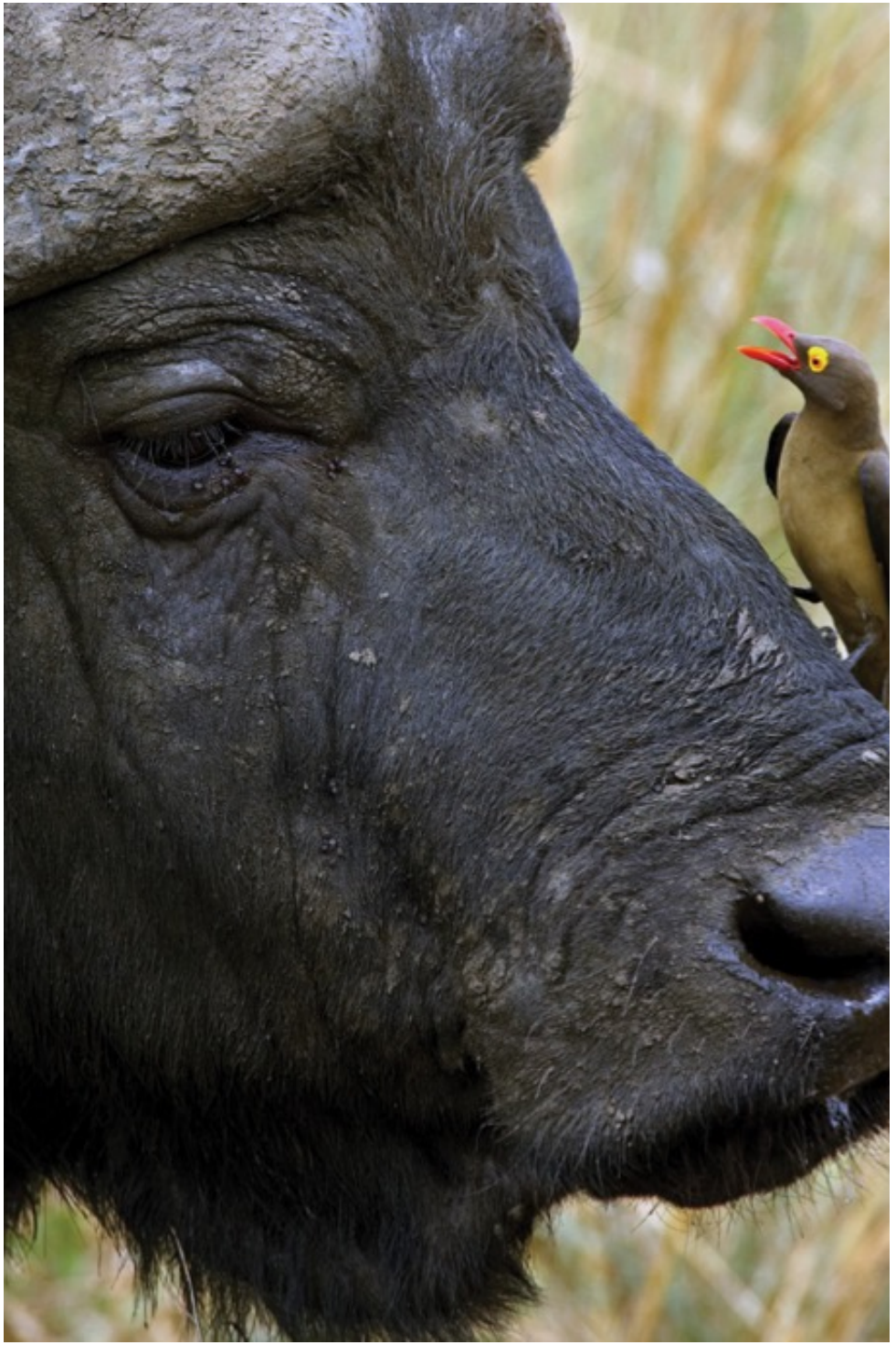
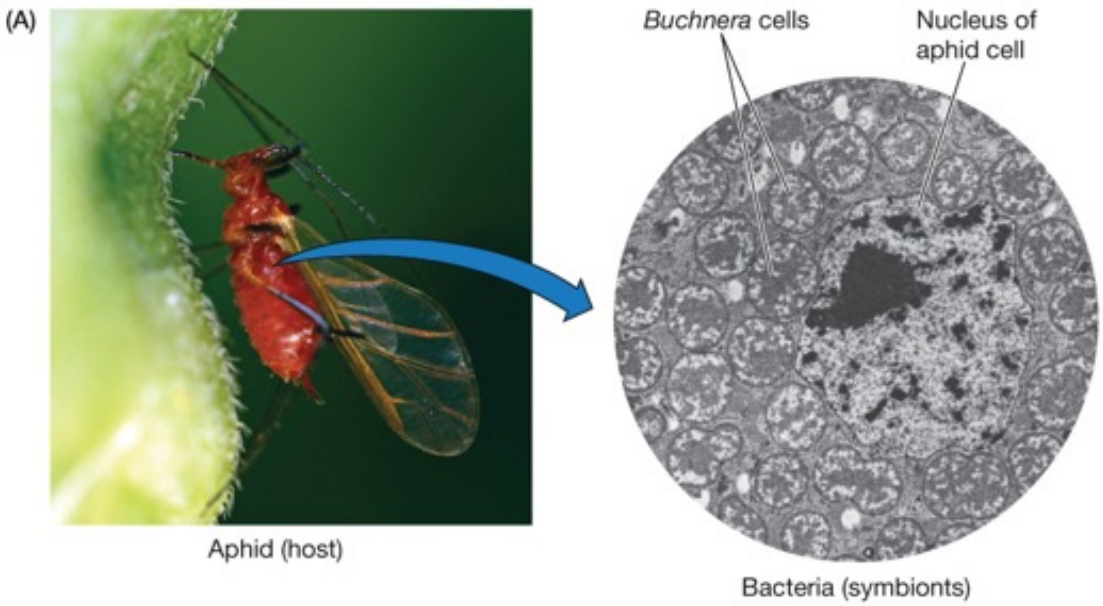
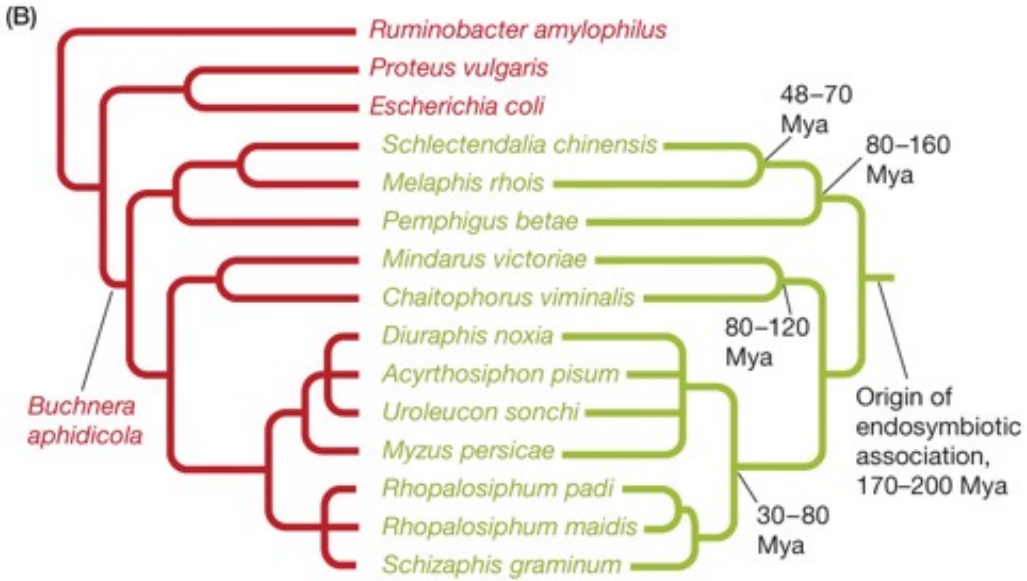
Coevolución

Dr. Luis Castañeda



Coevolución

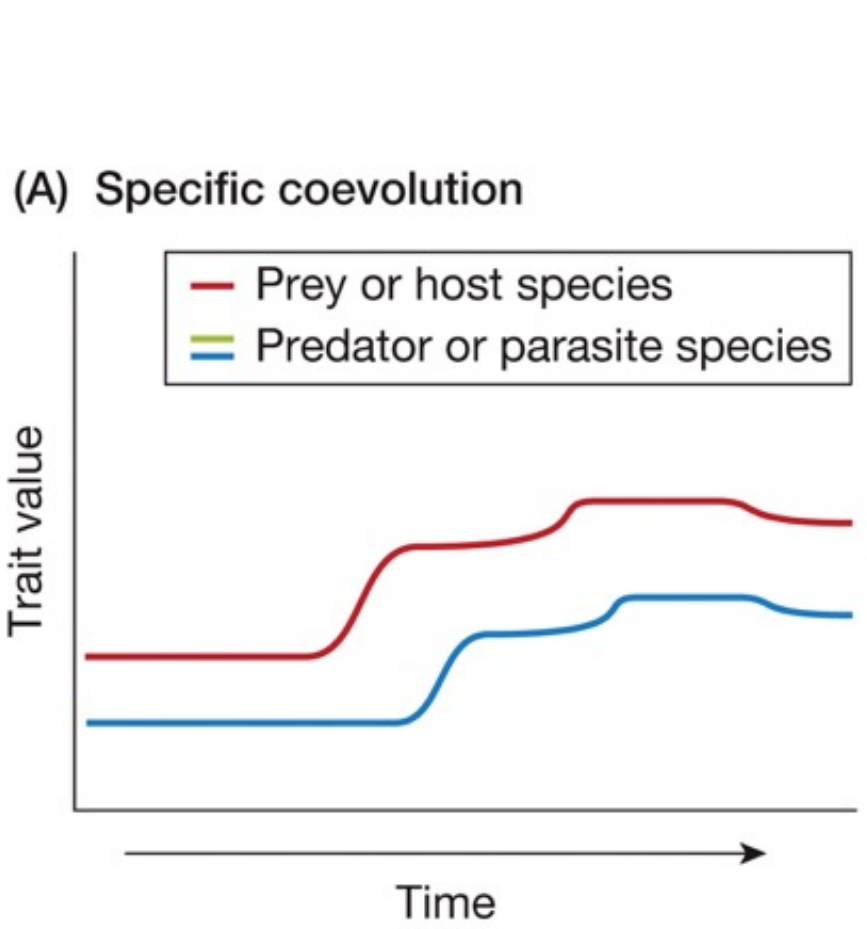




EVOLUTION 4e, Figure 13.4

~ 200 MYA !!!

Coevolución



EVOLUTION 4e, Figure 13.3 (Part 1)
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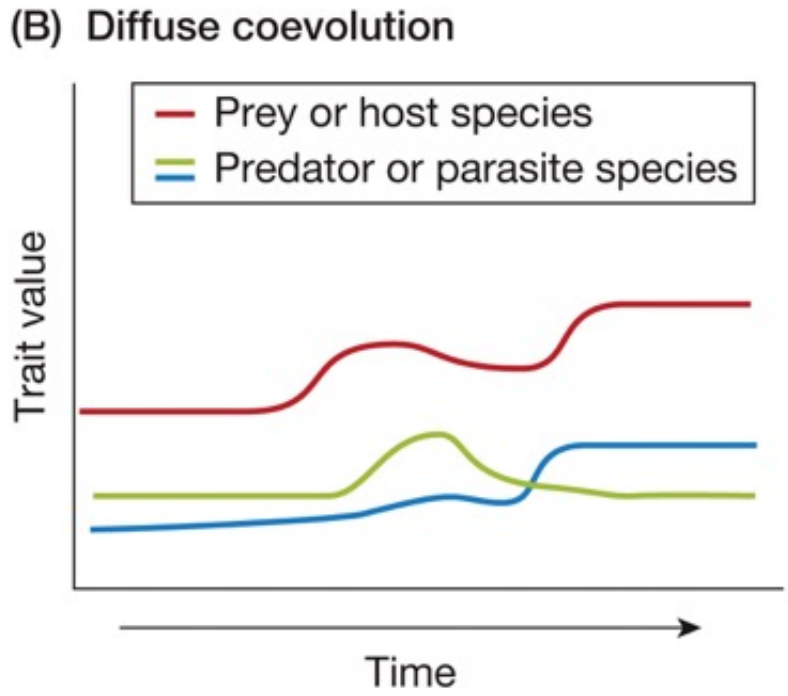
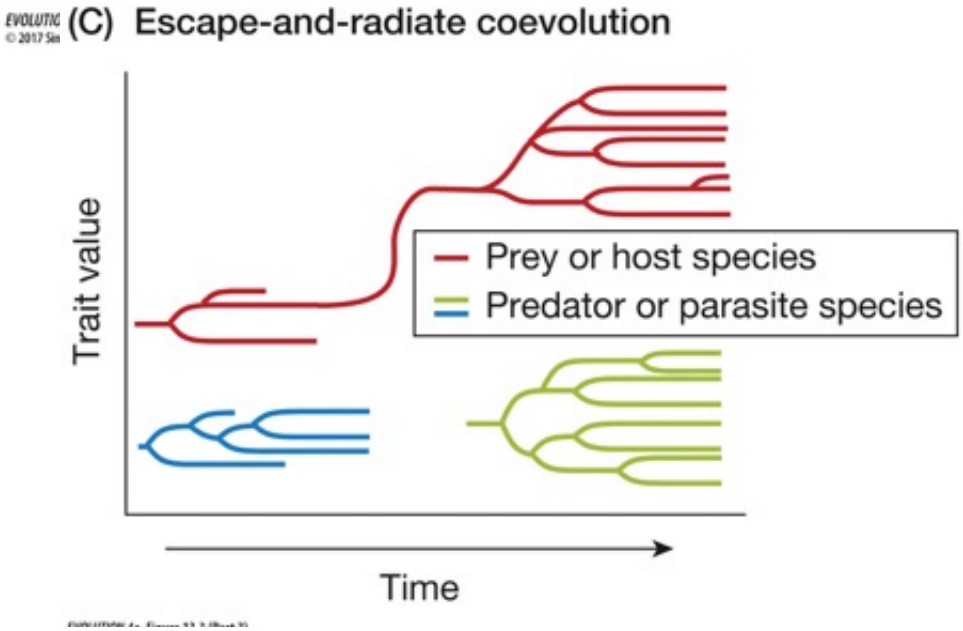
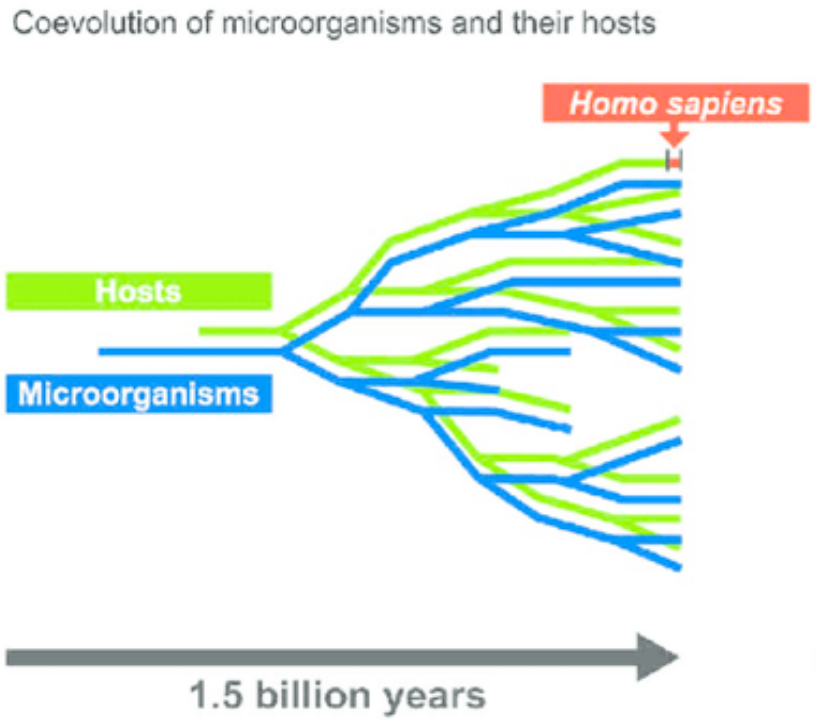




Coevolución

Cambio genético recíproco en especies que interactúan entre ellas debido a la selección natural impuesta por cada una de ellas sobre la otra especie (Futuyma & Kirkpatrick 2017).

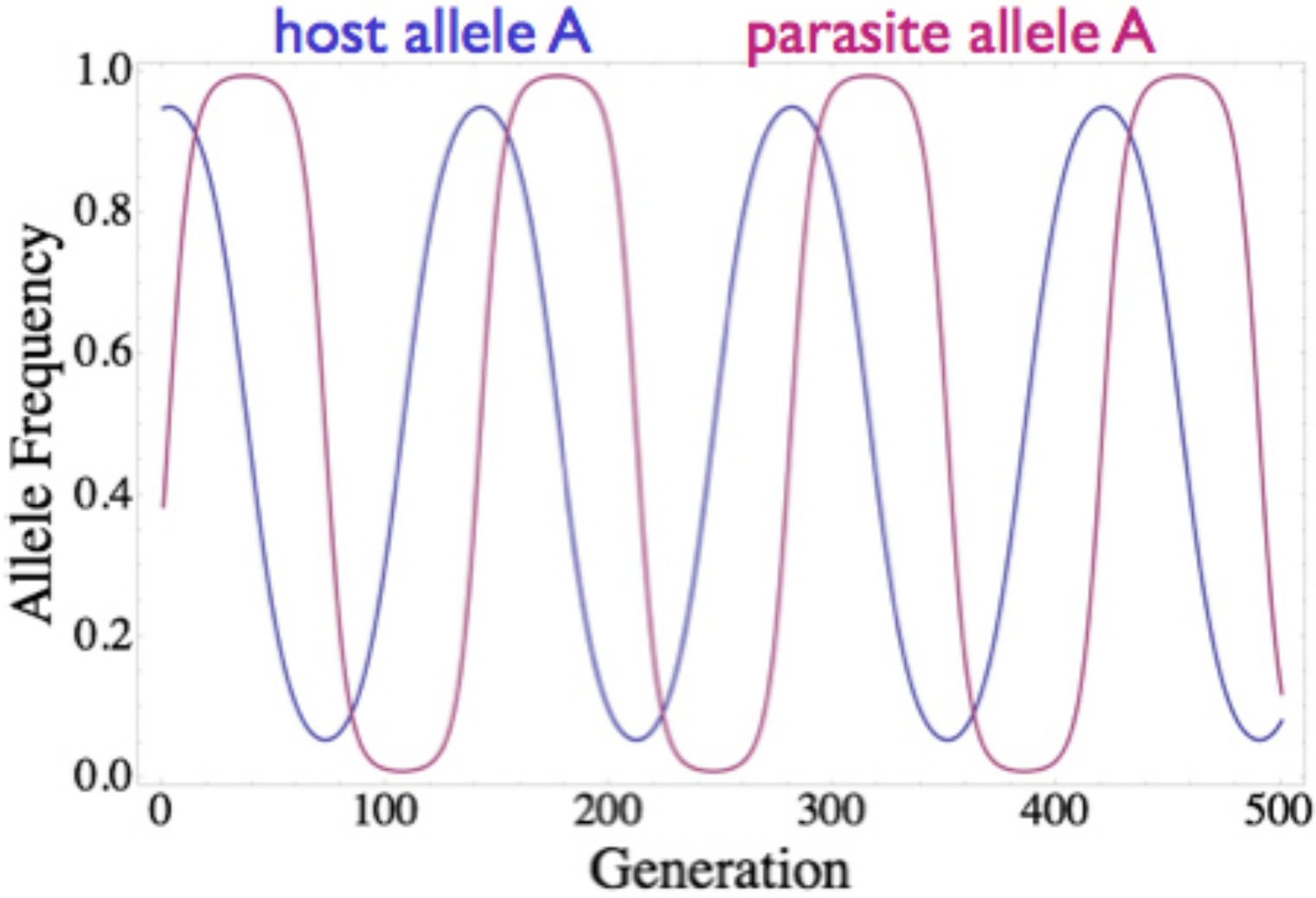


Hipótesis de la Reina Roja

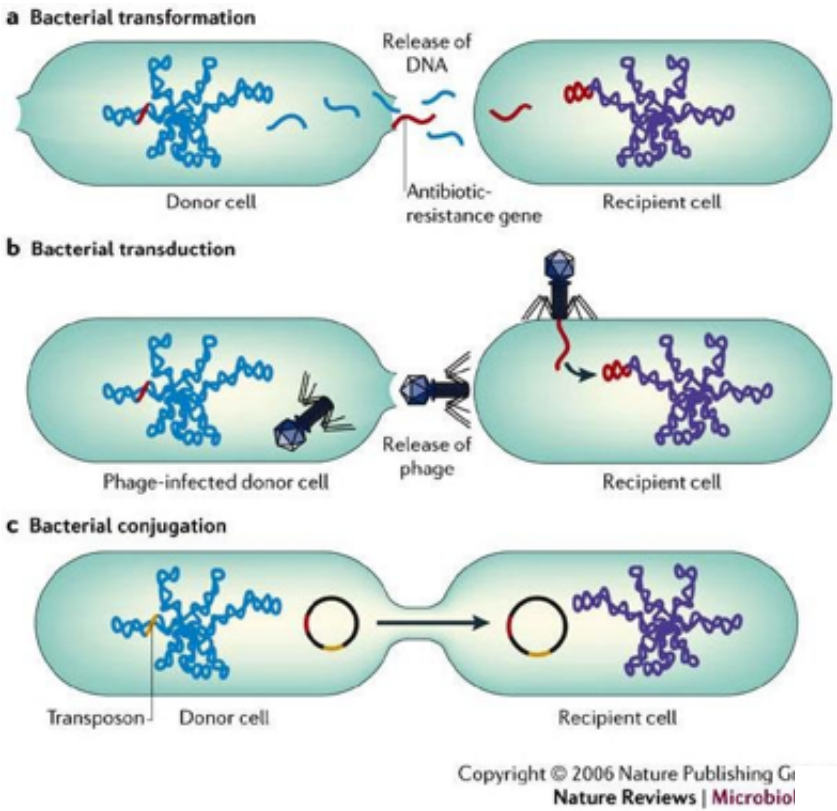
”No importa que tan rápido corras, siempre estarás en el mismo lugar”

“Para un sistema evolutivo, la mejora continua es necesaria para sólo mantener su ajuste a los sistemas con los que está coevolucionando”

Hipótesis de la Reina Roja



Coevolución parasito-humano

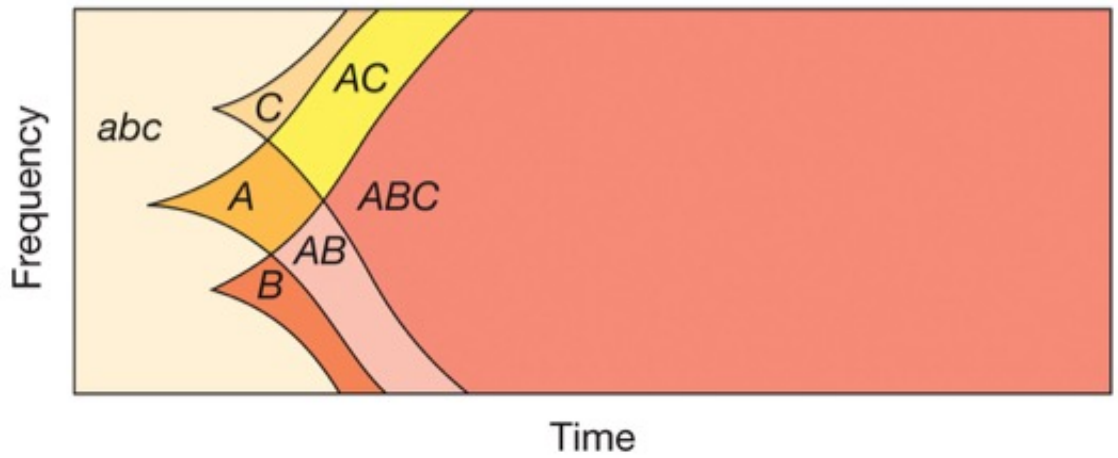


Tasa mutacional bacterias

3×10^{-5}

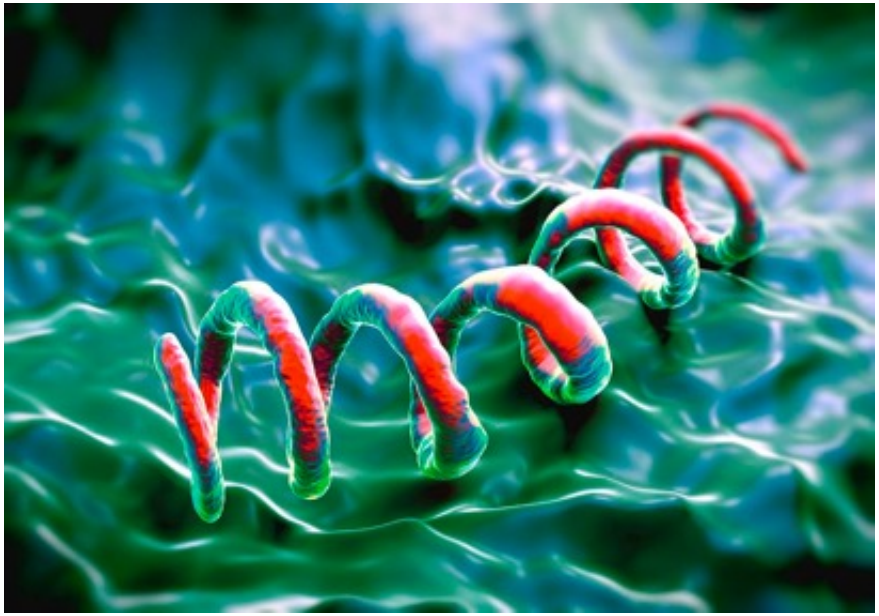
Tasa mutacional humanos

1×10^{-8}

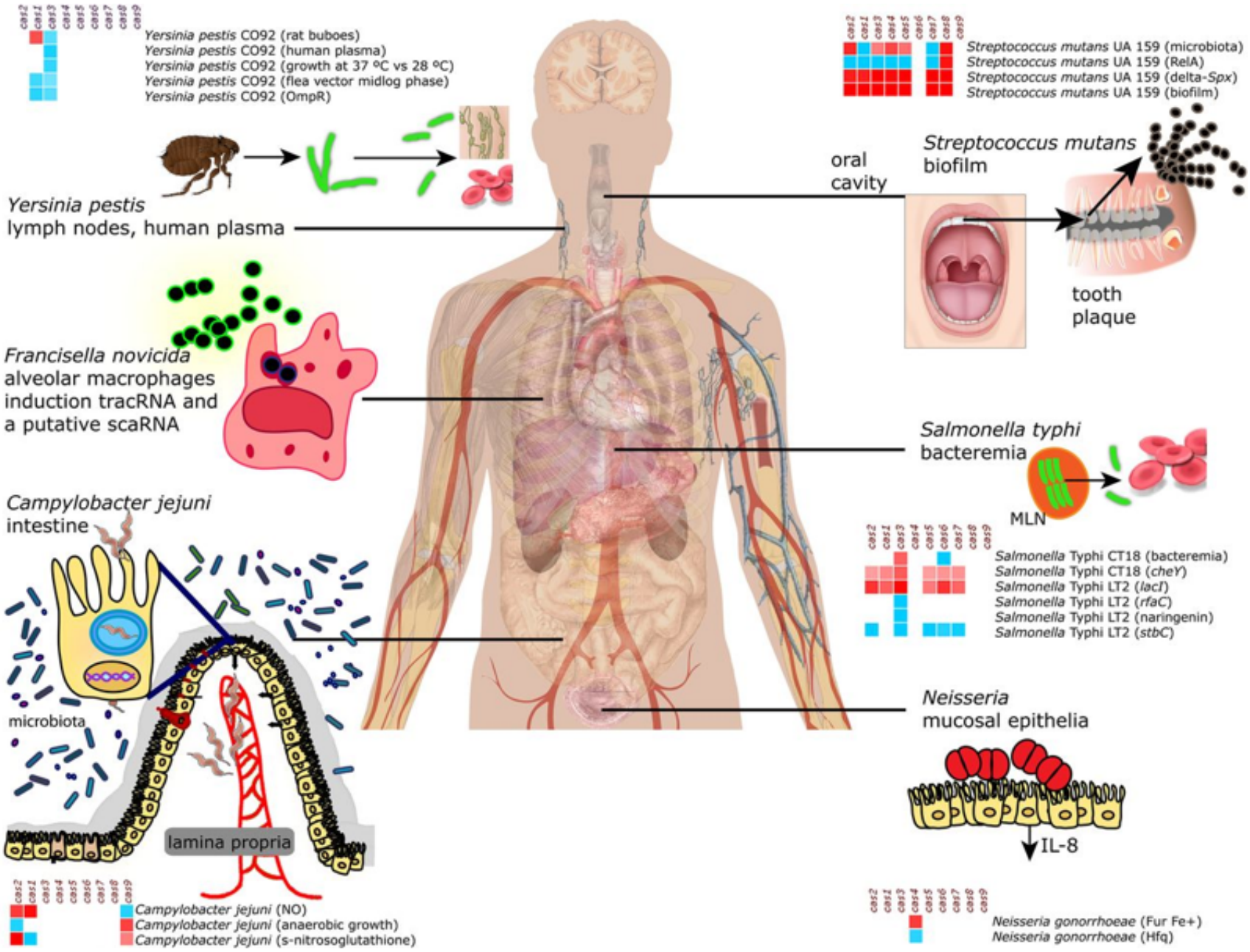


EVOLUTION 4e, Figure 10.23 (Part 2)

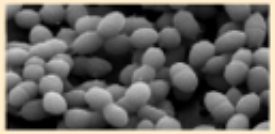
Humanos y especies asociadas



Humanos y especies asociadas

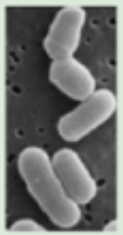


A map of diversity in the human microbiome

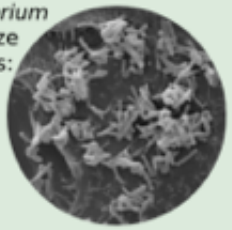


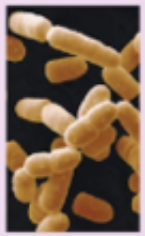
Streptococcus dominates the oral cavity with *S. mitis* > 75% in the cheek

Propionibacterium acnes lives on the skin and nose of most people



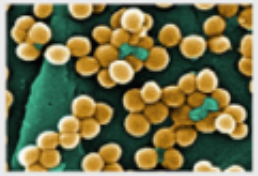
Many *Corynebacterium* species characterize different body sites:
C. matruchoti the plaque
C. accolens the nose
C. croppenstedtii the skin



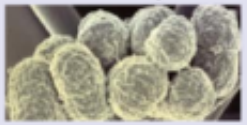


Lactobacillus species (*L. gasseri*, *L. jensenii*, *L. crispatus*, *L. iners*) are predominant but mutually exclusive in the vagina

Staphylococcus epidermidis colonizes external body sites

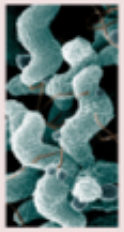


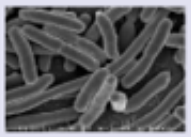
Several *Prevotella* species are present in the gastrointestinal tract. *P. copri* is present in 19% of the subjects and dominates the intestinal flora when present



Bacteroides is the most abundant genus in the gut of almost all healthy subjects

Campylobacter includes opportunistic pathogens, but members live in the oral cavities of most healthy people in the cohort





E. coli is present in the gut of the majority of healthy subjects but at very low abundance

Commensal microbes

Potential pathogens

The four most abundant phyla

- Actinobacteria
- Bacteroidetes
- Firmicutes
- Proteobacteria

Low abundance phyla

- Chloroflexi
- Cyanobacteria
- Euryarchaeota
- Fusobacteria
- Lentisphaerae
- Spirochaetes
- Synergistetes
- Tenericutes
- Thermi
- Verrucomicrobia

National Institutes of Health Human Microbiome Project

N. Segata & C. Huttenhower
http://huttenhower.sph.harvard.edu

Streptococcus
Corynebacterium
Actinomyces
Bifidobacterium
Lactobacillus
Porphyromonas
Prevotella
Staphylococcus
Bacteroides
Ruminococcus
Clostridium
Campylobacter
Neisseria
Anaerococcus
Acinetobacter
Selenomonas
Veillonella
Haemophilus
Fusobacterium
Escherichia

Phylogenetic map of the microbial species detected in the healthy human microbiome

0% 50% 100%

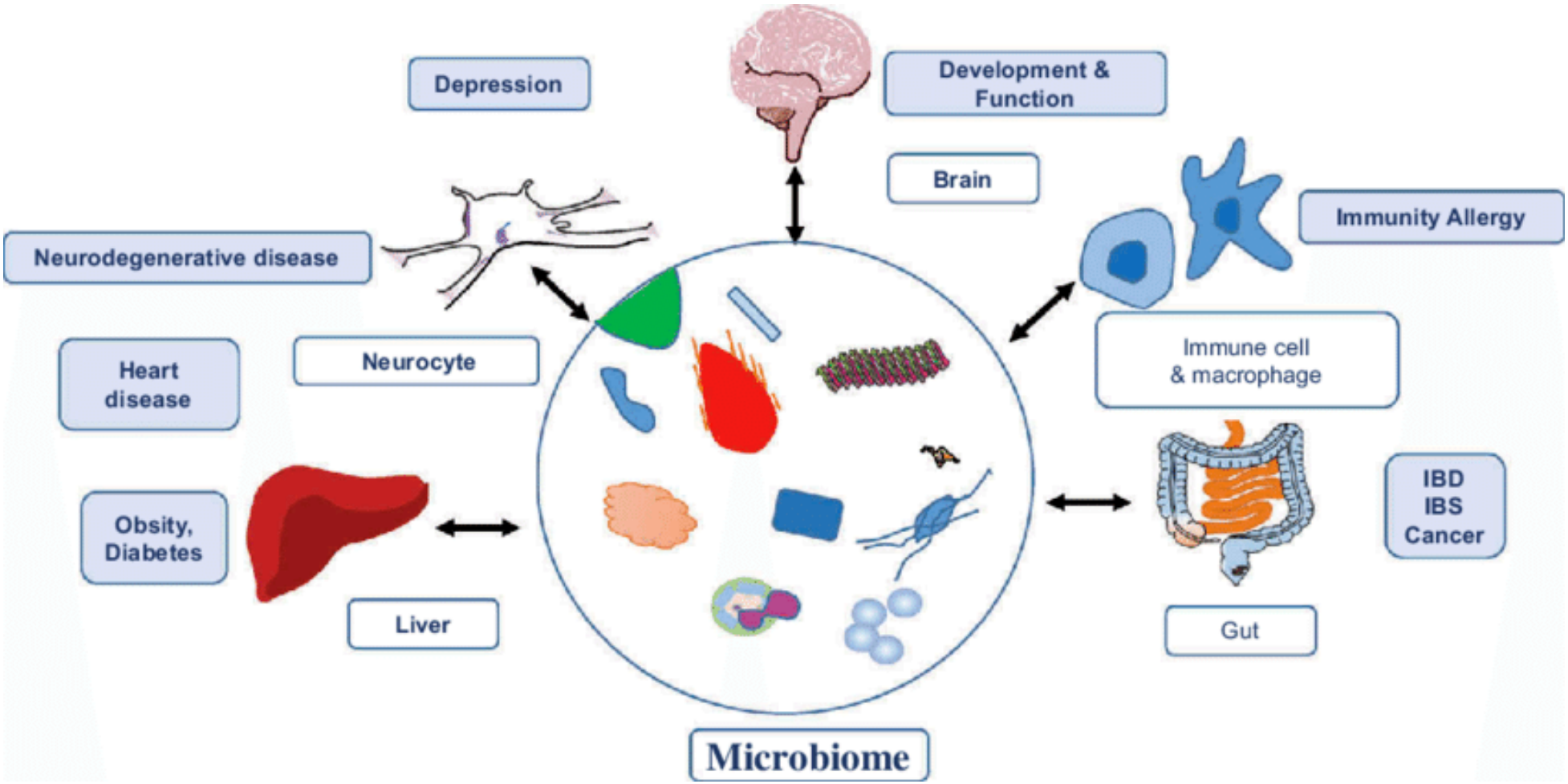
Intensity of external colors denotes species prevalence in each body site

Stool
Cheek
Plaque
Tongue
Nose
Vagina
Skin

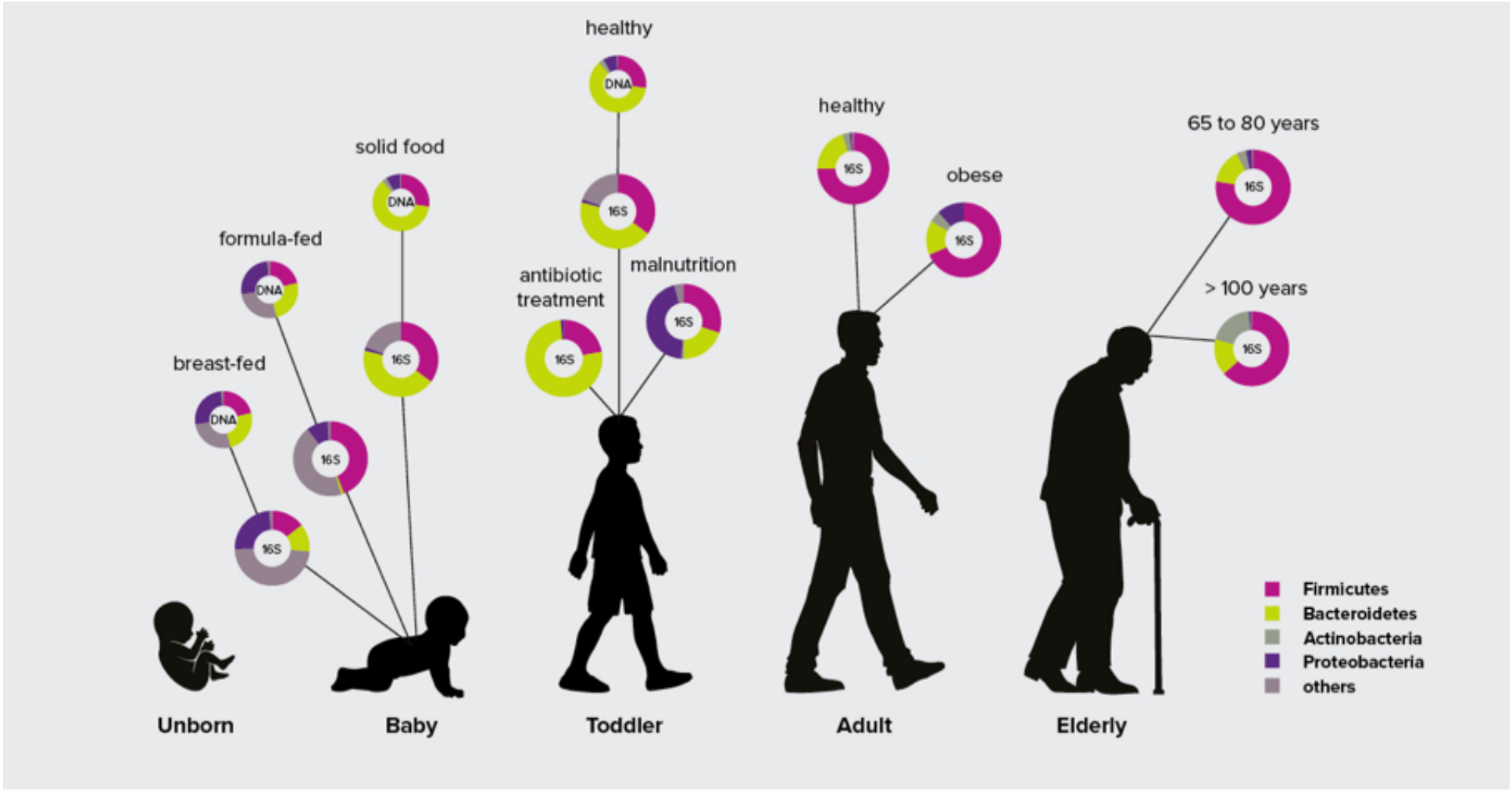
100% 75% 50% 25% 0%

Bar lengths indicate microbial abundance (colored by body site of greatest prevalence)

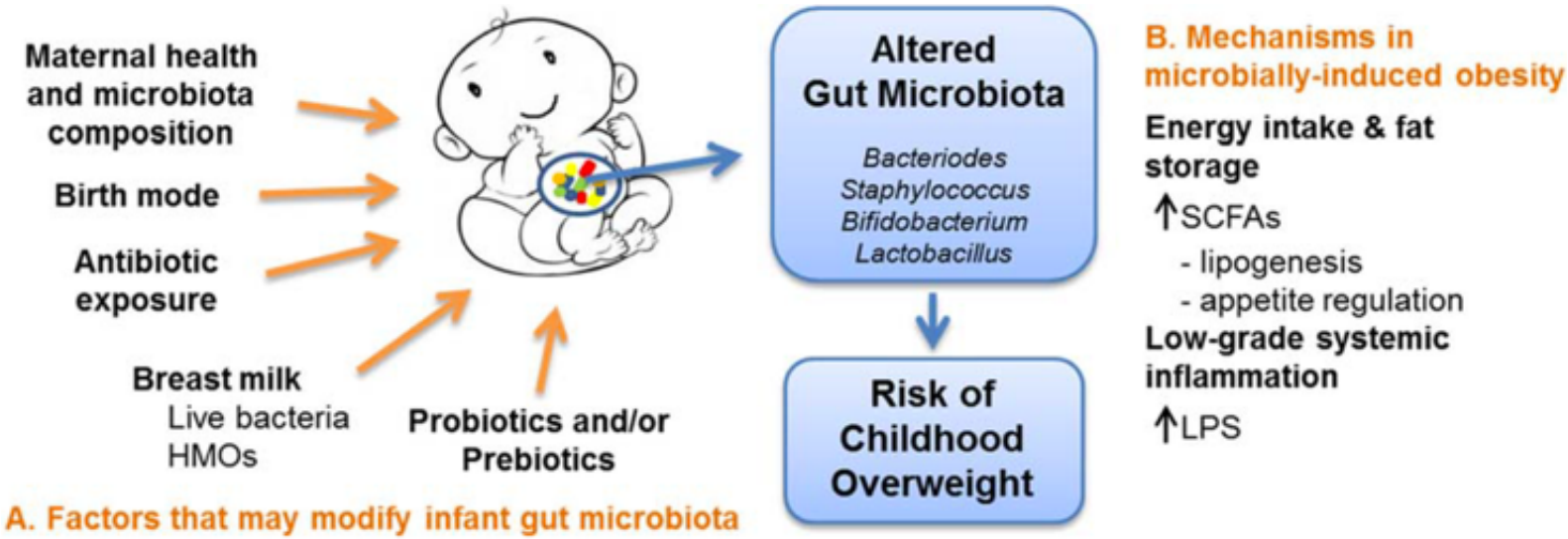
Microbiota intestinal en humanos

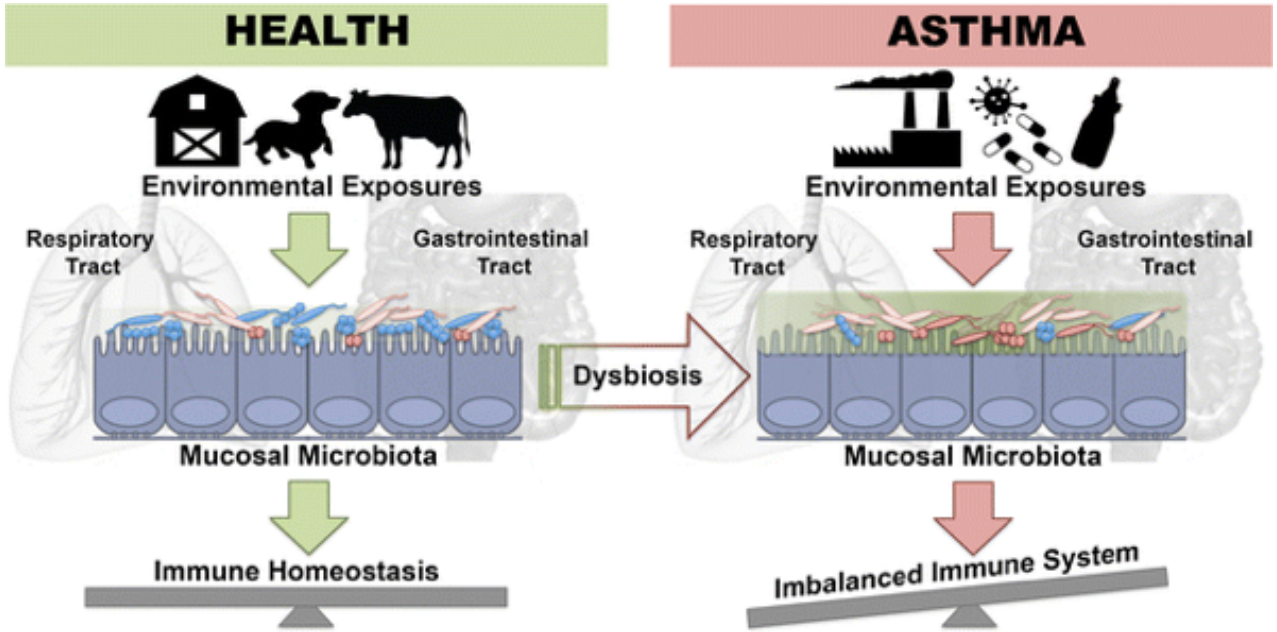


Microbiota intestinal en humanos



Microbiota en humanos

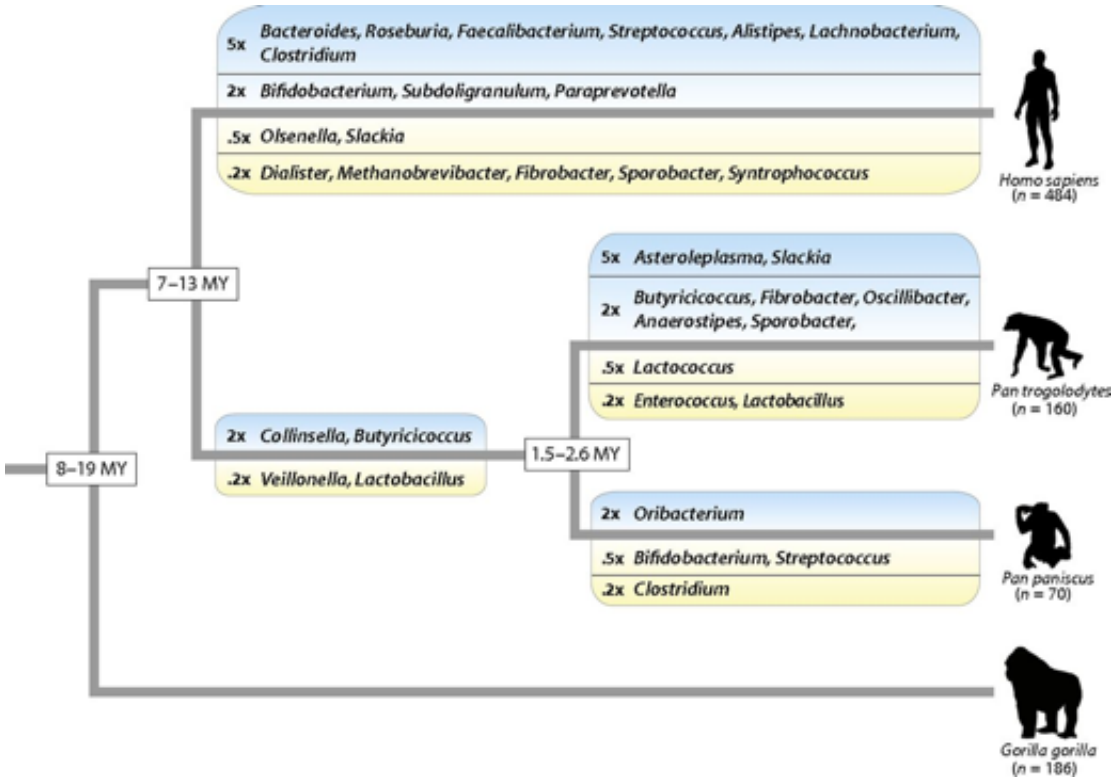


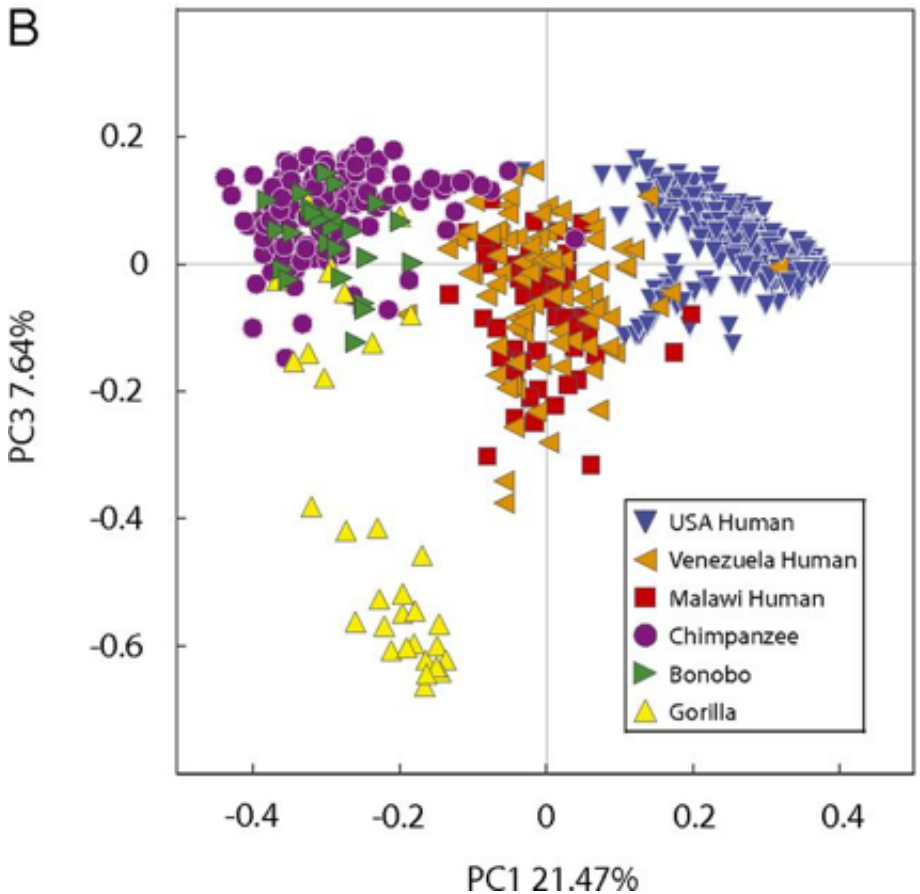


Coevolución microbioma-humano

Rapid changes in the gut microbiome during human evolution

Andrew H. Moeller[a,b], Yingying Li[c,d], Eitel Mpoudi Ngole[e], Steve Ahuka-Mundeke[f,g], Elizabeth V. Lonsdorf[h,i], Anne E. Pusey[j], Martine Peeters[g], Beatrice H. Hahn[c,1], and Howard Ochman[b,1]

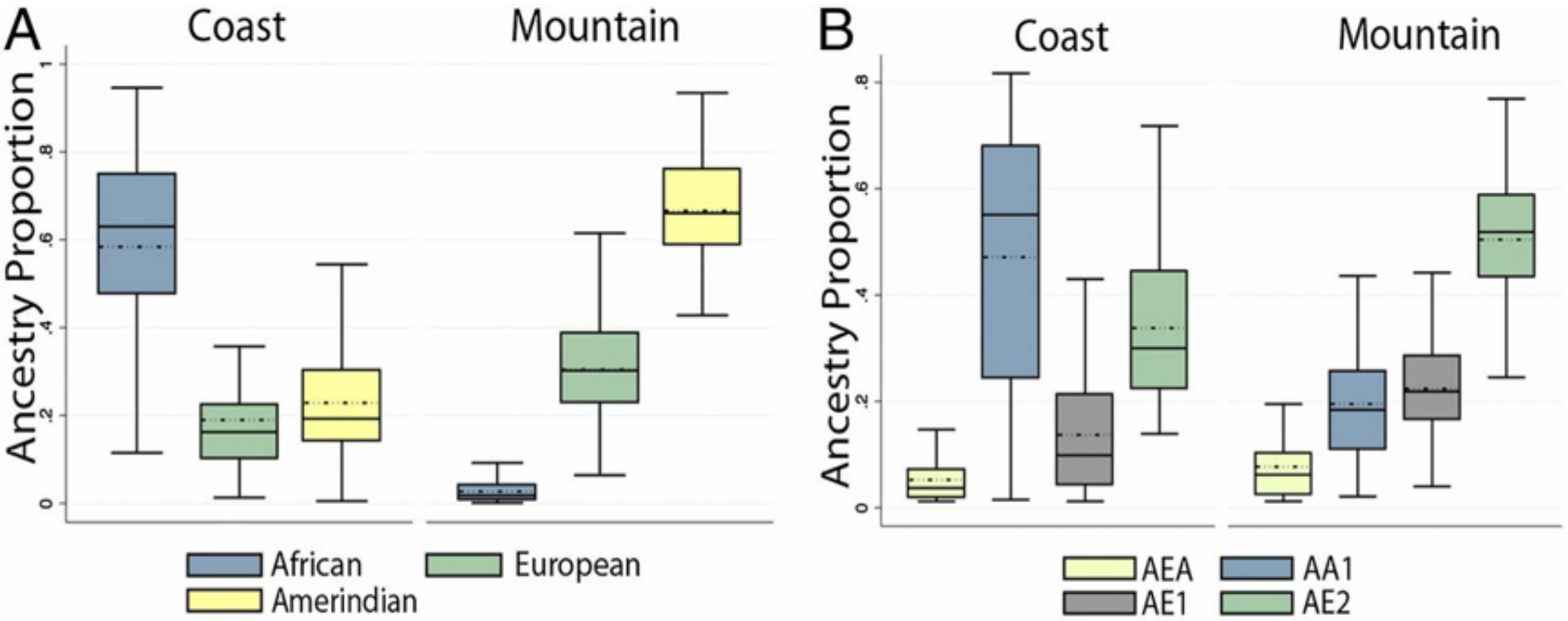




Coevolución microbioma-humano

Human and *Helicobacter pylori* coevolution shapes the risk of gastric disease

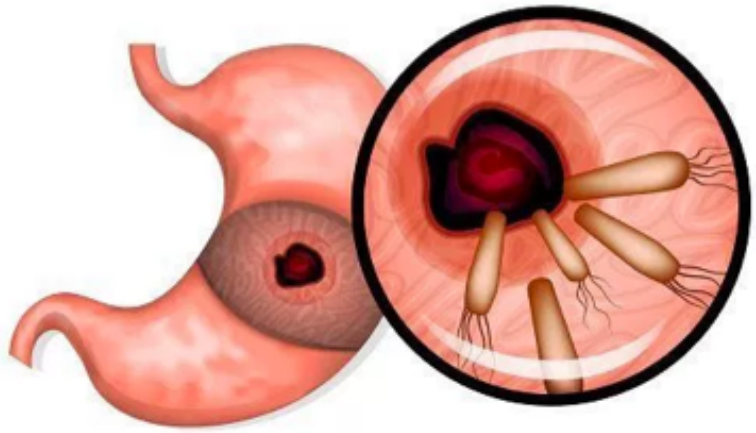
Nuri Kodaman[a,b,1], Alvaro Pazos[c,1], Barbara G. Schneider[d,2], M. Blanca Piazuelo[d], Robertino Mera[d], Rafal S. Sobota[a,b], Liviu A. Sicinschi[e], Carrie L. Shaffer[f], Judith Romero-Gallo[d], Thibaut de Sablet[d], Reed H. Harder[b], Luis E. Bravo[g], Richard M. Peek, Jr.[d], Keith T. Wilson[d,f,h,i], Timothy L. Cover[f,h,i,j], Scott M. Williams[a,b,3], and Pelayo Correa[d,3]

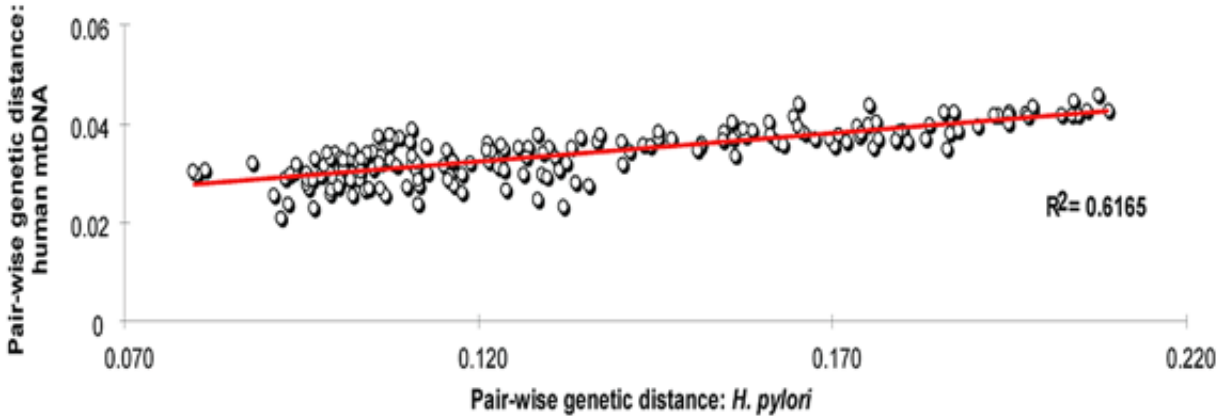


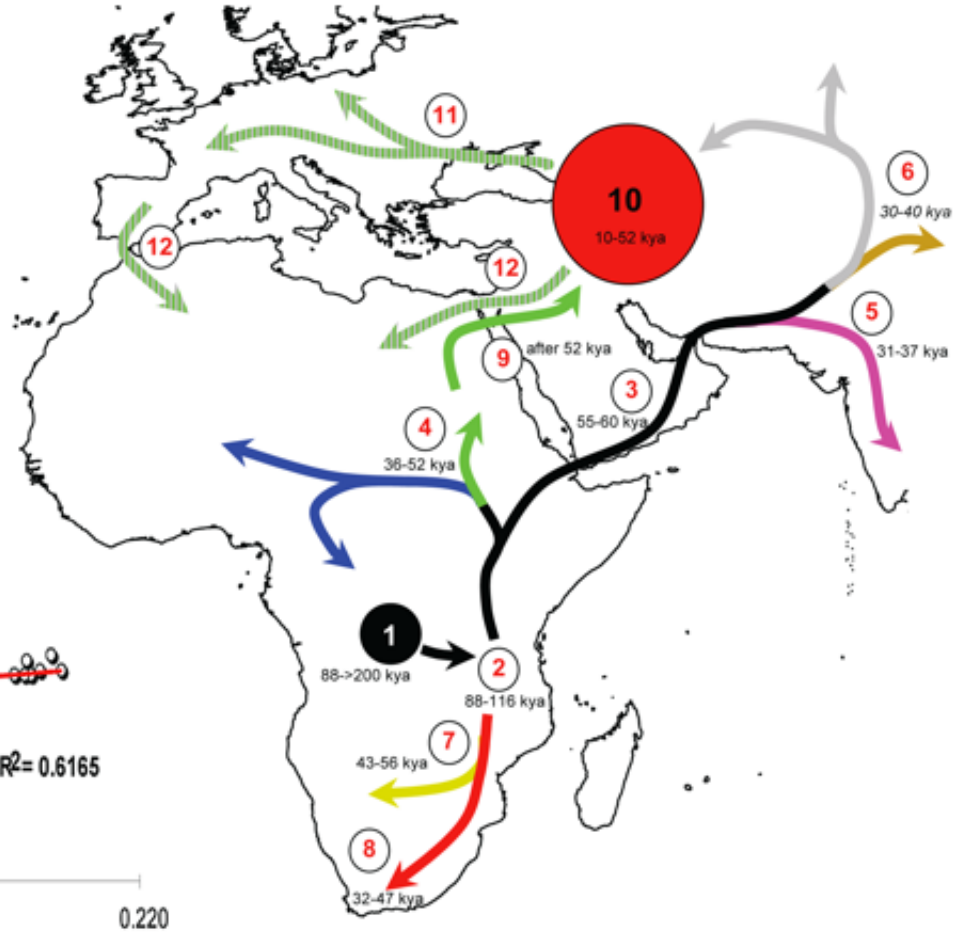
Coevolución microbioma-humano

Age of the Association between *Helicobacter pylori* and Man

Yoshan Moodley[1,2]*, Bodo Linz[1,3]*, Robert P. Bond[4], Martin Nieuwoudt[4], Himla Soodyall[5], Carina M. Schlebusch[5], Steffi Bernhöft[1], James Hale[6], Sebastian Suerbaum[7], Lawrence Mugisha[8], Schalk W. van der Merwe[4], Mark Achtman[1,6]*



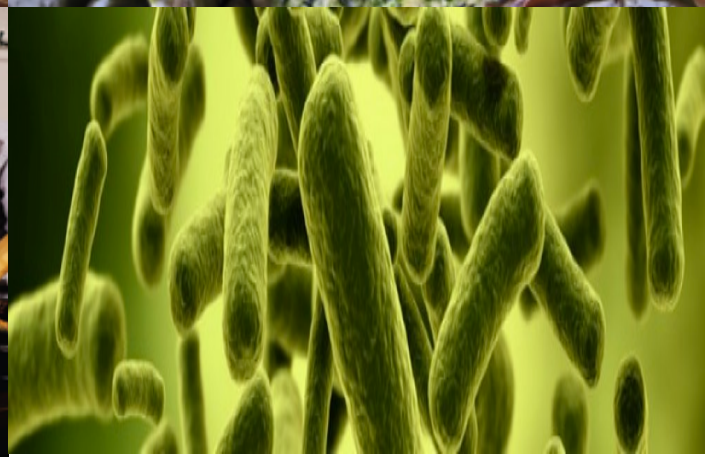




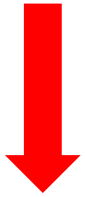
Coevolución microbioma-humano

Transfer of carbohydrate-active enzymes from marine bacteria to Japanese gut microbiota

Jan-Hendrik Hehemann[1,2]†, Gaëlle Correc[1,2], Tristan Barbeyron[1,2], William Helbert[1,2], Mirjam Czjzek[1,2] & Gurvan Michel[1,2]

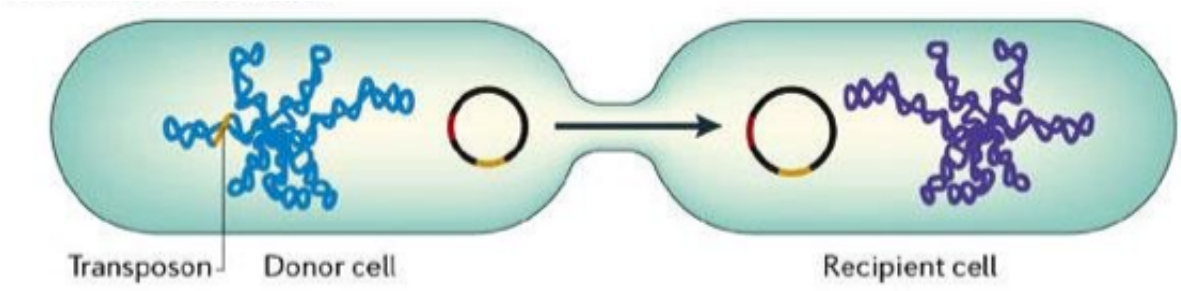


Zobellia galactanivorans



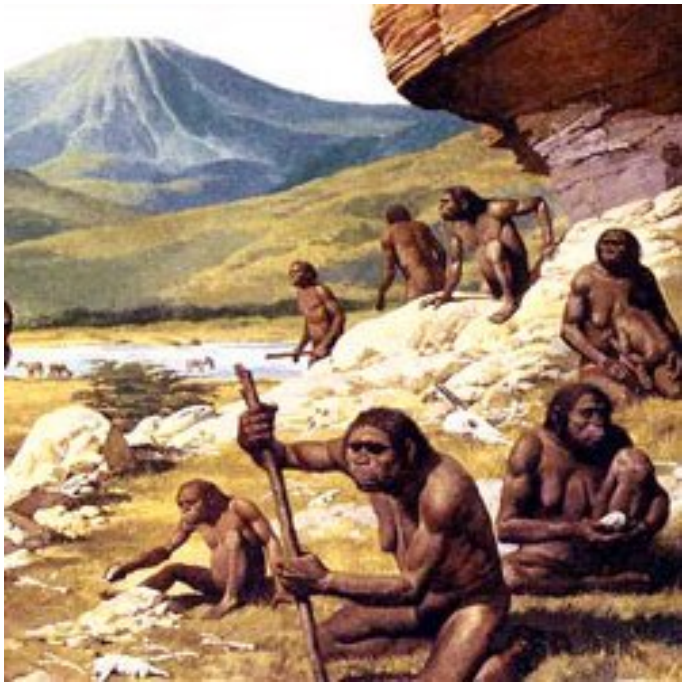
Bacteroides plebeius

Coevolución microbioma-humano



Zobellia galactanivorans → *Bacteroides plebeius*

Coevolución patógeno-humano



Coevolución entre humanos y patógenos que ha determinado los patrones de virulencia y transmisión de estos patógenos.

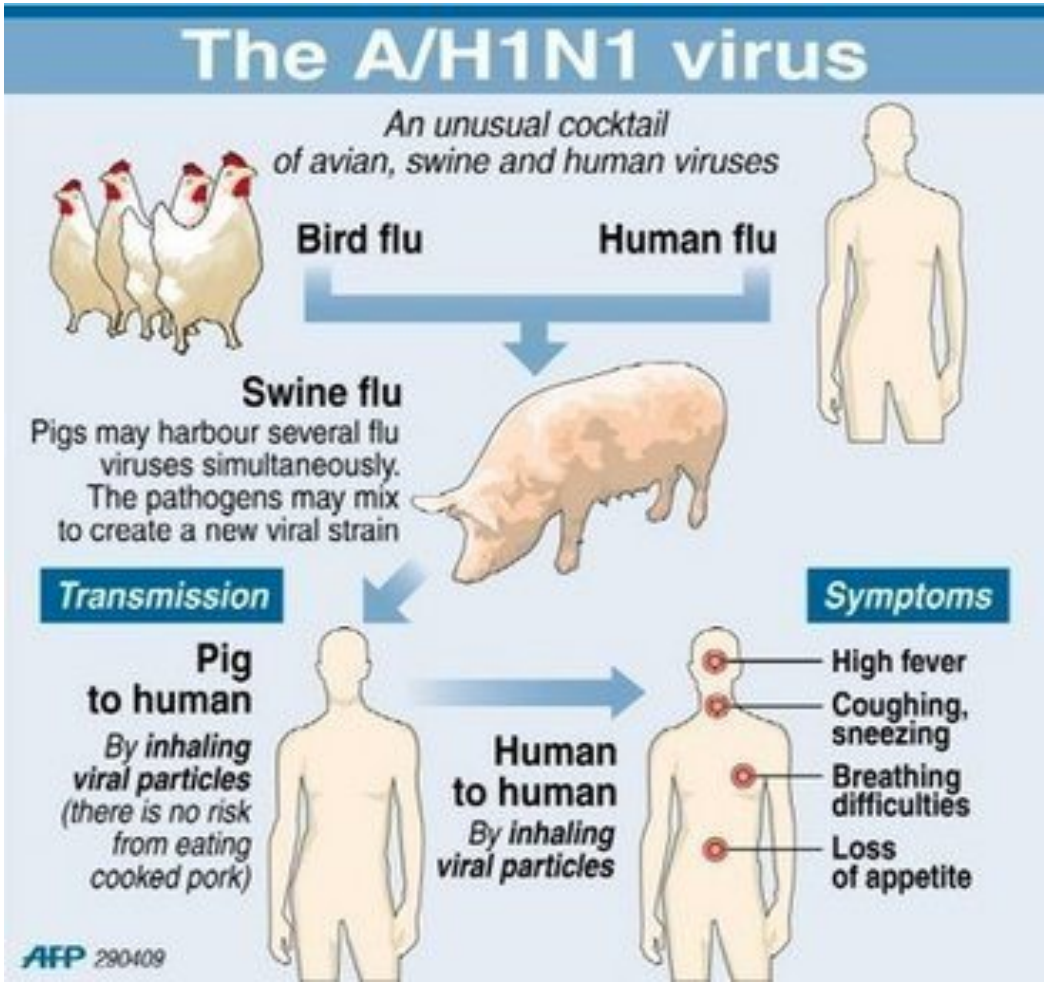
Coevolución patógeno-humano

Esquistosomiasis

- Dolor abdominal, diarrea.
- Falla renal y hepática, cáncer, déficit cognitivo.
- Baja virulencia, necesidad de un vector.

Coevolución patógeno-humano

Enfermedades zoonóticas



Alta virulencia

Coevolución patógeno-humano

- Un patógeno evolucionará hacia un equilibrio establecido por un compromiso entre su virulencia y su capacidad de transmisión.
- Esto maximizaría su capacidad de infectar nuevos hospederos.

- Patógenos altamente virulentos deben altamente transmisibles.
- Patógenos con baja virulencia pueden ser menos transmisibles.

Coevolución patógeno-humano

El compromiso entre virulencia y transmisión de un patógeno en un hospedero en particular dependerá tanto de factores asociados a ambas especies y de la historia coevolutiva entre ellas.

Classes of Human Pathogens

Taxonomic	Site of Propagation	Examples	Diseases
Prions	Intracellular	Prion protein	Creutzfeld- Jacob Disease
Viruses	Obligate Intracellular	Poliovirus	Poliomyelitis
Bacteria	1. Obligate Intracellular 2. Extracellular 3. Facultative intracellular	1. Chlamydia trachomatis 2. Strep pneumoniae 3. TB	Trachoma Pneumonia Tuberculosis
Fungi	1. Extracellular 2. Facultative intracellular	1. Candida albicans 2. Histoplasma capsulatum	Thrush Histoplasmosis
Protozoa	1. Extracellular 2. Facultative intracellular 3. Obligate intracellular	1. Trypanosoma gambiense 2. T. cruzi 3. Leishmania donovani	1. Sleeping sickness 2. Chagas dse 3. Kala- azar
Helminths	1. Extracellular 2. Intracellular	1. Wuchereria bancrofti 2. Trichinella spiralis	1. Filariasis 2. Trichinosis

Coevolución patógeno-humano

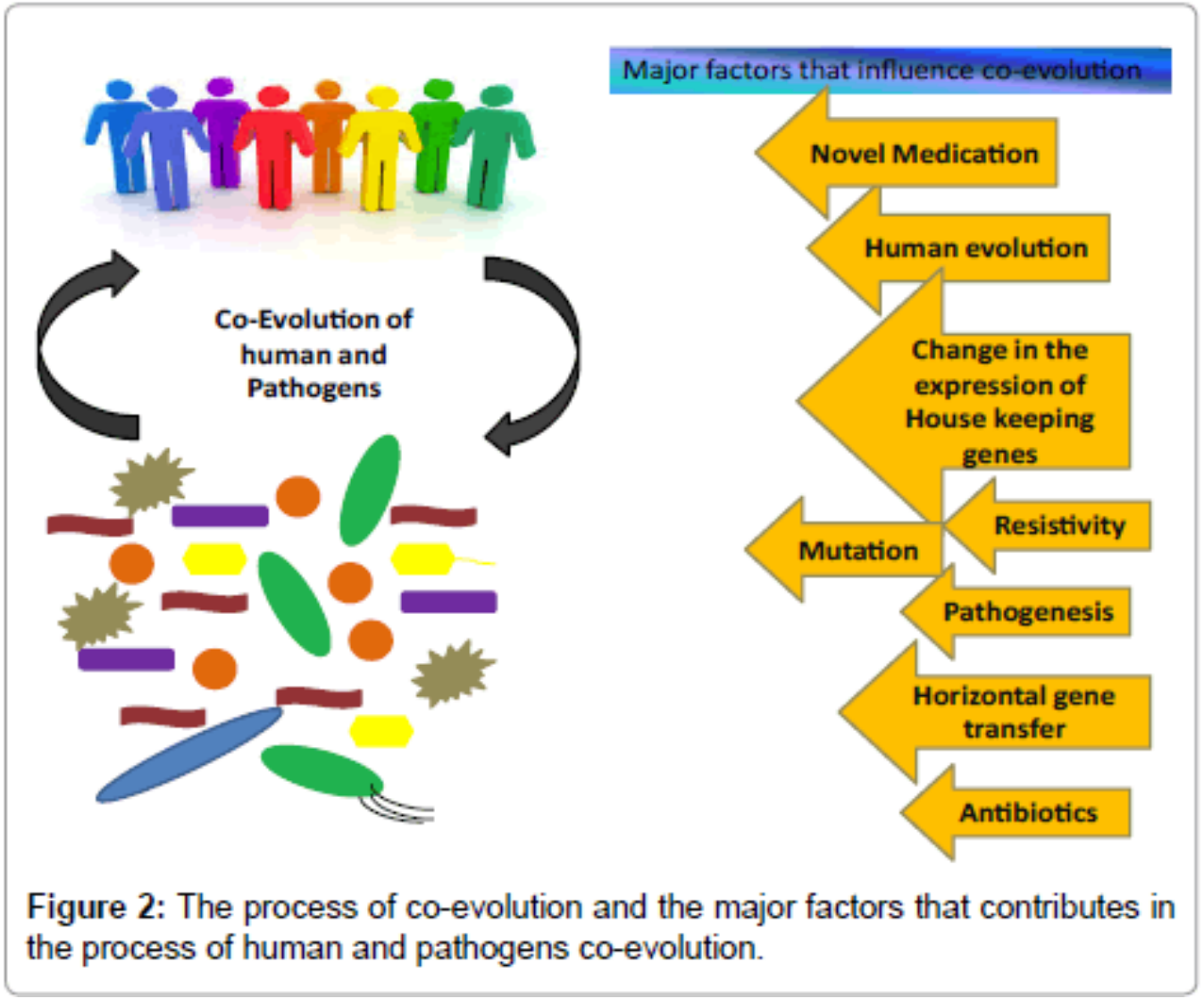
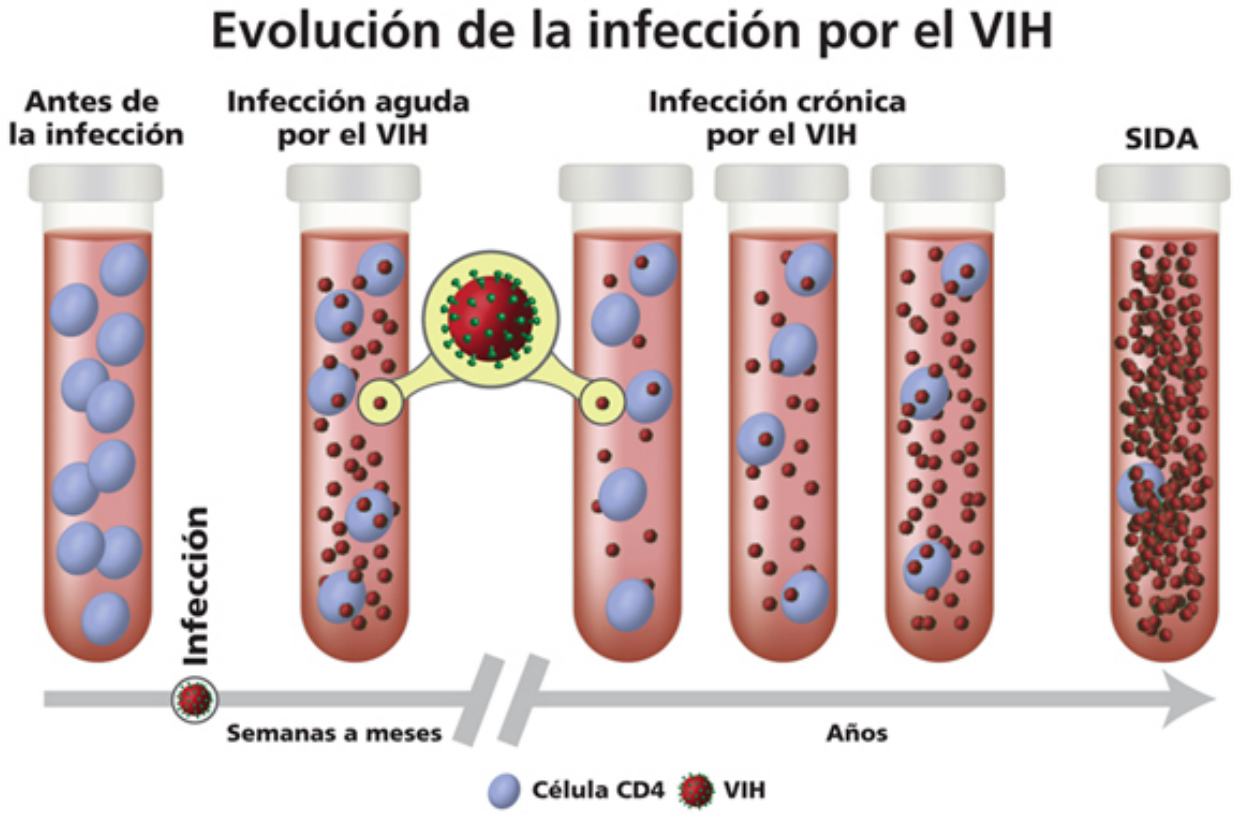


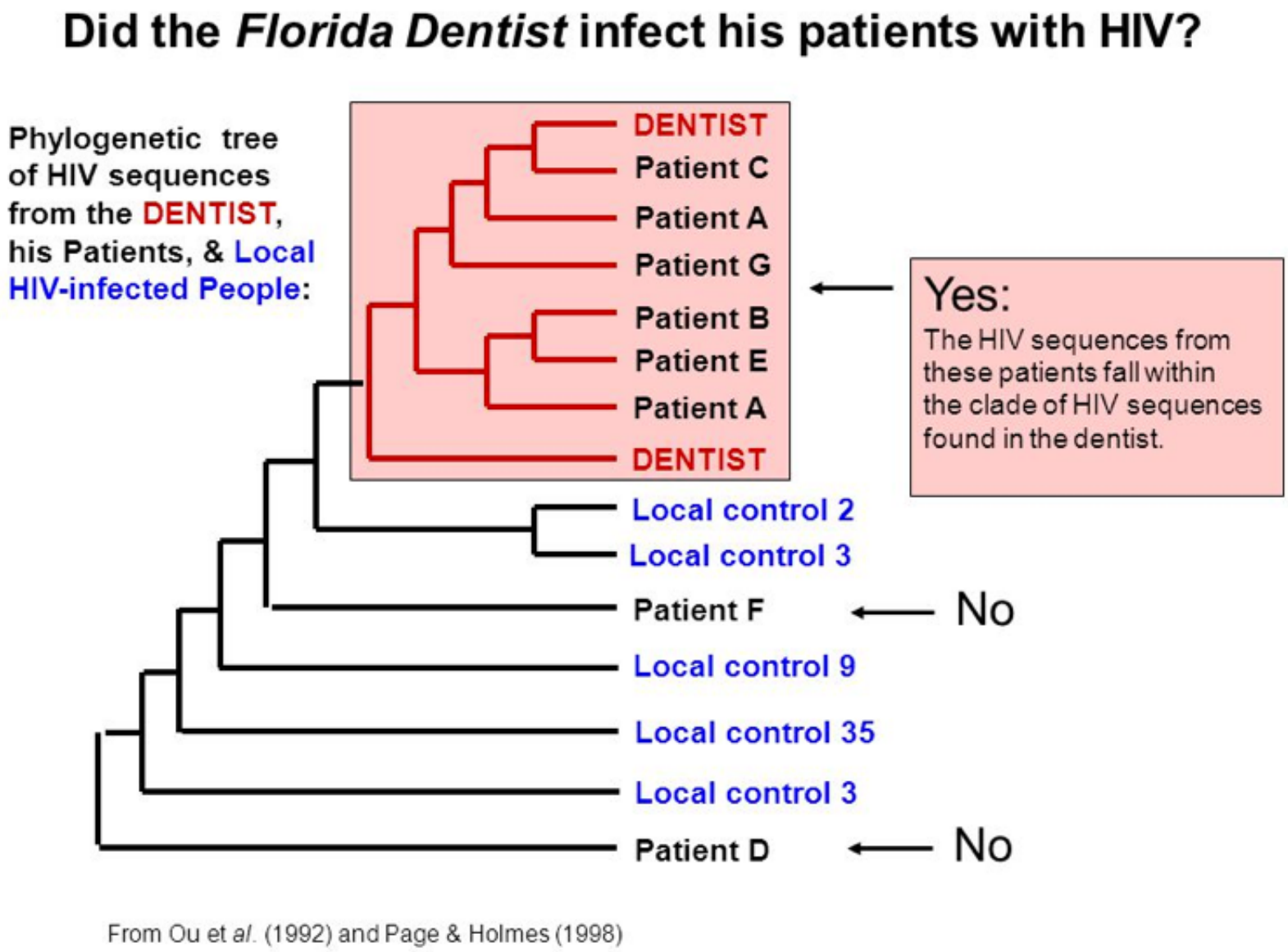
Figure 2: The process of co-evolution and the major factors that contributes in the process of human and pathogens co-evolution.

Coevolución patógeno-humano



- Baja mortalidad inmediata.
- Largo periodo asintomático que promueve la transmisión a través de contacto “directo” con infectados.

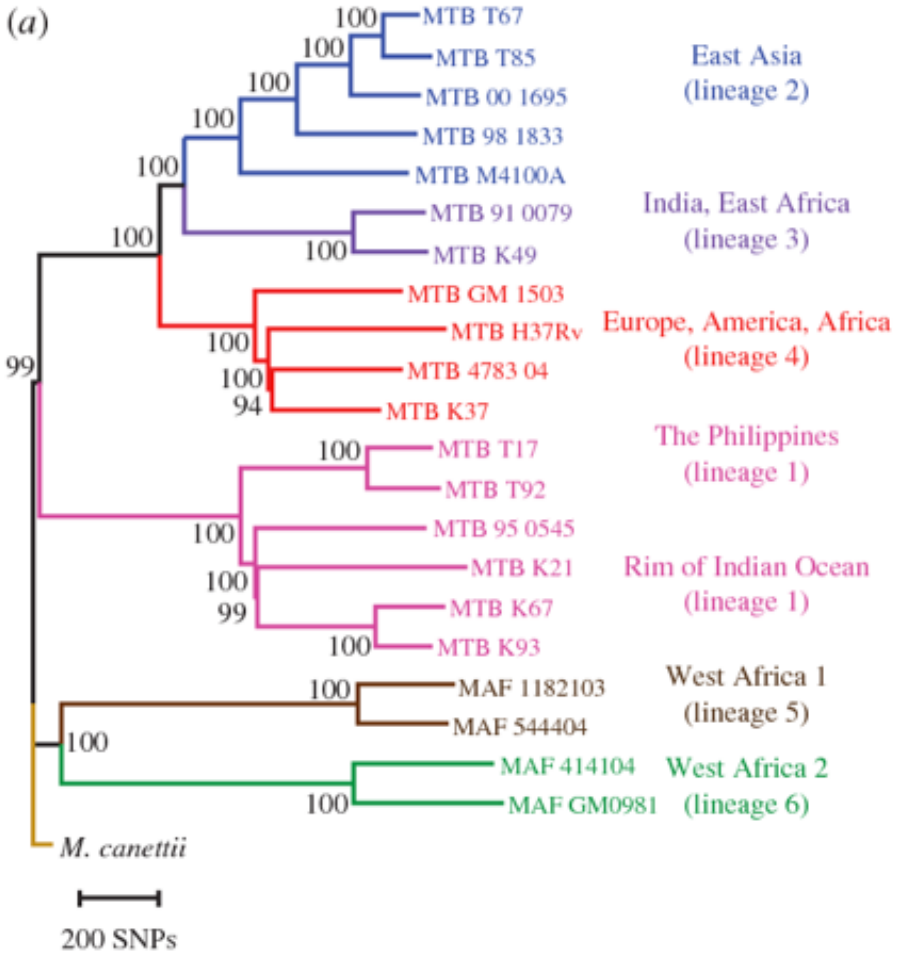
Coevolución patógeno-humano

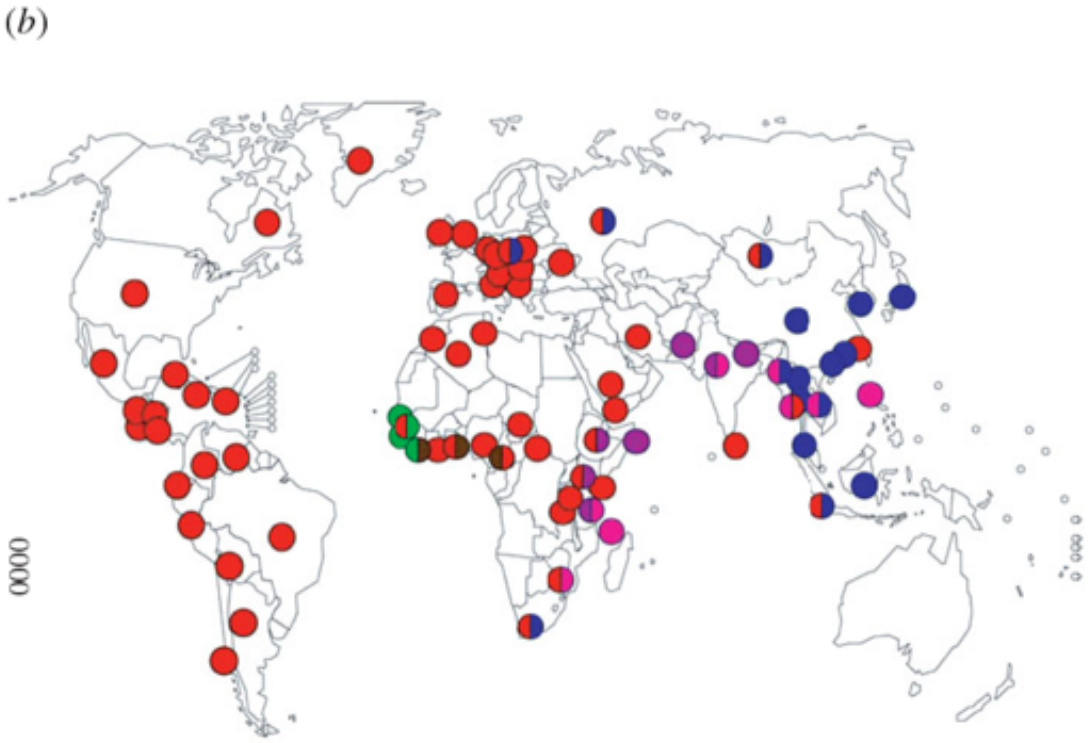


From Ou et *al*. (1992) and Page & Holmes (1998)

Coevolución patógeno-humano

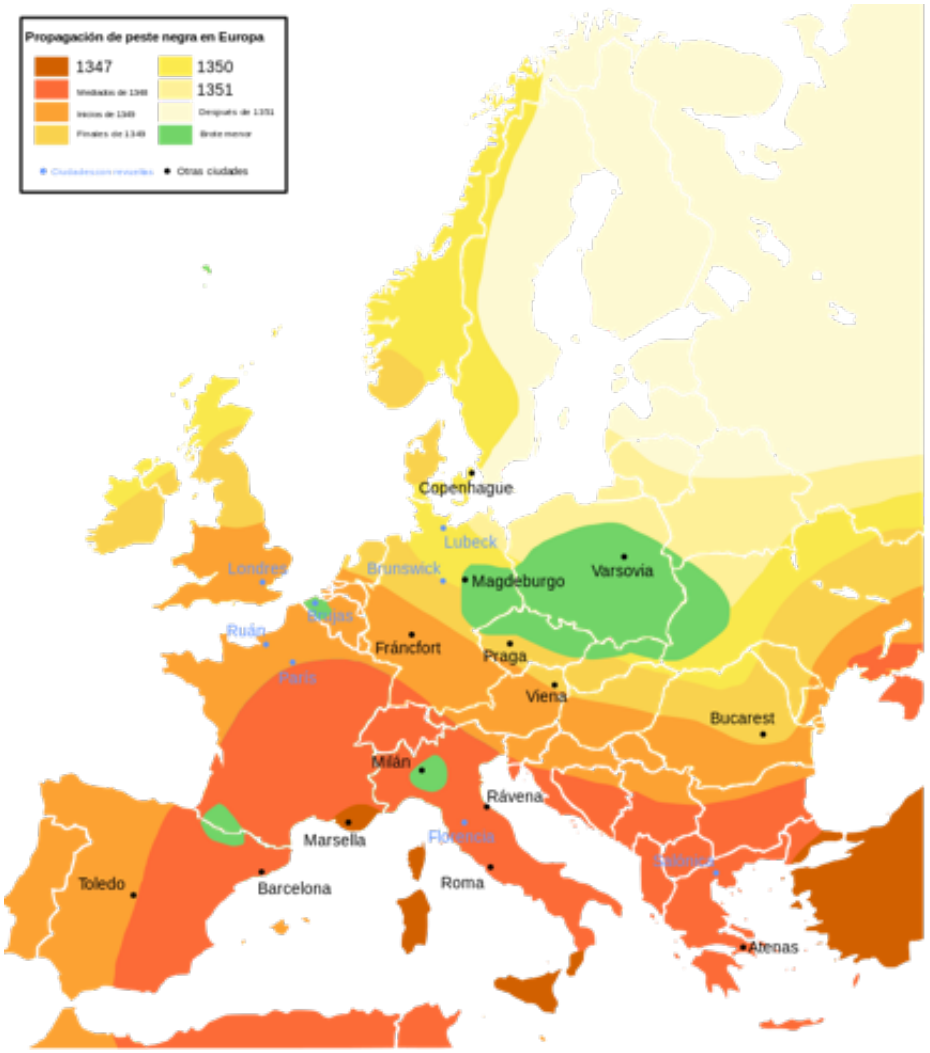
Mycobacterium tuberculosis



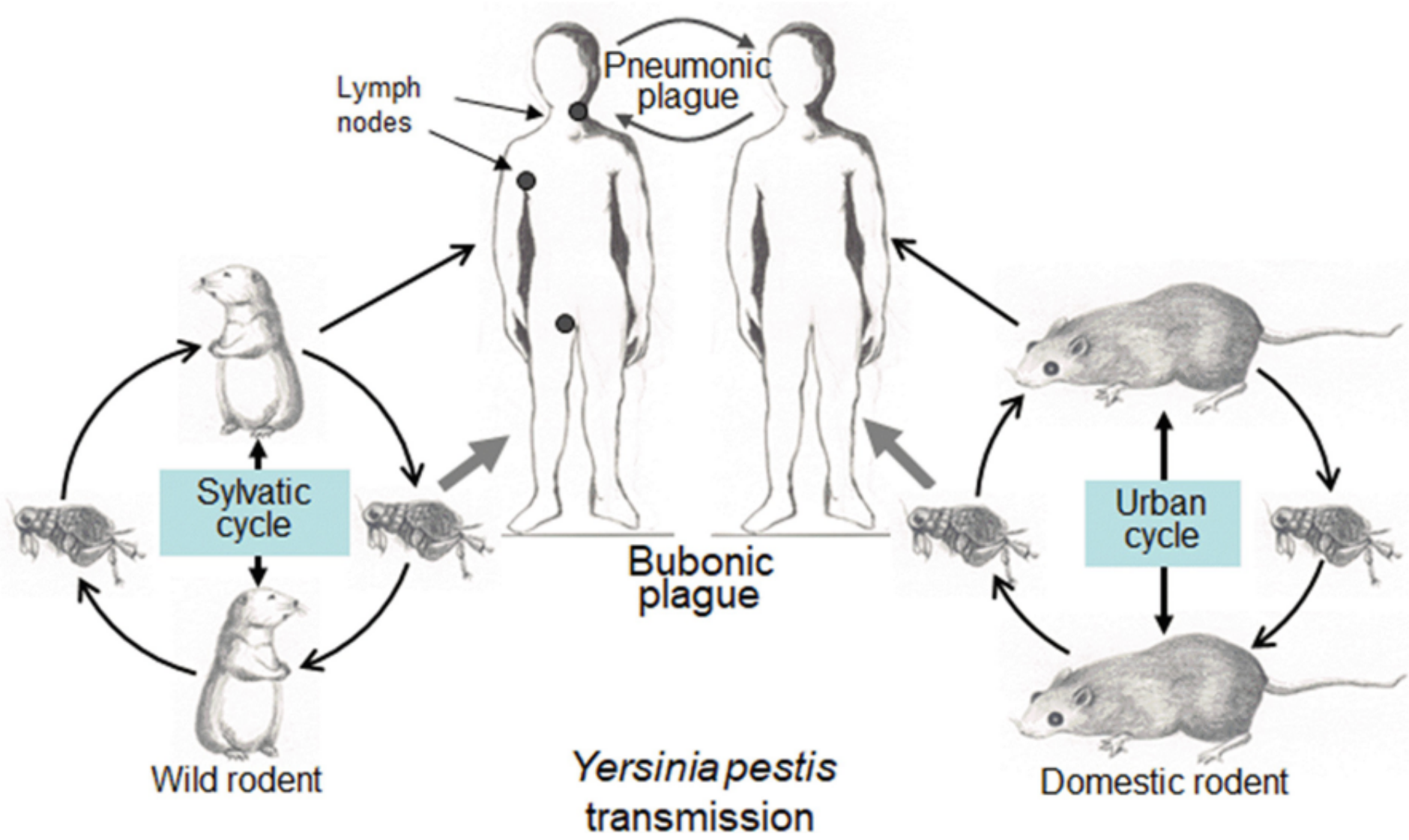


Coevolución patógeno-humano

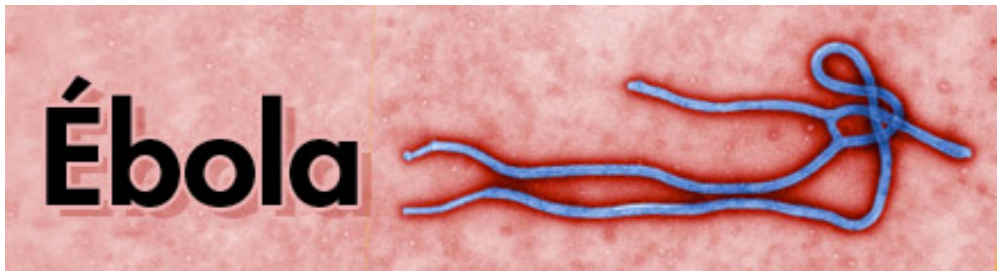
- Peste
- *Yersenia pestis*
- Peste negra
- 1/3 población europea
- Roedor – Pulgas/Piojos

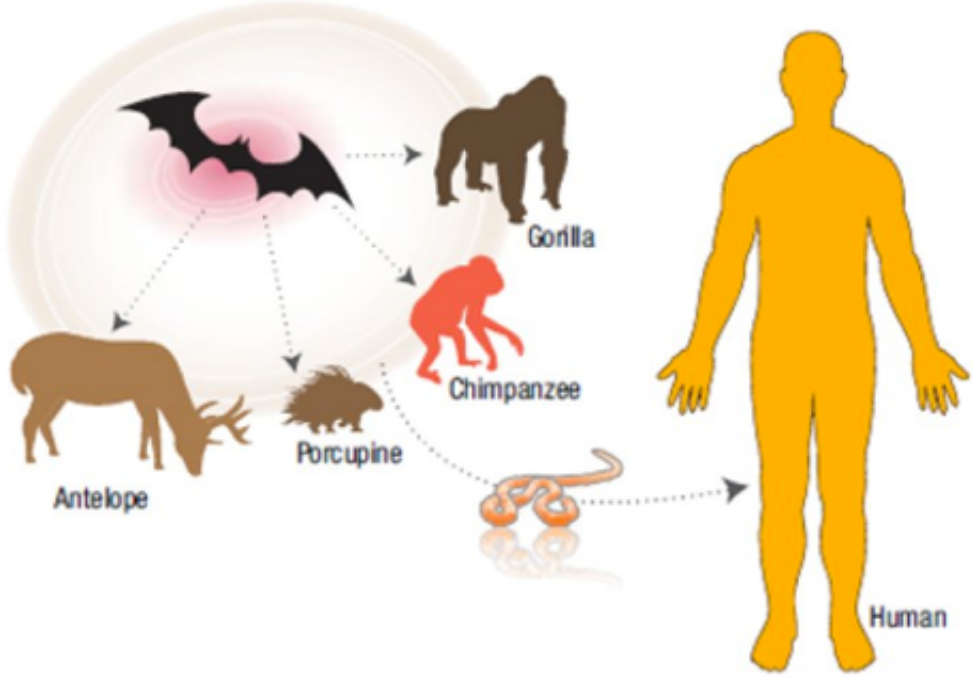


Coevolución patógeno-humano



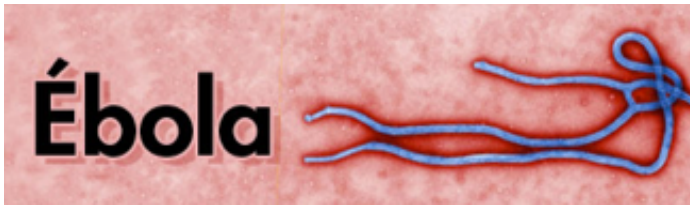
Coevolución patógeno-humano

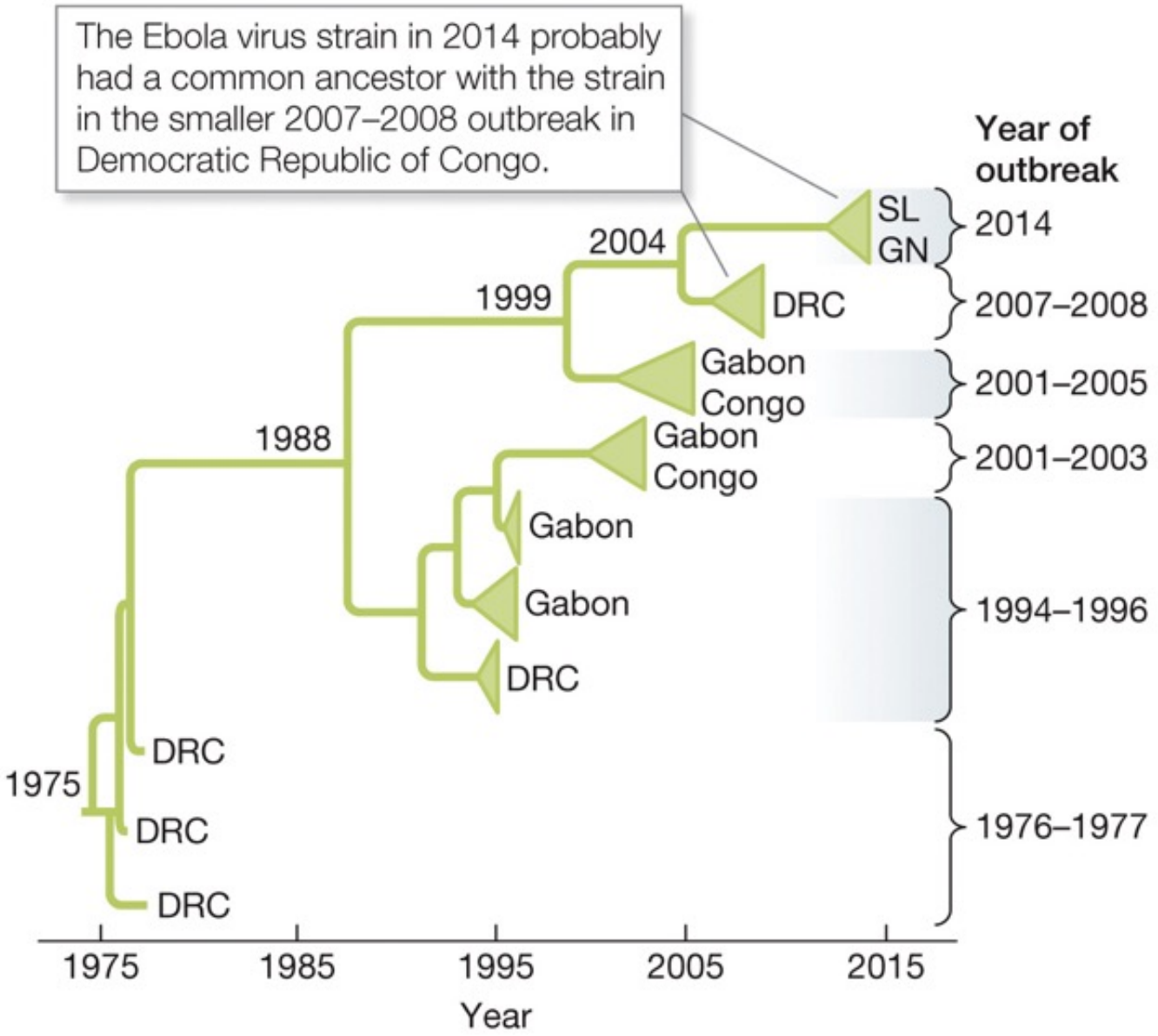




- Altamente contagioso.
- Alta mortalidad inmediata.
- Esta alta virulencia limita la habilidad del virus de dispersarse a un gran número de personas.
- Aislamiento y cuarentena son medidas efectivas para su control.

Coevolución patógeno-humano





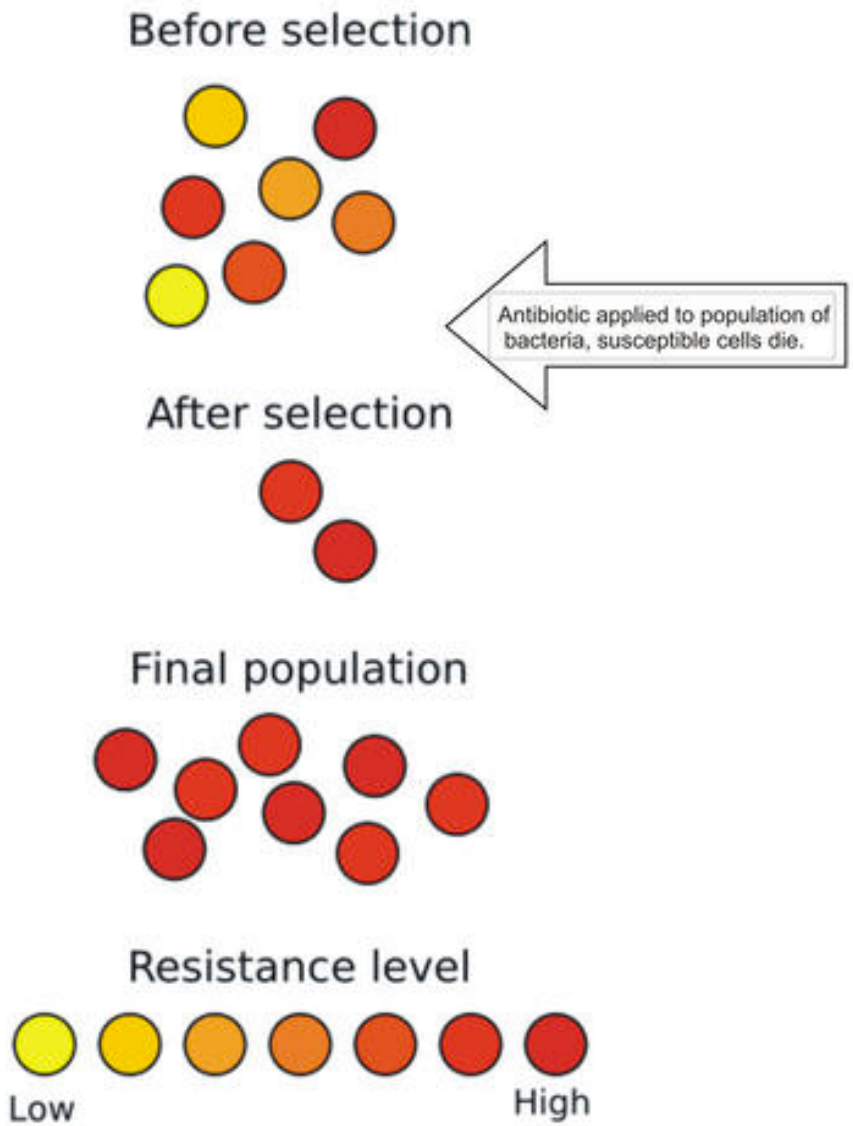
EVOLUTION 4e, Figure 16.21

Coevolución patógeno-humano

- Un patógeno evolucionará hacia un equilibrio establecido por un compromiso entre su virulencia y su capacidad de transmisión.
- Esto maximizaría su capacidad de infectar nuevos hospederos.

- Patógenos altamente virulentos deben altamente transmisibles.
- Patógenos con baja virulencia pueden ser menos transmisibles.

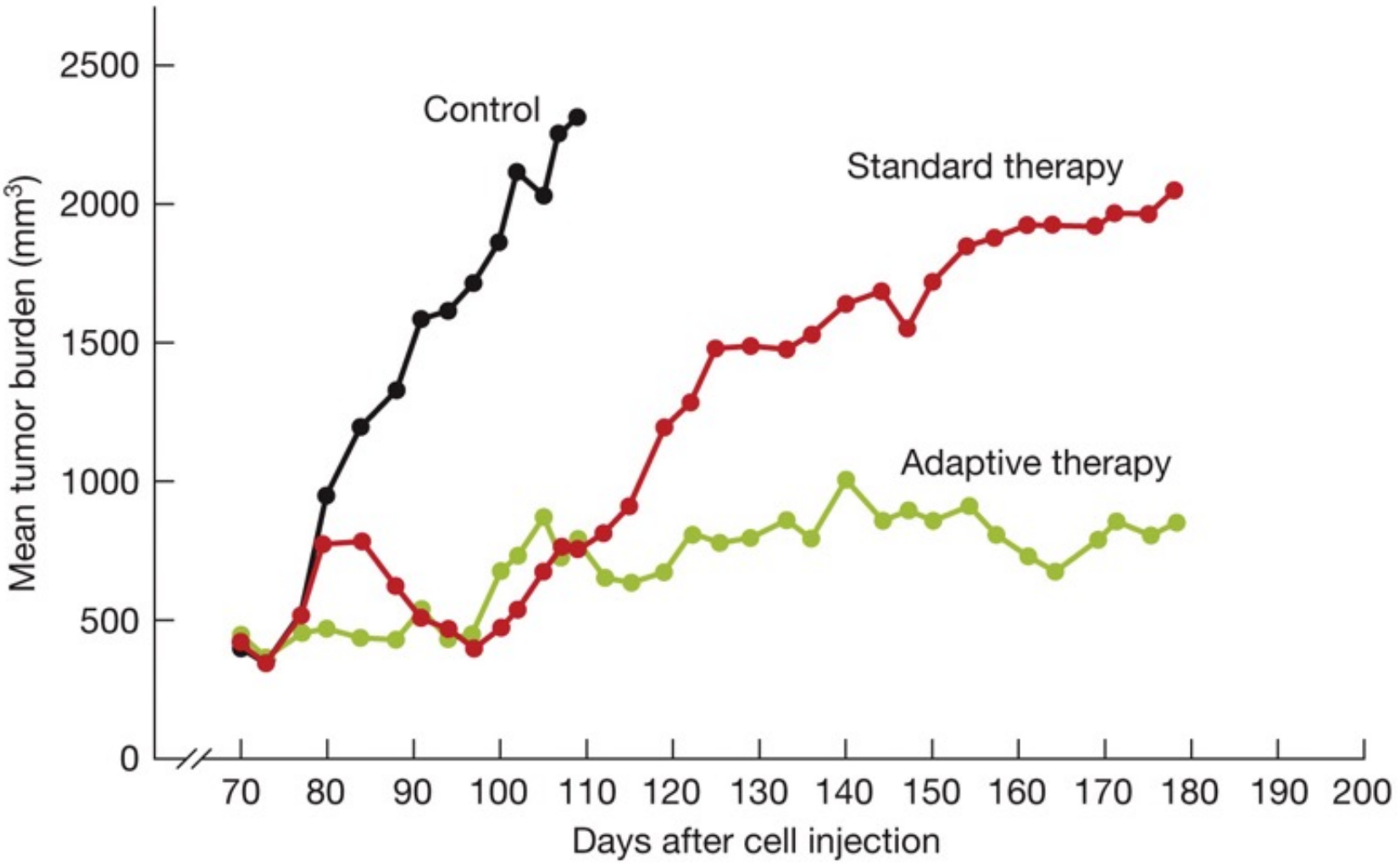
Coevolución patógeno-humano



- Tratamientos altamente agresivos podrían aumentar la virulencia.

- Tratamientos adaptativos podrían facilitar la competencia entre patógenos con distinto grado de virulencia.

Coevolución patógeno-humano



EVOLUTION 4e, Figure 22.5

Coevolución patógeno-humano

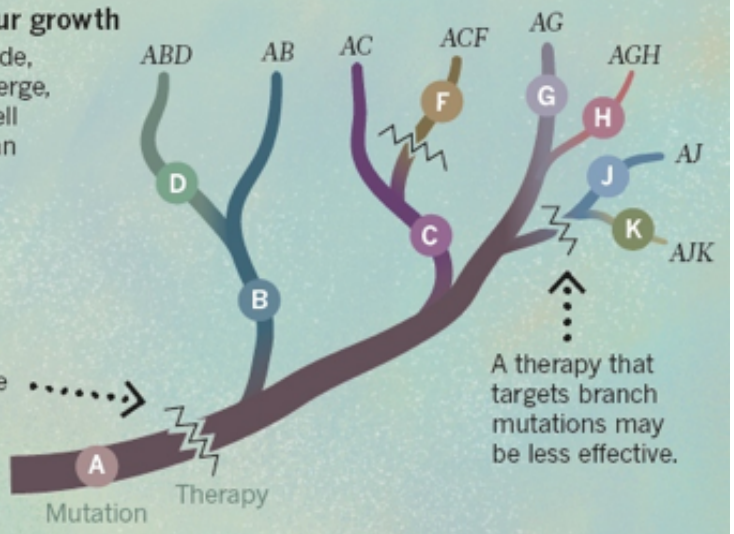
CANCER: AN EVOLVING THREAT

EVOLVING STRATEGIES

Oncologists are adapting cancer-treatment strategies to take into account how a tumour evolves.

Stemming tumour growth

As cancer cells divide, new mutations emerge, establishing new cell populations that can be mapped on an evolutionary tree.

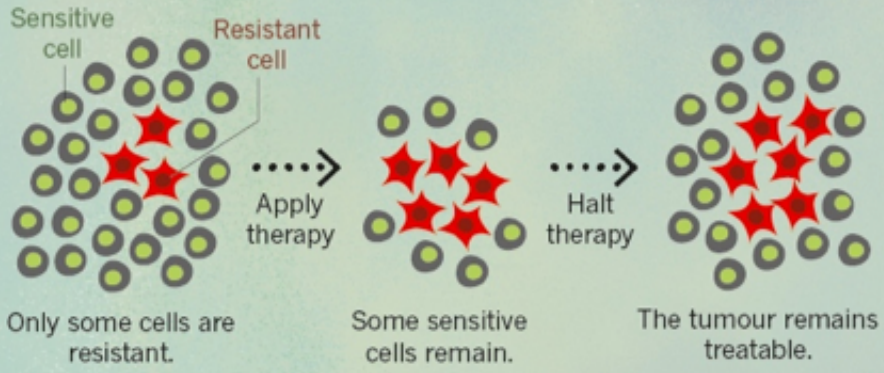


A therapy that targets mutations closer to the trunk has a better chance of eliminating cancer.

A therapy that targets branch mutations may be less effective.

Adapting for balance

Cancer-cell populations compete, so completely killing cells that are sensitive to a particular drug lets resistant cells grow unfettered. Adjusting dosage according to tumour response could maintain balance in the populations.



The double bind

Developing resistance to one treatment can leave tumours vulnerable to others. Evolutionary modelling can suggest the best way to apply multiple therapies to almost eradicate resistant cells.