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ABSTRACT

### Global Transposon Mutagenesis and a Minimal Mycoplasma Genome

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FULL TEXT

## Supplementary Material

Disrupted *Mycoplasma genitalium* genes (or *M. pneumoniae* homologs)

This table lists transposon insertion sites more than 9 bases downstream of the first base in the initiation codon, and located in the 5'-most 80% of the coding sequence (hits in the COOH-terminal 20% of proteins are considered potentially nondisruptive; see text). An *M. genitalium* gene is listed (MGXXX) if a presumptively disruptive hit has been identified in *M. genitalium* (g), its *M. pneumoniae* ortholog (p), or both (g/p). The second column lists the *M. pneumoniae* ortholog of the gene (MPYYY) where YYY corresponds to the gene designation in Fig. 2. The number of distinct sites in *M. genitalium* and *M. pneumoniae* (X and Y) at which such insertions have been observed are indicated by gX and/or pY in the column "Disrupted species". **Entries for genes in which we have observed more than one independent disruptive event are shown in red.** If the gene is a member of the proposed minimal gene set of Mushegian and Koonin (*I*), then the gene designation is underlined. Gene functions are from the current TIGR version of the *M. genitalium* annotation ([www.tigr.org/~clyde/Mggenes99.html](http://www.tigr.org/~clyde/Mggenes99.html)).

If the assignment of a gene to the minimal gene set (*I*) is based on a different functional assignment, then that assignment is also shown in square brackets, i.e., [alternate assignment]. The name of each functional class is followed by a fraction in parentheses. This fraction indicates the number of putative dispensable genes observed over the total number of genes within that functional class. For this analysis we have pooled the functional classes "Unknown" and "Hypothetical" into a class we call "Unknown function".

### Mycoplasma genes with Tn4001 insertions

*M. gen.* *M. pn.* Disrupted Gene function

gene gene species

Purines, pyrimidines, nucleosides, and nucleotides (5/19)

2'-Deoxyribonucleotide metabolism  
 MG231 MP513 p1 alpha chain (nrdE) ribonucleoside-diphosphate reductase,  
 MG227 MP517 p1 thymidylate synthase (thyA)  
 Salvage of nucleosides and nucleotides  
 MG049 MP092 g1 purine-nucleoside phosphorylase (deoD)  
 MG051 MP090 g1 thymidine phosphorylase (deoA)  
 MG052 MP089 g2 cytidine deaminase (cdd)  
 Fatty acid and phospholipid metabolism (1/8)  
 Degradation  
 MG310 MP395 g5 lipase/esterase, putative  
 Biosynthesis of cofactors, prosthetic groups, and carriers (1/4)  
 Lipoate  
 MG270 MP450 p1 lipoate protein ligase (lplA)  
 Central intermediary metabolism (3/7)  
 Other  
 MG293 MP420 g6 glycerophosphoryl diester phosphodiesterase, putative  
 MG299 MP412 p1 phosphotransacetylase (pta)  
 MG394 MP266 g1 serine hydroxymethyltransferase (glyA)  
 Energy metabolism (1/33)  
 Sugars  
 MG118 MP577 p1 UDP-glucose 4-epimerase (galE)  
 Transport and binding proteins (8/33)  
 Anions  
 MG410 MP233 g1/p2 phosphate ABC transporter, ATP-binding protein (pstB)  
 MG411 MP232 g4 phosphate ABC transporter, permease protein (pstA)  
 Carbohydrates, organic alcohols, and acids  
 MG033 MP111 g2 glycerol uptake facilitator (glpF)  
 MG062 MP077 g4/p1 PTS system, fructose-specific IIBC component (fruA)  
 Unknown substrate  
 MG014 MP136 g1 ABC transporter, ATP-binding protein  
 MG467 MP159 g1 ABC transporter, ATP-binding protein

**MG390 MP271** **g1/p2** **ABC transporter, ATP-binding protein**  
**MG291 MP422** **g1** **transport system permease protein P69**  
**DNA metabolism (6/29)**  
**DNA replication, recombination, and repair**  
**MG244 MP496** **p2** **DNA helicase II, putative**  
**MG261 MP460** **p1** **DNA polymerase III, subunit alpha (polC-2)**  
**MG339 MP351** **g3** **recA protein (recA)**  
**MG380 MP284** **g1** **glucose-inhibited division protein B gidB**  
**MG421 MP223** **g1/p1** **excinuclease ABC subunit A (uvrA)**  
**MG469 MP156** **p1** **chromosomal replication initiator protein (dnaA)**  
**Transcription (3/13)**  
**Transcription factors**  
**MG249 MP485** **p1** **RNA polymerase sigma-43 factor (rpoD)**  
**RNA processing**  
**MG017 MP134** **g2** **ATP-dependent RNA helicase, putative**  
**MG308 MP397** **g1** **ATP-dependent RNA helicase, putative**  
**Protein synthesis (6/90)**  
**tRNA aminoacylation**  
**MG345 MP322** **g1** **isoleucyl-tRNA synthetase (ileS)**  
**MG455 MP173** **p1** **tyrosyl-tRNA synthetase (tyrS)**  
**Ribosomal proteins: synthesis and modification**  
**MG426 MP218** **g1** **ribosomal protein L28 (rpL28)**  
**tRNA and rRNA base modification**  
**MG182 MP636** **g5** **pseudouridylate synthase I (hist)**  
**MG252 MP482** **p1** **rRNA methylase, putative**  
**MG346 MP321** **g1/p2** **rRNA methylase, putative**  
**Protein fate (4/21)**  
**Protein modification and repair**  
**MG106 MP588** **g1** **polypeptide deformylase (def)**  
**Protein folding and stabilization**  
**MG392 MP269** **p2** **heat shock protein (groEL)**  
**Degradation of proteins, peptides, and glycopeptides**  
**MG183 MP635** **g1** **oligoendopeptidase F (pepF)**  
**MG355 MP311** **p3** **ATP-dependent Clp protease, ATPase subunit (clpB)**  
**Regulatory functions (3/5)**  
**Other**  
**MG085 MP609** **g1** **hpr(ser) kinase, putative**  
**MG278 MP442** **p7** **guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase (spoT)**  
**MG408 MP235** **g2** **peptide methionine sulfoxide reductase (pmsR)**  
**Cell envelope (18/29)**  
**Lipoproteins**  
**MG040 MP102** **p1** **lipoprotein, putative**  
**MG045 MP096** **p1** **lipoprotein, putative [spermidine/putrescine periplasmic binding protein]**  
**MG067 MP256** **g3** **lipoprotein, putative**  
**MG068 MP255** **p1** **lipoprotein, putative**  
**MG149 MP670** **g1** **lipoprotein, putative**  
**MG185 MP633** **g1** **lipoprotein, putative**  
**MG186 MP022** **g2** **lipoprotein, putative**  
**MG260 MP552** **p2** **lipoprotein, putative**  
**MG307 MP404** **p1** **lipoprotein, putative**  
**MG338 MP352** **g1** **lipoprotein, putative**  
**MG395 MP250** **g40** **lipoprotein, putative**  
**MG412 MP231** **g3** **lipoprotein, putative**  
**MG440 MP199** **g2** **lipoprotein, putative**  
**Surface structures**  
**MG191 MP014** **g1/p1** **adhesin P1 (mgpB)**  
**MG192 MP013** **g1/p2** **mgpC protein (mgpC)**  
**MG218 MP527** **p4** **cytadherence accessory protein (hmw2)**  
**MG317 MP388** **g1** **cytadherence accessory protein (hmw3)**  
**Biosynthesis of surface polysaccharides and lipopolysaccharides**  
**MG137 MP558** **p2** **UDP-galactopyranose mutase (glf)**  
**Cellular processes (1/6)**  
**Adaptations to atypical conditions**  
**MG470 MP154** **g2** **soj protein (soj)**  
**Unknown function (69/180)**  
**MG002 MP152** **g1** **Unknown function (dnaJ-like protein)**  
**MG009 MP145** **g9** **Unknown function [uncharacterized ACR (metal-utilizing enzyme?)]**  
**MG010 MP140** **g1** **Unknown function**  
**MG011 MP139** **g8** **Unknown function**  
**MG024 MP128** **p2** **Unknown function (GTP-binding protein, putative)**  
**MG025 MP126** **g1** **Unknown function**  
**MG029 MP122** **g5** **Unknown function**  
**MG032 MP112** **g5** **Unknown function**  
**MG039 MP103** **p2** **Unknown function**  
**MG055 MP086** **p1** **Unknown function [preprotein translocase subunit (secE)]**  
**MG059 MP081** **p1** **Unknown function (small protein (smpB)) [LPS-heptosyl-2-transferase]**

