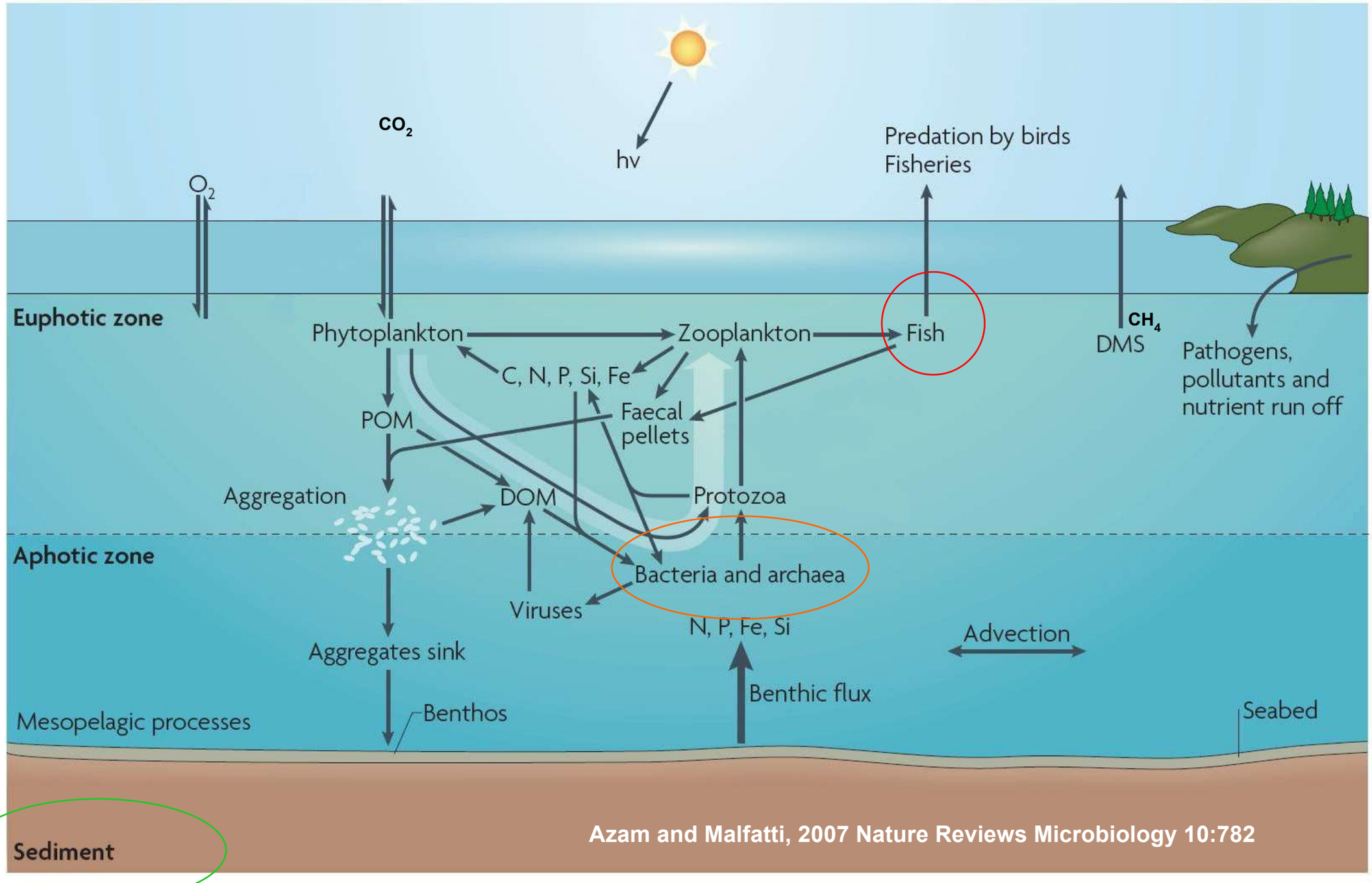
L03a: Diversity of Marine Bacteria, Archaea, Eukarya and Viruses

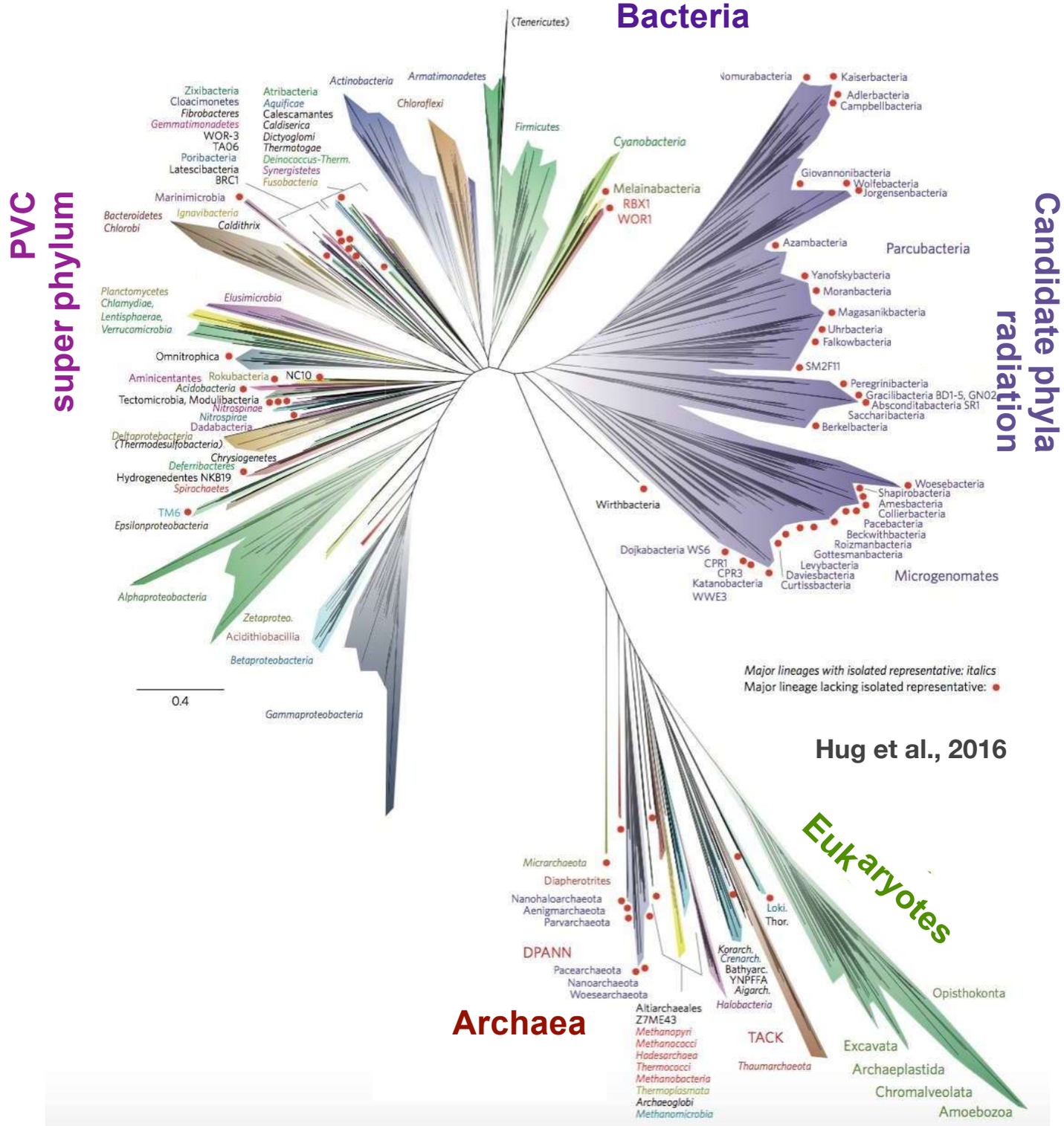
Marine microbes are highly diverse



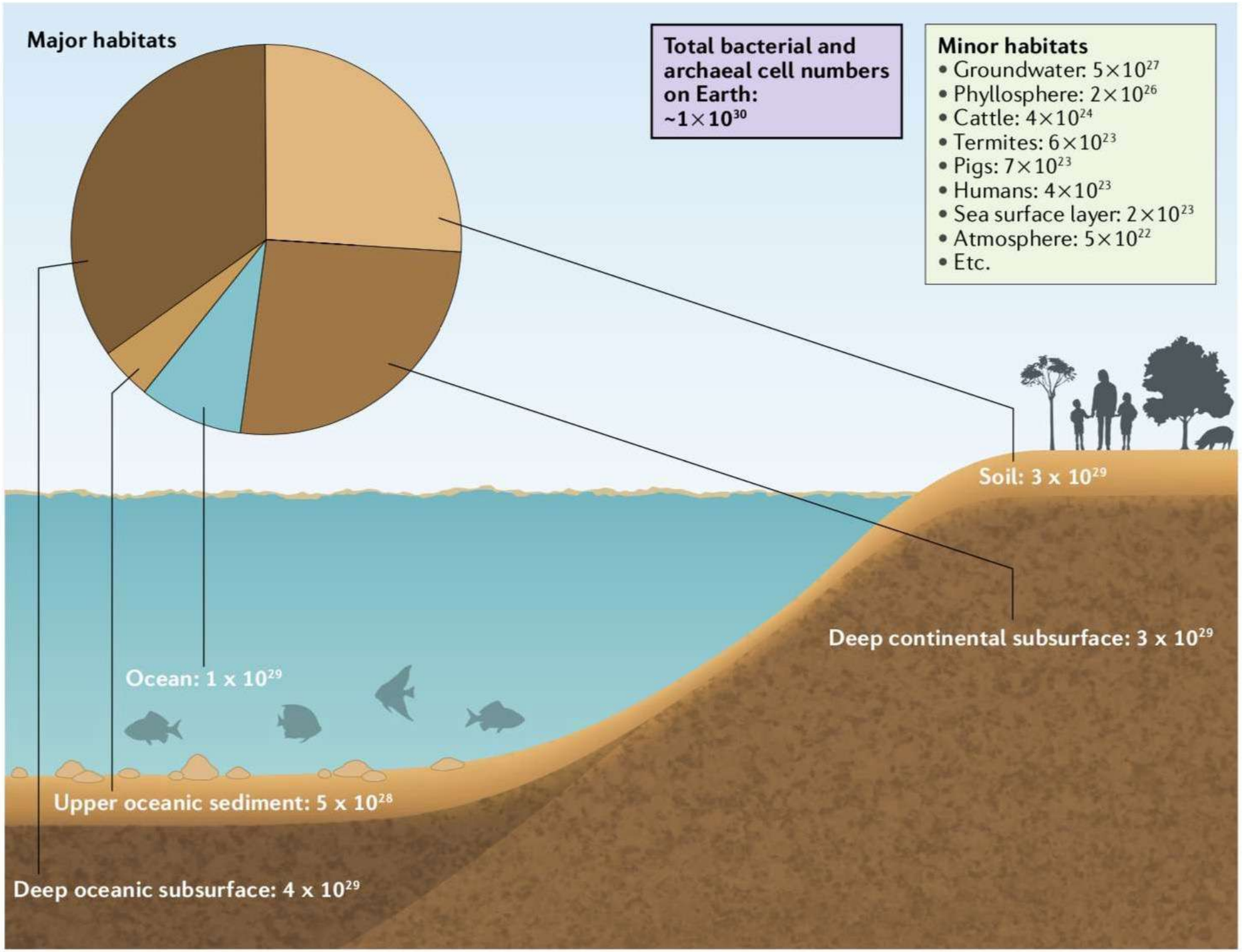
Azam and Malfatti, 2007 Nature Reviews Microbiology 10:782

Microbial diversity on Earth

- Still finding new microbes with massive sequencing approaches
- Deeper branching —> early in evolution
- Majority of microbes not cultivated, yet
- Not a species definition



Abundance of Bacteria and Archaea on Earth



Flemming & Wuertz, 2019

How many species? Ecologist Robert May remarked that “we have a catalog of all the celestial bodies our instruments can detect in the universe, but we ignore how many living beings share the Earth with us” (ISME meeting, Barcelona, 1992).

This ignorance is particularly large for life in the oceans.

Thus, the international initiative ‘Census of Marine Life’

Yarincik, K. and O’Dor, R. (2005) The census of marine life: goals, scope and strategy. Sci. Mar. 69(Suppl. 1), 201–208

Species

97% sequence similarity on the 16S rRNA gene

OTU, (Operational Taxonomic Unit)

A cluster of similar DNA sequencing reads grouped together based on a pre-defined **sequence similarity threshold**, traditionally set at **97%**

ASV, (Amplicon Sequence Variant)

An exact, unique DNA sequence inferred from high-throughput sequencing data after using statistical algorithms to remove sequencing errors. Instead of grouping reads by a 97% similarity cut-off, ASVs operate at **100% similarity (single-nucleotide resolution)**—sometimes called a "zero-radius OTU" (zOTU)

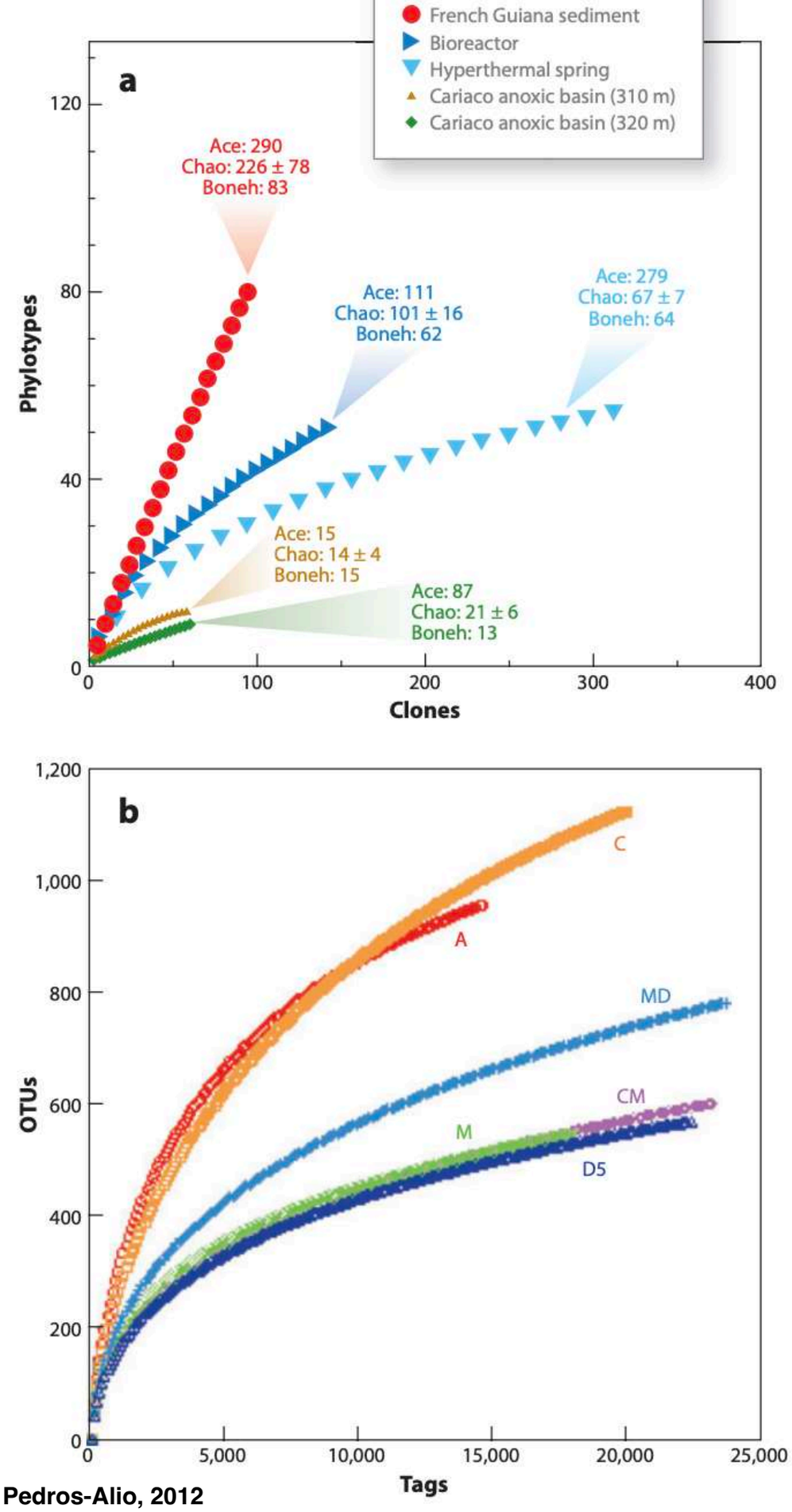
The Rare Bacterial Biosphere

Carlos Pedrós-Alió

Institut de Ciències del Mar, CSIC, 08003 Barcelona, Spain; email: cpedros@icm.csic.es

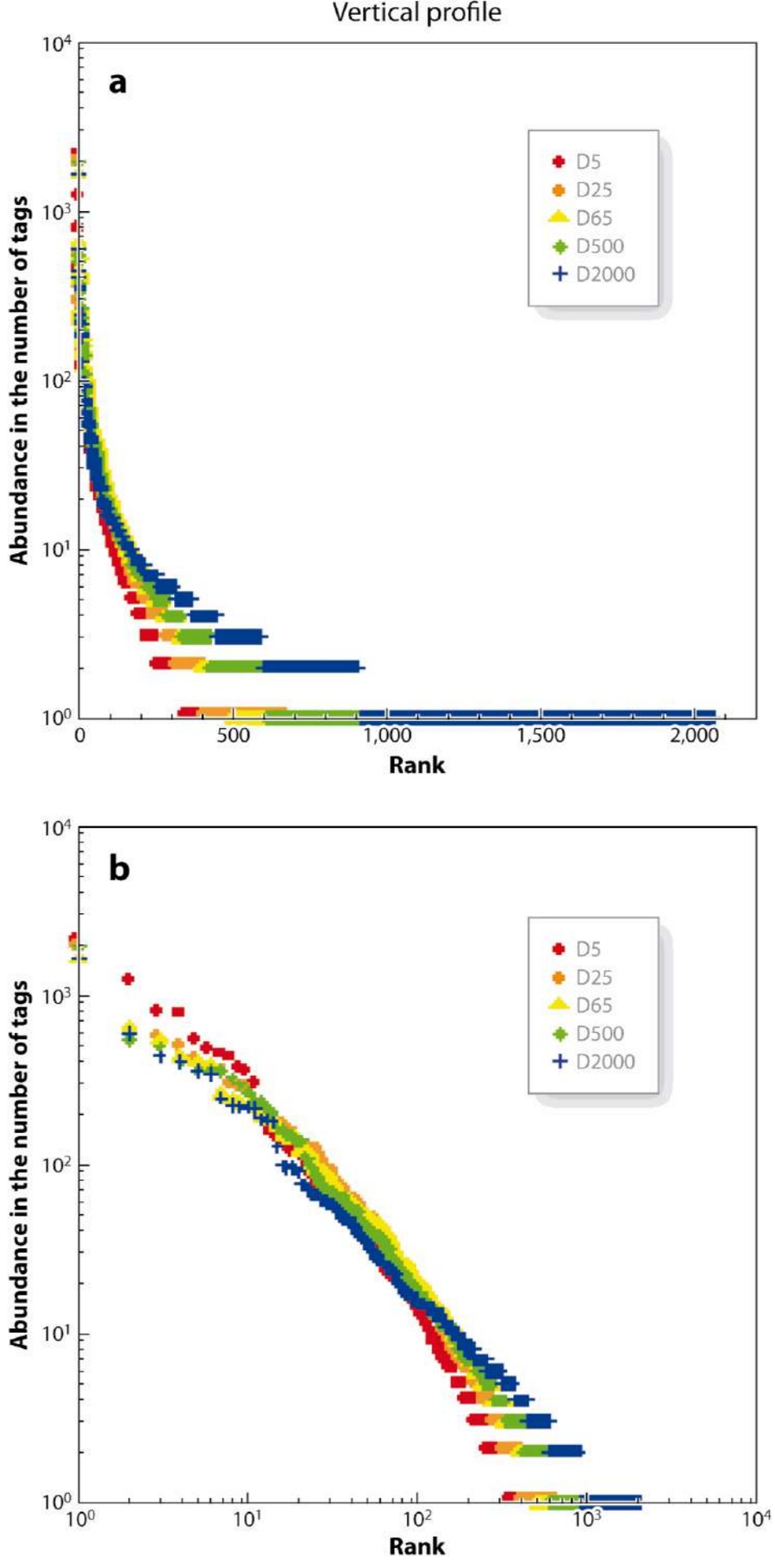
https://www.nature.com/scitable/knowledge/library/explaining-general-patterns-in-species-abundance-and-23162842/

Method to the madness



Collectors curves for bacteria obtained from (a) conventional clone libraries and (b) 454 pyrosequencing data. OTU, operational taxonomic unit; A, C, CM, M, MD, and D5 denote the stations sampled along a surface transect in the original study, from the shore (A) to the open Mediterranean Sea (D5)

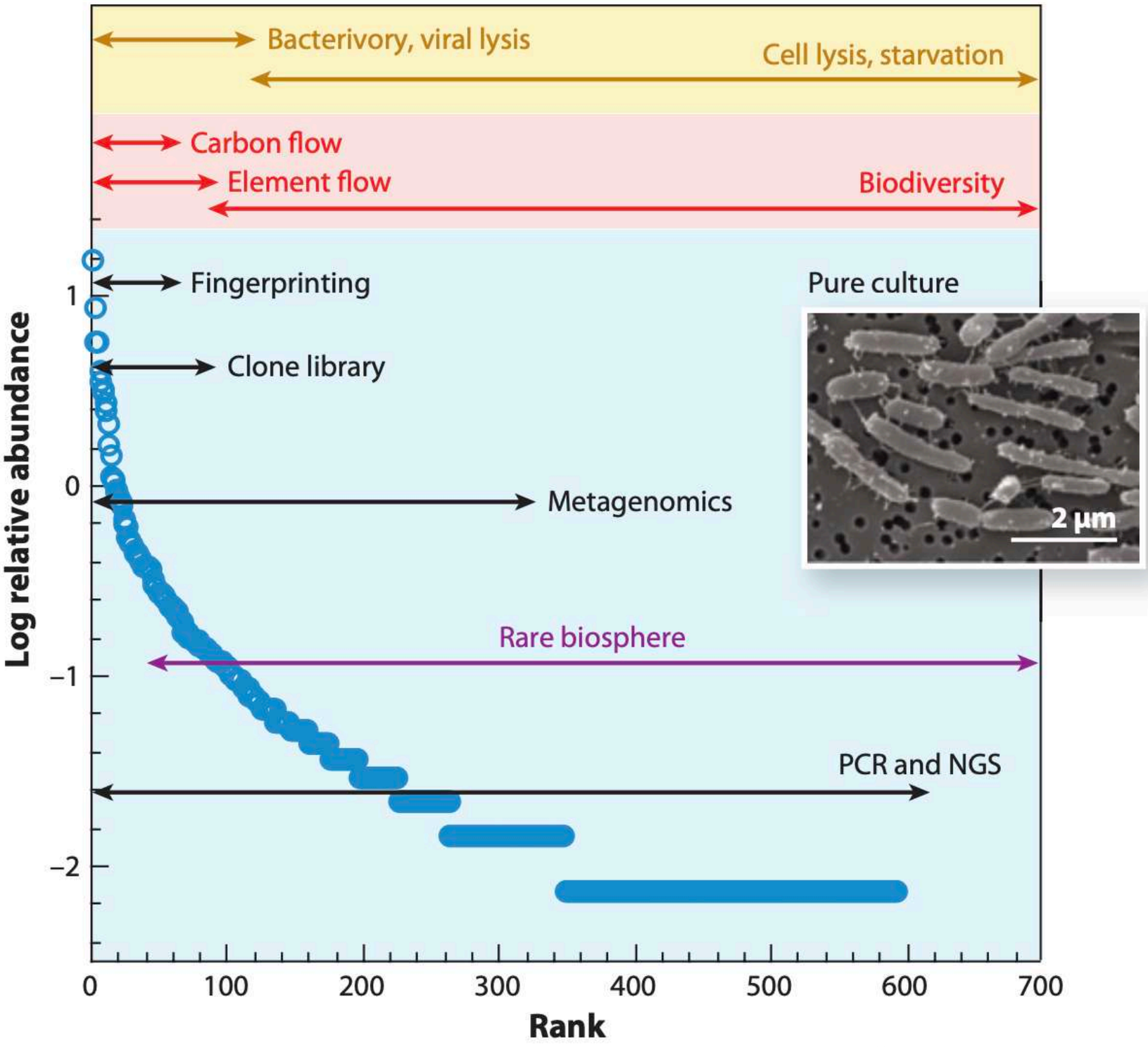
Rank-abundance curves for bacteria obtained with 454 pyrosequencing, shown with (*a*) a conventional semilog plot



Pedros-Alio, 2012

Pedrós-Alió C. 2012.
Annu. Rev. Mar. Sci. 4:449–66

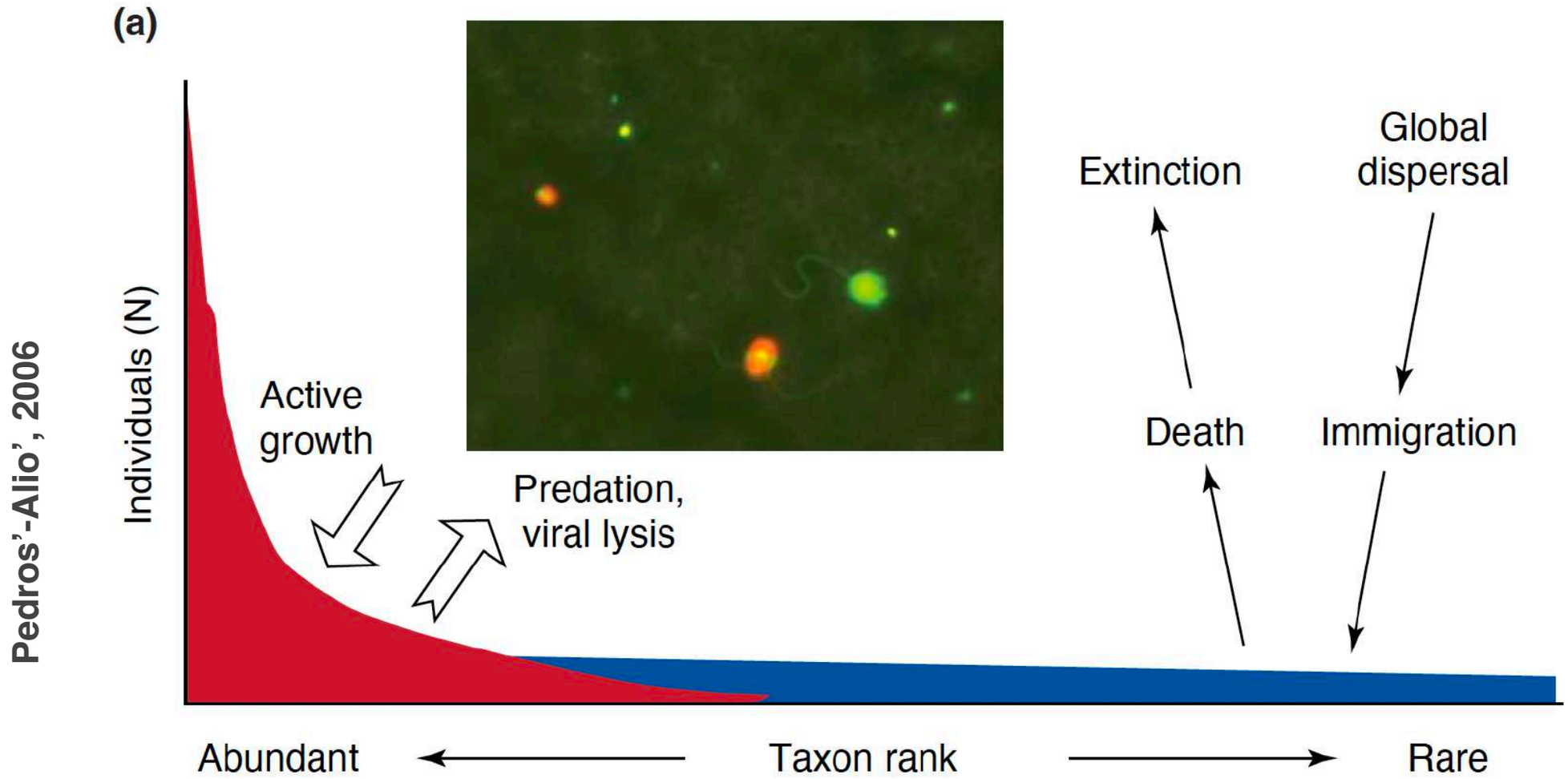
Continuum of microbial abundances



Rank-abundance curve for bacteria, showing the loss factors relevant in each part of the curve (gold), the ecological relevance (red), and the depth of sampling that different molecular techniques allow (black). The extent of the rare biosphere is shown in purple.

Pedros-Alio, 2012

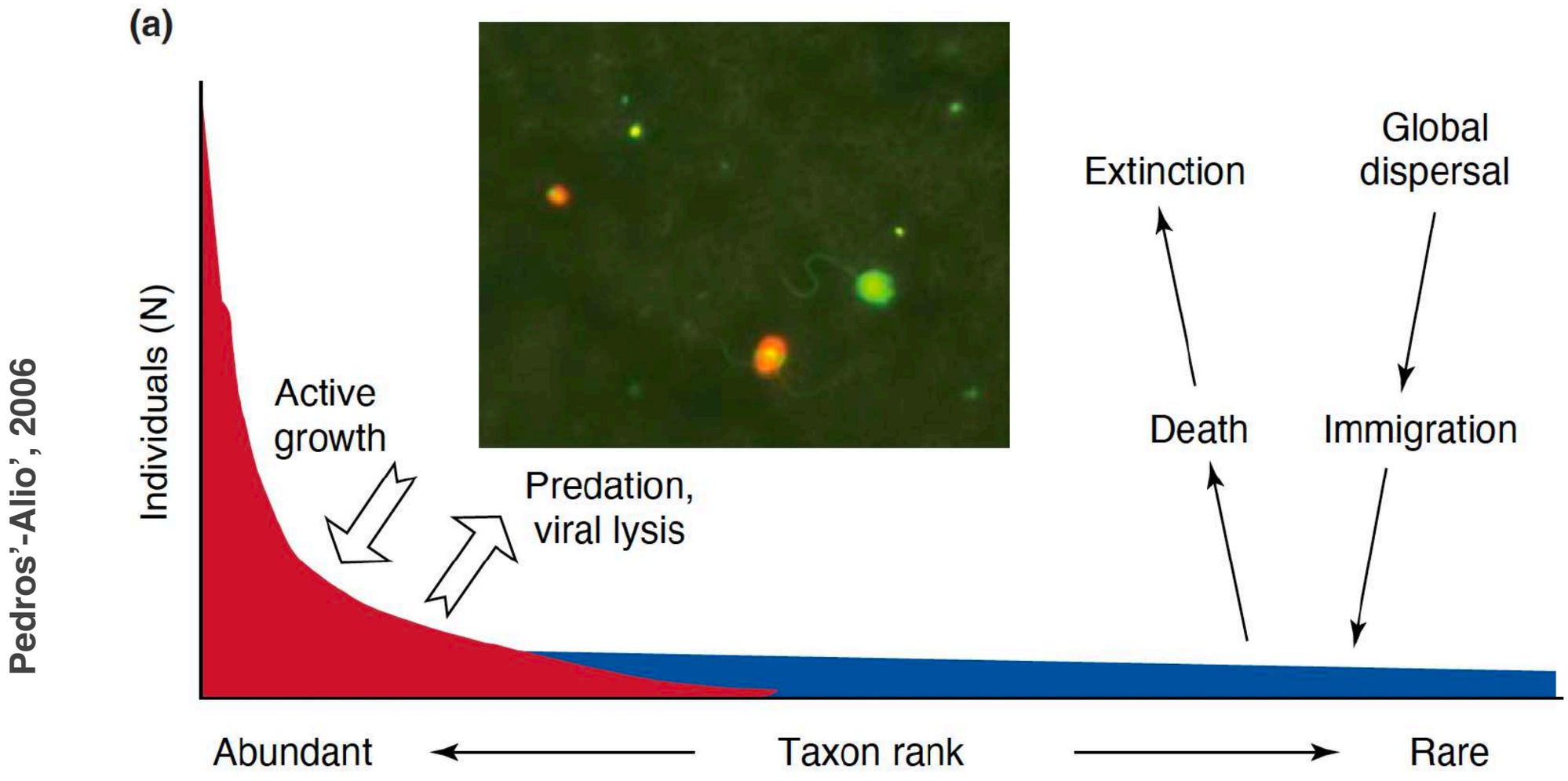
Microbial diversity fluctuations



(i) The red section curve: abundant taxa with active role in carbon and energy flow in ecosystem —> active growth and suffer losses because of predation and viral lysis

(ii) The blue section curve: rare taxa, which survive in ecosystem at low abundance (? with resting stages or spores) —> This 'seed bank' recruits new species through immigration

Microbial diversity: Individual vs. Taxon



- Because of easy dispersal of microbes, it is likely that essentially all microorganisms reach this ecosystem periodically
- By being rare, these microbes do not experience viral attack and predation is minimized; thus, extinction can only be a result of cell death
- Because extinction can be expected to be low while immigration is probably high, this part of the curve might be long and perhaps include the whole biodiversity of microbes

Table 1 Characteristics expected of abundant and rare bacteria

Property	Abundant bacteria	Rare bacteria
Contribution to ecosystem		
Abundance	≥1%	≤0.1%
Biomass	Major	Minor
Biodiversity	Minor	Major
Carbon flow	Major	Minor
Nutrient cycling	Major	Significant in some cases
Growth rate	High	Low
Losses and resistance		
Predation	High	Low
Predation resistance	Probably not	Passive (small size, palatability)
Viruses	High	Absent
Virus resistance	Some	No (betaproteobacteria?)
UV radiation	Intense at surface	Intense at surface
UV pigments and repair	Variable	Variable
Starvation	No	Yes
Starvation resistance stages	No	Some

Pedros-Alio, 2012

Everything is everywhere and environment selects (Baas Becking statement)

This “rare biosphere” is very ancient and may represent a nearly inexhaustible source of genomic innovation

Members of the rare biosphere are highly divergent from each other and, at different times in earth’s history, may have had a profound impact on shaping planetary processes

Newer and better methods will allow us to see more

Everything is not everywhere but environment selects