Genome Sizes

The genome of an organism is the complete set of genes specifying how its phenotype will develop (under a certain set of environmental conditions). In this sense, then, **diploid** organisms (like ourselves) contain two genomes, one inherited from our mother, the other from our father. Table of Genome Sizes (haploid)

_	Base pairs	Genes	Notes	
<u>Phi-X 174</u>	5,386	10	virus of E. coli	
Human mitochondrion	16,569	37		
Epstein-Barr virus (EBV)	172,282	80	causes mononucleosis	
nucleomorph of Guillardia theta	551,264	511	all that remains of the nuclear	
genome of a red alga (eukaryote) eng	ulfed long ago by	y another eukaryo	ote	
Mycoplasma genitalium	580,073	483	three of the smallest true	
organisms				
Ureaplasma urealyticum	751,719	652		
Mycoplasma pneumoniae	816,394	680		
Chlamydia trachomatis	1,042,519	936	most common sexually-	
transmitted disease (STD) bacterium in the U.S.				
Rickettsia prowazekii	1,111,523	834	bacterium that causes	
epidemic typhus				
Treponema pallidum	1,138,011	1,039	bacterium that causes syphilis	
Mimivirus	1,181,404	1,262	A virus (of an amoeba) with a	
conome larger than the six collular organisms above				

genome larger than the six cellular organisms above

Rickettsia conorii	1,268,755	1,374	causes Mediterranean spotted
fever			
Borrelia burgdorferi	1.44 x 106	1,738	bacterium that causes Lyme
disease [<u>Note</u>]			
Aquifex aeolicus	1,551,335	1,749	bacterium isolated from a hot
spring in Yellowstone National Park			
Thermoplasma acidophilum1,	564,905	1,509	an <u>archaean</u> that lacks a cell
wall			
Campylobacter jejuni	1,641,481	1,708	frequent cause of food
poisoning			
Helicobacter pylori	1,667,867	1,589	chief cause of stomach ulcers
(not stress and diet)			
Methanococcus jannaschii	1,664,970	1,783	These unicellular prokaryotes
look like typical bacteria but their gen	es are so differen	t from thos	e of either bacteria or eukaryotes that
they are classified in a third kingdom:	<u>Archaea</u> .		
Aeropyrum pernix	1,669,695	1,885	
Pyrococcus horikoshii1,	738,505	1,994	
Methanobacterium			
thermoautotrophicum	1,751,377	2,008	
<u>Haemophilus influenzae</u>	1,830,138	1,738	bacterium that causes middle ear
infections			
Thermotoga maritima	1,860,725	1,879	marine bacterium
Streptococcus pneumoniae	2,160,837	2,236	the <u>pneumococcus</u>
Archaeoglobus fulgidus	2,178,400	2,437	another member of the <u>Archaea</u>

epidemics of meningitis in less developed countries.Neisseria meningitidis2,272,3512,221Group B; the most frequent causeof meningitis in the U.S.Encephalitozoon cuniculi2,507,5191,997(plus 69 RNA genes); a parasiticeukaryote.Propionibacterium acnes2,560,2652,333Listeria meneoutogenes2,044,5282,0262,952 of these encode meneous	Neisseria meningitidis2,	184,406	2,185	Group A; causes occasional
of meningitis in the U.S.2,507,5191,997(plus 69 RNA genes); a parasiticEncephalitozoon cuniculi eukaryote.2,560,2652,333causes acne		ped countries.		
Encephalitozoon cuniculi2,507,5191,997(plus 69 RNA genes); a parasiticeukaryote.2,560,2652,333causes acne	Neisseria meningitidis2,	272,351	2,221	Group B; the most frequent cause
eukaryote.Propionibacterium acnes2,560,2652,333causes acne	of meningitis in the U.S.			
Propionibacterium acnes 2,560,265 2,333 causes acne	Encephalitozoon cuniculi	2,507,519	1,997	(plus 69 RNA genes); a parasitic
•	eukaryote.			
Listeria monosytegenes 2.044528 2.026 2.952 of these encode proteins, the	Propionibacterium acnes	2,560,265	2,333	causes acne
<u>Listeria monocytogenes</u> 2,944,528 2,920 2,855 of these encode proteins; the	Listeria monocytogenes	2,944,528	2,926	2,853 of these encode proteins; the
rest RNAs	rest RNAs			
Deinococcus radiodurans 3,284,156 3,187 on 2 chromosomes and 2 plasmids;	Deinococcus radiodurans	3,284,156	3,187	on 2 chromosomes and 2 plasmids;
bacterium noted for its resistance to radiation damage	bacterium noted for its resistance to ra-	diation damage		
Synechocystis3,573,4704,003a marine prokaryote, one of the	Synechocystis	3,573,470	4,003	a marine prokaryote, one of the
cyanobacteria ("blue-green algae")	cyanobacteria ("blue-green algae")			
Vibrio cholerae4,033,4603,890in 2 chromosomes; causes cholera	Vibrio cholerae	4,033,460	3,890	in 2 chromosomes; causes cholera
Mycobacterium tuberculosis 4,411,532 3,959 causes tuberculosis	Mycobacterium tuberculosis	4,411,532	3,959	causes tuberculosis
Mycobacterium leprae 3,268,203 1,604 causes leprosy	Mycobacterium leprae	3,268,203	1,604	causes leprosy
Bacillus subtilis 4,214,814 4,779 another bacterium	Bacillus subtilis	4,214,814	4,779	another bacterium
<u>E. coli</u> 4,639,221 4,377 4,290 of these genes encode	<u>E. coli</u>	4,639,221	4,377	4,290 of these genes encode
proteins; the rest RNAs	proteins; the rest RNAs			
Agrobacterium tumefaciens4,674,0625,419Useful vector for making	Agrobacterium tumefaciens	4,674,062	5,419	Useful vector for making
transgenic plants; shares many genes with Sinorhizobium meliloti				
Salmonella enterica var Typhi 4,809,037 4,395 + 2 plasmids with 372 active genes;	<u>Salmonella enterica var Typhi</u>	4,809,037	4,395	+ 2 plasmids with 372 active genes;
causes typhoid fever	causes typhoid fever			
Salmonella enterica var Typhimurium 4,857,432 4,450 + 1 plasmid with 102 active genes	Salmonella enterica var Typhimurium	4,857,432	4,450	+ 1 plasmid with 102 active genes

<u>Yersinia pestis</u>	4,826,100	4,052	on 1 chromosome + 3 plasmids;	
causes plague			-	
Schizosaccharomyces pombe	12,462,637	4,929	Fission yeast. A eukaryote with	
fewer genes than the five prokaryotes	below.			
E. coli O157:H7	5.44 x 106	5,416	strain that is pathogenic for humans	
Ralstonia solanacearum	5,810,922	5,129	soil bacterium pathogenic for many	
plants; 1681 of its genes on a huge plants;	asmid			
Pseudomonas aeruginosa	6.3 x 106	5,570	Increasingly common cause of	
opportunistic infections in humans.				
Streptomyces coelicolor	6,667,507	7,842	An actinomycete whose relatives	
provide us with many antibiotics				
Sinorhizobium meliloti	6,691,694	6,204	The <u>rhizobial symbiont</u> of alfalfa.	
Genome consists of one chromosome and 2 large plasmids.				
Saccharomyces cerevisiae	12,495,682	5,770	Budding yeast. A eukaryote.	
Cyanidioschyzon merolae	16,520,305	5,331	A unicellular <u>red alga</u> .	
<u>Plasmodium falciparum</u>	22,853,764	5,268	Plus 53 RNA genes. Causes the	
most dangerous form of malaria.				
Thalassiosira pseudonana	34.5 x 106	11,242	A diatom. Plus 144 chloroplast and	
40 mitochondrial genes encoding proteins				
Neurospora crassa	38,639,769	10,082	Plus 498 RNA genes.	
Caenorhabditis elegans	100,258,171	~19,000	The first multicellular eukaryote to	
be sequenced.				
Arabidopsis thaliana	115,409,949	25,498	a flowering plant (<u>angiosperm</u>) <u>See</u>	
<u>note.</u>				

Drosophila melanogaster	122,653,977	13,472	the "fruit fly"
Anopheles gambiae	278,244,063	13,683	Mosquito vector of malaria.
Humans	3.3 x 109	20,000-25	5,000 [Link to more details.]
Tetraodon nigroviridis (a pufferfish)	3.42 x 108 27,9	Alth Alth	ough Tetraodon seems to have about
the same number of genes as we do, it	has much less 💾	unk" DNA	so its total genome is about a tenth
the size of ours.			
Rice	4.3 x 108	~60,000	
Amphibians	109 - 1011 ?		
Psilotum nudum	2.5 x 1011 ?	Note	

Note: The gene total for **Borrelia burgdorferi** is based on 853 genes on its single chromosome (of 910,724 base pairs) plus 430 genes on 11 of the 17 <u>plasmids</u> it contains.

Arabidopsis thaliana is a plant (in the mustard family) that has the smallest genome known in the plant kingdom and for this reason has become a favorite of plant molecular biologists. The sequences of two of its five chromosomes (#2 and #4) were published in December 1999. The others were reported in December 2000.

Even though **Psilotum nudum** (sometimes called the "whisk fern") is a far simpler plant than Arabidopsis (it has no true leaves, flowers, or fruit), it has 3000 times as much DNA. No one knows why, but 80% or more of it is <u>repetitive DNA</u> containing no genetic information. This is also the case for some amphibians, which contain 30 times as much DNA as we do but certainly are not 30 times as complex.

The total amount of DNA in the haploid genome is called its **C value**. The lack of a consistent relationship between the C value and the complexity of an organism (e.g., amphibians vs. mammals) is called the <u>C value paradox</u>.