

Biodiversità delle popolazioni microbiche: tra adattamento e biotecnologia

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In questa presentazione

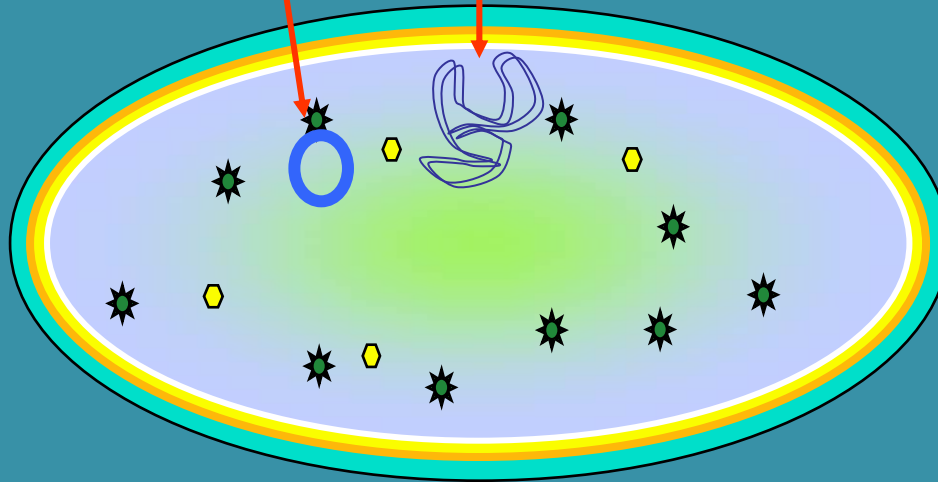
- Peculiarità del genoma dei procarioti
- Biodiversità nei procarioti
- Dalla biodiversità alla biotecnologia

IL PATRIMONIO GENETICO DEI PROCARIOTI

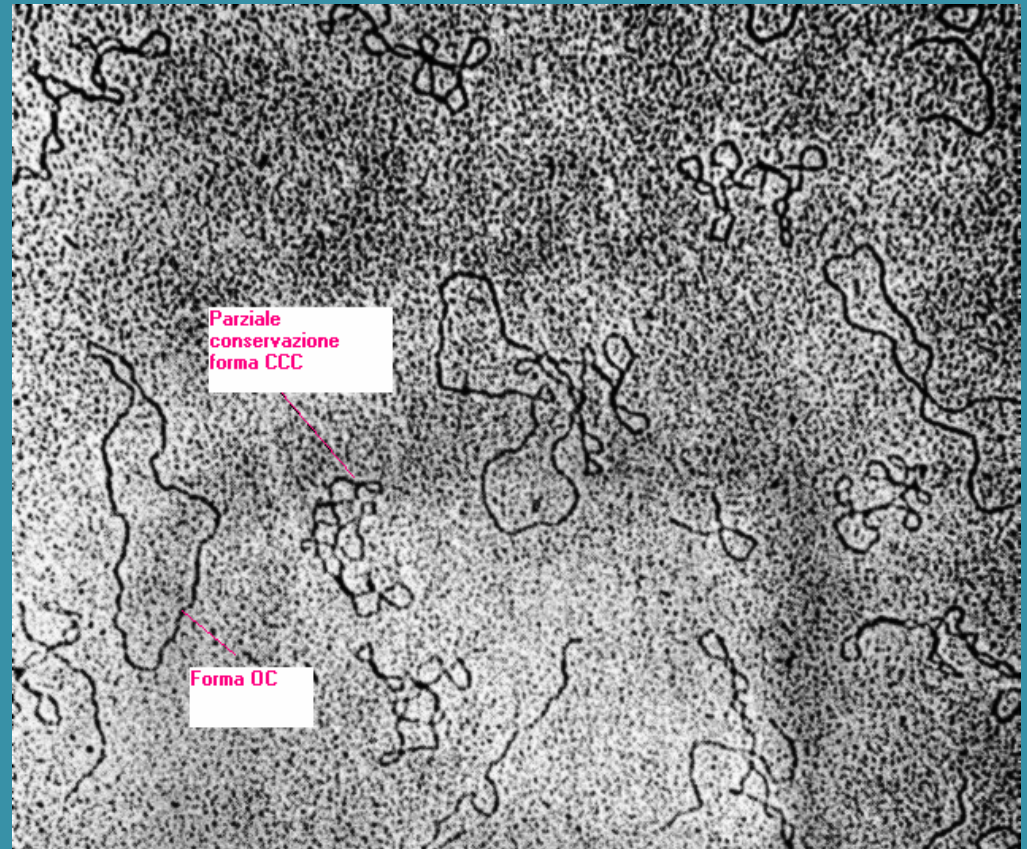
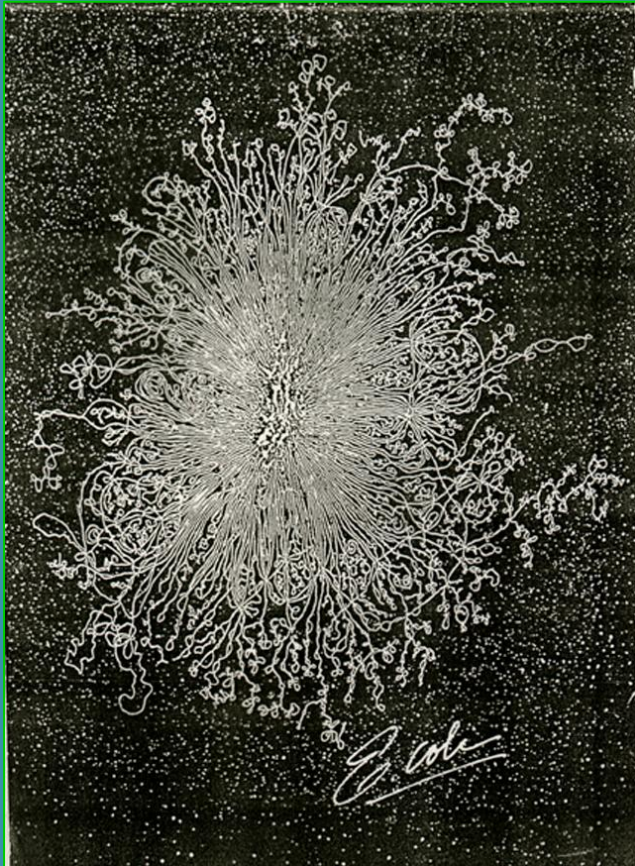
Repliconi e non repliconi

DNA extracromosomico
DNA non autoreplicativo

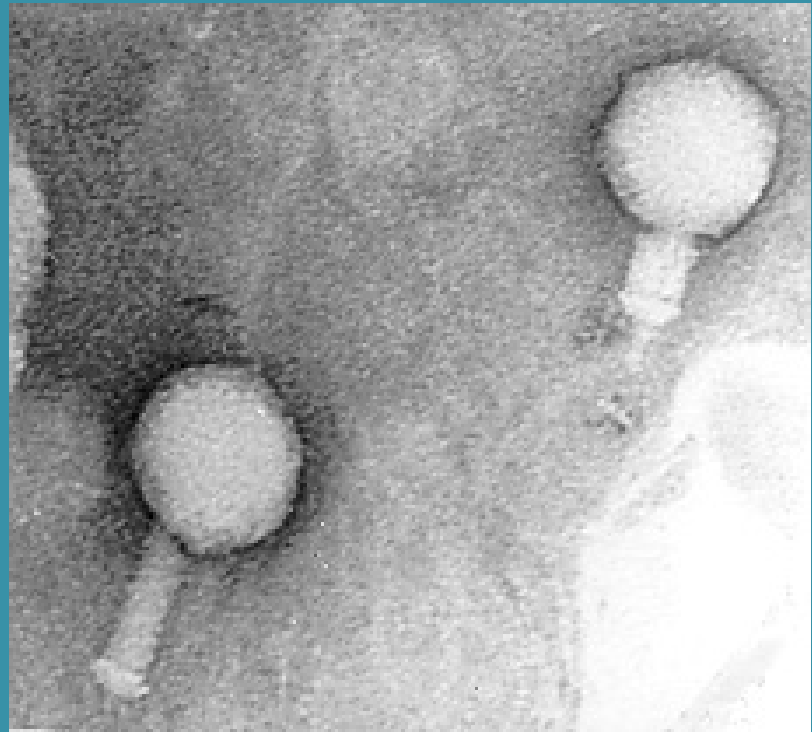
Cromosoma



Repliconi: cromosoma e plasmidi



| non repliconi: IS, Tn; Batteriofagi



Elementi di biodiversità : gene loss

CURING PLASMIDICO

Durante la divisione, ogni cellula figlia eredita almeno una copia del plasmide



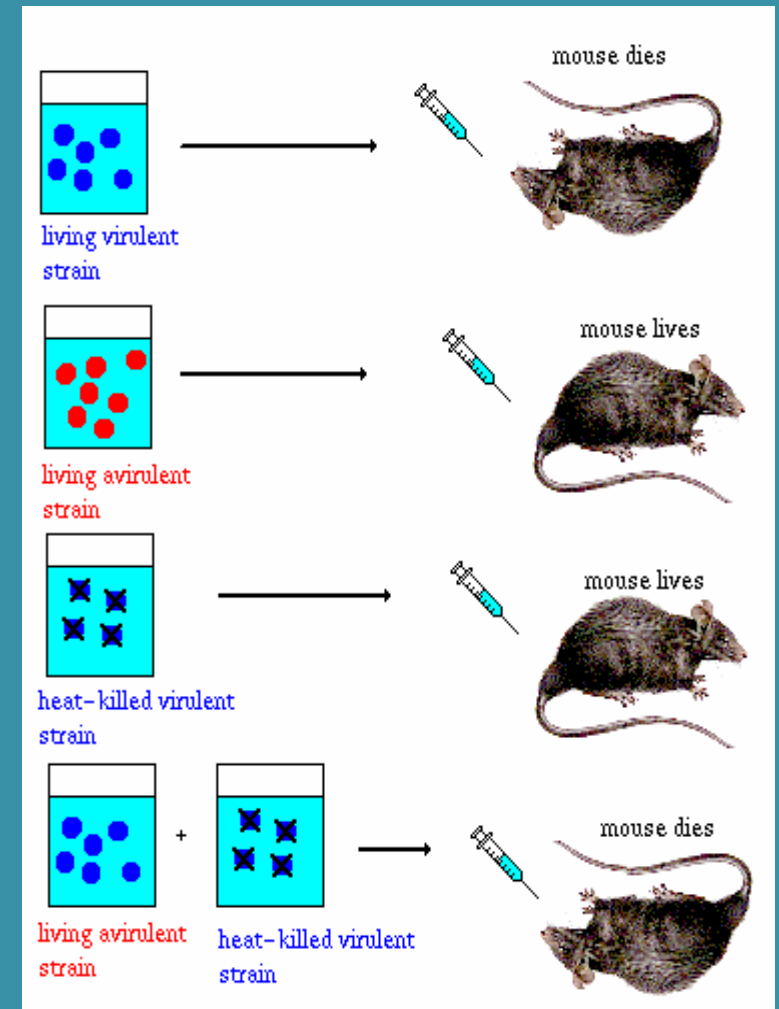
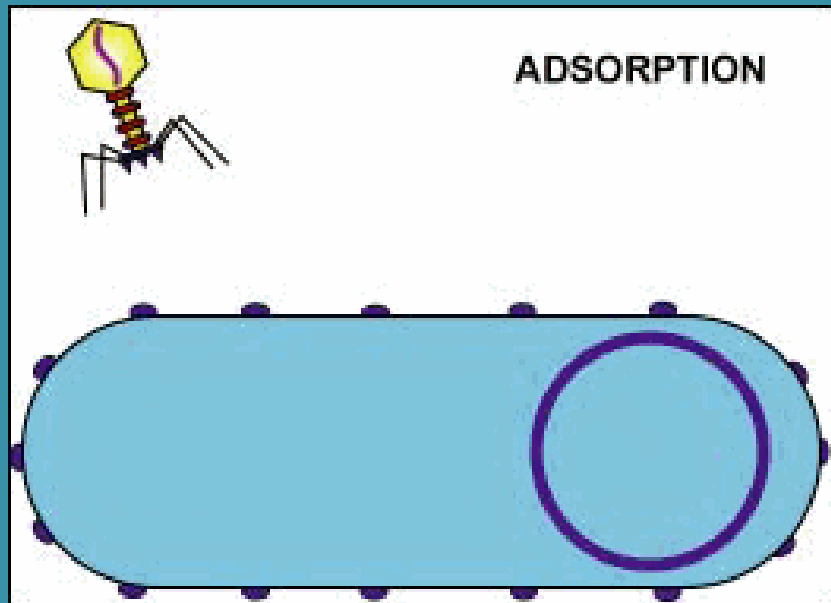
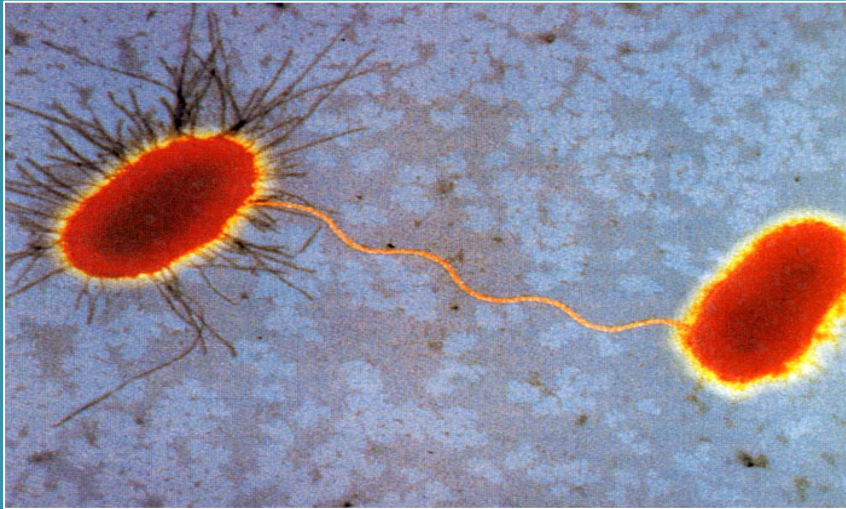
La cellula batterica possiede tre copie dello stesso plasmide



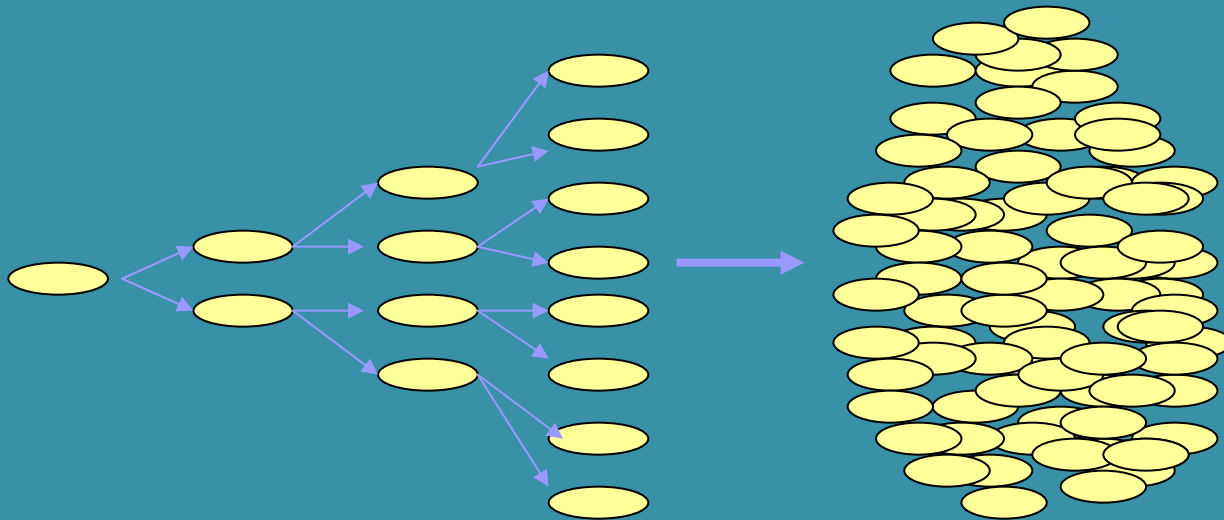
Invece, in questo caso, la cellula non riceve nessuna copia del plasmide; subisce quindi un "curing"



Elementi di biodiversità: HGT

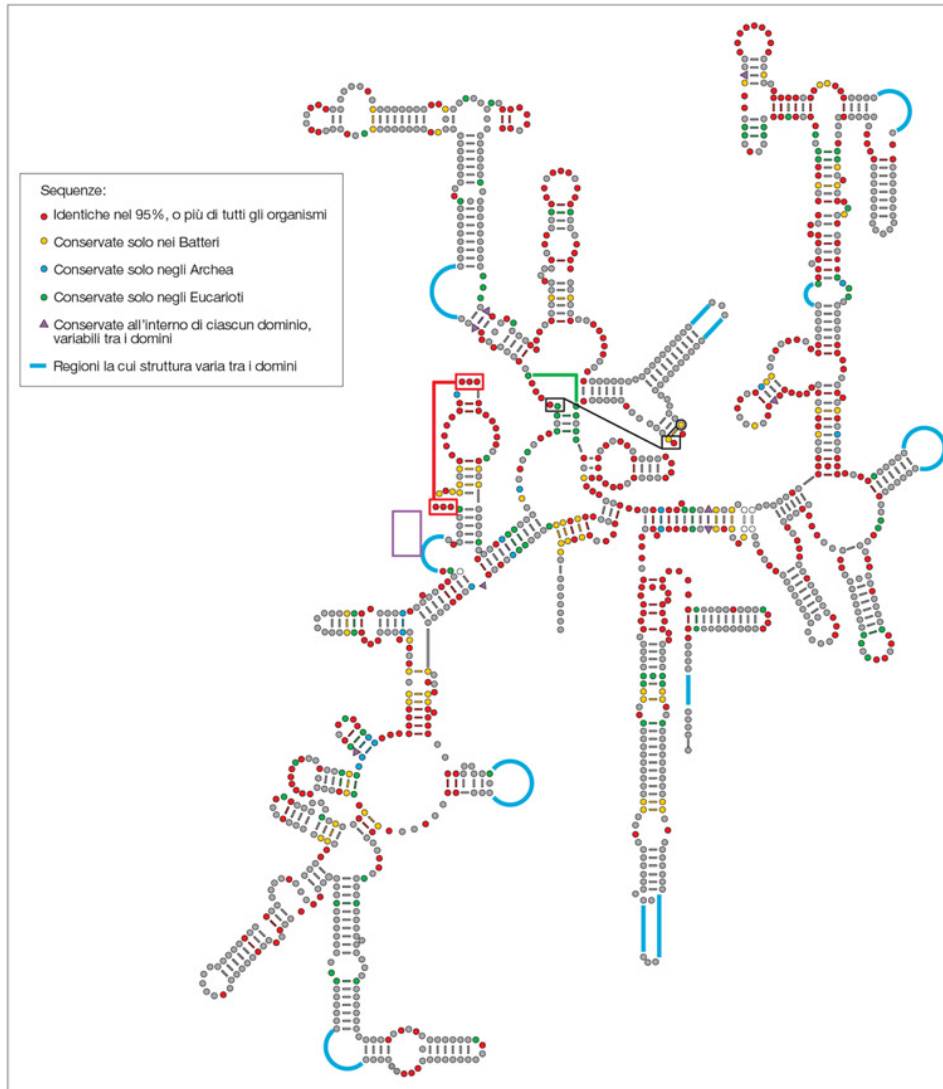


L'individuo batterico è una *popolazione che deriva da un singolo progenitore ancestrale*



La specie batterica

- La sequenza di DNA che codifica per l'RNA 16S (sub-unità più piccola del ribosoma) è usata come “misura” dell'omologia fra individui e gruppi batterici.
- E' presente in tutti i batteri, è sufficiente piccola (circa 1500 paia di basi) da poter essere studiata con facilità e sufficientemente lunga da poter contenere un numero di mutazioni significative della storia evolutiva della molecola e della cellula batterica che la contiene.
- Definisce la specie batterica



Ricordiamo alcuni concetti: a volte da un progenitore batterico A_0 possono derivare due individui non + identici:



Ma dalla prima biforcazione.....



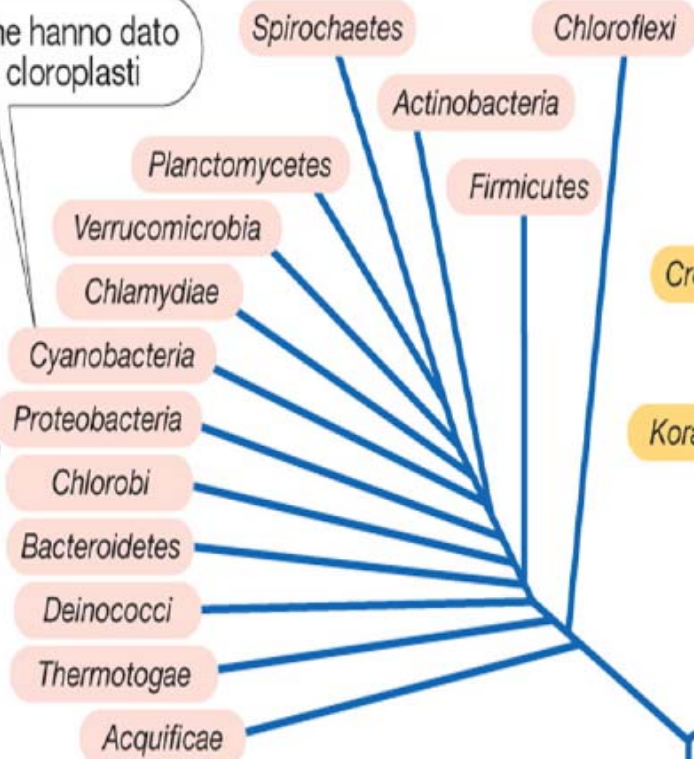
BACTERIA

ARCHAEA

EUKARYA

Batteri che hanno dato origine ai cloroplasti

Batteri che hanno dato origine ai mitocondri



Muffe mucillaginose acellulari

Muffe mucillaginose cellulari

Entamebe

Alghie rosse

Animali

Funghi

Piante

Eteroconti

Ciliati, dinoflagellati

Ameboflagellati

Parabasaliani

Microsporidi

Diplomonadi

In cerca di *LUCA* (*Last Universal Common Ancestor*) all'epoca della *comparative genomics*

Background: Comparative analysis of sequenced genomes reveals numerous instances of apparent horizontal gene transfer (HGT), at least in prokaryotes, and indicates that lineage-specific gene loss might have been even more common in evolution. This complicates the notion of a species tree, which needs to be re-interpreted as a prevailing evolutionary trend, rather than the full depiction of evolution, and makes reconstruction of ancestral genomes a non-trivial task.

In cerca di *LUCA* (*Last Universal Common Ancestor*) all'epoca della *comparative genomics*

Results: We addressed the problem of constructing parsimonious scenarios for individual sets of orthologous genes given a species tree. The orthologous sets were taken from the database of Clusters of Orthologous Groups of proteins (COGs). We show that the phyletic patterns (patterns of presence-absence in completely sequenced genomes) of almost 90% of the COGs are inconsistent with the hypothetical species tree. Algorithms were developed to reconcile the phyletic patterns with the species tree by postulating gene loss, COG emergence and HGT (the latter two classes of events were collectively treated as gene gains). We prove that each of these algorithms produces a parsimonious evolutionary scenario which can be represented as mapping of loss and gain events on the species tree. The distribution of the evolutionary events among the tree nodes substantially depends on the underlying assumptions of the reconciliation algorithm, e.g. whether or not independent gene gains (gain after loss after gain) are permitted. Biological considerations suggest that, on average, gene loss might be a more likely event than gene gain. Therefore different gain penalties were used and the resulting series of reconstructed gene sets for the last universal common ancestor (LUCA) of the extant life forms were analysed. The number of genes in the reconstructed LUCA gene sets grows as the gain penalty increases. However, qualitative examination of the LUCA versions reconstructed with different gain penalties indicates that, even with a gain penalty of 1 (equal weights assigned to a gain and a loss), the set of 572 genes assigned to LUCA might be nearly sufficient to sustain a functioning organism. Under this gain penalty value, the numbers of horizontal gene transfer and gene loss events are nearly identical. This result holds true for two alternative topologies of the species tree and even under random

**Evoluzione delle specie
batteriche e COGs non
coincidono in maniera diretta**

Filogenesi 16S vs evoluzione COGs

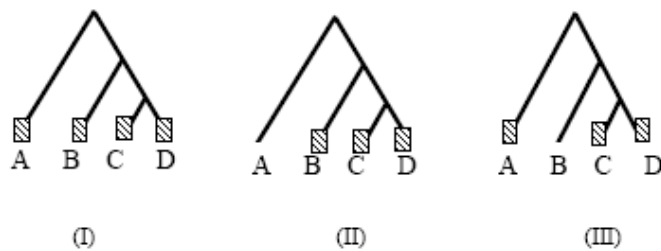


Figure 1

Phyletic patterns of presence/absence of genes (1), (2) and (3) at an evolutionary tree with four current species A, B, C, and D being the tree leaves. The gene presence is shown with the patterned box.

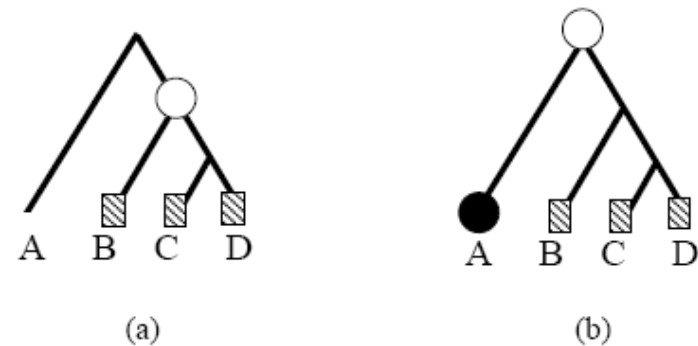
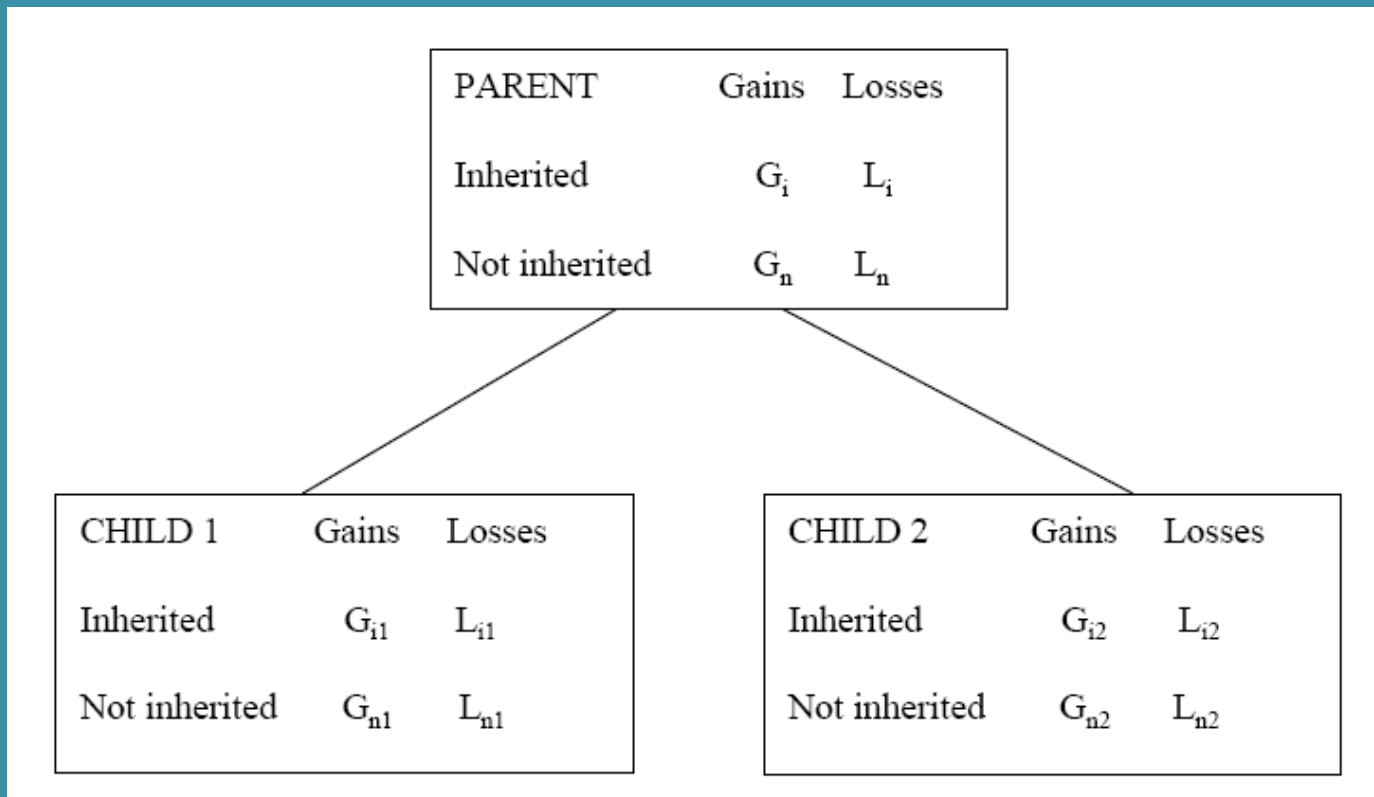


Figure 2

Two evolutionary scenarios leading to pattern II of Figure 1. The black circle represents gene loss and the white circle represents emergence of the COG.

COGs + HGT + gene loss

Filogenesi 16S vs evoluzione COGs

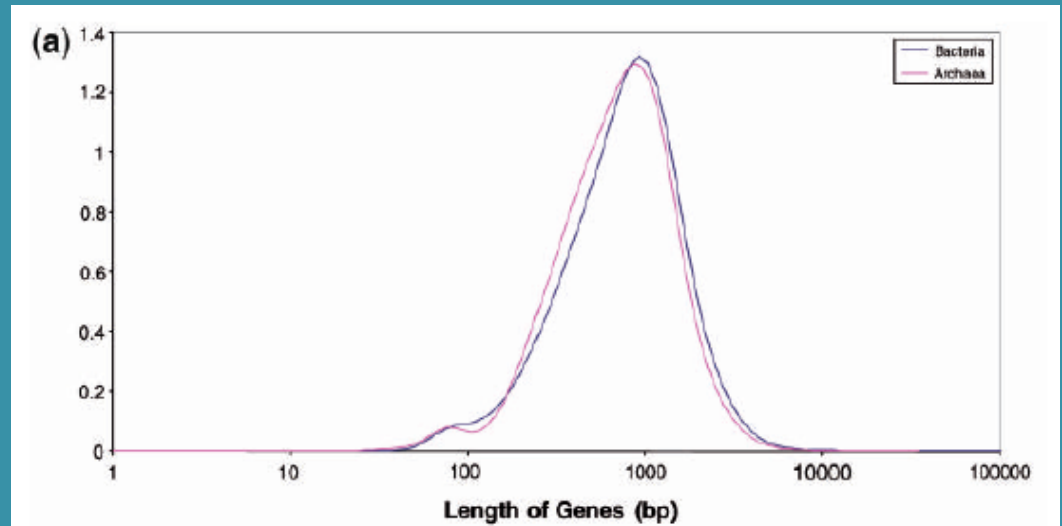
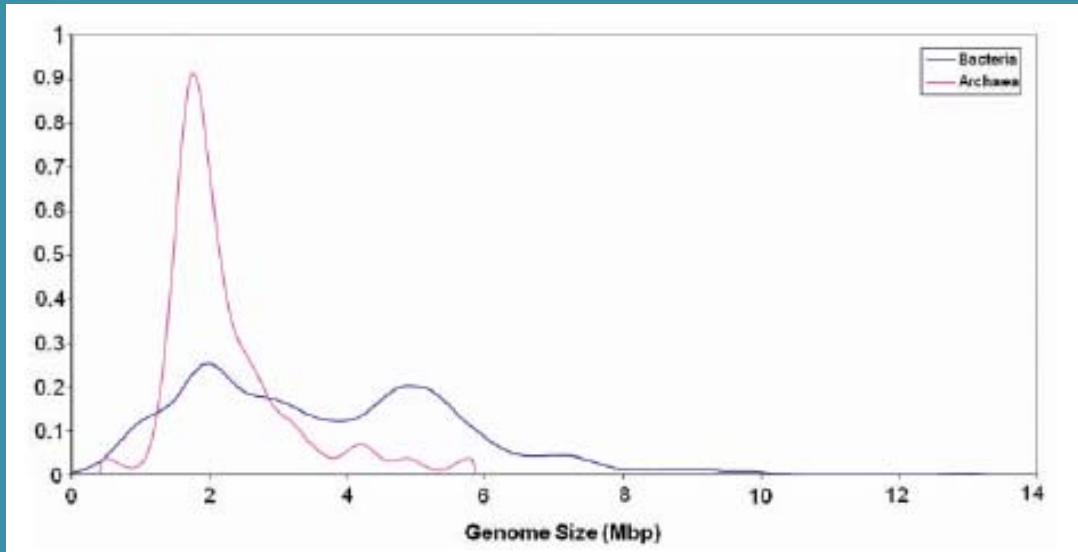


L'architettura del genoma procariote

Almost immediately after the release of the first complete genome sequences, it became apparent that the gene order in bacterial and archaeal genomes is relatively poorly conserved , dramatically less so than genes themselves .

Nucleic Acids Research, 2008, Vol. 36, No. 21

L'architettura del genoma procariote



ORFans: le percentuali della biodiversità batterica: 10-15% dei geni predetti



Figure 7. Common and rare genes in selected archaeal and bacterial genomes. Red, core; green, shell; light gray, cloud; dark gray, ORFans. The assignment of the genes from each genome to one of the four classes was based on their inclusion to the core, shell or cloud EggNOGs (Figure 6); the remaining genes were classified as ORFans.

the number of essential genes in bacteria between 300 and 700, depending on the life style

ORFans: le percentuali della biodiversità batterica: 10-15% dei geni predetti

The ORFans have also received the less flattering name ELF, Evil Little Fellow, and it has been argued that many of them are false predictions rather than actual protein-coding genes (45). Furthermore, it has been proposed that the majority of those ORFans that are real genes were derived from bacteriophages and, accordingly, are characterized by high horizontal mobility.

Recent estimates from metagenomic surveys of bacteriophages suggest that the diversity of phage sequences is vast and remains, largely, unexplored .

Therefore, it does seem plausible that a major fraction of bacterial and archaeal ORFans derives from the still poorly explored but, certainly, vast bacteriophage gene pool.

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Una prima conclusione

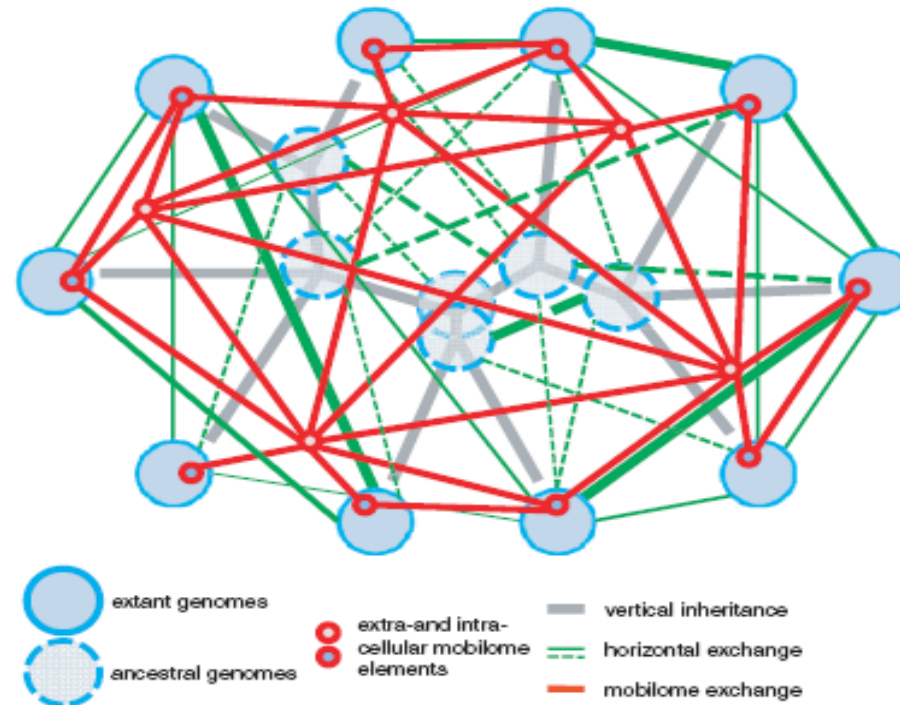


Figure 17. The dynamic view of the prokaryotic world. The figure is a conceptual schematic representation that is not based on specific data. The larger blue circles denote extant (solid lines) or ancestral (dashed lines) archaeal and bacterial genomes. The small red circles denote mobilome components such as plasmids or phages. Gray lines denote vertical inheritance of genes; green lines denote recent (solid) or ancient (dashed) HGT; red lines denote the permanent ongoing process of the exchange of genetic material between mobilome elements. The thickness of connecting lines reflects the intensity of gene transfer between the respective genetic elements.

Biodiversità della distribuzione spaziale: assenza di sintenia

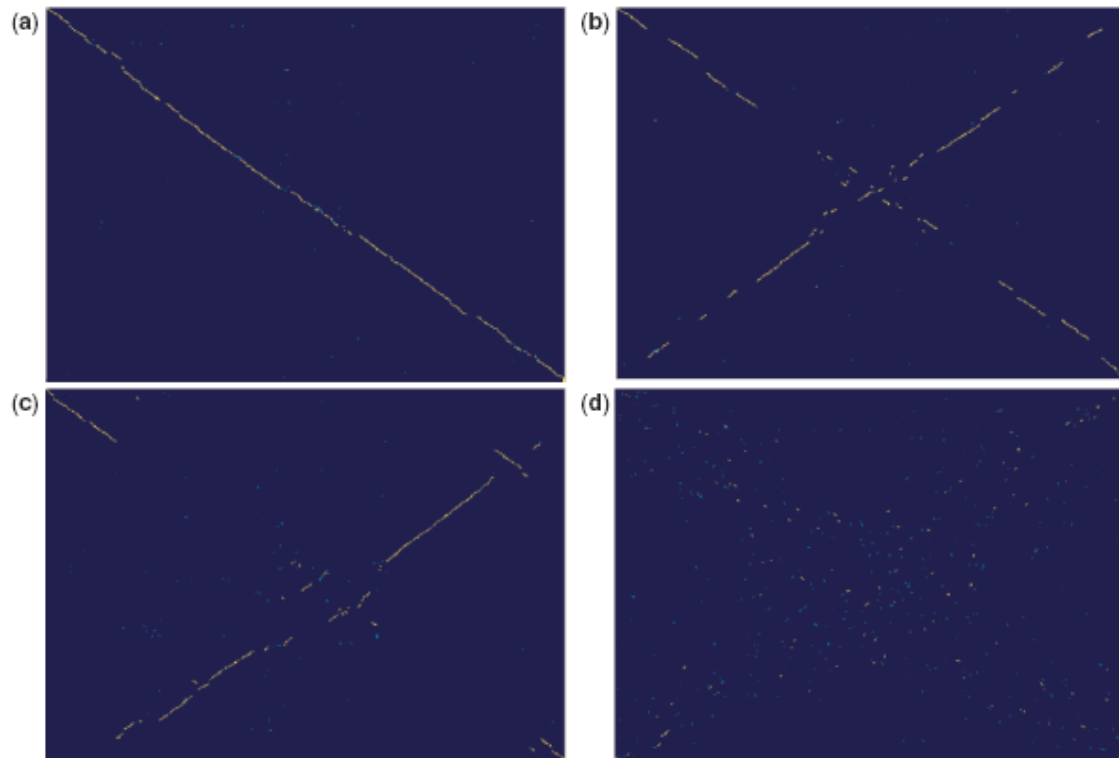


Figure 13. Evolution of gene order in bacteria and archaea: genomic dot-plots. (a) Colinearity with a few breakpoints between closely related bacteria: *Geobacillus thermodenitrificans* versus *Geobacillus kaustophilus*; (b) X-shaped pattern between moderately diverged bacteria: *Shewanella* sp. MR-4 versus *Shewanella oneidensis*; (c) X-shaped pattern between moderately diverged archaea: *Pyrococcus horikoshii* OT3 versus *Pyrococcus abyssi* GE5; and (d) No clear pattern between more distantly related bacteria: *Streptococcus gordonii* str. Challis versus *Streptococcus pneumoniae* R6. In each panel, the genome indicated first is plotted along the vertical axis.

Prospettive biotecnologiche per un *self cloning*
fra I domini procarioti

L'universo procariote è diviso fra *Archea* e *Eubacteria*

Gli Archea sono fonte di sostanze utili (*Taq* polimerasi)

Ma queste sostanze derivano da cloni eubatterici per problemi di produttività industriale

Questo limita l'uso *open field*

L'universo procariote è diviso fra *Archea* e *Eubacteria*

Ma è veramente diviso?

Prospettive biotecnologiche per un *self cloning* fra i domini procarioti

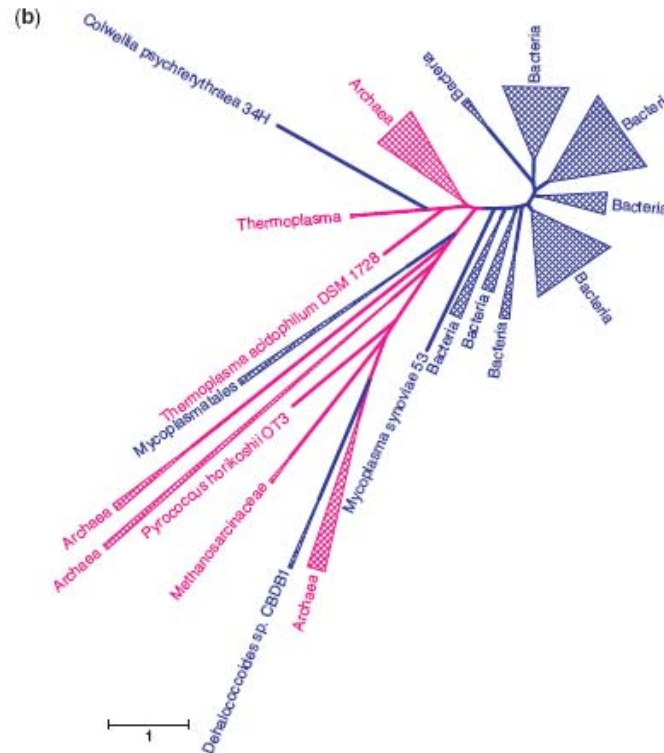
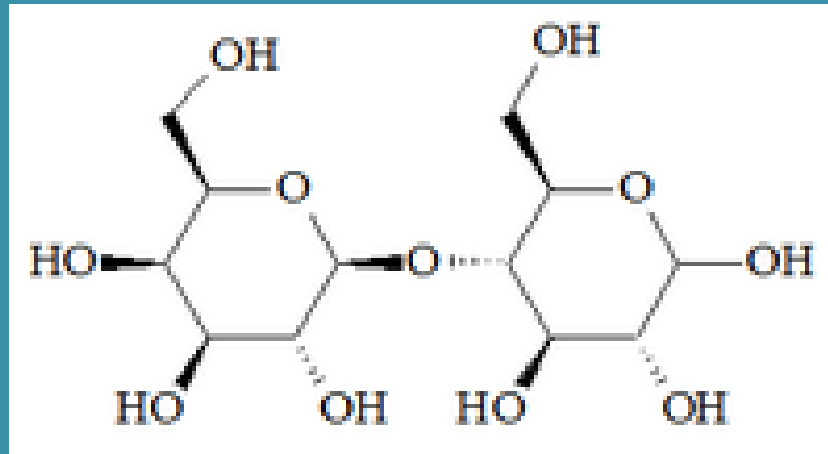


Figure 16. Two cases of readily demonstrable horizontal gene transfer between archaea and bacteria. (a) COG0030, dimethyladenosine transferase, an enzyme involved in rRNA methylation. (b) COG0206, FtsZ, a GTPase involved in cell division. Blue, bacteria; magenta, archaea. The trees were constructed using the maximum likelihood method implemented in the PhyML software (278) (WAG evolutionary model; γ -distributed site-specific rates with the shape parameter 1.0). The complete information on the analyzed sequences and the alignments are available from the authors upon request.

Prospettive biotecnologiche: il caso del lattosio

Il lattosio è un disaccaride tipico dei mammiferi, quindi relativamente *nuovo* per il mondo procariote



Prospettive biotecnologiche: il caso del lattosio

La possibilità di fermentare il lattosio (sistemi di trasporto e presenza dell'enzima idrolitico) segue alla comparsa dei mammiferi; questo fenotipo è talmente “recente” per il mondo procariote da essere ancora instabile (plasmidi , Tn).

La “tracciatura” della presenza dei due sistemi di utilizzazione del lattosio (ATP o PTS dipendente)

è indice di evoluzione e biodiversità

Ma la capacità di utilizzazione del lattosio è anche fenotipo di interesse tecnologico

A close-up photograph of a flowering branch, likely a cherry blossom, with clusters of pink and white flowers and green leaves. The text is overlaid in the center.

**FIORI PER LA VOSTRA
GENTILE ATTENZIONE**