

## Really Big Bacteria

bigger cells=larger vol in relation to surface area

surface area can't permit entry of nutrients to maintain vol

*Beijerinia giganta* (filamentous in sulfur rich env, low pH)

Hydrogen sulfide:  $\text{H}_2\text{S} + 2 \text{O}_2 \rightarrow \text{SO}_4^{2-} + 2 \text{H}^+$

Thiosulfate:  $\text{S}_2\text{O}_3^{2-} + \text{H}_2\text{O} + 2 \text{O}_2 \rightarrow 2 \text{SO}_4^{2-} + 2 \text{H}^+$

Both release ave. 736 kJ of energy/rxn

env. high in hydrogen sulfide

normally reduced to  $\text{H}_2\text{S}$

If hydrogen sulfide deficient, sulfur reduced to sulfuric acid

binds with carbonate ions = sulfate

Form mats to search for sulfur

*Epulopiscium fishelsoni*

originally thought of as a protist due to lg size, then rRNA analysis

first found in surgeon fish

Fruiting body: *Myxococcus xanthus*

G- rod in soil w/ pH 5-8 (5um x .5 um) motile w/o flagella

2nd lgst prokaryotic genome

predatory, not pathogenic

hunt in swarms

extracellular matrix: polysaccharides/proteins

LC: Starvation-->aggregation-->mound-->fruiting body-->myxospore, germ, vegetative

normal conditions: grow in swarms that spread

scarce nutrients: starvation-->mounds then fruiting body

spores-->encounter food and germinate

swarms kill prey/take up nutrients, produce antibiotics/enzymes

social motility: move as one w/ type IV pili extended and retracted

replicate DNA normally (not possible at other stages)

Scarce nutrients: A signal activates C signal

C signal=aggregation-->mounds--> fruiting bodies

10% cells remain undiff. rods-->scout for nutrients

20-90% lysed for nutrients, rest diff. into cocci spores

resistant heat/dessication, viable for long

nutrients cause spores to germinate and revert to swarm

## Archaeal Methanogens

many extremophiles/methanogens=not O<sub>2</sub> tolerant

grp 1 thermophiles, grp 2 everything else

*Methanopyrus* bridges btwn 2

equal or smaller than eubacteria

no junk DNA

gene products, polymerases and RNA introns similar to eukarya

unique ribosomes

Plasma membrane w/ unique lipids in monolayer, isoprenoid

protect against env., less permeable

glycero-ether lipids, not glycerol ester lipids

## methanogenesis

CO<sub>2</sub>, methanol, acetate pathways  
strict anaerobic process to ATP production, methane byproduct  
electron transfer/oxidation reduction rxn  
makes all ATP needed  
pathways diff. depending on material  
all pathways need H<sub>2</sub> gas and water

### CO<sub>2</sub> pathway

simplest, model system  
process spontaneous  
C loses 1 O at a time, first 1 H added, then 2 for CH<sub>3</sub>  
coenzyme M reduces methyl to make methane-->released

### Methanol pathway

1 methanol converted to CO<sub>2</sub> by reversing up chain  
used to convert 3 methanols into methane  
methyl-amines/methyl sulfides use same path

### Acetate Pathway

2/3 natural methane produced  
only 2 genera: Methanosarcina Methanotrix (this uses exclusively)  
needs ATP, 5 steps  
transport into cell, activation of acetate to acetyl-CoA  
cleavage of CS and CC bonds make CO<sub>2</sub> and CH<sub>3</sub>  
CH<sub>3</sub> transferred to coenzyme M  
reduce to methane  
can also use pyruvate and turn into acetyl coa  
produce methane using glucose through glycolysis  
only cells w/ acetate pathway can do this

Coenzyme M most important, responsible for energy transfer

Coenzyme F<sub>420</sub> main electron carrier, fluorescent blue green

Coenzyme F<sub>430</sub> secondary electron carrier w/ nickel required for growth  
ATP production

Co M make H gradient, to power ATP synthase

Found in wetlands, guts, hot spring, hydrothermal vents, deep earth's crust

Methanopyrus (hyperthermophilic), Methanosarcina acetivorans (model)

pyrus: see floor, very hot

acetivorans: 1<sup>st</sup> largest genome of archaea, 4<sup>th</sup> largest over all, uses all 3 pathways  
only archaea known to fix N

has molybdenum/iron containing, vanadium/iron, iron only

## nitrogenase

Methanoacterium thermotrophicum (thermophilic) Methanobrevibacter smithii

(gut)

therma: 35-70 C, 6.0-8.5 pH, rods or curved rods, G<sup>-</sup> non motile

smithii: methanogen in gut, correlates w/ obesity, facilitates pathogen

## growth

looks to produce renewable energy and control obesity, disease, cancer

Mycoplasmas: bacteria w/o walls--class Mollicutes

parasitic, commensals, saprotrophic  
facultative anaerobe and strict aerobe  
no flagella

motile and non

Used to think viruses or L form bacteria

no evolutionary descendants of G<sup>+</sup>, lost many genes, related to Lactobacillus,

Bacillus, Streptococcus, Clostridium

Smallest/simplest self-replicating orgs: 0.2–0.8 μm (E. coli 2 μm)

pass through bacteria filters--need electron microscopy

smallest genome: 580–1300 kb, coding capacity 700

lack many enzymatic activities/metabolic pathways

express housekeeping genes

low GC content 23–41%

UGA (universal stop codon) codes for tryptophan

*M. genitalium*: pathogenic, nongonococcal urethritis disease

smallest genome size: 580 kb 470 genes coding for proteins, 32% GC

model for minimal genes for independent existence

no wall, many shapes, fusion between membranes

β-lactam antibiotic resistance

membrane exposed, need exogenous sterols (unique)

capsule: in 10 species--acidic carbs or lipids, antiphagocytic properties

electronegative charges

prevent immunoglobulin deposition

parasitic: need amino acids, nucleotides, fatty acids, steroids

adhere to host cells w/ adhesion protein in terminal organelle

also used for gliding motility

contaminates in research labs

cause pneumonia, pelvic inflammation disease,

difficult to isolate

fried egg colonies

adherence

tip attachment: bind membrane glycolipids in host cell

accessory proteins: P40 and P90 assist localization of P1 to tip

mutant P1 scattered over surface of mycoplasma

HMW1, 2, 3 proline rich cytoskeleton proteins; anchor P1

cell invasion protects mycoplasmas

can damage hosts: competition, adherence, fusion, apoptosis

avoids immune system

molecular mimicry

phenotypic plasticity, immunoglobulin binding proteins

may cause cancer

Gliding

Predatory bacteria: *Bdellovibrio bacteriovorus*

G<sup>-</sup>, obligate aerobic, parasitic to G<sup>-</sup>

rod, small, single flagellum  
colide w/ prey--occupy intraperiplasmic space  
kills, digests, lyses prey  
3 hr predatory cycle  
random swimming find prey