

Genome Sequence of an Obligate Intracellular Pathogen of Humans: *Chlamydia trachomatis*

Stephens, R.S., Kalman, S., Lammel, C., Fan, J., Marathe, R., Aravind, L., Mitchell, W., Olinger, L., Tatusov, R., Zhao, Q., Koonin, E. V., Davis, R.W. (1998) *Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis*. *Science* 282: 754-759. [10.1126/science.282.5389.754](https://doi.org/10.1126/science.282.5389.754).

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November 12, 2013

Glycogen Metabolism and Glycolytic within Aerobic Respiration

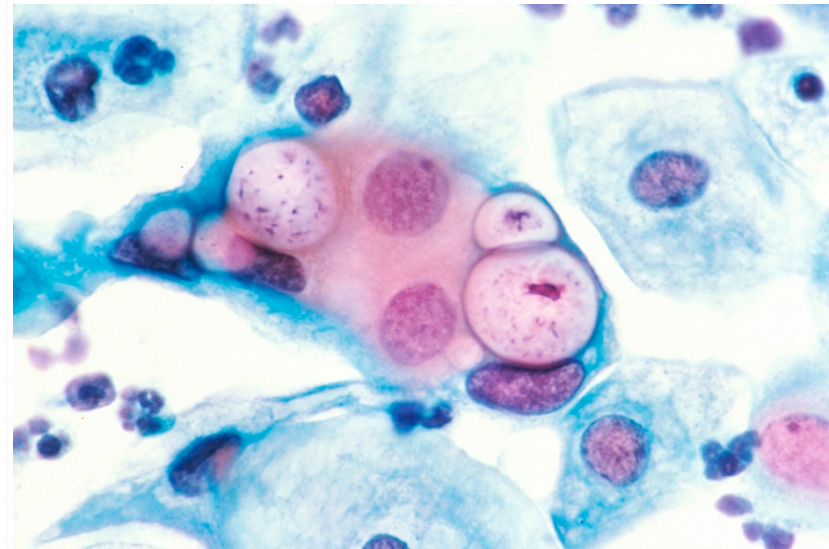
- 0 Central carbon source is likely glutamate
 - Glucose and 2-oxoglutarate play supplementary roles depending on the chlamydial development stage.
- 0 Contains complete glycogen synthesis and degradation system
 - Supports hypothesis of a central role for glucose or glucose derivatives as primary carbon source for some developmental stages.
- 0 Contain an intact glycolytic pathway
 - Exception is fructose-1,6-diphosphate aldolase not being identified.

TCA, Phospholipids, and Fatty Acid Biosynthesis in Aerobic Respiration

- 0 The tricarboxylic acid (TCA) cycle found to be incomplete because certain genes could not be identified.
 - However, the cycle could be fed by an uptake of glutamine or by uptake of 2-oxoglutarate.
- 0 Contains extensive number of genes for enzymes of fatty acid and phospholipid biosynthesis.
 - Suggests that chlamydiae synthesize fatty acids, phosphatidylethanolamine, and phosphatidylglycerol de novo.

Nutrient Uptake and the Vacuole

- 0 Chlamydia invade eukaryotic cells
 - Grow within an intracellular vacuole, called an inclusion (does not fuse with lysosomes).
- 0 Intracellular vacuolar inclusion is apparently not permeable to small compounds.
 - Process by which chlamydiae obtain required nutrients is unknown.
- 0 Transport operon identified in genome encodes certain proteins associated with vacuole.
 - Examples: TolB, TolQ, and ExbD-like proteins.



A majority of Chlamydial genes are a result of horizontal gene transfer.

Table 1

Horizontally transferred genes in *Chlamydia trachomatis*.

Chlamydial gene	Support for horizontal transfer
Topoisomerase I, COOH-terminal domain (CT643), and stand-alone SWIB protein (CT460)	The α -helical SWIB domain detected only in eukaryotic chromatin-associated proteins.
SET domain protein (CT737)	SET domain found only in numerous eukaryotic chromatin-associated proteins.
Methionyl-tRNA synthetase (Met-RS) (CT032)	Chlamydial Met-RS groups with eukaryotic ones in phylogenetic analysis. A C2C2 "little finger" domain is conserved in <i>Chlamydia</i> , Archaea, and eukaryotes, to the exclusion of the other bacteria. An accessory, COOH-terminal RNA-binding domain is present in bacterial Met-RS, but not in <i>Chlamydia</i> , Archaea, or eukaryotes.
Pyrophosphate-dependent phosphofructokinase 1 and 2 (CT205, CT207)	Much greater similarity to eukaryotic than to bacterial orthologs, with the exception of the spirochetes.
Glucose-1-phosphate adenylyltransferase (CT489)	Supported by phylogenetic analysis (39); likely chloroplast origin in plants.
Glycogen phosphorylase (CT248)	Supported by phylogenetic analysis (39).
UDP-glucose pyrophosphorylase (CT715)	No easily detectable bacterial homologs.
Adenine nucleotide translocases 1 and 2 (CT495, CT065)	ATP/ADP translocases of this family are detectable only in <i>Rickettsia</i> and in plants.

Tracing the Phylogeny of enoyl-acyl carrier protein reductase

