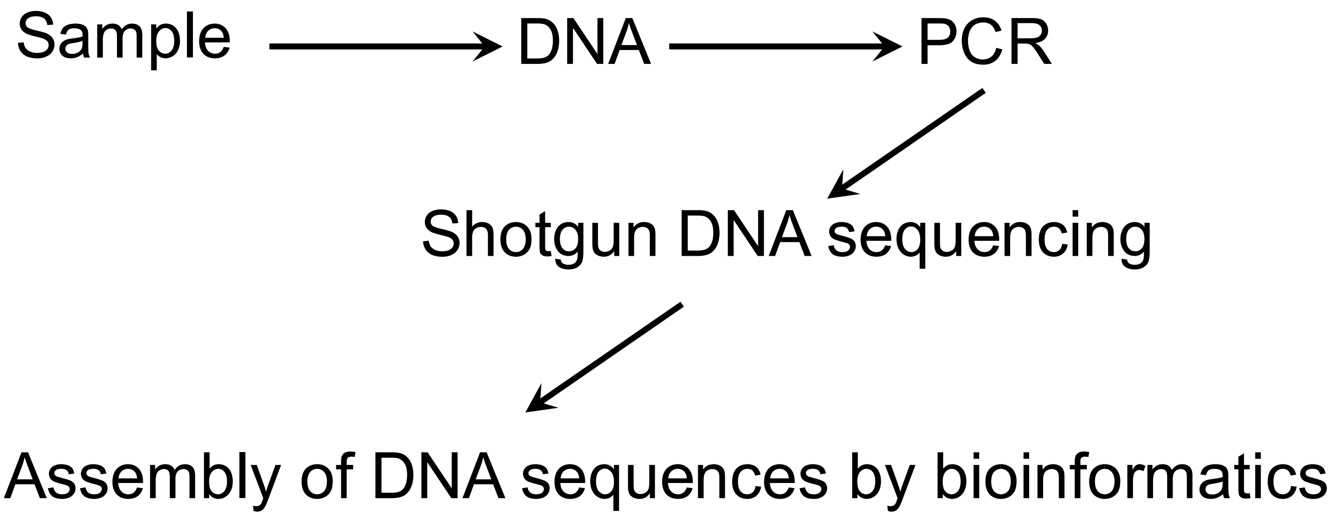
Metagenomics - Revolution in the study of non-cultivable microorganisms



Sample → DNA → PCR

Shotgun DNA sequencing

Assembly of DNA sequences by bioinformatics

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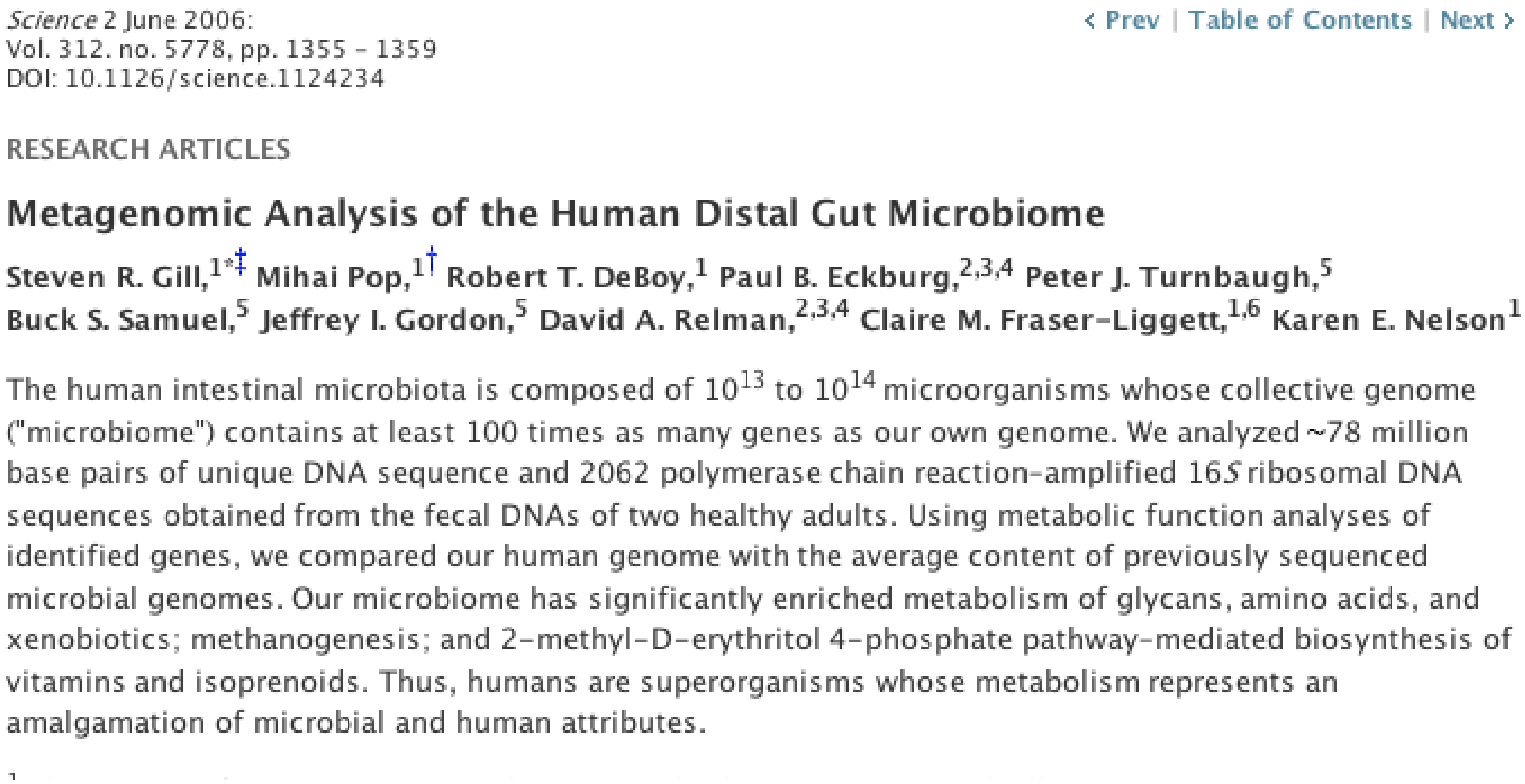

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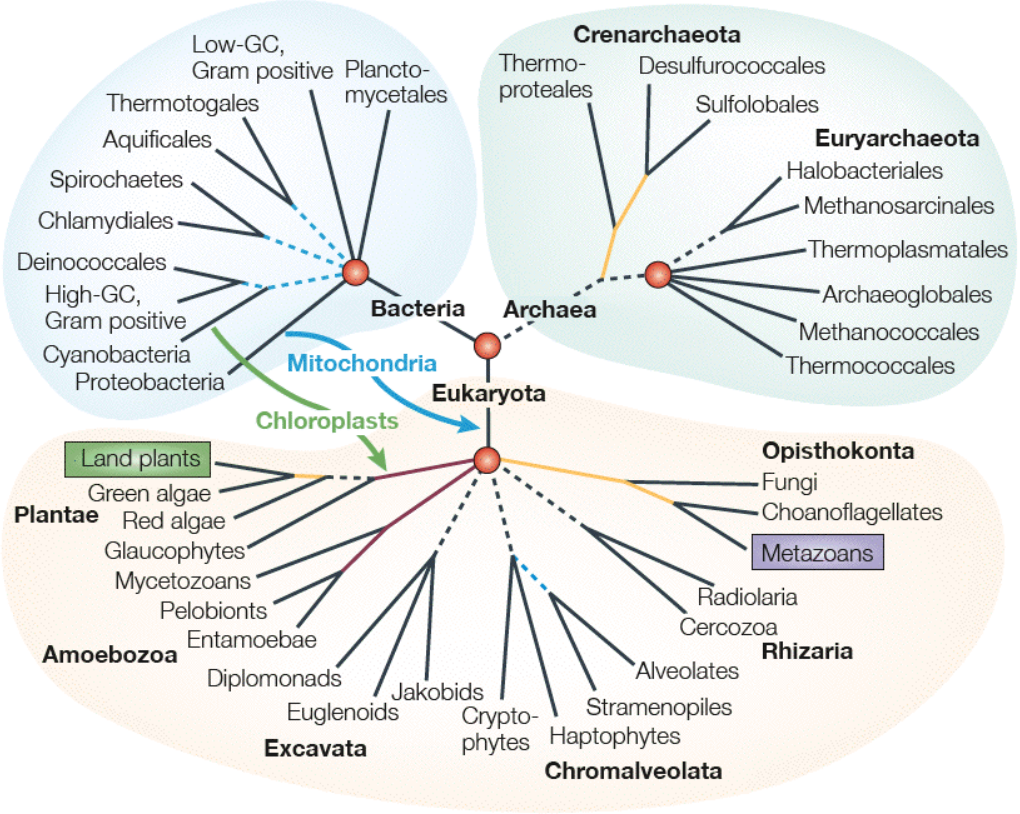
RESEARCH ARTICLES

Metagenomic Analysis of the Human Distal Gut Microbiome

Steven R. Gill,[1*‡] Mihai Pop,[1†] Robert T. DeBoy,[1] Paul B. Eckburg,[2,3,4] Peter J. Turnbaugh,[5] Buck S. Samuel,[5] Jeffrey I. Gordon,[5] David A. Relman,[2,3,4] Claire M. Fraser-Liggett,[1,6] Karen E. Nelson[1]

The human intestinal microbiota is composed of 10^{13} to 10^{14} microorganisms whose collective genome ("microbiome") contains at least 100 times as many genes as our own genome. We analyzed ~78 million base pairs of unique DNA sequence and 2062 polymerase chain reaction-amplified 16*S* ribosomal DNA sequences obtained from the fecal DNAs of two healthy adults. Using metabolic function analyses of identified genes, we compared our human genome with the average content of previously sequenced microbial genomes. Our microbiome has significantly enriched metabolism of glycans, amino acids, and xenobiotics; methanogenesis; and 2-methyl-D-erythritol 4-phosphate pathway-mediated biosynthesis of vitamins and isoprenoids. Thus, humans are superorganisms whose metabolism represents an amalgamation of microbial and human attributes.

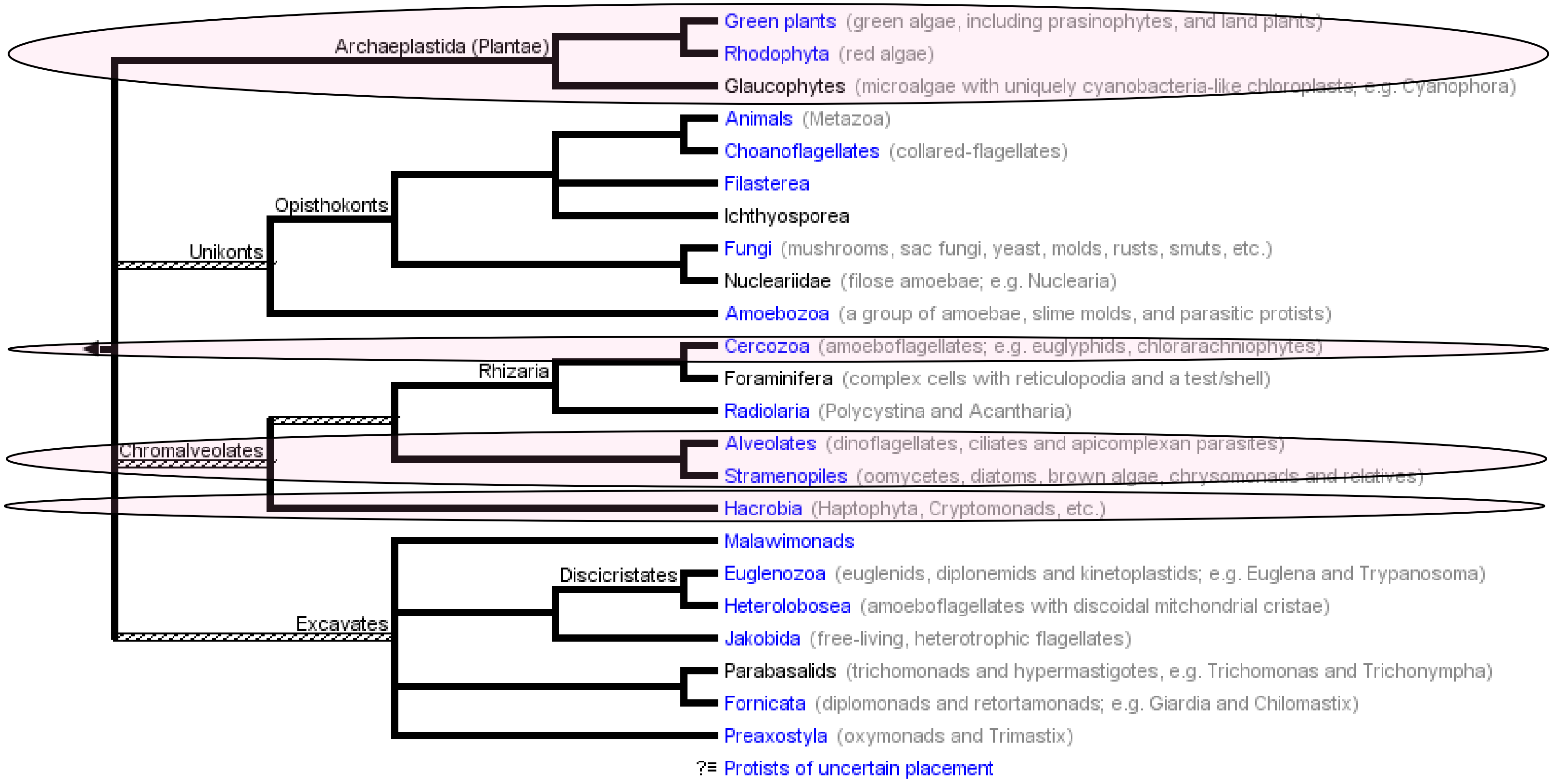
Life Domains (rRNA + Comparative genomics)



Delsuc *et al.(2005) Nature Rev. Genetics* **6**: 361-375
Adl, S.M. et al. (2005). *J. Eukaryot. Microb.* **52**, 399-451.

Superkingdom *Eukaryota*

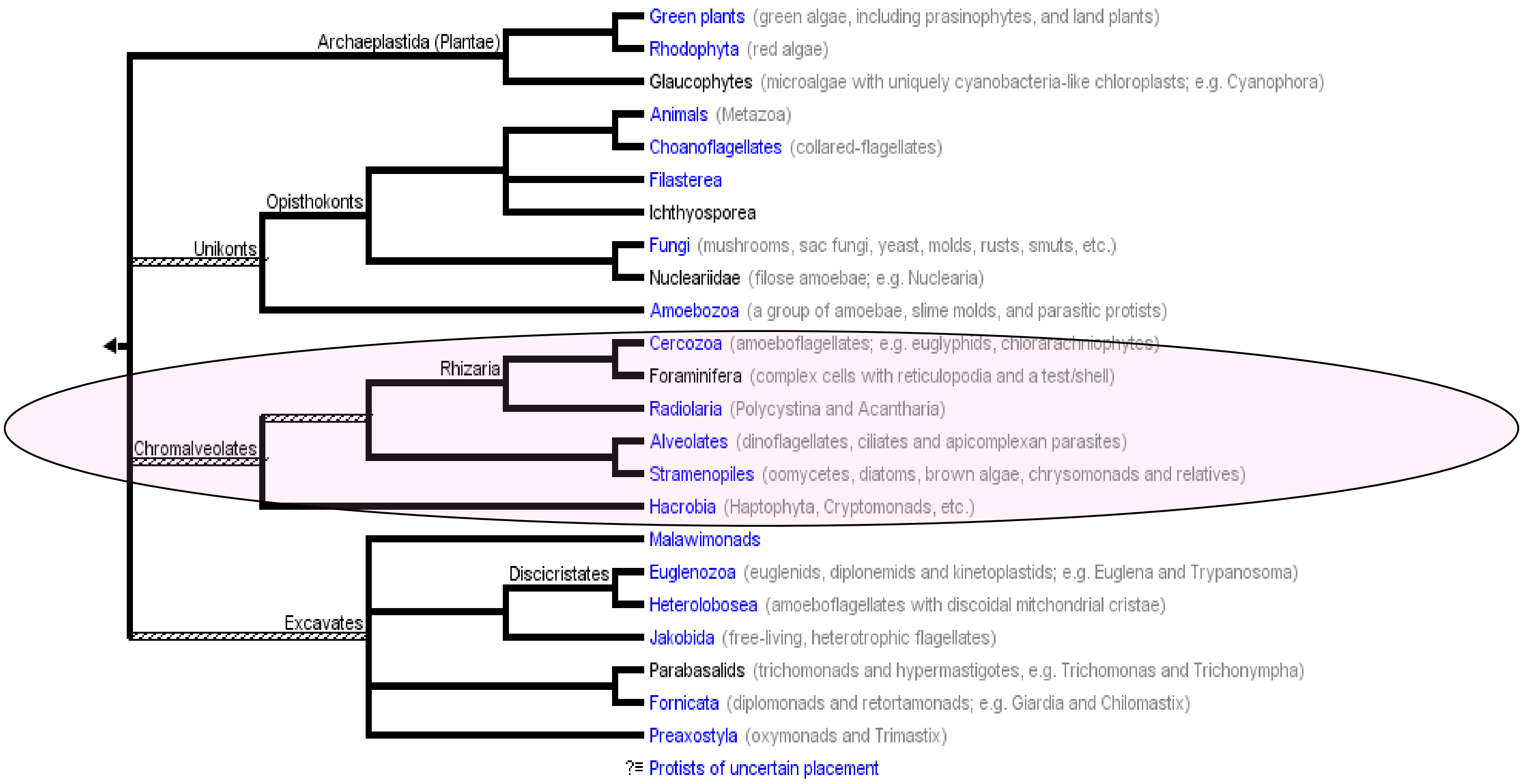
(NCBI Taxonomy Browser + Tree of Life)



Archaeplastida (Plantae)
Green plants (green algae, including prasinophytes, and land plants)
Rhodophyta (red algae)
Glaucophytes (microalgae with uniquely cyanobacteria-like chloroplasts; e.g. Cyanophora)
Unikonts
Opisthokonts
Animals (Metazoa)
Choanoflagellates (collared-flagellates)
Filasterea
Ichthyosporea
Fungi (mushrooms, sac fungi, yeast, molds, rusts, smuts, etc.)
Nucleariidae (filose amoebae; e.g. Nuclearia)
Amoebozoa (a group of amoebae, slime molds, and parasitic protists)
Rhizaria
Cercozoa (amoeboflagellates; e.g. euglyphids, chlorarachniophytes)
Foraminifera (complex cells with reticulopodia and a test/shell)
Radiolaria (Polycystina and Acantharia)
Chromalveolates
Alveolates (dinoflagellates, ciliates and apicomplexan parasites)
Stramenopiles (oomycetes, diatoms, brown algae, chrysomonads and relatives)
Hacrobia (Haptophyta, Cryptomonads, etc.)
Excavates
Malawimonads
Discicristates
Euglenozoa (euglenids, diplonemids and kinetoplastids; e.g. Euglena and Trypanosoma)
Heterolobosea (amoeboflagellates with discoidal mitchondrial cristae)
Jakobida (free-living, heterotrophic flagellates)
Parabasalids (trichomonads and hypermastigotes, e.g. Trichomonas and Trichonympha)
Fornicata (diplomonads and retortamonads; e.g. Giardia and Chilomastix)
Preaxostyla (oxymonads and Trimastix)
?≡ Protists of uncertain placement

http://tolweb.org/Eukaryotes/3

“Kingdom” *Chromalveolata*



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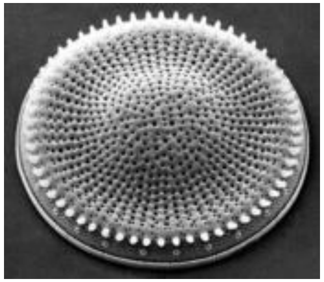
“Kingdom” *Chromalveolata*

Macrocystis
Stramenopiles
Phaeophyta



Stephanodiscus
Stramenopiles
Bacillariophyta

Gymnodinium
Alveolata
Dinophyceae

Bursaria
Alveolata
Ciliophora

Gymnochlora
Cercozoa
Chlorarachniophyta

- predominantly unicellular eukaryotes with auto- and heterotrophic sub-lineages
- chloroplast mainly by endosymbiosis with a rhodophyte that has become a cryptoplast or that has been lost in heterotrophic sub-lineages
- genes shared with unusual evolutionary histories (e.g., horizontal gene transfer, HGT)

http://tolweb.org/Eukaryotes/3