Data Article

Data on genome analysis of *Mycoplasma gallisepticum* during intracellular infection

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**Abstract**

The genus *Mycoplasma* relates to Gram-positive bacteria that lack a cell wall and are capable of causing chronic disease in humans and animals. Among the agents of infection and disease in domestic poultry and wild birds, *Mycoplasma gallisepticum* is the most important mycoplasma species, causing considerable losses in the poultry industry. In the present paper, we provide data on adaptation of *M. gallisepticum* to the eukaryotic host cells on the genomic level. The major changes were predominantly localized in the VlhA-hemagglutinin genes which are important components of pathogenesis. The ability of mycoplasmas to change dramatically the repertoire of surface antigens and to vary the immunogenicity of these components allows them to remain undetected by the immune system of the host. The data presented in this article are related to the article entitled “Phase Transition of the Bacterium upon Invasion of a Host Cell as a Mechanism of Adaptation: a *Mycoplasma gallisepticum* Model.” (Matyushkina et al., 2016) [1]. Data posted in repository [https://www.ncbi.nlm.nih.gov/bioproject/315515](https://www.ncbi.nlm.nih.gov/bioproject/315515). Bioproject ID: PRJNA315515.

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### Specifications Table

| Subject area     | Biology       |
|------------------|---------------|
| More specific subject area | Genomics     |
| Type of data     | Table         |
| How data was acquired | Data was acquired on Ion Torrent PGM (Life Technologies) and 454 GS FLX + (Roche) |
| Data format      | Raw, processed|
| Experimental factors | Mycoplasma gallisepticum S6 cells were cultured as described previously [2]. Chicken erythroblast cell line HD3 (clone A6 of line LSCC [3,4]) was cultivated as described in [5]. The gentamicin invasion assay and isolation of intracellular mycoplasma were carried out as described in [1]. Genomic DNA from individual clones was isolated as previously described [2]. |
| Experimental features | Sequencing was performed according to Life Technologies and Roche protocols for DNA-seq. |
| Data source location | N/A          |
| Data accessibility | Data is within this article and raw data was deposited at NCBI repository https://www.ncbi.nlm.nih.gov/bioproject/315515. Bioproject ID: PRJNA315515. |

### Value of the data

- This data set will be of value for the scientific community working in the area of host-pathogen interaction since it represents the genome changes of bacterium *Mycoplasma gallisepticum* upon invasion of a host cell.
- The data will also be of value for studies in the area of infection and immunity because basic genome changes were predominantly localized in the VlhA-hemagglutinin genes which are the primary strategy for survival among bacterial pathogens.
- These data may have implications for the development of preventive strategies.

### 1. Data

The data represents the genomic polymorphisms of *Mycoplasma gallisepticum* clones after infection and isolation from HD3 cells. Table 1 represent data obtained during acute (24 h) infection. Table 2 represent data obtained during chronic (7 weeks) infection. In analysis were taken 10 different colonies of mycoplasma isolated from HD3 cells after acute infection, 10 different colonies of mycoplasma isolated from HD3 cells after chronic infection and 12 different colonies of control laboratory strain.

### 2. Experimental design, materials and methods

#### 2.1. Cell culturing

*M. gallisepticum* S6 cells were cultured as described previously [2]. Chicken erythroblast cell line HD3 (clone A6 of line LSCC [3,4]) was cultivated as described in [5]. The gentamicin invasion assay and isolation of intracellular mycoplasma were carried out as described in [1]. Genomic DNA from individual cultures was isolated as previously described [2].
2.2. Genome sequencing and analysis

Genomic DNA from individual cultures was isolated as previously described [2]. The DNA (100 ng for each sample) was disrupted into 200–300 bp fragments using the Covaris S220 System (Covaris, Woburn, Massachusetts, USA). Barcode shotgun libraries for mycoplasma isolated from eukaryotic cells (MIEC) were prepared by the Ion Xpress™ Plus Fragment Library Kit (Life Technologies). PCR emulsion was performed by the Ion PGM™ Template OT2 200 Kit (Life Technologies). DNA sequencing was performed by the Ion Torrent PGM (Life Technologies) with the Ion 318 chip v2 and the Ion PGM™ Sequencing 200 Kit v2 (Life Technologies). Control *M. gallisepticum* S6 strain was sequenced by using the Roche 454 Life Sciences Genome Sequencer FLX following the manufacturer’s instructions (Roche 454 Life Science, USA). Assembly of raw sequencing reads with an average length of 540 bases was performed by the GS de novo assembly software version 2.8 (Roche 454 Life Science, USA).

For the detection of nucleotide variants relatively to the reference, a reference-based mapping approaches via bowtie2 [6] and samtools mpileup [7] tools were used. On average 93% of reads mapped to the reference genome. We skipped alignments with mapping quality (mapQ) less than

| ORF name       | Gene name                                  | Position  | Ref     | MIEC   | Quality | Combined depth across samples | Mean allele frequency across samples |
|----------------|--------------------------------------------|-----------|---------|--------|---------|-------------------------------|--------------------------------------|
| GCW_00395      | 23S ribosomal RNA                           | 83344     | T       | C      | 68.3    | 422                           | 1                                    |
| GCW_01160      | VlhA.I.01 variable lipoprotein family protein | 264070    | C       | T,A    | 999     | 239                           | 1                                    |
| GCW_01340      | 23S ribosomal RNA                           | 317111    | T       | C      | 37.2    | 431                           | 1                                    |
| GCW_01345      | 5S ribosomal RNA                            | 318386    | G       | A      | 999     | 479                           | 1                                    |
| GCW_01455      | Upstream of mobile element protein          | 348358    | A       | T      | 999     | 229                           | 1                                    |
| GCW_01960      | VlhA, cluster 2                             | 465075    | A       | G      | 999     | 92                            | 1                                    |
| GCW_02037      | Phenylalanyl-tRNA synthetase (PheRS) beta chain core domain | 465216    | T       | A      | 55.7    | 128                           | 1                                    |
| GCW_92457      | VlhA, cluster 3                             | 483621    | A       | T,G    | 999     | 85                            | 0.8354                               |
| GCW_03335      | VlhA, cluster 4                             | 588982    | G       | A,C    | 999     | 162                           | 1                                    |
| GCW_03371      | Serine protease                             | 816612    | G       | T      | 999     | 121                           | 1                                    |
| GCW_00585      | Upstream of VlhA, cluster 4                 | 816905    | A       | T      | 999     | 595                           | 1                                    |
| GCW_91948      | Upstream of VlhA, cluster 2                | 817621    | G       | T,A    | 999     | 762                           | 1                                    |
| GCW_92433      | Upstream of VlhA, cluster 3                | 817733    | A       | G      | 999     | 935                           | 1                                    |
| GCW_92454      | VlhA, cluster 3                             | 818171    | C       | A,G    | 999     | 89                            | 1                                    |
| GCW_93372      | Upstream of VlhA, cluster 4                | 818493    | T       | G      | 999     | 449                           | 1                                    |
| GCW_00985      | Serine protease                             | 137223    | G       | A      | 999     | 836                           | 0.6297                               |
| GCW_91948      | Upstream of VlhA, cluster 2                | 462290    | G       | A      | 999     | 168                           | 0.7728                               |
| GCW_92433      | Upstream of VlhA, cluster 3                | 577485    | G       | T      | 999     | 384                           | 0.6192                               |
| GCW_92454      | VlhA, cluster 3                             | 586155    | G       | T      | 999     | 238                           | 0.5183                               |
| GCW_03035      | 3OS ribosomal protein S12                  | 722693    | C       | A      | 999     | 438                           | 0.654                                |
| GCW_03140      | Major facilitator superfamily permease      | 750922    | G       | C      | 999     | 489                           | 0.6667                               |
| GCW_03470      | Asparagine synthase                         | 839170    | A       | G      | 999     | 907                           | 0.6487                               |

MIEC – mycoplasma isolated from eukaryotic cells; Ref – references strain of *M. gallisepticum* S6.
Variants were called using the samtools mpileup command with options `-C50 -D -S`. Variants were filtered using the following criteria: (1) the depth of high-quality coverage larger than 20, (2) in average across all samples at least 50% of reads at the site supporting the call, (3) at least 5 samples have the variant, (4) a homozygous call under a diploid model. We identified nucleotide polymorphisms by comparing calls between the control genomes and the MIEC genomes.

### Table 2
Comparative genomic analysis of *M. gallisepticum* isolated from HD3 cells after chronic (7 weeks) infection with laboratory strain of *M. gallisepticum* S6.

| ORF name      | Gene name                                      | Position | Ref    | MIEC | Quality | Combined depth across samples | Mean allele frequency across samples |
|---------------|------------------------------------------------|----------|--------|------|---------|-------------------------------|-------------------------------------|
| GCW_00633     | Upstream of mobile element protein             | 152250   | A      | T,G  | 999     | 7417                          | 1                                   |
| GCW_01160     | vlhA, cluster 1                                | 264070   | C      | TA   | 999     | 1465                          | 1                                   |
| GCW_01345     | 5S ribosomal RNA                               | 318386   | G      | A    | 999     | 6909                          | 1                                   |
| GCW_01395     | Asparaginyl-tRNA synthetase                     | 332883   | G      | T    | 999     | 2712                          | 0.9444                              |
| GCW_01520     | M42 glutamyl-aminopeptidase family protein     | 359323   | T      | C    | 999     | 1107                          | 0.9444                              |
| GCW_01960     | vlhA, cluster 2                                | 465075   | A      | G    | 999     | 2067                          | 1                                   |
|               |                                                | 465125   | T      | A    | 999     | 429                           | 1                                   |
|               |                                                | 465131   | A      | T,G  | 159     | 301                           | 1                                   |
|               |                                                | 465137   | G      | A    | 171     | 326                           | 1                                   |
|               |                                                | 465154   | C      | G    | 999     | 531                           | 1                                   |
|               |                                                | 465159   | C      | G    | 175     | 702                           | 1                                   |
|               |                                                | 465166   | T      | C    | 999     | 867                           | 1                                   |
|               |                                                | 465216   | T      | A    | 999     | 2494                          | 1                                   |
| GCW_92037     | Phenylalanyl-tRNA synthetase (PheRS) beta chain core domain | 483621   | A      | G,T  | 999     | 703                           | 1                                   |
| GCW_02455     | Upstream of VlhA, cluster 3                    | 588982   | G      | A    | 999     | 1135                          | 1                                   |
| GCW_03040     | 30S ribosomal protein S4                       | 723019   | T      | C    | 999     | 6594                          | 1                                   |
| GCW_03045     | Hypothetical protein DUF3682, eukaryotic protein | 724257   | G      | C    | 999     | 7035                          | 0.9444                              |
| GCW_03335     | Upstream of VlhA family protein               | 801100   | T      | C    | 999     | 5441                          | 1                                   |
| GCW_93371     | vlhA, cluster 4                                | 816612   | G      | T    | 999     | 5428                          | 1                                   |
|               |                                                | 816905   | A      | T    | 999     | 6345                          | 1                                   |
|               |                                                | 817733   | A      | G    | 999     | 7904                          | 1                                   |
|               |                                                | 818171   | C      | A,G  | 999     | 1297                          | 1                                   |
|               |                                                | 818177   | A      | T,G  | 30.6    | 1407                          | 1                                   |
|               |                                                | 818179   | C      | T,G  | 50.5    | 1371                          | 1                                   |
|               |                                                | 818184   | T      | G    | 87.6    | 1185                          | 1                                   |
|               |                                                | 818186   | T      | A    | 77.6    | 1097                          | 1                                   |
|               |                                                | 818187   | G      | T    | 51.6    | 1038                          | 1                                   |
|               |                                                | 818188   | G      | T    | 88.5    | 1024                          | 1                                   |
|               |                                                | 818193   | G      | C    | 41.6    | 908                           | 1                                   |
|               |                                                | 818194   | G      | C    | 50.6    | 874                           | 1                                   |
|               |                                                | 818202   | T      | A    | 47.7    | 576                           | 1                                   |
|               |                                                | 818225   | T      | G    | 94.2    | 251                           | 1                                   |
|               |                                                | 818226   | G      | TA   | 95.8    | 261                           | 1                                   |
|               |                                                | 818228   | A      | G    | 106     | 331                           | 1                                   |
|               |                                                | 818255   | T      | CA   | 999     | 991                           | 1                                   |

**MIEC** – mycoplasma isolated from eukaryotic cells; **Ref** – references strain of *M. gallisepticum* S6.

10. Variants were called using the samtools mpileup command with options `-C50 -D -S`. Variants were filtered using the following criteria: (1) the depth of high-quality coverage larger than 20, (2) in average across all samples at least 50% of reads at the site supporting the call, (3) at least 5 samples have the variant, (4) a homozygous call under a diploid model. We identified nucleotide polymorphisms by comparing calls between the control genomes and the MIEC genomes.

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**Transparency document. Supplementary material**

Transparency data associated with this article can be found in the online version at: http://dx.doi.org/10.1016/j.dib.2016.12.006.

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