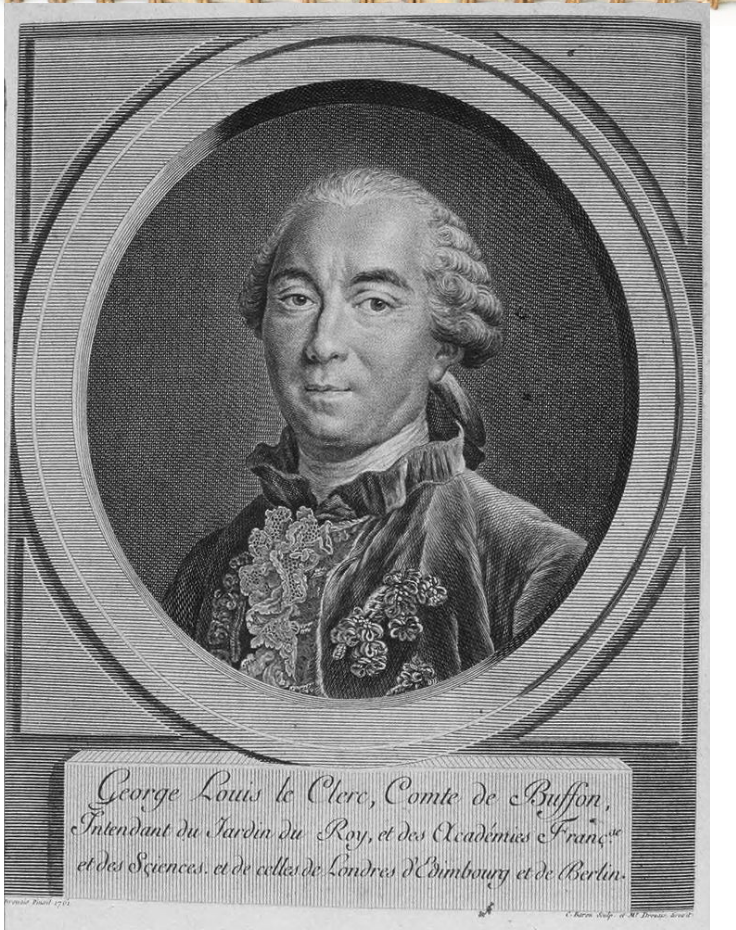
HISTOIRE NATURELLE,
GENERALE ET PARTICULIERE,
AVEC LA DESCRIPTION
DU CABINET DU ROY.

(Georges Louis Leclerc, comte de Buffon) Buffon

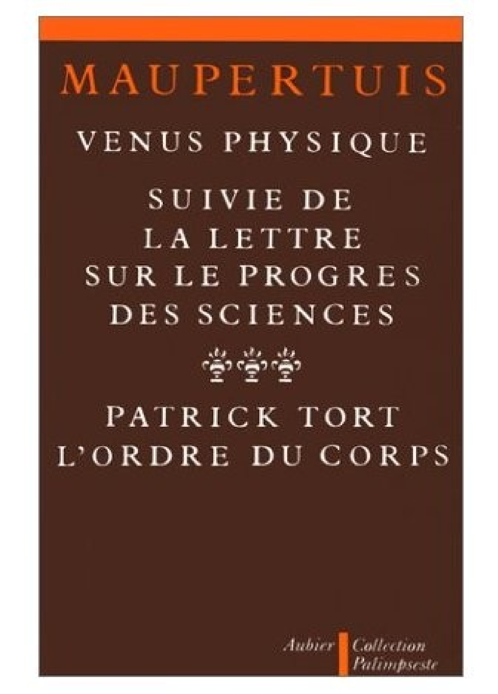
Tome Premier.

A PARIS,
DE L'IMPRIMERIE ROYALE.
M. DCCXLIX.
1749

(1707-1788)



George Louis le Clerc, Comte de Buffon,
Intendant du Jardin du Roy, et des Académies Franç.se
et des Sciences. et de celles de Londres d'Edimbourg et de Berlin.



MAUPERTUIS

VENUS PHYSIQUE

SUIVIE DE
LA LETTRE
SUR LE PROGRES
DES SCIENCES

* * *

PATRICK TORT
L'ORDRE DU CORPS

Aubier
Collection
Palimpseste

Louis Moreau de Maupertuis

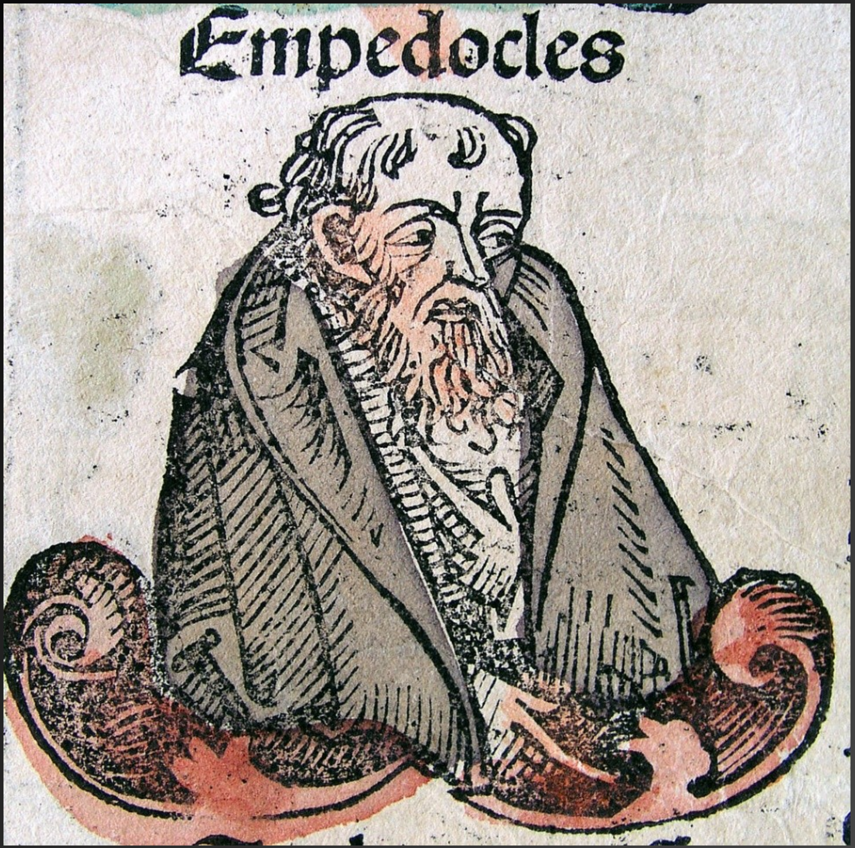
(1698-1759)

“Could one not say that, in the fortuitous combinations of the productions of nature, as there must be some characterized by a certain relation of fitness which are able to subsist, it is not to be wondered at that this fitness is present in all the species that are currently in existence? Chance, one would say, produced an innumerable multitude of individuals; a small number found themselves constructed in such a manner that the parts of the animal were able to satisfy its needs; in another infinitely greater number, there was neither fitness nor order: all of these latter have perished. Animals lacking a mouth could not live; others lacking reproductive organs could not perpetuate themselves... The species we see today are but the smallest part of what blind destiny has produced...”.

[*Système de la Nature*, 1756]

Chance, one might say, turned out a vast number of individuals; a small proportion of these were organized in such a manner that the animals' organs could satisfy their needs. A much greater number showed neither adaptation nor order; these last have all perished. . . . Thus the species which we see to-day are but a small part of all those that a blind destiny has produced. "

[Vénus Physique, 1745]



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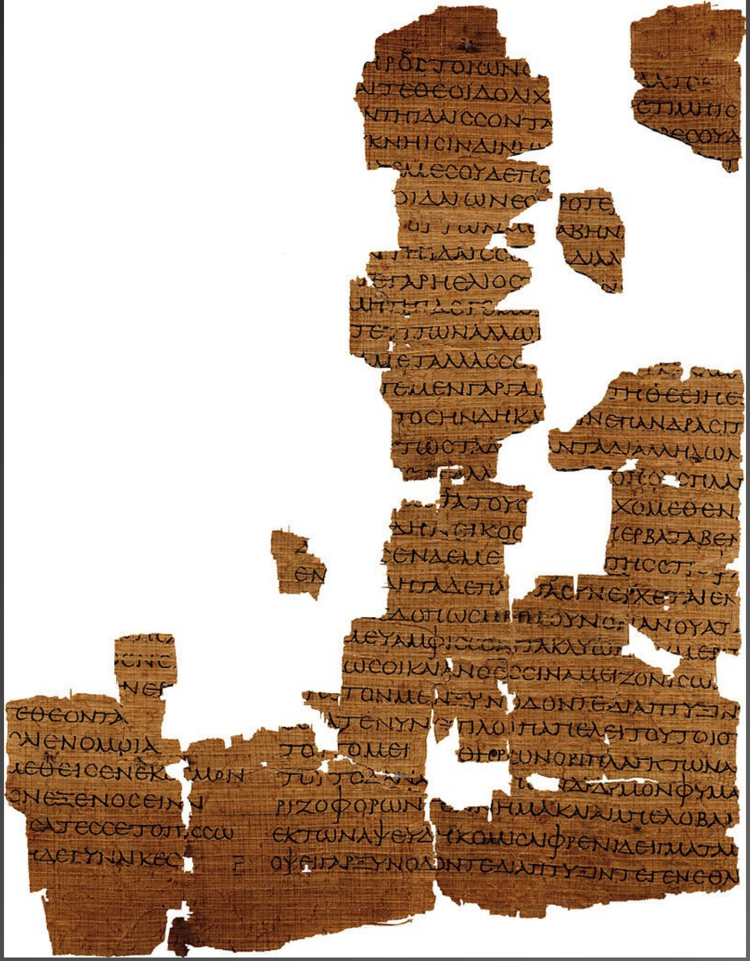
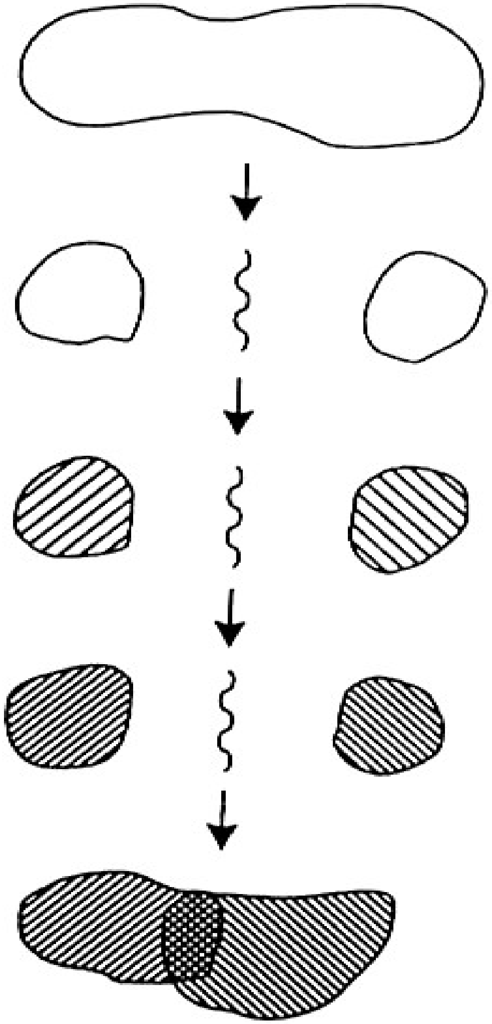
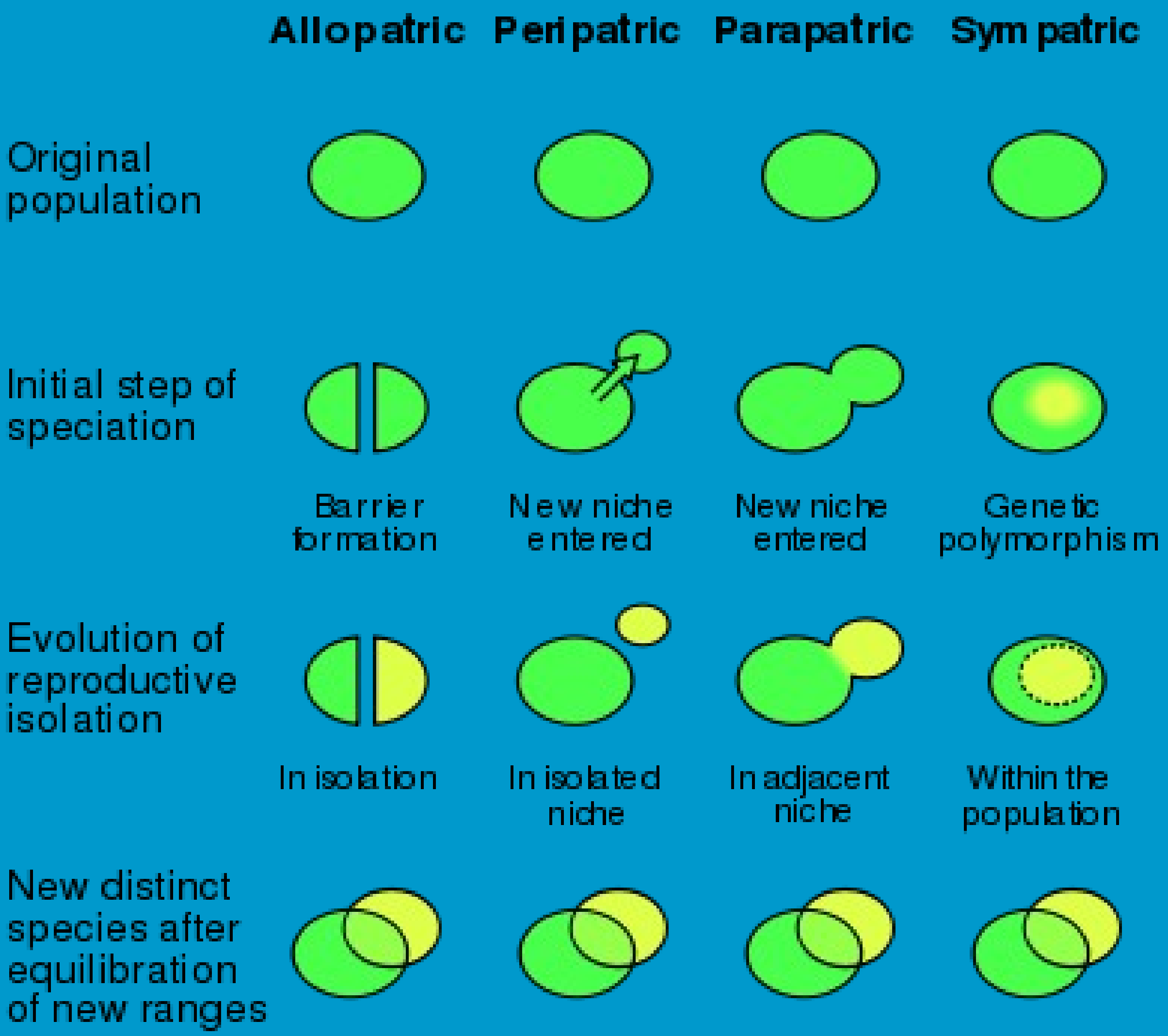
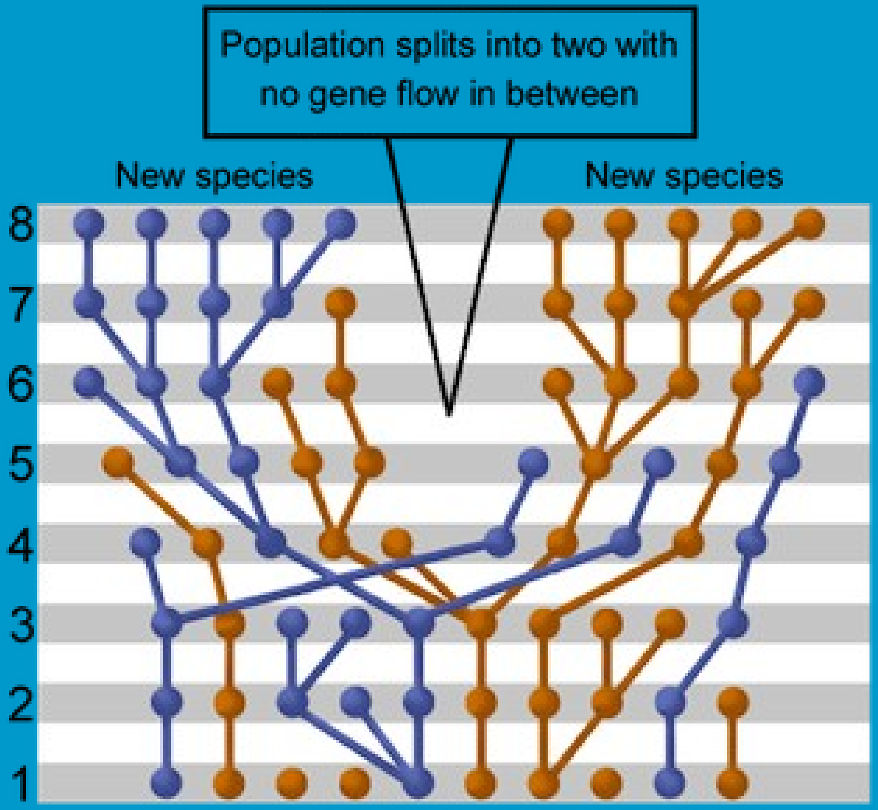






	Allopatric	Peripatric	Parapatric	Sympatric
Original population				
Initial step of speciation	Barrier formation	New niche entered	New niche entered	Genetic polymorphism
Evolution of reproductive isolation	In isolation	In isolated niche	In adjacent niche	Within the population
New distinct species after equilibration of new ranges				

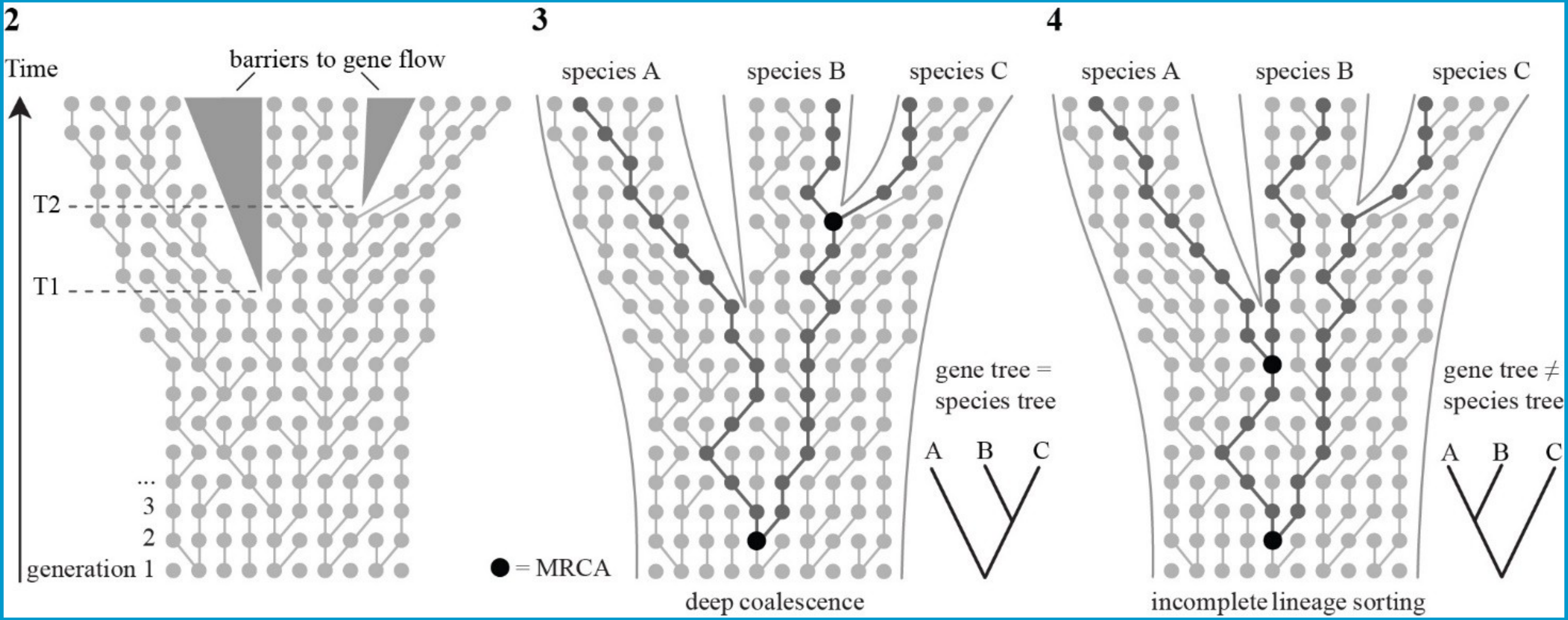


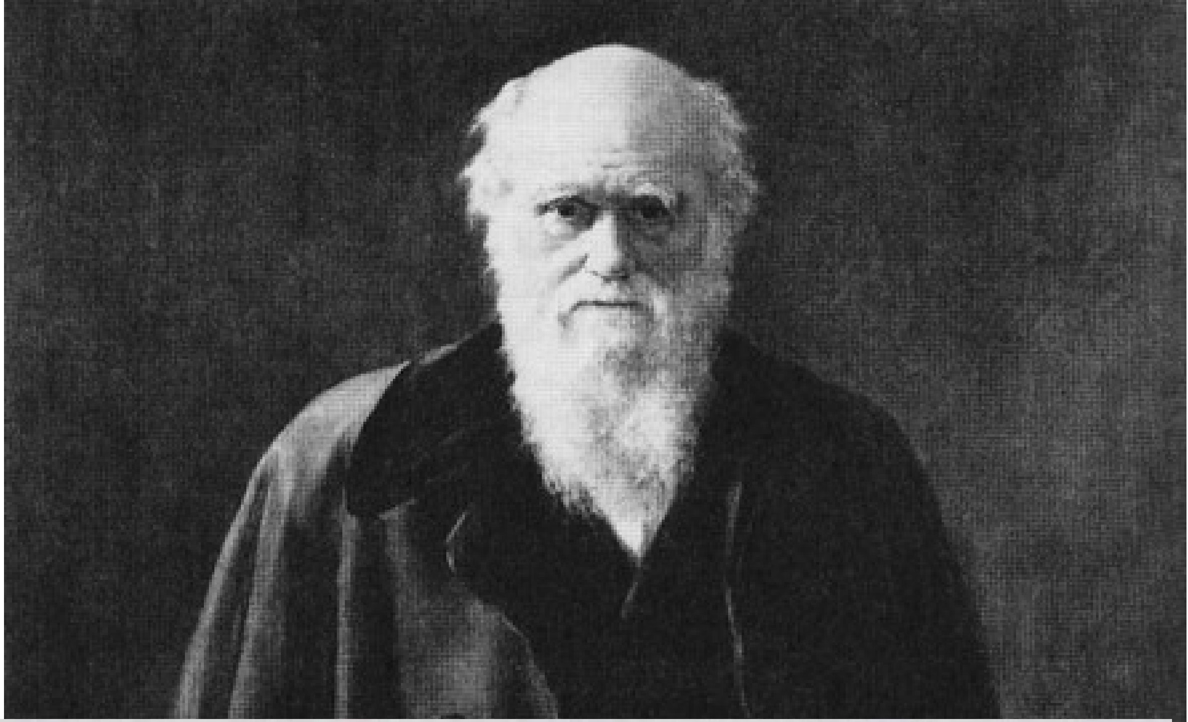
Population splits into two with no gene flow in between

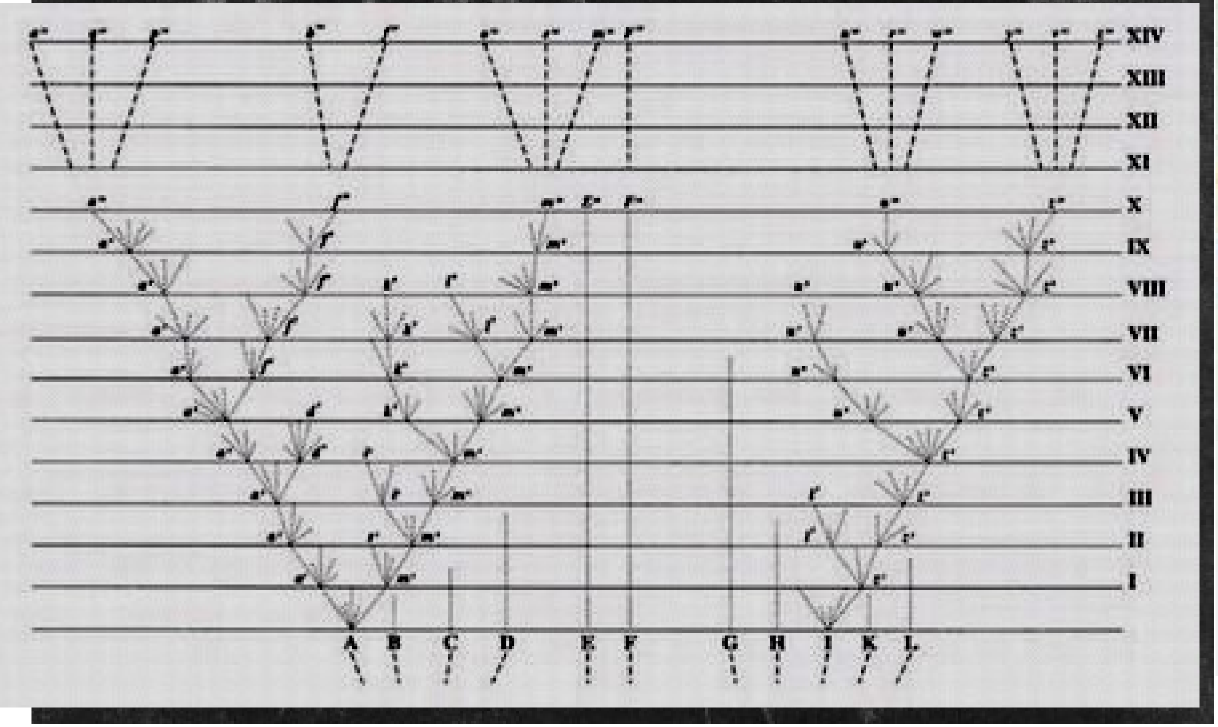
#'s refer to generations

Either because of ramdom chance or (genetic drift) or adaptation to different environments (natural selection), allele frequencies can change

The single ancestral species is polymorphic for a certain allele, and gene flow is possible throughout the species


2
Time
barriers to gene flow
T2
T1
...
3
2
generation 1
3
species A
species B
species C
gene tree =
species tree
A
B
C
● = MRCA
deep coalescence
4
species A
species B
species C
gene tree ≠
species tree
A
B
C
incomplete lineage sorting

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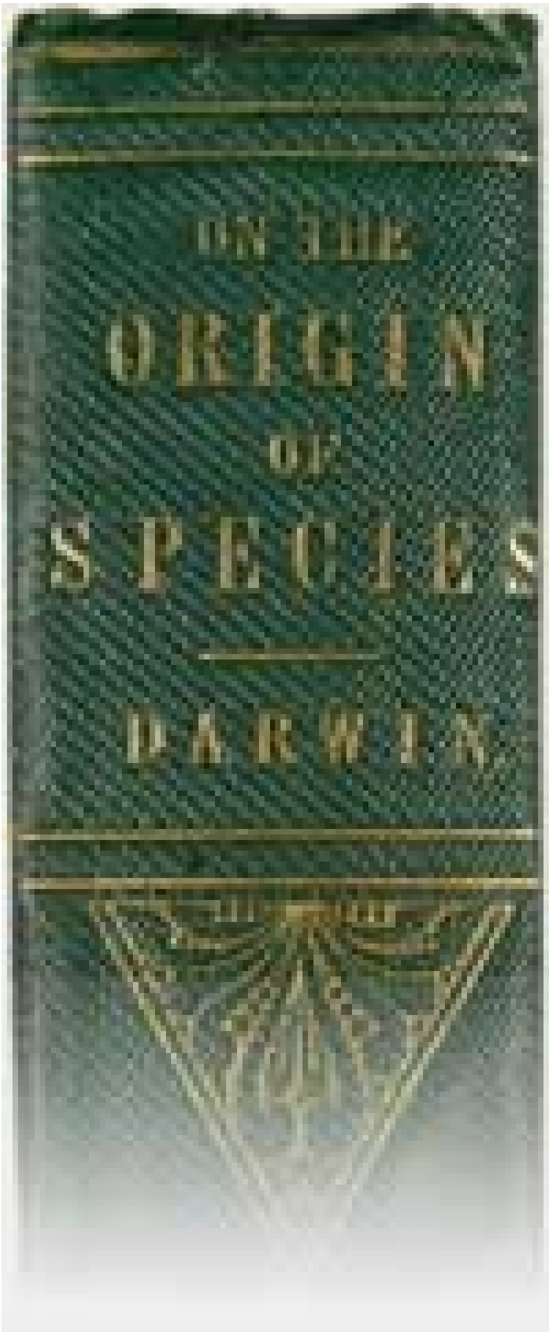
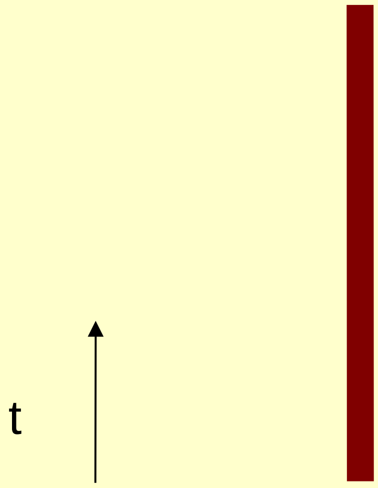

ON THE
ORIGIN
OF
SPECIES
DARWIN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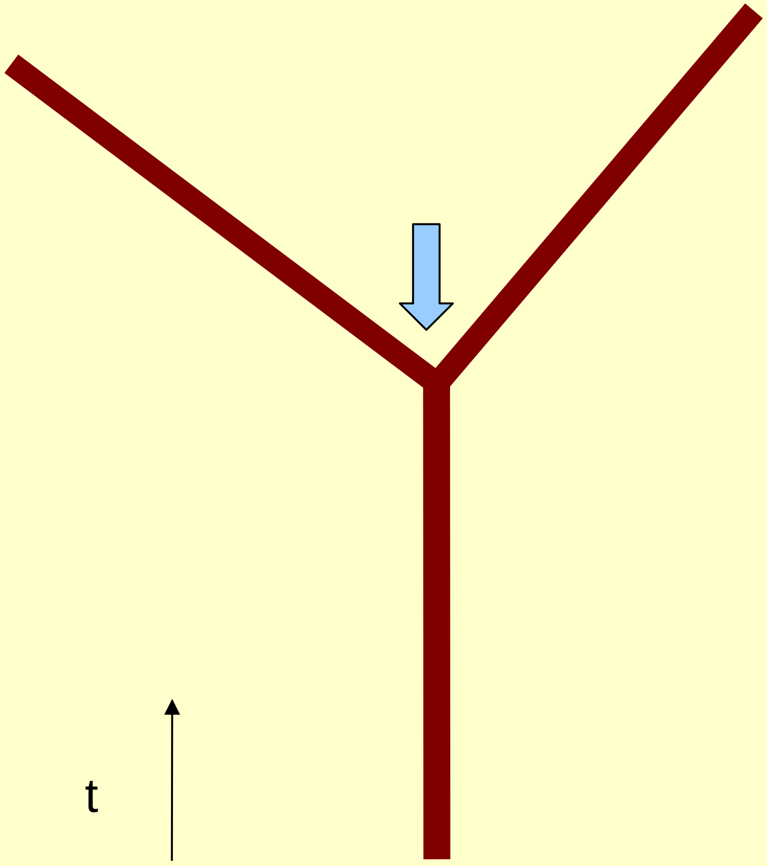
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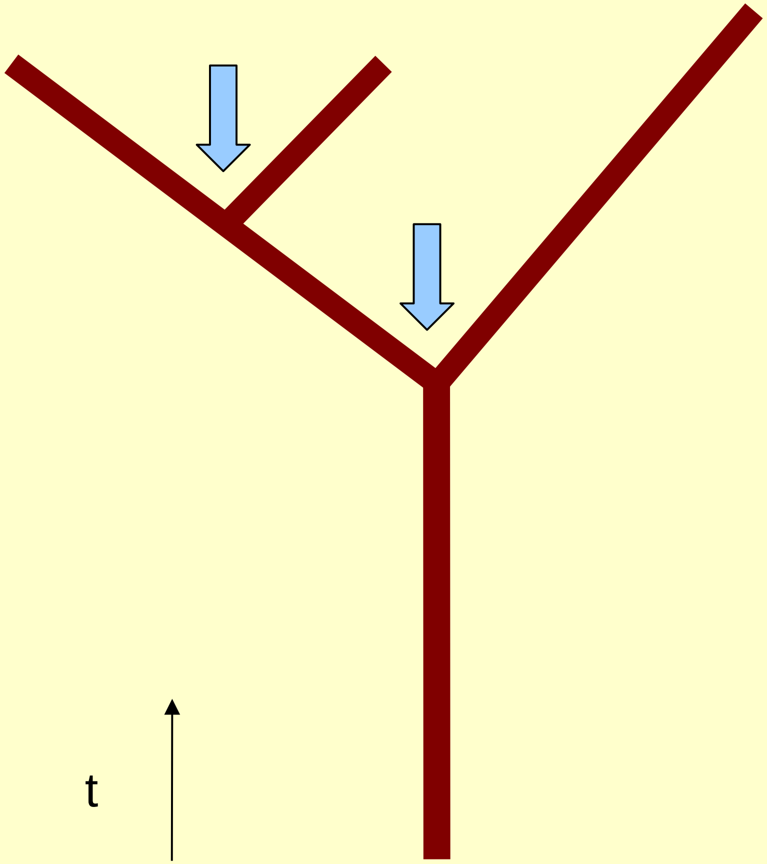
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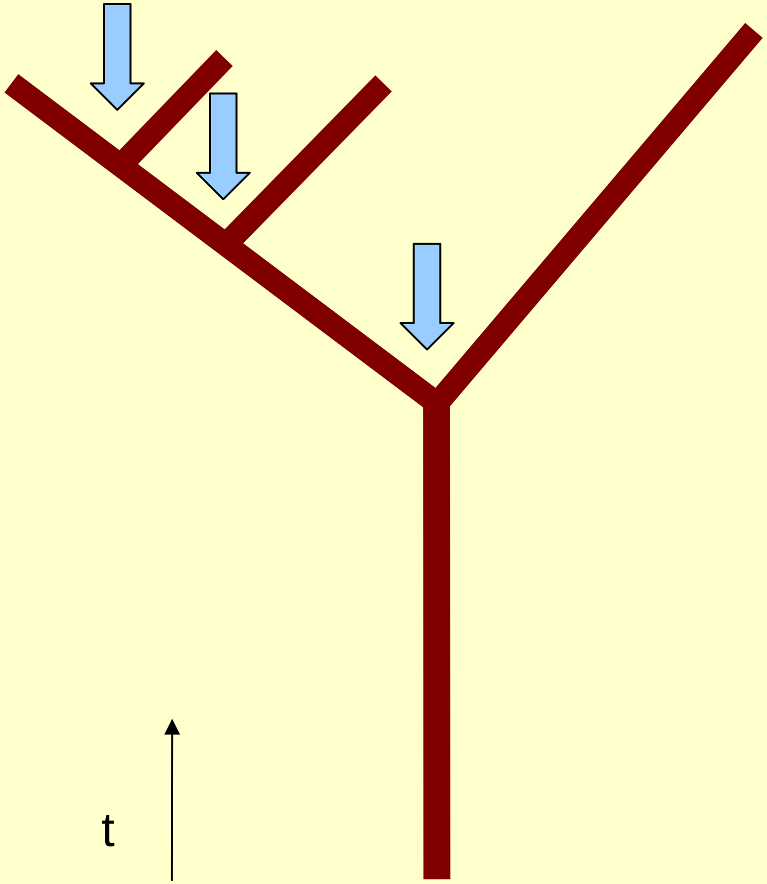
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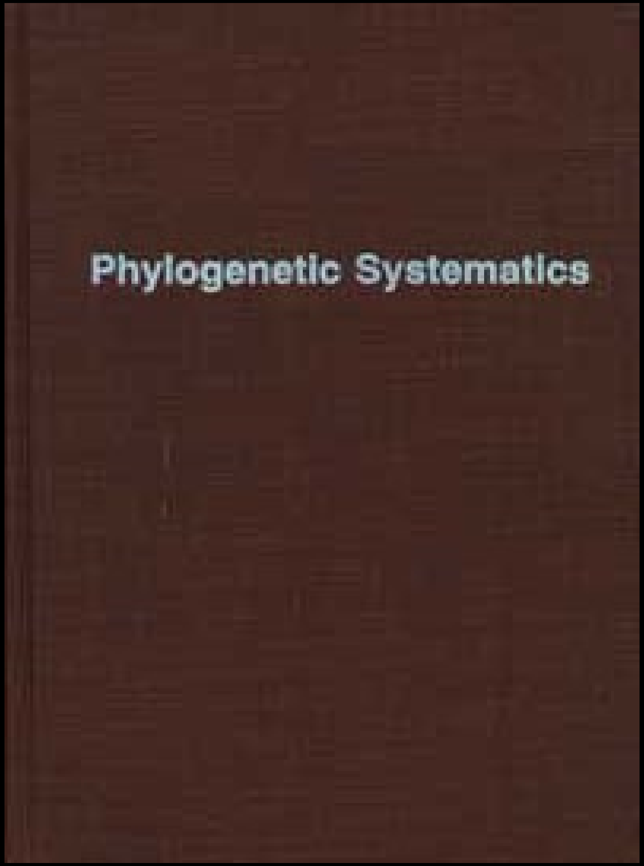
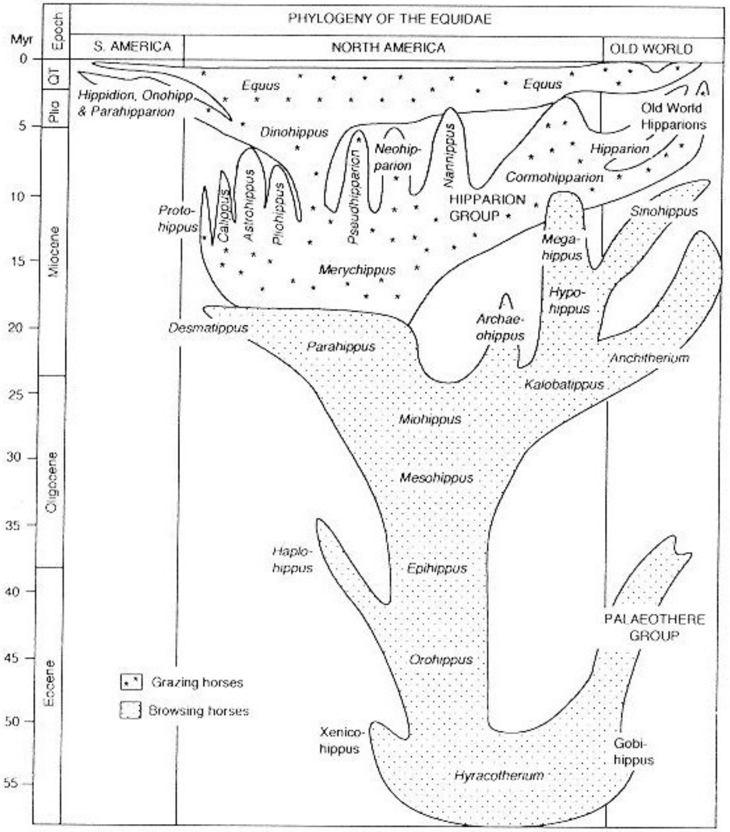
Willi Hennig



Phylogenetic Systematics



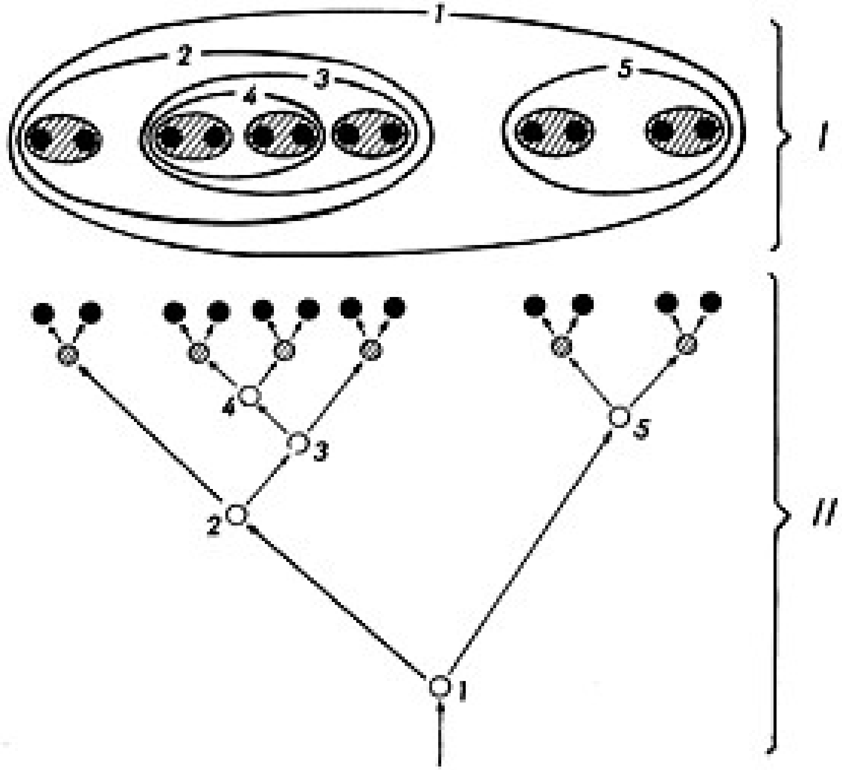
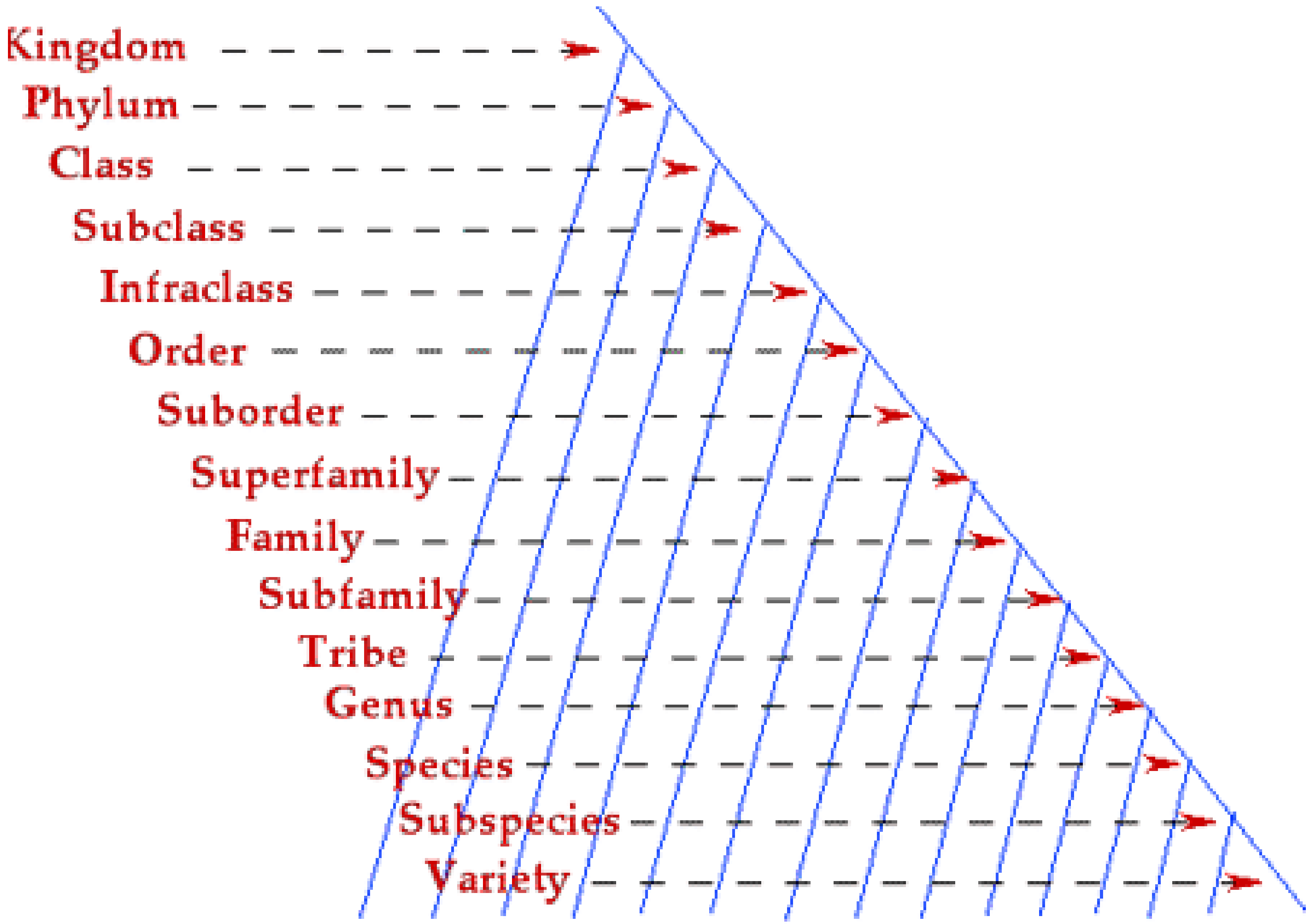


Figure 18. The phylogenetic kinship relations between the species of a monophyletic group, represented in two different ways.


Kingdom
Phylum
Class
Subclass
Infraclass
Order
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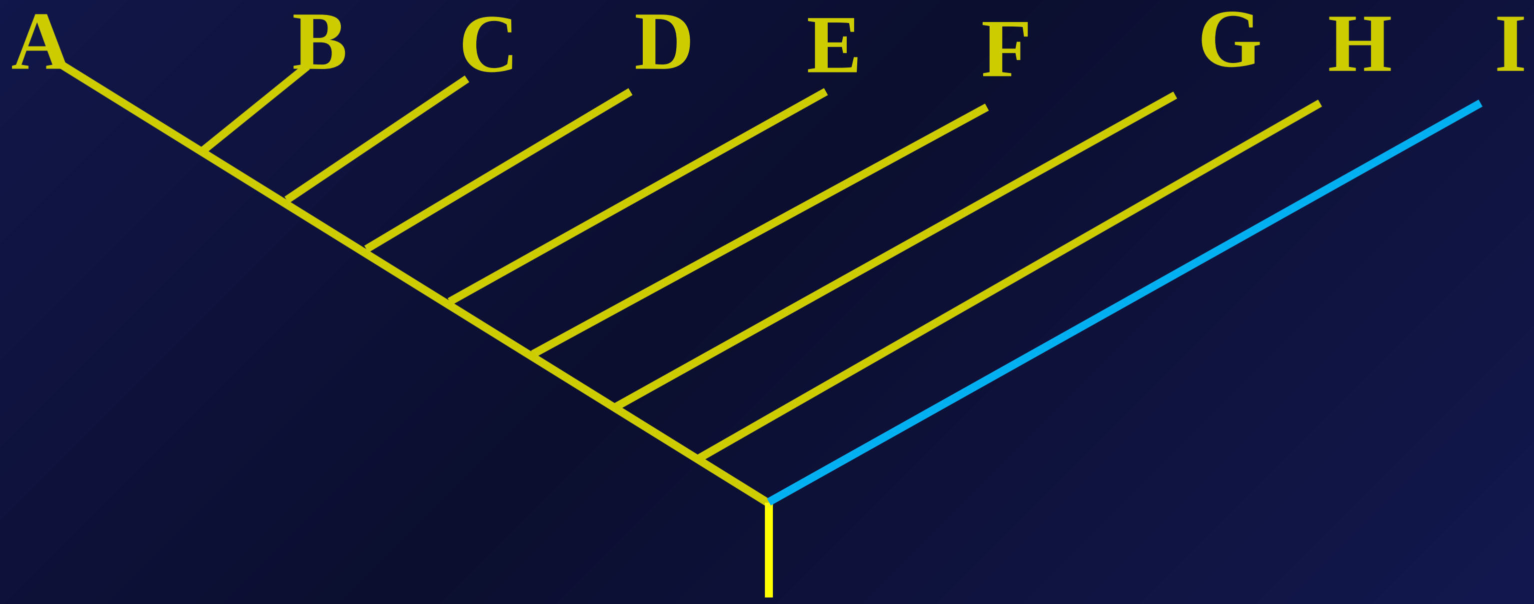
Superfamily
Family
Subfamily
Tribe
Genus
Species
Subspecies
Variety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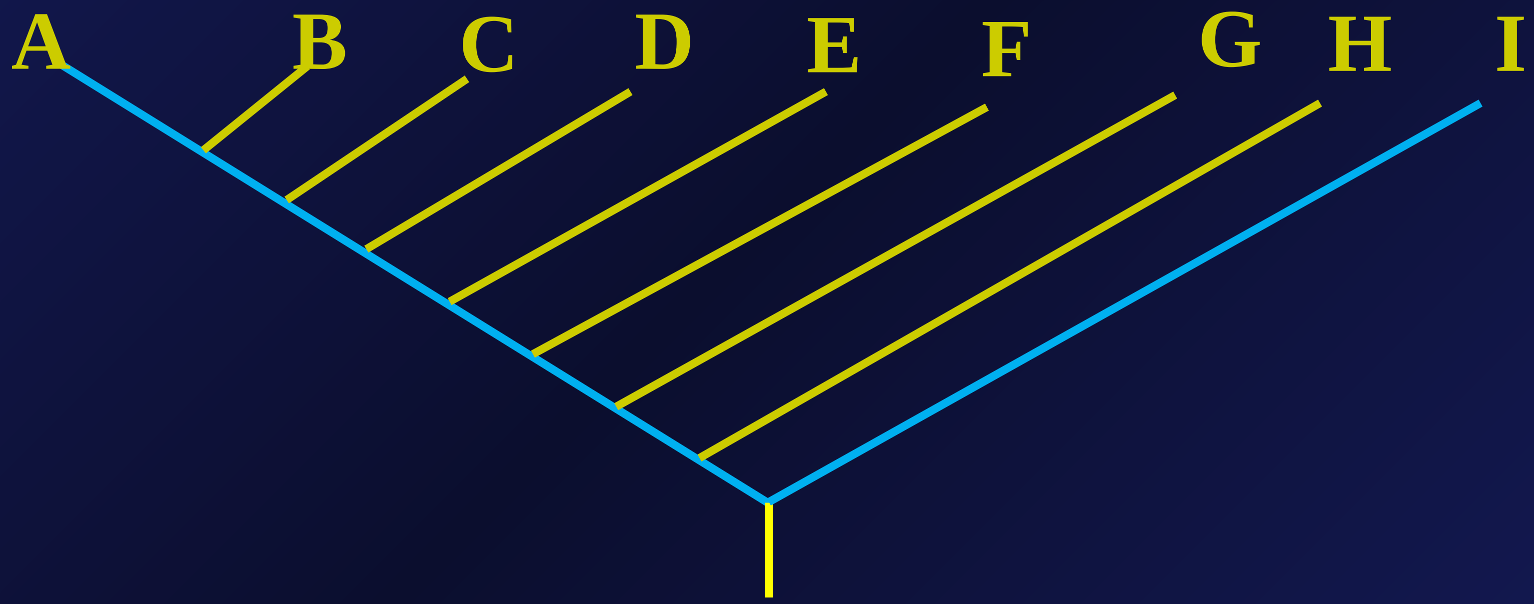
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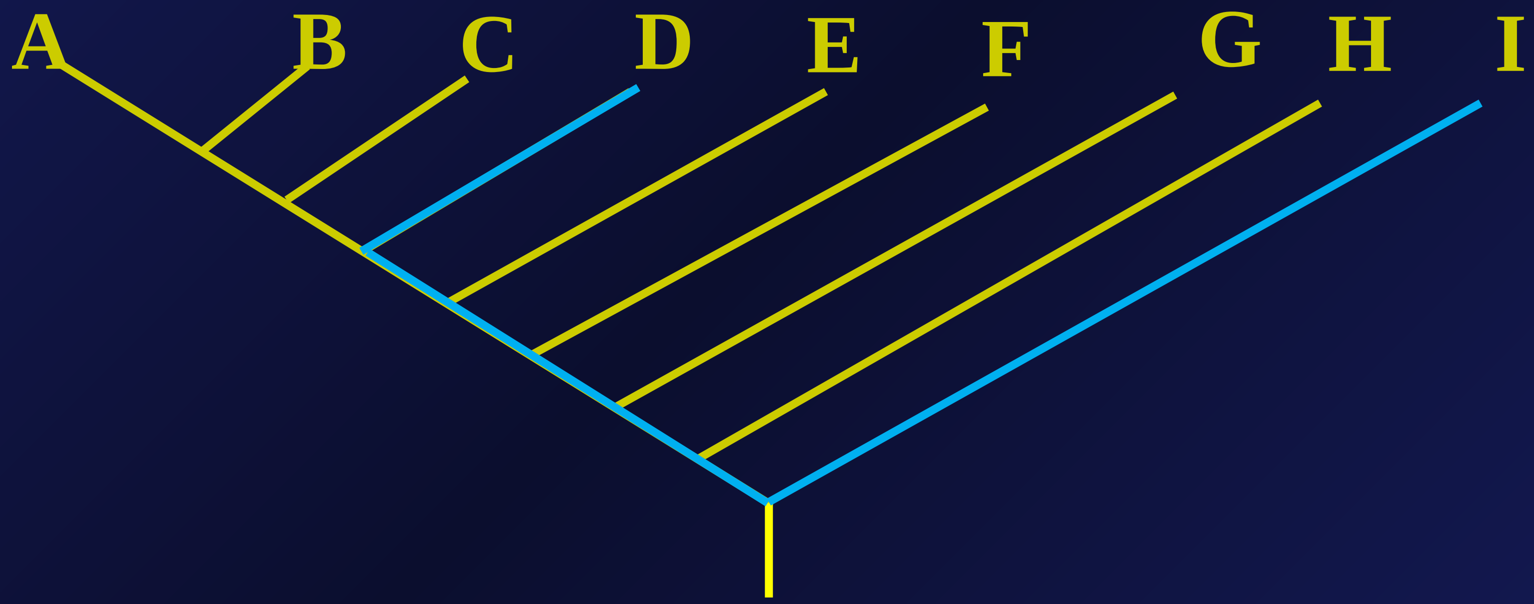
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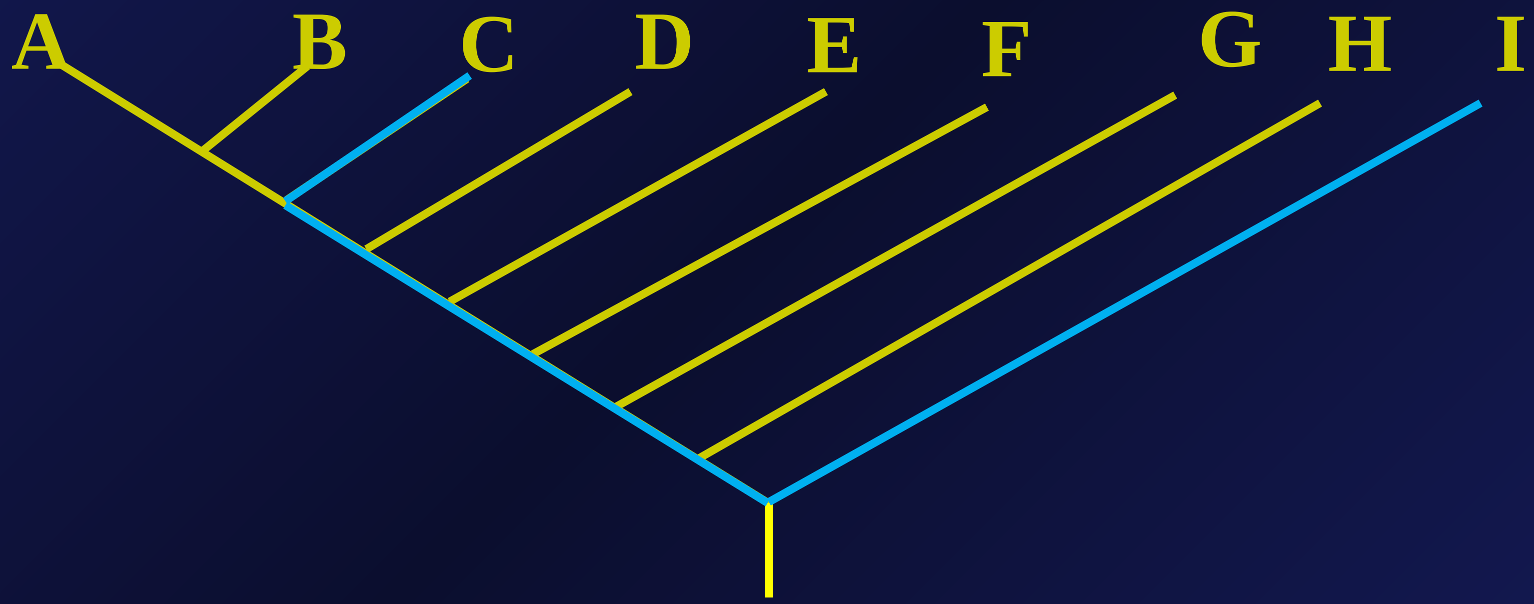
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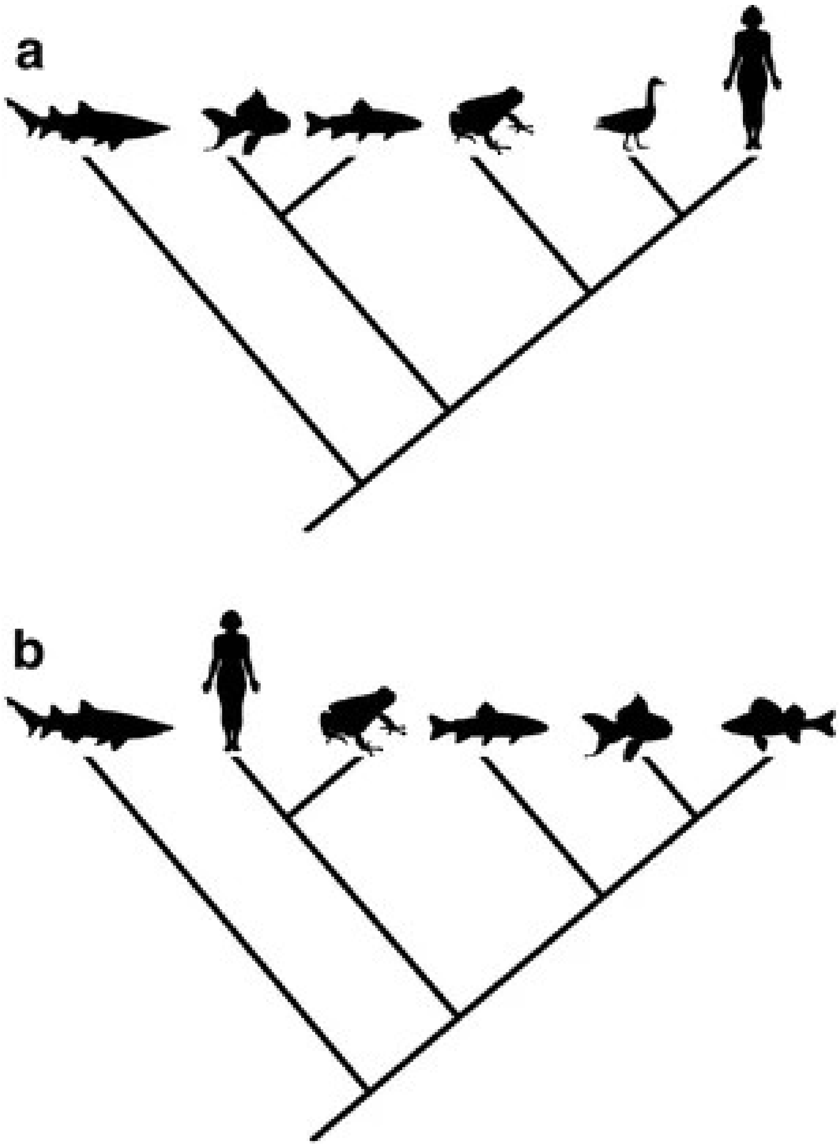
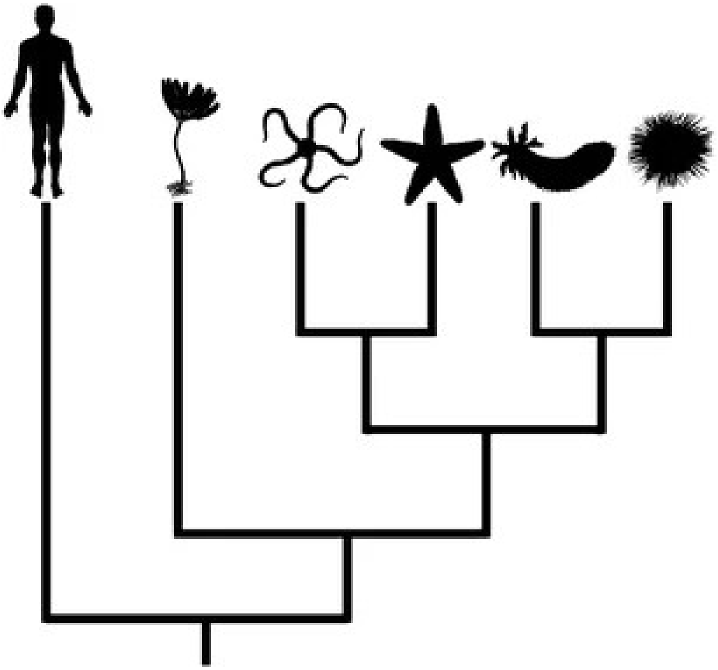
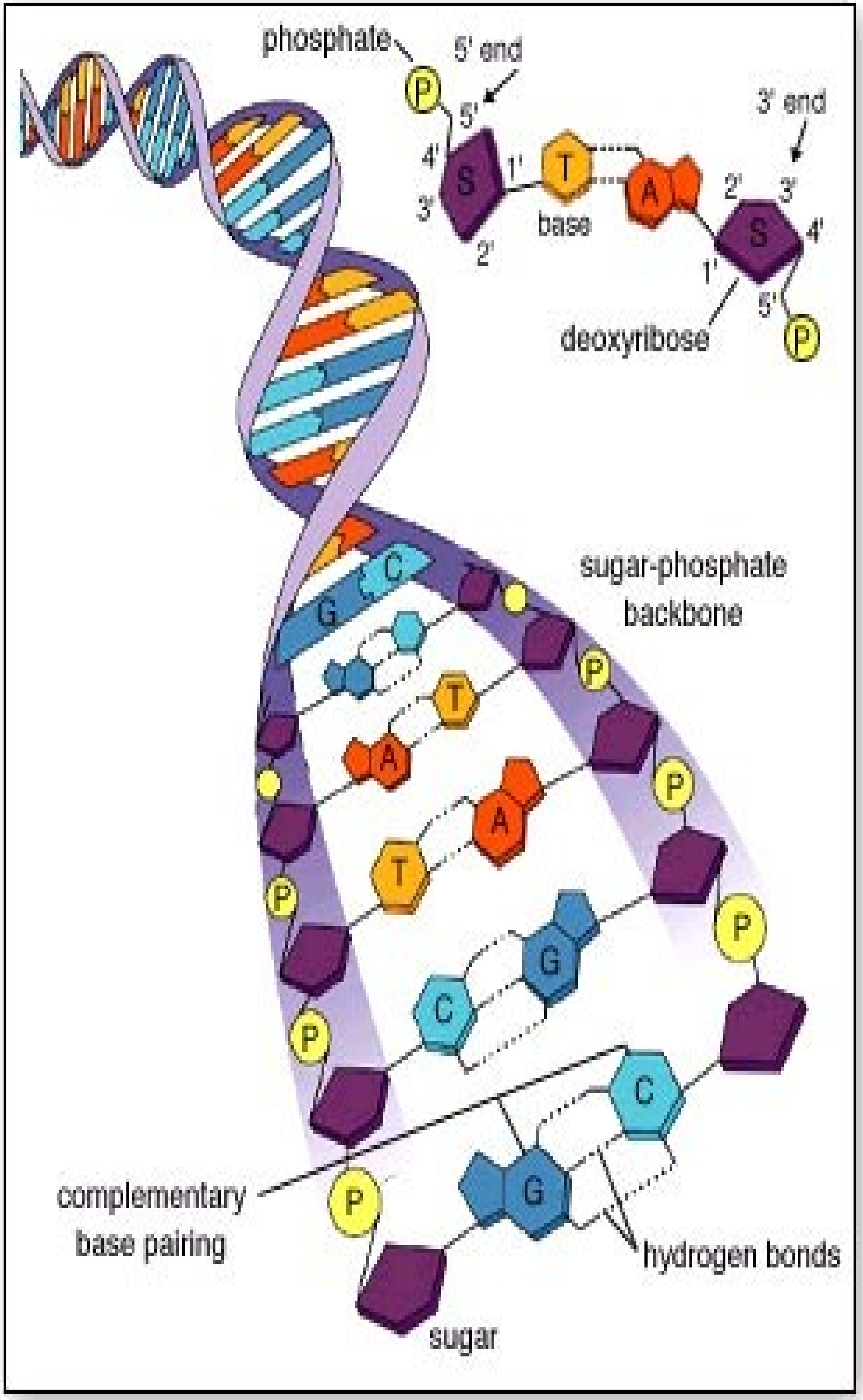

a
b

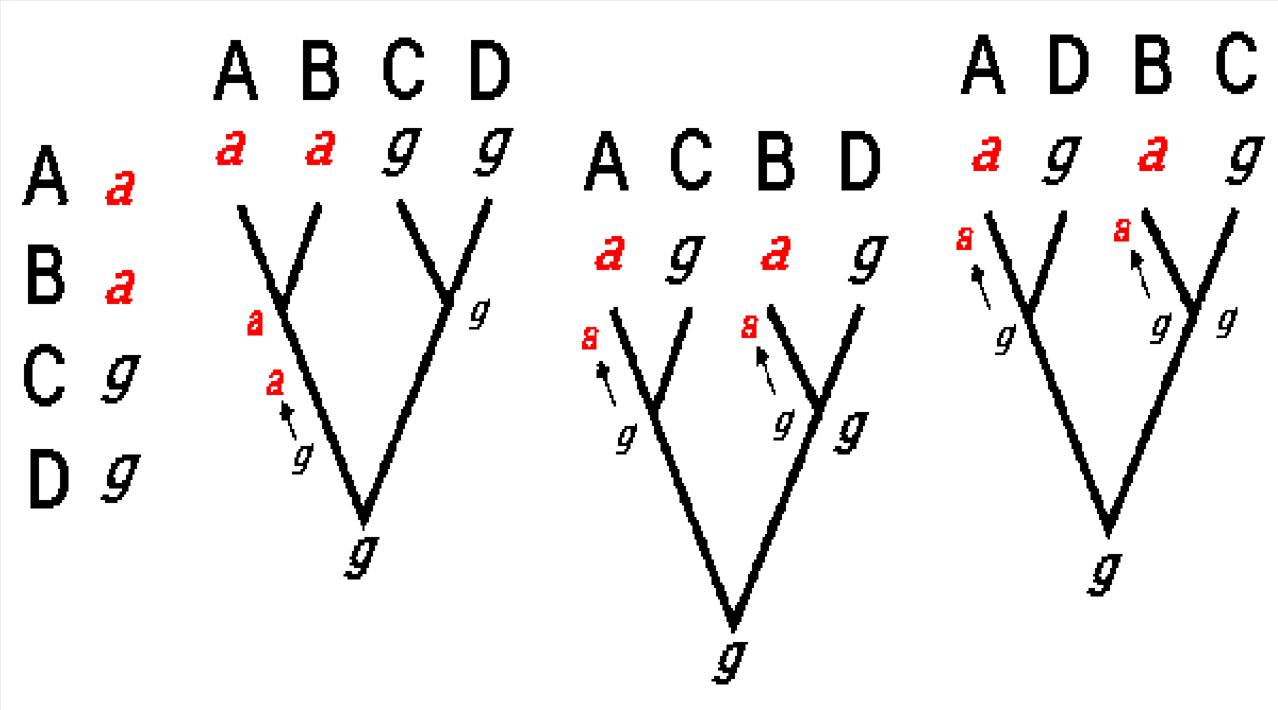


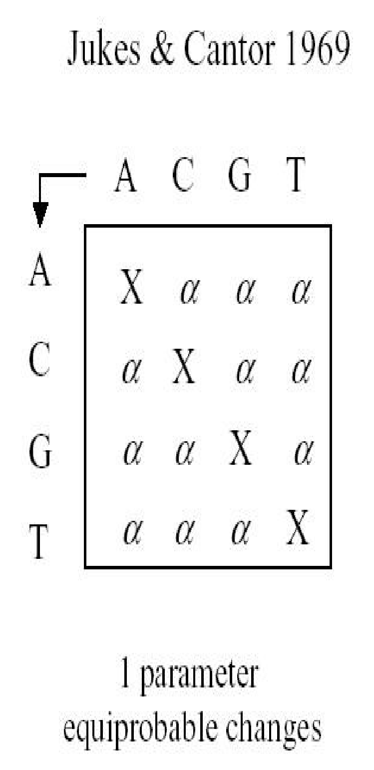

phosphate
5' end
P
5'
4'
S
3'
2'
1'
T
base
A
3' end
2'
3'
S
4'
1'
5'
deoxyribose
P
sugar-phosphate
backbone
G
C
P
T
A
A
T
P
P
G
C
P
P
C
complementary
base pairing
P
G
hydrogen bonds
sugar

infA	10528-10896	☑	🟩
matK	10897-12783	☑	🟦
ndhA	12784-13914	☑	🟥
ndhB	13915-15474	☑	🟥

relevant r...

relevant region to discuss

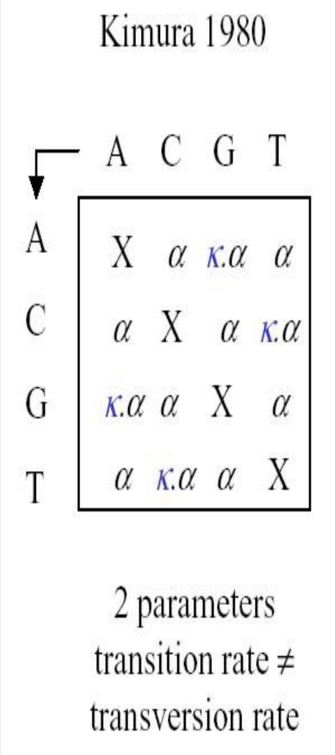

A a
B a
C g
D g
A B C D
a a g g
a
a
g
g
g
A C B D
a g a g
a
g
a
g
g
g
A D B C
a g a g
a
g
a
g
g
g



Jukes & Cantor 1969

$$\begin{array}{c|cccc} & A & C & G & T \\ \hline A & X & \alpha & \alpha & \alpha \\ C & \alpha & X & \alpha & \alpha \\ G & \alpha & \alpha & X & \alpha \\ T & \alpha & \alpha & \alpha & X \end{array}$$

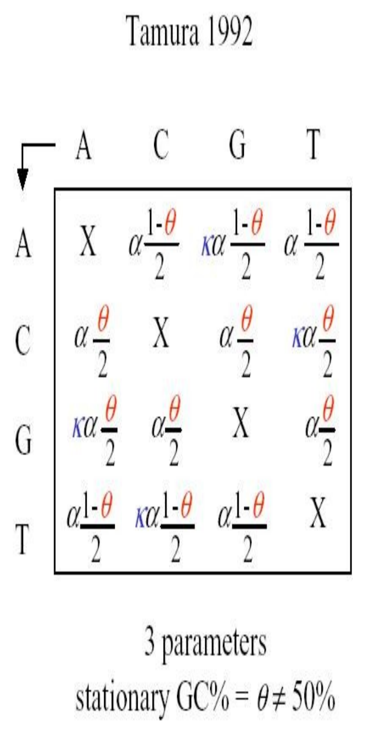
1 parameter
equiprobable changes



Kimura 1980

$$\begin{array}{c|cccc} & A & C & G & T \\ \hline A & X & \alpha & \kappa.\alpha & \alpha \\ C & \alpha & X & \alpha & \kappa.\alpha \\ G & \kappa.\alpha & \alpha & X & \alpha \\ T & \alpha & \kappa.\alpha & \alpha & X \end{array}$$

2 parameters
transition rate ≠
transversion rate



Tamura 1992

$$\begin{array}{c|cccc} & A & C & G & T \\ \hline A & X & \alpha\frac{1-\theta}{2} & \kappa\alpha\frac{1-\theta}{2} & \alpha\frac{1-\theta}{2} \\ C & \alpha\frac{\theta}{2} & X & \alpha\frac{\theta}{2} & \kappa\alpha\frac{\theta}{2} \\ G & \kappa\alpha\frac{\theta}{2} & \alpha\frac{\theta}{2} & X & \alpha\frac{\theta}{2} \\ T & \alpha\frac{1-\theta}{2} & \kappa\alpha\frac{1-\theta}{2} & \alpha\frac{1-\theta}{2} & X \end{array}$$

3 parameters
stationary GC% = $\theta \neq 50\%$

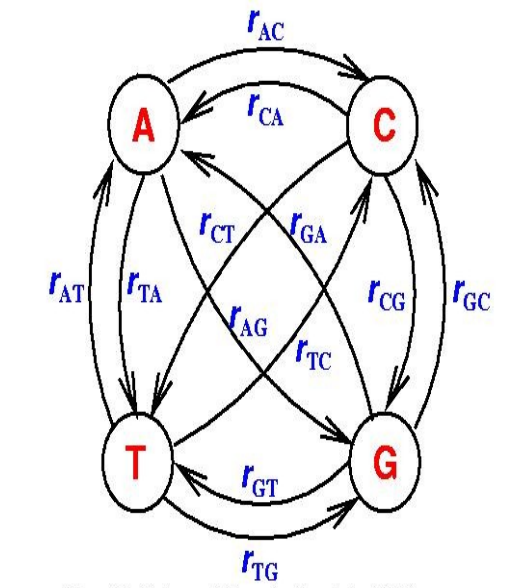
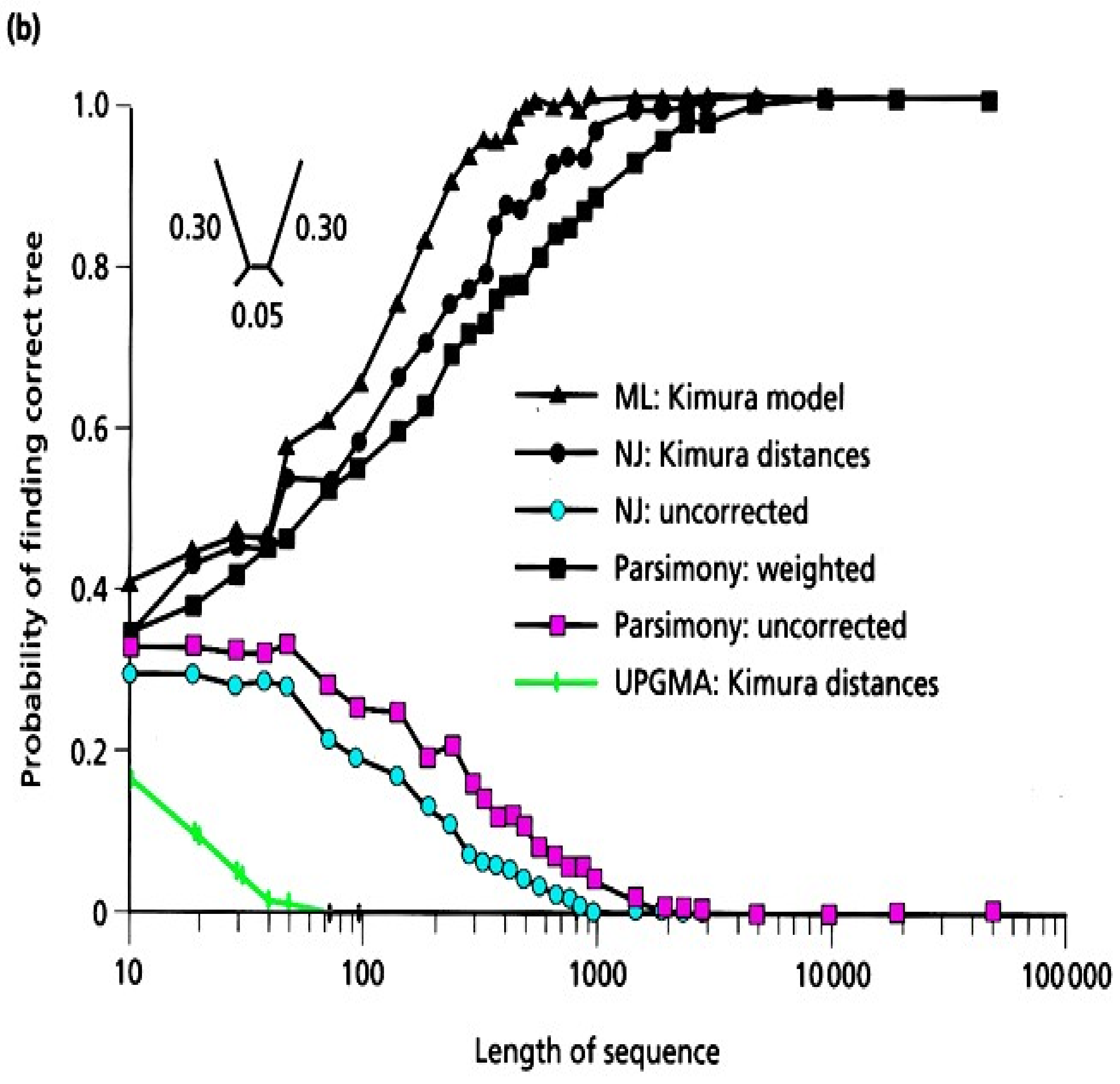


Figure 2.2: Markov model for nucleotide evolution in DNA sequences


(b)
0.30
0.30
0.05
ML: Kimura model
NJ: Kimura distances
NJ: uncorrected
Parsimony: weighted
Parsimony: uncorrected
UPGMA: Kimura distances
Probability of finding correct tree
1.0
0.8
0.6
0.4
0.2
0
10
100
1000
10000
100000
Length of sequence

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Cladistics 19 (2003) 120–127

Cladistics

www.elsevier.com/locate/yclad

Cladistic analysis of languages: Indo-European classification based on lexicostatistical data

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Accepted 15 July 2002

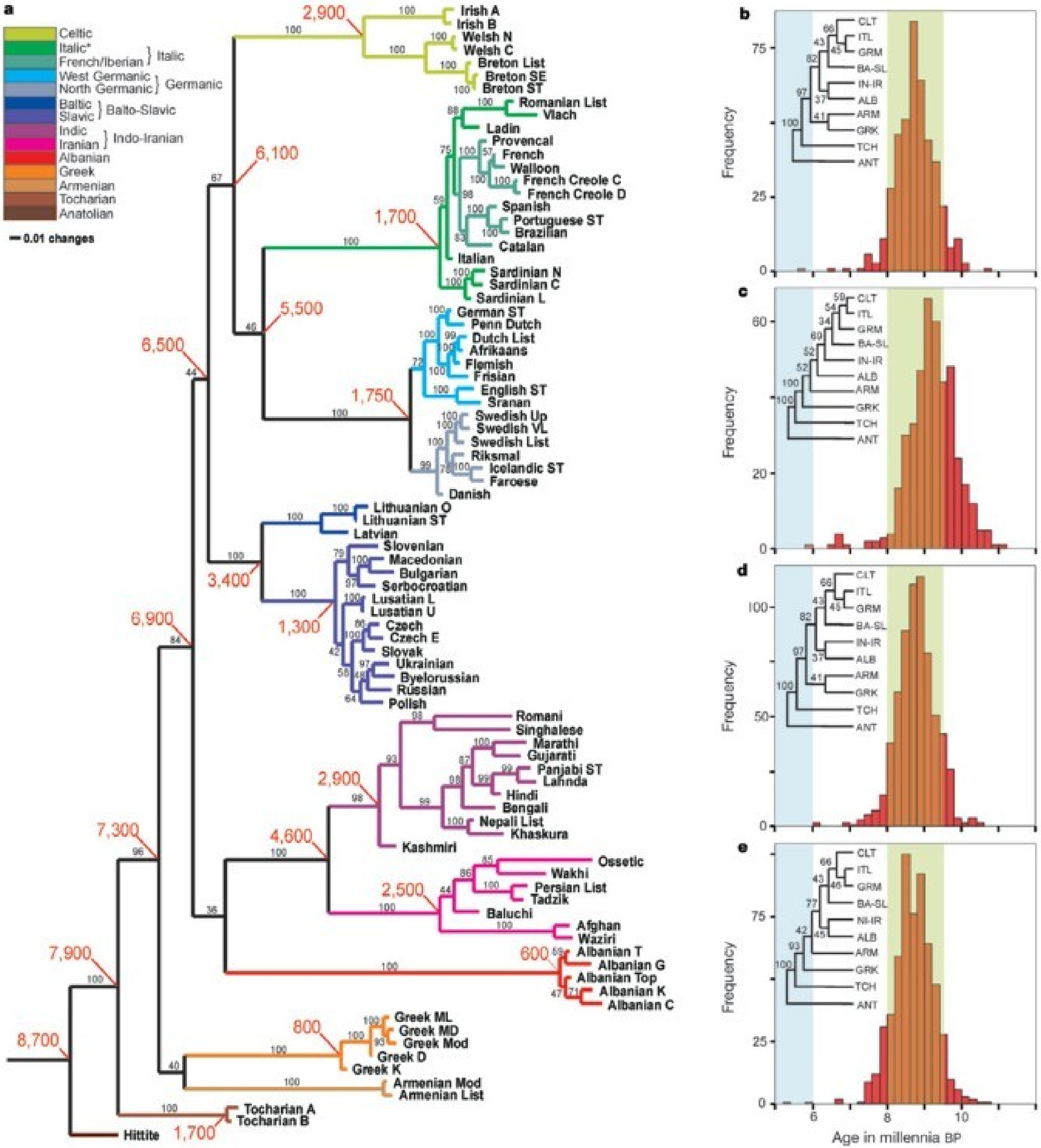
Abstract

The phylogeny of the Indo-European (IE) language family is reconstructed by application of the cladistic methodology to the lexicostatistical dataset collected by Dyen (about 200 meanings, 84 speech varieties, the Hittite language used as a functional outgroup). Three different methods of character coding provide trees that show: (a) the presence of four groups, viz., Balto-Slavonic clade, Romano-Germano-Celtic clade, Armenian-Greek group, and Indo-Iranian group (the two last groups possibly paraphyletic); (b) the unstable position of the Albanian language; (c) the unstable pattern of the basalmost IE differentiation; but (d) the probable existence of the Balto-Slavonic–Indo-Iranian ("satem") and the Romano-Germano-Celtic (+Albanian?) superclades. The results are compared with the phenetic approach to lexicostatistical data, the results of which are significantly less informative concerning the basal pattern. The results suggest a predominantly branching pattern of the basic vocabulary phylogeny and little borrowing of individual words. Different scenarios of IE differentiation based on archaeological and genetic information are discussed.

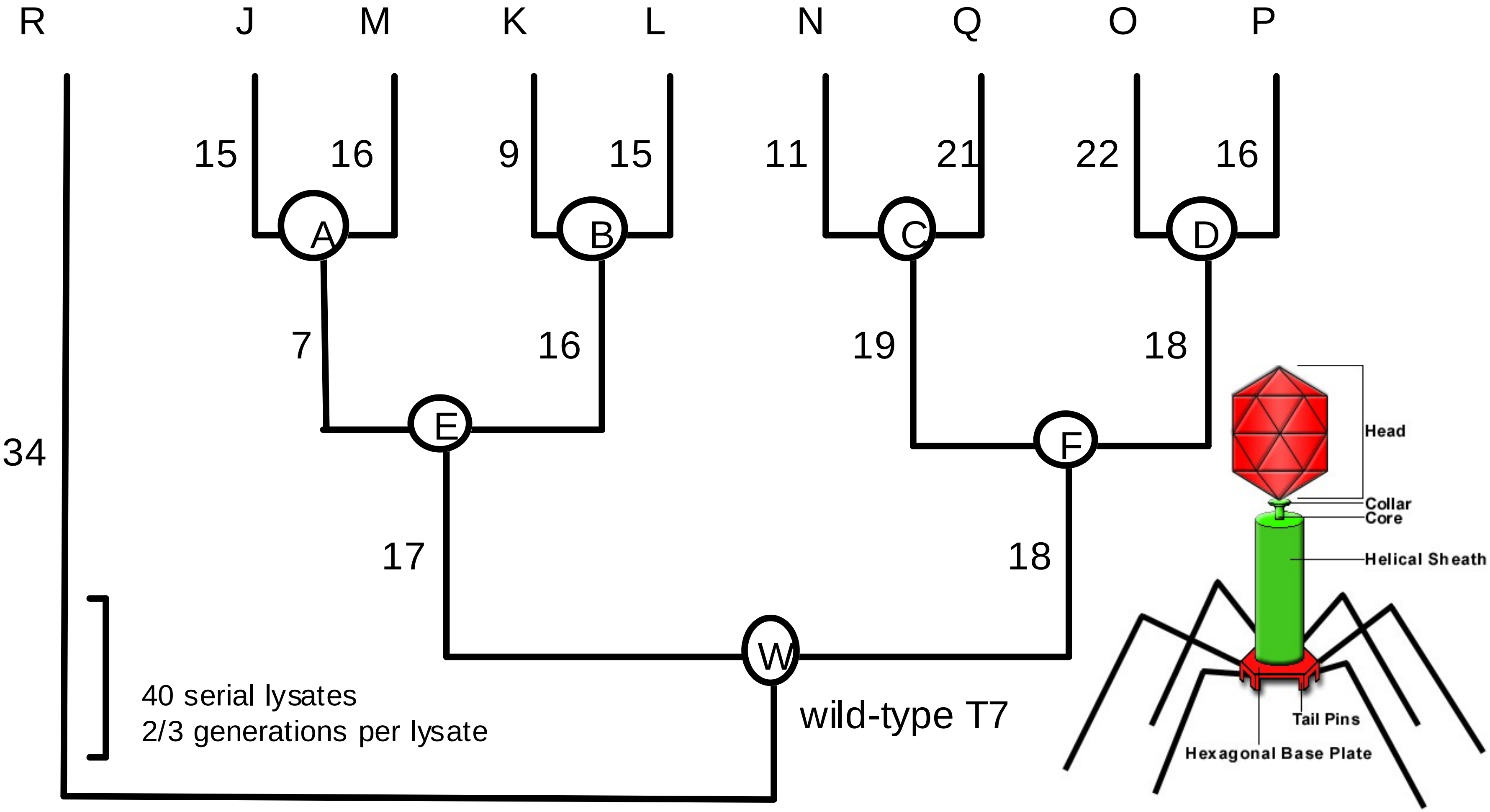
Introduction

The story of language confusion in Babel written in

introduced into comparative linguistics for the evaluation of lexical data. The only exceptions are the recent studies by Gray and Jordan (2000) on Austronesian


a
Celtic
Italic*
French/Iberian
Italic
West Germanic
North Germanic
Germanic
Baltic
Slavic
Balto-Slavic
Indic
Iranian
Indo-Iranian
Albanian
Greek
Armenian
Tocharian
Anatolian
0.01 changes
8,700
7,900
7,300
6,900
6,500
6,100
5,500
4,600
3,400
2,900
2,900
2,500
1,750
1,700
1,700
1,300
800
600
Irish A
Irish B
Welsh N
Welsh C
Breton List
Breton SE
Breton ST
Romanian List
Vlach
Ladin
Provencal
French
Walloon
French Creole C
French Creole D
Spanish
Portuguese ST
Brazilian
Catalan
Italian
Sardinian N
Sardinian C
Sardinian L
German ST
Penn Dutch
Dutch List
Afrikaans
Flemish
Frisian
English ST
Sranan
Swedish Up
Swedish VL
Swedish List
Riksmal
Icelandic ST
Faroese
Danish
Lithuanian O
Lithuanian ST
Latvian
Slovenian
Macedonian
Bulgarian
Serbocroatian
Lusatian L
Lusatian U
Czech
Czech E
Slovak
Ukrainian
Byelorussian
Russian
Polish
Romani
Singhalese
Marathi
Gujarati
Panjabi ST
Lahnda
Hindi
Bengali
Nepali List
Khaskura
Kashmiri
Ossetic
Wakhi
Persian List
Tadzik
Baluchi
Afghan
Waziri
Albanian T
Albanian G
Albanian Top
Albanian K
Albanian C
Greek ML
Greek MD
Greek Mod
Greek D
Greek K
Armenian Mod
Armenian List
Tocharian A
Tocharian B
Hittite
b
c
d
e
CLT
ITL
GRM
BA-SL
IN-IR
NI-IR
ALB
ARM
GRK
TCH
ANT
Frequency
0
25
75
20
60
50
100
6
8
10
Age in millennia BP

Experimental phylogenetics



40 serial lysates
2/3 generations per lysate

wild-type T7

T7 bacteriophage in presence of *N*-methyl-*N'*-nitro-*N*-nitroguanidine

BMC Biology

BioMed Central

Research article

Open Access

Pair of lice lost or parasites regained: the evolutionary history of anthropoid primate lice

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Accepted: 7 March 2007

Abstract

Background: The parasitic sucking lice of primates are known to have undergone at least 25 million years of coevolution with their hosts. For example, chimpanzee lice and human head/body lice last shared a common ancestor roughly six million years ago, a divergence that is contemporaneous with their hosts. In an assemblage where lice are often highly host specific, humans host two different genera of lice, one that is shared with chimpanzees and another that is

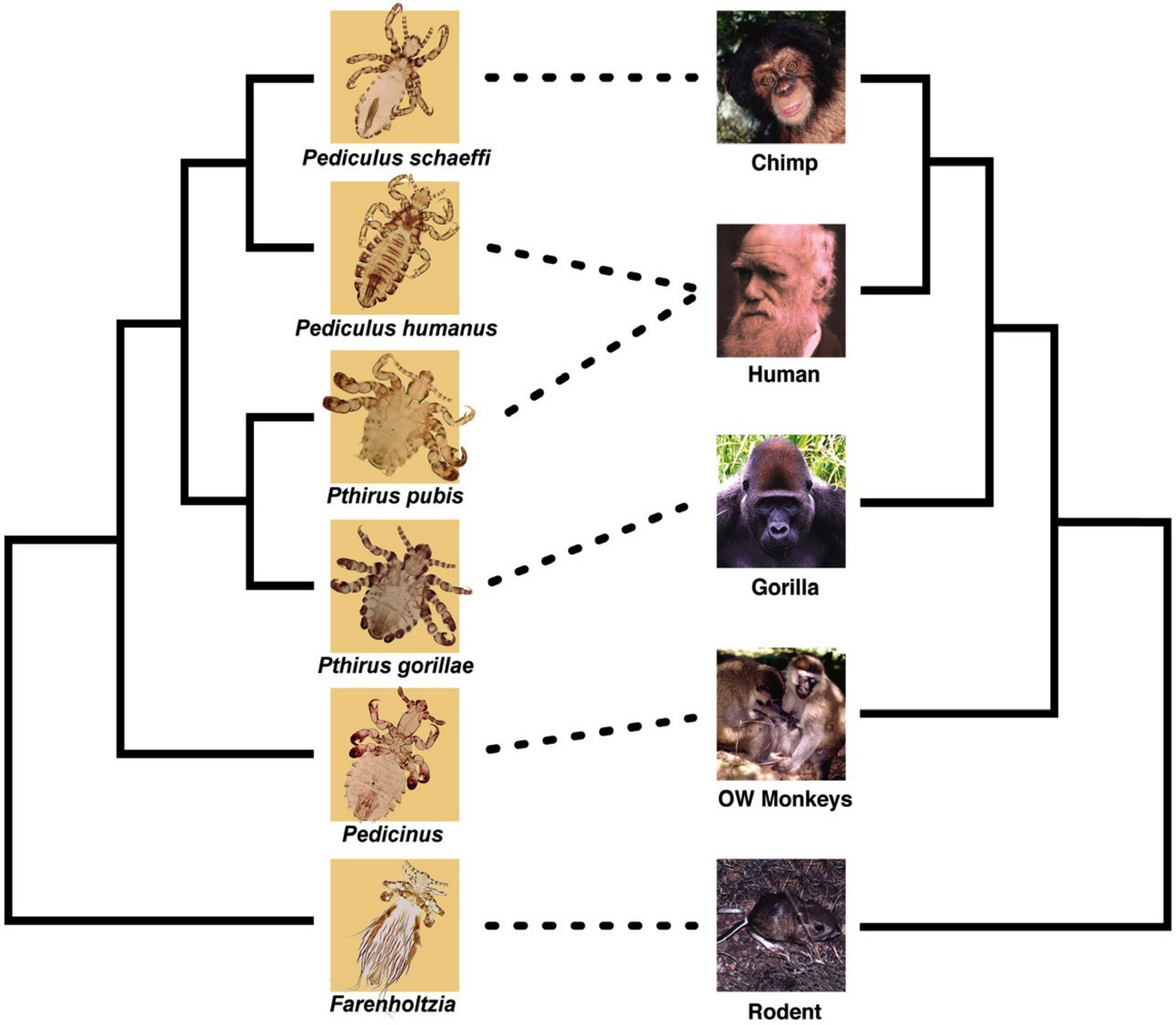
A tale of three lice

- Lice are highly specialized blood sucking parasites that live on a single host species.
- Each of our ape relatives hosts one louse species, but humans host three types of lice.

The head louse,
Pediculus humanus capitus

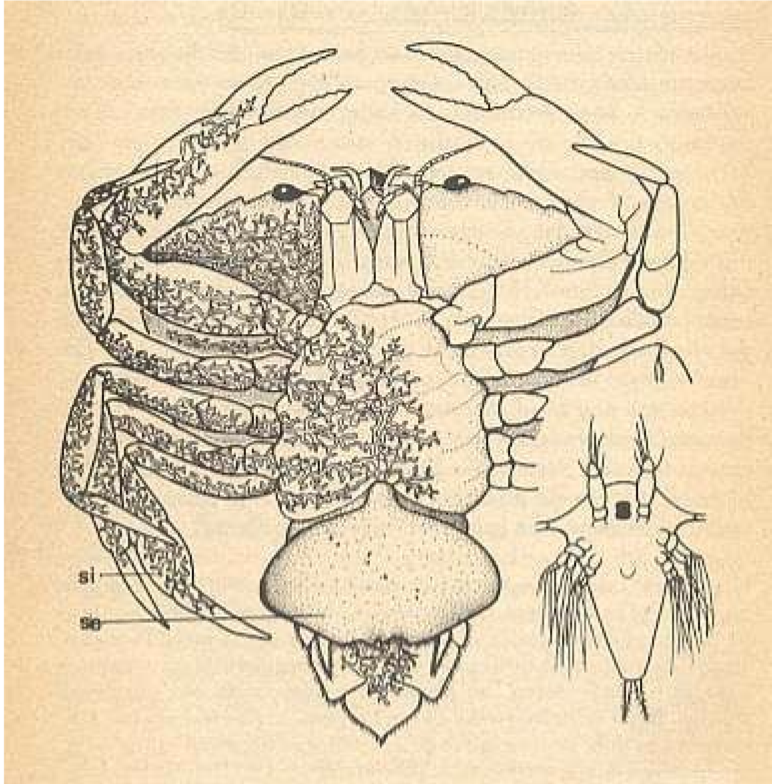
The pubic louse,
Phthirus pubis

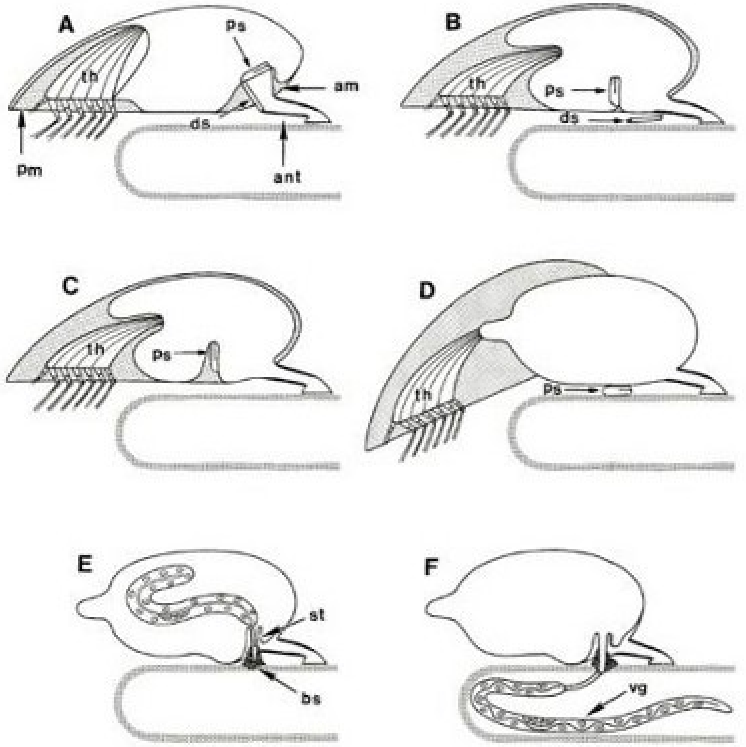
The body louse,
Pediculus humanus corporis

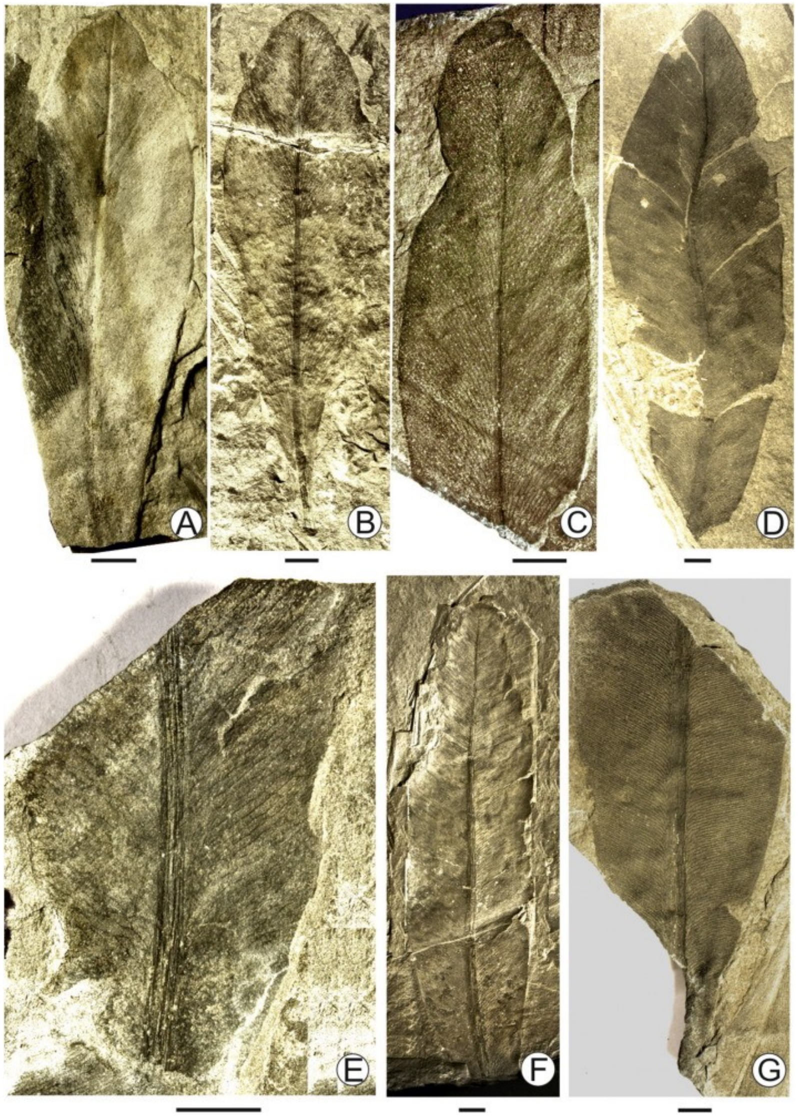

Pediculus schaeffi
Pediculus humanus
Pthirus pubis
Pthirus gorillae
Pedicinus
Farenholtzia
Chimp
Human
Gorilla
OW Monkeys
Rodent


A


Foto di Rocco Mussat Sartor
© Università degli Studi di Torino

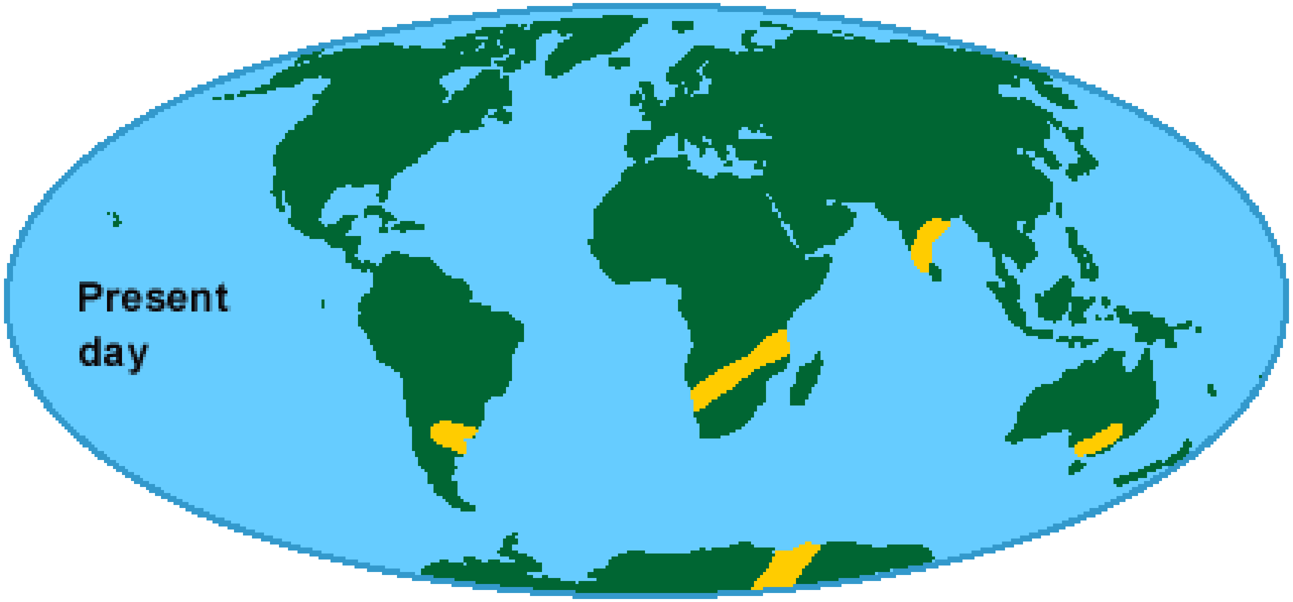

si
se

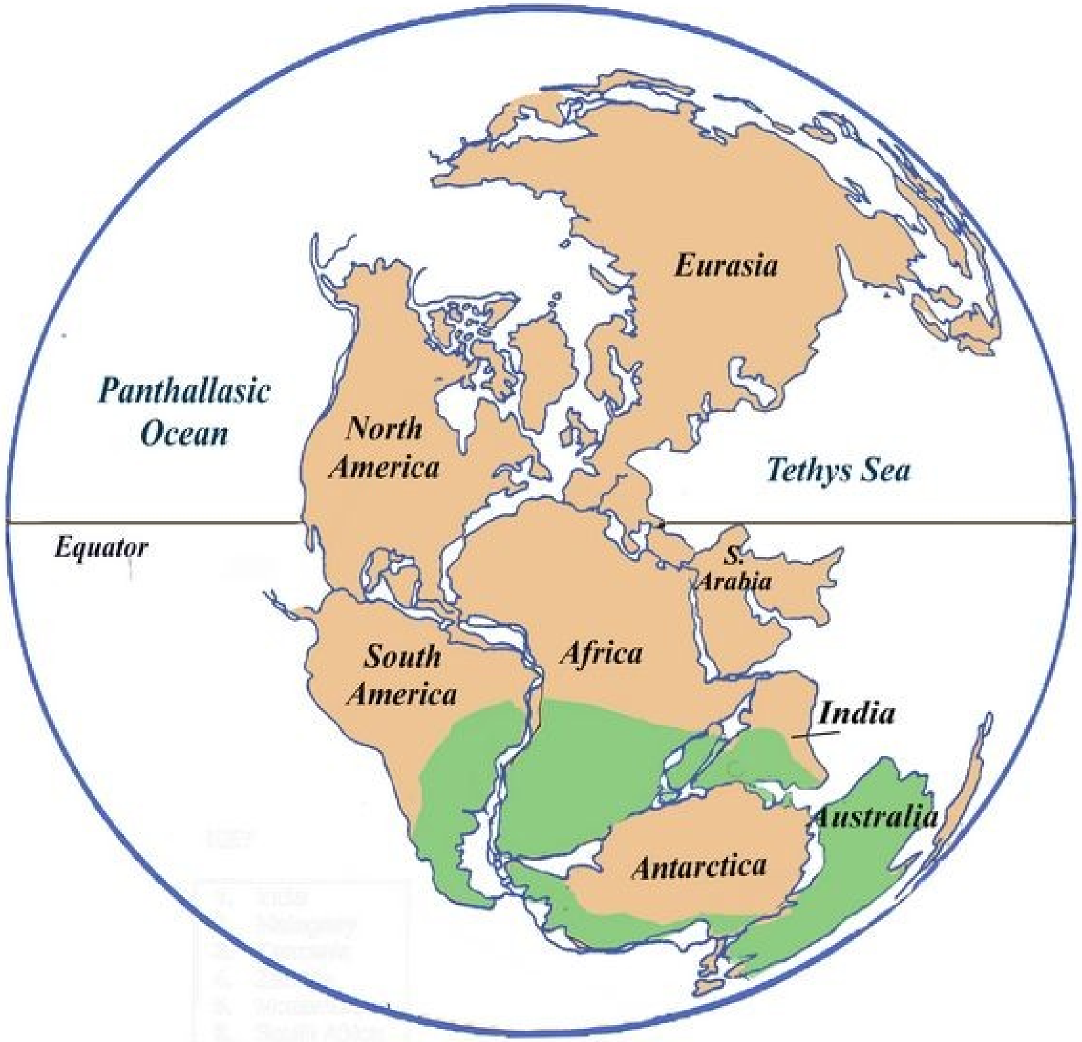

A
ps
th
am
ds
pm
ant
B
th
ps
ds
C
th
ps
D
th
ps
E
st
bs
F
vg



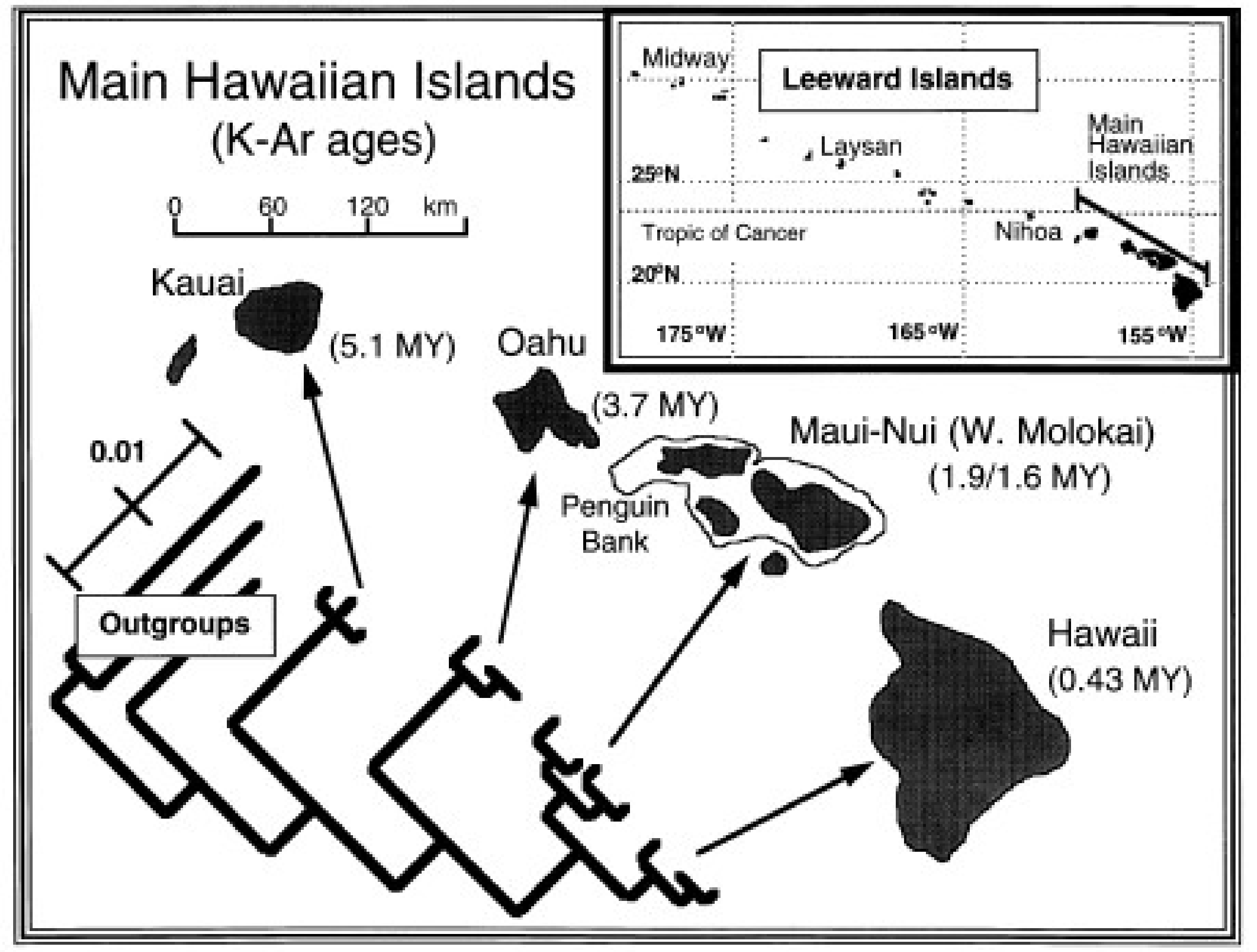
Glossopteris

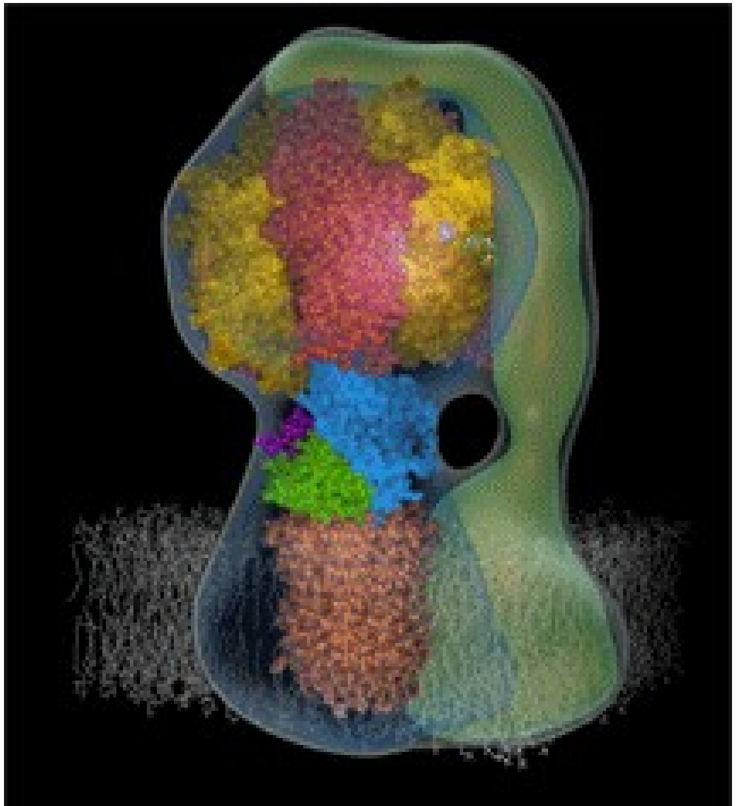
Tewari et al., 2015


Present
day

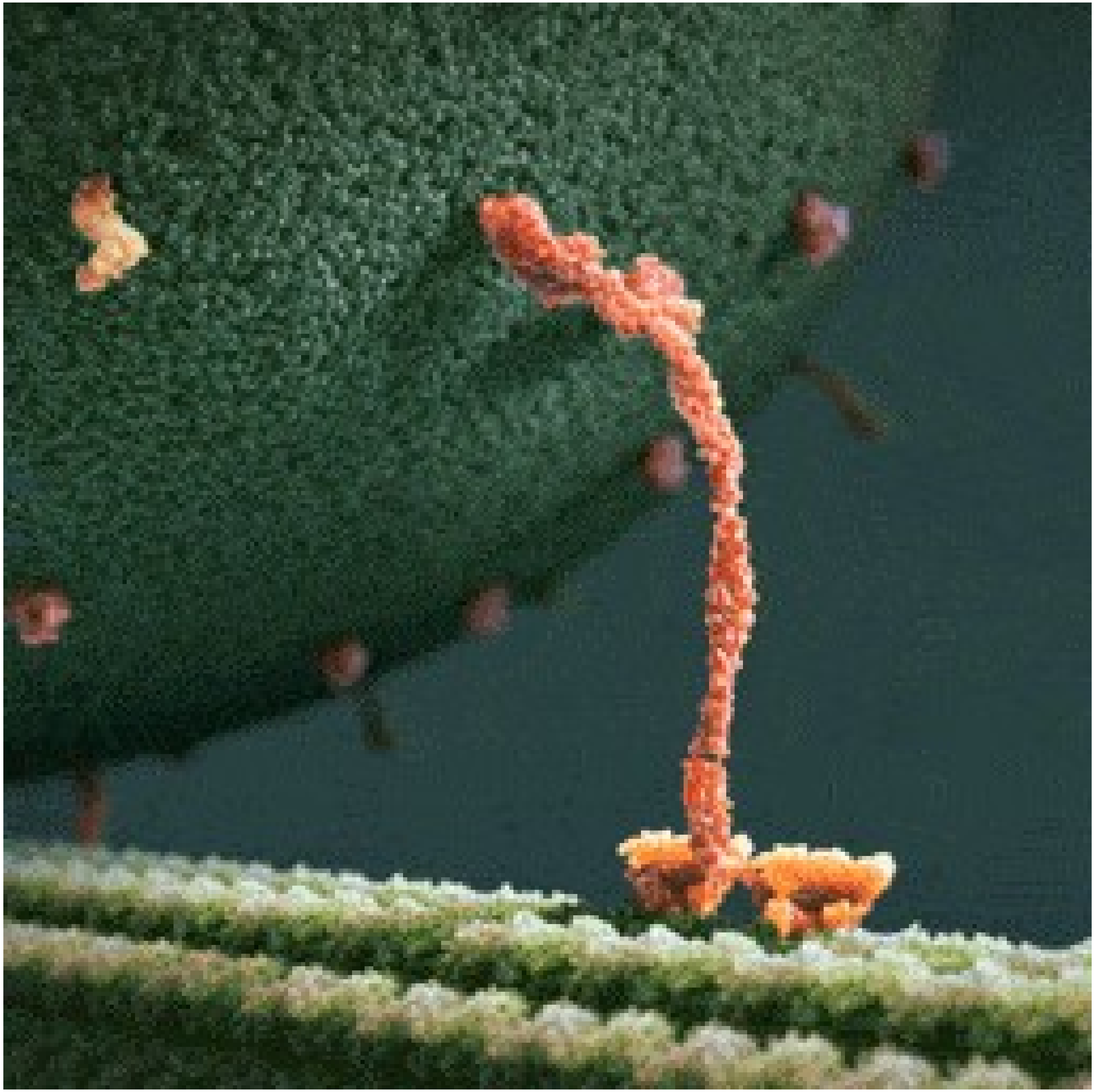


Distribution of *Glossopteris* in the Permian period

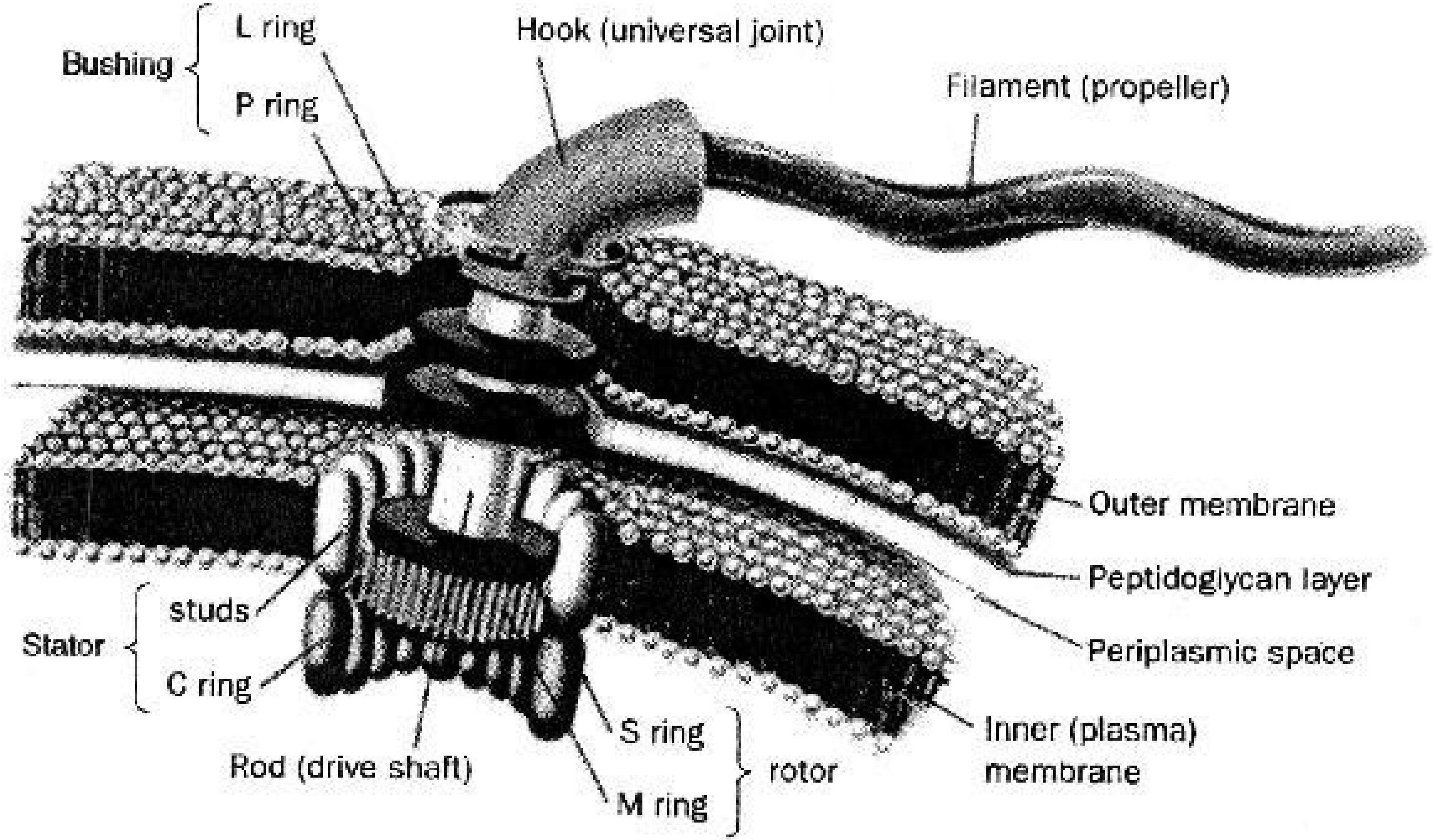

Main Hawaiian Islands
(K-Ar ages)
0
60
120
km
Kauai
(5.1 MY)
Oahu
(3.7 MY)
Maui-Nui (W. Molokai)
(1.9/1.6 MY)
Penguin
Bank
Hawaii
(0.43 MY)
0.01
Outgroups
Midway
Leeward Islands
Laysan
Main
Hawaiian
Islands
25°N
Tropic of Cancer
Nihoa
20°N
175°W
165°W
155°W

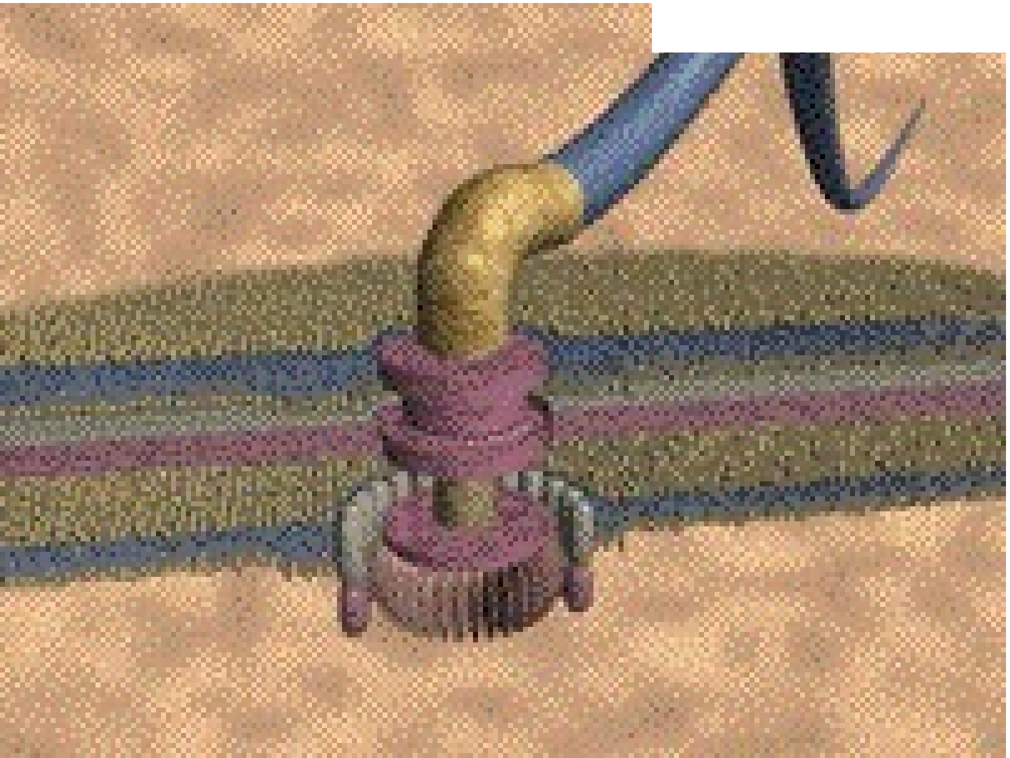


Mitochondrial ATP synthase



Kinesin protein walking on microtubule


Bushing
L ring
P ring
Hook (universal joint)
Filament (propeller)
Outer membrane
Peptidoglycan layer
Periplasmic space
Inner (plasma) membrane
Stator
studs
C ring
Rod (drive shaft)
S ring
M ring
rotor



GENETIC VARIABILITY, TWIN HYBRIDS AND CONSTANT HYBRIDS, IN A CASE OF BALANCED LETHAL FACTORS

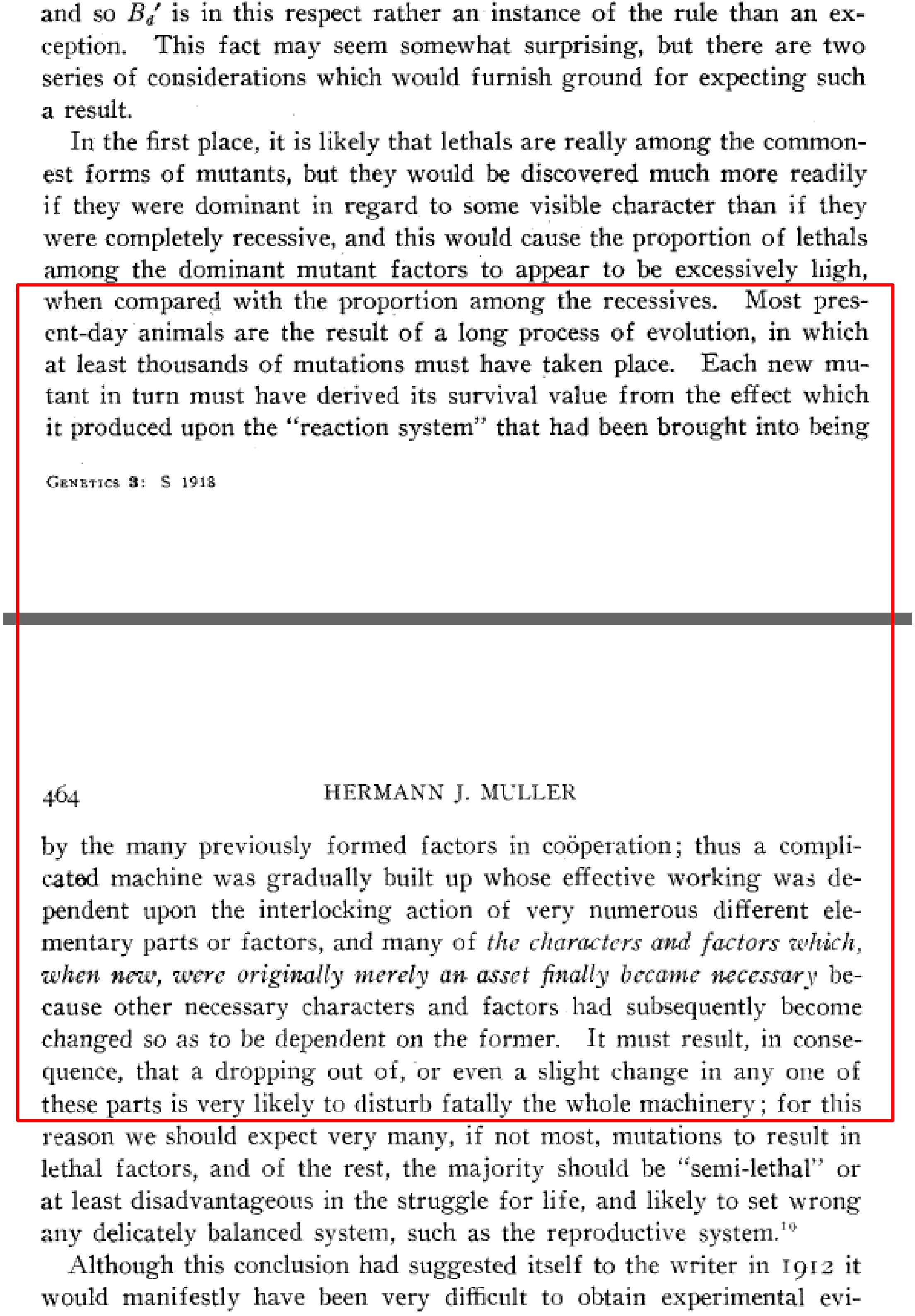
HERMANN J. MULLER
The Rice Institute, Houston, Texas.

[Received January 14, 1918]

TABLE OF CONTENTS

THE PROBLEM OF FACTOR VARIABILITY AND THE CASE OF BEADED WINGS

In numerous breeding experiments there is positive evidence that the factors concerned undergo no sensible fluctuation, nor sensible contamination during segregation. But, unfortunately for a clear and simple proof or disproof of the generality of these principles, Mendelian theory demands, and experiment has proved, that not infrequently multiple factors and other complications quite consistent with factor constancy



and so B_d' is in this respect rather an instance of the rule than an exception. This fact may seem somewhat surprising, but there are two series of considerations which would furnish ground for expecting such a result.

In the first place, it is likely that lethals are really among the commonest forms of mutants, but they would be discovered much more readily if they were dominant in regard to some visible character than if they were completely recessive, and this would cause the proportion of lethals among the dominant mutant factors to appear to be excessively high, when compared with the proportion among the recessives. Most present-day animals are the result of a long process of evolution, in which at least thousands of mutations must have taken place. Each new mutant in turn must have derived its survival value from the effect which it produced upon the "reaction system" that had been brought into being

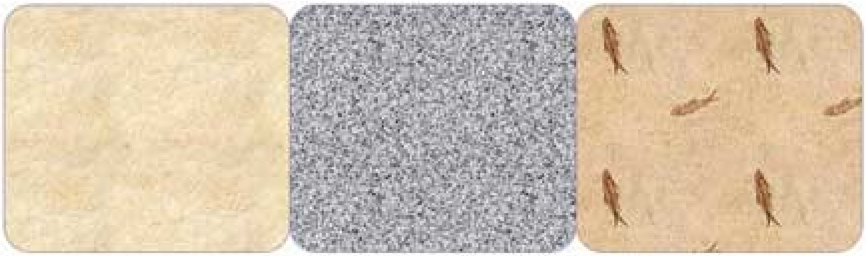
GENETICS 3: S 1918

464 HERMANN J. MULLER

by the many previously formed factors in coöperation; thus a complicated machine was gradually built up whose effective working was dependent upon the interlocking action of very numerous different elementary parts or factors, and many of *the characters and factors which, when new, were originally merely an asset finally became necessary* because other necessary characters and factors had subsequently become changed so as to be dependent on the former. It must result, in consequence, that a dropping out of, or even a slight change in any one of these parts is very likely to disturb fatally the whole machinery; for this reason we should expect very many, if not most, mutations to result in lethal factors, and of the rest, the majority should be "semi-lethal" or at least disadvantageous in the struggle for life, and likely to set wrong any delicately balanced system, such as the reproductive system.[10]

Although this conclusion had suggested itself to the writer in 1912 it would manifestly have been very difficult to obtain experimental evi-

“Each new mutation must have derived its survival value from the effect it produced upon the "reaction system” that had been brought into being by the many previously formed factors in cooperation; thus a complicated machine was gradually built up whose effective working was dependent upon the interlocking action of very numerous different elementary parts or factors, and ***many of the characters and factors which, when new, were originally merely an asset finally became necessary*** because other other necessary characters and factors had subsequently become changed so as to be dependent upon the former. It must result, in consequence, that ***a dropping***



condição precursora: ponte formada por três pedras

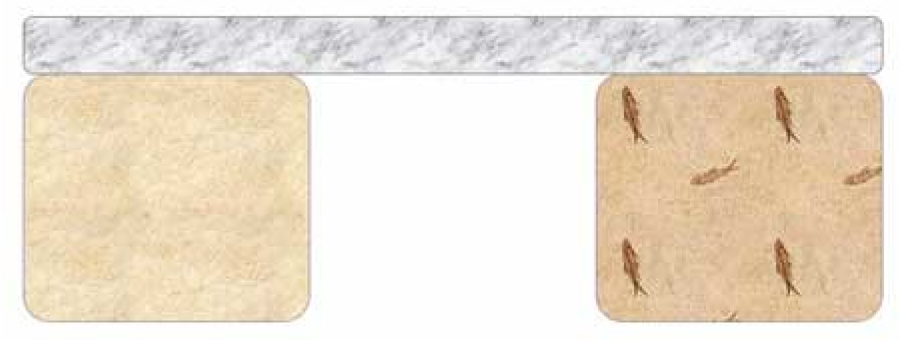
condição precursora:
ponte formada por três
pedras

passo 1: adição de uma
pedra contínua por cima

condição precursora:
ponte formada por três
pedras

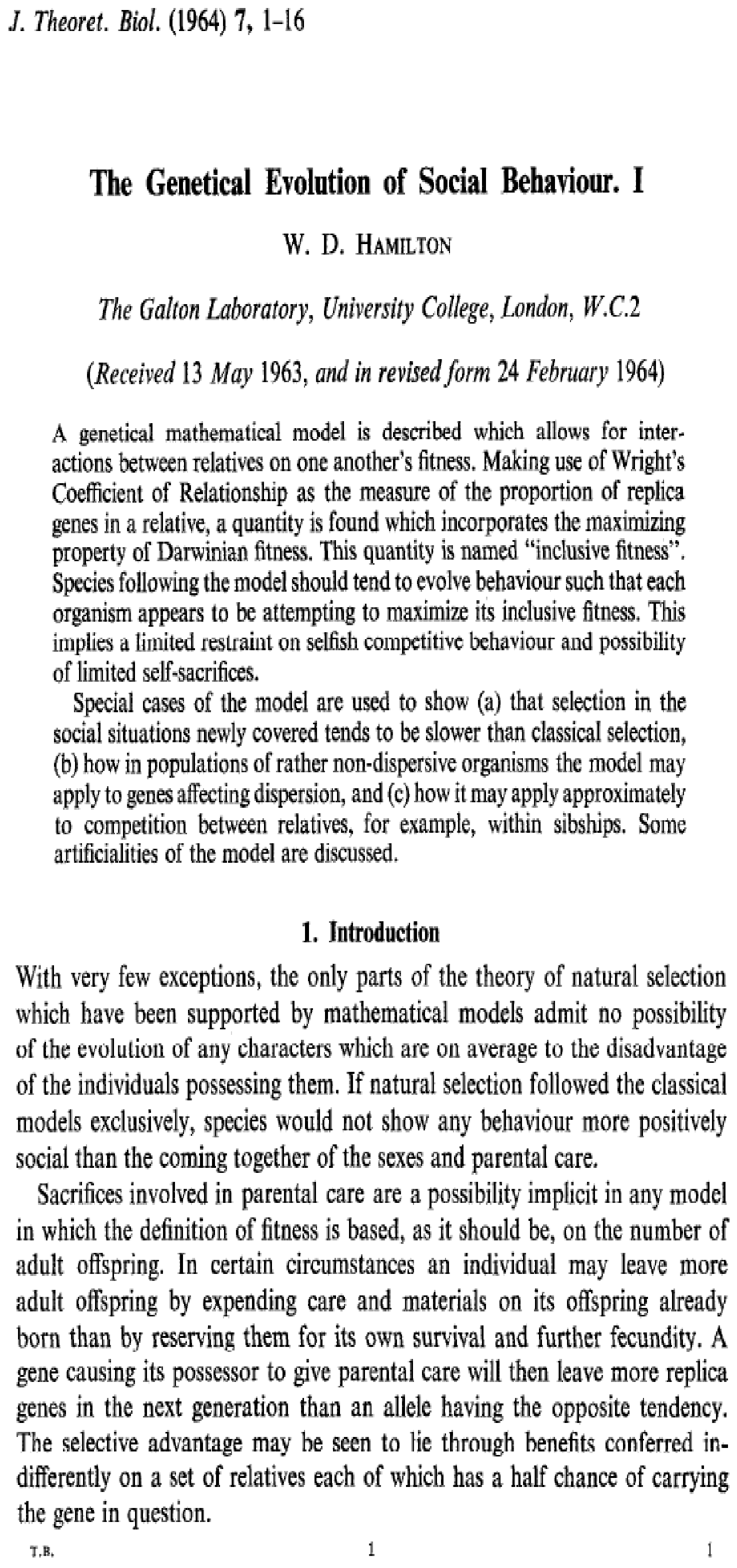
passo 1: adição de uma
pedra contínua por cima

passo 2: retirada da
Pedra intermediária



resultado: complexidade irredutível!

Nenhuma pedra pode ser retirada sem perda de funcionalidade. Cada um dos três elementos é indispensável para a funcionalidade do sistema.



J. Theoret. Biol. (1964) 7, 1–16

The Genetical Evolution of Social Behaviour. I

W. D. Hamilton

The Galton Laboratory, University College, London, W.C.2

(*Received* 13 *May* 1963, *and in revised form* 24 *February* 1964)

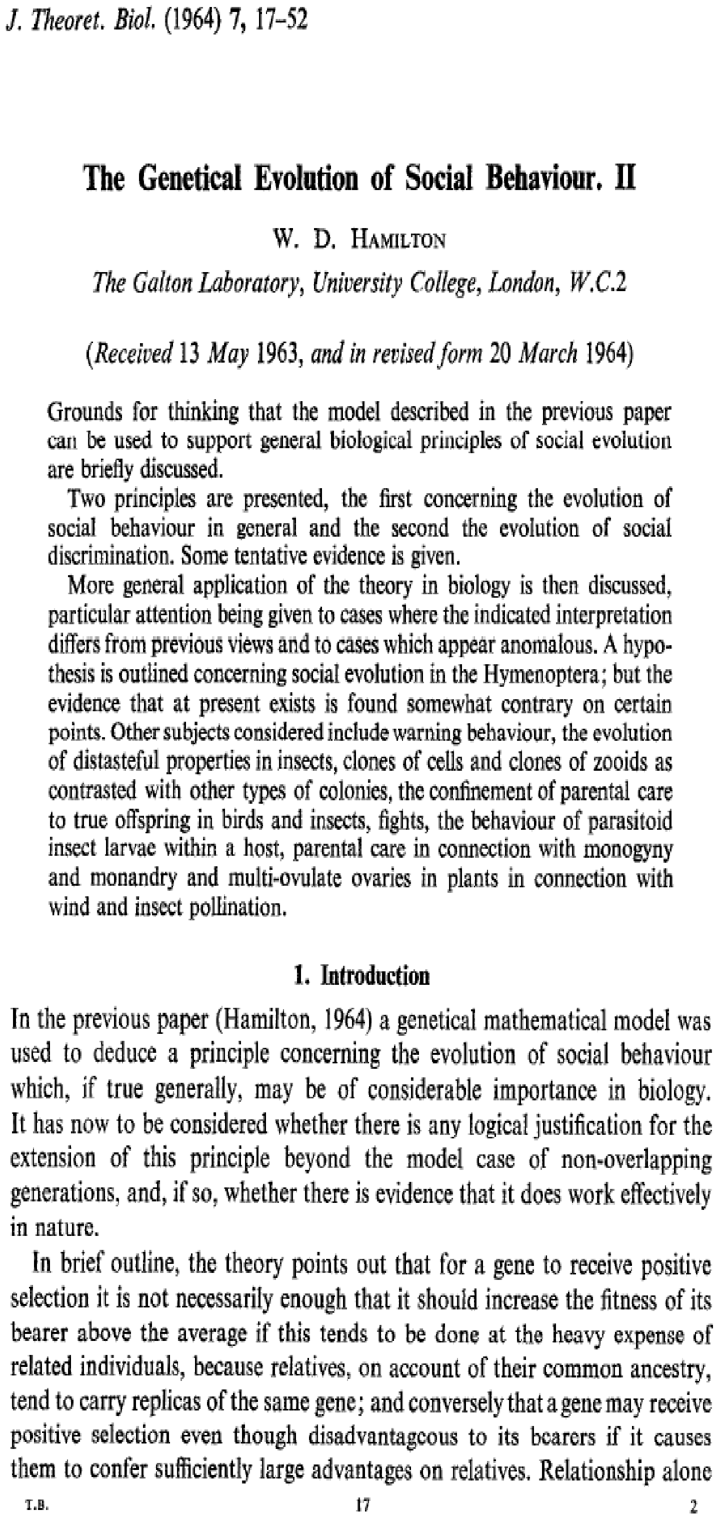
A genetical mathematical model is described which allows for interactions between relatives on one another's fitness. Making use of Wright's Coefficient of Relationship as the measure of the proportion of replica genes in a relative, a quantity is found which incorporates the maximizing property of Darwinian fitness. This quantity is named "inclusive fitness". Species following the model should tend to evolve behaviour such that each organism appears to be attempting to maximize its inclusive fitness. This implies a limited restraint on selfish competitive behaviour and possibility of limited self-sacrifices.

Special cases of the model are used to show (a) that selection in the social situations newly covered tends to be slower than classical selection, (b) how in populations of rather non-dispersive organisms the model may apply to genes affecting dispersion, and (c) how it may apply approximately to competition between relatives, for example, within sibships. Some artificialities of the model are discussed.

1. Introduction

With very few exceptions, the only parts of the theory of natural selection which have been supported by mathematical models admit no possibility of the evolution of any characters which are on average to the disadvantage of the individuals possessing them. If natural selection followed the classical models exclusively, species would not show any behaviour more positively social than the coming together of the sexes and parental care.

Sacrifices involved in parental care are a possibility implicit in any model in which the definition of fitness is based, as it should be, on the number of adult offspring. In certain circumstances an individual may leave more adult offspring by expending care and materials on its offspring already born than by reserving them for its own survival and further fecundity. A gene causing its possessor to give parental care will then leave more replica genes in the next generation than an allele having the opposite tendency. The selective advantage may be seen to lie through benefits conferred indifferently on a set of relatives each of which has a half chance of carrying the gene in question.



J. Theoret. Biol. (1964) 7, 17–52

The Genetical Evolution of Social Behaviour. II

W. D. Hamilton

The Galton Laboratory, University College, London, W.C.2

(*Received* 13 *May* 1963, *and in revised form* 20 *March* 1964)

Grounds for thinking that the model described in the previous paper can be used to support general biological principles of social evolution are briefly discussed.

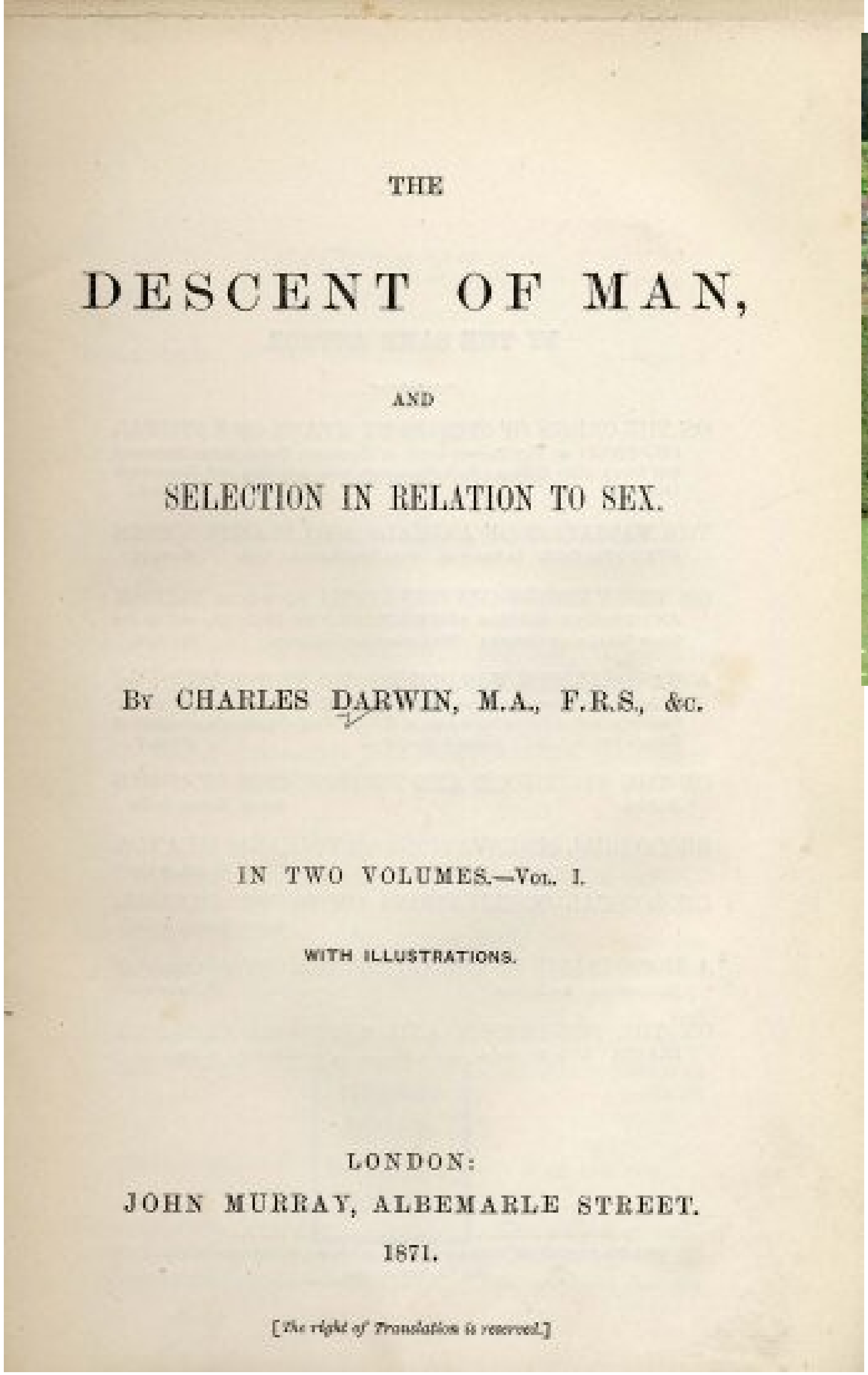
Two principles are presented, the first concerning the evolution of social behaviour in general and the second the evolution of social discrimination. Some tentative evidence is given.

More general application of the theory in biology is then discussed, particular attention being given to cases where the indicated interpretation differs from previous views and to cases which appear anomalous. A hypothesis is outlined concerning social evolution in the Hymenoptera; but the evidence that at present exists is found somewhat contrary on certain points. Other subjects considered include warning behaviour, the evolution of distasteful properties in insects, clones of cells and clones of zooids as contrasted with other types of colonies, the confinement of parental care to true offspring in birds and insects, fights, the behaviour of parasitoid insect larvae within a host, parental care in connection with monogyny and monandry and multi-ovulate ovaries in plants in connection with wind and insect pollination.

1. Introduction

In the previous paper (Hamilton, 1964) a genetical mathematical model was used to deduce a principle concerning the evolution of social behaviour which, if true generally, may be of considerable importance in biology. It has now to be considered whether there is any logical justification for the extension of this principle beyond the model case of non-overlapping generations, and, if so, whether there is evidence that it does work effectively in nature.

In brief outline, the theory points out that for a gene to receive positive selection it is not necessarily enough that it should increase the fitness of its bearer above the average if this tends to be done at the heavy expense of related individuals, because relatives, on account of their common ancestry, tend to carry replicas of the same gene; and conversely that a gene may receive positive selection even though disadvantageous to its bearers if it causes them to confer sufficiently large advantages on relatives. Relationship alone



THE

DESCENT OF MAN,

AND

SELECTION IN RELATION TO SEX.

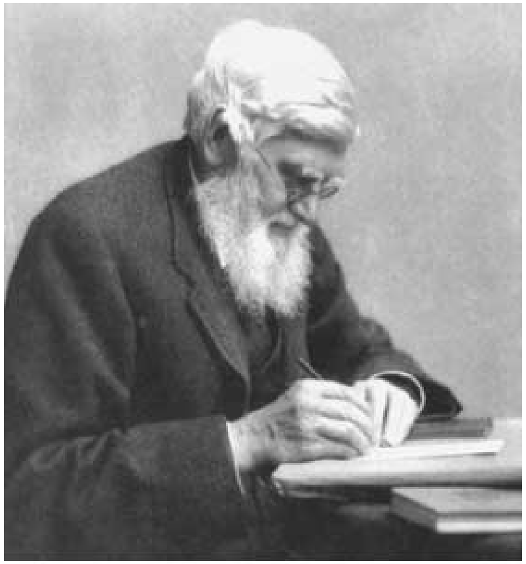
By CHARLES DARWIN, M.A., F.R.S., &c.

IN TWO VOLUMES.—Vol. I.

WITH ILLUSTRATIONS.

LONDON:
JOHN MURRAY, ALBEMARLE STREET.
1871.

[*The right of Translation is reserved.*]



Library of Congress

Vol. XCIX, No. 909 The American Naturalist November-December, 1965

EVOLUTION IN SEXUAL AND ASEXUAL POPULATIONS*

JAMES F. CROW AND MOTOO KIMURA

University of Wisconsin, Madison, Wisconsin, and National Institute
of Genetics, Mishima-shi, Shizuoka-ken, Japan

It has often been said that sexual reproduction is advantageous because of the enormous number of genotypes that can be produced by a recombination of a relatively small number of genes (for example, *Issues in Evolution*, p. 114-115). The number of potential combinations is indeed great, but the number produced in any single generation is limited by the population size, and gene combinations are broken up by recombination just as effectively as they are produced by it. Furthermore, for a given amount of variability, the efficiency of selection is greater in an asexual population than in one with free recombination since the rate is measured by the total genotypic variance rather than by just the additive component thereof.

On the other hand, unless new mutations occur, an asexual population has a selection limit determined by the best existing genotype, whereas directional selection in a sexual population can progress far beyond the initial extreme, as has been demonstrated by selection experiments. The purpose of this article is to compare sexual and asexual systems as to the rate at which favorable gene combinations can be incorporated into the population, considering the effect of gene interaction, mutation rate, population size, and magnitude of gene effect. Most of the material is not new, but the various ideas have not been brought together in this context and we have introduced some refinements.

HISTORICAL

The question was first discussed from the viewpoint in which we are here interested by Fisher (1930) and Muller (1932). We shall follow mainly the argument given by Muller.

In an asexual population, two beneficial mutants can be incorporated into the population only if the second occurs in a descendant of the individual in which the first occurred. On the other hand, in a sexual population the various mutants can get into the same individual by recombination. Only if the mutation rate were so low or the population so small that each mutant became established before another favorable mutant occurred would the two systems be equivalent.

The situation is illustrated in figure 1, adapted from Muller's original drawings. The three mutants, A, B, and C are all beneficial. In the asexual

---

*Paper number 987 from the Division of Genetics, University of Wisconsin; also contribution number 534 from the National Institute of Genetics, Mishima-shi, Japan. This work was aided by grants from the National Institutes of Health (RG-8217 and RG-7666).

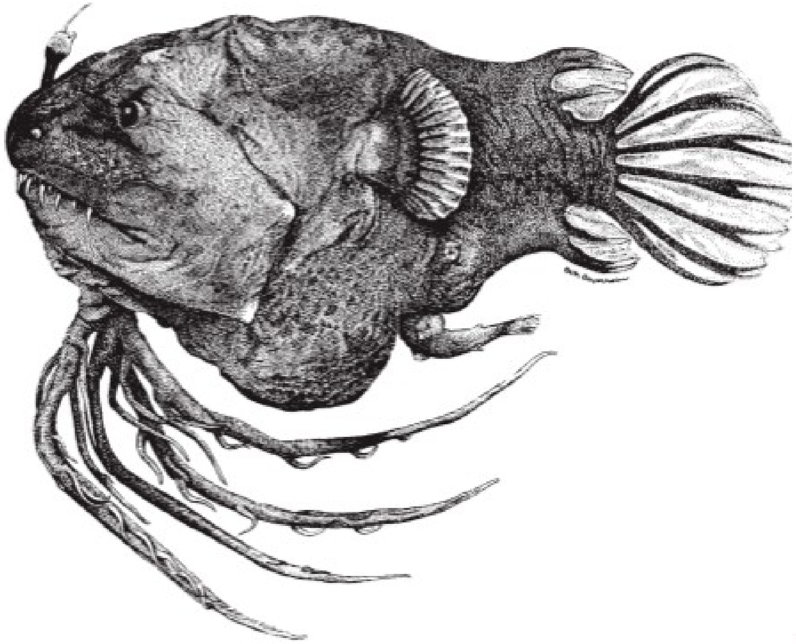


Fig. 22. *Linophryne brevibarbata*, 100-mm female, with an 18.5-
parasitic male, BMNH 1995.1.18.4. (Drawing by Elisabeth Beyerho
after Bertelsen, 1980a)

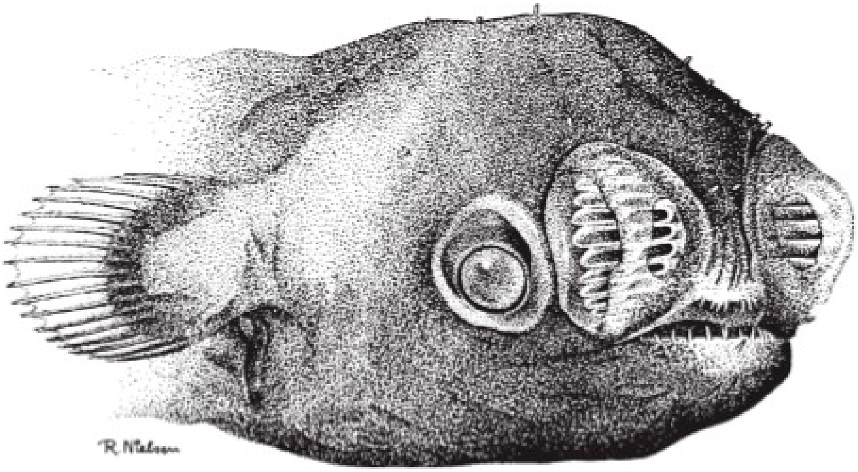
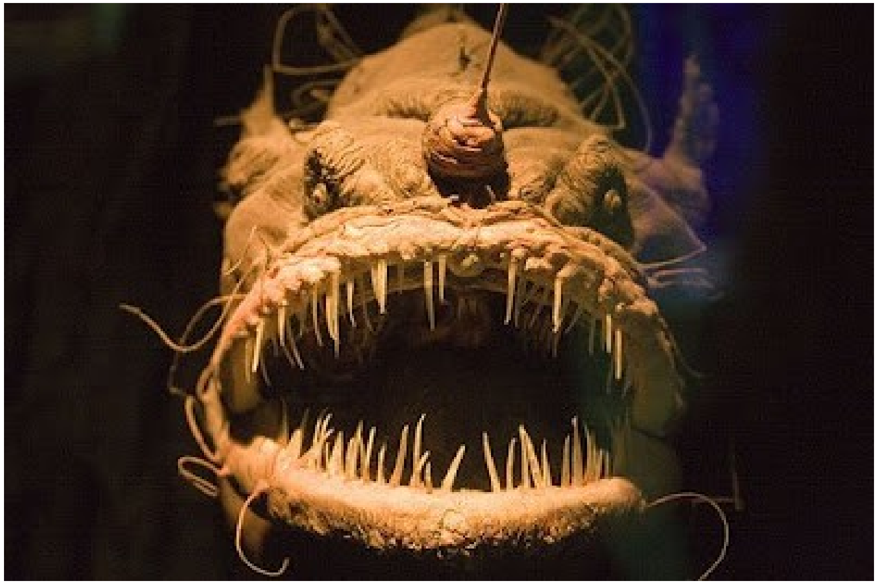


Fig. 18. Free-living male of *Linophryne arborifera*-group, 18.5 mm, BMNH 2004.7.5.1, showing extremely well-developed eyes and nostrils (Drawing by R. Nielsen; after Bertelsen, 1980a)

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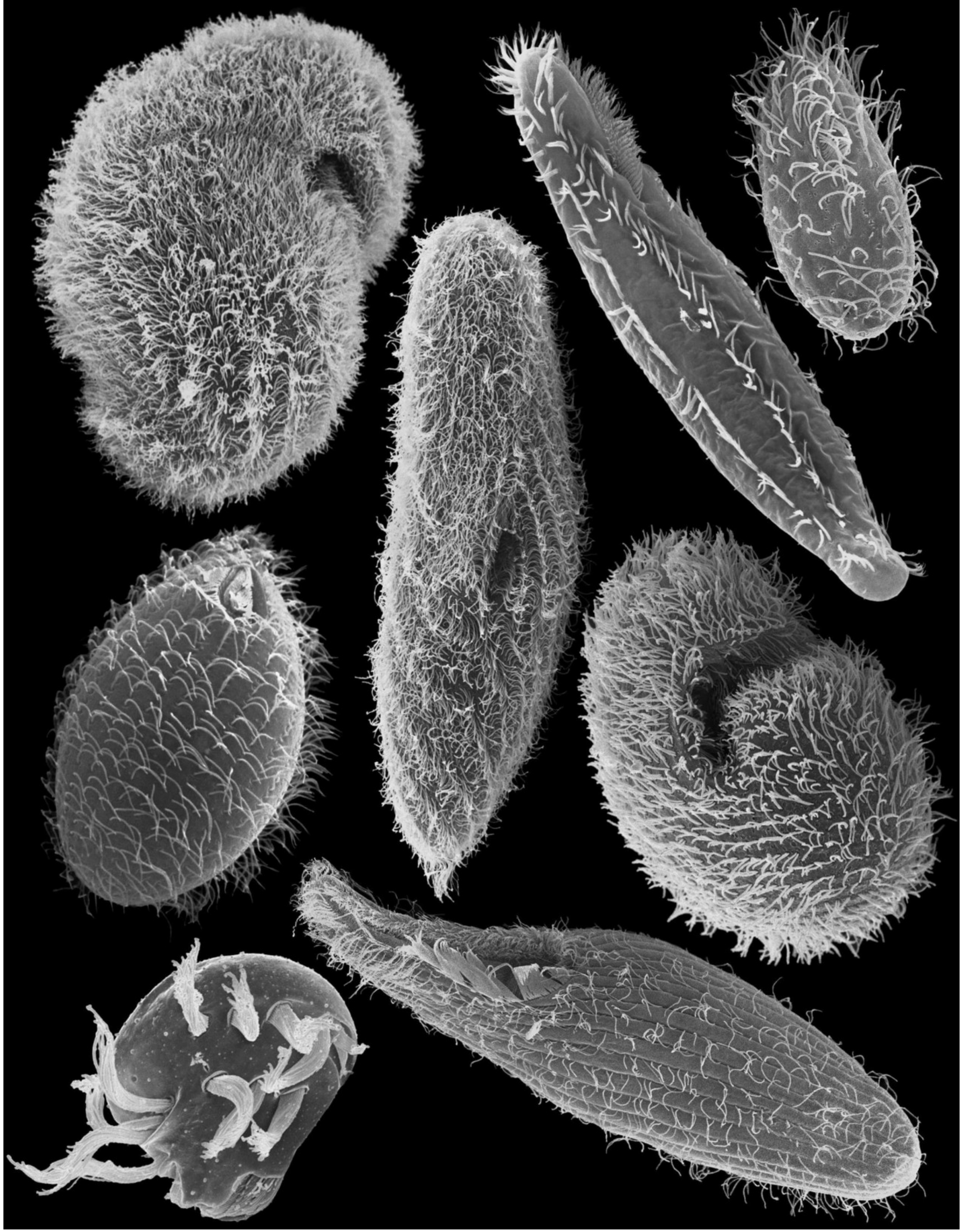
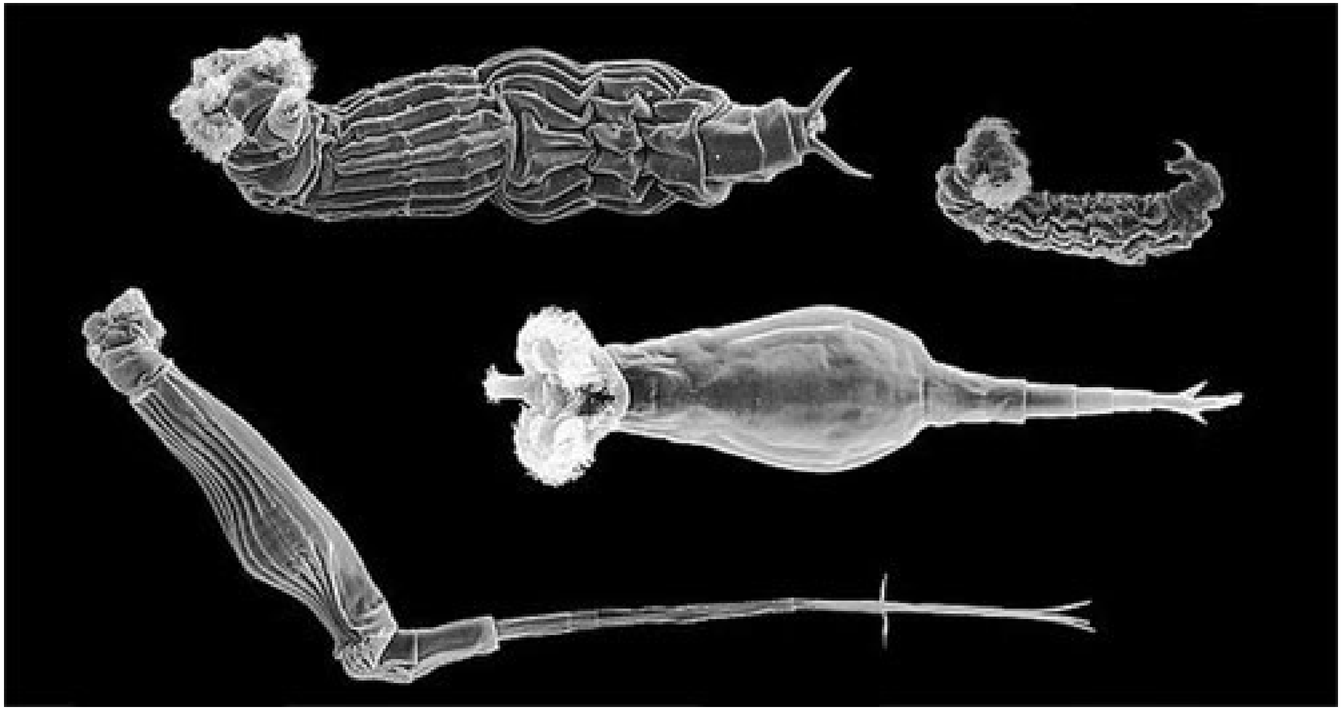
Cnemidophorus neomexicanus

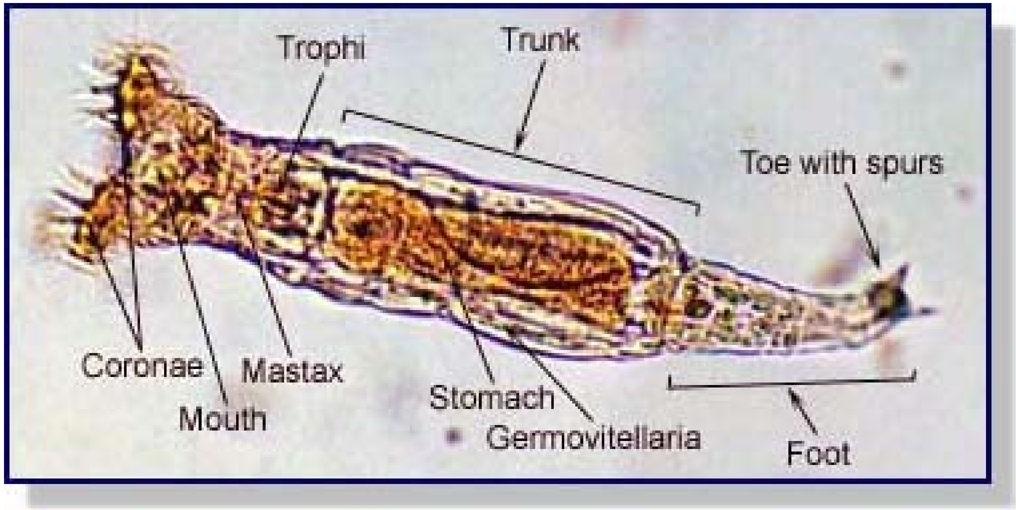
Poecilia formosa

Photo by Slaboch, R.

Cupressus dupreziana






Trophi
Trunk
Toe with spurs
Coronae
Mastax
Mouth
Stomach
Germovitellaria
Foot

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PLoS BIOLOGY

Independently Evolving Species in Asexual Bdelloid Rotifers

Diego Fontaneto[1☯], Elisabeth A. Herniou[2,3☯], Chiara Boschetti[4], Manuela Caprioli[1], Giulio Melone[1], Claudia Ricci[1], Timothy G. Barraclough[2,3,5*]

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Asexuals are an important test case for theories of why species exist. If asexual clades displayed the same pattern of discrete variation as sexual clades, this would challenge the traditional view that sex is necessary for diversification into species. However, critical evidence has been lacking: all putative examples have involved organisms with recent or ongoing histories of recombination and have relied on visual interpretation of patterns of genetic and phenotypic variation rather than on formal tests of alternative evolutionary scenarios. Here we show that a classic asexual clade, the bdelloid rotifers, has diversified into distinct evolutionary species. Intensive sampling of the genus *Rotaria* reveals the presence of well-separated genetic clusters indicative of independent evolution. Moreover, combined genetic and morphological analyses reveal divergent selection in feeding morphology, indicative of niche divergence. Some of the morphologically coherent groups experiencing divergent selection contain several genetic clusters, in common with findings of cryptic species in sexual organisms. Our results show that the main causes of speciation in sexual organisms, population isolation and divergent selection, have the same qualitative effects in an asexual clade. The study also demonstrates how combined molecular and morphological analyses can shed new light on the evolutionary nature of species.

Citation: Fontaneto D, Herniou EA, Boschetti C, Caprioli M, Melone G, et al. (2007) Independently evolving species in asexual bdelloid rotifers. PLoS Biol 5(4): e87. doi:10.1371/journal.pbio.0050087

Introduction

Species are fundamental units of biology, but there remains uncertainty on both the pattern and processes of species existence. Are species real evolutionary entities or convenient figments of taxonomists' imagination [1–3]? If they exist, what are the main processes causing organisms to diversify [1,4]? Despite considerable debate, surprisingly few studies have formally tested the evolutionary status of species [1,5,6].

One central question concerning the nature of species has been whether asexual organisms diversify into species [1]. The traditional view is that species in sexual clades arise mainly because interbreeding maintains cohesion within species, whereas reproductive isolation causes divergence between species [7]. If so, asexuals might not diversify into distinct species, because there is no interbreeding to maintain cohesive units above the level of the individual. However, if other processes were more important for maintaining cohesion and causing divergence, for example, specialization into distinct niches, then asexuals should diversify in a

Although horizontal gene transfer can occur between distantly related bacteria, homologous recombination occurs only at appreciable frequency between closely related strains [20,21]. Therefore, clusters in these bacteria could arise from similar processes to interbreeding and reproductive isolation in sexual eukaryotes [20]. Aside from issues of sexuality, previous studies looking for distinct clusters have been descriptive, relying on visual interpretation of plots of genetic or phenotypic variation rather than on formal tests of predictions under null and alternative evolutionary scenarios [1].

Here, we demonstrate that a classic asexual clade, the bdelloid rotifers, has diversified into independently evolving and distinct entities arguably equivalent to species. Bdelloids are abundant animals in aquatic or occasionally wet terrestrial habitats and represent one of the best-supported clades of ancient asexuals [22–24]. They reproduce solely via parthenogenetic eggs, and no males or traces of meiosis have ever been observed. Molecular evidence that bdelloid

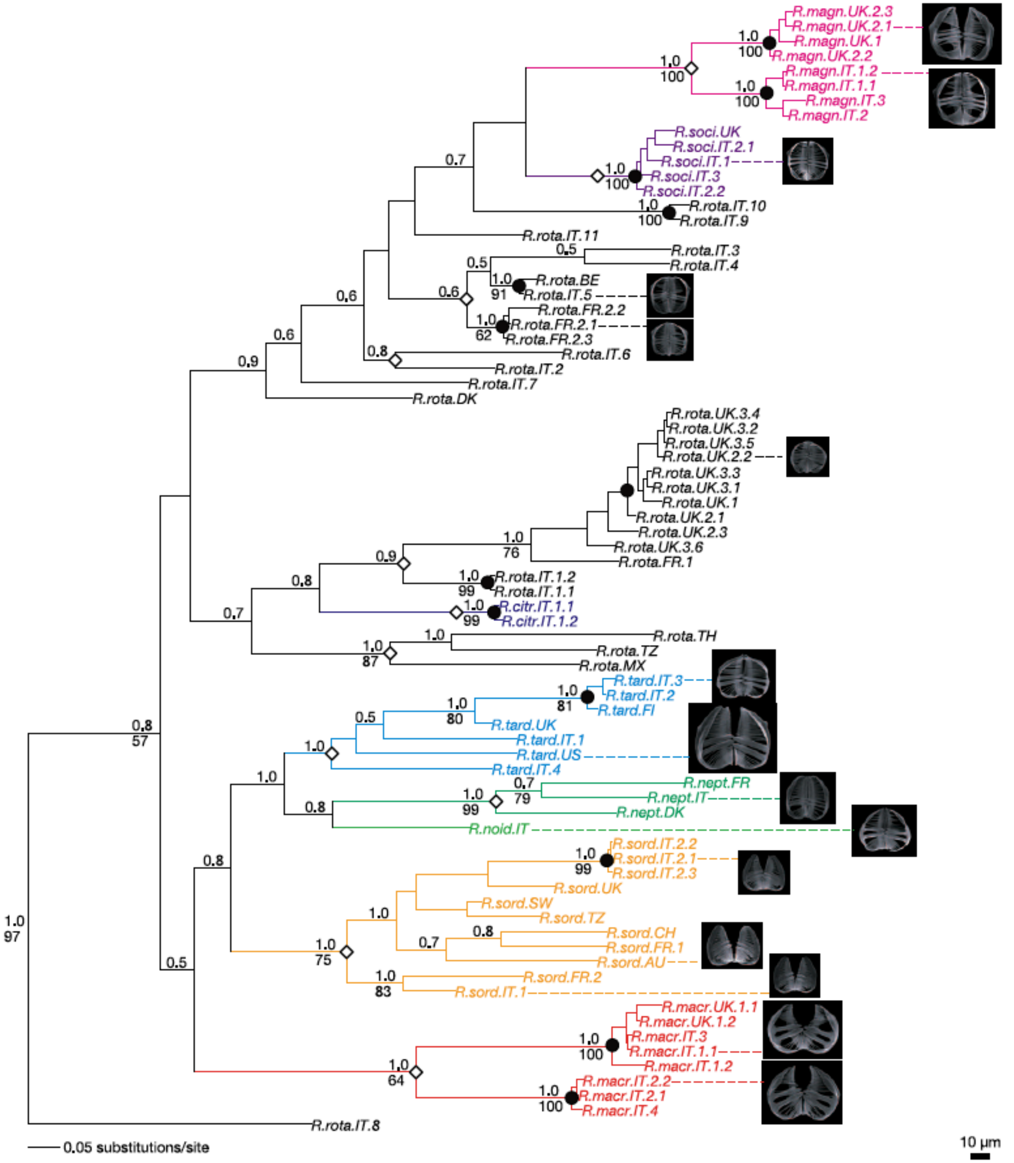
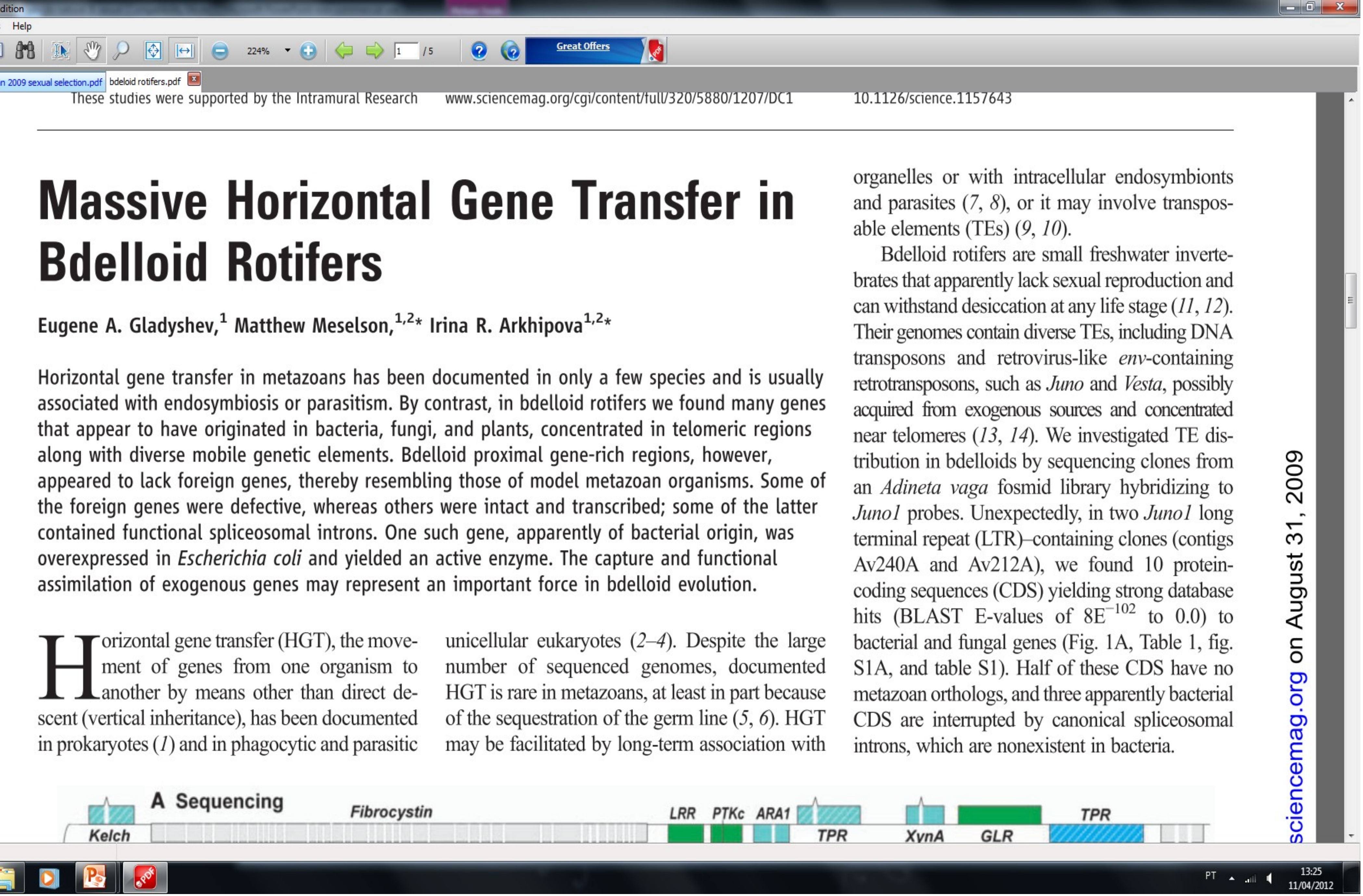


Figure 3. Phylogenetic Relationships in the Genus *Rotaria*

The consensus of 80,000 sampled trees from Bayesian analysis of the combined *cox1* and *28S* rDNA data sets is shown, displaying all compatible groupings and with average branch lengths proportional to numbers of substitutions per site under a separate GTR + invgamma substitution model for the *cox1* and *28S* partitions. Posterior probabilities above 0.5 and bootstrap support above 50% from a maximum parsimony bootstrap analysis are shown above and below each branch, respectively. Support values for within-species relationships are not shown for very short branches but are shown in Figures S1 through S3. Closed circles indicate clusters identified by the clustering analysis. Colors represent traditional species memberships. Diamonds indicate taxonomic species and monophyletic groups of *Rotaria*. Names refer to the species, the country, the number of site within that country for that species, and the number of individual from that site if several were isolated; for example, R.macr.IT.1.1 refers to the first individual from site 1 in Italy for *R. macrura*. Pictures of trophi from one individual from each cluster are shown to scale: Representatives of all sampled populations are shown in Figure S4. A full list of names and localities of samples is available in Table S1.
doi:10.1371/journal.pbio.0050087.g003



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10.1126/science.1157643

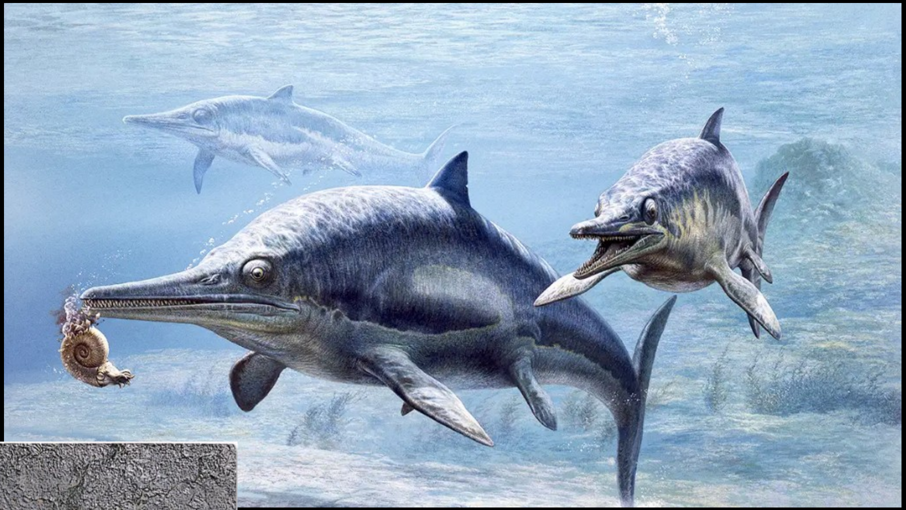
Massive Horizontal Gene Transfer in Bdelloid Rotifers

Eugene A. Gladyshev,[1] Matthew Meselson,[1,2]* Irina R. Arkhipova[1,2]*

Horizontal gene transfer in metazoans has been documented in only a few species and is usually associated with endosymbiosis or parasitism. By contrast, in bdelloid rotifers we found many genes that appear to have originated in bacteria, fungi, and plants, concentrated in telomeric regions along with diverse mobile genetic elements. Bdelloid proximal gene-rich regions, however, appeared to lack foreign genes, thereby resembling those of model metazoan organisms. Some of the foreign genes were defective, whereas others were intact and transcribed; some of the latter contained functional spliceosomal introns. One such gene, apparently of bacterial origin, was overexpressed in *Escherichia coli* and yielded an active enzyme. The capture and functional assimilation of exogenous genes may represent an important force in bdelloid evolution.

Horizontal gene transfer (HGT), the movement of genes from one organism to another by means other than direct descent (vertical inheritance), has been documented in prokaryotes (*1*) and in phagocytic and parasitic unicellular eukaryotes (*2–4*). Despite the large number of sequenced genomes, documented HGT is rare in metazoans, at least in part because of the sequestration of the germ line (*5*, *6*). HGT may be facilitated by long-term association with organelles or with intracellular endosymbionts and parasites (*7*, *8*), or it may involve transposable elements (TEs) (*9*, *10*).

Bdelloid rotifers are small freshwater invertebrates that apparently lack sexual reproduction and can withstand desiccation at any life stage (*11*, *12*). Their genomes contain diverse TEs, including DNA transposons and retrovirus-like *env*-containing retrotransposons, such as *Juno* and *Vesta*, possibly acquired from exogenous sources and concentrated near telomeres (*13*, *14*). We investigated TE distribution in bdelloids by sequencing clones from an *Adineta vaga* fosmid library hybridizing to *Juno1* probes. Unexpectedly, in two *Juno1* long terminal repeat (LTR)–containing clones (contigs Av240A and Av212A), we found 10 protein-coding sequences (CDS) yielding strong database hits (BLAST E-values of $8E^{-102}$ to 0.0) to bacterial and fungal genes (Fig. 1A, Table 1, fig. S1A, and table S1). Half of these CDS have no metazoan orthologs, and three apparently bacterial CDS are interrupted by canonical spliceosomal introns, which are nonexistent in bacteria.



Euphorbia (Euphorbiaceae)

Astrophytum (Cactaceae)

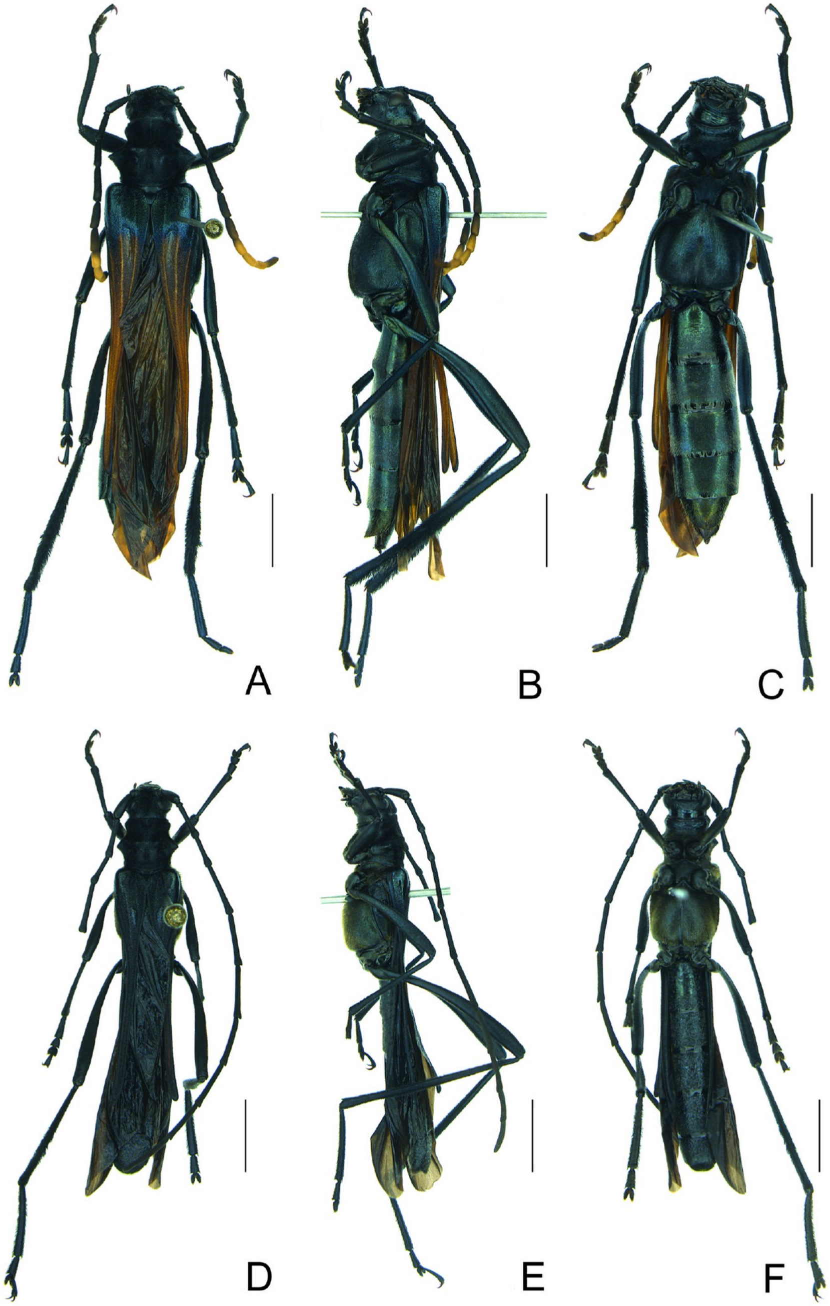
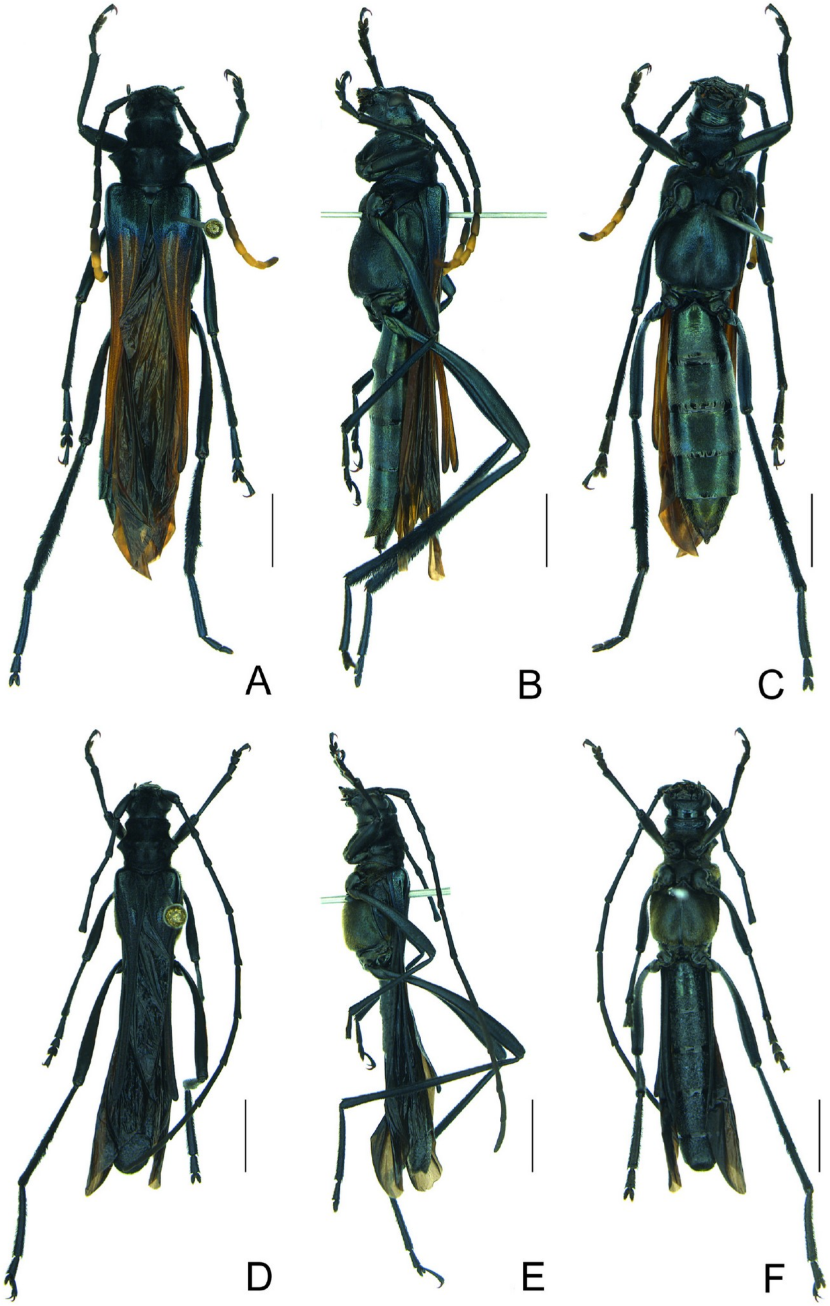


FIGURE 1A–F. *Parahephaestion mimicus* **sp. nov.** Habitus. Holotype female, A–C: A—Dorsal; B—Lateral; C—Ventral. Paratype male, D–F: D—Dorsal; E—Lateral; F—Ventral. Scale bars: (A–C) 5 mm, (D–F) 4 mm.



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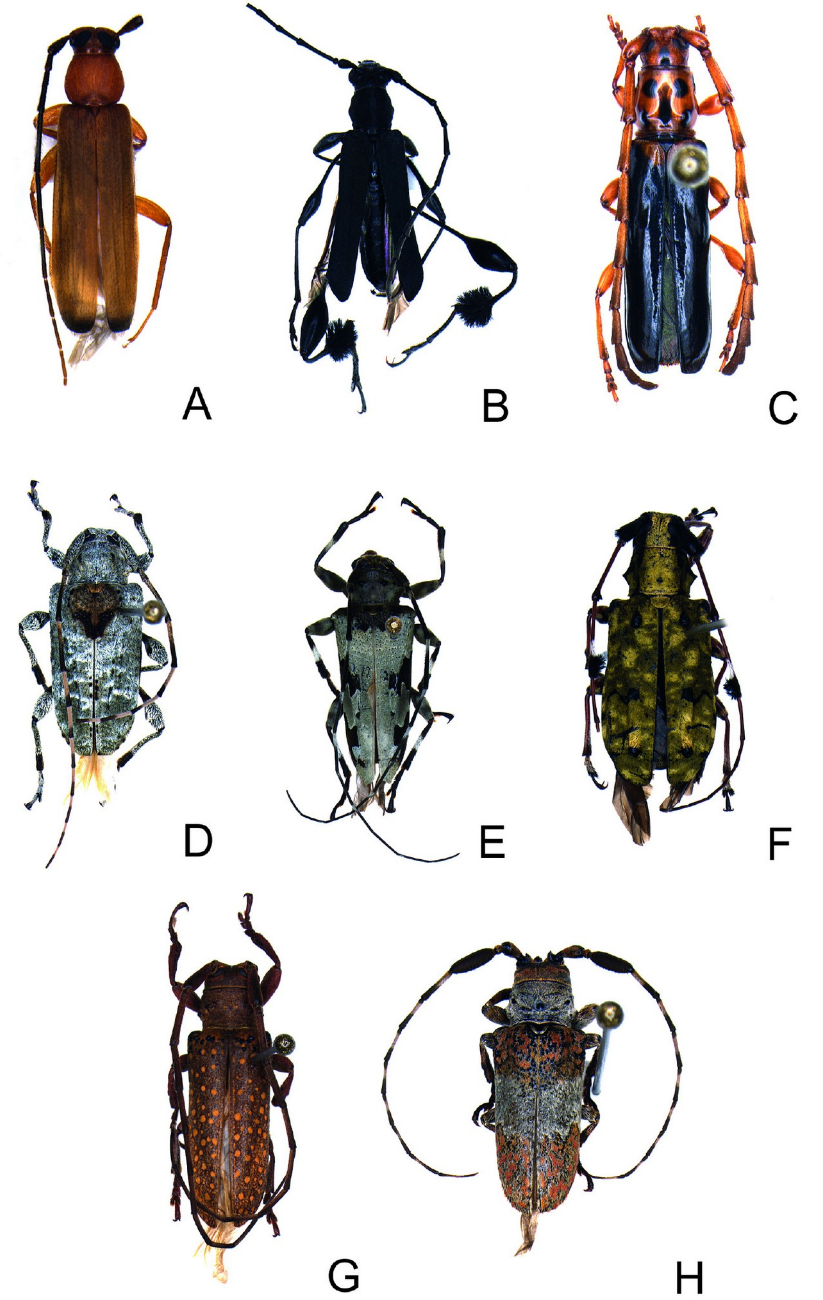

FIGURE 3A–H. New records in Cerambycidae. Dorsal habitus. A—*Sphalloeme costipennis* Melzer, 1928; B—*Thalusia atrata* (Melzer, 1918); C—*Trachelissa pustulata* (Audinet-Serville, 1834); D—*Ateralphus dejeani* (Lane, 1973); E—*Oreodera omissa* Melzer, 1932; F—*Phacellocera plumicornis* (Klug, 1825); G—*Oncideres impluviata* (Germar, 1823); H—*Psyllotoxus griseocinctus* Thomson, 1868.

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Article

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New species of the wasp-mimic *Parahephaestion* Melzer, 1930 (Coleoptera: Cerambycidae), from Minas Gerais, Brazil, with new records

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**Corresponding author*

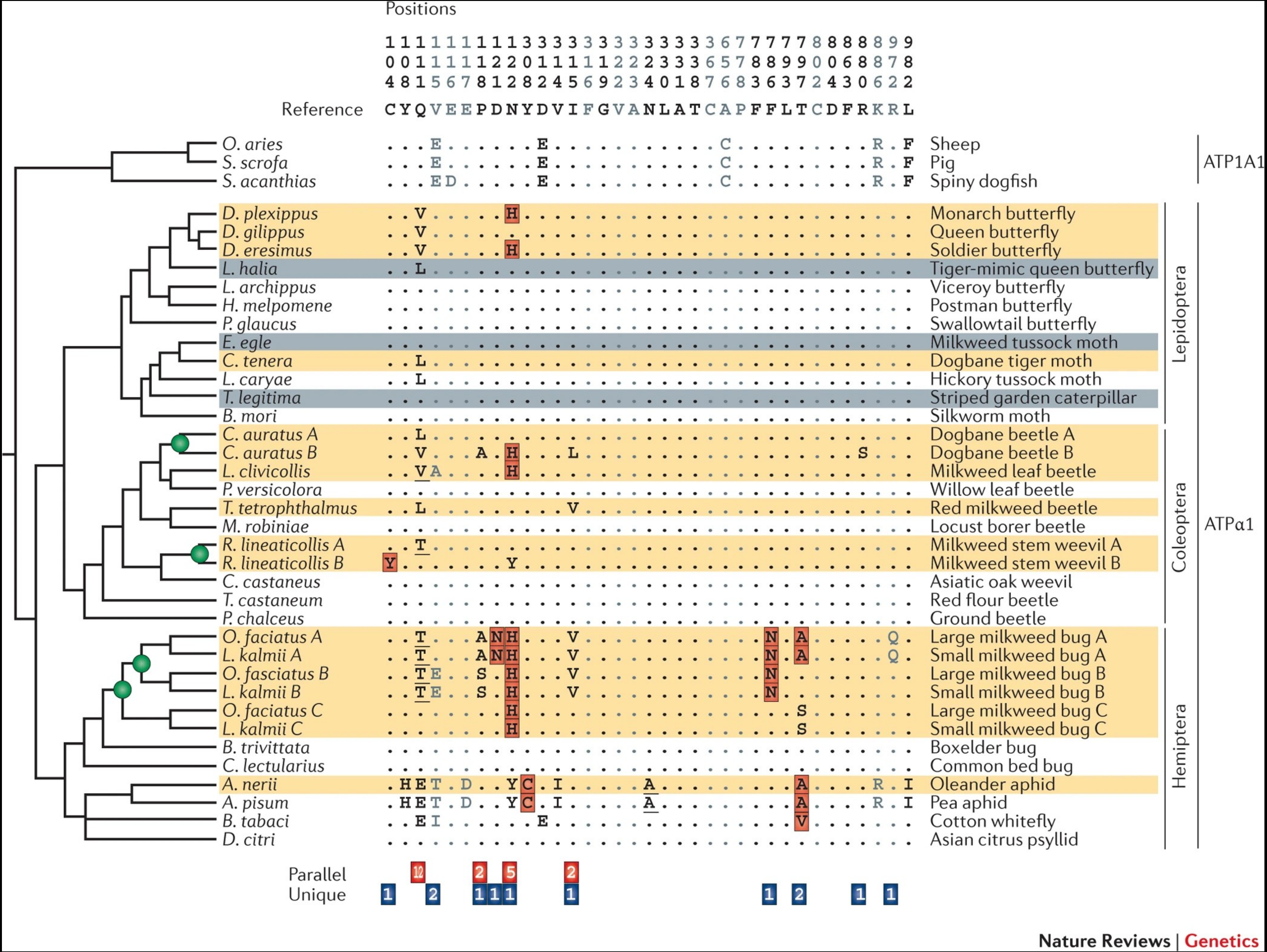
Abstract

A new species, *Parahephaestion mimicus* **sp. nov.**, is described. Two species are newly recorded for the Brazilian state of Minas Gerais: *Sphalloeme costipennis* Melzer, 1928 (Cerambycinae, Oemini) and *Oreodera omissa* Melzer, 1932 (Lamiinae, Acrocinini). Six species are new records for the RPPN Sanctuary of Caraça, (Brazil, Minas Gerais): *Thalusia atrata* (Melzer, 1918) (Cerambycinae, Rhopalophorini), *Trachelissa pustulata* (Audinet-Serville, 1834) (Cerambycinae, Trachyderini), *Ateralphus dejeani* (Lane, 1973) (Lamiinae, Acanthoderini), *Phacellocera plumicornis* (Klug, 1825) (Lamiinae, Anisocerini), *Oncideres impluviata* (Germar, 1823), and *Psyllotoxus griseocinctus* Thomson, 1868 (Lamiinae, Onciderini).

Key word: Longhorn beetles, Pompilidae, Neotropical, Batesian mimicry, Necydalinae

Introduction

Eight subfamilies have been historically included in Cerambycidae: Cerambycinae, Dorcasominae, Lamiinae, Lepturinae, Necydalinae, Parandrinae, Prioninae, and Spondylidinae (Haddad *et al*. 2018). More recently, Necydalinae and Parandrinae have been recognized as part of Lepturinae and Prioninae, respectively, reducing the number of subfamilies to six (Nie *et al*. 2021).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Reference CYQVEEPDNYDVIFGVANLATCAPFFLTCDFRKRL
O. aries ...E......E...........C.........R.F Sheep
S. scrofa ...E......E...........C.........R.F Pig
S. acanthias ...ED.....E...........C.........R.F Spiny dogfish
D. plexippus ..V.....H.......................... Monarch butterfly
D. gilippus ..V................................ Queen butterfly
D. eresimus ..V.....H.......................... Soldier butterfly
L. halia ..L................................ Tiger-mimic queen butterfly
L. archippus .... Viceroy butterfly
H. melpomene .... Postman butterfly
P. glaucus .... Swallowtail butterfly
E. egle .... Milkweed tussock moth
C. tenera ..L................................ Dogbane tiger moth
L. caryae ..L................................ Hickory tussock moth
T. legitima .... Striped garden caterpillar
B. mori .... Silkworm moth
C. auratus A ..L................................ Dogbane beetle A
C. auratus B ..V...A.H...L..................S... Dogbane beetle B
L. clivicollis ..VA....H.......................... Milkweed leaf beetle
P. versicolora .... Willow leaf beetle
T. tetrophthalmus ..L.........V...................... Red milkweed beetle
M. robiniae .... Locust borer beetle
R. lineaticollis A ..T................................ Milkweed stem weevil A
R. lineaticollis B Y.......Y.......................... Milkweed stem weevil B
C. castaneus .... Asiatic oak weevil
T. castaneum .... Red flour beetle
P. chalceus .... Ground beetle
O. faciatus A ..T...ANH...V............N.A.....Q. Large milkweed bug A
L. kalmii A ..T...ANH...V............N.A.....Q. Small milkweed bug A
O. fasciatus B ..TE..S.H...V............N......... Large milkweed bug B
L. kalmii B ..TE..S.H...V............N......... Small milkweed bug B
O. faciatus C ........H..................S....... Large milkweed bug C
L. kalmii C ........H..................S....... Small milkweed bug C
B. trivittata .... Boxelder bug
C. lectularius .... Common bed bug
A. nerii .HET.D..YC.I.....A.........A....R.I Oleander aphid
A. pisum .HET.D..YC.I.....A.........A....R.I Pea aphid
B. tabaci ..EI......E................V....... Cotton whitefly
D. citri .... Asian citrus psyllid
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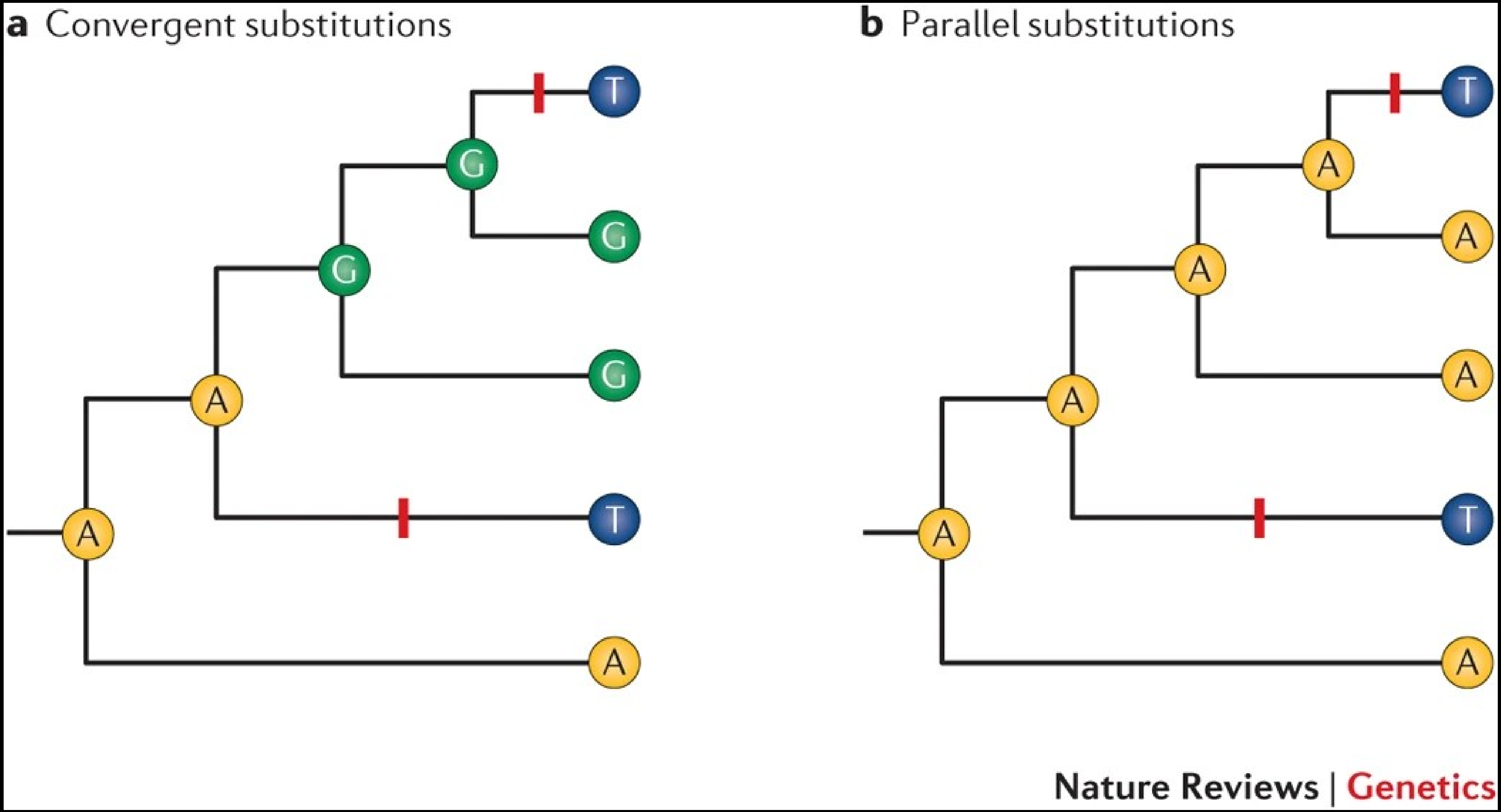
Nature Reviews | Genetics



From Storz (2016)

nature ecology & evolution

Article

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The nature of the last universal common ancestor and its impact on the early Earth system

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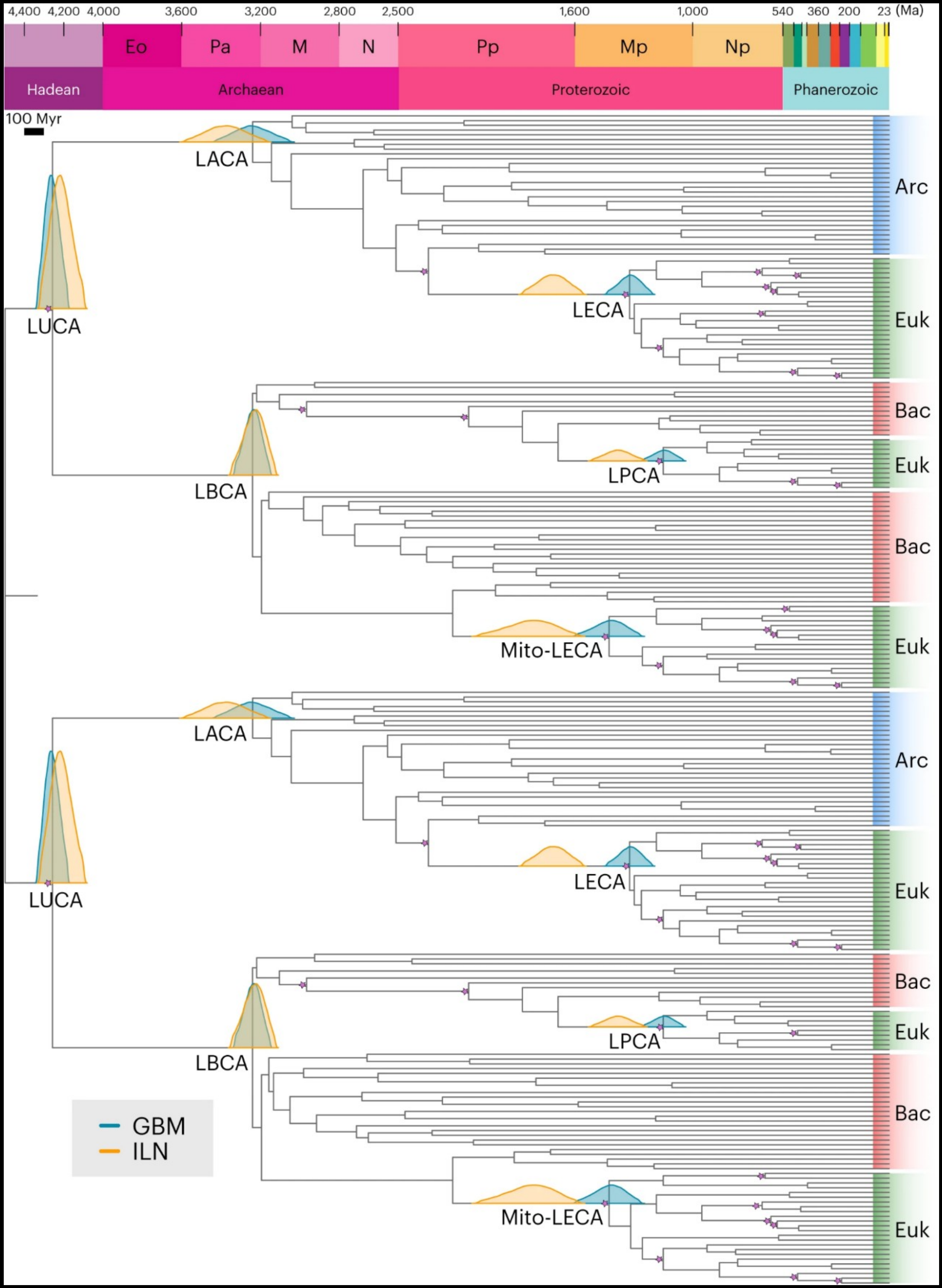
The nature of the last universal common ancestor (LUCA), its age and its impact on the Earth system have been the subject of vigorous debate across diverse disciplines, often based on disparate data and methods. Age estimates for LUCA are usually based on the fossil record, varying with every reinterpretation. The nature of LUCA's metabolism has proven equally contentious, with some attributing all core metabolisms to LUCA, whereas others reconstruct a simpler life form dependent on geochemistry. Here we infer that LUCA lived ~4.2 Ga (4.09–4.33 Ga) through divergence time analysis of pre-LUCA gene duplicates, calibrated using microbial fossils and isotope records under a new cross-bracing implementation. Phylogenetic reconciliation suggests that LUCA had a genome of at least 2.5 Mb (2.49–2.99 Mb), encoding around 2,600 proteins, comparable to modern prokaryotes. Our results suggest LUCA was a prokaryote-grade anaerobic acetogen that possessed an early immune system. Although LUCA is sometimes perceived as living in isolation, we infer LUCA to have been part of an established ecological system. The metabolism of LUCA would have provided a niche for other microbial community members and hydrogen recycling by atmospheric photochemistry could have supported a modestly productive early ecosystem.

The common ancestry of all extant cellular life is evidenced by the universal genetic code, machinery for protein synthesis, shared chirality of the almost-universal set of 20 amino acids and use of ATP as a common energy currency[1]. The last universal common ancestor (LUCA) is the node on the tree of life from which the fundamental prokaryotic domains (Archaea and Bacteria) diverge. As such, our understanding of

it inhabit and when? Previous estimates of LUCA are in conflict either due to conceptual disagreement about what LUCA is[2] or as a result of different methodological approaches and data[3–9]. Published analyses differ in their inferences of LUCA's genome, from conservative estimates of 80 orthologous proteins[10] up to 1,529 different potential gene families[4]. Interpretations range from little beyond an information-processing


4,400
4,200
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540
360
200
23
(Ma)
Eo
Pa
M
N
Pp
Mp
Np
Hadean
Archaean
Proterozoic
Phanerozoic
100 Myr
LUCA
LACA
LECA
LBCA
LPCA
Mito-LECA
Arc
Euk
Bac
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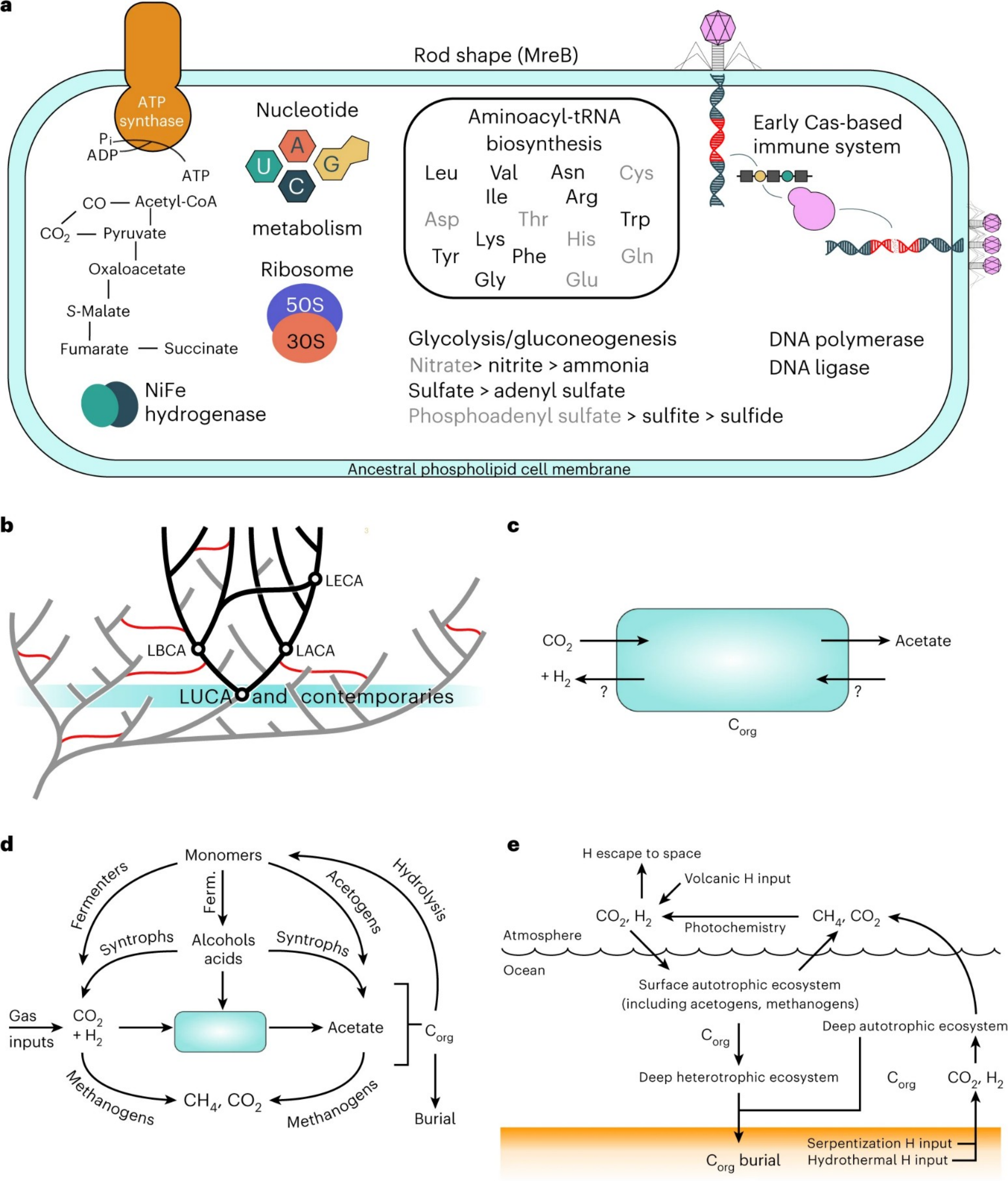
a
Rod shape (MreB)
ATP synthase
P_i
ADP
ATP
CO — Acetyl-CoA
CO_2 — Pyruvate
Oxaloacetate
S-Malate
Fumarate — Succinate
NiFe hydrogenase
Nucleotide metabolism
A
U
G
C
Ribosome
50S
30S
Aminoacyl-tRNA biosynthesis
Leu
Val
Asn
Cys
Ile
Arg
Asp
Thr
Trp
Lys
His
Tyr
Phe
Gln
Gly
Glu
Early Cas-based immune system
Glycolysis/gluconeogenesis
Nitrate> nitrite > ammonia
Sulfate > adenyl sulfate
Phosphoadenyl sulfate > sulfite > sulfide
DNA polymerase
DNA ligase
Ancestral phospholipid cell membrane
b
LECA
LBCA
LACA
LUCA and contemporaries
c
CO_2
+ H_2
?
Acetate
?
C_{org}
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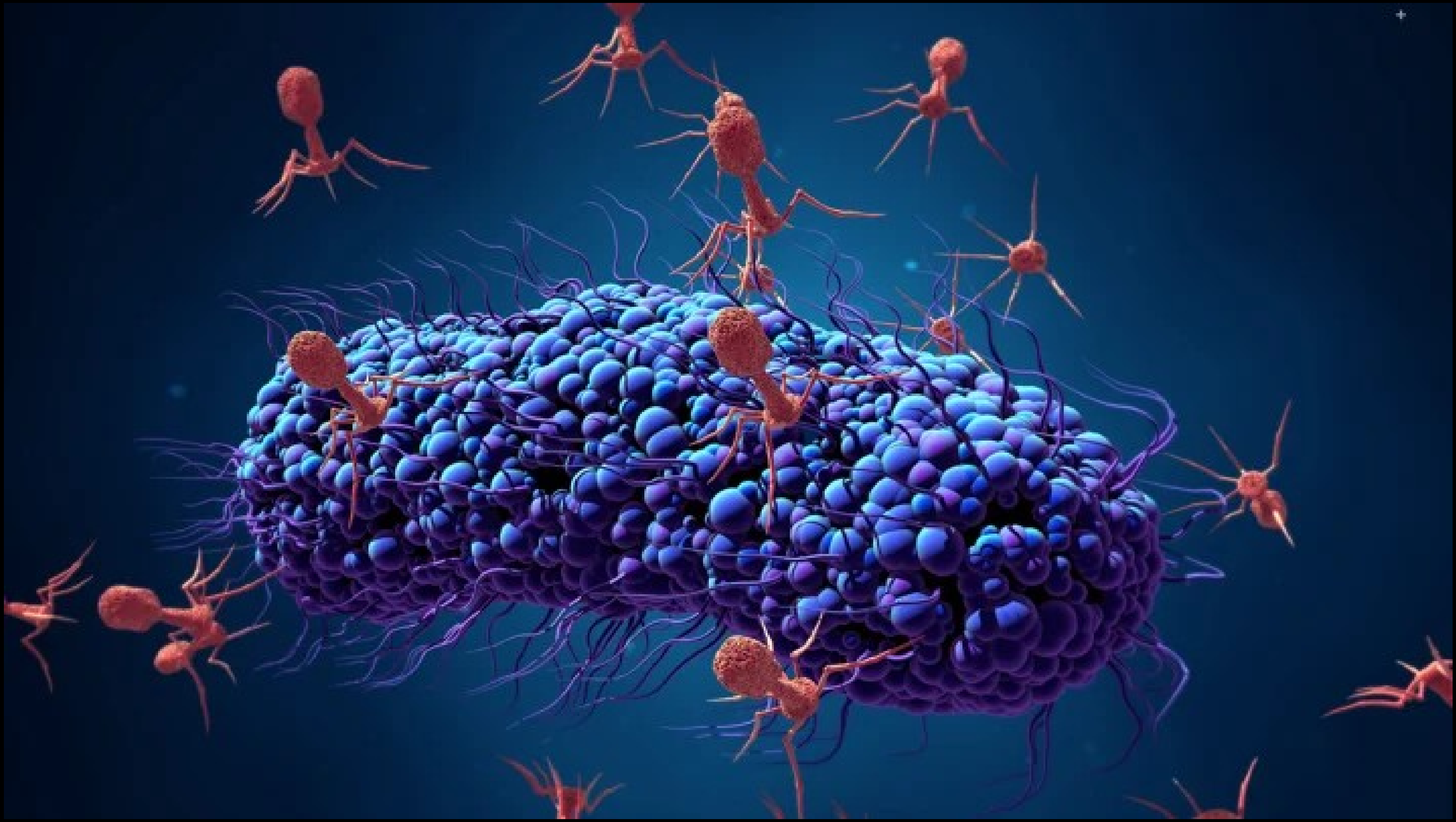
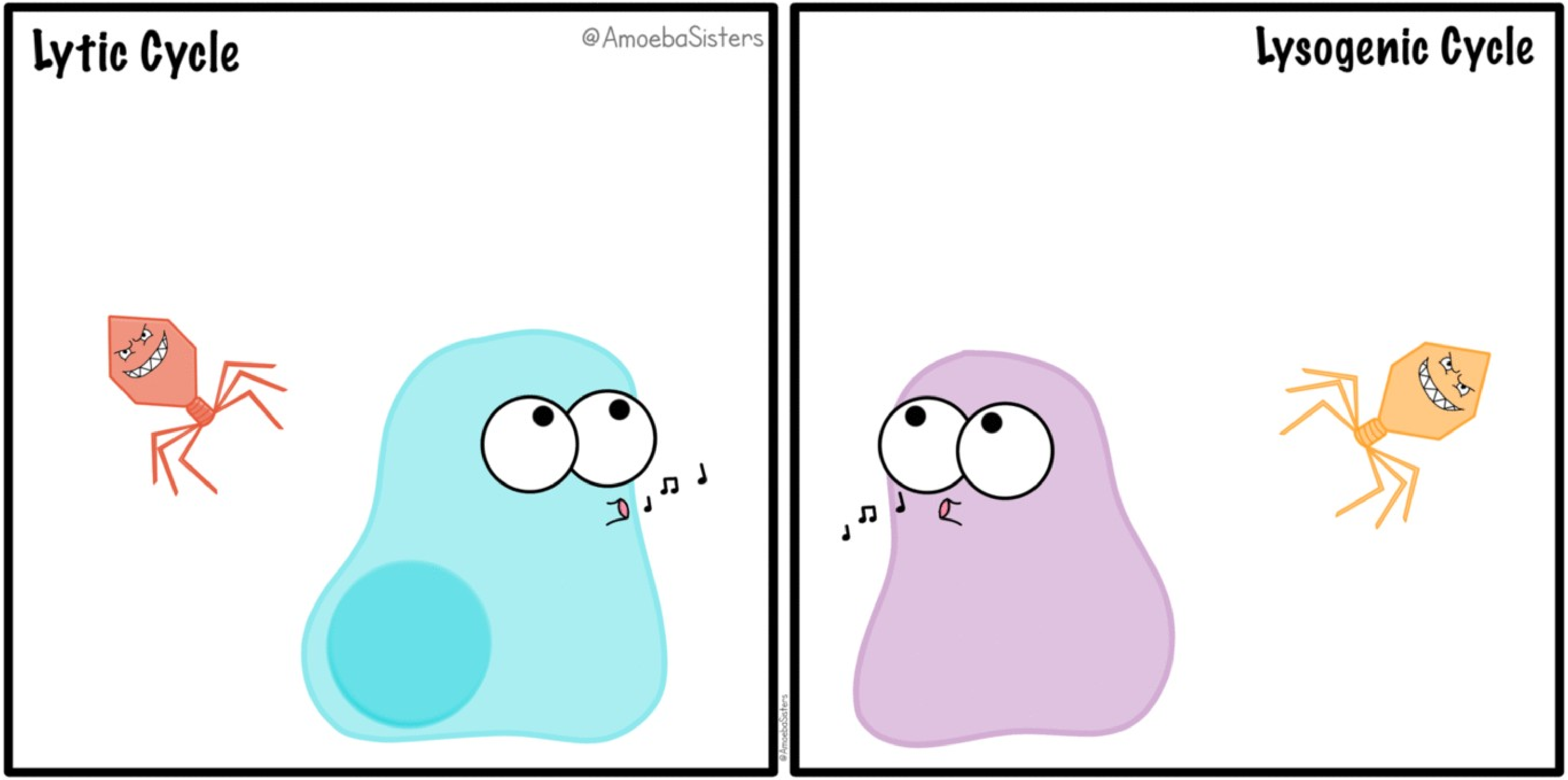
Monomers
Fermenters
Ferm.
Acetogens
Hydrolysis
Syntrophs
Alcohols acids
Syntrophs
Gas inputs
CO_2 + H_2
Acetate
C_{org}
Methanogens
CH_4, CO_2
Methanogens
Burial
e
H escape to space
Volcanic H input
CO_2, H_2
Photochemistry
CH_4, CO_2
Atmosphere
Ocean
Surface autotrophic ecosystem (including acetogens, methanogens)
C_{org}
Deep autotrophic ecosystem
Deep heterotrophic ecosystem
C_{org}
CO_2, H_2
C_{org} burial
Serpentization H input
Hydrothermal H input

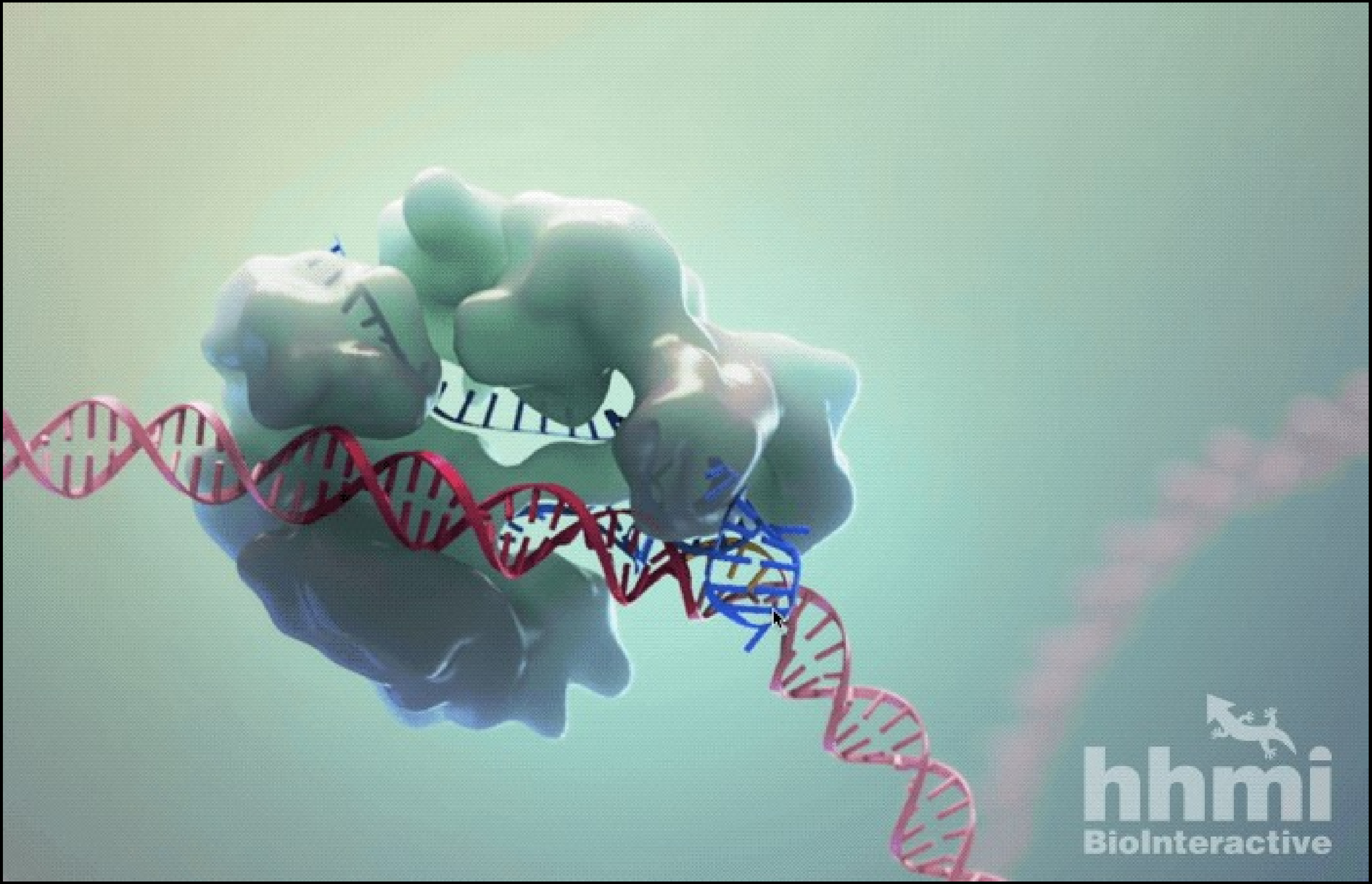


Lytic vs Lysogenic Cycles



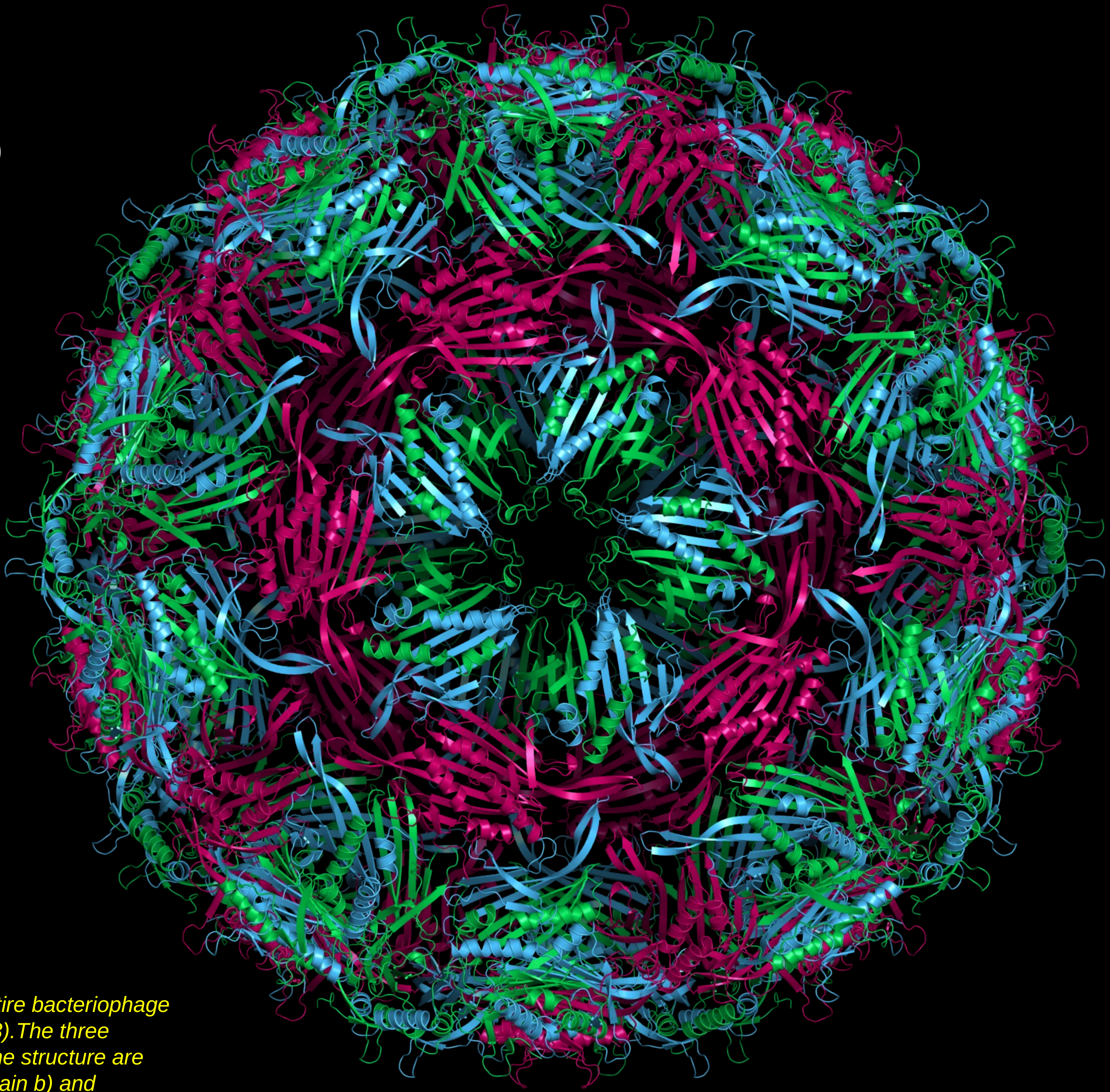
Lytic Cycle

Lysogenic Cycle

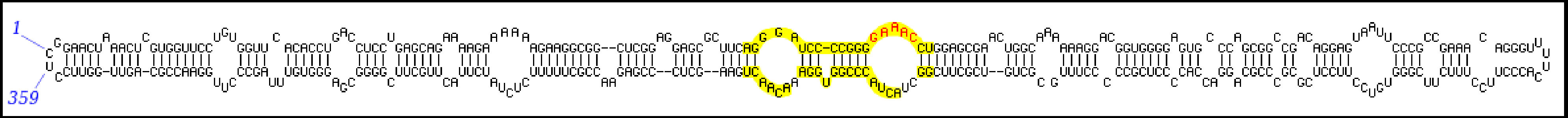


In the genome editing technology known as CRISPR-Cas9, RNA (blue) forms a complex with the protein Cas9 (bumpy structure). Cas9 unwinds target DNA (red) and acts as a molecular scalpel, slicing both strands. Cas13, a related protein, cuts RNA instead of DNA. Credit: HHMI BioInteractive, CRISPR-Cas 9 Mechanism & Applications

3569 nucleotides
(single-stranded RNA)
-> 4 proteins



Cartoon representation of the entire bacteriophage MS2 protein capsid (pdb id 1AQ3).The three quasi-equivalent conformers in the structure are labelled blue (chain a), green (chain b) and magenta (chain c). The view is approximately down an icosahedral 5-fold symmetry axis.)



(By Jakub Friedl)

Putative secondary structure of the PSTV (potato spindle tuber viroid)

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Emergence and natural selection of drug-resistant prions

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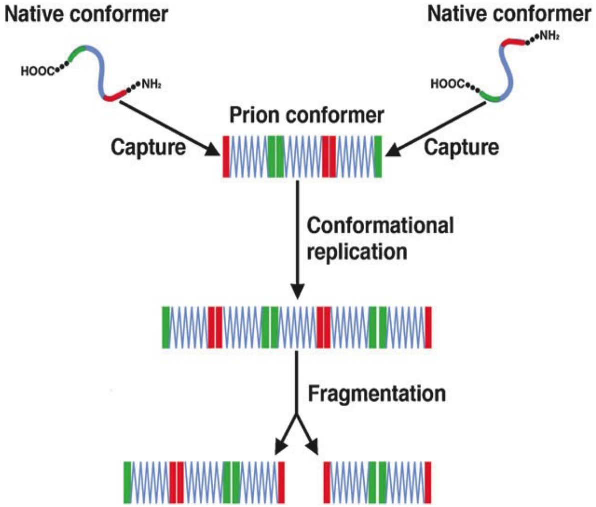
Drug resistance is a refractory barrier in the battle against many fatal diseases caused by rapidly evolving agents, including HIV, apicomplexans and specific cancers. Emerging evidence suggests that drug resistance might extend to lethal prion disorders and related neurodegenerative amyloidoses. Prions are self-replicating protein conformers, usually 'cross-β' amyloid polymers, which are naturally transmitted between individuals and promote phenotypic change. Prion conformers are catalytic templates that specifically convert other copies of the same protein to the prion form. Once in motion, this chain reaction of conformational replication can deplete all non-prion copies of a protein. Typically, prions exist as ensembles of multiple structurally distinct, self-replicating forms or 'strains'. Each strain confers a distinct phenotype and replicates at different rates depending on the environment. As replicators, prions are units of selection. Thus, natural selection inescapably enriches or depletes various prion strains from populations depending on their conformational fitness (ability to self-replicate) in the prevailing environment. The most successful prions confer advantages to their host as with numerous yeast prions. Here, I review recent evidence that drug-like small molecules can antagonize some prion strains but simultaneously select for drug-resistant prions composed of mammalian PrP or the yeast prion protein, Sup35. For Sup35, the drug-resistant strain configures original intermolecular amyloid contacts that are not ordinarily detected. Importantly, a synergistic small-molecule cocktail counters prion diversity by eliminating multiple Sup35 prion strains. Collectively, these advances illuminate the plasticity of prionogenesis and suggest that synergistic combinatorial therapies might circumvent this pathological vicissitude.

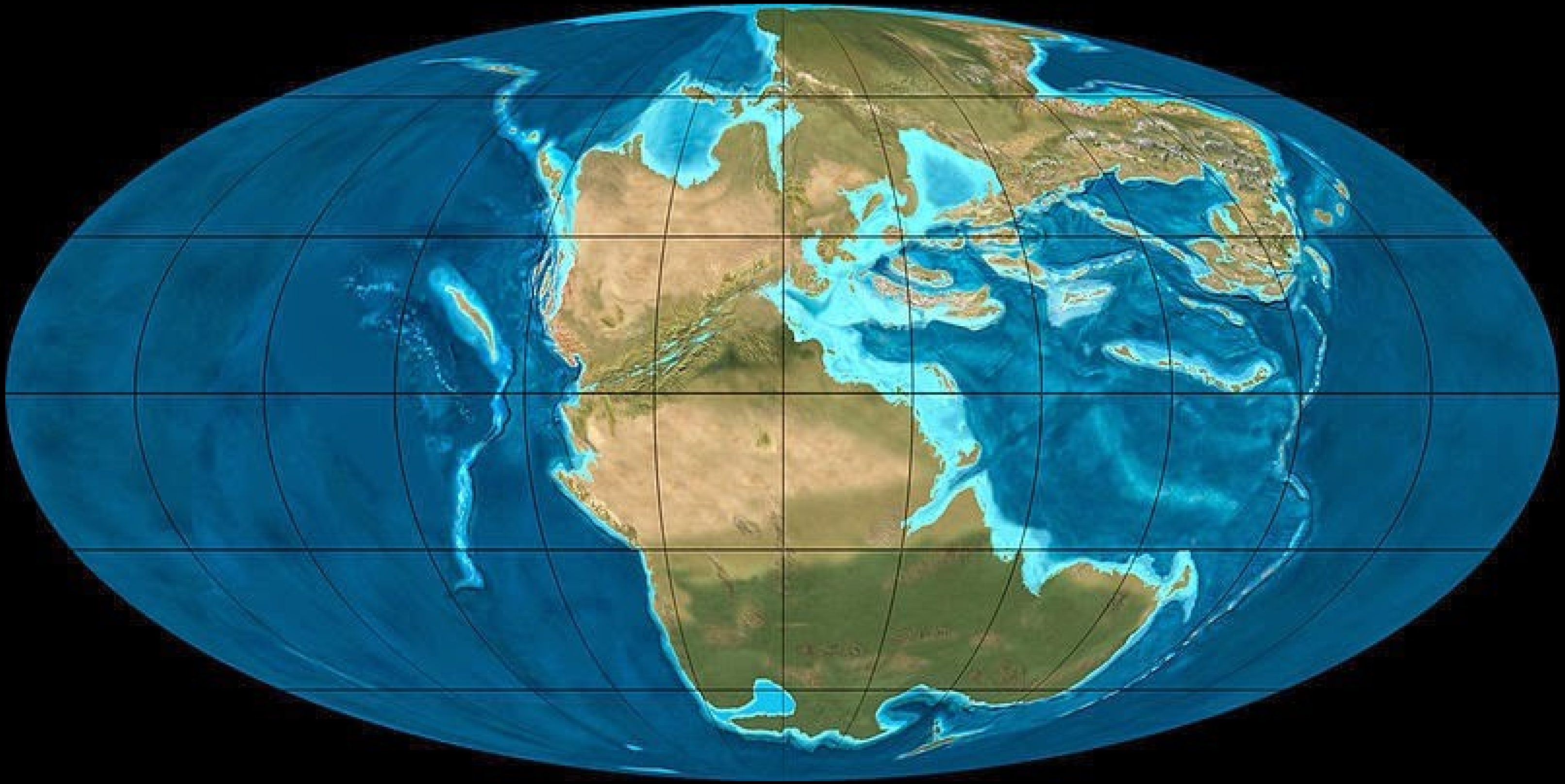


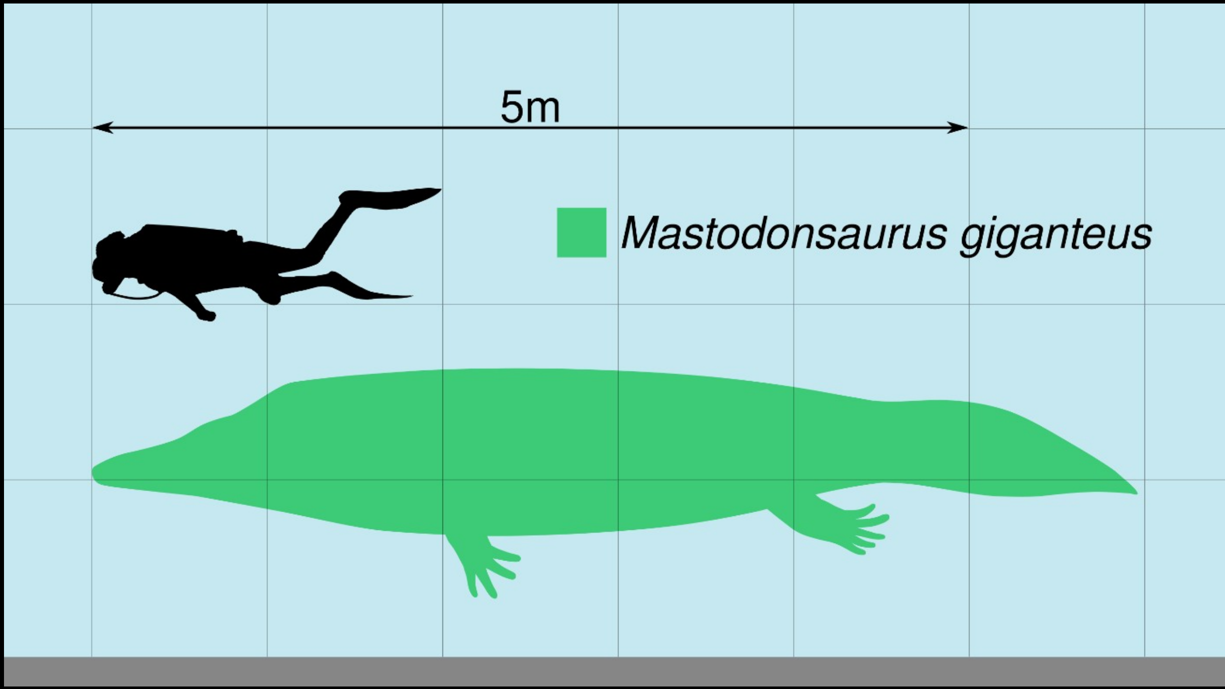
1. Introduction to prion phenomena

1.1 Prions are replicators that store and transmit biological information

Life is based upon the replication, transfer and evolution of specific heritable information. The information that encodes

replicate itself and become infectious.[5,6] Typically, the self-replicating prion conformation is an amyloid template: a 'cross-β' fibrous structure in which the β-sheet strands align orthogonal to the fiber axis.[5–16] This highly stable conformation resists chaotropes, detergents, proteases and mechanical stress,[17–19] and confers the inherent specificity of the self-

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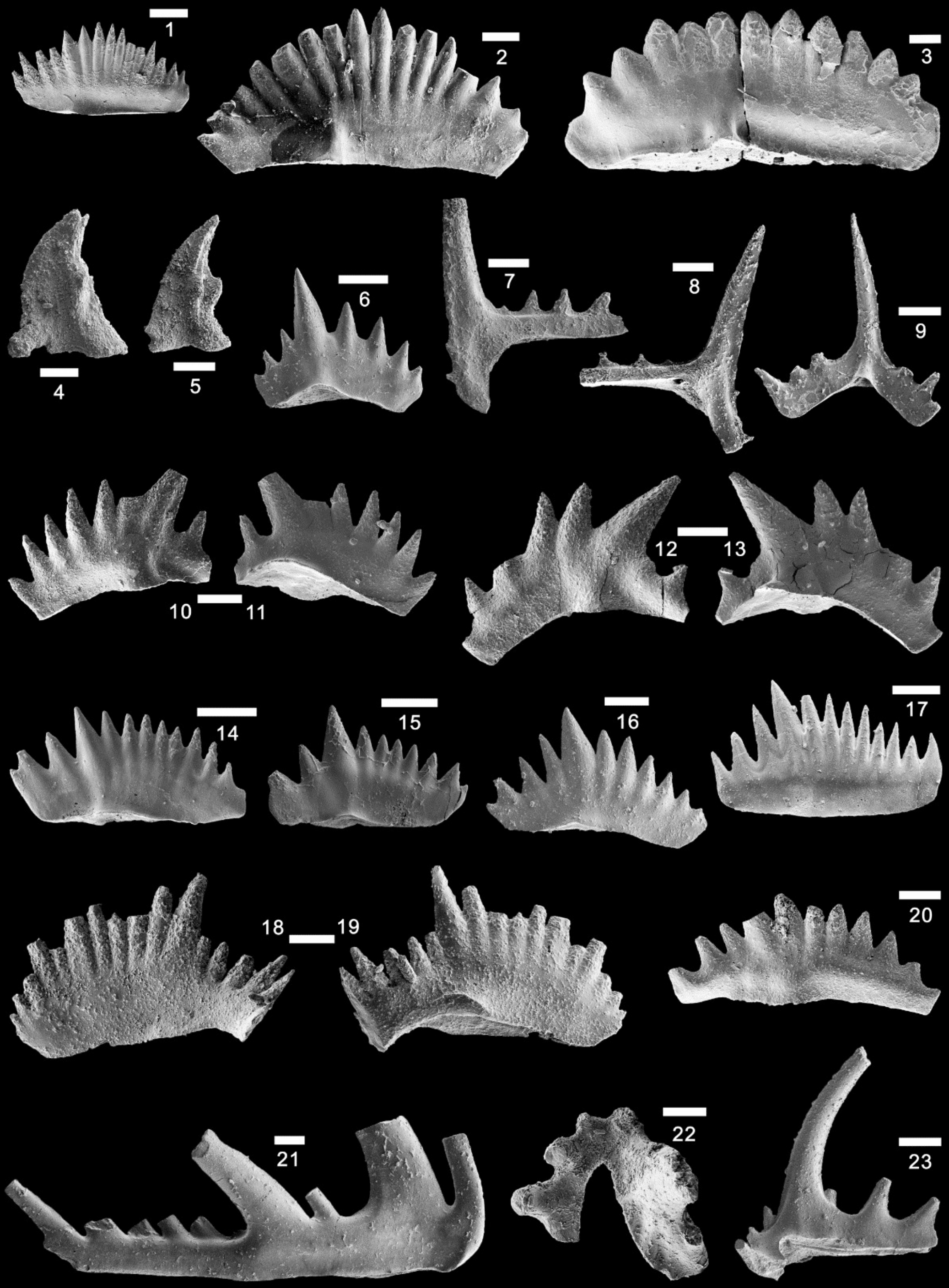

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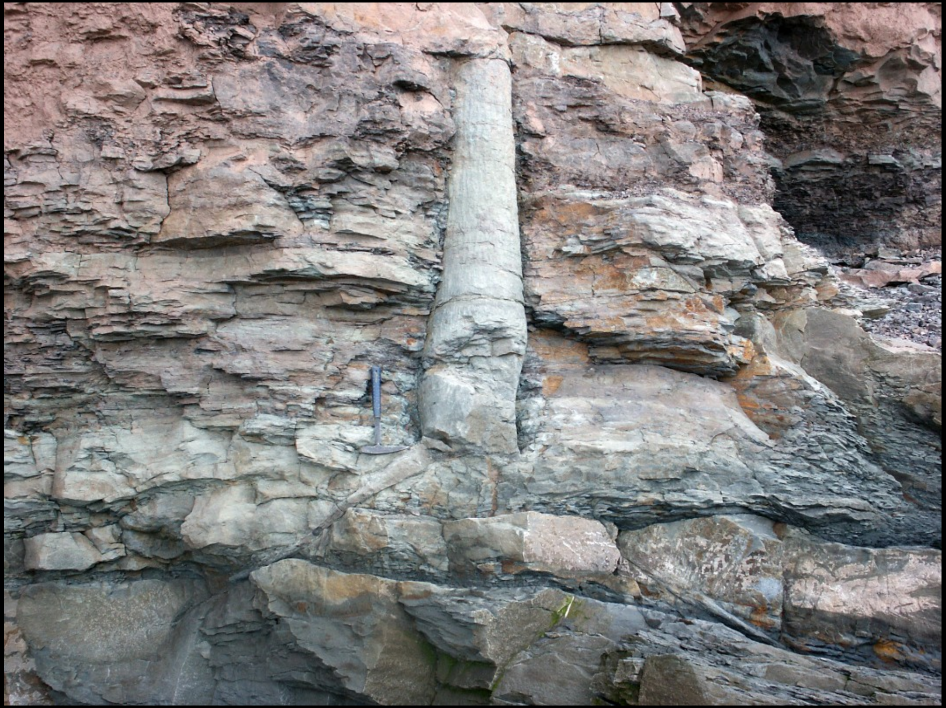

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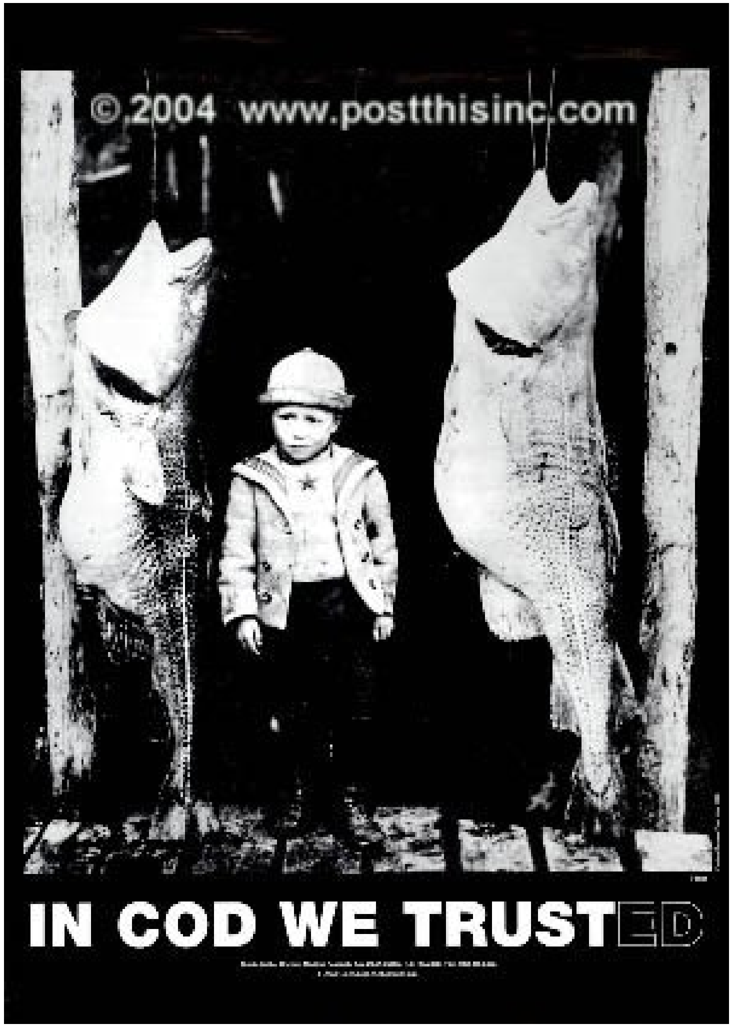

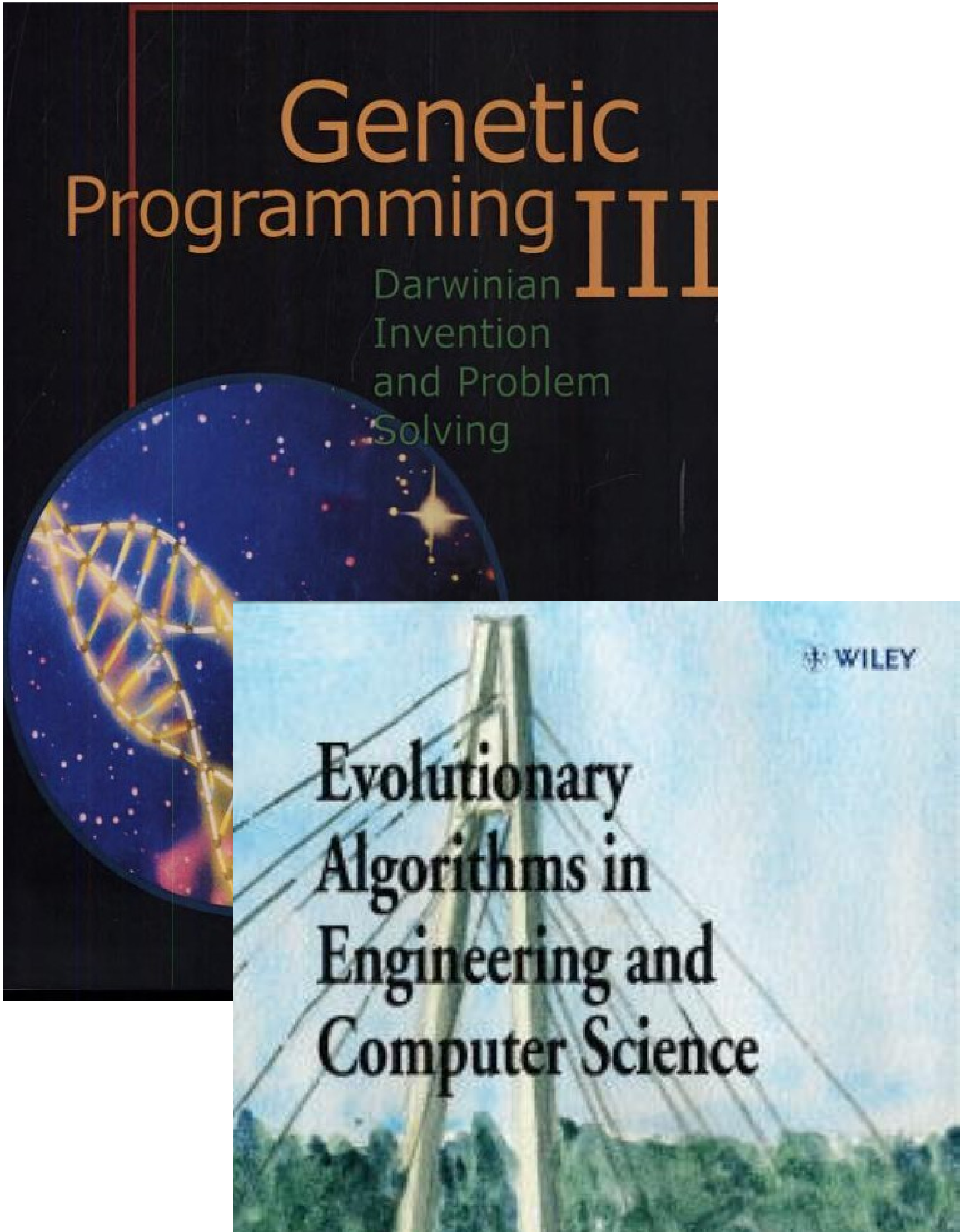
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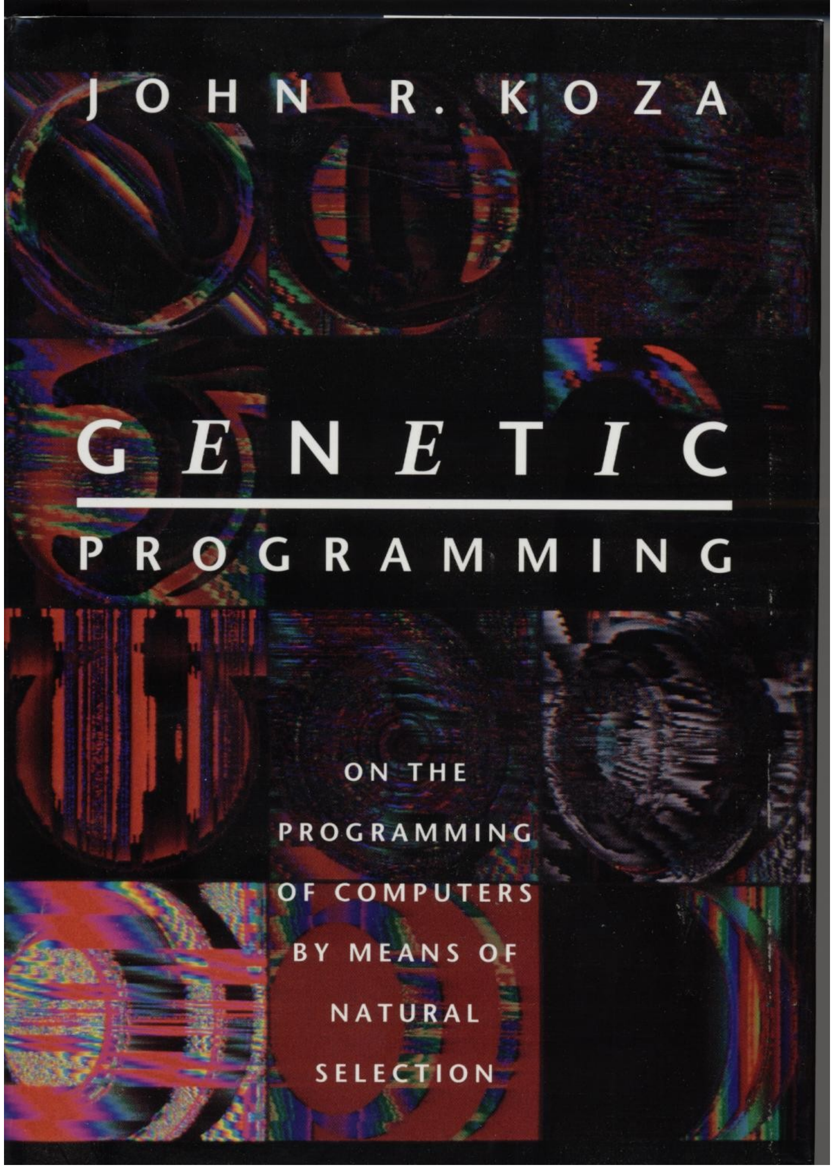
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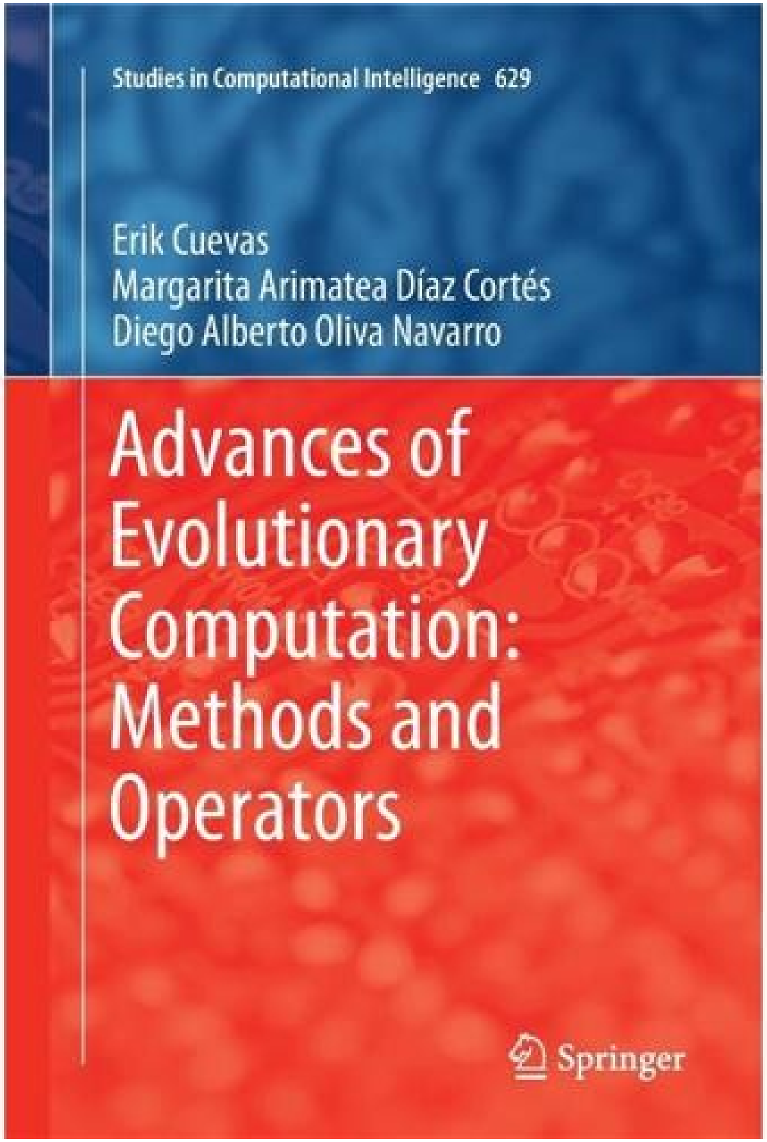

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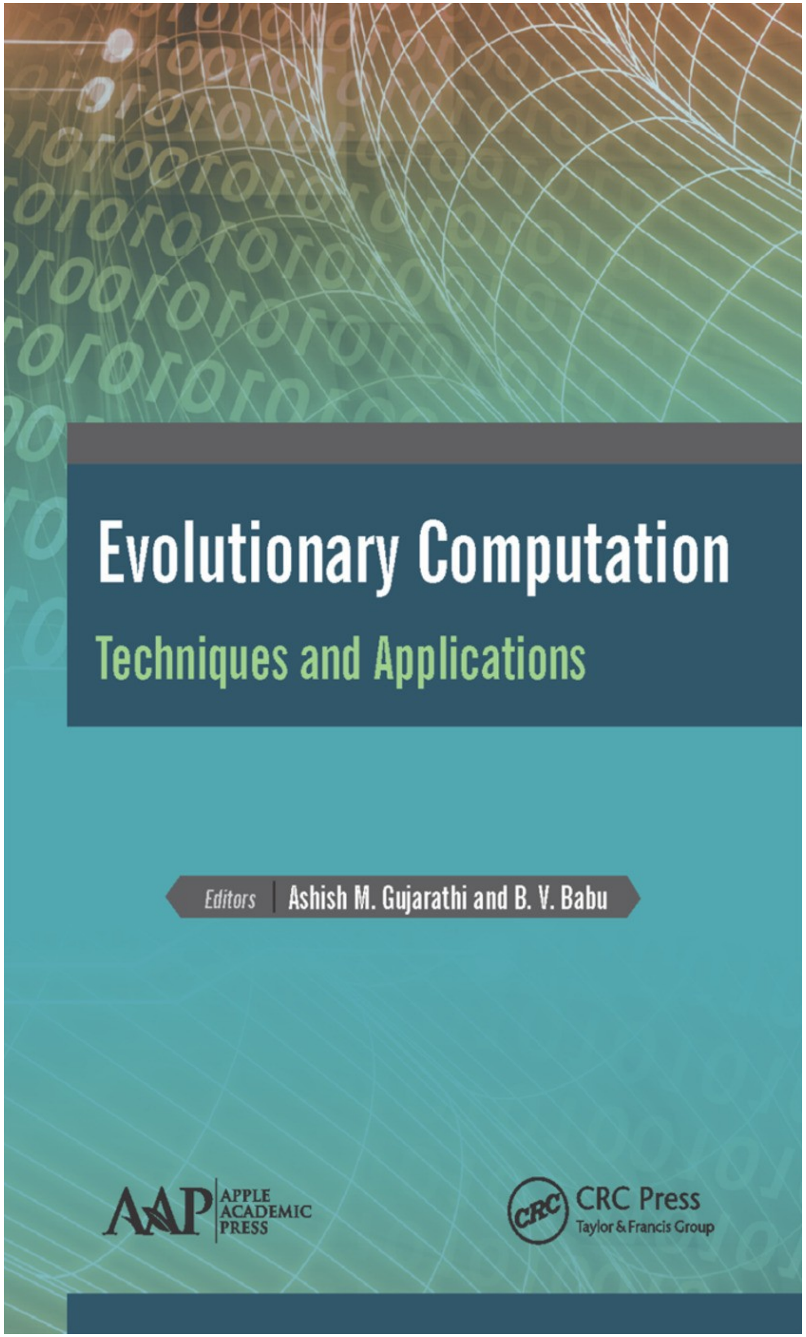

Evolutionary Computation

Techniques and Applications

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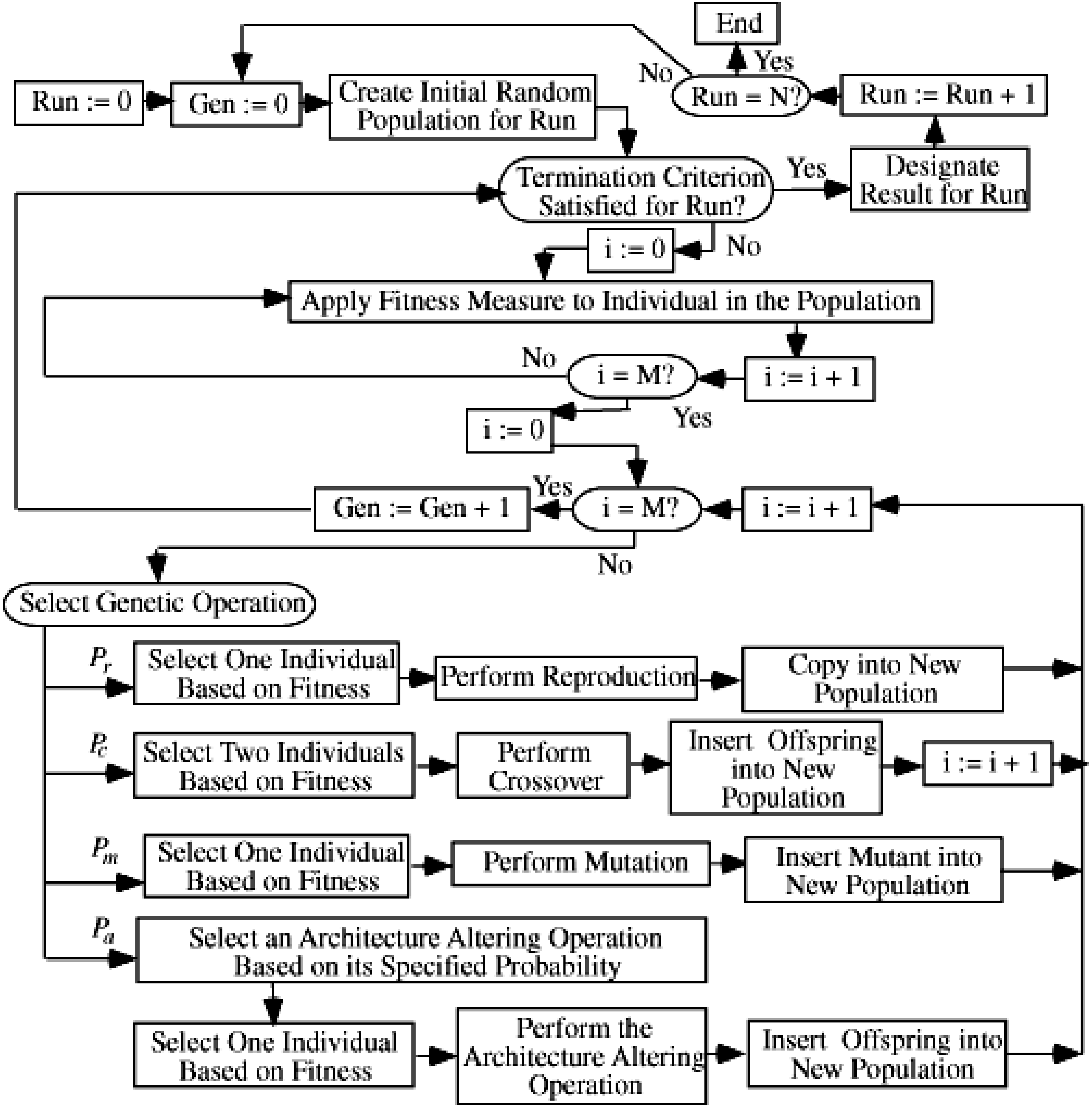

End
Yes
No
Run = N?
Run := Run + 1
Run := 0
Gen := 0
Create Initial Random Population for Run
Termination Criterion Satisfied for Run?
Yes
Designate Result for Run
i := 0
No
Apply Fitness Measure to Individual in the Population
No
i = M?
i := i + 1
i := 0
Yes
Yes
Gen := Gen + 1
i = M?
i := i + 1
No
Select Genetic Operation
P_r
Select One Individual Based on Fitness
Perform Reproduction
Copy into New Population
P_c
Select Two Individuals Based on Fitness
Perform Crossover
Insert Offspring into New Population
i := i + 1
P_m
Select One Individual Based on Fitness
Perform Mutation
Insert Mutant into New Population
P_a
Select an Architecture Altering Operation Based on its Specified Probability
Select One Individual Based on Fitness
Perform the Architecture Altering Operation
Insert Offspring into New Population

“Programação Genética realiza a síntese automática de programas usando a seleção natural Darwiniana e operações biologicamente-inspiradas, como recombinação, mutação, inversão, duplicação e deleção gênicas.”

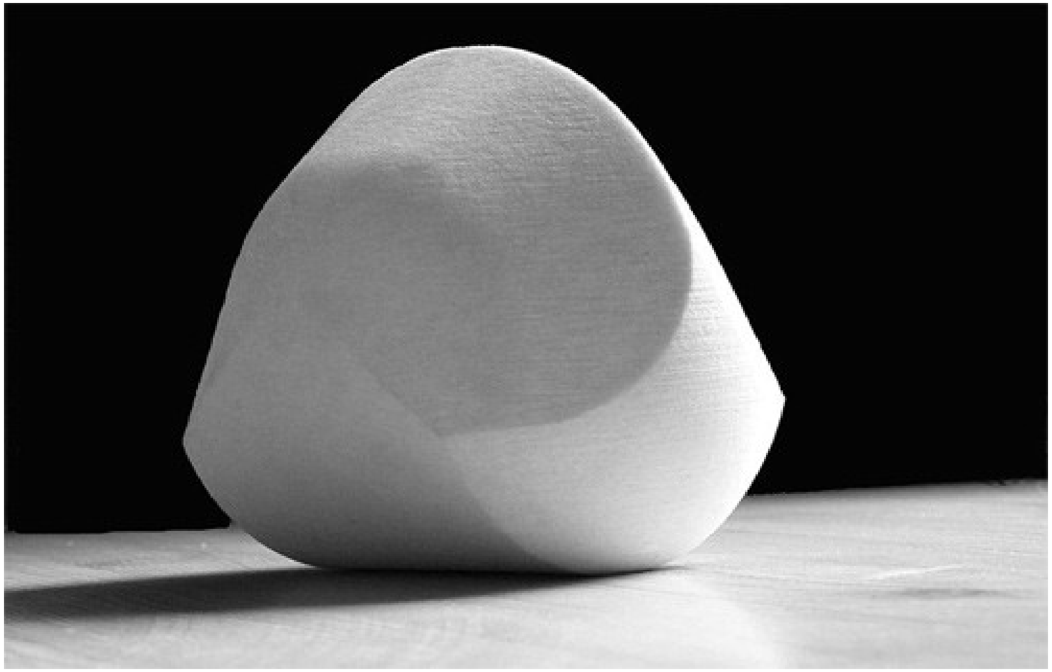
Evolved Antenna

Among the new technologies to be tested aboard the ST5 spacecraft is an antenna that was designed by a computer running a simulation of Darwinian evolution. This evolved antenna was discovered by an evolutionary algorithm running for days on a supercomputer. Its unusual shape is expected because most human antenna designers would never think of such a design. However, this design works very well in meeting the mission requirements. In addition, this particular design was rapidly evolved after the orbit changed from the original orbit. Each ST5 spacecraft will have one evolved antenna installed.

Back

an **evolved antenna** is an antenna designed fully or substantially by an automatic computer design program that uses an evolutionary algorithm that mimics Darwinian evolution. This procedure has been used in recent years to design a few antennas for mission-critical applications involving stringent, conflicting, or unusual design requirements, such as unusual radiation patterns, for which none of the many existing antenna types are adequate.

the computer repeats the procedure, generating a successive population (using operators such as mutation, crossover, and selection) from which the higher-scoring designs are selected. After a number of iterations, the population of antennas is evaluated and the highest-scoring design is chosen. The resulting antenna often outperforms the best manual designs, because it has a complicated asymmetric shape that could not have been found with traditional manual design methods.



Gábor Domokos and Péter Várkonyi

“We discovered it with mathematics, but evolution got there first.”