

Comparing Prokaryotic and Eukaryotic Cells

Basic chemical components/elements of a cell.

CHOPKNS CaFe (its) Mg (ood)

TABLE 3.2 Chemical comp	osition of a prokaryotic cell*		"	Rem: 70-85% Water		
Molecule	Percent	t of dry weight	Mo	lecules per cell.	Different kinds	
Total macromolecules	•	96		24,610,000	~2500	
Protein		55		2,350,000	~1850	
Polysaccharide		5		4,300	25 🗲	
Lipid		9.1		22,000,000	44	
Lipopolysaccharide		3.4		1,430,000	1	
DNA		3.1		2.1	1	
8 RNA		20.5		255,500	6660 ·	
Total monomers		3.0			~350	
Amino acids and precursors		0.5			~100	
Sugars and precursors		2			~50	
Nucleotides and precursors		0.5			~200	
Inorganic ions		1 .			18	
Total		100%				
a Data from Neidhardt, F. C., et al. (eds. American Society for Microbiology, Was b Dry weight of an actively growing cei c Assuming peptidoglycan and glycog d There are several classes of phosphol between species and because of differe	hington, DC. 1 of E. coli ≈ 2 m to be the main pids, each of y	chia coli and Salmonella t 2.6 × 10 ⁻¹³ g; total weig ajor polysaccharides pr which exists in many ki	ht (70% v resent.	vater) = 9.5×10^{-13} g.		
Protein ~ Lipid ~	50% 10%	Cel	l Wa	ll 10–20%	, 0	

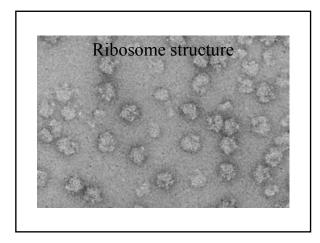
Take Home Message:

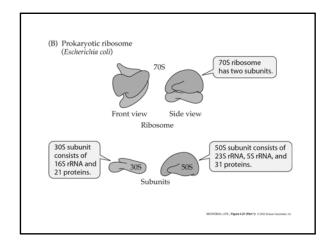
Proteins are #1 by weight

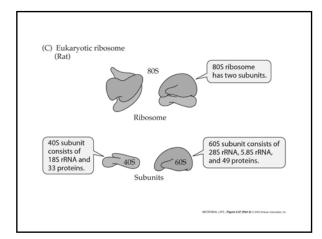
Lipids are #1 by number

Peptidoglycan is 1 jumbo molecule

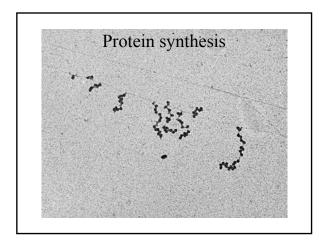
Comparing Prokaryotic and Eukaryotic Cells Classification of prokaryotic cellular features: Invariant (or common to all) Ribosomes: Sites for protein synthesis – aka the grand translators. Cell Membranes: The barrier between order and chaos. Nucleoid Region: Curator of the Information.







Property	Prokaryote	Eukaryote	
Overall size	705	80S	
Small subunit	305	40S	
Number of proteins	~21	~30	
RNA size (number of bases)	16S (1500)	18S (2300)	
Large subunit	505	605	
Number of proteins	~34	~50	
RNA size	235 (2900)	285 (4200)	
(number of bases)	5S (120)	5.8S (160)	
		5S (120)	



Importance of a Molecular Biological Approach

- **Traditional culturing** techniques isolate ~1% of the total bacteria in marine ecosystems, thereby severely underestimating diversity and community structure.
- Because nutrient-rich **culture media** have been historically used during enrichment procedures, bacteria which may be dominant in natural communities are selected against in favor of copiotrophic (weedy) bacteria.
- SSU rRNAs and their respective genes are excellent descriptors of microbial taxa based on phylogeny.

