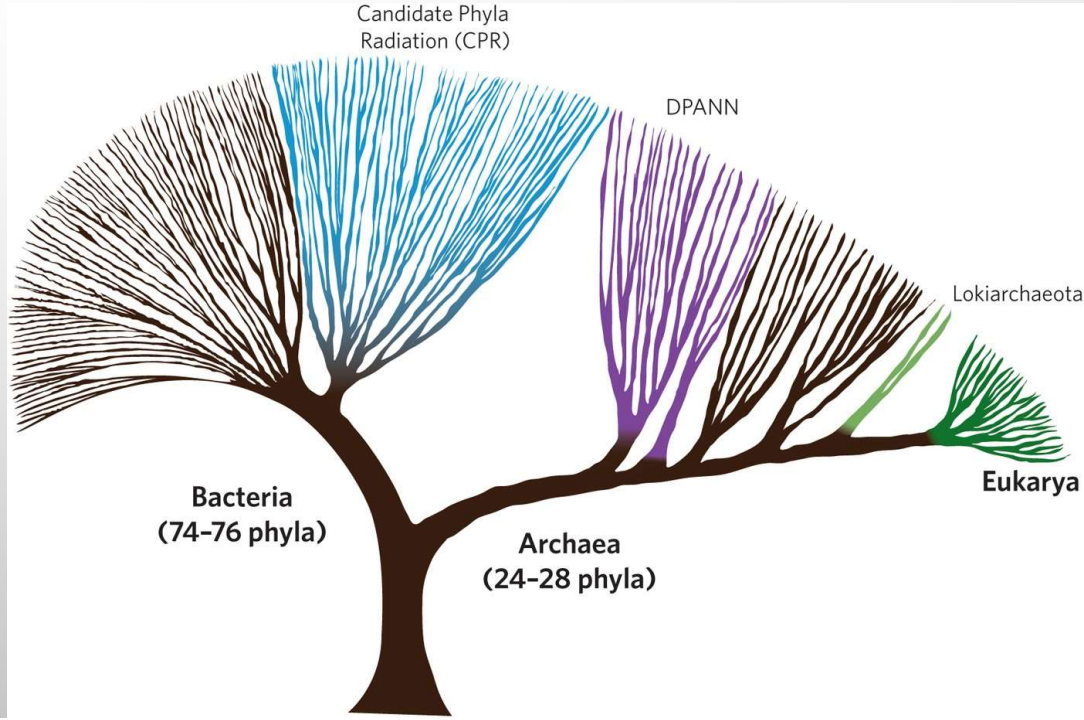
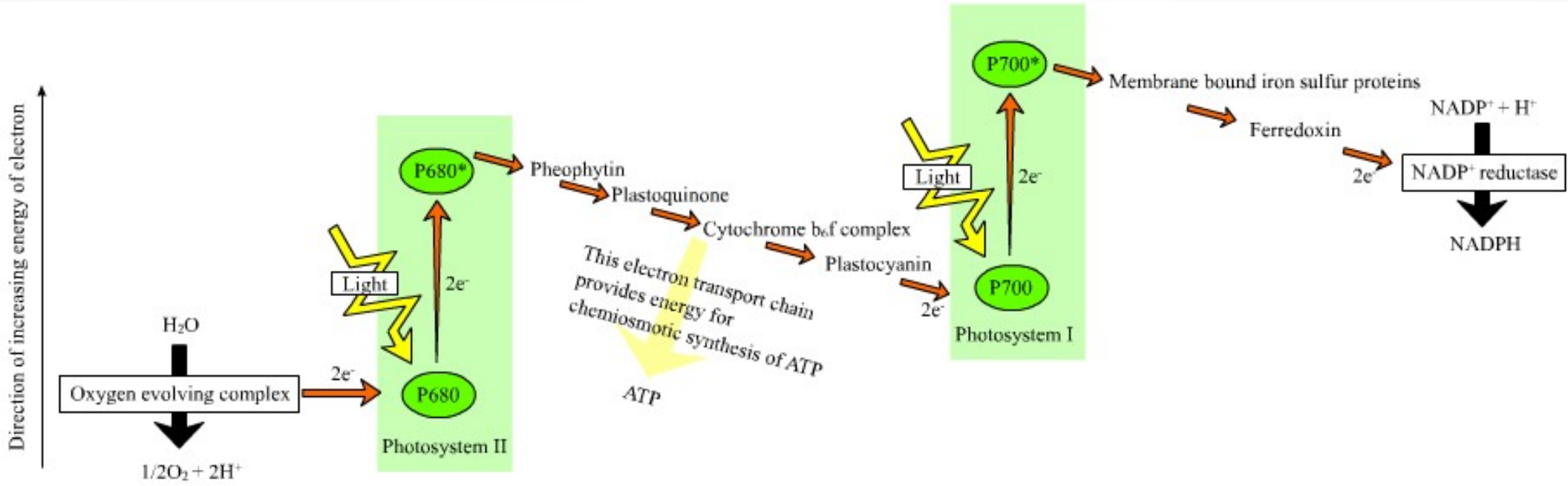
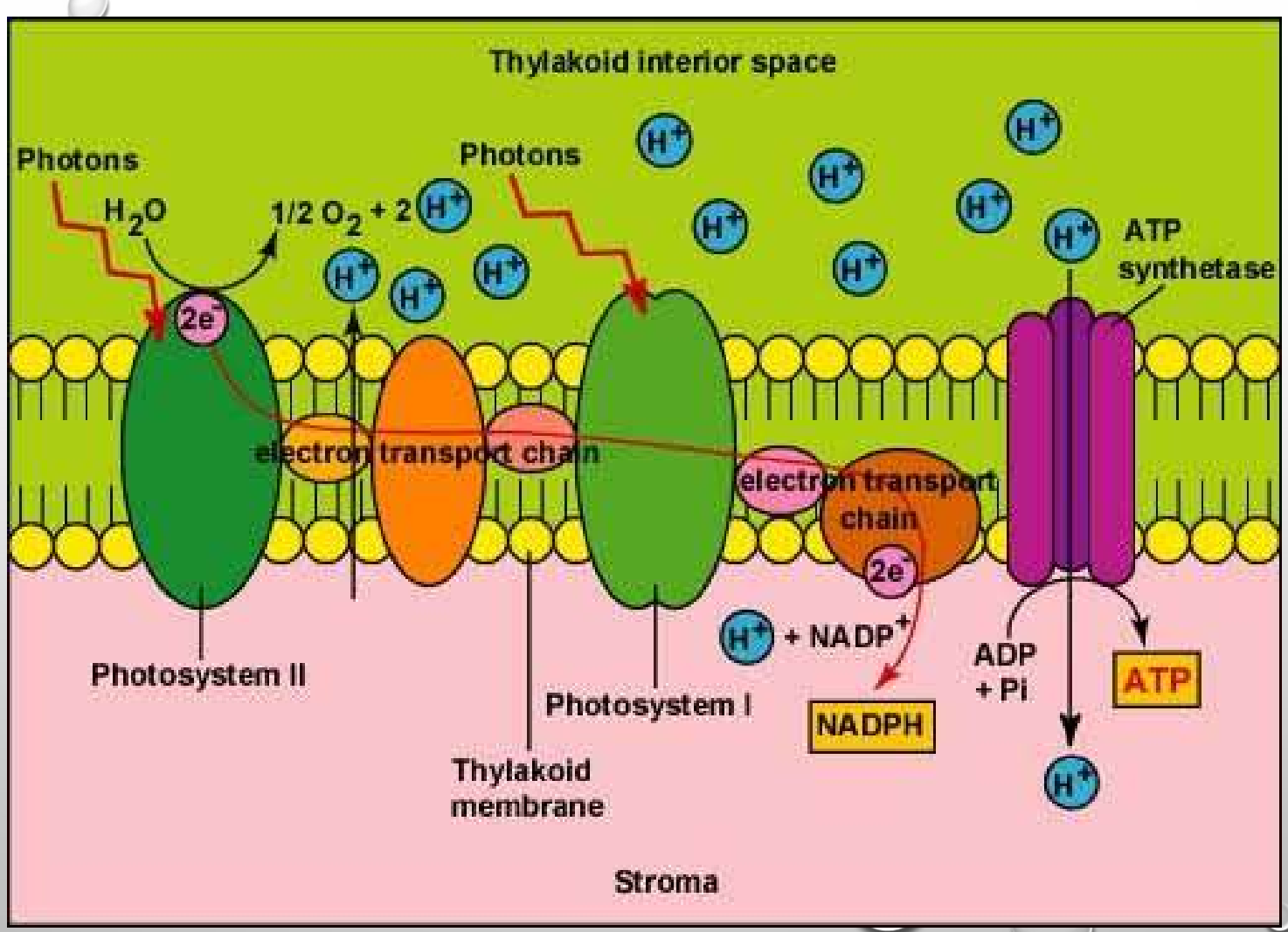
MOLECULAR INVENTIONS AND THE TREE OF LIFE

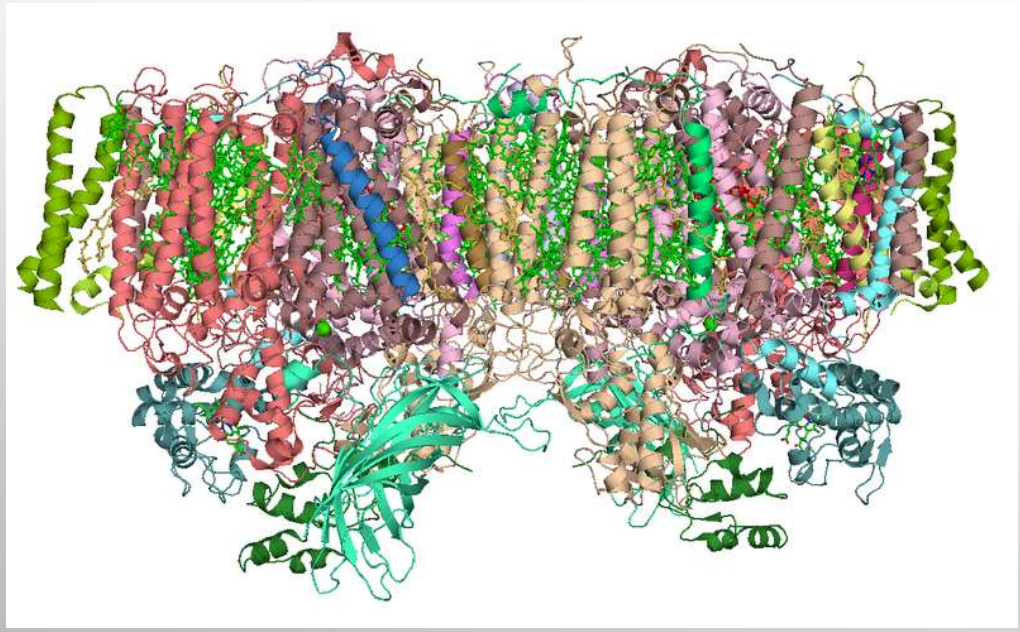
SPRING 2024



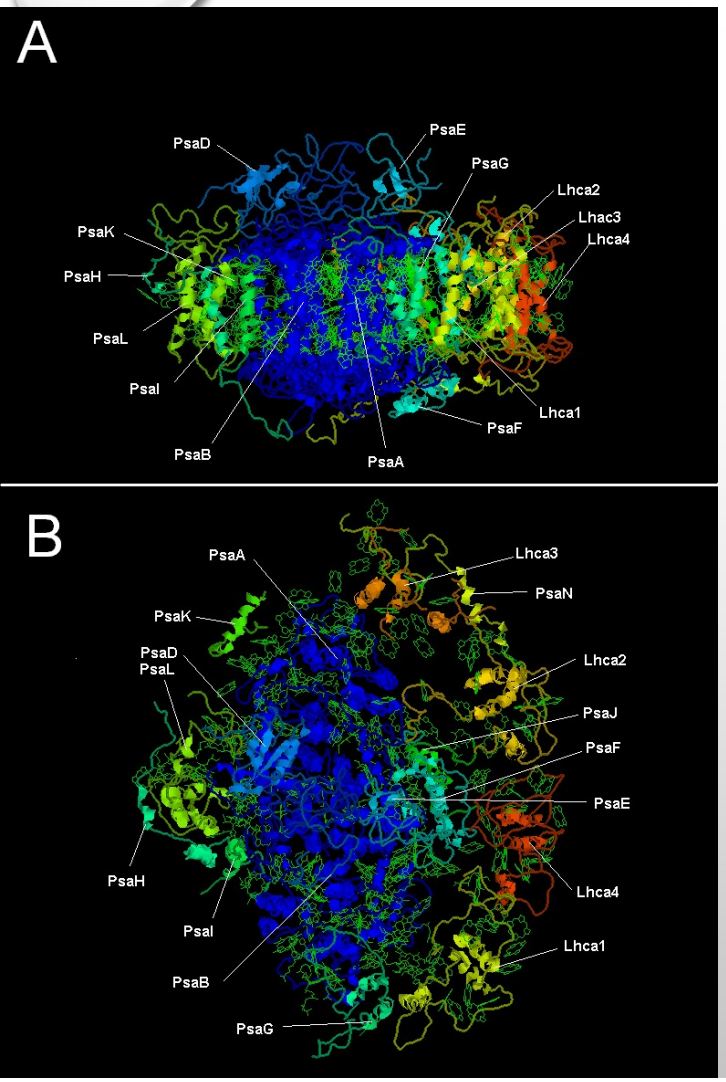

Direction of increasing energy of electron
H2O
Oxygen evolving complex
1/2O2 + 2H+
2e-
Light
2e-
P680*
P680
Photosystem II
Pheophytin
Plastoquinone
Cytochrome b6f complex
Plastocyanin
This electron transport chain provides energy for chemiosmotic synthesis of ATP
ATP
2e-
Light
2e-
P700*
P700
Photosystem I
Membrane bound iron sulfur proteins
Ferredoxin
2e-
NADP+ + H+
NADP+ reductase
NADPH


Thylakoid interior space
Photons
H_2O
1/2 O_2 + 2 H^+
Photons
ATP synthetase
$2e^-$
electron transport chain
electron transport chain
$2e^-$
H^+ + $NADP^+$
NADPH
ADP + Pi
ATP
Photosystem II
Photosystem I
Thylakoid membrane
Stroma

PHOTOSYNTHESIS SYSTEM II



- AT LEAST 24 PROTEINS
- AT LEAST 60 AUXILIARY PROTEINS INVOLVED IN ASSEMBLY, STABILITY AND REPAIR
- AT LEAST 5 PIGMENTS
- AT LEAST 20 LIPIDS



PHOTOSYNTHESIS SYSTEM I

- AT LEAST 17 PROTEINS
- AT LEAST 4 LIPIDS
- 5 PIGMENTS
- AT LEAST 3 COFACTORS

CYANOBACTERIA

- MOST NUMEROUS AND WIDESPREAD MICROBES
- THE ONLY OXYGEN-RELEASING PHOTOSYNTHETIC BACTERIA
- CONTRIBUTE ALMOST HALF OF THE EARTH'S TOTAL PRIMARY PRODUCTION
- CYANOBACTERIA ARE ARGUABLY THE MOST SUCCESSFUL GROUP OF MICROORGANISMS ON EARTH
- THEY ARE THE MOST GENETICALLY DIVERSE
- CAN BE FOUND IN ALMOST EVERY TERRESTRIAL AND AQUATIC HABITAT – OCEANS, FRESH WATER, DAMP SOIL, TEMPORARILY MOISTENED ROCKS IN DESERTS, BARE ROCK AND SOIL, AND EVEN ANTARCTIC ROCKS

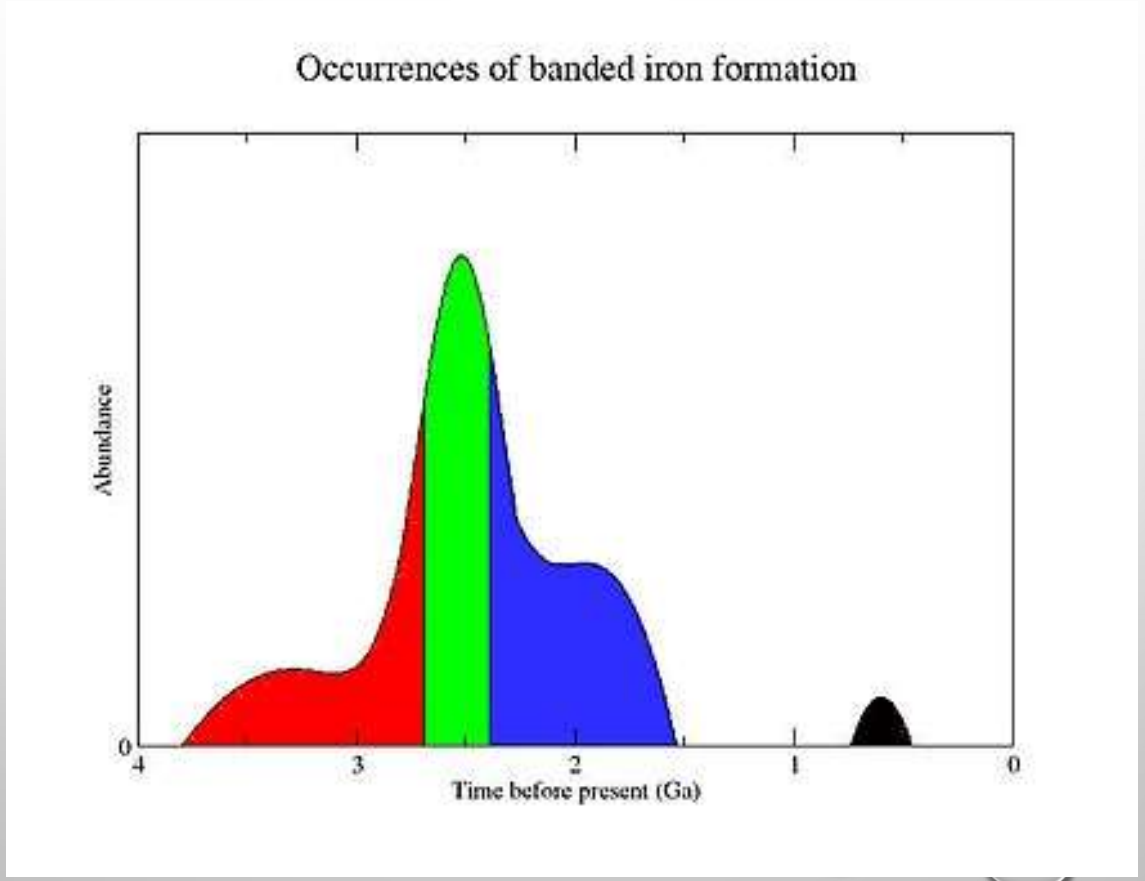
CYANOBACTERIA AND THE GREAT OXYGENATION EVENT

- THEY MOST LIKELY GO BACK TO AT LEAST 2.7 BILLION YEARS AGO (GA: GIGA YEARS AGO)
- SOME RESEARCHERS PROPOSE THAT THEY GO BACK 3.3 GA
- THEY START DUMPING OXYGEN INTO THE ENVIRONMENT
- EVIDENCE: BANDED IRON FORMATION

BANDED IRON FORMATIONS

- SEDIMENTARY ROCK CONSISTING OF ALTERNATING LAYERS OF IRON OXIDES AND IRON-POOR SEDIMENT
- BANDED IRON FORMATIONS ARE THOUGHT TO HAVE FORMED IN SEA WATER AS THE RESULT OF OXYGEN PRODUCTION BY CYANOBACTERIA
- THE OXYGEN COMBINED WITH DISSOLVED IRON IN EARTH'S OCEANS TO FORM INSOLUBLE IRON OXIDES, WHICH PRECIPITATED OUT
- THEY ARE FOUND WORLDWIDE
- BANDED IRON FORMATIONS ACCOUNT FOR MORE THAN 60% OF GLOBAL IRON RESERVES

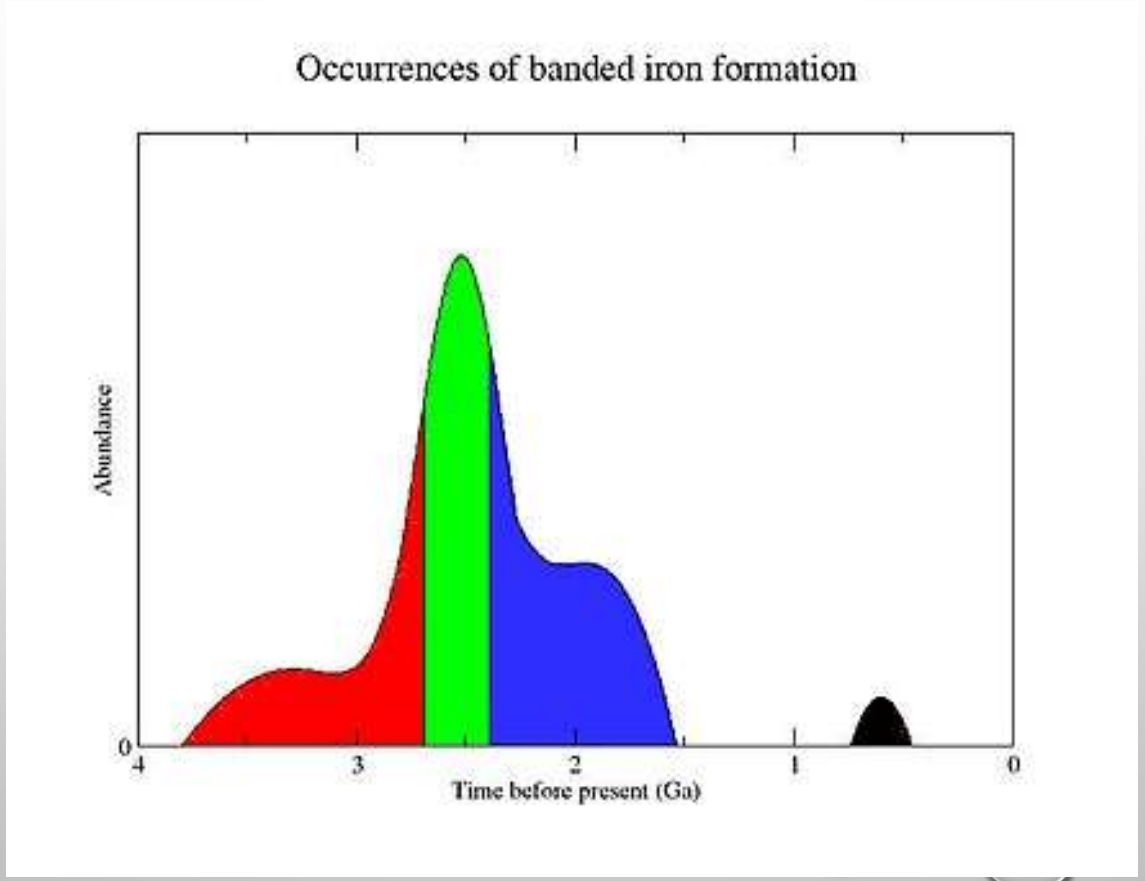
BANDED IRON FORMATIONS



WAS IT OXYGENIC PHOTOSYNTHESIS THAT LED TO BANDED IRON FORMATIONS?

- DEPOSITION OF A BANDED IRON FORMATION REQUIRES BOTH AN ANOXIC DEEP OCEAN CAPABLE OF TRANSPORTING IRON IN SOLUBLE FERROUS FORM, AND AN OXIDIZED SHALLOW OCEAN WHERE THE FERROUS IRON IS OXIDIZED TO INSOLUBLE FERRIC IRON AND PRECIPITATES ONTO THE OCEAN FLOOR
- THEY COULD FORM BY DIRECT OXIDATION OF IRON BY MICROBIAL ANOXYGENIC PHOTOSYNTHESIS
- HOWEVER, THE OXIDATION OF Fe^{2+} TO Fe^{3+} YIELDS VERY LITTLE ENERGY TO THE CELL → THE CELL MUST OXIDIZE LARGE AMOUNTS OF Fe^{2+} TO FULFILL ITS METABOLIC REQUIREMENTS
- IRON-OXIDIZING METABOLISM WOULD HAVE MADE A REMARKABLE CONTRIBUTION TO THE FORMATION OF BANDED IRON DEPOSIT BEFORE THE ADVENT OF OXYGENIC PHOTOSYNTHESIS

BANDED IRON FORMATIONS



THE GLITCH EXPLAINED: "SNOWBALL EARTH" HYPOTHESIS

- FOR SUCH IRON-RICH ROCKS TO BE DEPOSITED THERE WOULD HAVE TO BE ANOXIA IN THE OCEAN, SO THAT MUCH DISSOLVED IRON COULD ACCUMULATE BEFORE AN OXIDANT WOULD PRECIPITATE IT AS FERRIC OXIDE
- BUT AT THAT TIME, THE ATMOSPHERE WAS OXYGENATED
- FOR THE OCEAN TO BECOME ANOXIC IT MUST HAVE LIMITED GAS EXCHANGE WITH THE OXYGENATED ATMOSPHERE
- THIS COULD HAPPEN IN AN OCEAN SEALED BY SEA-ICE
- THE PLANET'S SURFACE BECAME ENTIRELY OR NEARLY ENTIRELY FROZEN WITH NO LIQUID OCEANIC OR SURFACE WATER EXPOSED TO THE ATMOSPHERE
- THE PERIOD OF SUCH GLOBAL GLACIATION IS BELIEVED TO HAVE OCCURRED SOMETIME BEFORE 650 MILLION YEARS AGO

SNOWBALL EARTH

- TRIGGERS:
  - ERUPTION OF A SUPERVOLCANO
  - A REDUCTION IN THE ATMOSPHERIC CONCENTRATION OF GREENHOUSE GASES
  - CHANGES IN SOLAR ENERGY OUTPUT
- REGARDLESS OF THE TRIGGER, INITIAL COOLING RESULTS IN AN INCREASE IN THE AREA OF EARTH'S SURFACE COVERED BY ICE AND SNOW
- THE ADDITIONAL ICE AND SNOW REFLECTS MORE SOLAR ENERGY BACK TO SPACE → ALBEDO EFFECT, LEADING TO FURTHER COOLING
- THIS 'RUNAWAY' POSITIVE FEEDBACK LOOP COULD EVENTUALLY PRODUCE A FROZEN EQUATOR AS COLD AS MODERN ANTARCTICA.

SNOWBALL EARTH

SNOWBALL GLOBAL ICE AGES ARE TEMPORARY IN NATURE

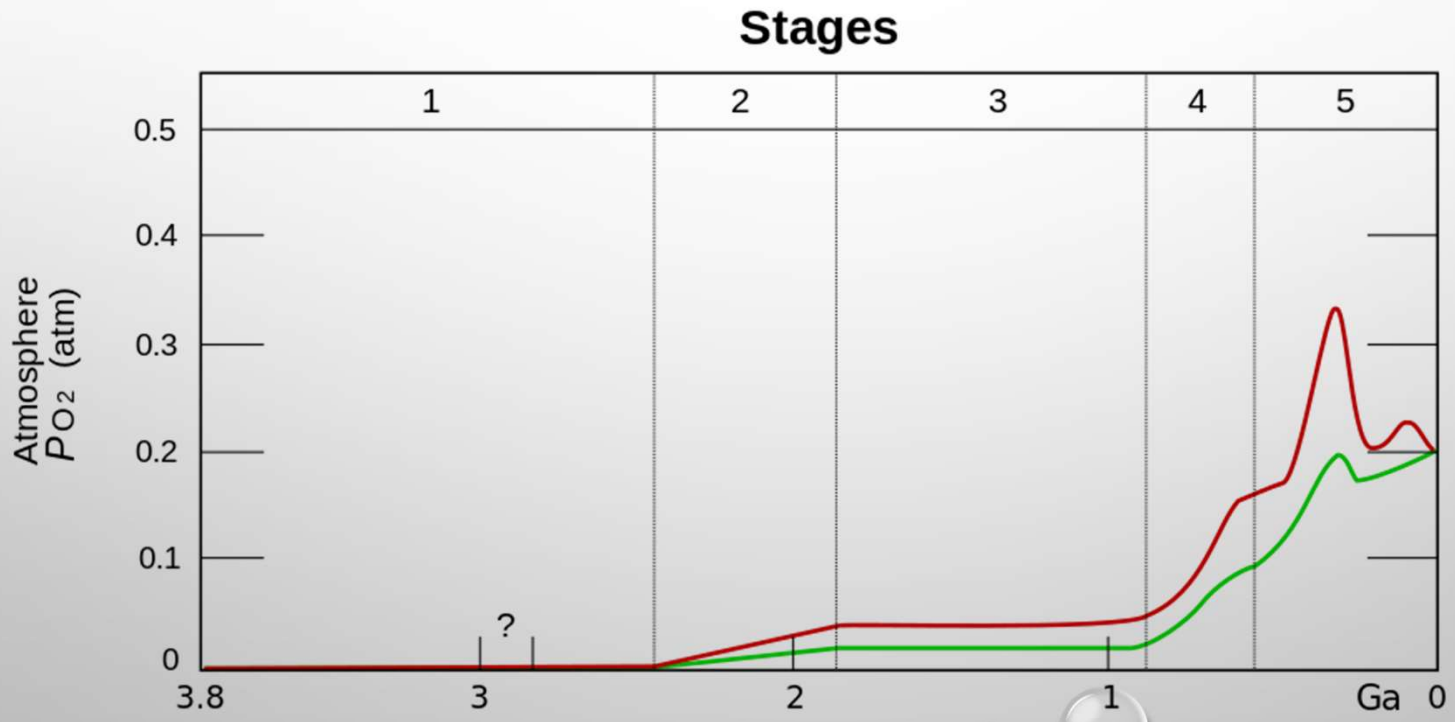
OVER 4 TO 30 MILLION YEARS, ENOUGH CO_2 AND METHANE, EMITTED BY VOLCANOES AND PRODUCED BY MICROBES WOULD ACCUMULATE TO FINALLY CAUSE ENOUGH GREENHOUSE EFFECT TO MAKE SURFACE ICE MELT

CYANOBACTERIA FACE A CONUNDRUM

- OXYGEN IS A VERY REACTIVE CHEMICAL SPECIES
- TOXIC EFFECTS THROUGH THE PRODUCTION OF PEROXIDES AND FREE RADICALS THAT CAN DAMAGE ALL COMPONENTS OF THE CELL, INCLUDING PROTEINS, LIPIDS AND DNA
- THE FIRST CYANOBACTERIA HAD EVOLVED THE CAPACITY TO CARRY OUT OXYGEN-PRODUCING PHOTOSYNTHESIS BUT HAD NOT YET EVOLVED MECHANISMS TO COUNTERACT OXIDATIVE DAMAGE
- THEY WOULD HAVE BEEN PROTECTED FROM THEIR OWN POISONOUS OXYGEN WASTE THROUGH ITS RAPID REMOVAL VIA THE HIGH LEVELS OF REDUCED FERROUS IRON, FE(II), IN THE EARLY OCEAN

- TO COPE WITH OXIDATIVE STRESS THERE ARE ENZYMES THAT EVOLVED TO NEUTRALIZE THE REACTIVE OXYGEN SPECIES
- THIS ENDED SELF-POISONING AND PRODUCED A POPULATION EXPLOSION IN THE CYANOBACTERIA THAT RAPIDLY OXYGENATED THE OCEAN AND ENDED BANDED IRON FORMATION DEPOSITION
- BY ~1.8 GA THESE REDUCTANTS HAD LARGELY BEEN TITRATED, AND MOLECULAR O_2 LEVELS GRADUALLY ROSE IN THE ATMOSPHERE
- ATMOSPHERIC O_2 STABILIZED AT ~10% OF CONTEMPORARY LEVELS, BEFORE IT FINALLY ROSE AGAIN STARTING 0.8 GA

THE RISE OF OXYGEN IN THE ATMOSPHERE



EARTH'S ATMOSPHERE CHANGES

- WHEN THE EARTH WAS FORMED AROUND 4.5 BILLION YEARS AGO, IT HAD VASTLY DIFFERENT CONDITIONS
- AT THAT TIME, THE EARTH HAD A REDUCING ATMOSPHERE, CONSISTING OF CARBON DIOXIDE, METHANE AND WATER VAPOR
- EVENTUALLY, OXYGEN STARTED TO ACCUMULATE IN THE ATMOSPHERE
- OXYGEN LIKELY OXIDIZED ATMOSPHERIC METHANE (A STRONG GREENHOUSE GAS) TO CARBON DIOXIDE (A WEAKER ONE) AND WATER
- THIS WEAKENED THE GREENHOUSE EFFECT OF THE EARTH'S ATMOSPHERE, CAUSING PLANETARY COOLING
- THIS TRIGGERED A SERIES OF ICE AGES KNOWN AS THE HURONIAN GLACIATION, BRACKETING AN AGE RANGE OF 2.45–2.22 GA

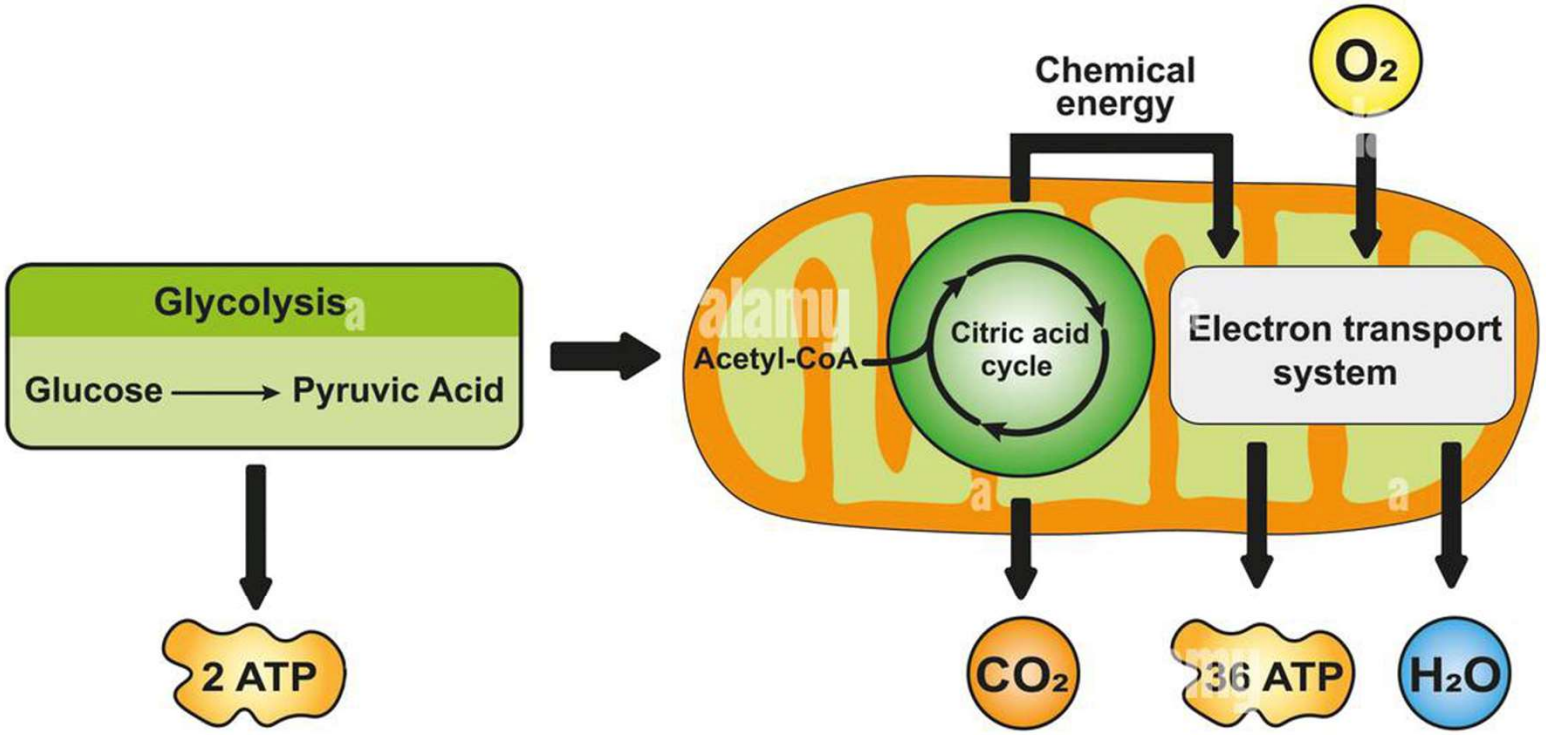
EFFECTS OF THE HURONIAN GLACIATION

- THE COMBINATION OF INCREASING FREE OXYGEN (WHICH CAUSES OXIDATIVE DAMAGE TO ORGANIC COMPOUNDS) AND CLIMATIC STRESSES LIKELY CAUSED AN **EXTINCTION EVENT**
- THIS WAS THE FIRST AND LONGEST LASTING IN THE EARTH'S HISTORY
- IT WIPED OUT MOST OF THE ANAEROBE AND ARCHAEAL POPULATIONS AND MICROBIAL MATS BOTH ON THE EARTH'S SURFACE AND IN SHALLOW WATERS

OXYGEN'S SILVER LINING: RESPIRATION

- **RESPIRATION** IS THE PROCESS BY WHICH BIOLOGICAL FUELS ARE MORE EFFICIENTLY METABOLIZED TO CONVERT CHEMICAL ENERGY FROM NUTRIENTS INTO ATP
- THE OVERALL REACTION OCCURS IN A SERIES OF BIOCHEMICAL STEPS
- THE SLOW, CONTROLLED RELEASE OF ENERGY FROM THE SERIES OF REACTIONS IS USED TO PRODUCE ATP

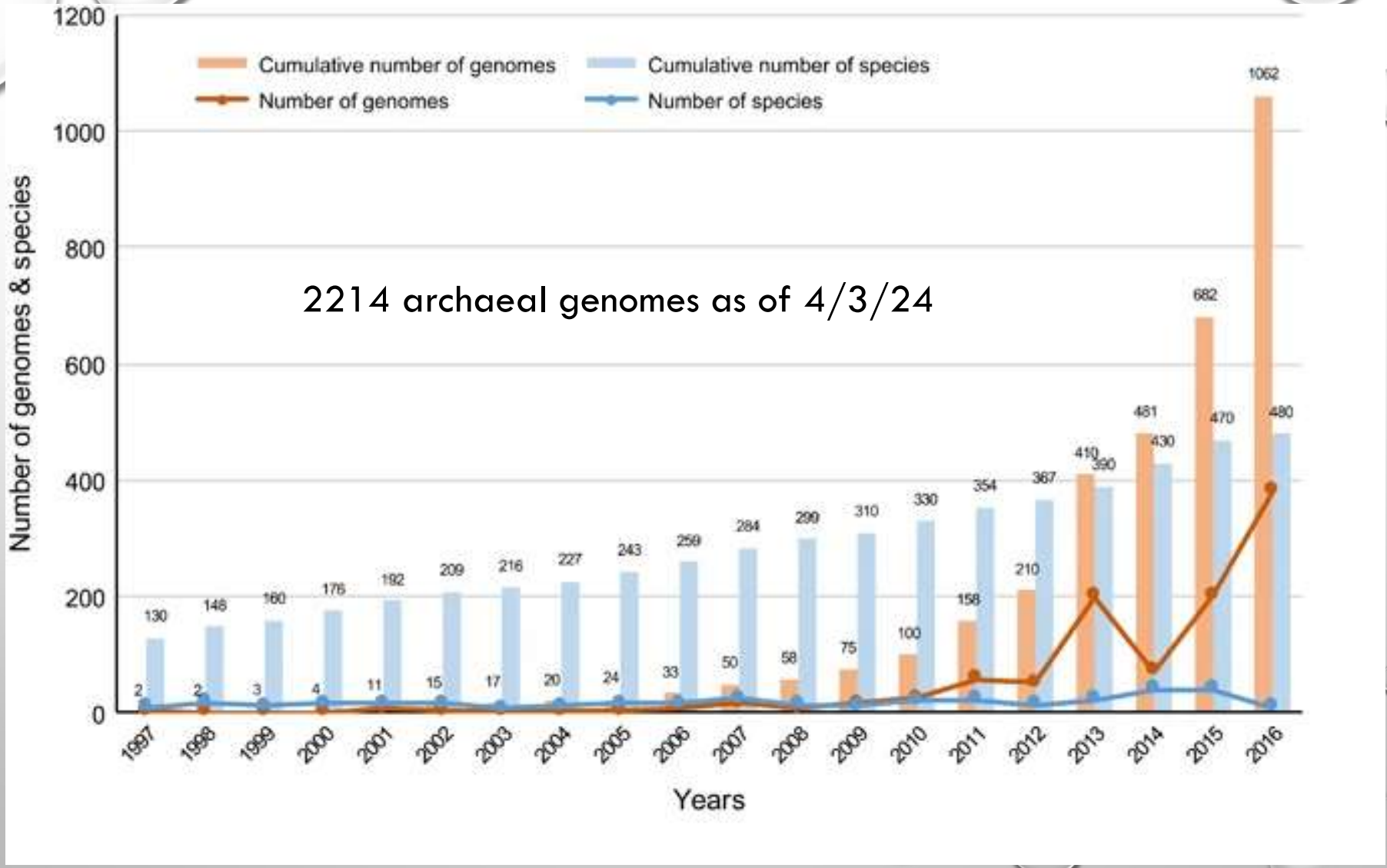
Aerobic respiration



MICROBIAL DIVERSIFICATION

- THE INCREASED OXYGEN CONCENTRATIONS PROVIDED A NEW OPPORTUNITY FOR BIOLOGICAL DIVERSIFICATION
- LIFE HAD REMAINED ENERGETICALLY LIMITED UNTIL THE WIDESPREAD AVAILABILITY OF OXYGEN
- THE AVAILABILITY OF OXYGEN GREATLY INCREASED THE FREE ENERGY AVAILABLE TO LIVING ORGANISMS, WITH GLOBAL ENVIRONMENTAL IMPACTS
- AFTER THE COMBINED IMPACT OF OXIDIZATION AND CLIMATE CHANGE DEVASTATED THE ANAEROBIC BIOSPHERE, AEROBIC ORGANISMS CAPABLE OF OXYGEN RESPIRATION WERE ABLE TO PROLIFERATE RAPIDLY AND EXPLOIT THE ECOLOGICAL NICHES VACATED BY ANAEROBES IN MOST ENVIRONMENTS

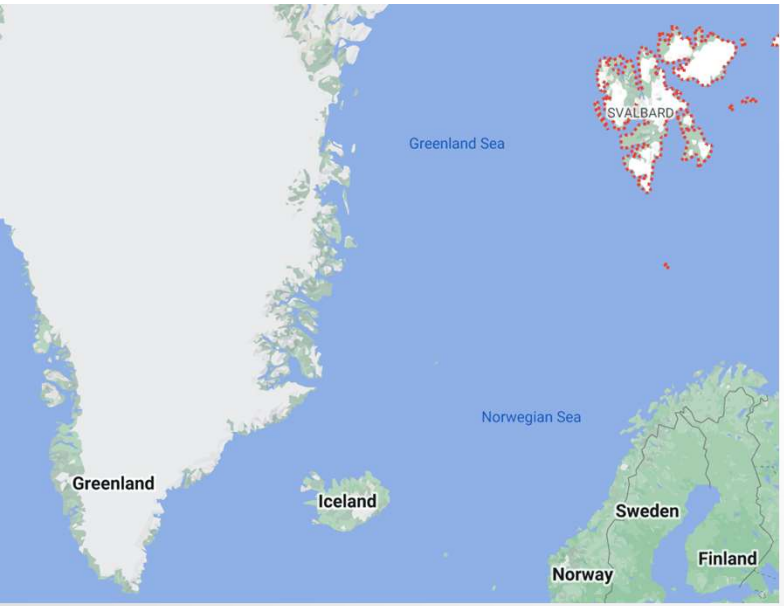
WHILE BACTERIA WERE EVOLVING TO PRODUCE AND USE OXYGEN, WHAT WAS HAPPENING IN THE ARCHAEAL/EUKARYAL BRANCH?

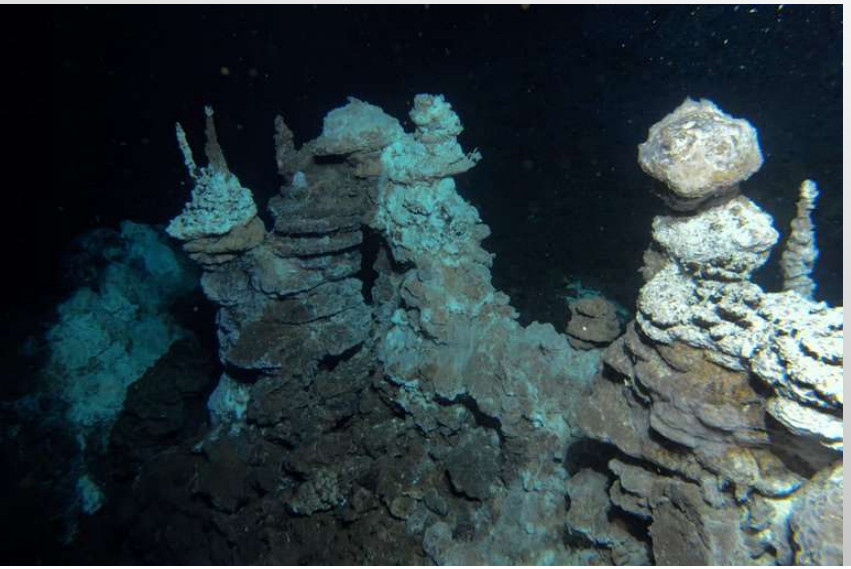

Cumulative number of genomes
Cumulative number of species
Number of genomes
Number of species
2214 archaeal genomes as of 4/3/24
Number of genomes & species
Years
1200
1000
800
600
400
200
0
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
130
148
160
176
192
209
216
227
243
259
284
299
310
330
354
367
390
430
470
480
2
2
3
4
11
15
17
20
24
33
50
58
75
100
158
210
410
461
682
1062

Altiarchaeales archaeon SM1-MS
Altiarchaeales archaeon SM1-CG
Candidatus Altiarchaeales archaeon WOR SM1 SCG
Euryarchaeota archaeon SCGC AAA252-I15
Altiarchaeales archaeon MC4
Altiarchaeia (SM1) (C/P?)
Methanococcoides jannaschii DSM 2661
Methanotorris igneus Kol 5
Methanothermococcus thermolithotrophicus DSM 2095
Methanococcus vannielii SB
Methanococci
Methanopyrus kandleri AV19
Methanopyri
Methanothermus fervidus DSM 2088
Methanothermobacter thermautotrophicus str. Delta H
Methanobrevibacter smithii ATCC 35061
Methanobacterium formicicum
Methanobacteria
Methanomada (SC)
(Class I methanogens)
Euryarchaeota
Palaeococcus pacificus DY20341
Thermococcus sibiricus MM 739
Thermococcus kodakarensis KOD1
Pyrococcus furiosus DSM 3638
Thermococci
Thermoplasmatales archaeon DG-70-1
Thermoplasmatales archaeon DG-70
Theionarchaea (Z7ME43)
Arc I group archaeon U1ls0528 Bin089
Arc I group archaeon U1ls0528 Bin055
Arc I group archaeon B03fssc0709 Meth Bin005
Arc I group archaeon ADurb1013 Bin02101
Methanofastidiosa (WSA2/ArcI)
Acherontia (SC)
Hadesarchaea archaeon YNP N21
Hadesarchaea archaeon DG-33.1
Hadesarchaea archaeon YNP 45
Hadesarchaea archaeon DG-33
Hadesarchaea (SAGMEG)
candidate division MSBL1 archaeon SCGC-AAA259J03
candidate division MSBL1 archaeon SCGC-AAA259D14
candidate division MSBL1 archaeon SCGC-AAA259E19
candidate division MSBL1 archaeon SCGC-AAA259A05
Persephonarchaea (MSBL-1)
Stygia (SC)
Candidatus Heimdallarchaeota archaeon LC_3
Candidatus Heimdallarchaeota archaeon LC_2
Candidatus Heimdallarchaeota archaeon AB_125
Heimdallarchaeota (P)
Thorarchaeota archaeon SMTZ1-83
Thorarchaeota archaeon SMTZ-45
Candidatus Thorarchaeota archaeon AB_25
Thorarchaeota archaeon SMTZ1-45
Thorarchaeota (MBG-B) (P)
Asgard (SP)
Candidatus Odinarchaeota archaeon LCB_4
Odinarchaeota (P)
Candidatus Lokiarchaeota archaeon CR_4
Lokiarchaeum sp. GC14 75
Lokiarchaeota (DSAG) (P)
Candidatus Korarchaeum cryptofilum OPF8
Korarchaeota (P)
Methanosuratus petracarbonis V4
Methanomethylicus oleusabulum V3
Methanomethylicus mesodigestum V2
Verstraetearchaeota (TMCG) (P)
crenarchaeote JGI-OTU-1
Geoarchaeota archaeon OSPB-1
Geoarchaeota (NAG1)
Thermofilum pendens Hrk 5
Vulcanisaeta moutnovskia 768-28
Thermoproteus tenax Kra 1
Ignicoccus hospitalis KIN4 I
Hyperthermus butylicus DSM 5456
Metallosphaera sedula DSM 5348
Sulfolobus tokodaii str. 7
Pyrodictium fontis Kam040
Caldisphaera lagunensis DSM 15908
Crenarchaeota (P)
Cluster I
2
1
TACK/Proteoarchaeota
Candidatus Bathyarchaeota archaeon B25
Candidatus Bathyarchaeota archaeon B24
miscellaneous Crenarchaeota group-15 archaeon DG-45
Candidatus Bathyarchaeota archaeon B26-2
Candidatus Bathyarchaeota archaeon BA2
Bathyarchaeota (MCG) (P)
Candidatus Caldarchaeum subterraneum
Thaumarchaeota archaeon JGI OTU-3
Thaumarchaeota archaeon JGI OTU-1
Candidatus Calditenuis aerotheumensis
Aigarchaeota (HWCG-I) (P)
Thaumarchaeota archaeon DS1
Dragon
Thaumarchaeota archaeon BS4
Thaumarchaeota archaeon BS1
Beowulf
Archaeon Thaum-Fn1
Fn1
Thaumarchaeota archaeon MY3
Candidatus Nitrosotenuis cloacae
Candidatus Nitrosopelagicus brevis
Thaumarchaeota archaeon SCGC AAA007-O23
Thaumarchaeota archaeon SCGC AAA287-E17
Cenarchaeum symbiosum A
Thaumarchaeota archaeon SCGC AAA282-K18
Candidatus Nitrosopumilus koreensis AR1
Thaumarchaeota (P)
Archaeoglobus veneficus SNP6
Archaeoglobus fulgidus DSM 4304
Ferroglobus placidus DSM 10642
Geoglobus ahangari
Archaeoglobi
uncultured archaeon ANME-1
Methanophagales (ANME-1)
Candidatus Syntrophoarchaeum butanivorans
Candidatus Syntrophoarchaeum caldarius
Syntropharchaeales (GoM-Arch87)
Methermicoccus shengliensis DSM 16856
Methanosaeta concilii GP6
Candidatus Methanoperedens nitroreducens
Methanococcoides burtonii DSM 6242
Methanosarcina mazei Go1
Methanosarcinales
Methanofollis liminatans DSM 4140
Methanoculleus bourgensis MS2
Methanoregula boonei 6A8
Methanocorpusculum labreanum Z
Methanomicrobiales
Methanoflorens stordalenmirensis
Methanoflorentaceae (RC-II)
Methanomicrobia
(Class II methanogens)
Methanotecta (SC)
Methanocella arvoryzae MRE50
Methanocella conradii HZ254
Methanocella paludicola SANAE
Methanocellales (RC-I)
Natrinema pellirubrum DSM 15624
Halomicrobium mukohataei DSM 12286
Haloferax mediterranei ATCC 33500
Halorubrum lacusprofundi ATCC 49239
Halobacteria
Euryarchaeota
Cluster II
Thermoplasmatales archaeon SCGC AB-539-N05
Thermoplasmatales archaeon SM1-50
Thermoplasmatales archaeon SG8-52-4
Thermoplasmatales archaeon SG8-52-3
Izemarchaea (MBG-D)
uncultured marine group II euryarchaeote
MGII Guaymas28
MGII Guaymas29
MGII Cayman51_deep
Thalassoarchaea (MG-II)
MGIII Guaymas32
MGIII Guaymas31
MGIII Cayman93 deep
MGIII Cayman92 shallow
Pontarchaea (MG-III)
Aciduliprofundum sp. MAR08-339
Aciduliprofundum boonei T469
Aciduliprofundales (DHVE-2)
Thermoplasmatales archaeon I-plasma
Thermoplasma volcanium GSS1
Ferroplasma acidarmanus fer1
Thermoplasmatales archaeon E-plasma
Thermoplasmatales archaeon A-plasma
Thermoplasmatales
Thermoplasmata
Diaforarchaea (SC)
Archaeon TMEG-Bg1
TMEG
Euryarchaeota archaeon SG8-5
SG8-5
Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1
Methanomassiliicoccales Mx2 EMMG1001
Methanomassiliicoccales Mx3 EMMG1002
Candidatus Methanoplasma termitum
Candidatus Methanomethylophilus alvus Mx1201
Methanomassiliicoccales (RC-III)
Tree scale: 0.1

LOKI

- AS DEPICTED IN AN 18TH-CENTURY ICELANDIC MANUSCRIPT
- SHAPE-SHIFTING NORSE GOD
- A TRICKSTER
- LOKI WAS THOUGHT TO BE THE CAUSER OF KNOTS/TANGLES/LOOPS, OR HIMSELF A KNOT/TANGLE/LOOP
- HE HAS BEEN DESCRIBED AS "A STAGGERINGLY COMPLEX, CONFUSING, AND AMBIVALENT FIGURE WHO HAS BEEN THE CATALYST OF COUNTLESS UNRESOLVED SCHOLARLY CONTROVERSIES"

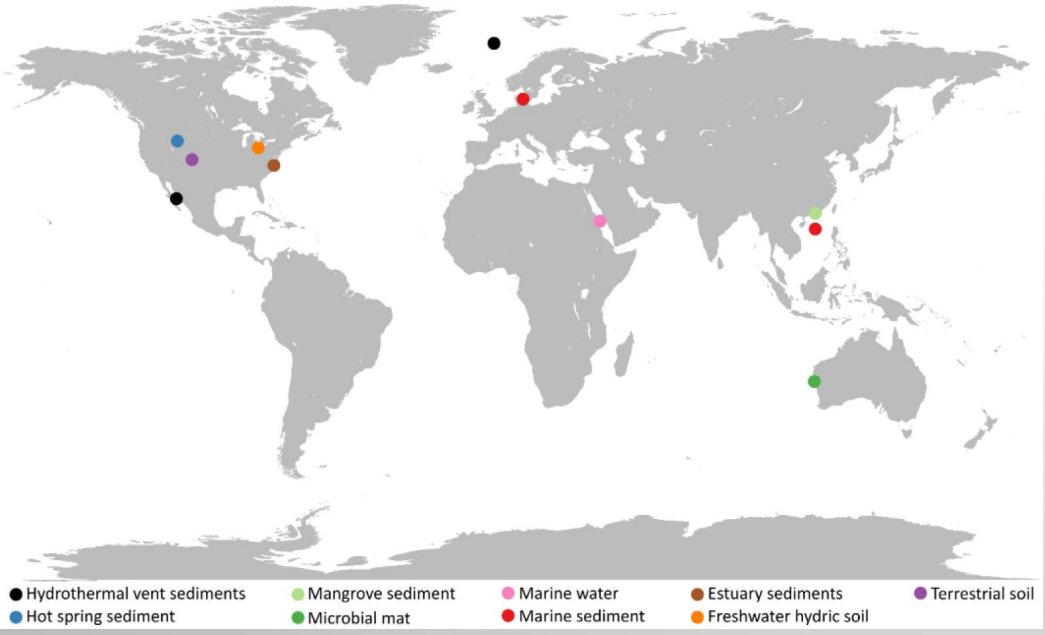




LOKI'S CASTLE

- **LOKI'S CASTLE** IS A FIELD OF FIVE ACTIVE HYDROTHERMAL VENTS LOCATED AT 73 DEGREES NORTH ON THE MID-ATLANTIC RIDGE BETWEEN ICELAND AND SVALBARD (NORWAY) AT A DEPTH OF 2,352 METRES (7,717 FT)
- THEY ARE THE MOST NORTHERLY BLACK SMOKER VENTS, DISCOVERED IN JULY 2008
- NAMED FOR THE SHAPE-SHIFTING NORSE GOD LOKI, IN AN ALLUSION TO THE HYDROTHERMAL VENT COMPLEX FROM WHICH THE FIRST GENOME SAMPLE ORIGINATED
- IT IS THE HOST SITE OF A BIOLOGICALLY DISTINCT ARCHAEA, THE LOKIARCHAEOTA, A BRANCH OF THE ASGARD SUPERGROUP

SINCE THEN



- DESCRIBED IN 2015
- 2 CULTURED IN 2019
- 59 WHOLE GENOME SEQUENCES AS OF 3/4/24
- ALL GROUPS ARE GIVEN NORSE MYTHOLOGY NAMES, HENCE ‘ASGARD’, THE RESIDENCE OF THE GODS

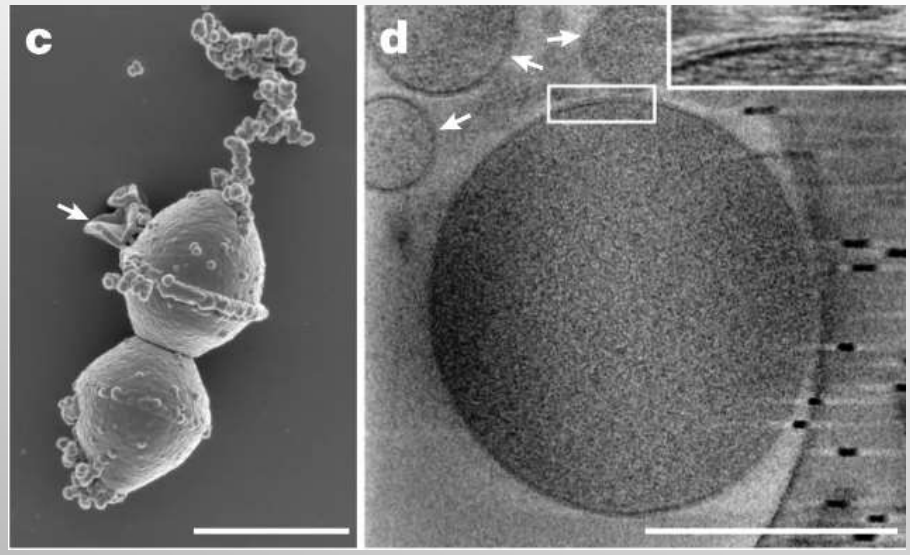
SURPRISES FROM THE FIRST AVAILABLE ASGARD SEQUENCE

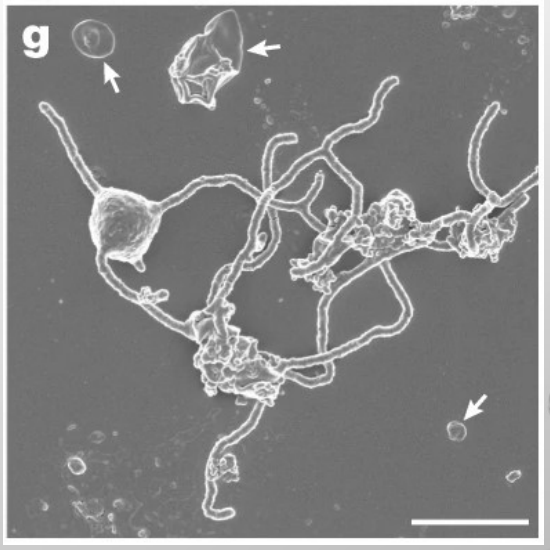
- THE GENOME CONSISTS OF 5,381 PROTEIN CODING GENES
- OF THESE, ROUGHLY 32% DO NOT CORRESPOND TO ANY KNOWN PROTEIN
- 26% CLOSELY RESEMBLE ARCHAEAL PROTEINS
- 29% CORRESPOND TO BACTERIAL PROTEINS
- THIS SITUATION IS CONSISTENT WITH: (I) PROTEINS FROM A NOVEL PHYLUM (WITH FEW CLOSE RELATIVES, OR NONE) ARE DIFFICULT TO ASSIGN; AND (II) EXISTING RESEARCH THAT SUGGESTS THERE HAS BEEN SIGNIFICANT INTER-DOMAIN HORIZONTAL GENE TRANSFER BETWEEN BACTERIA AND ARCHAEA
- **A SMALL, BUT SIGNIFICANT PORTION OF THE PROTEINS (175, 3.3%) THAT THE GENES CODE FOR ARE VERY SIMILAR TO EUKARYOTIC PROTEINS**
- **SUBSEQUENT ASGARD GENOMES HAVE VALIDATED THE OBSERVATION**

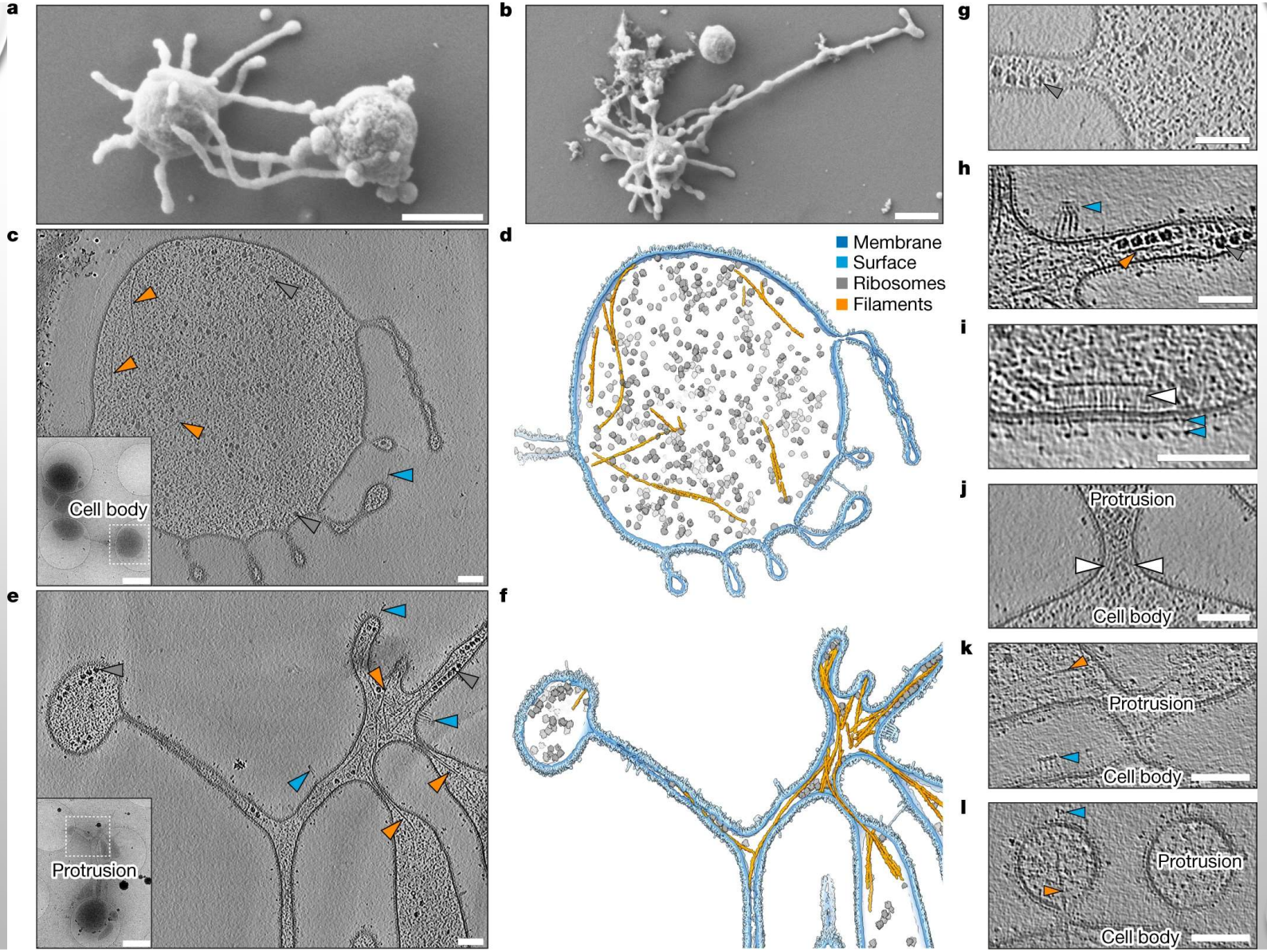
THE EUKARYOTIC COMPONENT

- EUKARYOTIC SIGNATURE PROTEINS (ESP) INVOLVED IN A BROAD RANGE OF EUKARYOTIC PROCESS (**THESE REPRESENT A STAGGERING 50% OF ALL ESP'S**) INCLUDING MEMBRANE-RELATED PROCESSES AND CELL SHAPE DYNAMICS
- PROTEINS INVOLVED IN EUKARYOTIC MEMBRANE TRAFFICKING MACHINERY
- EUKARYOTIC-LIKE STRUCTURAL AND CYTOSKELETON PROTEINS
- SORTING COMPLEX REQUIRED FOR TRANSPORT ACROSS CELL MEMBRANE
- EUKARYOTIC-LIKE RIBOSOMAL PROTEIN
- THE FUNCTION OF THESE SHARED PROTEINS INCLUDE CELL MEMBRANE DEFORMATION, CELL SHAPE FORMATION, AND A DYNAMIC PROTEIN CYTOSKELETON
- ANOTHER SHARED PROTEIN, ACTIN, IS ESSENTIAL FOR PHAGOCYTOSIS (THE ABILITY TO ENGULF AND CONSUME ANOTHER PARTICLE) IN EUKARYOTES

SOME PIX REVEAL SMALL COCCOID CELLS WITH EXTENSIVE PROTRUSIONS






a
b
c
Cell body
d
Membrane
Surface
Ribosomes
Filaments
e
Protrusion
f
g
h
i
j
Protrusion
Cell body
k
Protrusion
Cell body
l
Protrusion
Cell body

THE EUKARYOTES' ANCESTOR: AN EMERGING PICTURE

- THE ASGARD ARCHAEA EVOLVED MORE THAN 2 BILLION YEARS AGO
- ALTOGETHER, THE ASGARD ARCHAEAL ANCESTOR OF EUKARYOTES HAD, COMPARED WITH OTHER ARCHAEA, A RELATIVELY LARGE GENOME THAT RESULTED MAINLY FROM MORE NUMEROUS GENE DUPLICATIONS
- IT IS TEMPTING TO SPECULATE THAT THE INCREASED GENE DUPLICATION RATES OBSERVED ARE AN ANCESTRAL FEATURE AND THAT IT REMAINED THE PREDOMINANT MODE OF GENOME EVOLUTION DURING THE EARLY STAGES OF EUKARYOGENESIS
- ALTHOUGH ASGARD ARCHAEA PROBABLY HAD A THERMOPHILIC ANCESTRY, THE LINEAGE FROM WHICH EUKARYOTES EVOLVED WAS ADAPTED TO MESOPHILIC CONDITIONS. THIS FINDING IS COMPATIBLE WITH A GENERALLY ASSUMED MESOPHILIC ANCESTRY OF EUKARYOTES
- COMPLEX PATHWAYS INVOLVED IN PROTEIN TARGETING AND MEMBRANE TRAFFICKING AND IN GENOME MAINTENANCE AND EXPRESSION IN EUKARYOTES WERE PRESENT IN THE ASGARD ARCHAEAL ANCESTOR
- POTENTIAL FOR MEMBRANE DEFORMATION, CYTOSKELETON PROTEINS AND THE ABILITY TO DO PHAGOCYTOSIS WOULD BE INSTRUMENTAL IN THE EVOLUTION OF EUKARYOTES

THE EMERGING TREE OF LIFE