Seminario Virtual de

Ciencias Biológicas

Re-Expedición Colombia:

Ecología, Evolución y Conservación Tras un Siglo de Cambio en las Aves y sus Hábitats

Dr. Carlos Daniel Cadena

Departamento de Ciencias Biológicas

Universidad de los Andes

Universidad de los Andes

Facultad de Ciencias

Jueves 26 de marzo de 2020

12:30 p.m.

https://cornell.zoom.us/j/513106519

Miércoles 25 de marzo

Instrucciones

La primera media hora de la clase la vamos a dedicar a ver un vídeo de una conferencia dictada por Trevor Bedford, uno de los cerebros detrás de Nexstrain, un proyecto de acceso libre que busca explotar el potencial científico y de salud pública de datos genómicos de patógenos. Vea por su cuenta la conferencia titulada "Real-time Tracking of Virus Evolution" y nos encontraremos en la ventana de **clase remota** a las 10 am. Anote cualquier pregunta que le surja para discturir en el espacio de reunión virtual que tendremos.

Desarrollo

Luego de que los estudiantes vieron la conferencia, hicimos un pequeño sondeo. Una pregunta apuntaba a examinar si habían prestado atención, y a conectar con un mensaje que quería dejarles hoy y que describo más adelante. Otra pregunta buscaba mostrarles que la terminología que se usa en sistemática filogenética es aplicable al caso del estudio de epidemias. Si bien varios no contestaron correctamente esta última, en la discusión demostramos la correcta utilización de los conceptos de monofilia y parafilia con base en ejemplos de filogenias de los virus de Zika y Ebola.

Luego, conectando con la primera pregunta del sondeo, ilustramos lo que parece ser un patrón común en epidemias: los virus circulan en poblaciones humanas tiempo antes de que se manifiesten con efectos evidentes en la salud humana. Así sucedió con (1) HIV en los Estados Unidos en los 70s, (2) Zika en Brasil en 2014-2015 y (3) COVID-19 en el estado de Washington, Estados Unidos, en 2020. El COVID-19 circuló sin ser detectado por semanas en Washington, pero el caso de Zika en Brasil tomó un año y medio y el de HIV en Estados Unidos varios años. Este mensaje motivó preguntas de los estudiantes y nos permitió discutir brevemente sobre la importancia de las pruebas de diagnóstico para efectos de vigilancia epidemiológica. Mencionamos, en respuesta a una pregunta, que la demora entre la llegada de los virus a un lugar y su efecto evidente en salud pública puede deberse tanto a las demoras en la incubación de la enfermedad en los infectados (como en COVID-19) como a posibles cambios en el virus que incrementan su virulencia o transmisibilidad (como en HIV).

Cerramos la cesión haciéndoles ver a los estudiantes que para inferir cuál fue el momento de introducción de un agente infeccioso a un lugar tenemos que hacer suposiciones que se basan en principios de evolución. Por esto mañana nos encontraremos para una clase virtual sobre bases de evolución molecular necesarias para continuar estudiando este tema.

The History in Our Genes

Learning Objectives

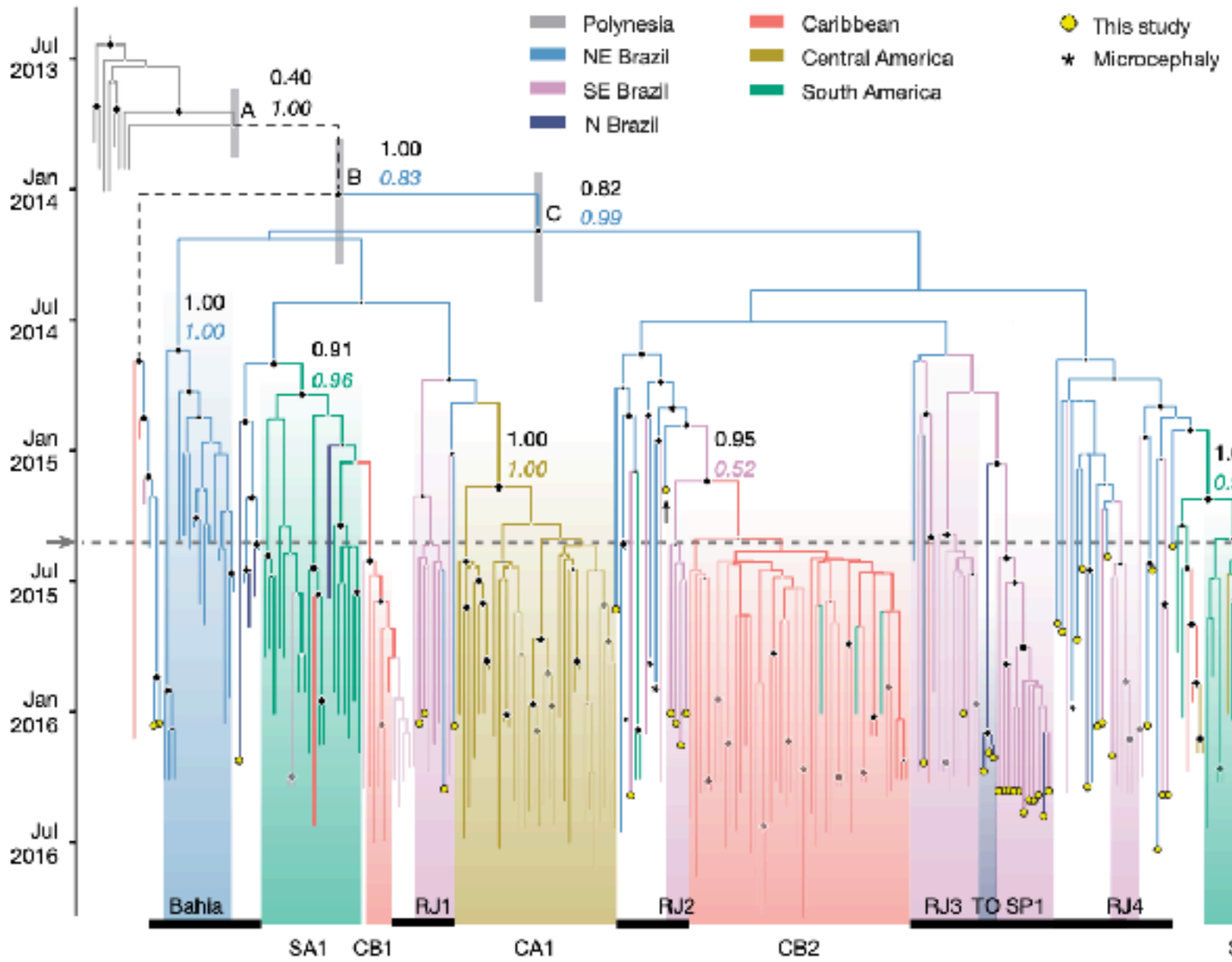
- Explain how and why gene trees can be different from species trees.
- Explain coalescence.
- Describe the methods scientists use to construct phylogenetic trees.
- Describe three examples of how DNA has been used to examine phylogenetic relationships.
- Compare and contrast neutral evolution and natural selection.
- Explain how molecular clocks can be used to deduce the timing of evolutionary events.
- Compare the effects of positive and purifying selection on synonymous and replacement substitutions within a pseudogene.

LETTER

doi:10.1038/nature22401

Establishment and cryptic transmission of Zika virus in Brazil and the Americas

N. R. Faria[1,2]*, J. Quick[2]*, I. M. Claro[3]*, J. Thézé[3]*, J. G. de Jesus[3]*, M. Giovanetti[3,4]*, M. U. G. Kraemer[1,5,6]*, S. C. Hill[3]*, A. Black[3,7]*, A. C. da Costa[4], L. C. Franco[2], S. P. Silva[2], C.-H. Wu[1], J. Raghwani[1], S. Cauchemez[1,2,3], L. du Plessis[1], M. P. Verotti[11], W. K. de Oliveira[12,13], E. H. Carmo[17], G. E. Coelho[18,19], A. C. F. S. Santelli[18,20], L. C. Vinhal[18], C. M. Henriques[17], J. T. Simpson[21], M. Loose[22], K. G. Andersen[23], N. D. Grubaugh[23], S. Somasekar[24], C. Y. Chiu[24], J. E. Muñoz-Medina[25], C. R. Gonzalez-Bonilla[25], C. F. Arias[26], L. L. Lewis-Ximenez[27], S. A. Baylis[28], A. O. Chieppe[29], S. F. Aguiar[29], C. A. Fernandes[29], P. S. Lemos[2], B. L. S. Nascimento[2], H. A. O. Monteiro[2], I. C. Siqueira[2], M. G. de Queiroz[2], T. R. de Souza[30,31], J. F. Bezerra[31,32], M. R. Lemos[31], G. F. Pereira[33], D. Loudal[1,3], L. C. Moura[33], R. Dhalia[34], R. F. França[34], T. Magalhães[34,35], E. T. Marques Jr[34], T. Jaenisch[37], G. L. Wallau[34], M. C. de Lima[38], V. Nascimento[38], E. M. de Cerqueira[38], M. M. da Lima[39], D. L. Mascarenhas[40], J. P. Moura Neto[40], A. S. Levin[4], T. R. Tozetto-Mendoza[4], S. N. Fonseca[41], M. C. Mendes-Correa[4], F. P. Milagres[41], A. Segurado[4], E. C. Holmes[44], A. Rambaut[45,46], T. Bedford[9], M. R. T. Nunes[2,47]§, E. C. Sabino[3]§, L. C. J. Alcantara[3]§, N. J. Loman[7]§ & O. G. Pybus[1,48]§

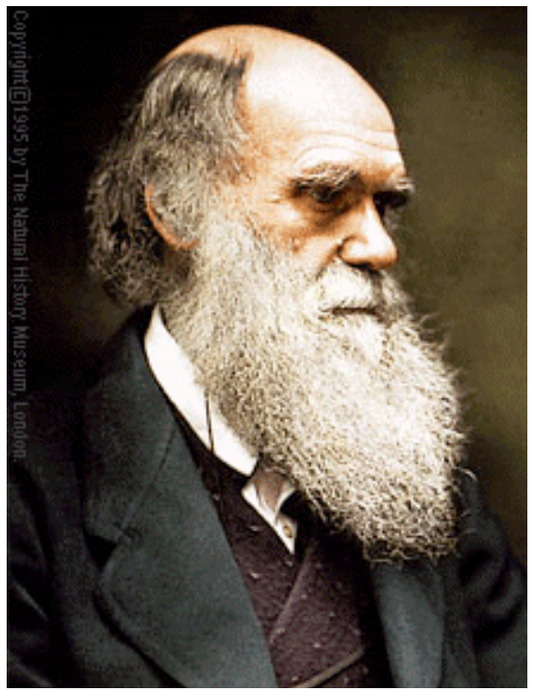


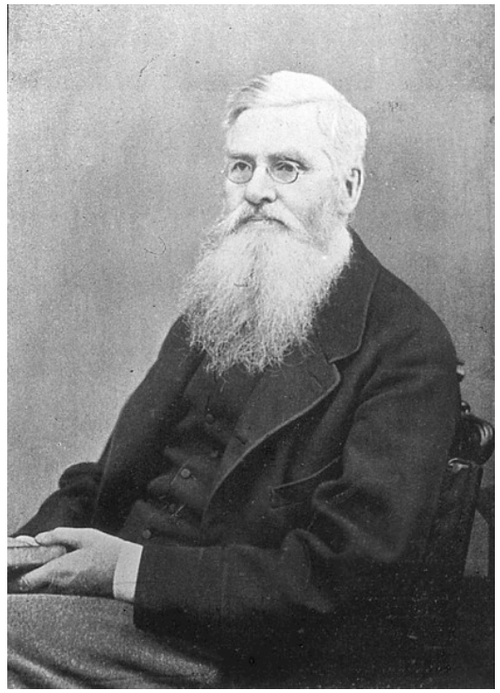
https://bedford.io/pdfs/papers/faria-zika-in-brazil.pdf

¿qué más podemos aprender con datos como estos?

definición de evolución:

el cambio a través del tiempo, en una población, en la proporción de organismos con diferencias genéticas en uno o más rasgos (cambio de frecuencias de genotipos)





Síntesis Moderna (1930-1950)

R. A. Fisher

J. B. S. Haldane

S. Wright

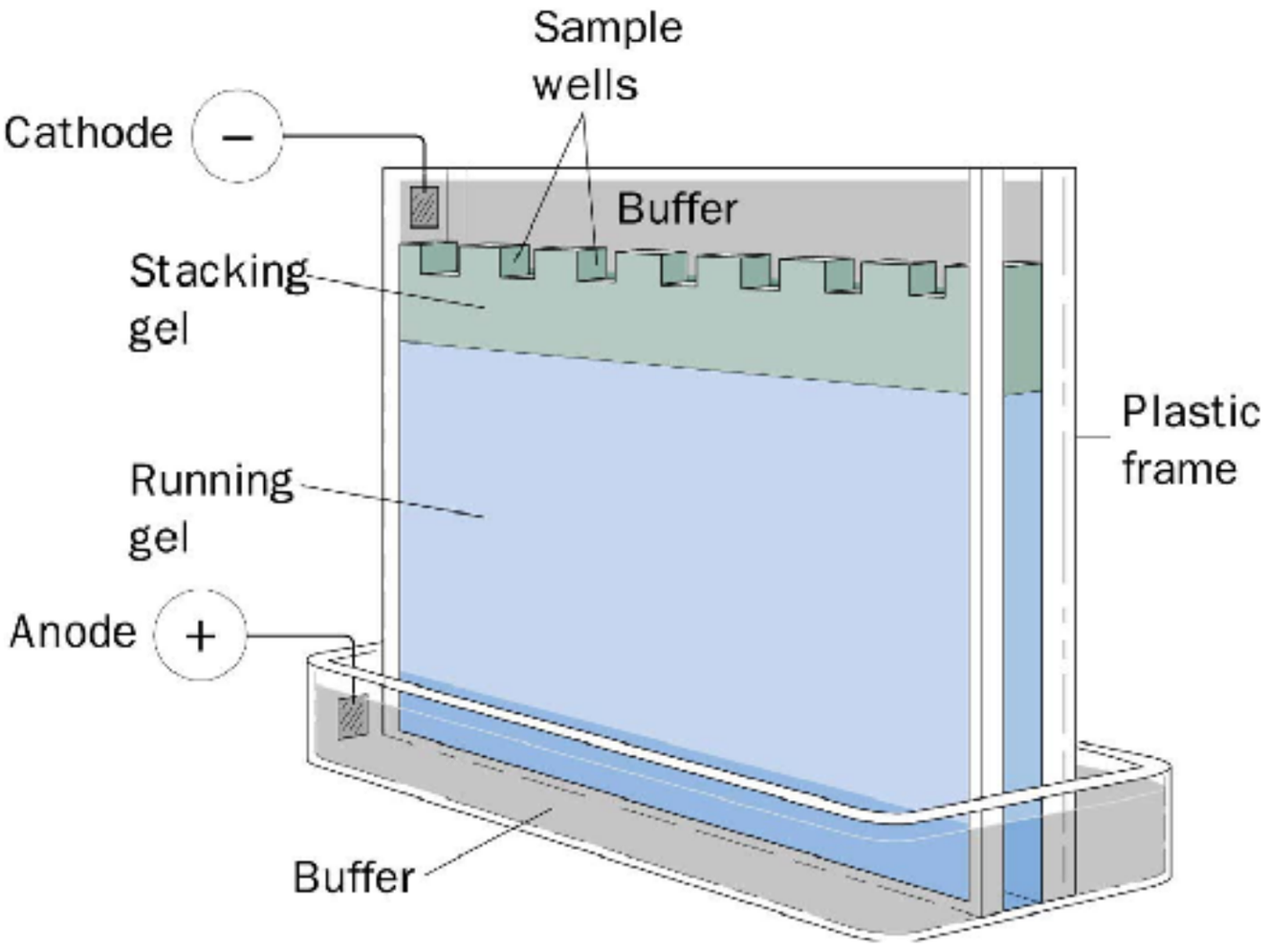
E. Mayr

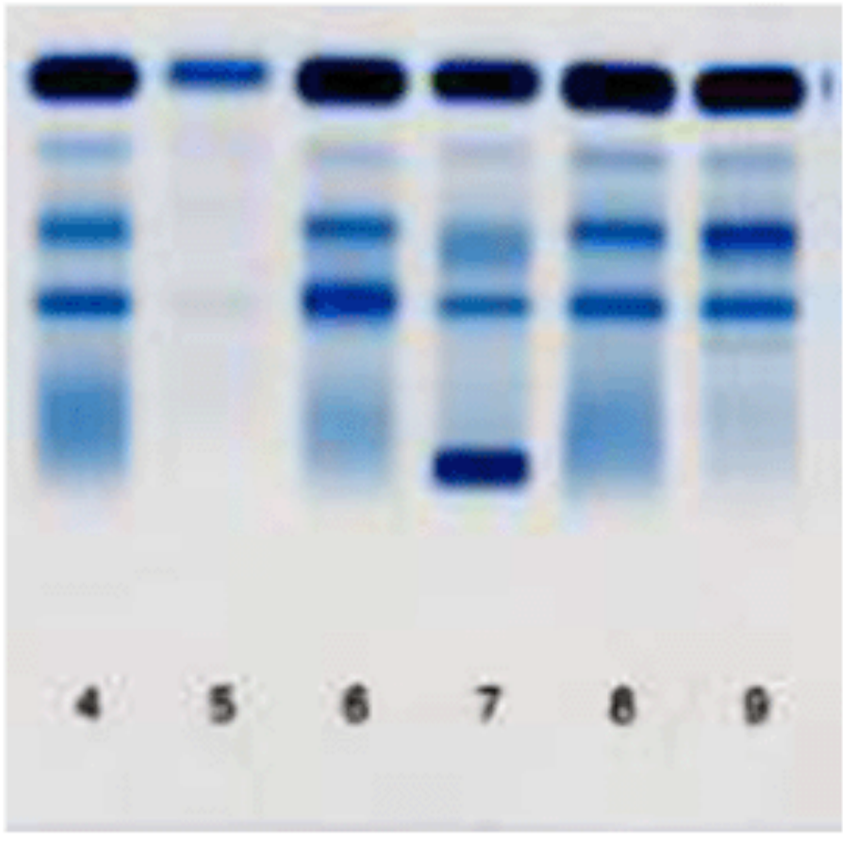
G. L. Stebbins G. G. Simpson T. Dobzhansky

El cambio evolutivo (modificación del acervo genético de las poblaciones) se explica por:

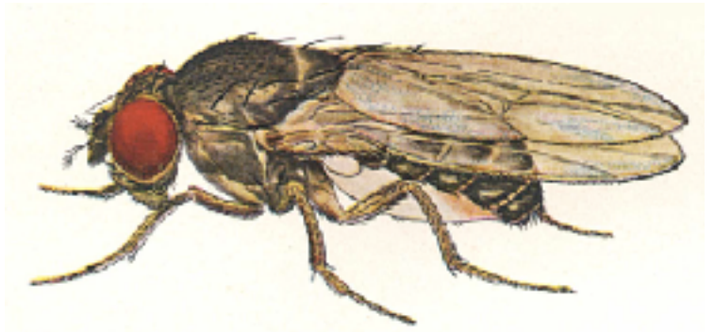
mutación, (recombinación), deriva, selección, migración

1960's: electroforesis de proteínas





Richard Lewontin y el estudio de la variación genética en poblaciones



A MOLECULAR APPROACH TO THE STUDY OF GENIC HETEROZYGOSITY IN NATURAL POPULATIONS. II. AMOUNT OF VARIATION AND DEGREE OF HETEROZYGOSITY IN NATURAL POPULATIONS OF *DROSOPHILA PSEUDOOBSCURA*[1]

R. C. LEWONTIN AND J. L. HUBBY

Using genetic differences in electrophoretic mobility, demonstrated by HUBBY and LEWONTIN (1966) to be single Mendelian alternatives, we have surveyed the allelic variation in samples from five natural populations of *D. pseudoobscura*. Out of 18 loci randomly chosen, seven are shown to be clearly polymorphic in more than one population and two loci were found to have a rare local variant segregating. Thus, 39% of loci in the genome are polymorphic over the whole species. The average population is polymorphic for 30% of all loci. The estimates of gene frequency at these loci enable us to estimate the proportion of all loci in an individual's genome that will be in heterozygous state. This value is between 8% and 15% for different populations, with an average of 12%. A suggestion of a relationship has been observed between the extent of this heterogeneity and the amount of inversion polymorphism in a population.—An examination of the various biases in the experiment shows that they all conspire to make our estimate of polymorphism and heterozygosity lower than the true value. There is no simple explanation for the maintenance of such large amounts of genic heterozygosity.

Genetics 54: 595–609 August 1966.

http://www.youtube.com/watch?v=iBZJWyGh1EI

Motoo Kimura (1924-1994) y la Teoría Neutral de Evolución Molecular

Evolutionary Rate at the Molecular Level

by
MOTOO KIMURA

National Institute of Genetics,
Mishima, Japan

Calculating the rate of evolution in terms of nucleotide substitutions seems to give a value so high that many of the mutations involved must be neutral ones.

Finally, if my chief conclusion is correct, and if the neutral or nearly neutral mutation is being produced in each generation at a much higher rate than has been considered before, then we must recognize the great importance of random genetic drift due to finite population number[23] in forming the genetic structure of biological populations. The significance of random genetic drift has been deprecated during the past decade. This attitude has been influenced by the opinion that almost no mutations are neutral, and also that the number of individuals forming a species is usually so large that random sampling of gametes should be negligible in determining the course of evolution, except possibly through the "founder principle"[24]. To emphasize the founder principle but deny the importance of random genetic drift due to finite population number is, in my opinion, rather similar to assuming a great flood to explain the formation of deep valleys but rejecting a gradual but long lasting process of erosion by water as insufficient to produce such a result.

NATURE, VOL. 217, FEBRUARY 17, 1968

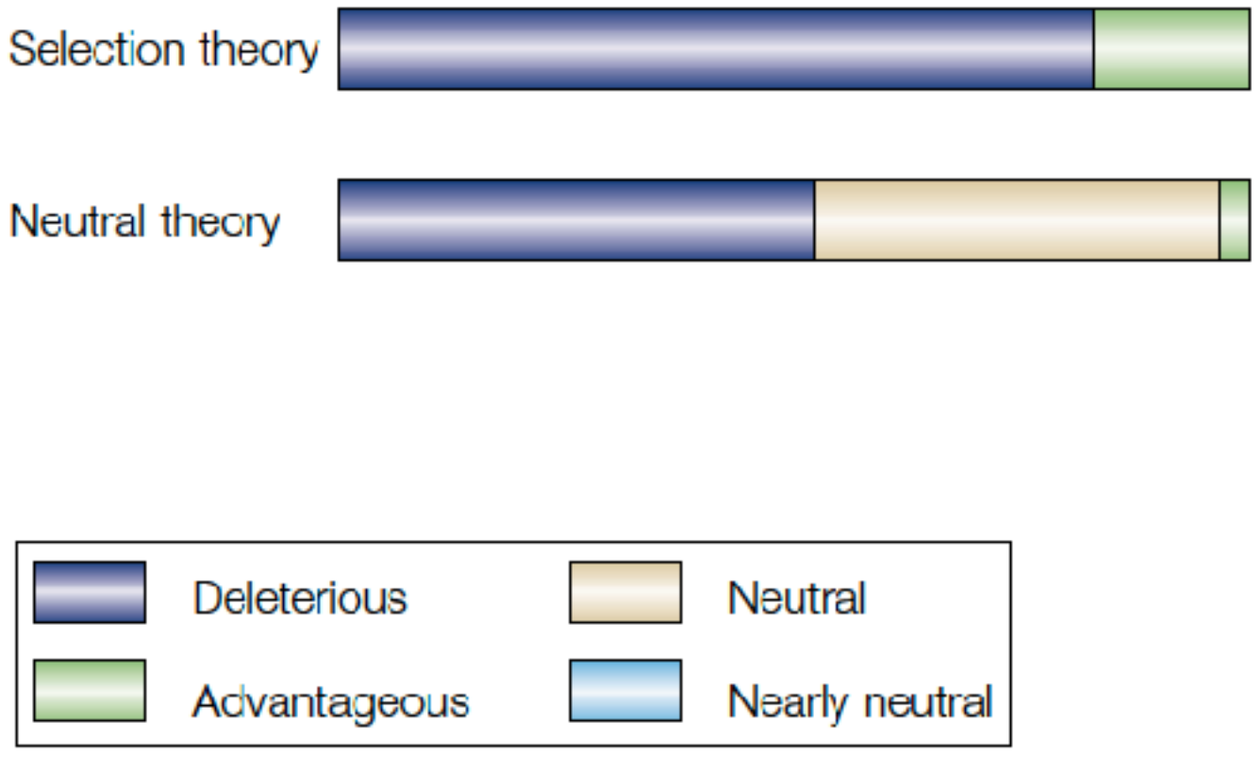
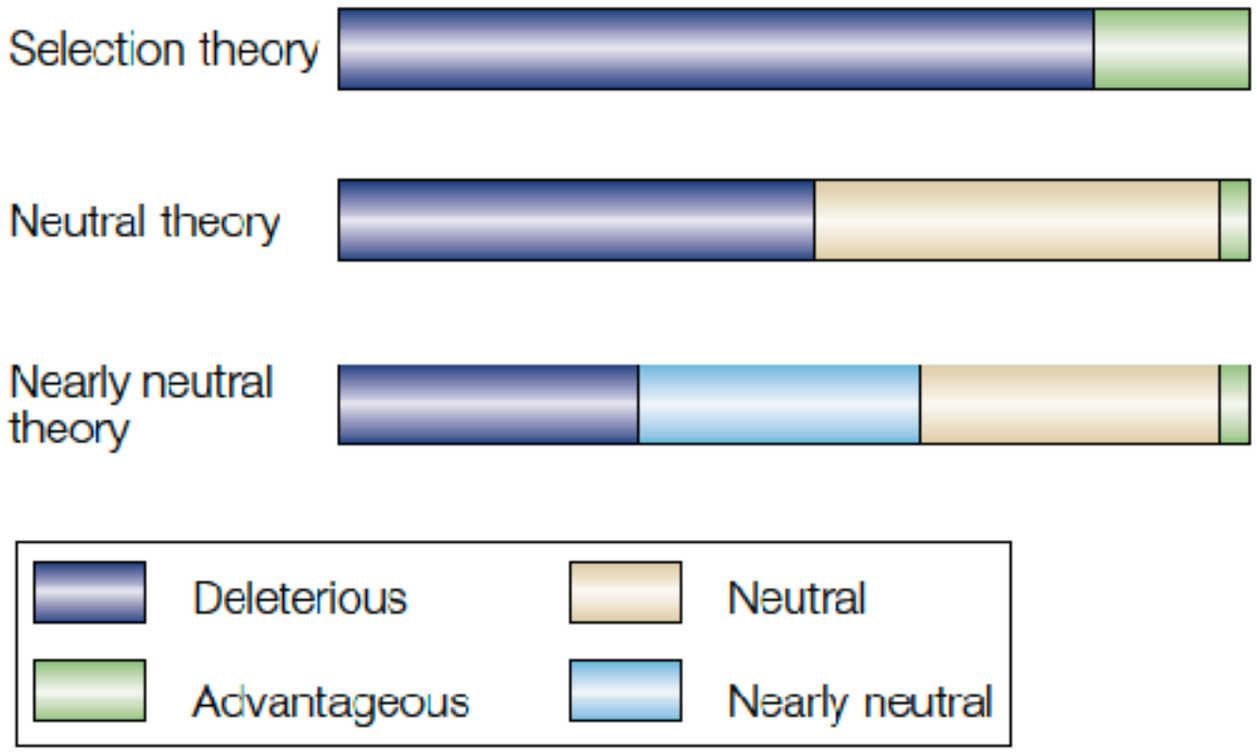


Figure 1 | **Selectionist, neutral and nearly neutral theories.** **a** | Selectionist theory: early neo-Darwinian theories assumed that all mutations would affect fitness and, therefore, would be advantageous or deleterious, but not neutral. **b** | Neutral theory: the neutral theory considered that, for most proteins, neutral mutations exceeded those that were advantageous, but that differences in the relative proportions of neutral sites would influence the rate of molecular evolution (that is, more neutral sites would produce a faster overall rate of change)



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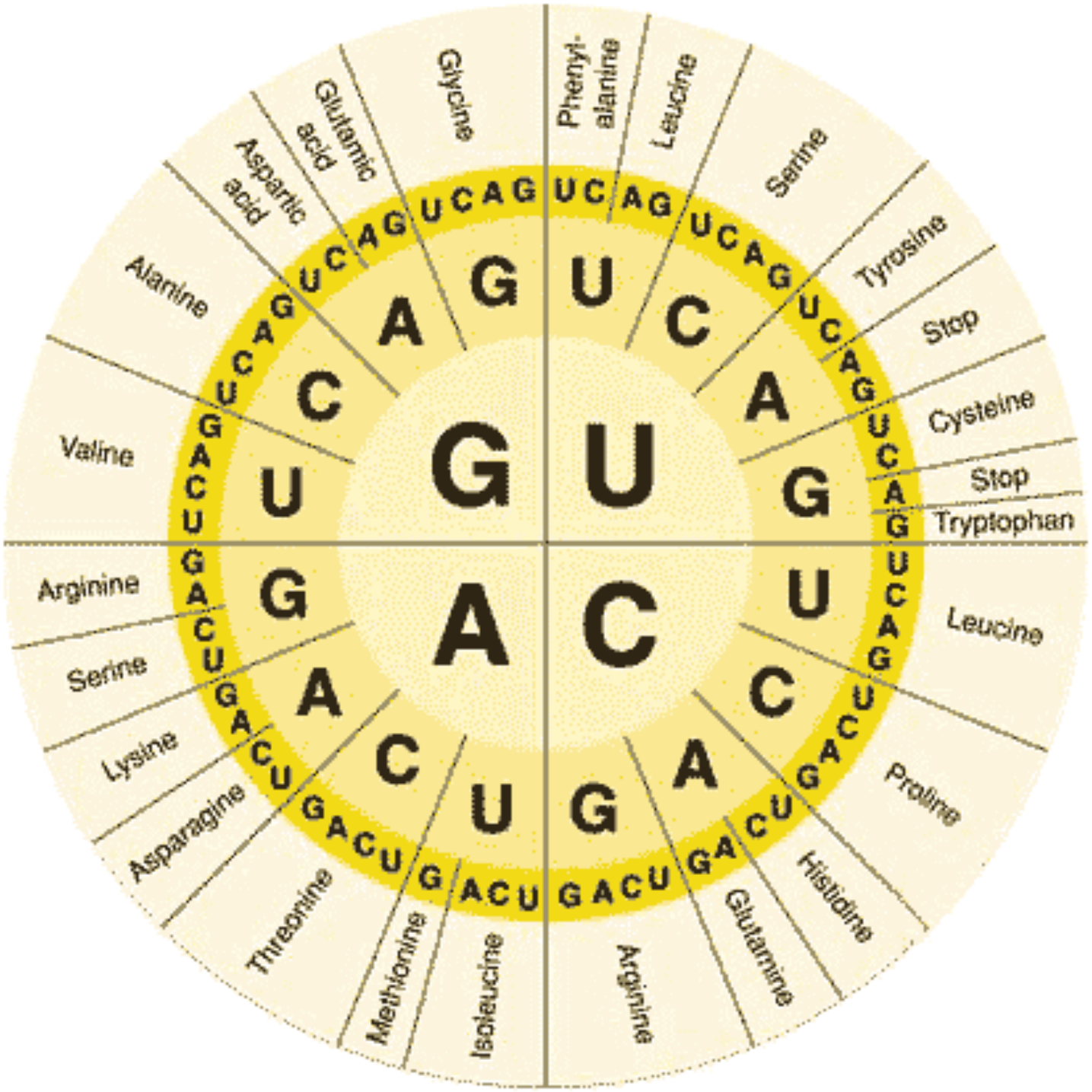
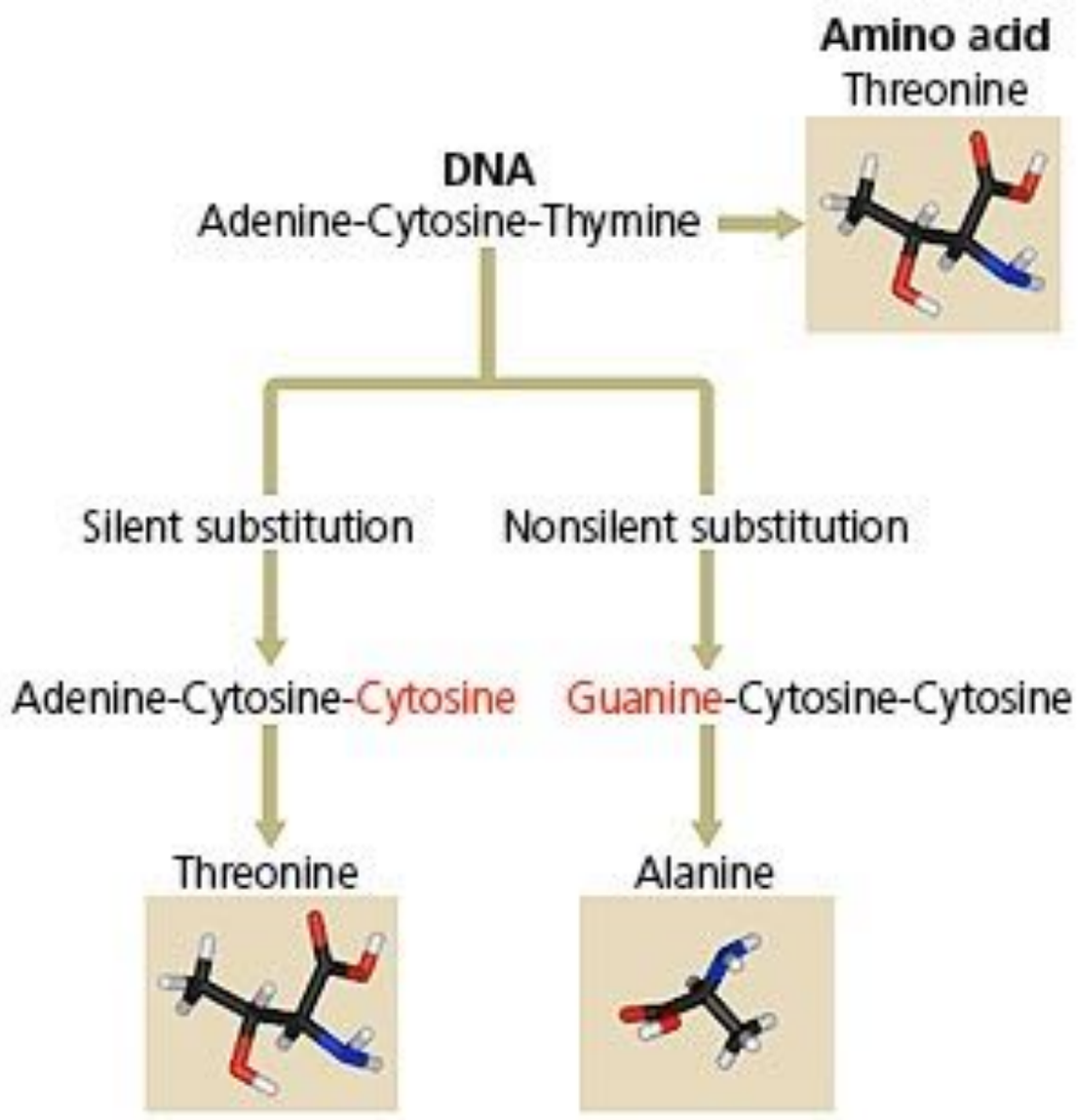
Box 4 | The nearly neutral theory: population size and the molecular clock

Tomoko Ohta[22–24] provided an important extension of the neutral theory by recognizing the crucial role of effective population size in the influence of selection. Slightly deleterious mutations will tend to be removed by selection in very large populations; however, they can be fixed by chance in smaller populations in which selection can be overpowered by random sampling events (GENETIC DRIFT). Ohta showed that the fixation of these nearly neutral mutations with small selection coefficients (s), whether positive or negative, would be governed by chance events in small populations, just as if they were neutral. So, a mutation would be effectively neutral if $|s| < 1/4N_e$, where N_e is the effective population size. In other words, whether a mutation behaves according to the neutral expectation is determined not simply by the selection properties of the mutation (s), but also the size of the population in which it arises (N_e). Ohta then considered the fate of a range of slightly deleterious or slightly advantageous mutations with a VARIANCE on their selection coefficients (σ_s) — some will be slightly deleterious and some slightly advantageous. Mutations are divided into three categories: mutations for which selection is the predominant force ($4N_e\sigma_s > 3$); nearly neutral mutations, which are governed by both selection and drift ($3 \geq 4N_e\sigma_s \leq 0.2$); and effectively neutral mutations, the fate of which is determined only by drift ($4N_e\sigma_s < 0.2$). So, the nearly neutral theory describes how the rate of molecular evolution can vary not only with changes in the mutation rate, but also through the changing balance between selection and drift.

El Código Genético es “Redundante”: Implicaciones



Lectura de Procesos Evolutivos en Alfabeto ACTG



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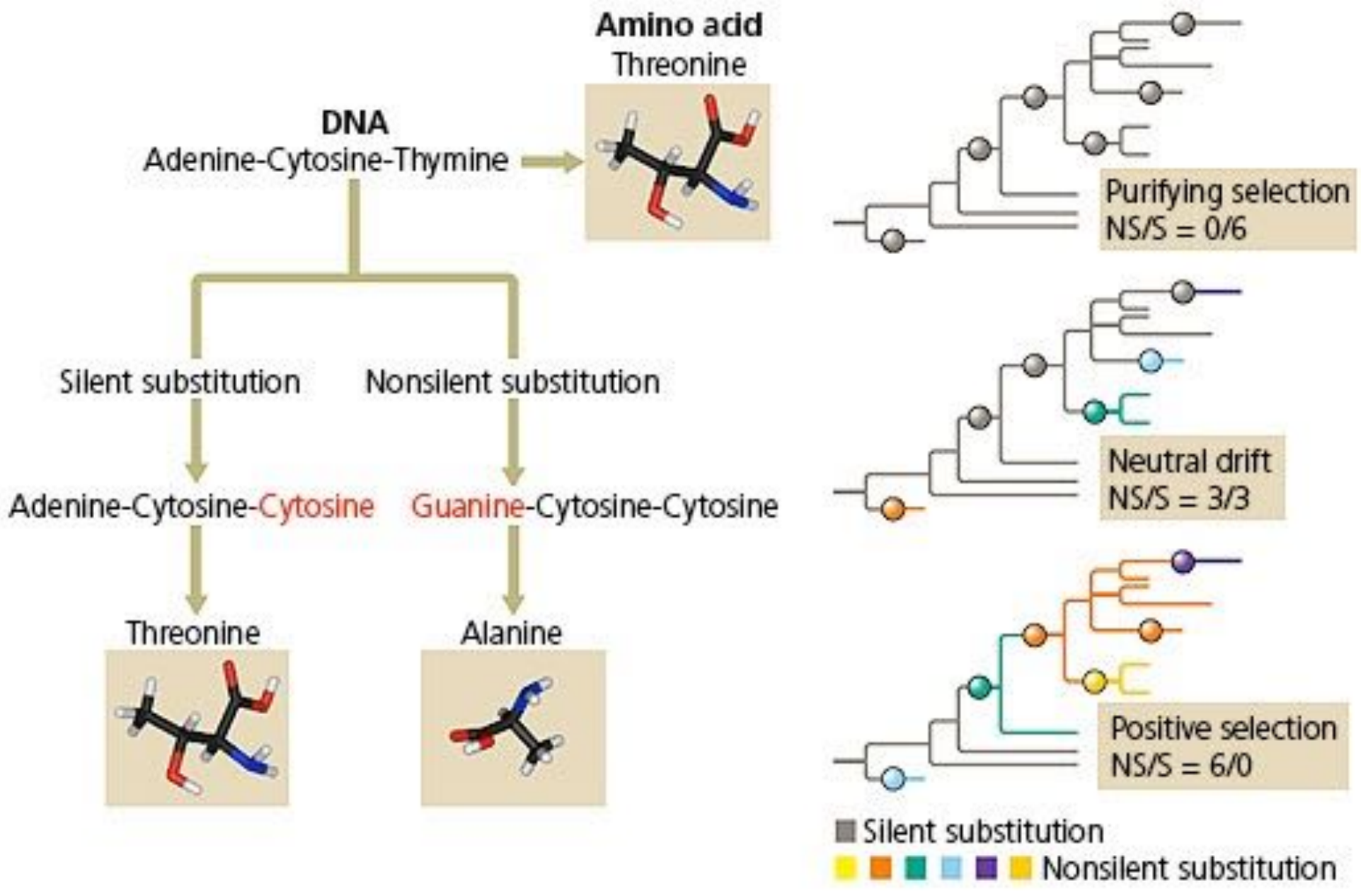

evaluación de la teoría neutral:
la mayoría de genes parecen evolucionar por selección purificadora

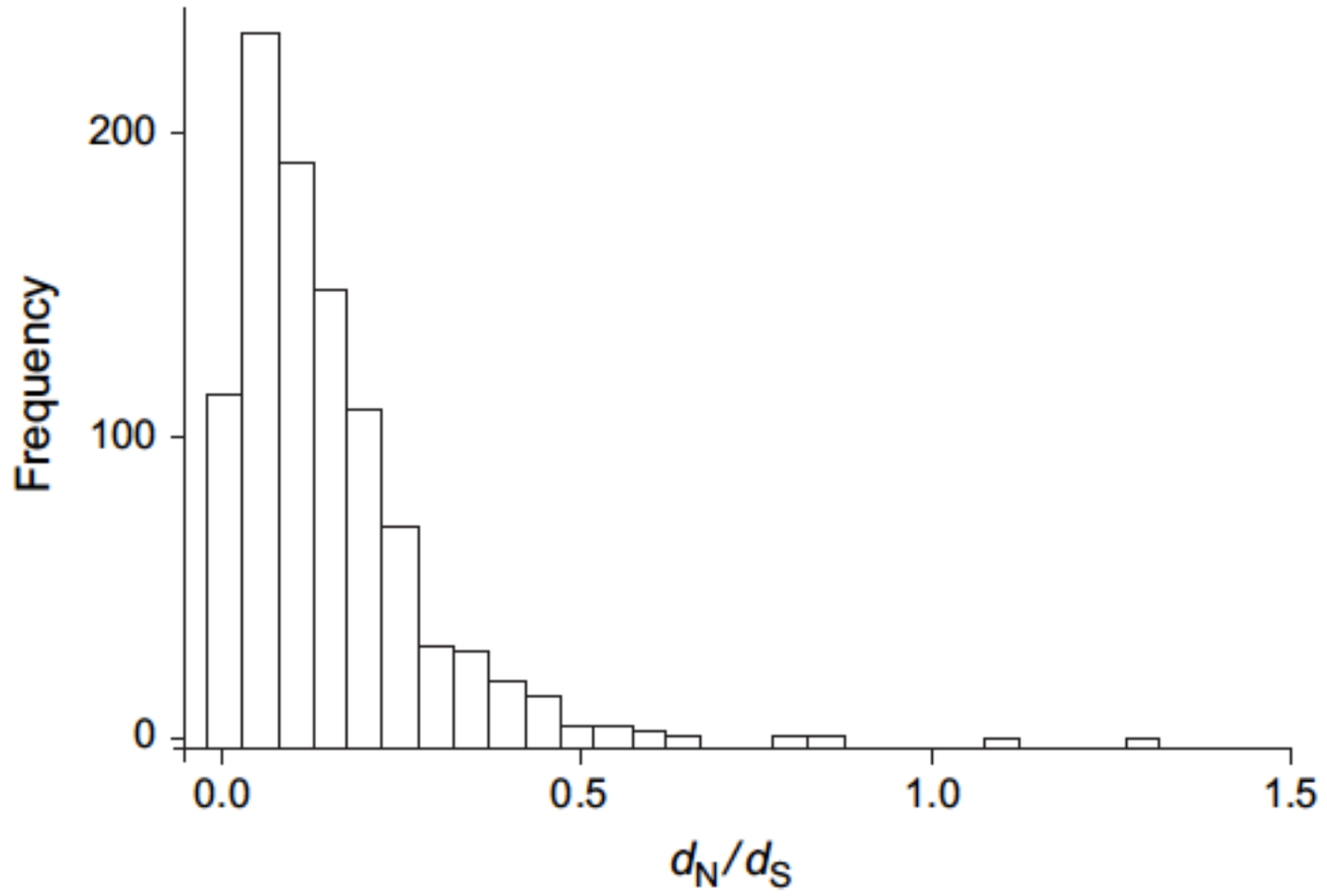

FIG. 3.—Ratios of nonsynonymous/synonymous divergence nucleotide substitutions (d_N/d_S) for 1,000 randomly chosen orthologous genes between humans and mice. The d_N and d_S values were computed by the method of Nei and Gojobori (1986). The median and mean values were 0.113 and 0.146, respectively.

Selectionism and Neutralism in Molecular Evolution

Masatoshi Nei

Mol. Biol. Evol. 22(12):2318–2342. 2005

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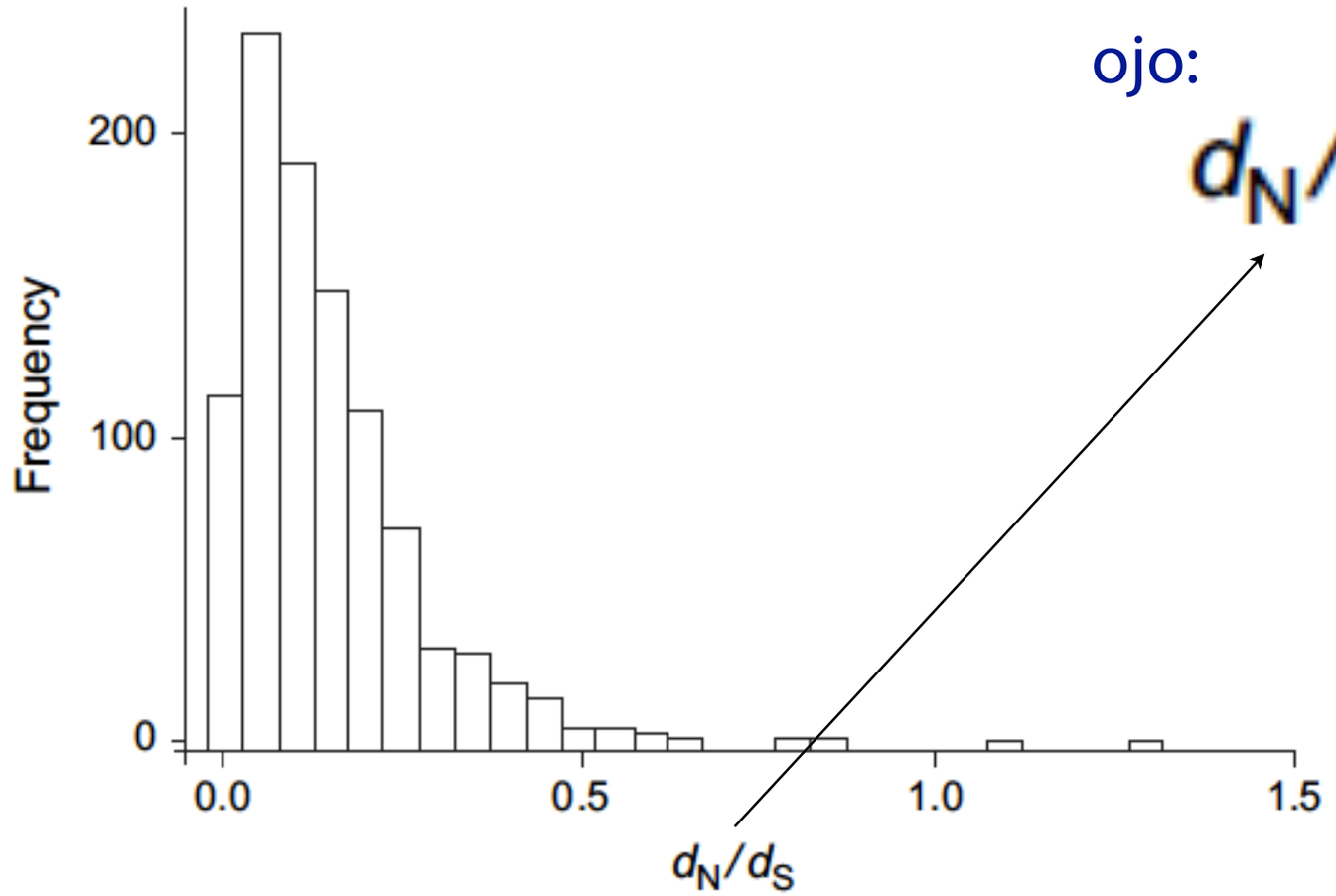

ojo:

d_N/d_S

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scans del genoma y búsqueda de señales de selección

S. Ramírez et al. (In prep.)

http://en.wikipedia.org/wiki/Tajima's_D