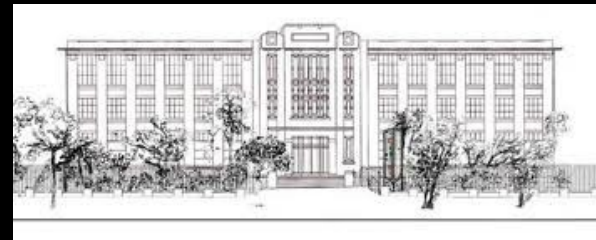


Escola de Astrobiologia

Observatório Nacional

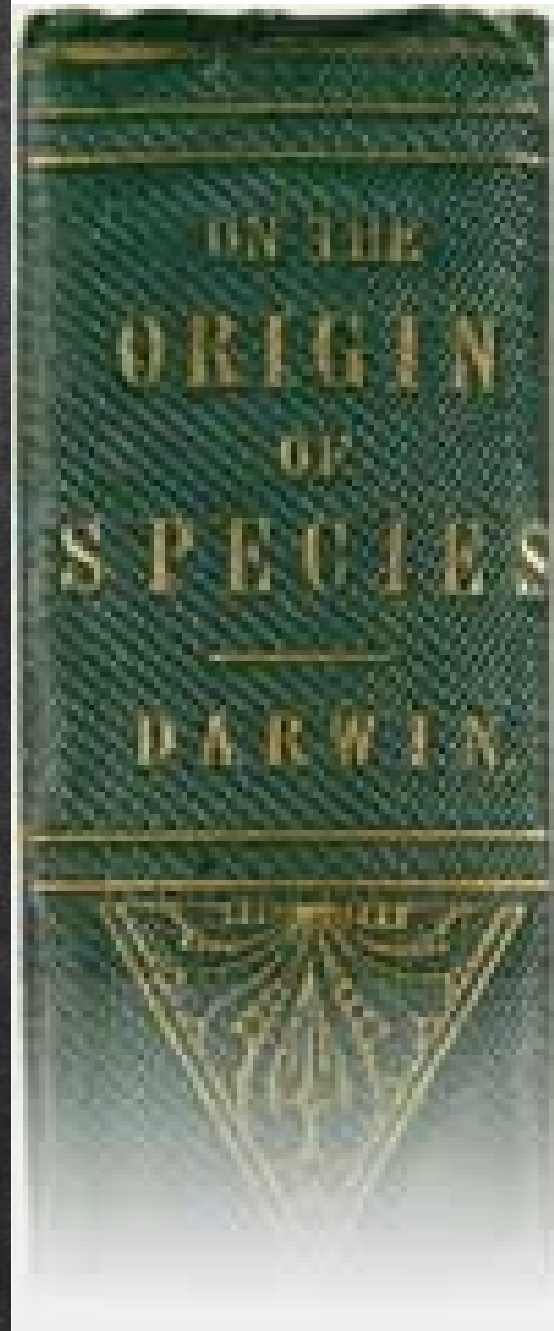
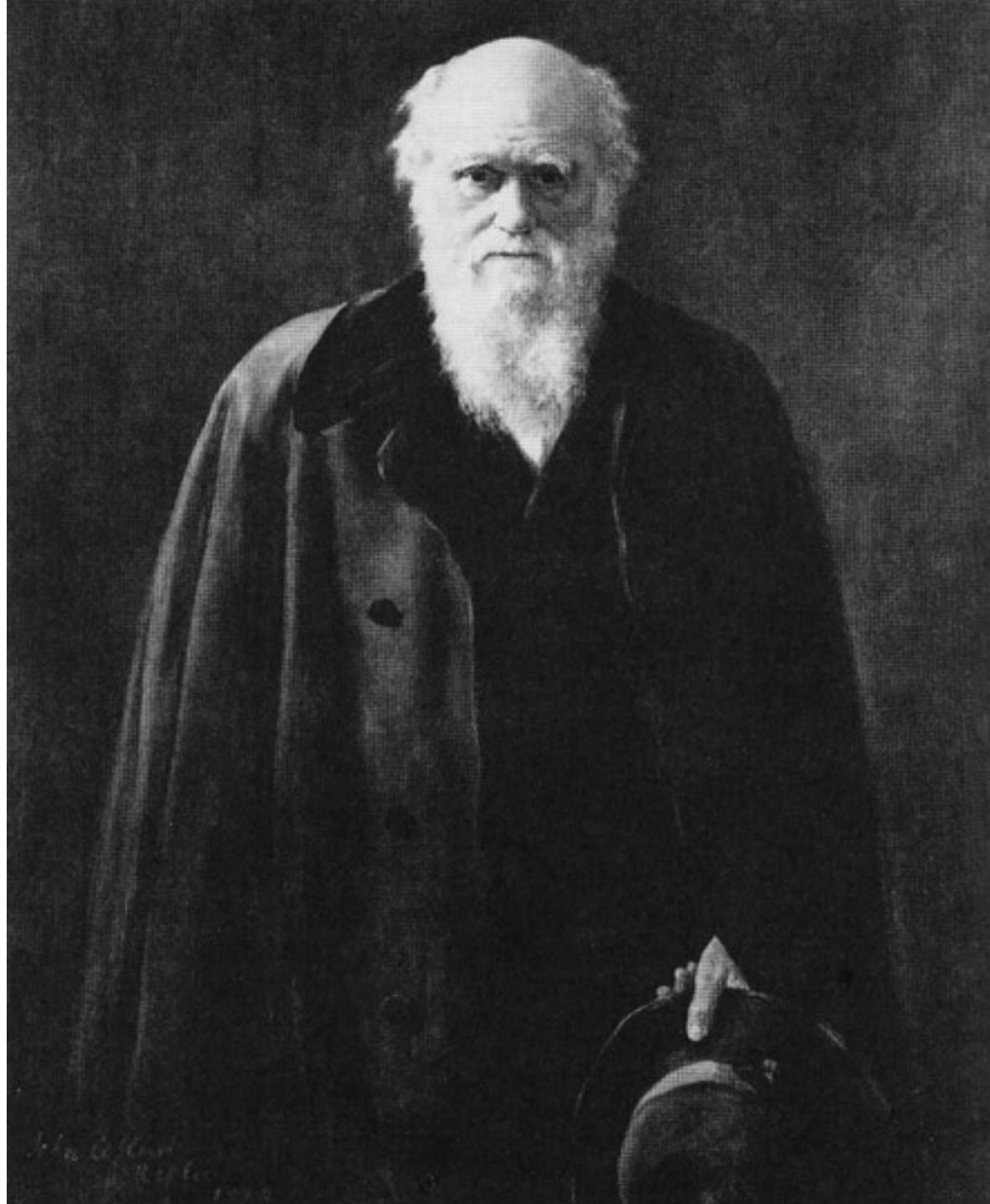
Rio de Janeiro, 16 setembro 2026

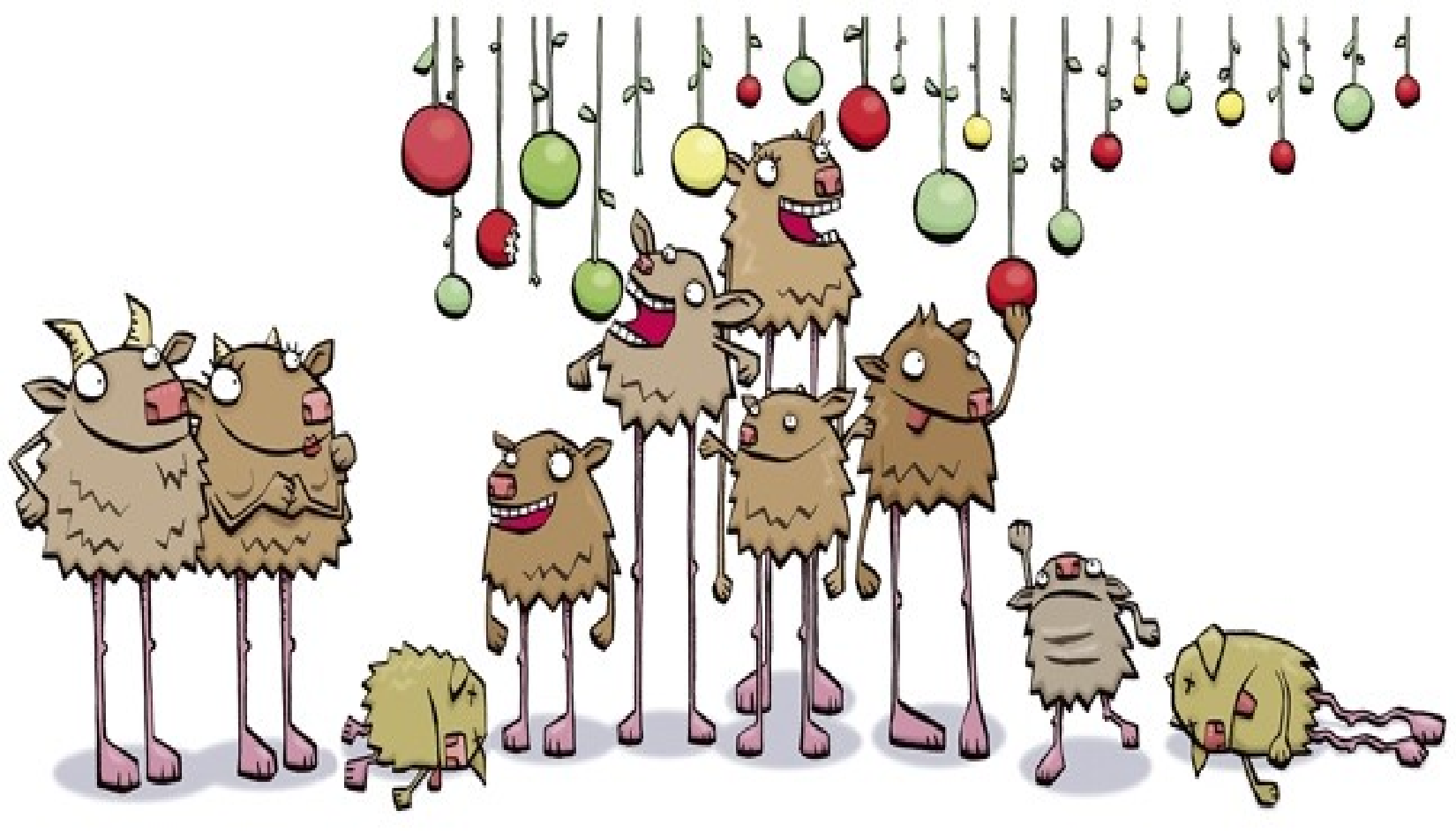
Mário de Pinna
Museu de Zoologia
Universidade de São Paulo



EDEVO  DARWIN
EVOLUÇÃO, DIVULGAÇÃO E EPISTEMOLOGIA DA EVOLUÇÃO BIOLÓGICA

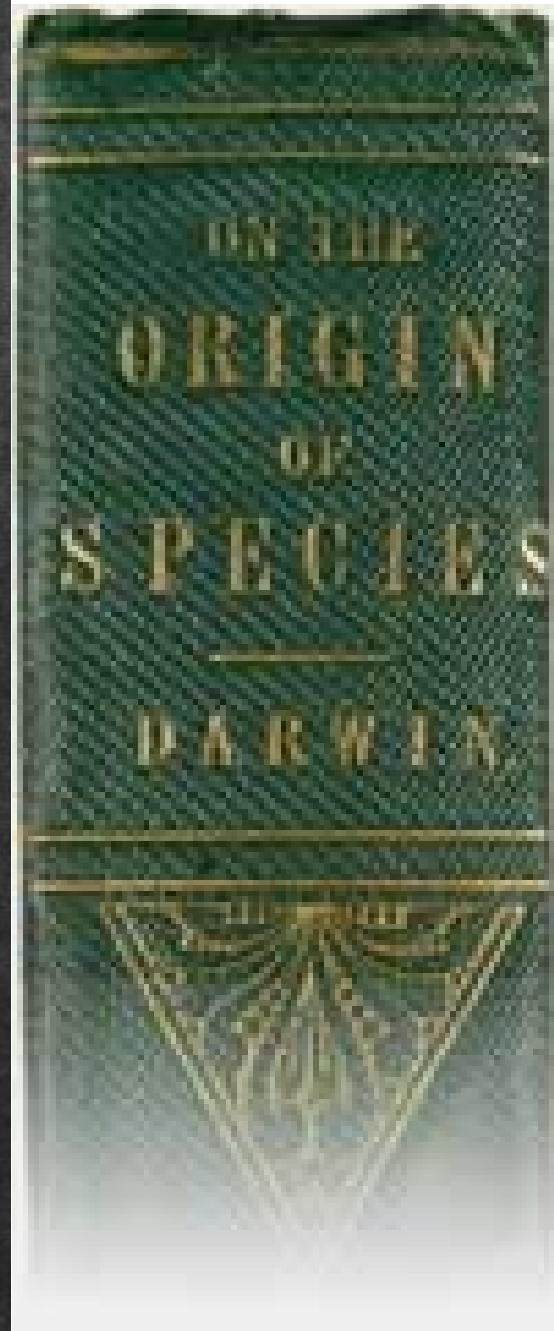
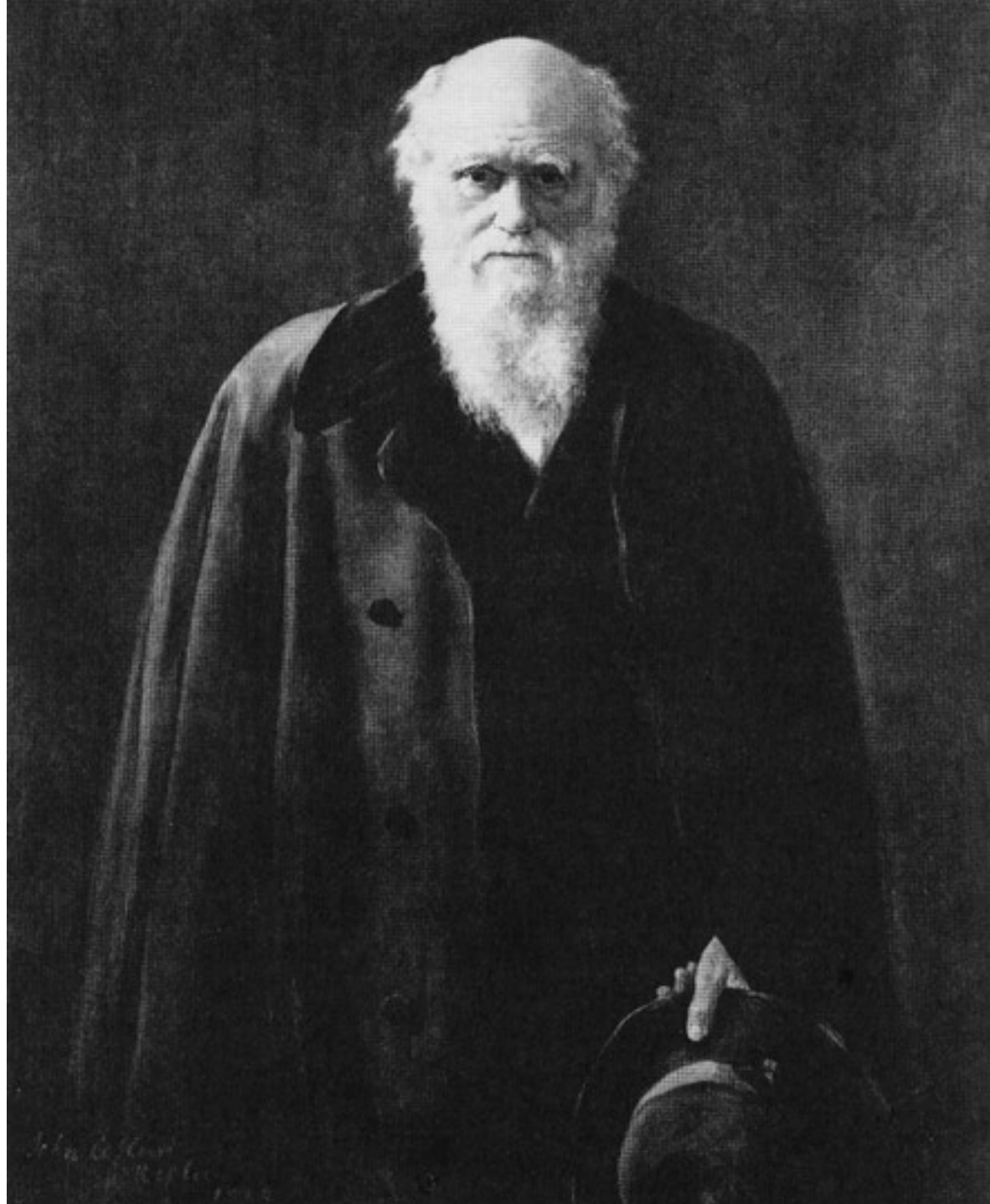
EDEVO  DARWIN





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.



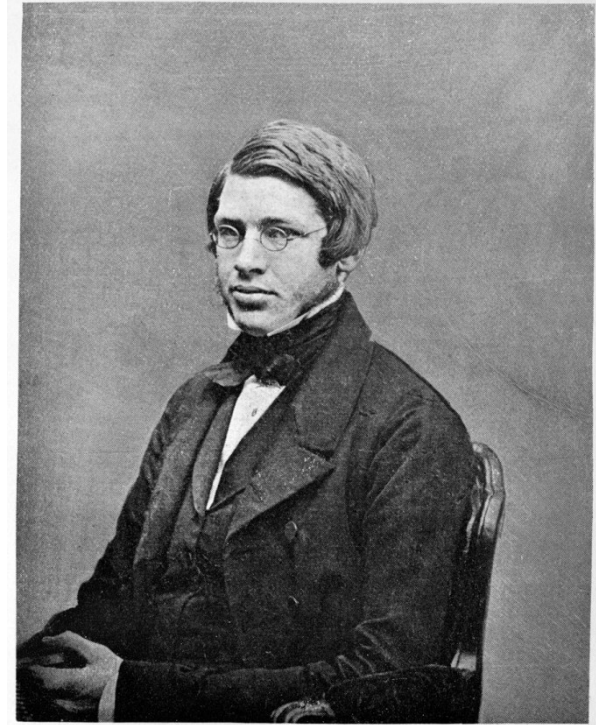
[*From the JOURNAL of the PROCEEDINGS OF THE LINNEAN SOCIETY for
August 1858.*]

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
SELECTION.**

TRUSTING to your
every man should have
hope you will give p
following communication

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 man
forms a selection, and sponte," in organic
discovery recently published as "the results
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 London, 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-boats
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 instinctiv
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.

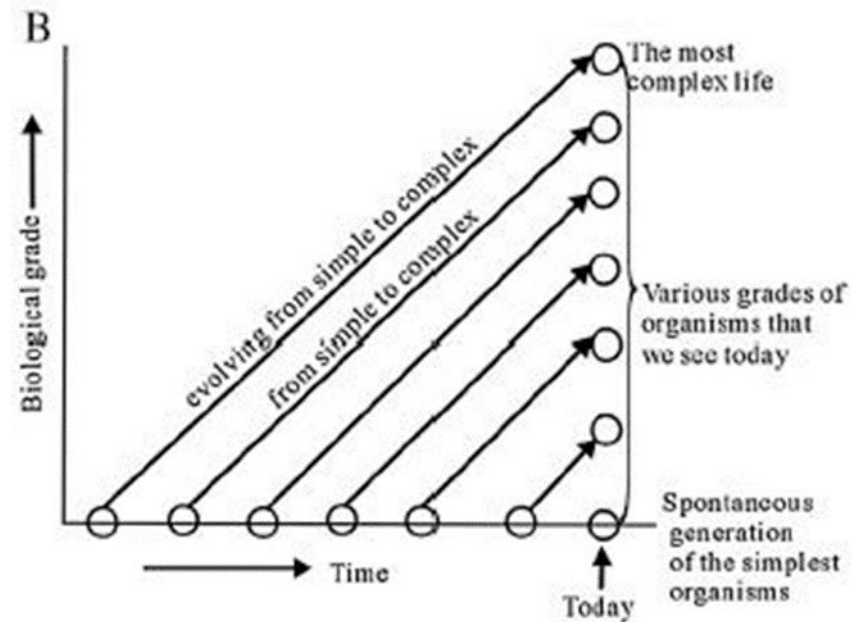
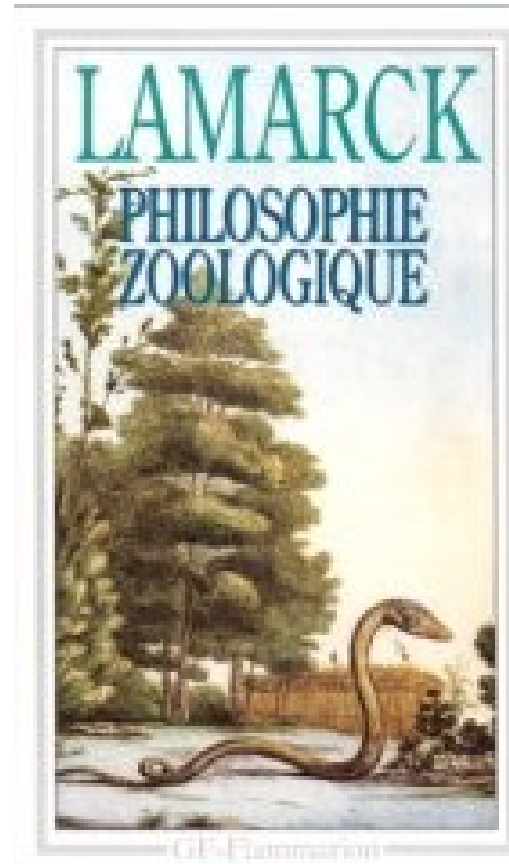
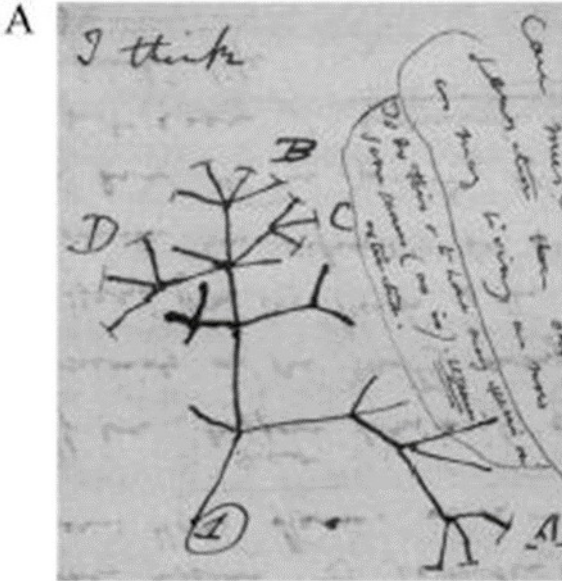
BY THE LATE WILLIAM CHARLES WELLS,
M.D. F.R.S. L. & E.

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.

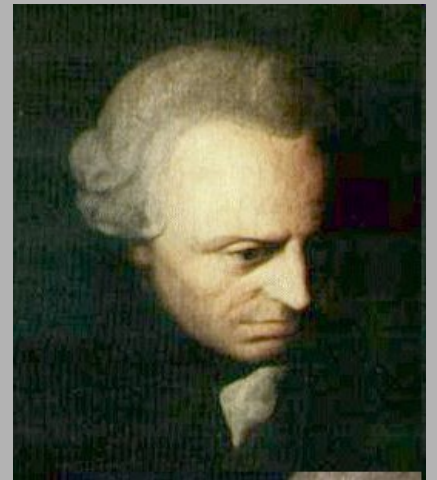
"[What was done for animals artificially] seems to be done with equal efficiency, though more slowly, by nature, in the formation of varieties of mankind, fitted for the country which they inhabit. Of the accidental varieties of man, which would occur among the first scattered inhabitants, some one would 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."

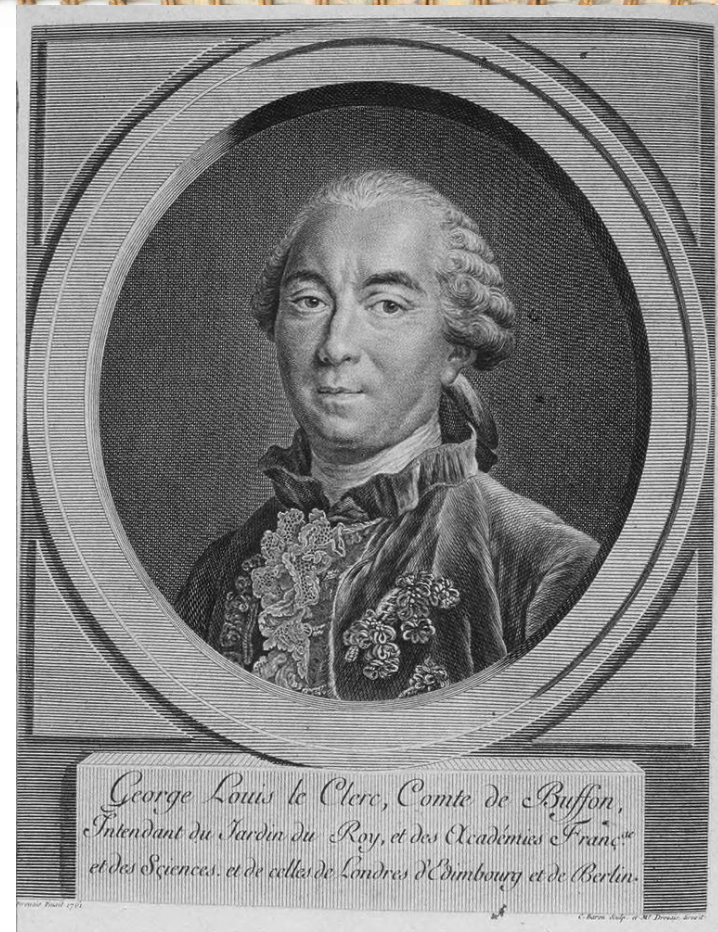
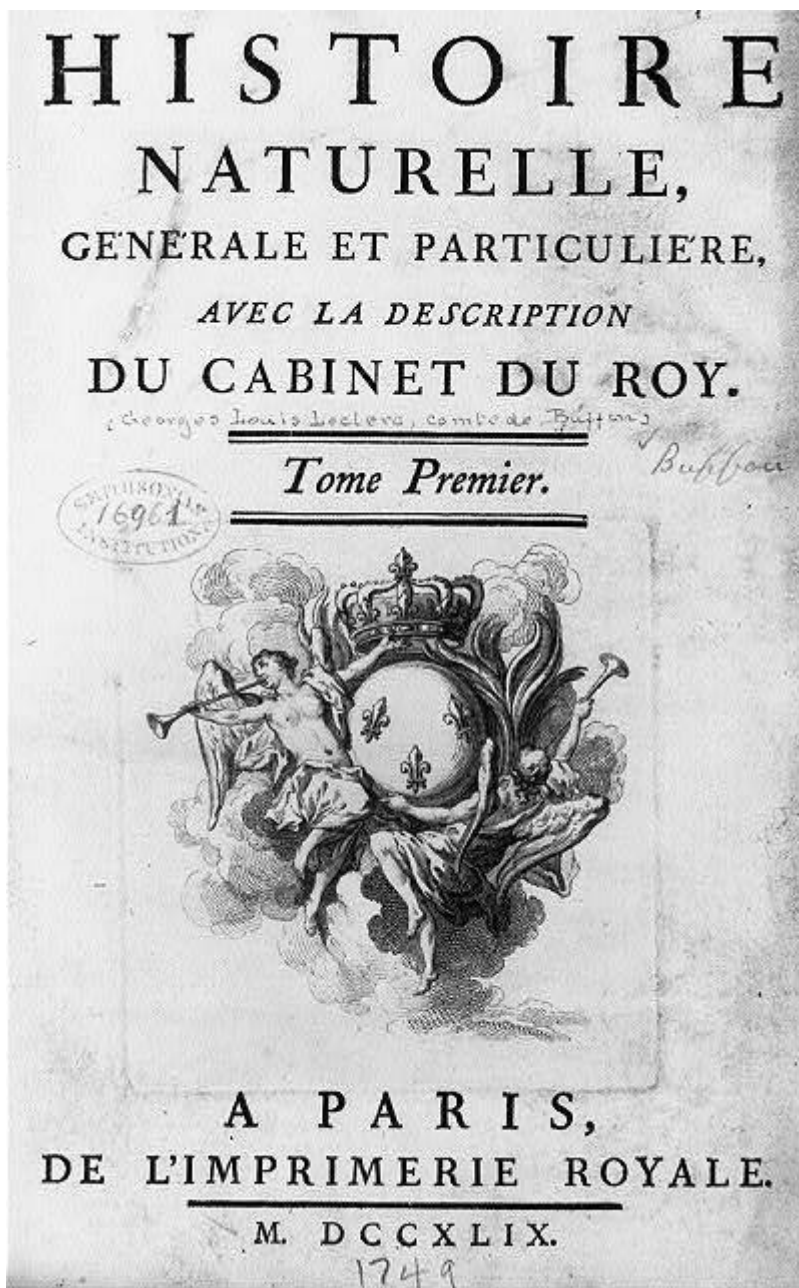
Jean-Baptiste Lamarck (1744-1829)



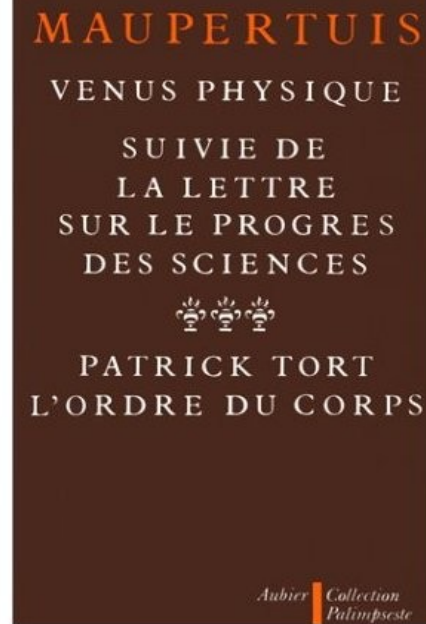
“This analogy of forms supports the supposition that there is among them a real blood relationship, due to the derivation from a common progenitor; a supposition reached by the observation of the gradual approximation of one class of animals to another”

Kant (1790)





(1707-1788)



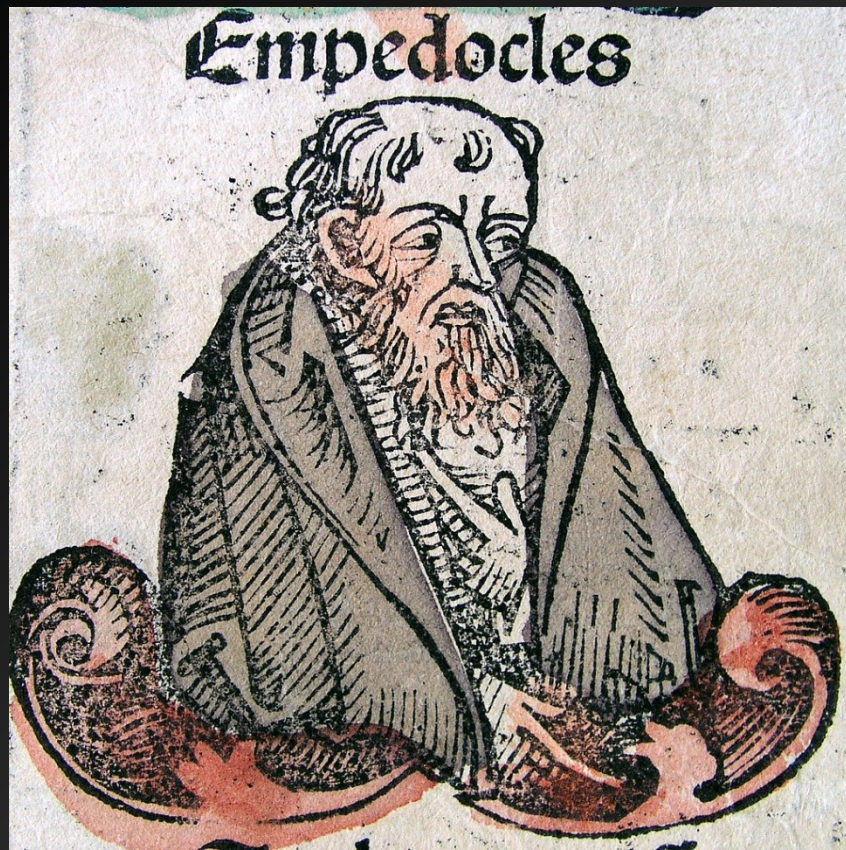
Louis Moreau de Maupertuis
(1698-1759)

“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...”.

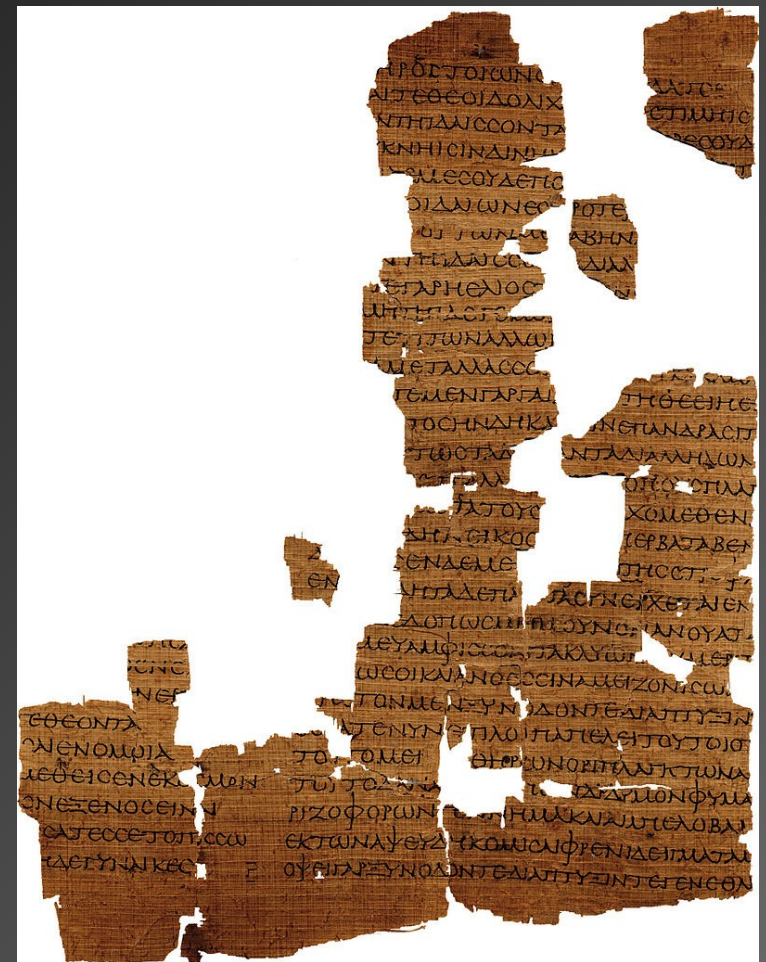
[*Système de la Nature*, 1756]

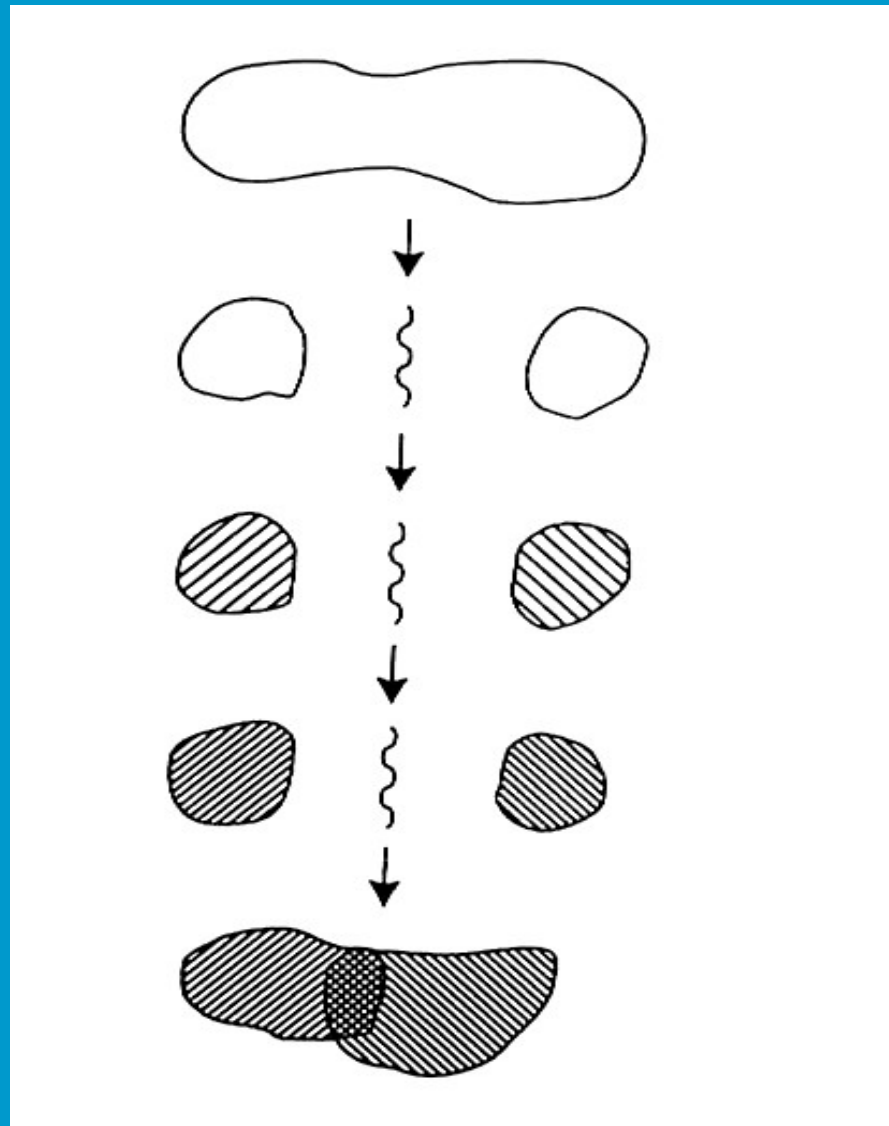
Chance, one might say, turned out a vast number of individuals; a small proportion of these were organized in such a manner that the animals' organs could satisfy their needs. A much greater number showed neither adaptation nor order; these last have all perished. . . . Thus the species which we see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

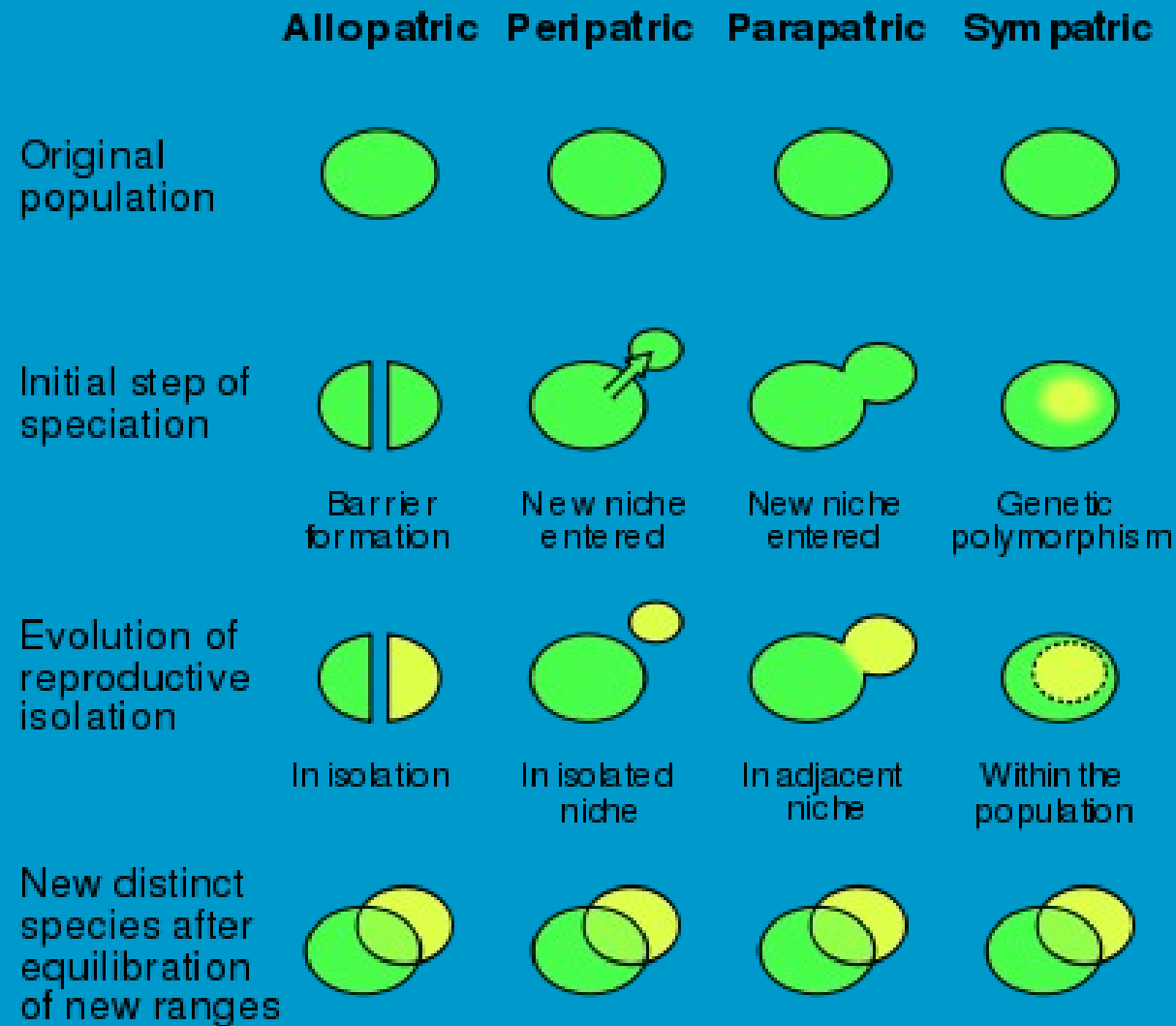
[*Vénus Physique*, 1745]

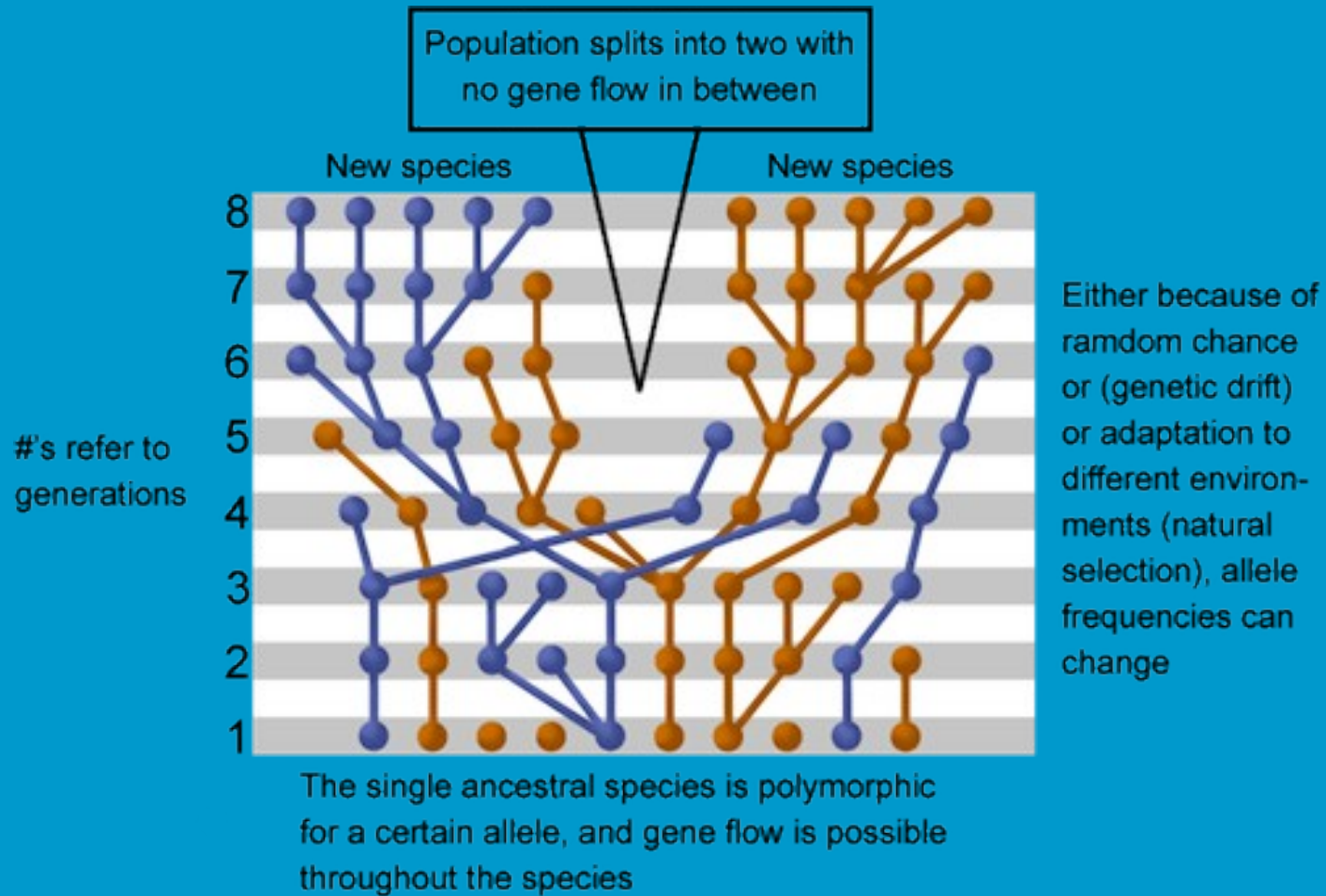


495 BC-430BC

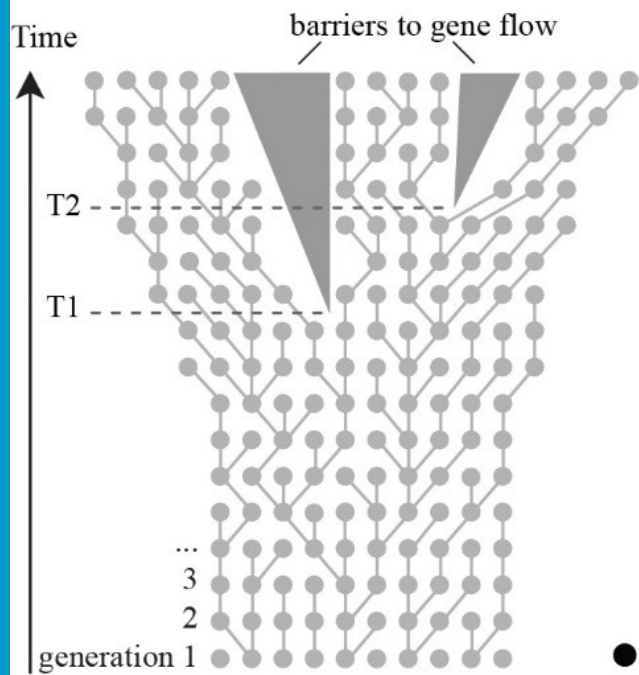




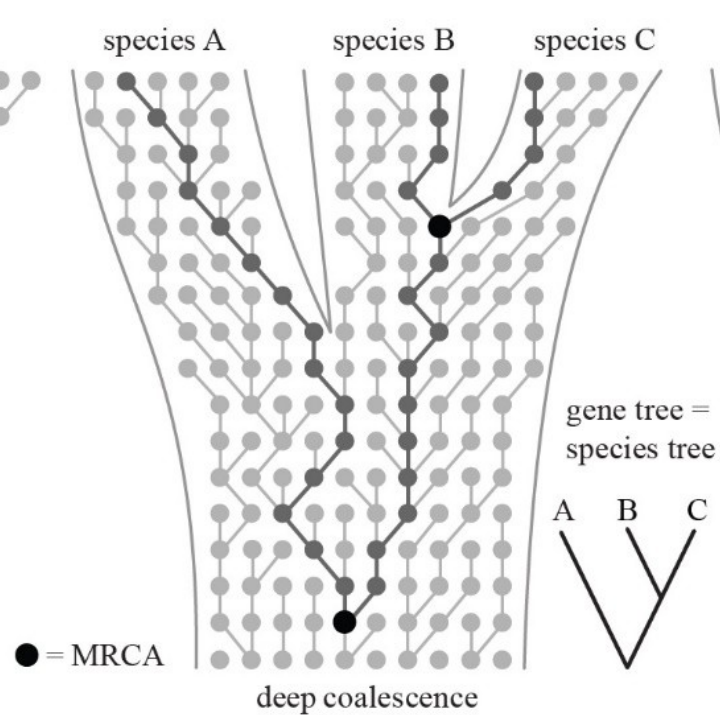




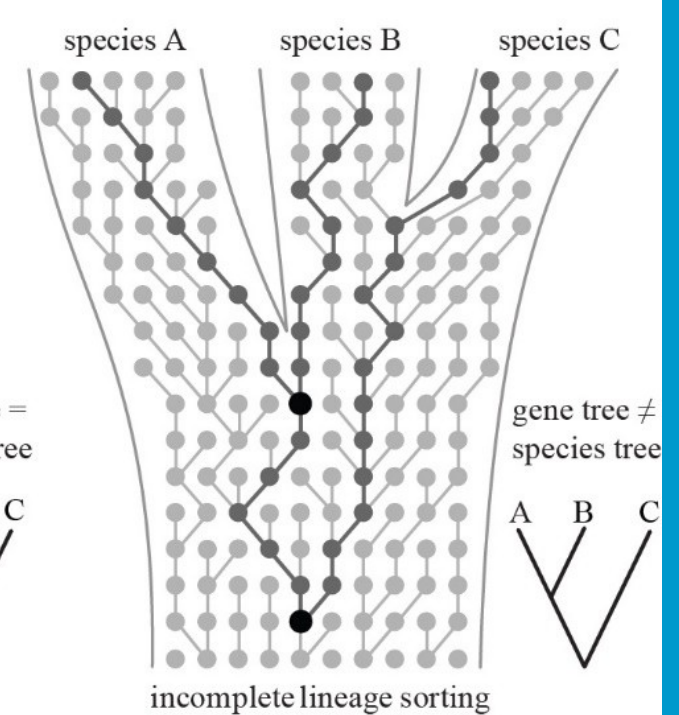
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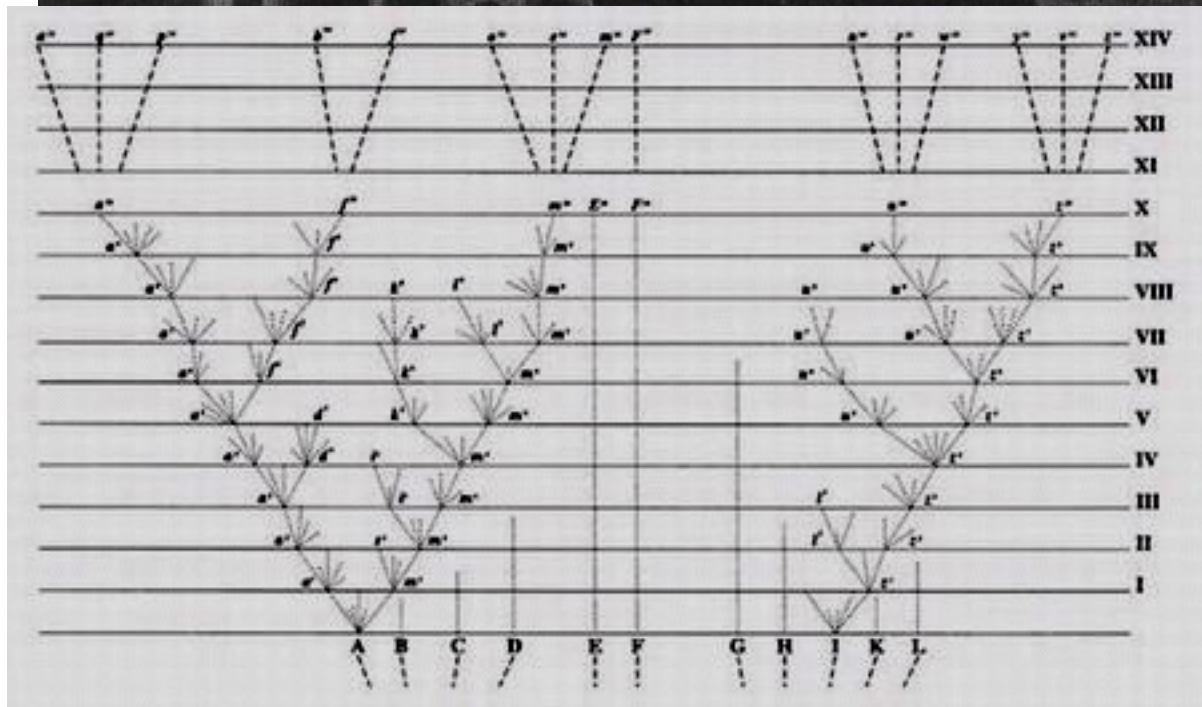
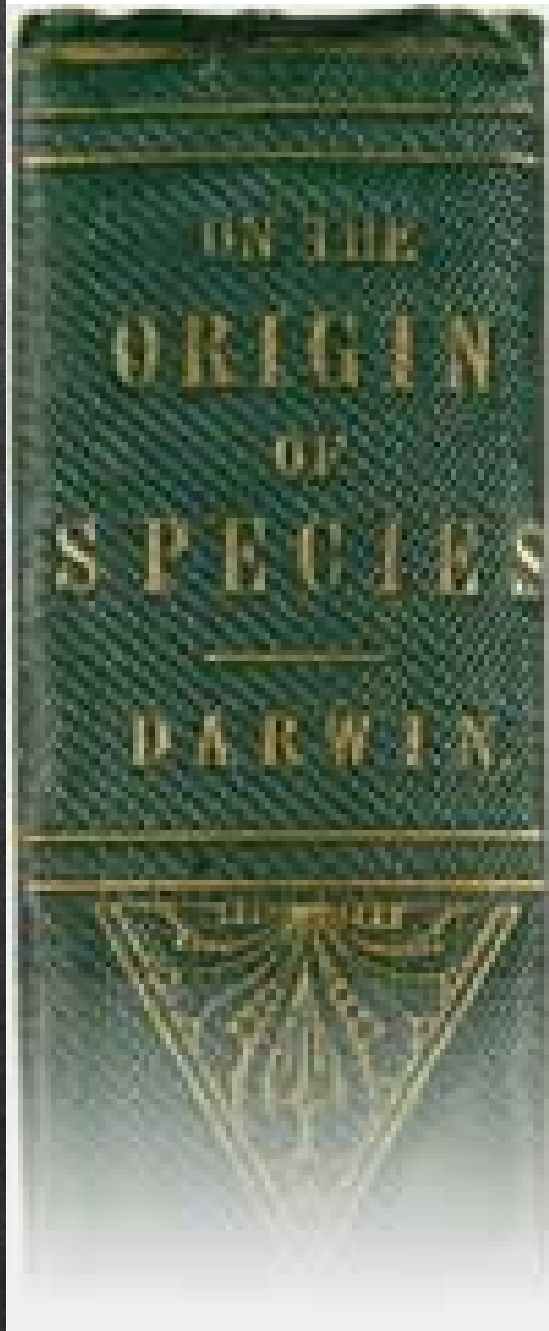
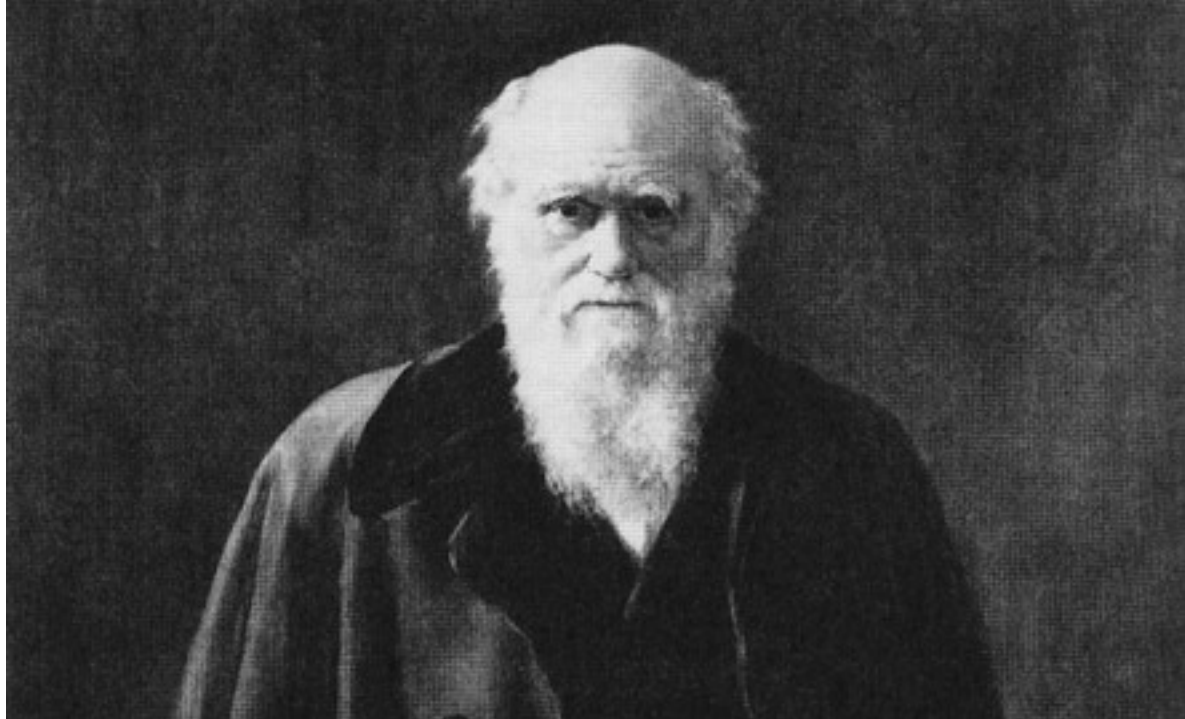


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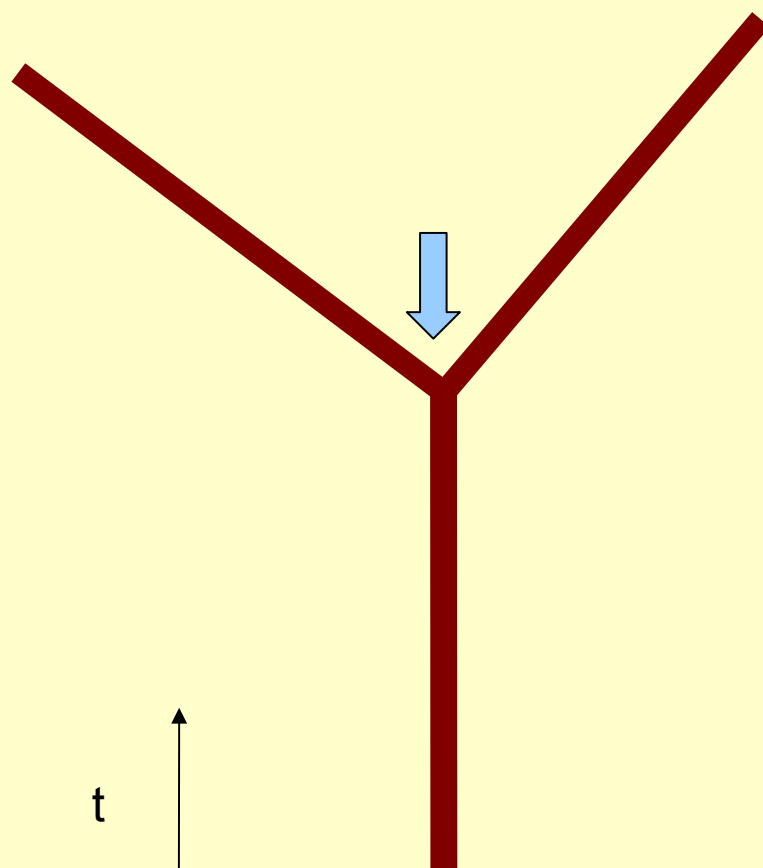
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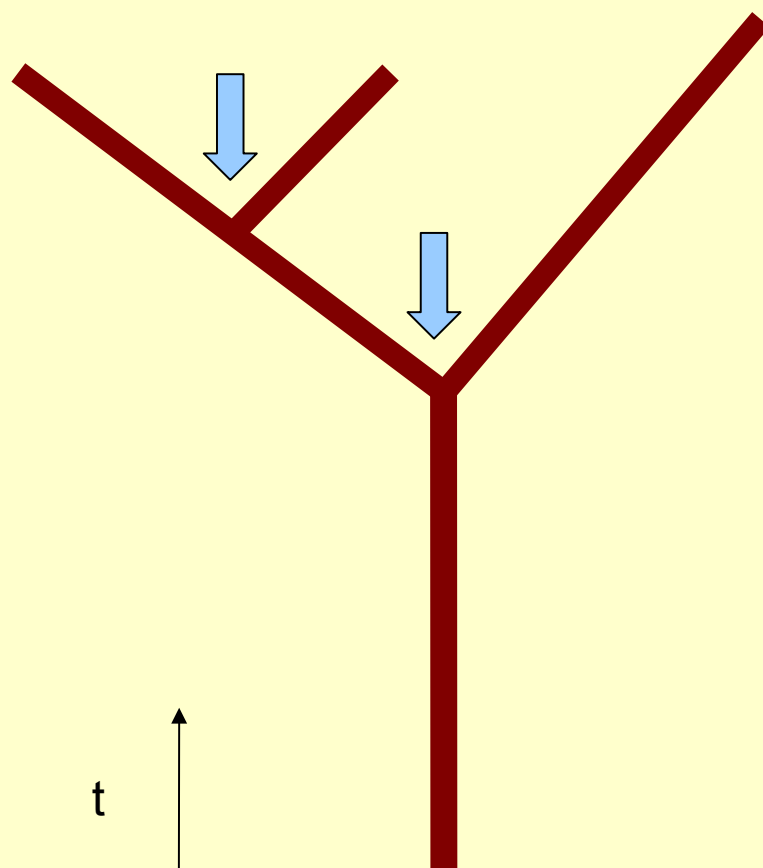


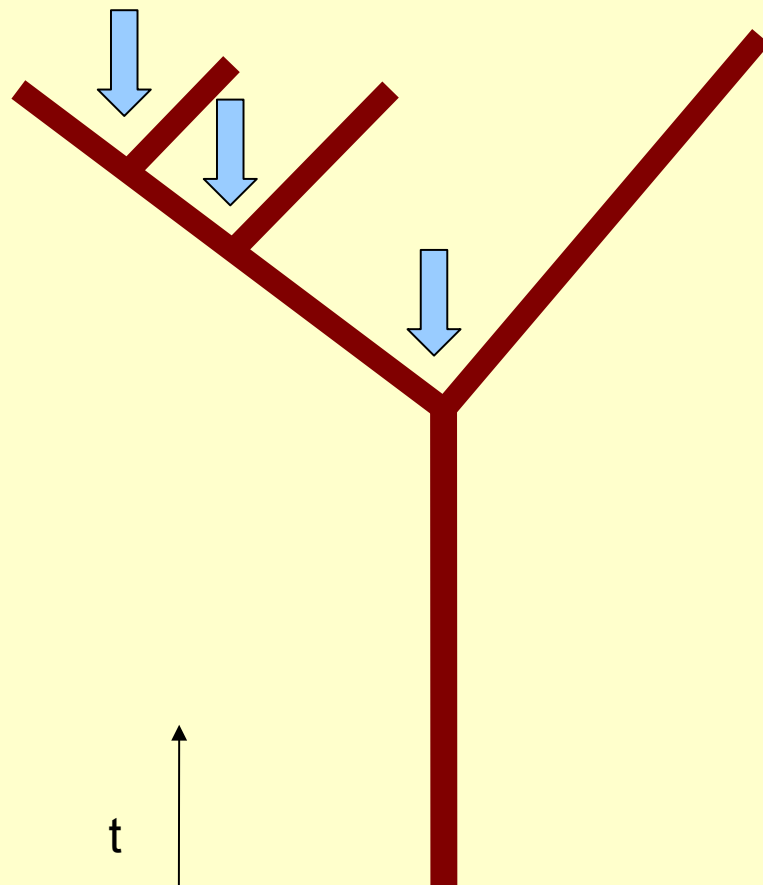


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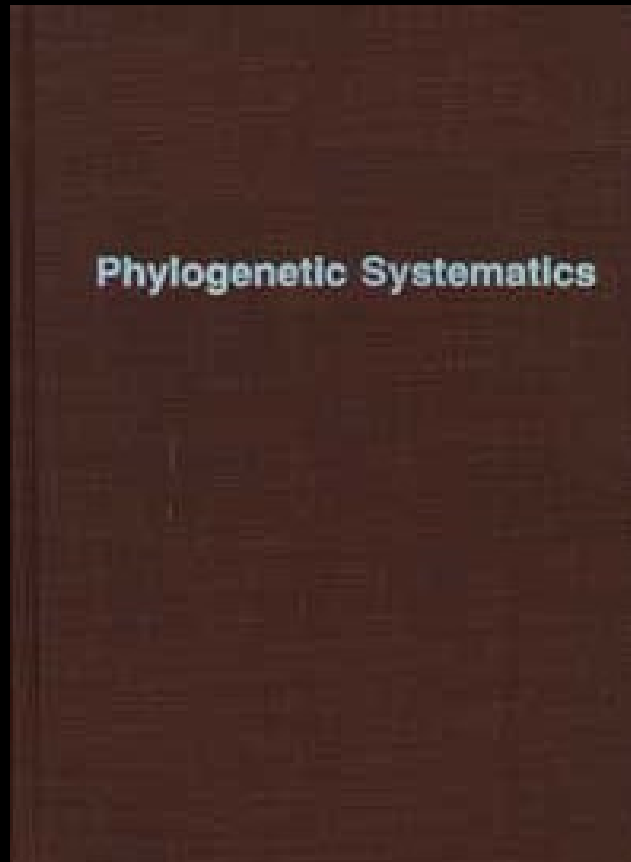








Willi Hennig



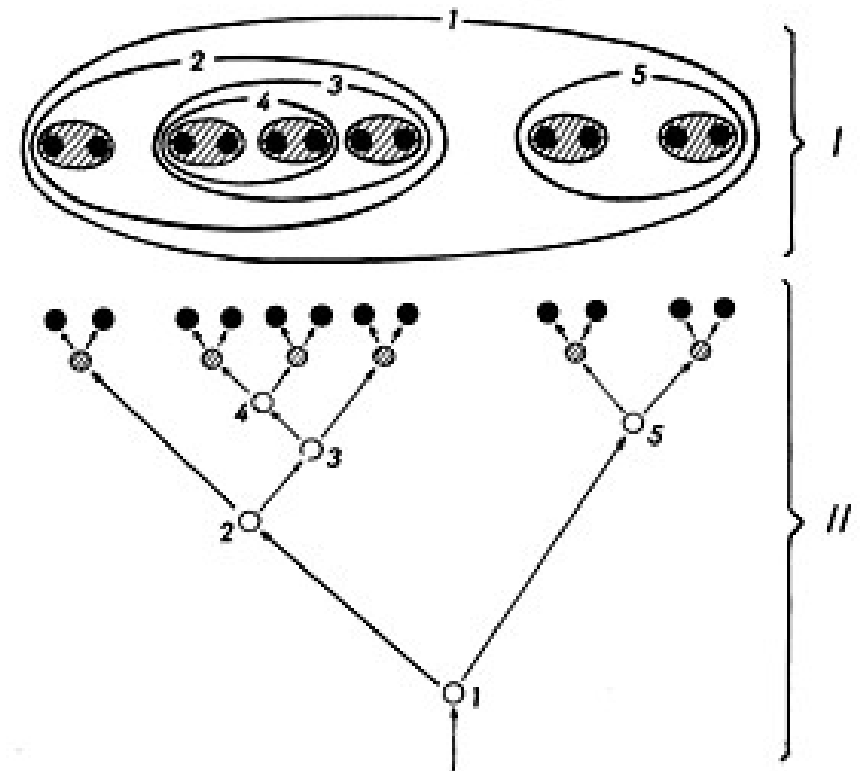
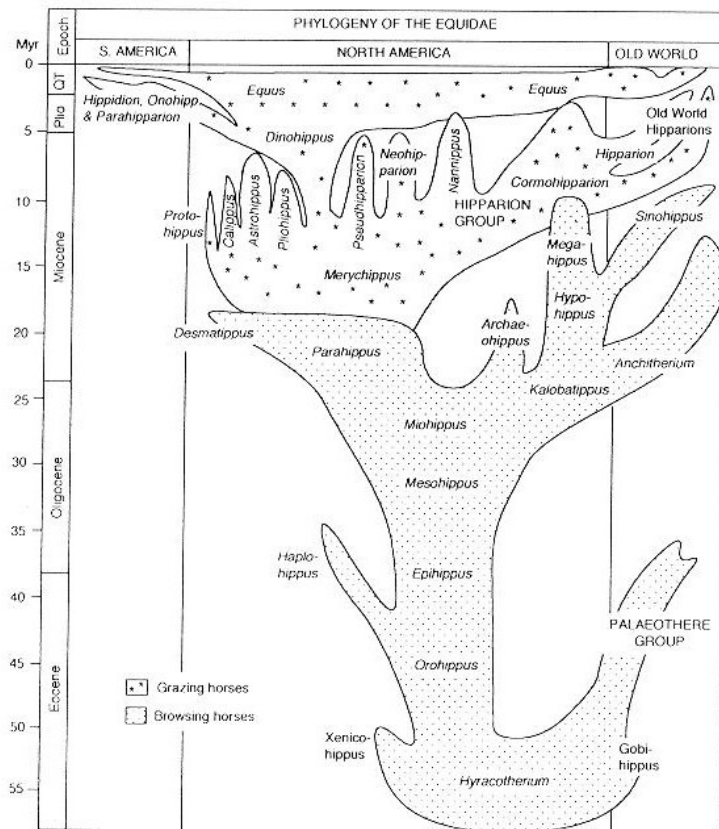
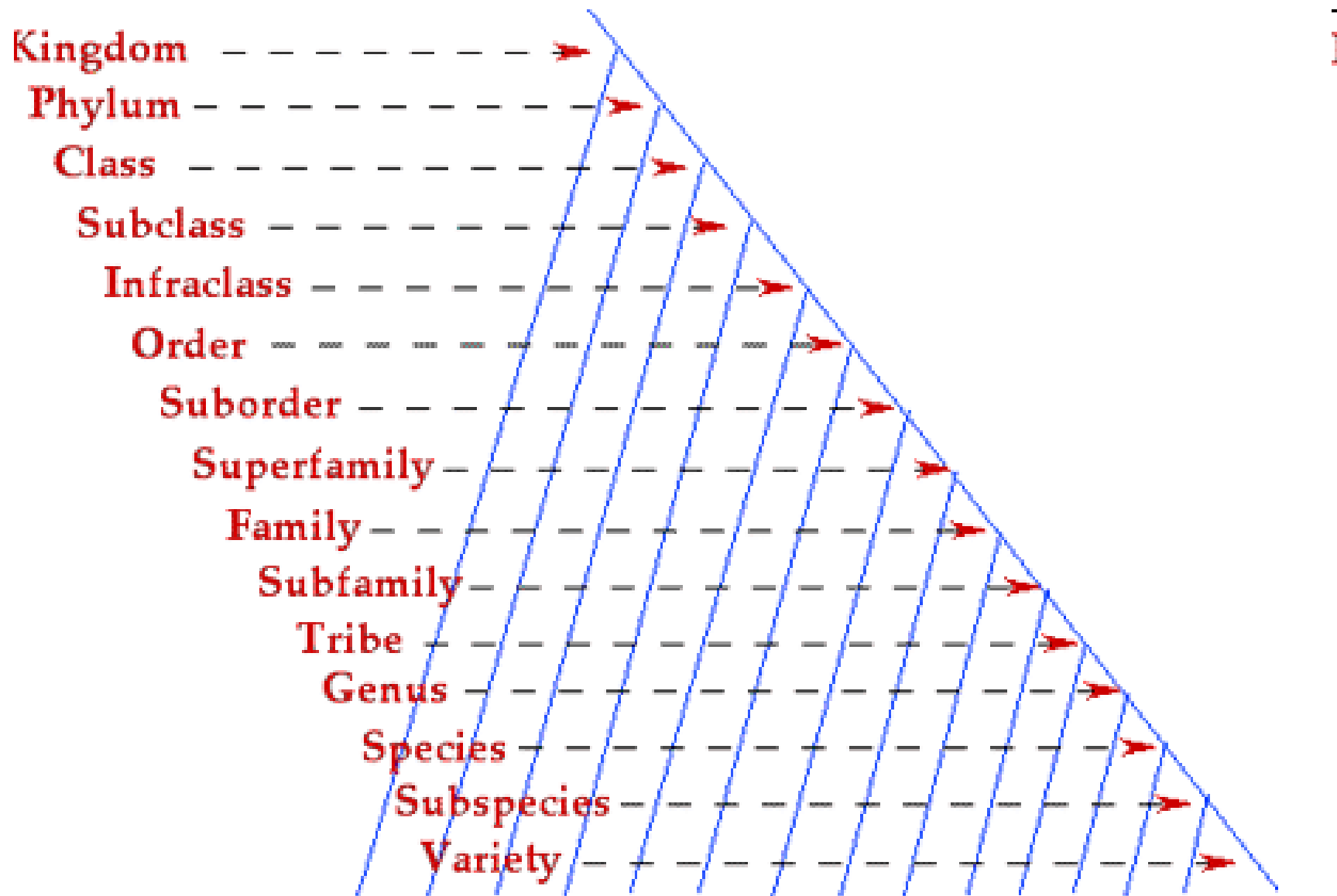
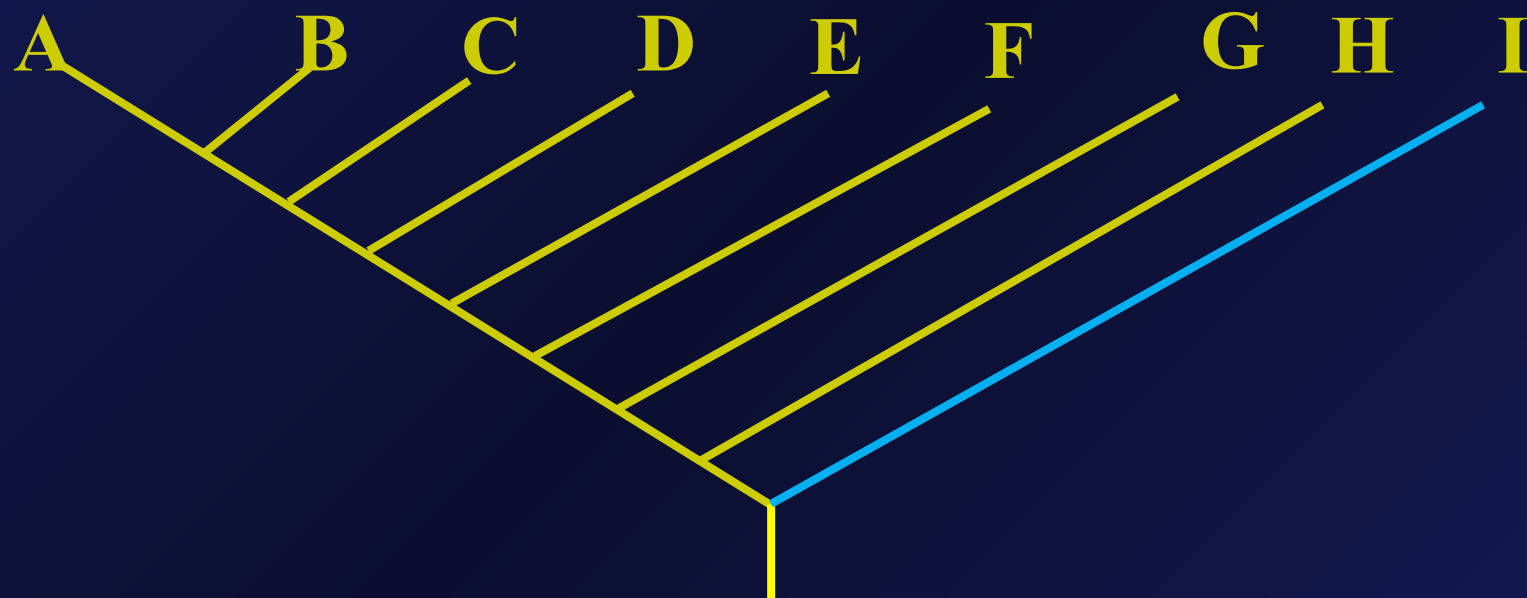
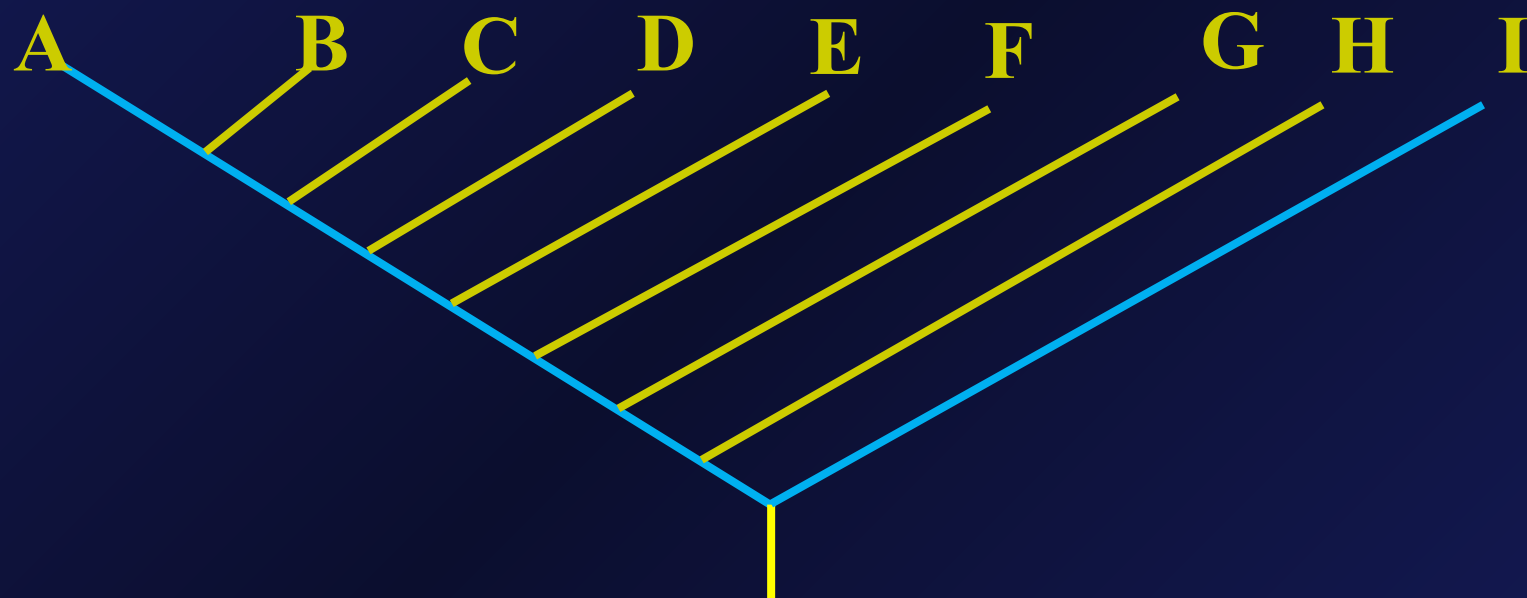
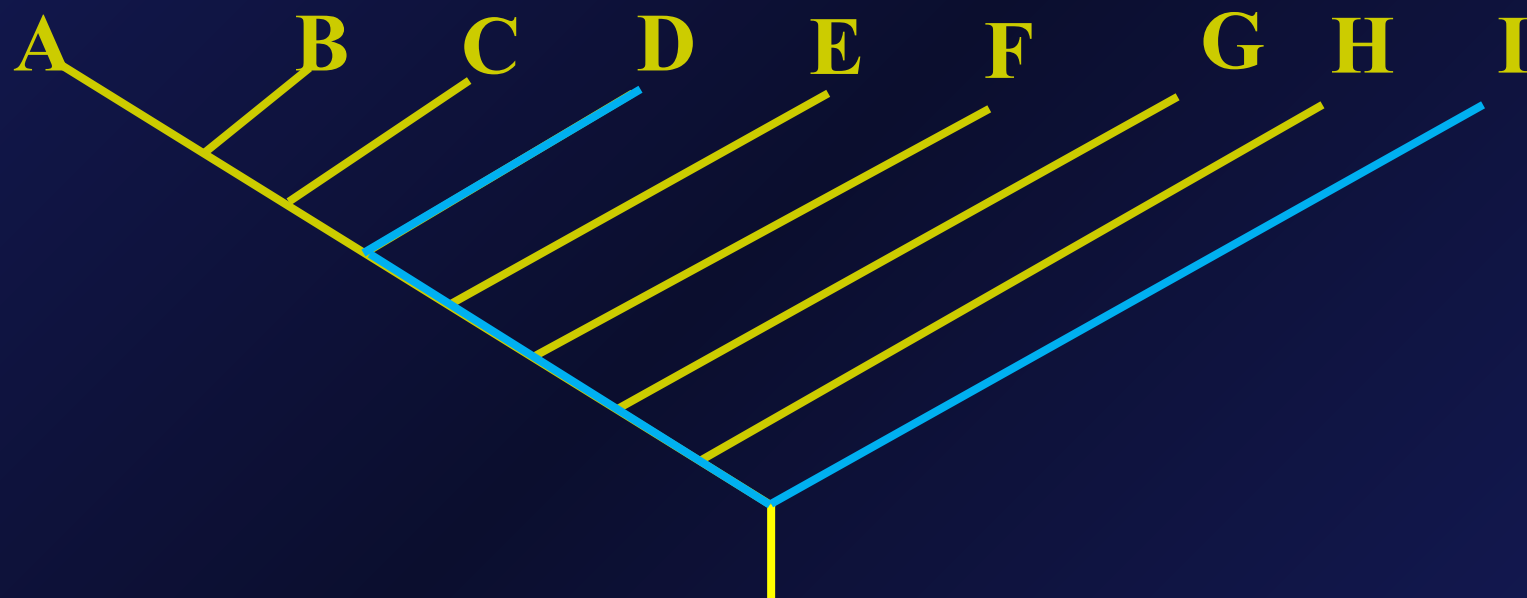


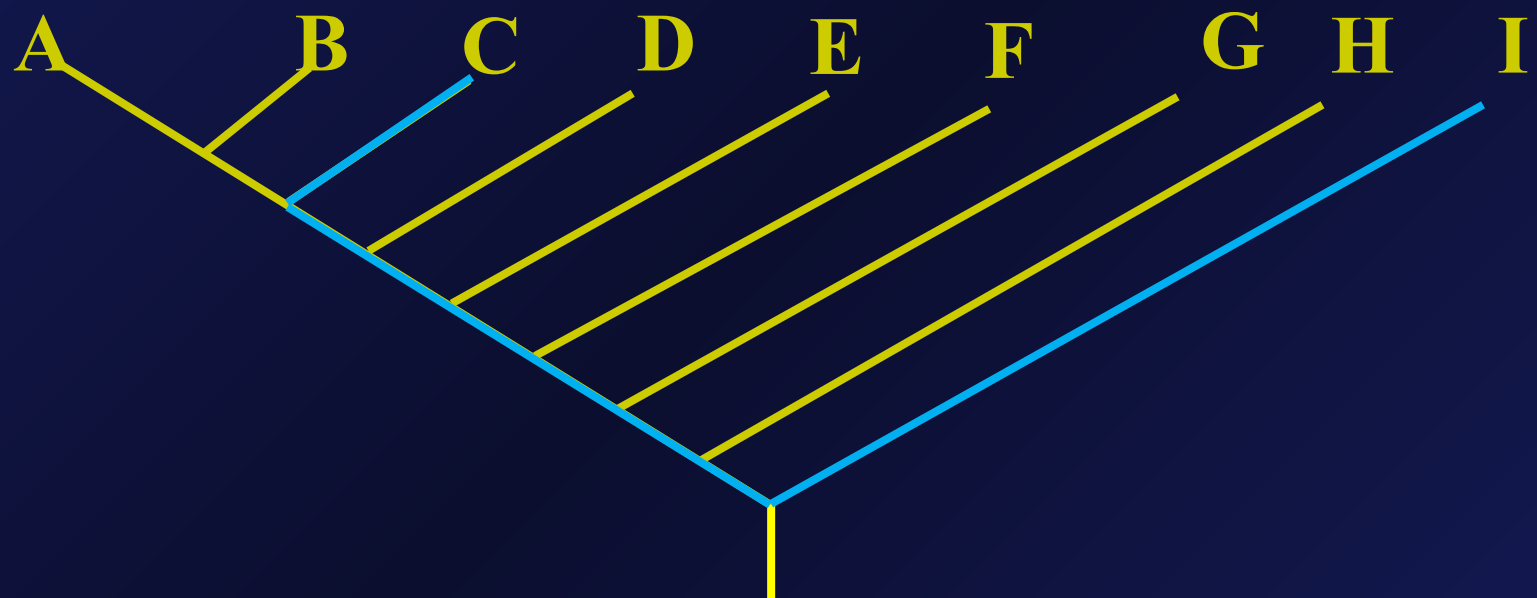
Figure 18. The phylogenetic linkage relations between the species of a monophyletic group, represented in two different ways.

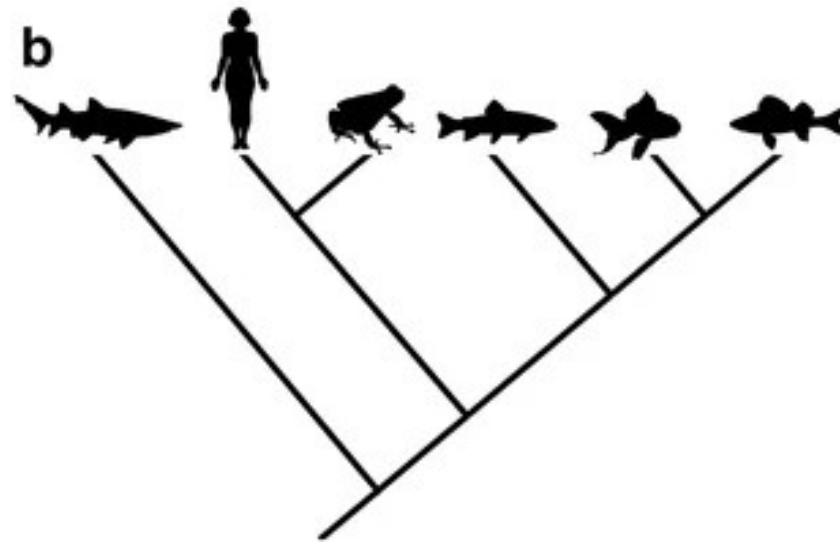
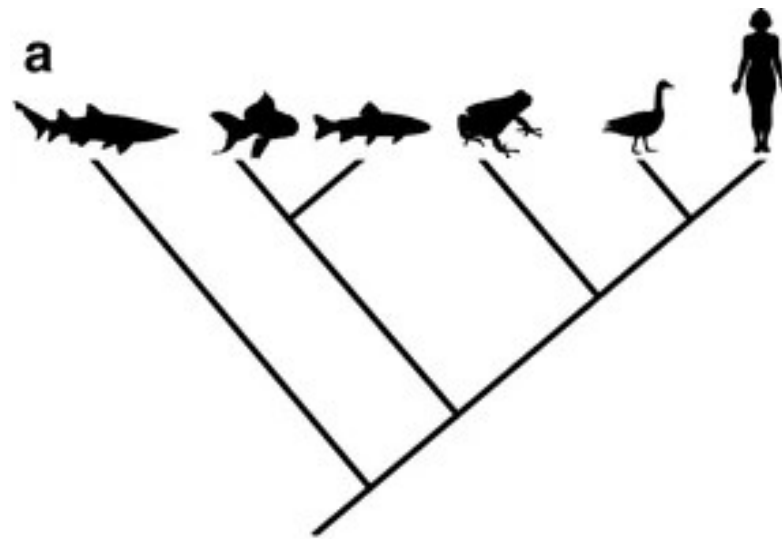


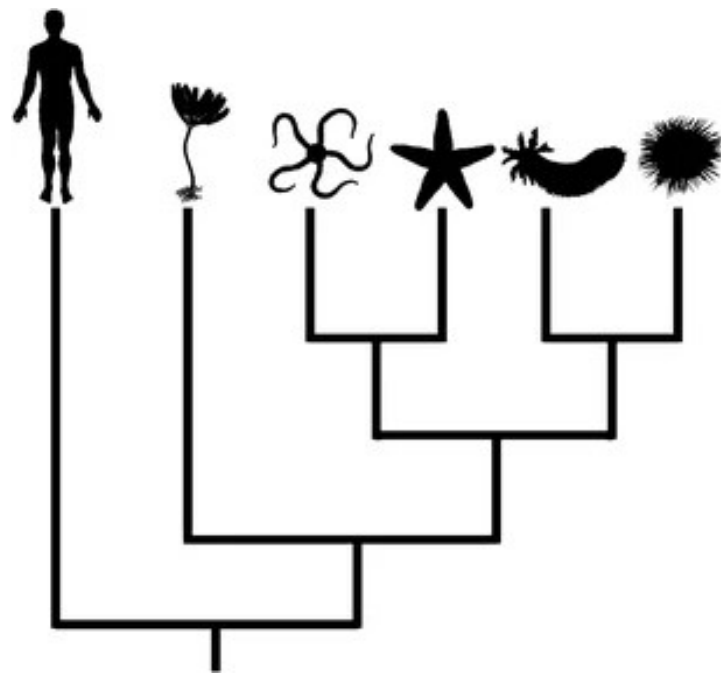


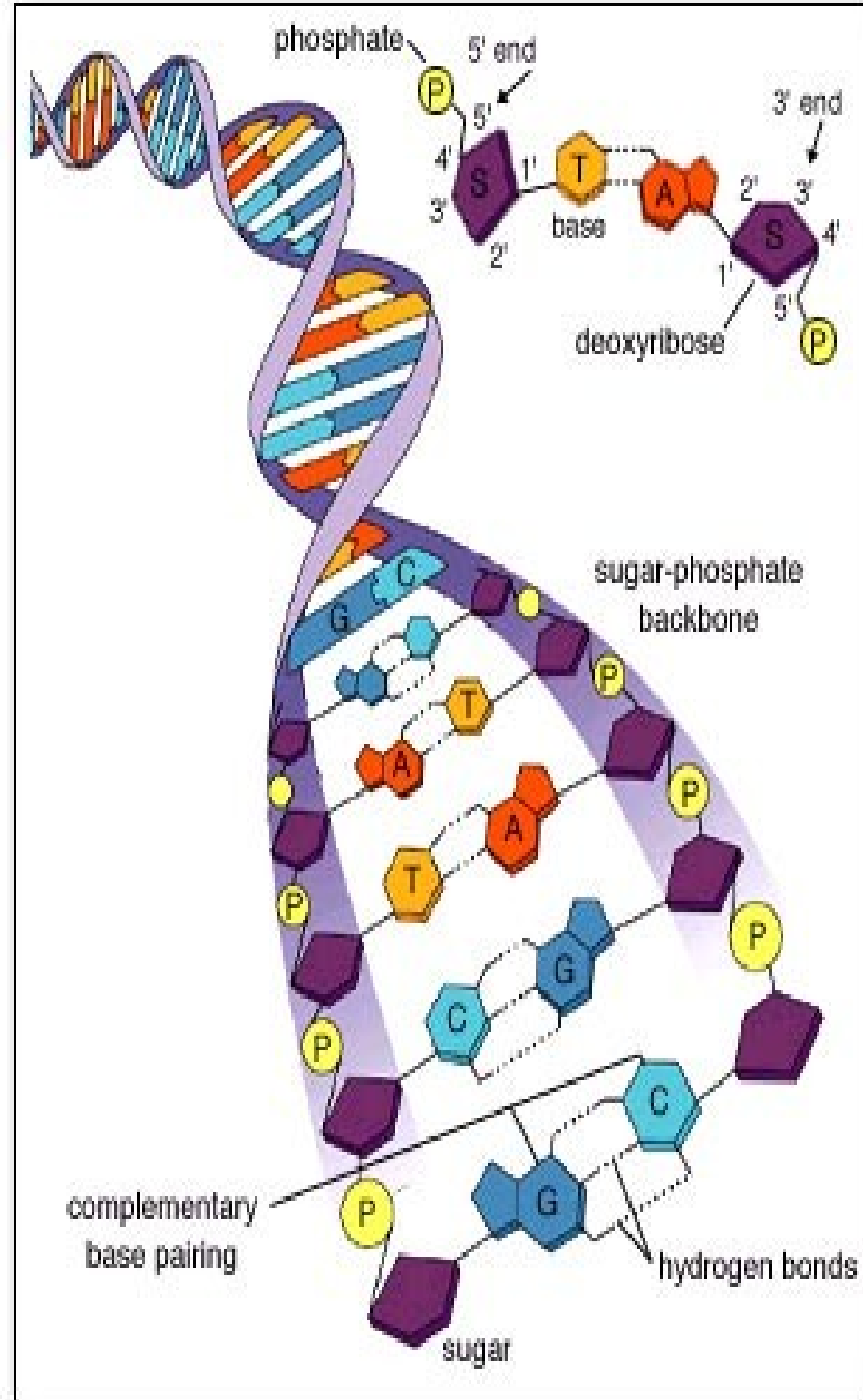






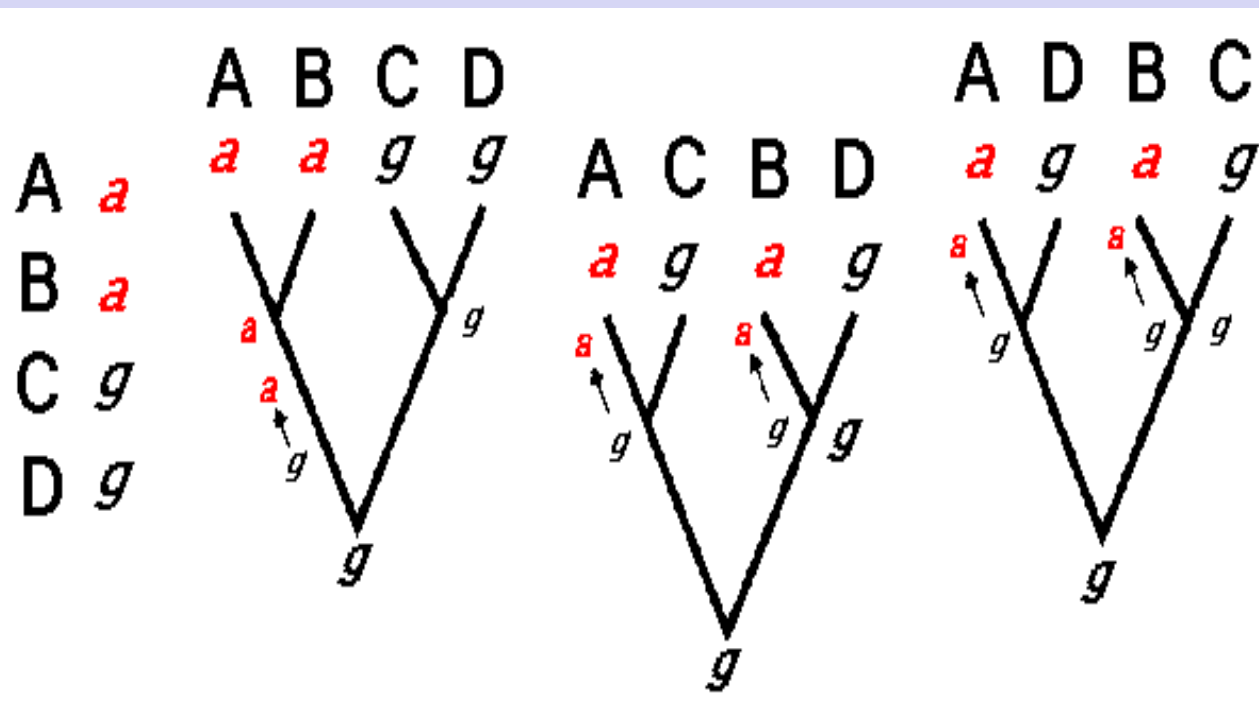






infrA	10528-10896	☒	
matK	10897-12783	☒	
ndhA	12784-13914	☒	
ndhB	13915-15474	☒	

Name &	8930	8940	8950	8960	8970	8980	8990	9000	9010	59950	59960
Acoamer	G A T T T A C T C C C C T C C C A	T A T C T T G C A T C T A T A	G T A T T T T T G C C C T G G T G G G T C T C T C T C T C A T T T A A T A A G A G	C A G A C T T . . . G G T G C A A C							
Acocal	G A T T T A C T C C A	T A T C T T G C A T C T A T A	G T A T T T T T G C C C T G G T G G G T C T C T C T C T C A T T T A A T A A G A G	C A G A C T T . . . G G T G C A A C							
Amborella	C A T T G A C T T C A	T A T C T T G C A T C T A T A	G T T T T T C T G C C C T G G G G A A T T T C T C T A T C A T T T A A T A A A A G	C A G A C T T . . . G G C A C A A C							
Anethum	C A T T C A A C C T A	T A T C T T G C A T C T A T A	G T A T T T T T G C C C T G G T G G A T T T C T C T C T C A T T T A A T A A A A G	C A G A C T T . . . G G T A C A A C							
Arabidopsis	C A T T C A T T C T T	T A T T T T C T A T C T A T A	G T C T T T T T G C C C T G G T T G A T C T C T C T C T G C T G T A A T A A A A G	C A G A C T T . . . G G T A C A A C							
Atropa	C A T T C A C T C T C	T A T C T T G C A T C T A T A	G T A T T T T T G C C C T G G T G G A T T T C T T T C T C A G T T A A T A A A T G	C A G A C T G . . . G G T A C A A C							
Brassica	C A T T C A T T C C T T T	T A T T T T A C A T C T A T A	G T C T T T T T G C C C T G G T T G A T C T C T C T C T G C T G T A A T A A A A G	C A G A C T T . . . G G T A C A A C							
Buxus	C A T T C A C T T C C C T	T A T C T T G C A T C T A T A	G T T T T T T T G C C C T G G T G G A T C T C T C T C T C A T T T A A T A A A T G	T A G A C T T . . . G G T A C A A C							
Calycanthus	C A T T G A C T C C C T T C C C A	T A T C T T G C A T C T A T A	G T T T T T T T G C C C T G G T G G A T C T C T C T C T C A T T T A C C A A A A G	C C G A C T T . . . G G T G A A A A							
Chloranthus	A A T C G A C C C C C C T C C C A T T C C C A	T A T C T T G C A T C T A T A	G T A T T G T T G C C C T G G T G G A T T T C T C T T T C A T T T A A G A A A T G	C A G A C T T . . . G G T G C A A C							
Citrus	C A T C C A T T C C C C T T A G A	T A T C T T T C A T C T A T A G T A T T T G T A G T A T T T T T G C C C T G G T G G A T C C C T C T C T C A T T T A A T A A A A G	C C G G C T T . . . G G T A C A A C								
Coffea	C A T T C A C T C C C C T T T T A	T A T C T T G T A T C T A T A	G T A T T T T T G C C C T G G T G G C T T T C T C T C T C A T T T A A T A A A A G	T A G A C T T . . . G G T A C A A C							
Cucumis	C A T T T C T T C C T C T T C T A	T A T C T T A C A T C T A T A	G T A T T T T T G C C C T G G T G G A T C T C T C T C T C A T T T A A T A A A A G	T C G A C T T . . . G G T G C A A C							
Cycas	C A T T A G C T T C C C T A C G A	T A C C T T G C A T G T C T A	G T A T T C C T G C C C T G G G G A A T C T C T A T T T C A T T C C A G A A A G G	T A G A C T T . . . G G T A T A A C							
Daucus	C A T T C A C C T C T C T T T T A	T A T C T T G C A T C T A T A	G T A T T T T T G C C C T G G T G G A T T T C T C T C T C A T T T A A T A A A A G	C A G A C T T . . . G G T A C A A C							
Dioscorea	C A T T G A T T T C C A T A C C A	T A T C T T G T A T C T A T A	G T A T T T T T G C C C T G G T G G G T C T C T C T C T C A T T T A A T A A A A G	C A G A C T T . . . G G T A C A A C							
Drimys	C A T T G A C T C C C C T C C C A	T A T C T T G C A T C T A T A	G T C T T T T T G C C C T G G T G G A T C T C T C T C T C A T T T A A T A A A A G	C C G A C T T . . . G G T G C A A A							
Ehretia	T A T T C A C T C C C C T T T T C	T A T C T T G C A T C T A T A	G T A T T T T T G C C C T G G T G G A T T T C T C T C T C A T T T A A T A A A A G	C A G A C T T . . . G G T A C A A C							
Elaeis	C C T T G G T C T C C C T C C C A	T A T A T T T C A T C C A T A	A T A T T T T T G C C C T G G T G G G T C T C T C T C T C A T T T A A T A A A T G	C A G A C T T . . . G G T A C A A C							
Eucalyptus	C A T T T C T T C C T C T T L	Y L T S I	V F L P W W I S L S F N K S	R L . . . G T T T							
Ginkgo	T A T C A G C T T C C C T A C A A	T A T C T C G C A T T T L	V F L P W G I S I S F Q E G	R L . . . G V T T							
Glycine	C A T T C A T T C C C C T T C T A	T A T C T T A C A T C T A T A	G T C T T T L P W C I S F T F K K S	R L . . . G T T T							
Gossypium	C A T T C A C T C C C C T T C T A	T A T C T T G C A T C T A T A	G T A T T T L P W W I S C T C T C A T T T A A T A A A A G	C A G A C T T . . . G G T A C A A C							
Helianthus	C A T T C A C T C C T C T T T T A	T A T C T T G T A T C T A T C	G T A T T T L P W W I S C T C T T A T T T C A A A A A G	C A G A C T T . . . G G T A C A A C							
Hordeum	C A T T G C C T T C T T T A C T A	T A T C T T G T A T T T A T C	G T A C T T L P W G V S T C C T C A T T T A A C A A A T G	C A G A C T T . . . G G T A C A A C							
Illicium	C A T T G A C T C C C T T C C C A	T A T C T T G C A T C T A T A	G T A T T T L P W G I S C T C T C A T T T A A T A A A A G	C A G A C T T . . . G G T A C A A C							
Ipomoea	C A T T C A C T C C T C T T T T C	T A T C T T T C A T T T A T A	G T C T T T L P W W I S T T C T C A T T T A A G A A A T G	C A G A C T T . . . G G T A C A A C							
Jasminum	C A T T C A C T C C T C T T T T G	T A T T T T G C A T C T A T A	G T C T T T L P W W I S C T C T C A T T T A C G A A A A G	C A G A C T T . . . G G T A C A A C							
Lactuca	C A T T C A C T C C T C T T T T A	T A T C T T G C A T C T A T A	A T A T T T L P W W I S C T C T C A T T T C A A A A A G	C A G A C T T . . . G G T A C A A C							
Liriodendron	C A T T G A C T C C C C T C C C A	T A T C T T G C A T C T A T A	G T C T T T L P W W I S A T C T C A T T T A A T A A A A G	C C G A C T T G G T G G A G A A A A							
Lotus	C A T C T A T T C C C T T T C T A	T C T C T C A C A T C T A T A	G T C T T T L P W C I S T T T A C A T G T A A G A A A G G	C A G A C T T . . . G G T A C A A C							
Medicago	C A T T C A T T C C C C T T C T A	T G T C T T A C A T C T A T A	G T C T T T L P W C I S T T T A C A T T T A A G A A A A G	C A G A C T T . . . G G T A C A A C							
Musa	C A T C G G C C T C C C T C C C A	T A T C T C G C A T C T A T A	G T A T T T L P W W V S T T C T C A T T T A A T A A A T G	C A G A C T T . . . G G T A C A A C							
Nicsyl	C A T T C A C T C C T C T T T T C	T A T C T T G C A T C T A T A	G T A T T T L P W W I S T T C T C A G T T A A T A A A T G	C A G A C T G . . . G G T A C A A C							
Nictab	C A T T C A C T C C T C T T T T C	T A T C T T G C A T C T A T A	G T A T T T T T G C C C T G G T G G A T T T C T T T C T C A G T T A A T A A A T G	C A G A C T G . . . G G T A C A A C							
Nictom	C A T T C A C T C C T C T T T T C	T A T C T T G C A T C T A T A	G T A T T T T T G C C C T G G T G G A T T T C T T T C T C A G T T A A T A A A T G	C A G A C T G . . . G G T A C A A C							
Nuphar	C A T T G A A T C C C . L . P	Y . L . A . S . I	V . F . L . P . W . G . I . S . L . S . F . N . K . S	. R . L G . T . T							
Nymphaea	C A T T G A A T C C C . L . P	Y . L . A . S . I	V . F . L . P . W . G . I . S . L . S . F . N . K . S	. R . L G . T . T							
Oenothera	A A T T C C T T C C G . L . L	Y . L . T . A . I	V . F . F . P . W . W . I . S . L . L . F . N . K . G	. R . L G . T . T							
Oryza	C A T T G C C T T C T . F . L	Y . L . V . F . I	V . L . L . P . W . G . V . S . F . S . F . N . K . C	. R . L G . T . T							
Panax	C A T T C A C T C C T . L . L	Y . L . A . S . L	V . F . L . P . W . W . I . S . L . S . F . N . K . S	. R . L G . T . T							



Jukes & Cantor 1969

	A	C	G	T
A	X	α	α	α
C	α	X	α	α
G	α	α	X	α
T	α	α	α	X

1 parameter
equiprobable changes

Kimura 1980

	A	C	G	T
A	X	α	$\kappa\alpha$	α
C	α	X	α	$\kappa\alpha$
G	$\kappa\alpha$	α	X	α
T	α	$\kappa\alpha$	α	X

2 parameters
transition rate $\neq$
transversion rate

Tamura 1992

	A	C	G	T
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

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

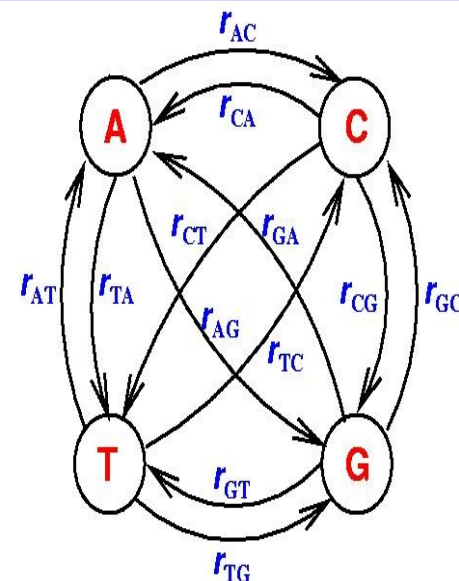
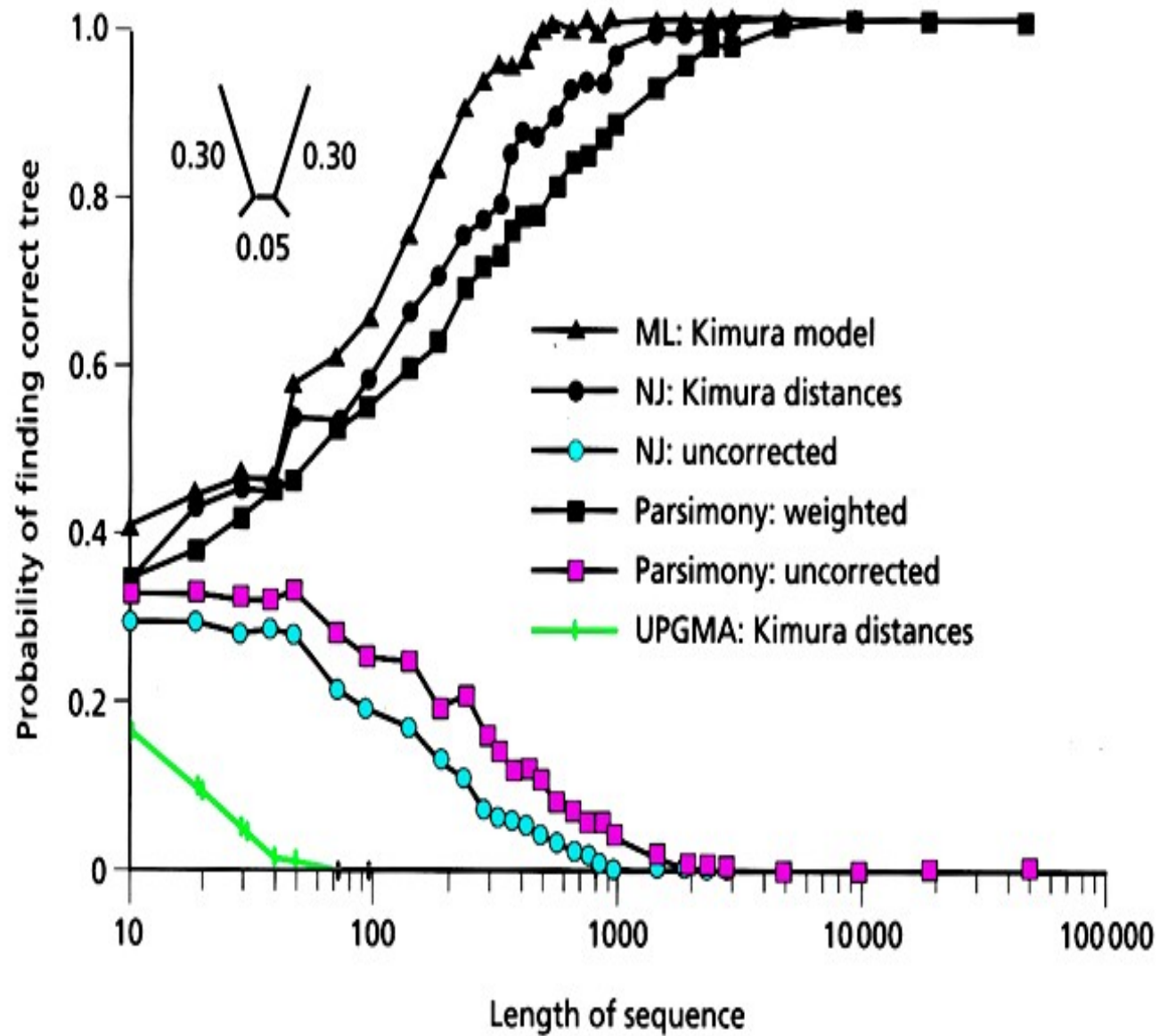


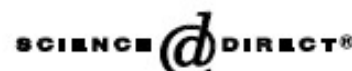
Figure 2.2: Markov model for nucleotide evolution in DNA sequences

(b)





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Cladistics 19 (2003) 120–127

Cladistics

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

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Accepted 15 July 2002

Abstract

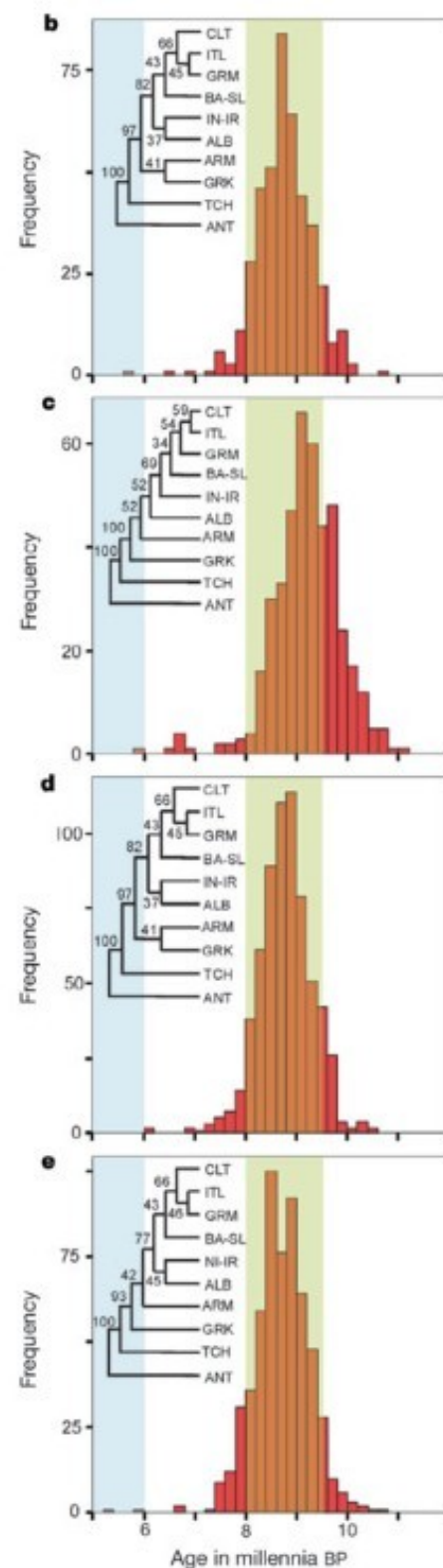
The phylogeny of the Indo-European (IE) language family is reconstructed by application of the cladistic methodology to the lexicostatistical dataset collected by Dyen (about 200 meanings, 84 speech varieties, the Hittite language used as a functional outgroup). Three different methods of character coding 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.

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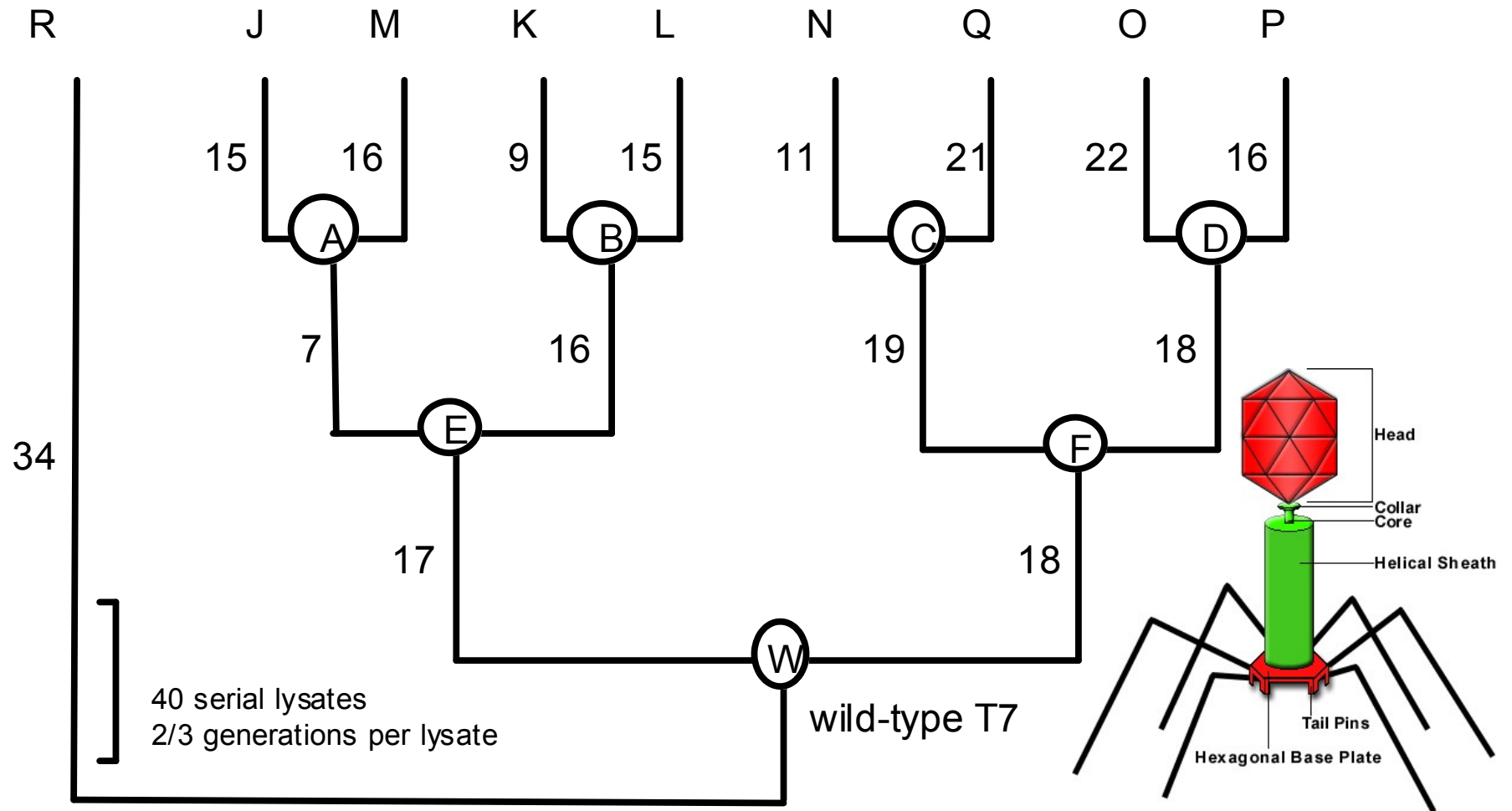
Introduction

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



Experimental phylogenetics



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



Research article

Open Access

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

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Email: David L Reed* - dreed@flmnh.ufl.edu; Jessica E Light - jlight@flmnh.ufl.edu; Julie M Allen - juliema@ufl.edu; Jeremy J Kirchman - jkirchma@mail.nysed.gov

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Abstract

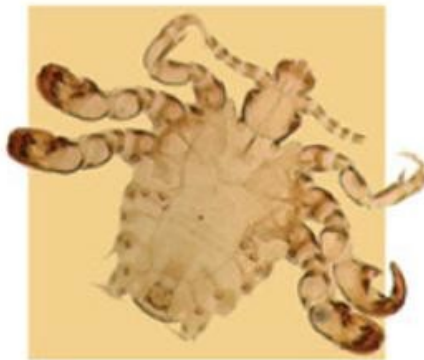
Background: The parasitic sucking lice of primates are known to have undergone at least 25 million years of coevolution with their hosts. For example, chimpanzee lice and human head/body lice last shared a common ancestor roughly six million years ago, a divergence that is contemporaneous with their 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

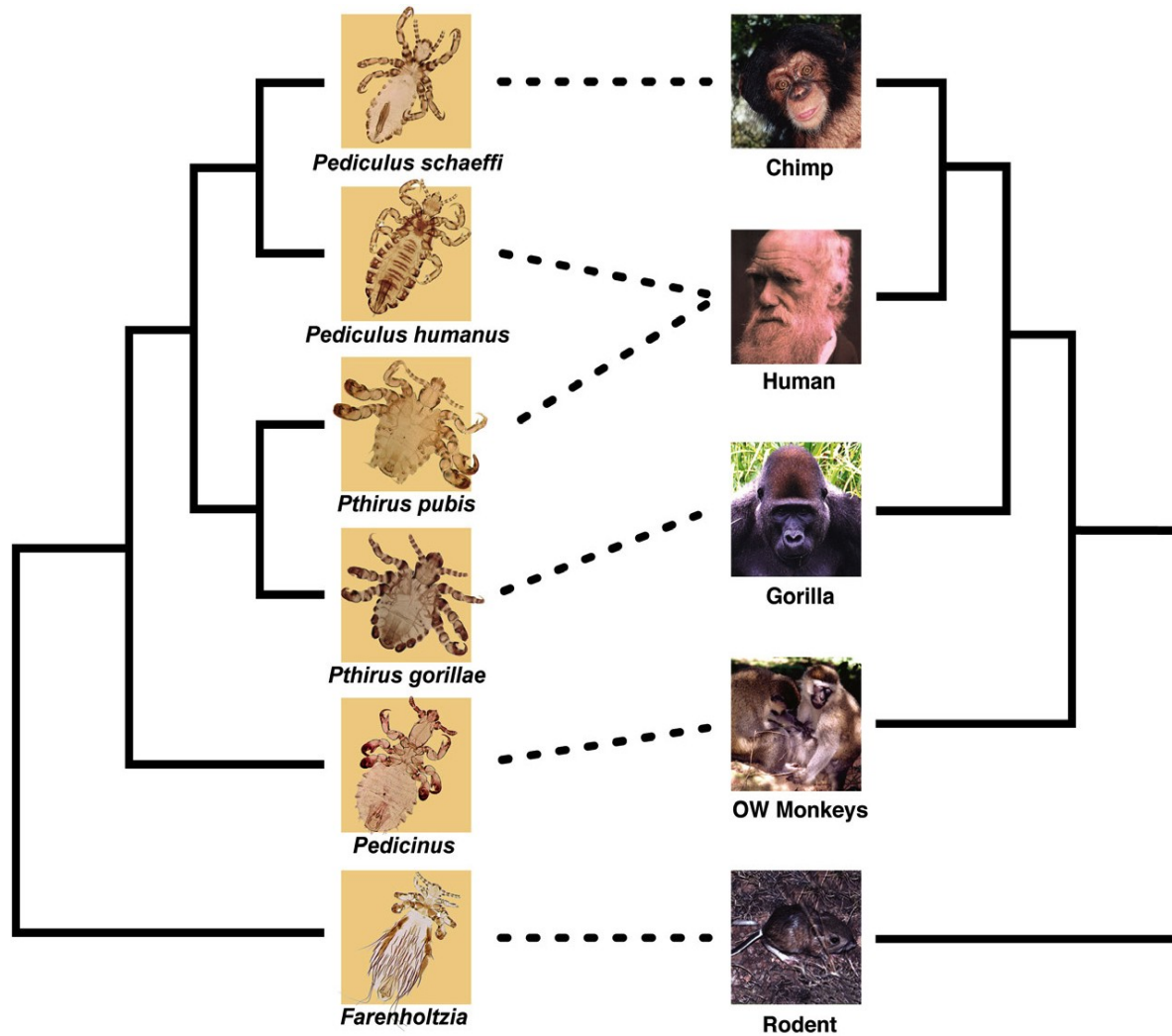
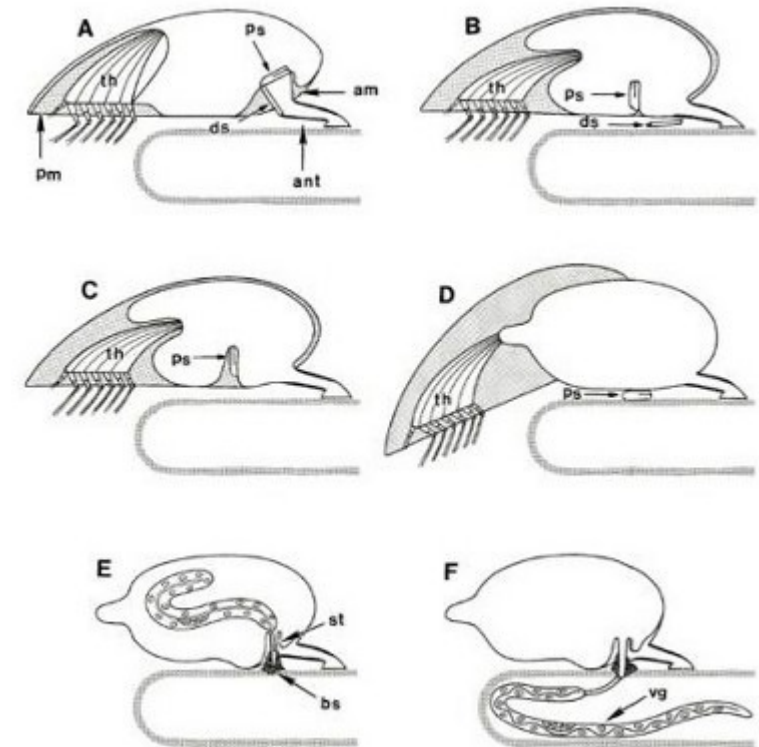
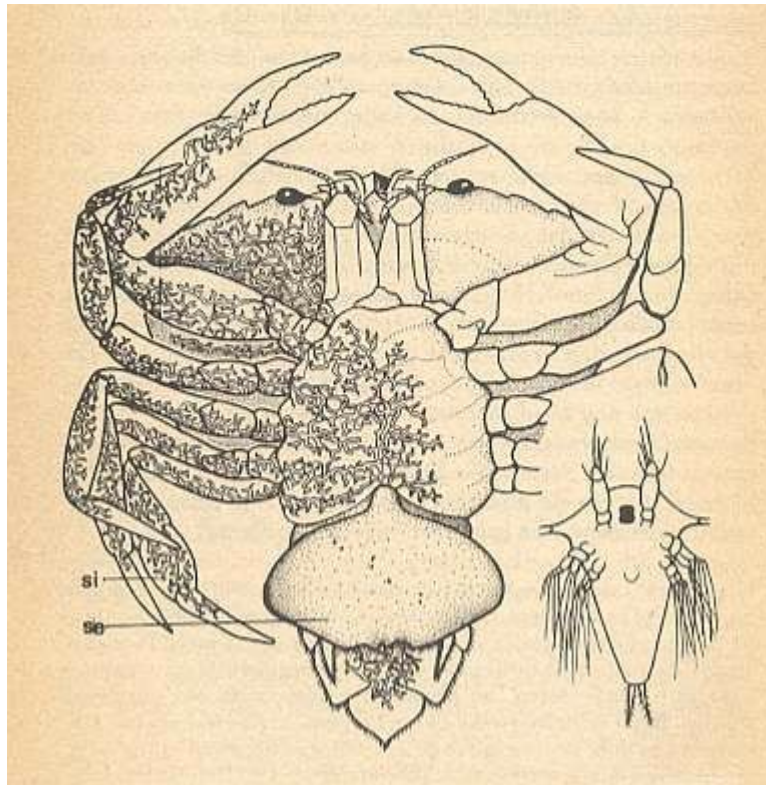
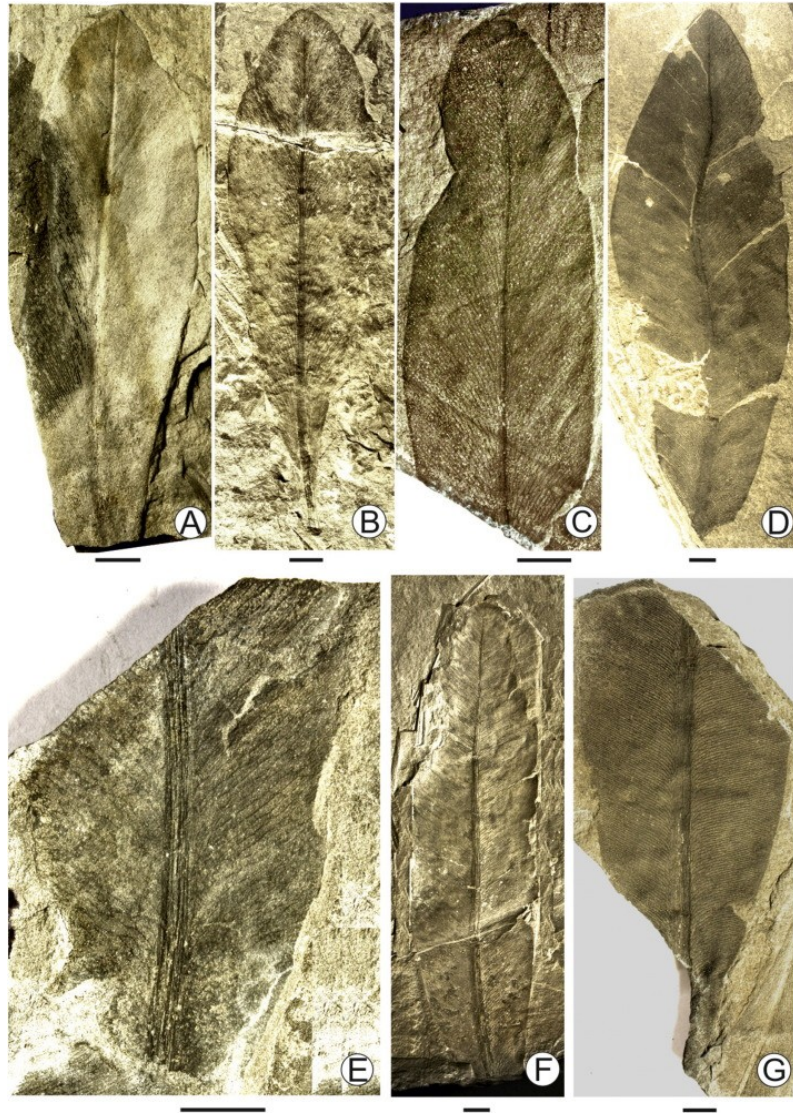




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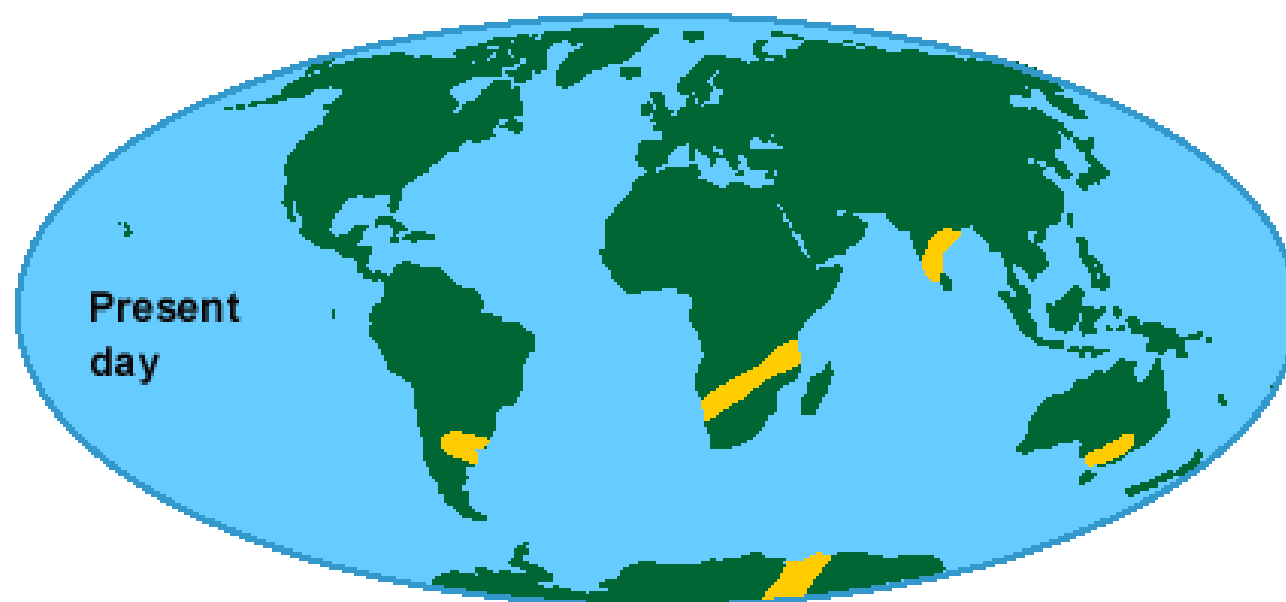


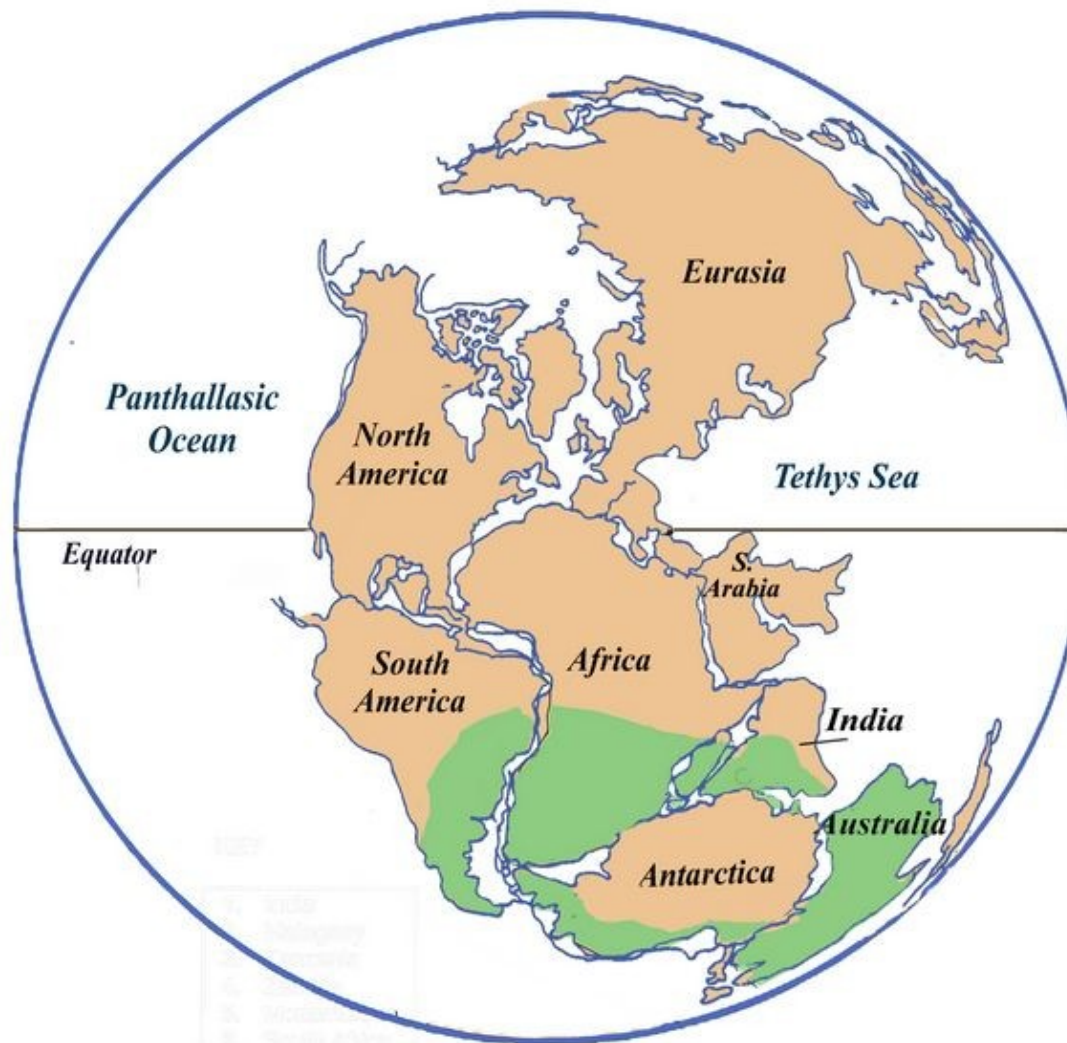




Glossopteris

Tewari et al., 2015

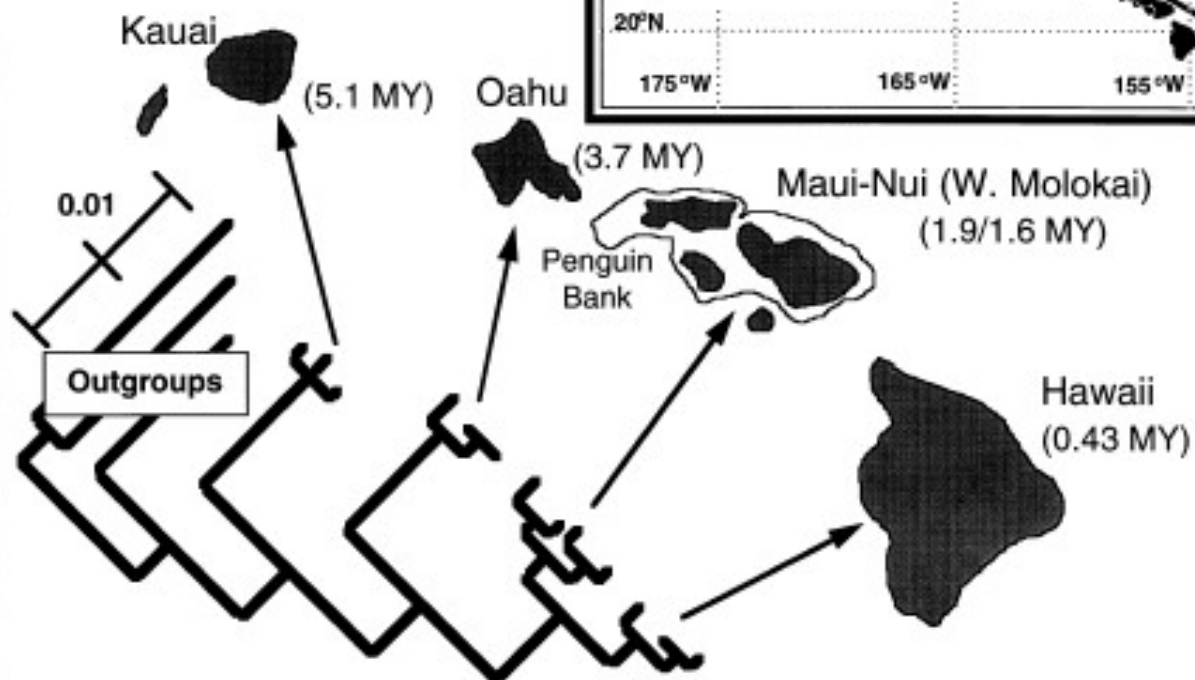


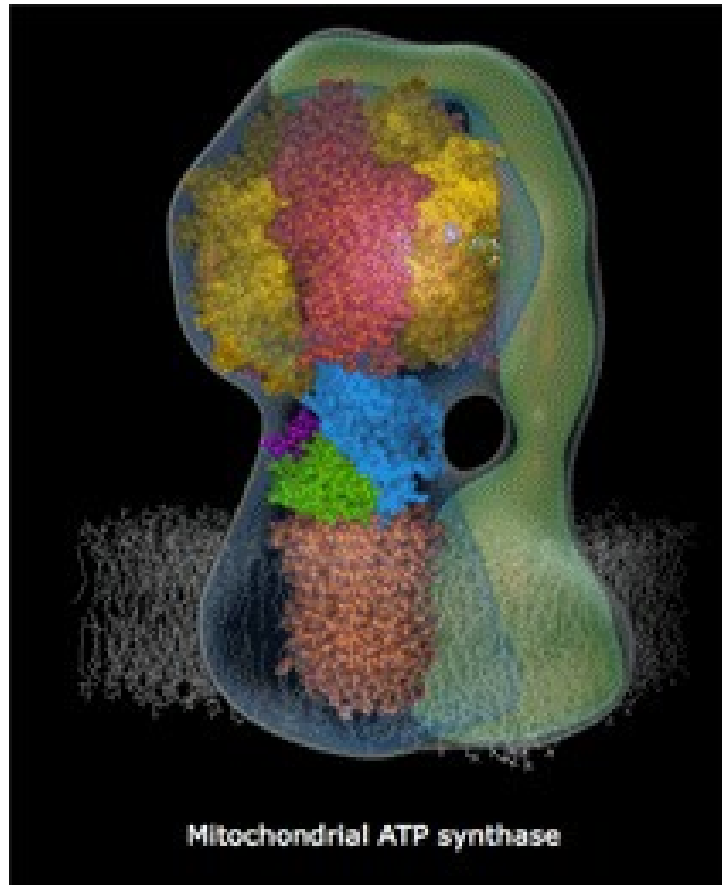


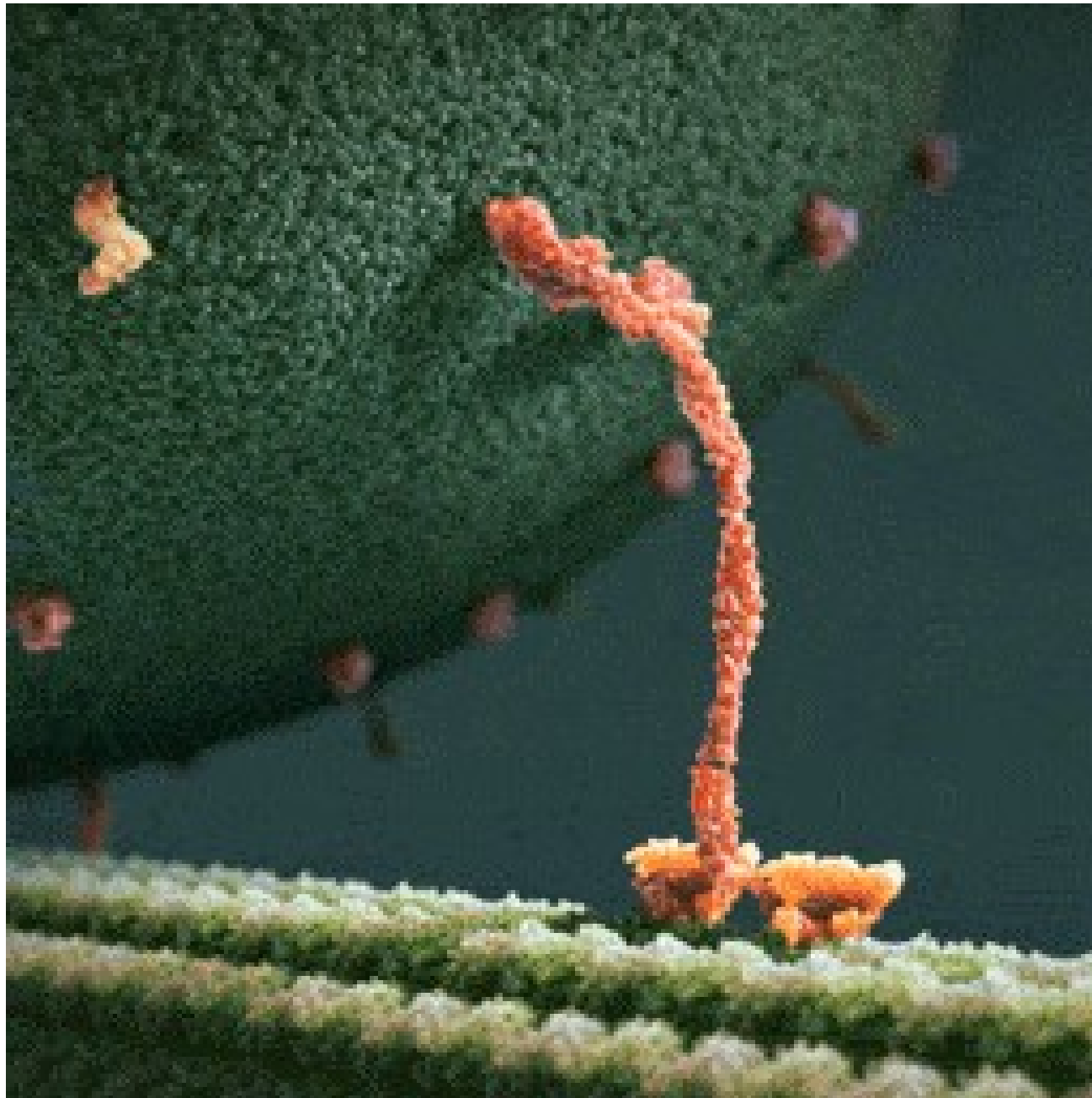
Distribution of *Glossopteris* in the Permian period

Main Hawaiian Islands (K-Ar ages)

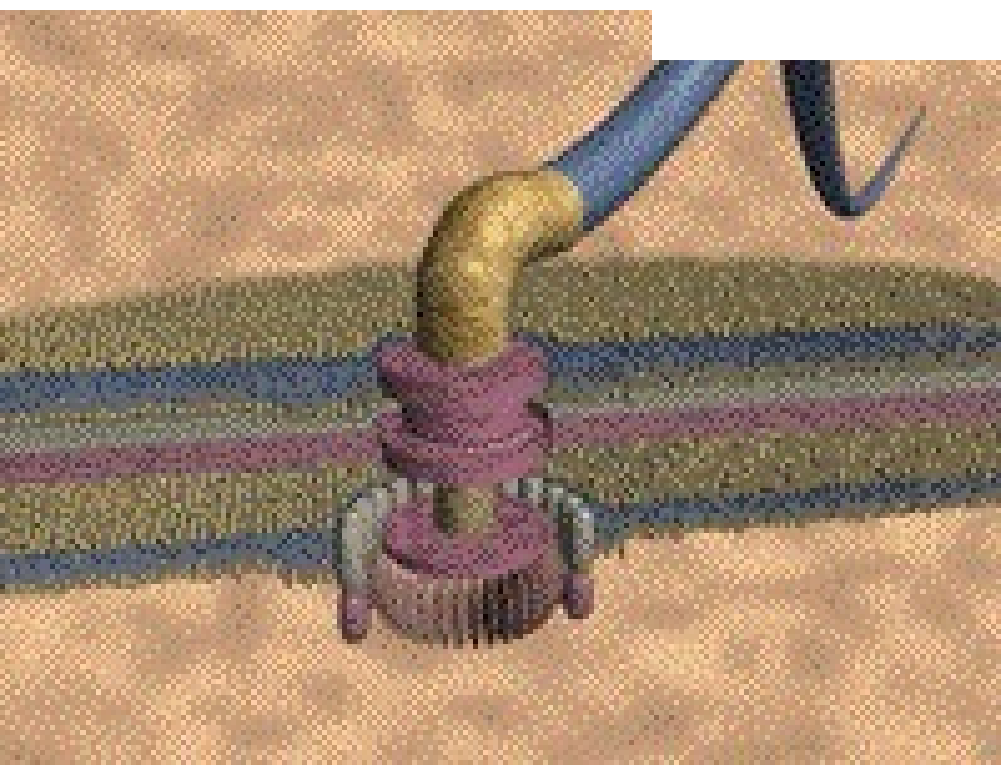
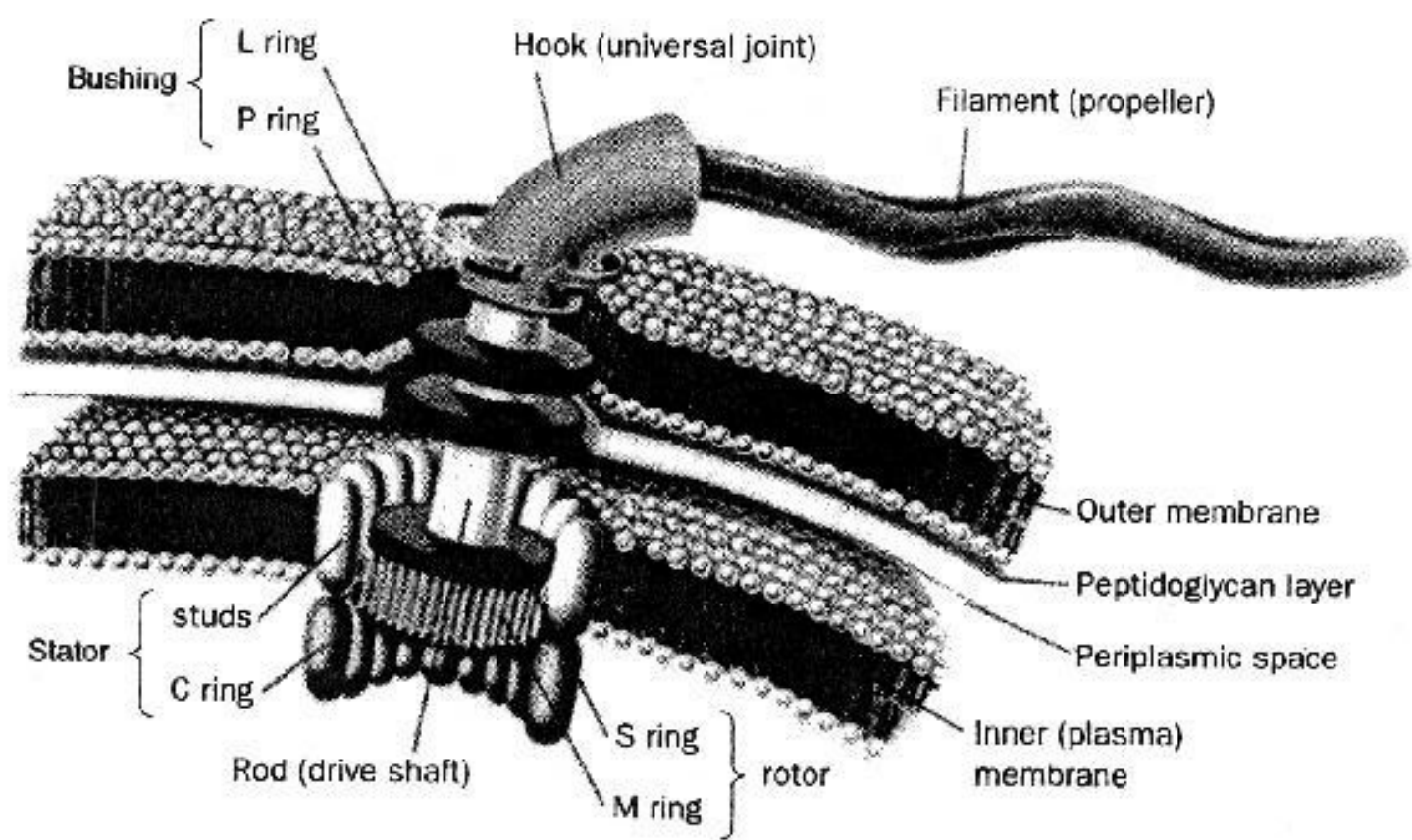
0 60 120 km







Kinesin protein walking on microtubule



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

	PAGE
THE PROBLEM OF FACTOR VARIABILITY AND THE CASE OF BEADED WINGS.....	422
PRELIMINARY CROSSES AND FORMULATION OF A WORKING HYPOTHESIS.....	428
SUBSTANTIATION OF THE HYPOTHESIS, AND CORRELATIVE EXPERIMENTS.....	437
(1) Existence of two kinds of chromosomes in beaded stock verified.....	437
(2) Crossover frequencies of the two chromosomes; position of beaded....	440
(3) The lethal effect of the chromosome containing B_d'	441
(4) Analysis of the C' -bearing chromosome.....	443
(5) Origin of the factor C_b'	450
(6) Modifying factors	452
(7) Other factors for beaded.....	458
CONSIDERATION OF RELATED PHENOMENA, AND GENERAL DISCUSSION.....	460
(1) The lethal effect of dominant mutants.....	460
(2) The balancing lethal	467
(3) Effects of balanced lethals on crosses.....	468
(4) Other cases of enforced heterozygosis.....	471
(5) The reason for the origin of enforced heterozygosis.....	476
(6) Effect of the continued heterozygosis on the chromosomes and on the evolution of the race	479
(7) Special results obtainable with lethal factors.....	486
(8) The variability of the character beaded.....	489
(9) General considerations concerning factor variability.....	491
(10) Contamination of factors	494
SUMMARY	495
LITERATURE CITED	497

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

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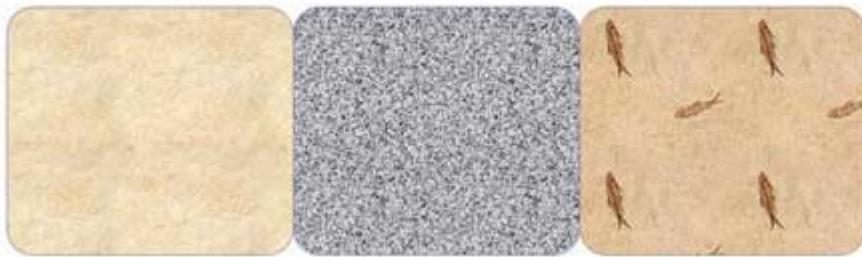
464

HERMANN J. MULLER

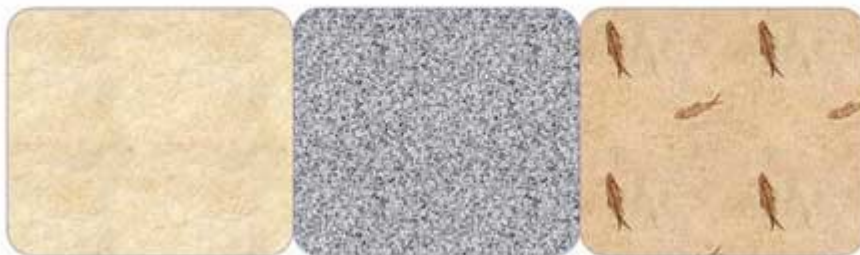
by the many previously formed factors in coöperation; thus a complicated machine was gradually built up whose effective working was dependent upon the interlocking action of very numerous different elementary parts or factors, and *many of the characters and factors which, when new, were originally merely 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***



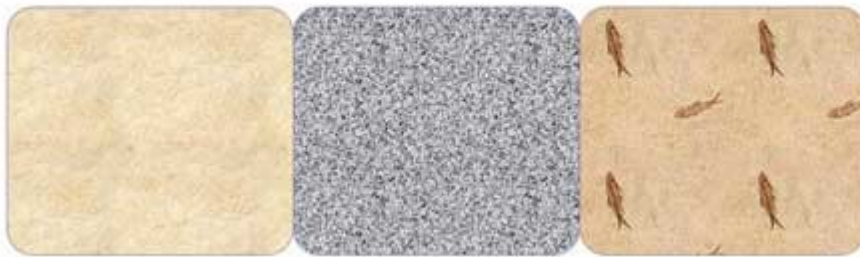
condição precursora:
ponte formada por três
pedras



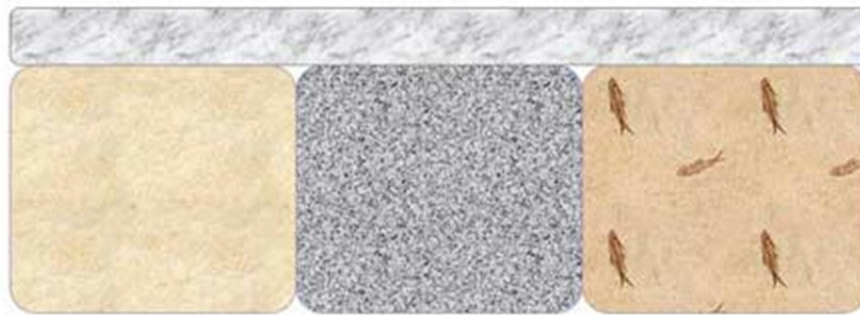
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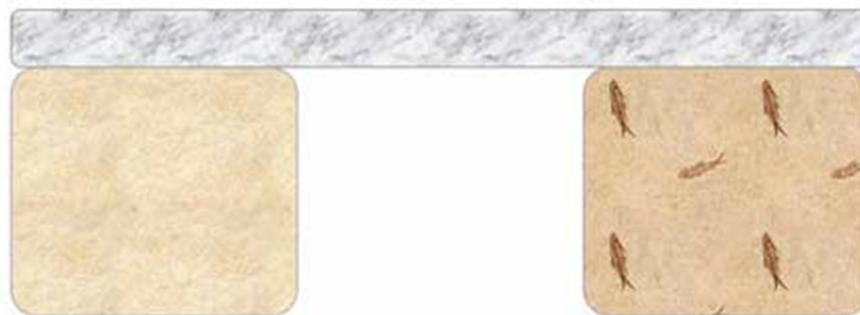
passo 1: adição de uma
pedra contínua por cima



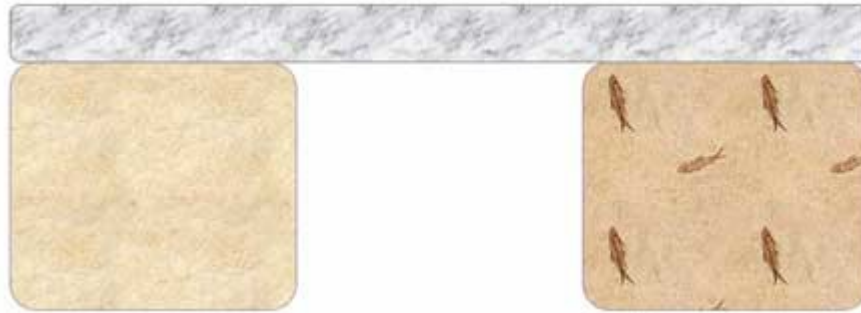
condição precursora:
ponte formada por três
pedras



passo 1: adição de uma
pedra contínua por cima



passo 2: retirada da
Pedra intermediária



resultado: **complexidade irreduzível!**

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

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.

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.

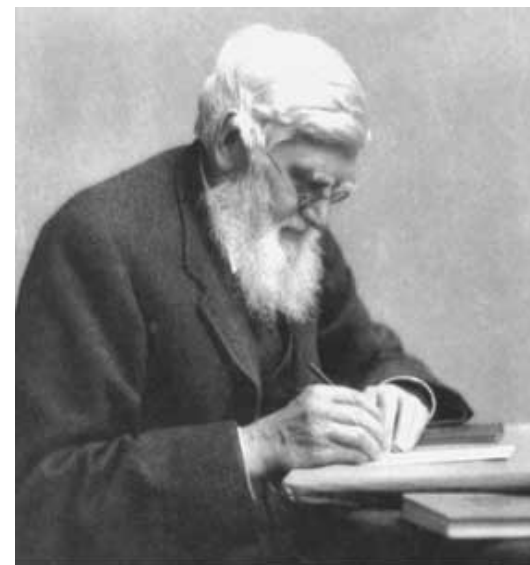
By CHARLES DARWIN, M.A., F.R.S., &c.

IN TWO VOLUMES.—Vol. I.

WITH ILLUSTRATIONS.

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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).



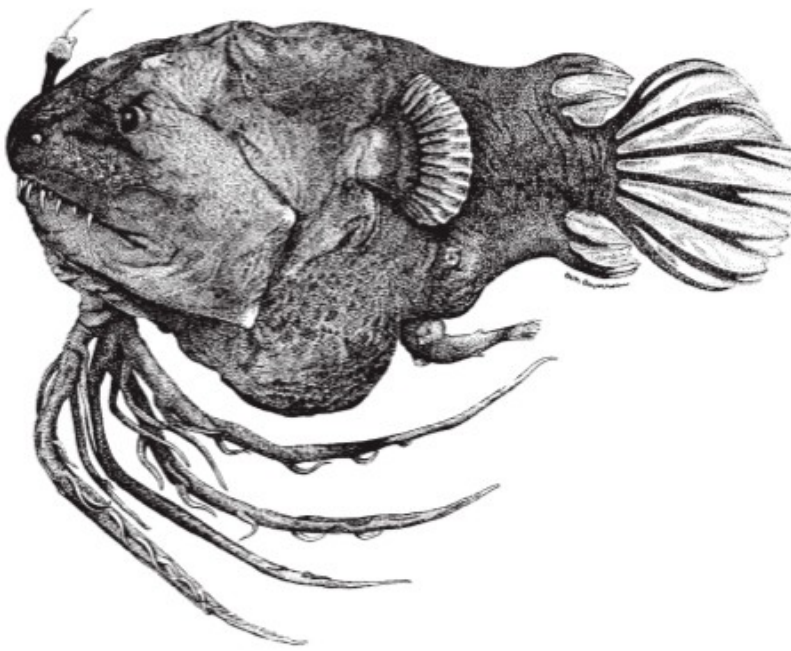


Fig. 22. *Linophryne brevibarbata*, 100-mm female, with an 18.5-mm parasitic male, BMNH 1995.1.18.4. (Drawing by Elisabeth Beyerhagen after Bertelsen, 1980a)

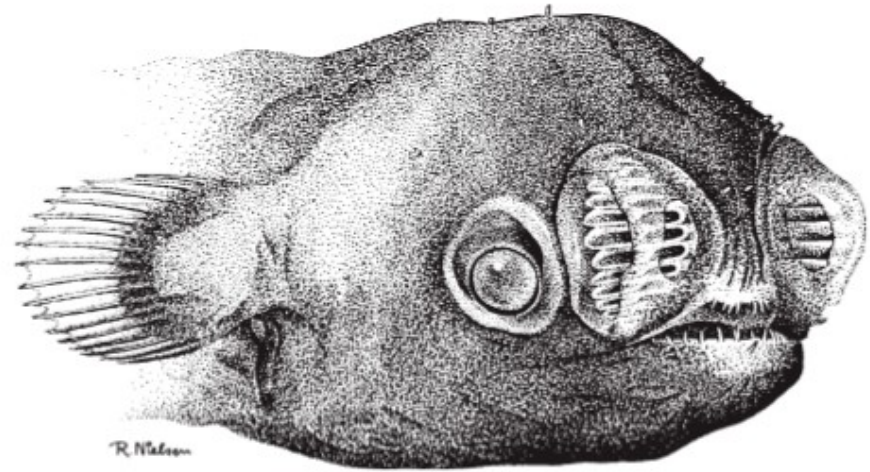
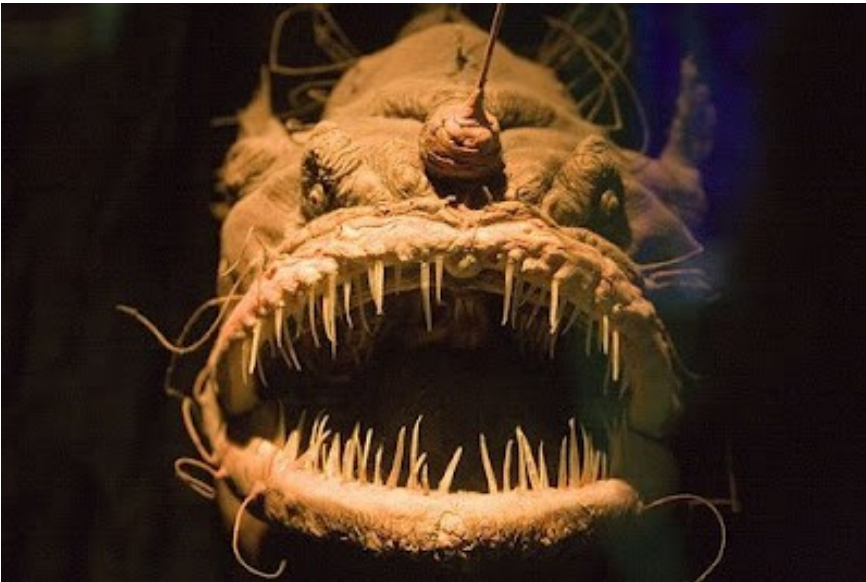


Fig. 18. Free-living male of *Linophryne arborifera*-group, 18.5 mm, BMNH 2004.7.5.1, showing extremely well-developed eyes and nostrils (Drawing by R. Nielsen; after Bertelsen, 1980a)













Cnemidophorus neomexicanus



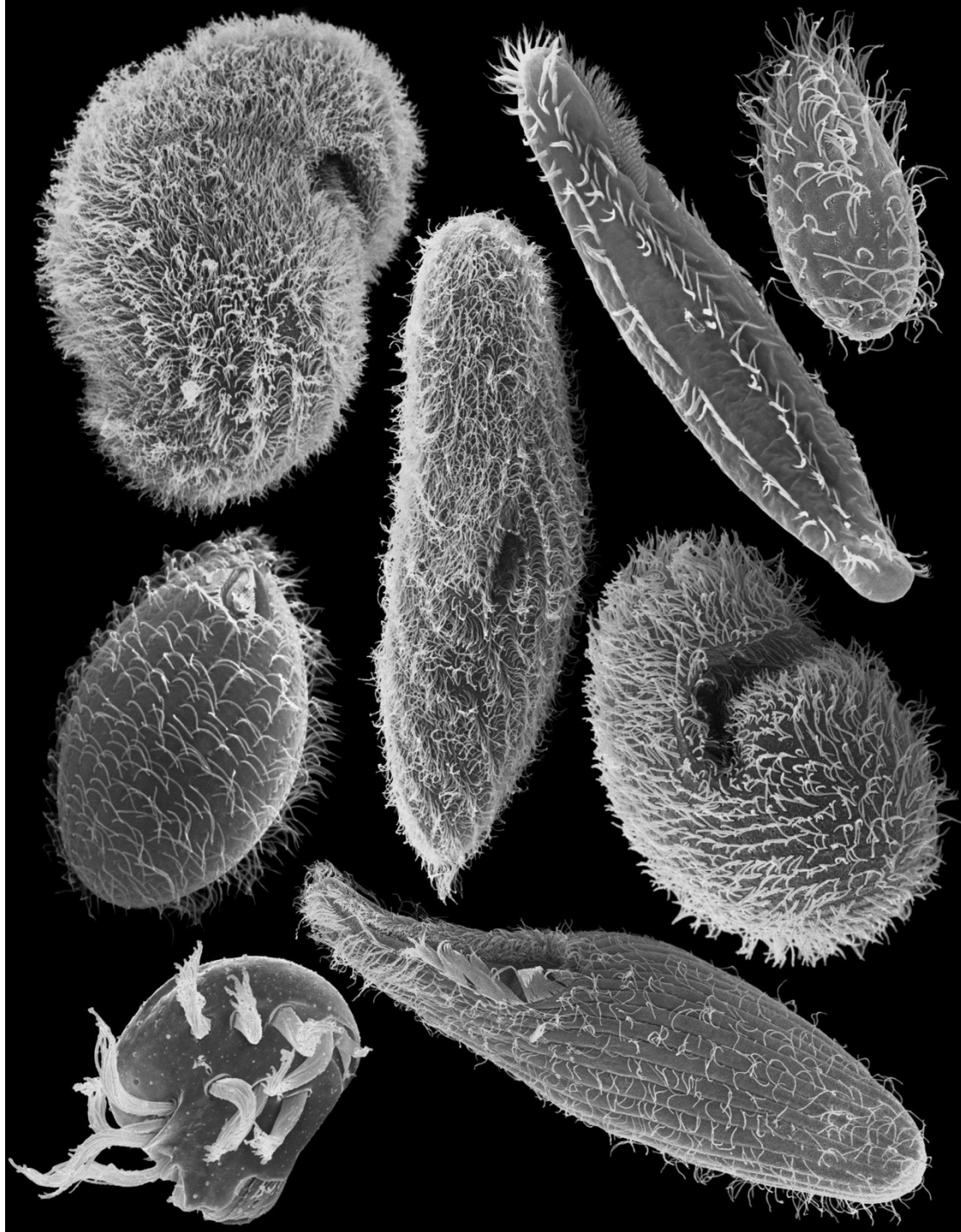


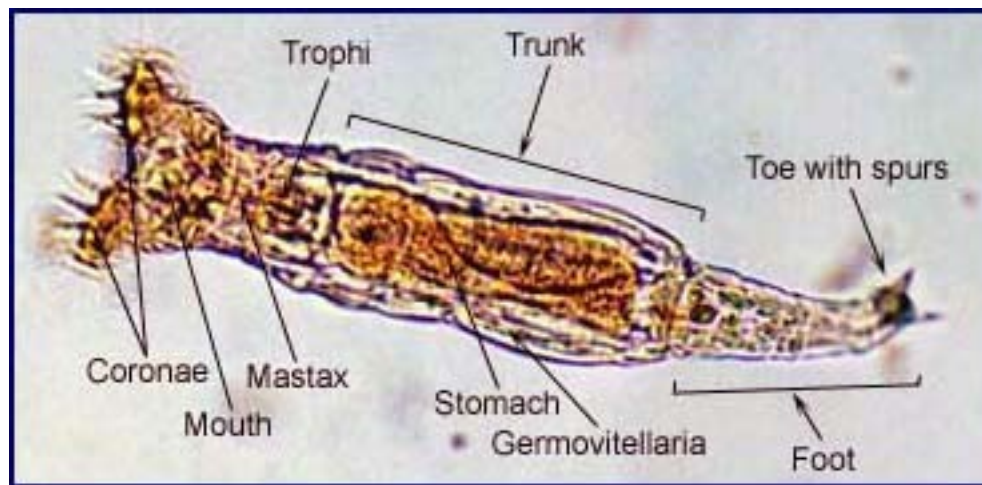
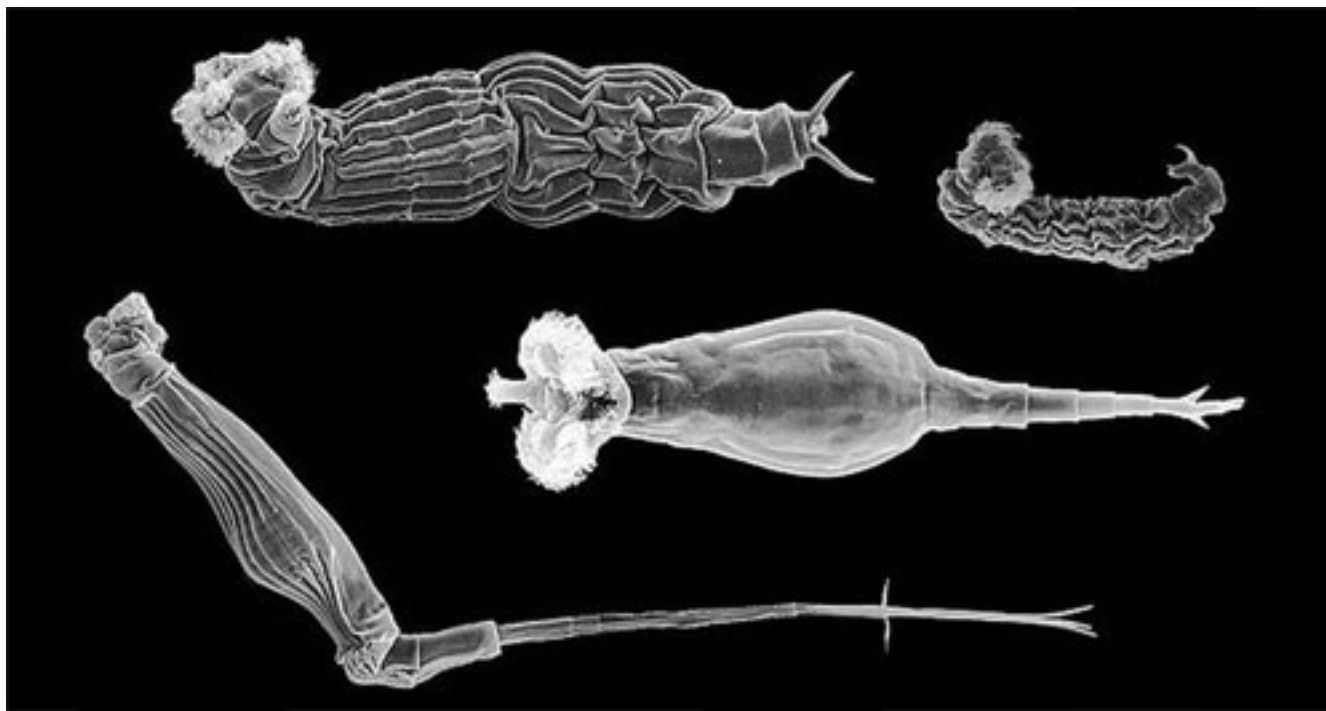
Poecilia formosa

Photo by Slaboch, R.



Cupressus dupreziana





Independently Evolving Species in Asexual Bdelloid Rotifers

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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

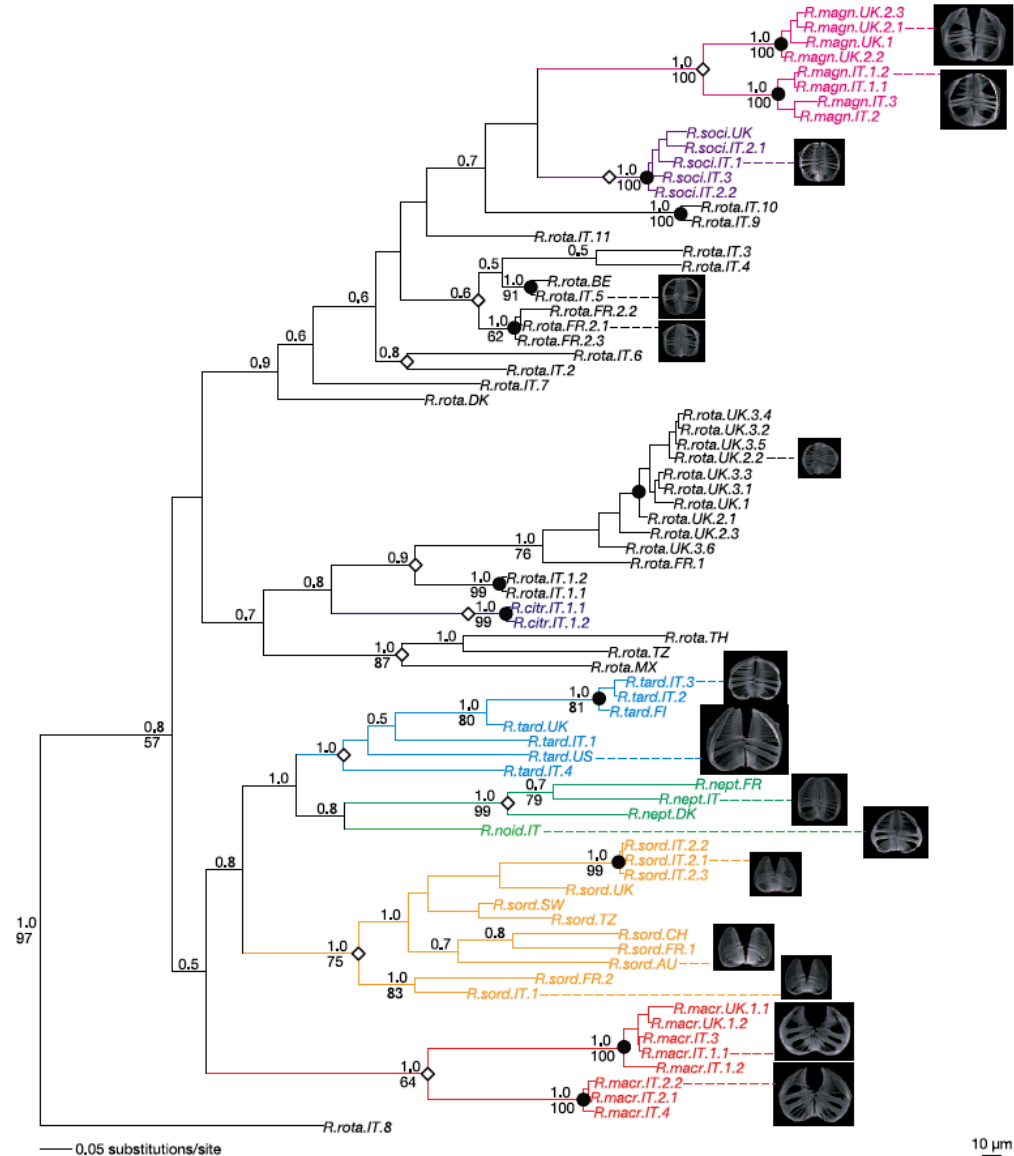


Figure 3. Phylogenetic Relationships in the Genus *Rotaria*

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

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.

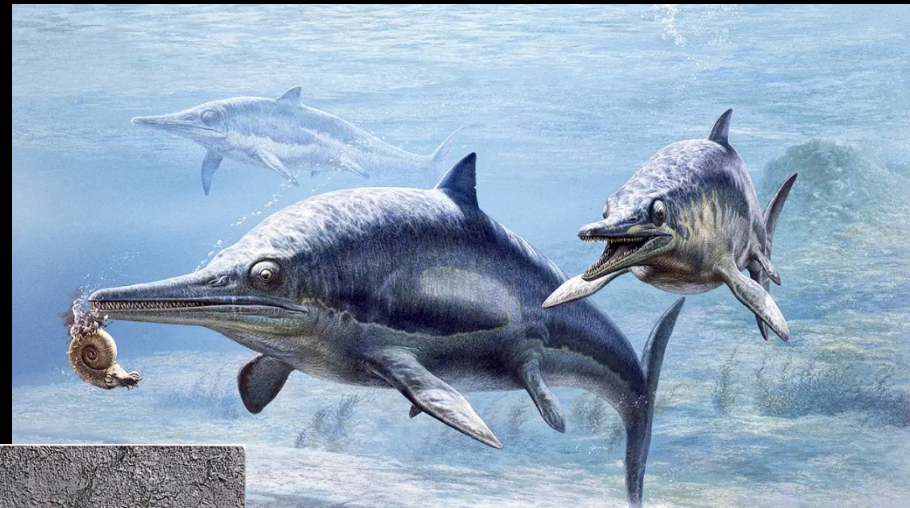
Horizontal gene transfer (HGT), the movement of genes from one organism to another by means other than direct descent (vertical inheritance), has been documented in prokaryotes (1) and in phagocytic and parasitic

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)





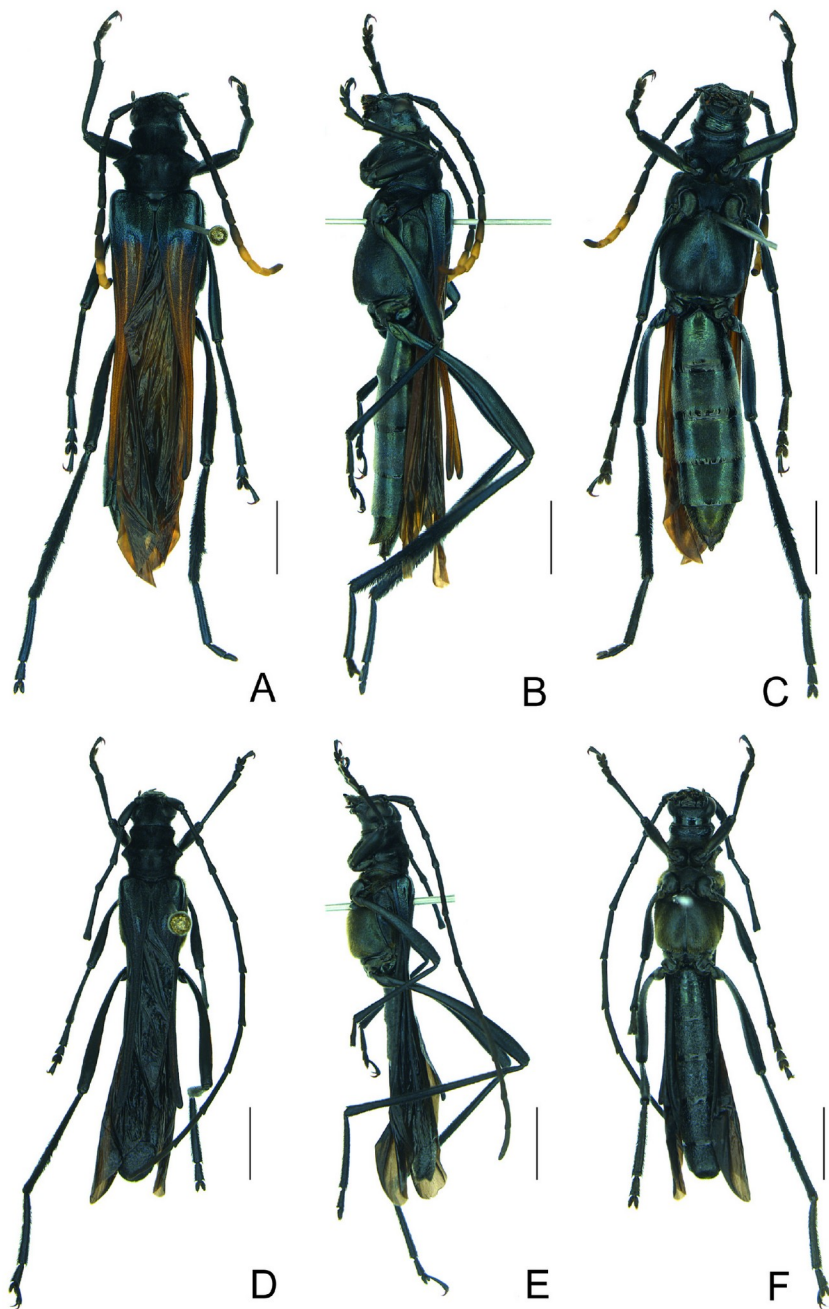


FIGURE 1A–F. *Parahephaestion mimicus* sp. nov. Habitus. Holotype female, A–C: A—Dorsal; B—Lateral; C—Ventral. Paratype male, D–F: D—Dorsal; E—Lateral; F—Ventral. Scale bars: (A–C) 5 mm, (D–F) 4 mm.

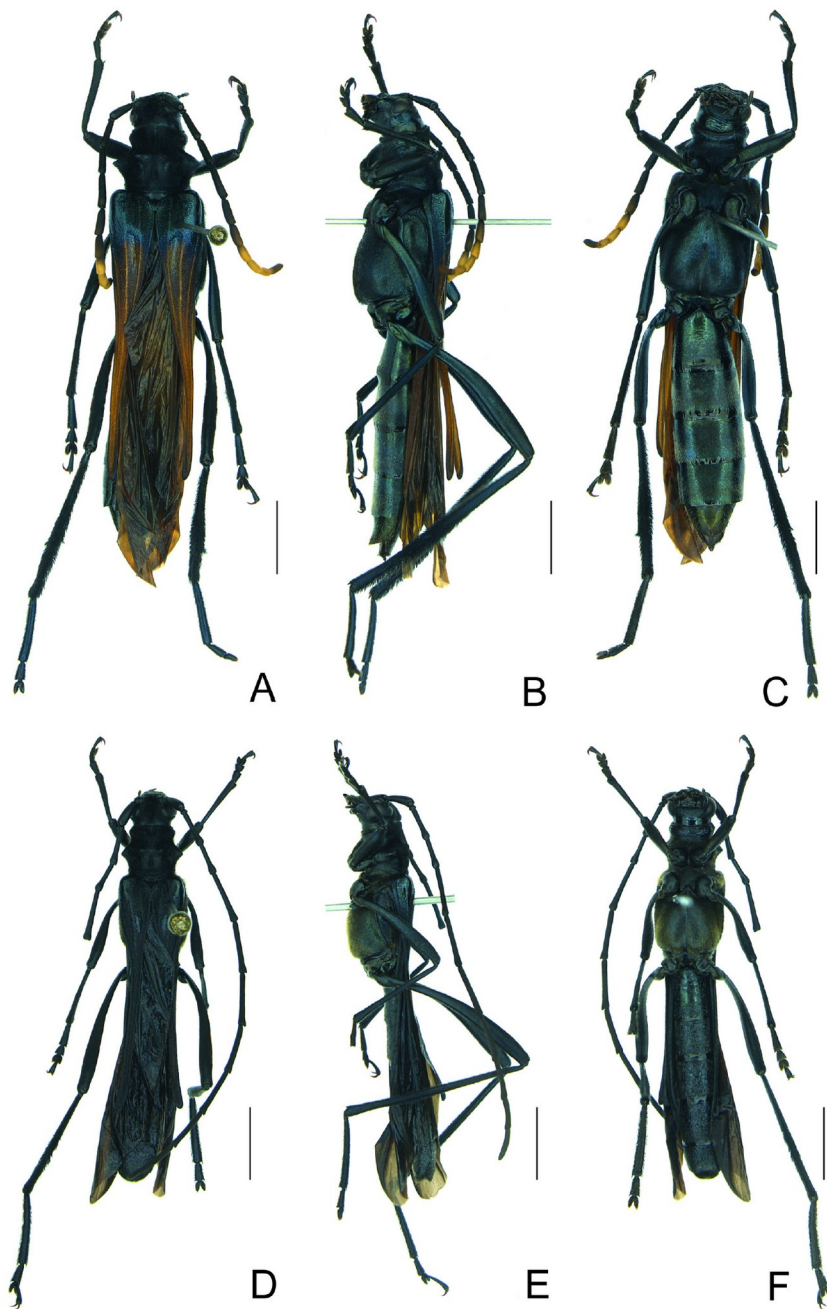


FIGURE 1A–F. *Parahephaeston mimicus* sp. nov. Habitus. Holotype female, A–C: A—Dorsal; B—Lateral; C—Ventral. Paratype male, D–F: D—Dorsal; E—Lateral; F—Ventral. Scale bars: (A–C) 5 mm, (D–F) 4 mm.

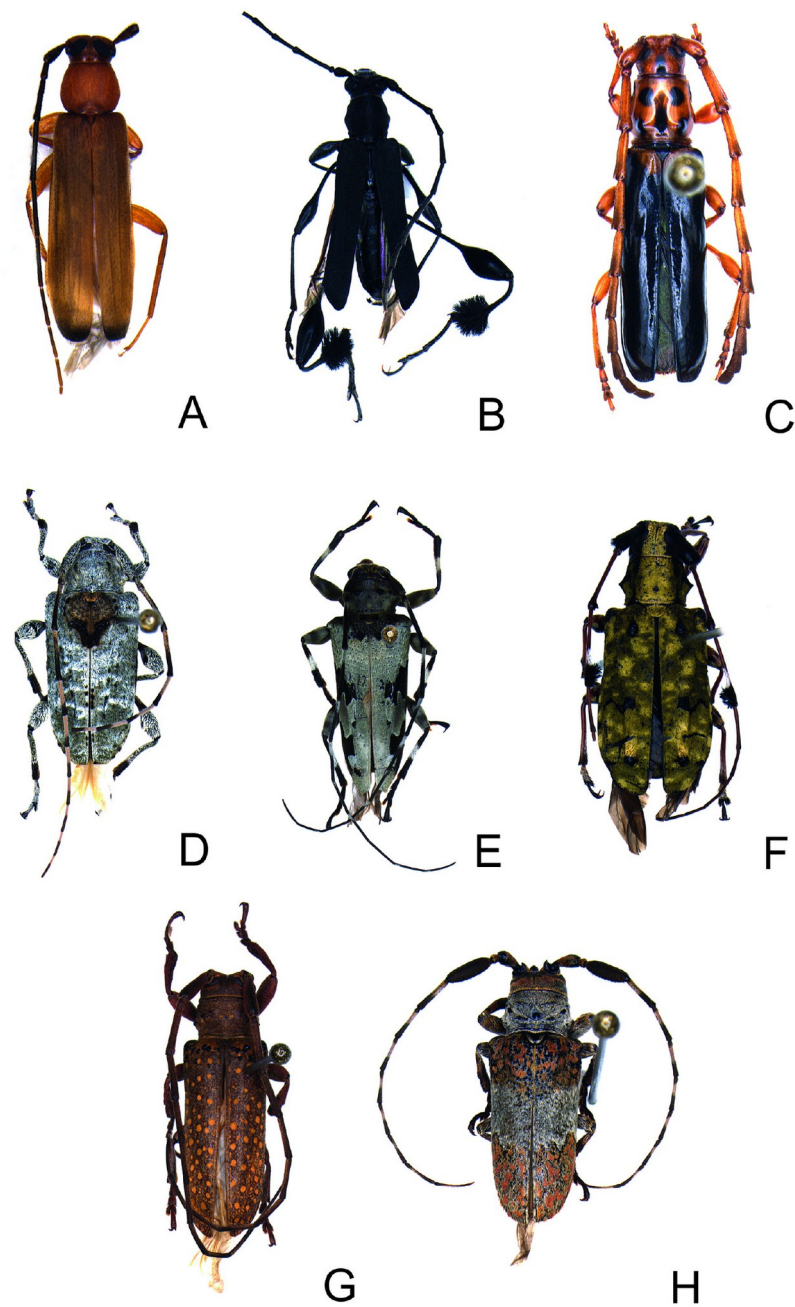


FIGURE 3A–H. New records in Cerambycidae. Dorsal habitus. A—*Sphalloeme costipennis* Melzer, 1928; B—*Thalusia atrata* (Melzer, 1918); C—*Trachelissa pustulata* (Audinet-Serville, 1834); D—*Ateralphus dejeani* (Lane, 1973); E—*Oreodera omissa* Melzer, 1932; F—*Phacellocera plumicornis* (Klug, 1825);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

<https://doi.org/10.11646/zootaxa.5418.3.7>

<http://zoobank.org/urn:lsid:zoobank.org:pub:80F6B5A7-0F3A-4AD5-9A21-73E161834F29>

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

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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

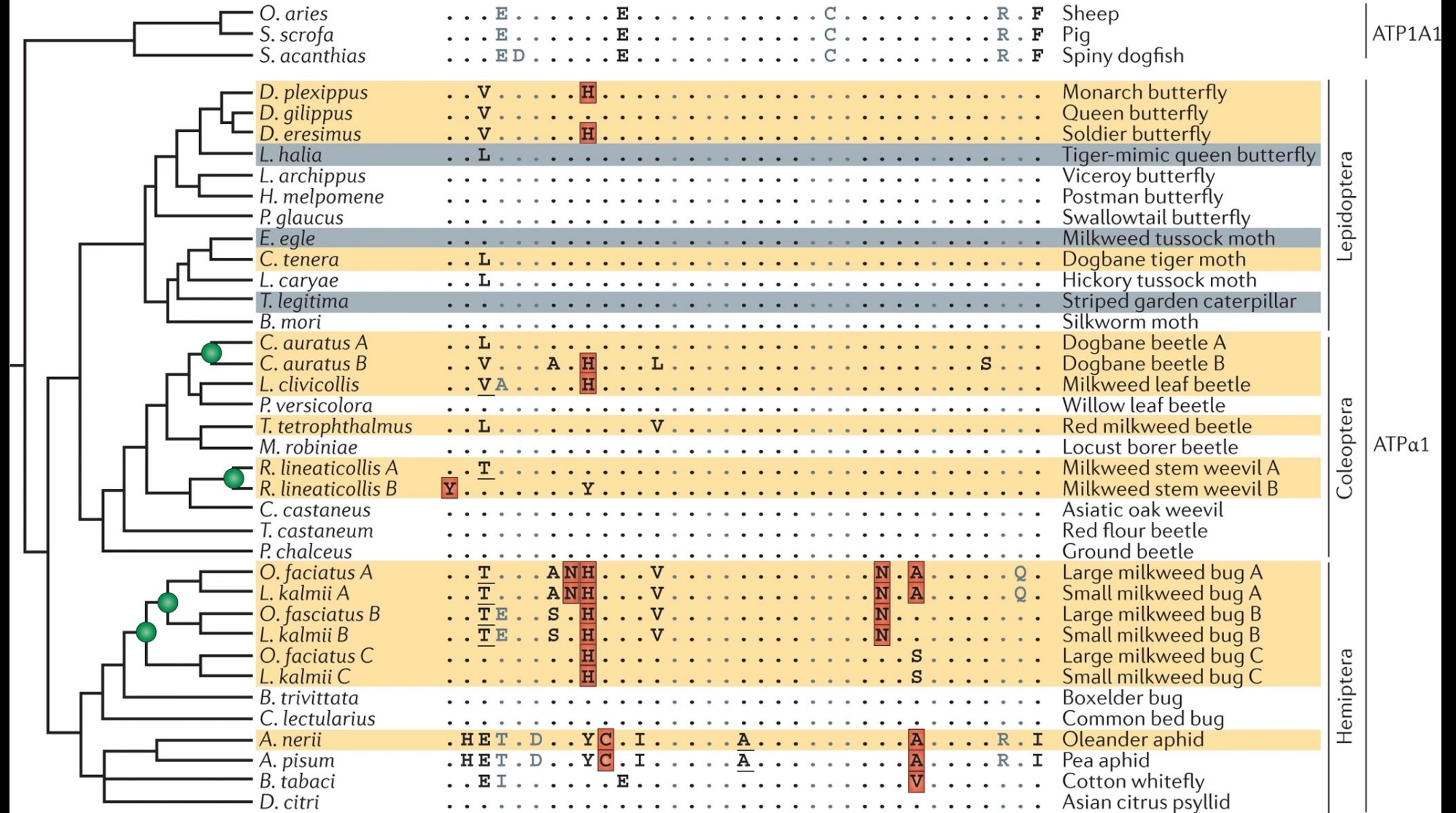
Eight subfamilies have been historically included in Cerambycidae: Cerambycinae, Dorcasominae, Lamiinae, Lepturinae, Necydalinae, Parandrinae, Prioninae, and Spondylidinae (Haddad *et al.* 2018). More recently, Necydalinae and Parandrinae have been recognized as part of Lepturinae and Prioninae, respectively, reducing the number of subfamilies to six (Nie *et al.* 2021).

Positions

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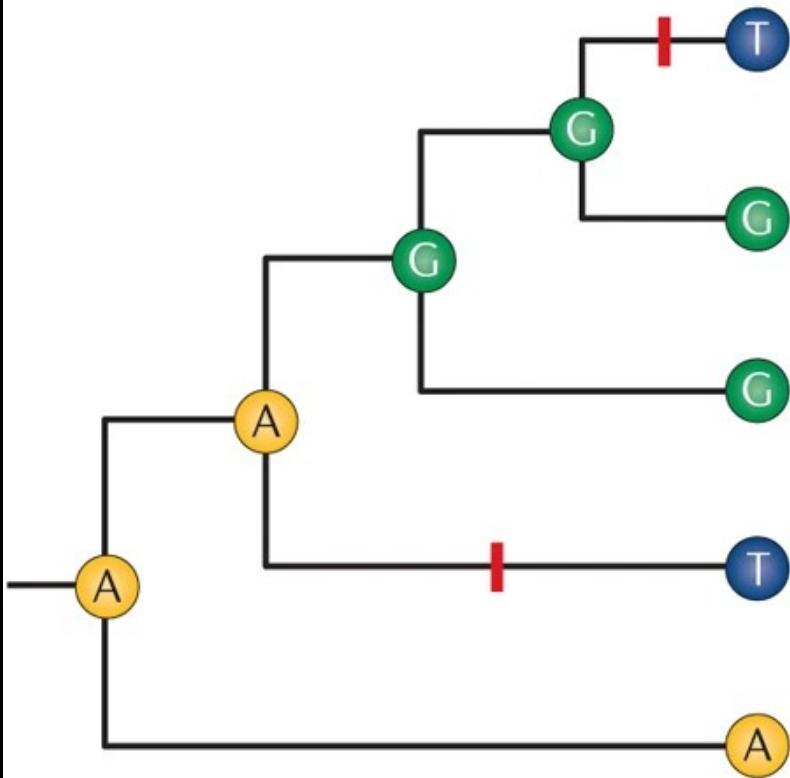
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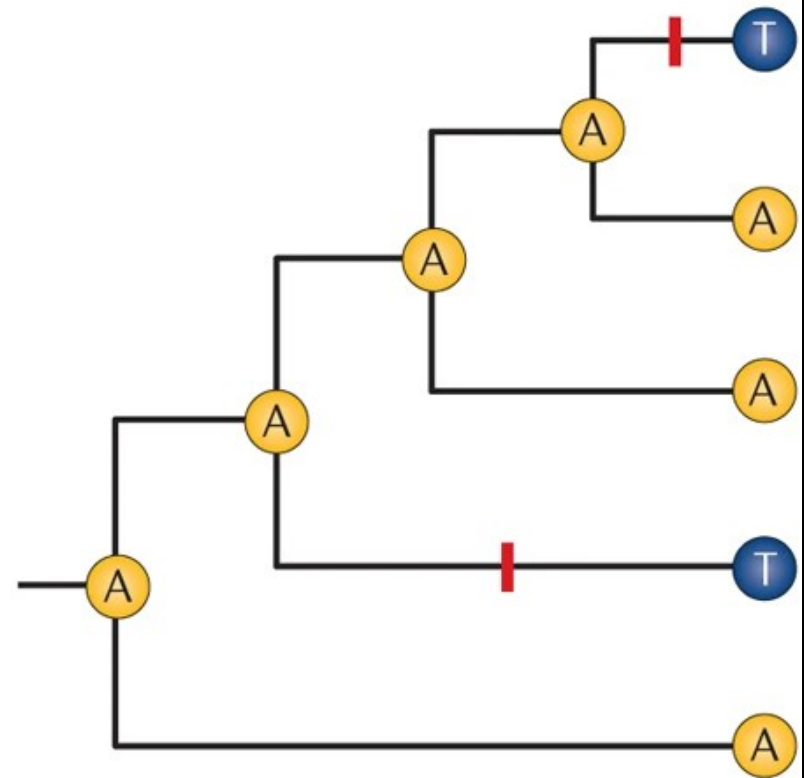
Parallel
Unique

1 12 2 2 5 1 1 1 2 1 2 1 1

a Convergent substitutions



b Parallel substitutions



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

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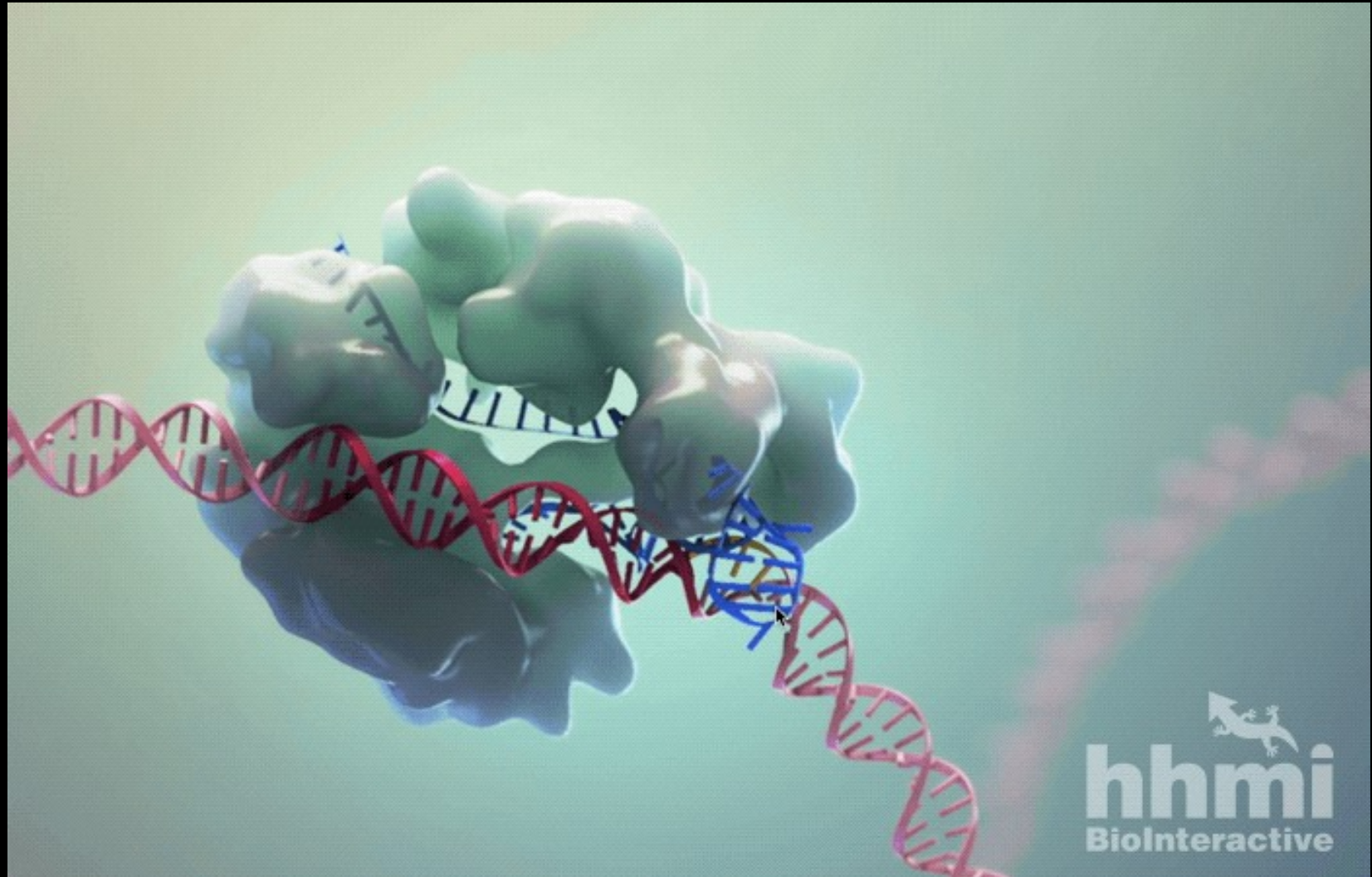
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Edmund R. R. Moody¹✉, Sandra Álvarez-Carretero¹,
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The nature of the last universal common ancestor (LUCA), its age and its impact on the Earth system have been the subject of vigorous debate across 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.

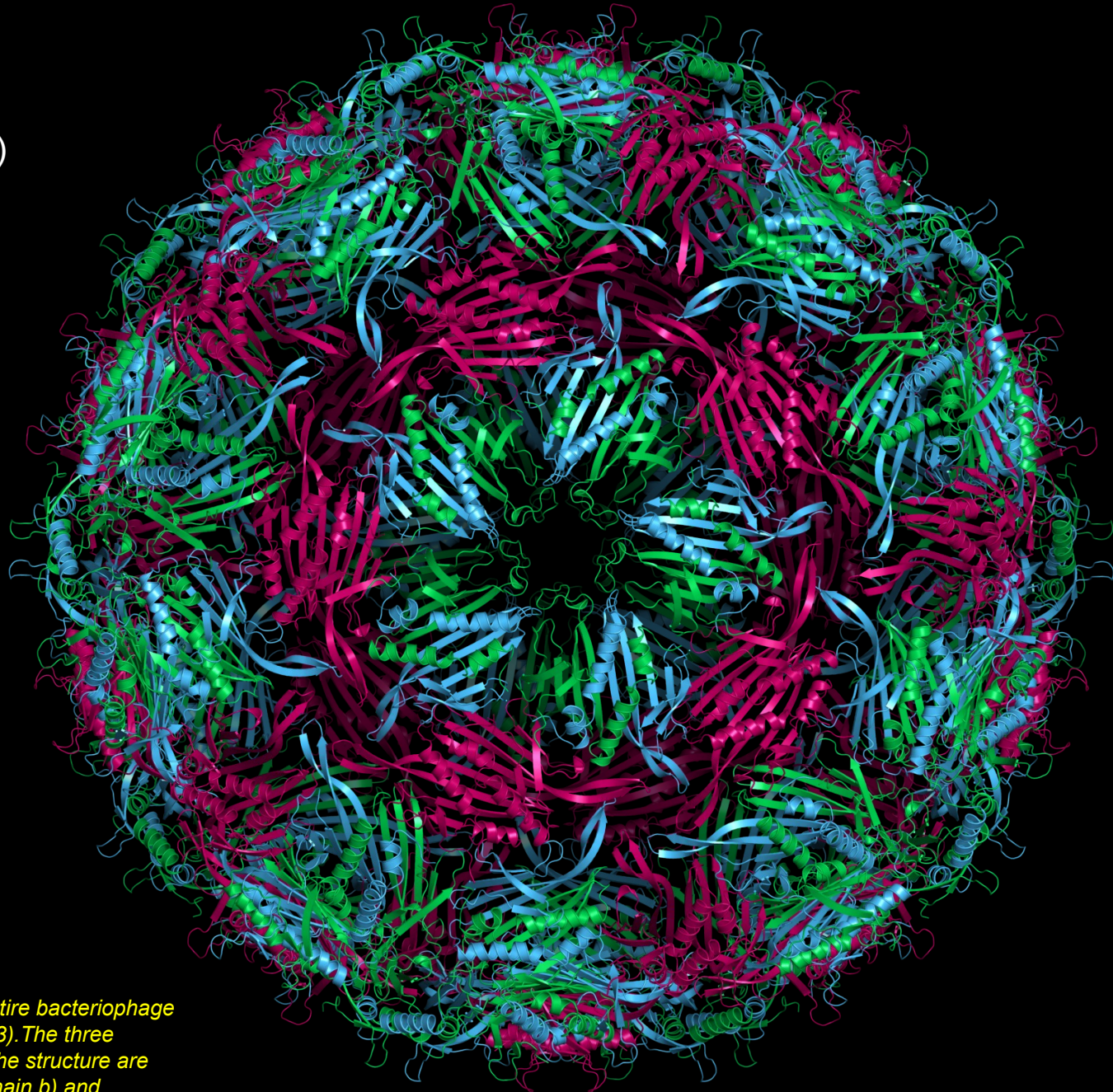
The common ancestry of all extant cellular life is evidenced by the universal genetic code, machinery for protein synthesis, shared chirality of the almost-universal set of 20 amino acids and use of ATP as a common energy currency¹. The last universal common ancestor (LUCA) is the node on the tree of 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 is² 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 proteins¹⁰ up to 1,529 different potential gene families⁴. Interpretations range from little beyond an information-processing



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.)

Emergence and natural selection of drug-resistant prions

James Shorter*

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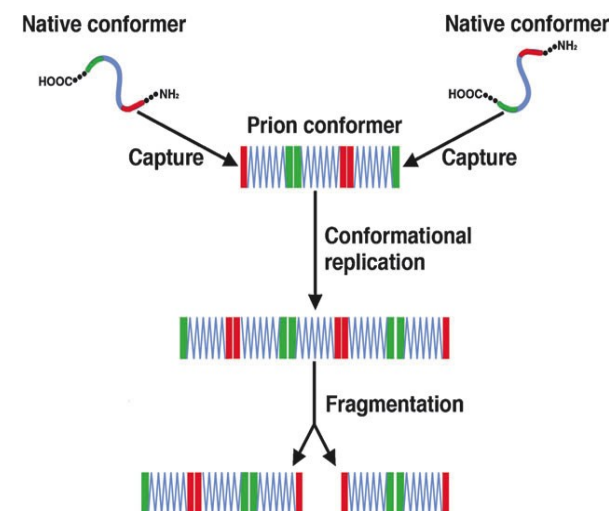
Drug resistance is a refractory barrier in the battle against many fatal diseases caused by rapidly evolving agents, including HIV, apicomplexans and specific cancers. Emerging evidence suggests that drug resistance might extend to lethal prion disorders and related neurodegenerative amyloidoses. Prions 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 the

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-replicating process.^{5,6,17} Fibers elongate at both ends by











<https://thenaturalhistorian.com/2013/12/31/>

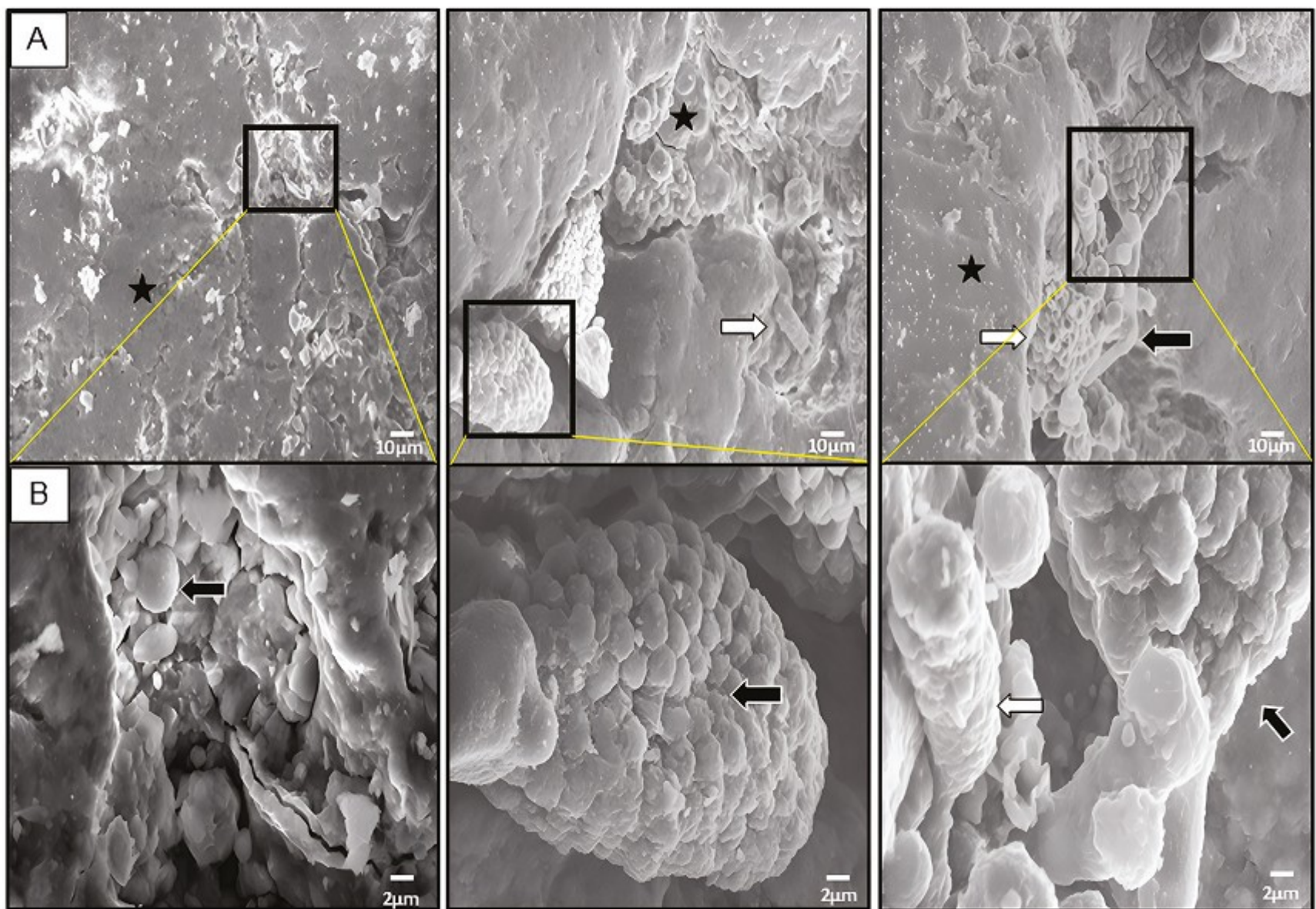


Figure 2 Analysis of varnish surface by SEM. A, Micrographs show many microorganisms morphologies embedded in the varnish such as: botryoidal biofilm (black star), ascomycetes colonies, hyphae and spores (black arrows), and tubular cells (white arrows). B, Magnification areas delimited by black rectangle (in A). Scale is indicated at bottom right by white bar (10 μm in A and 2 μm in B, respectively) (from: Aguirre Ramírez et al., 2025)