

**Next Generation Sequencing –  
The Role of New Sequence Technologies in Shaping  
the Future of Veterinary Science**

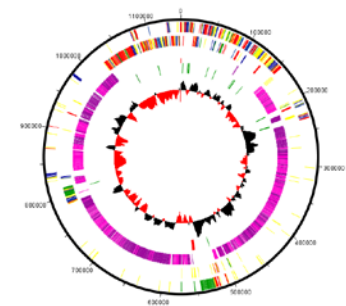
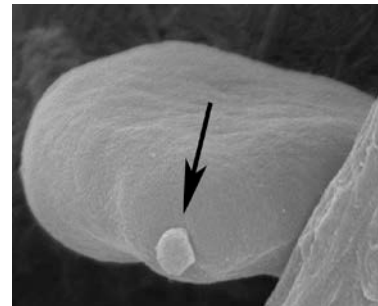
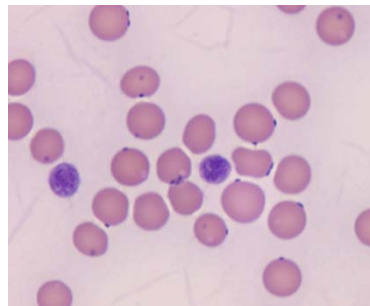
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# Feline Haemoplasmosis

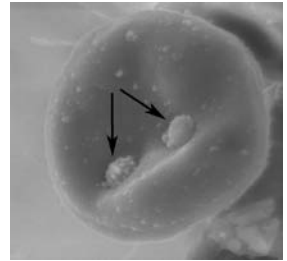
Using genome sequencing to shed light on a highly unusual genus



# 🌟 What are haemoplasmas?

- **Bacteria**

- Phylogenetically clustered within the *Mycoplasma* genus (previously *Haemobartonella* and *Eperythrozoon* genera)
- Share similarities with mucosal mycoplasmas
  - No cell wall = resistant to families of antibiotics e.g. penicillins
  - Very small genome & physical size
  - Fastidious growth requirements or are uncultivable



- **Red blood cell tropic**

- Cause of infectious anaemia in a variety of mammalian species

- **Worldwide distribution**



# Mammalian Hosts



**Zoonotic** – emerging infectious disease

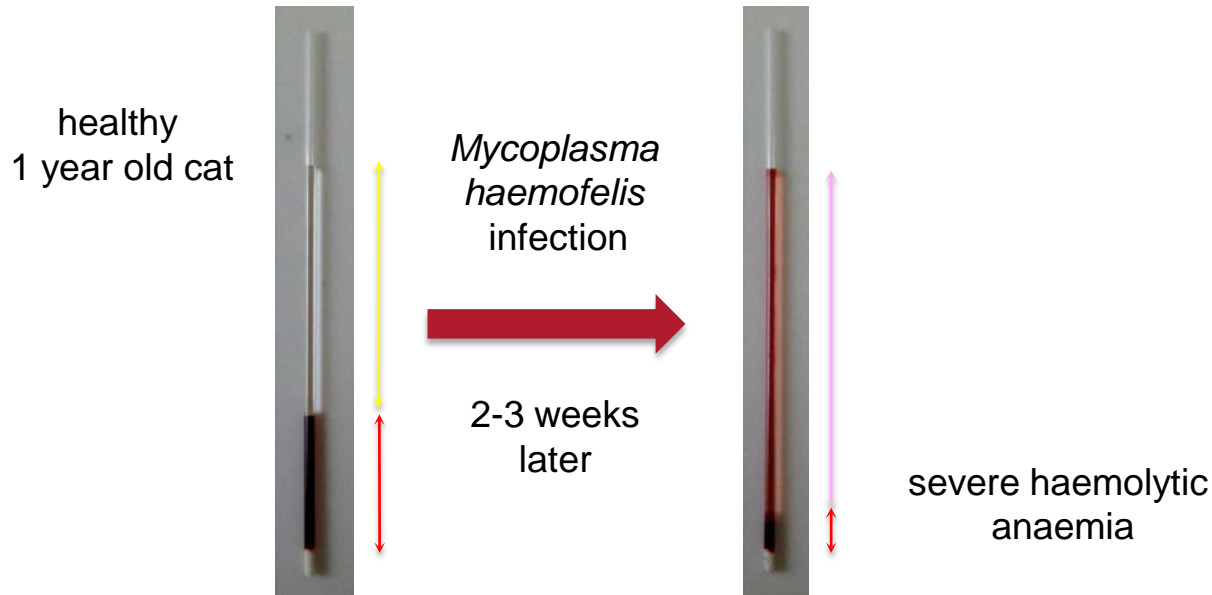


# 🌿 Feline haemoplasma infection

- Is really common!
  - *Mycoplasma haemofelis*: 0.4 – 46.6%
  - 'Candidatus Mycoplasma haemominutum': 10 – 46.7%
  - 'Candidatus Mycoplasma turicensis': 0.4 – 26%
- Can rapidly result in fatal disease

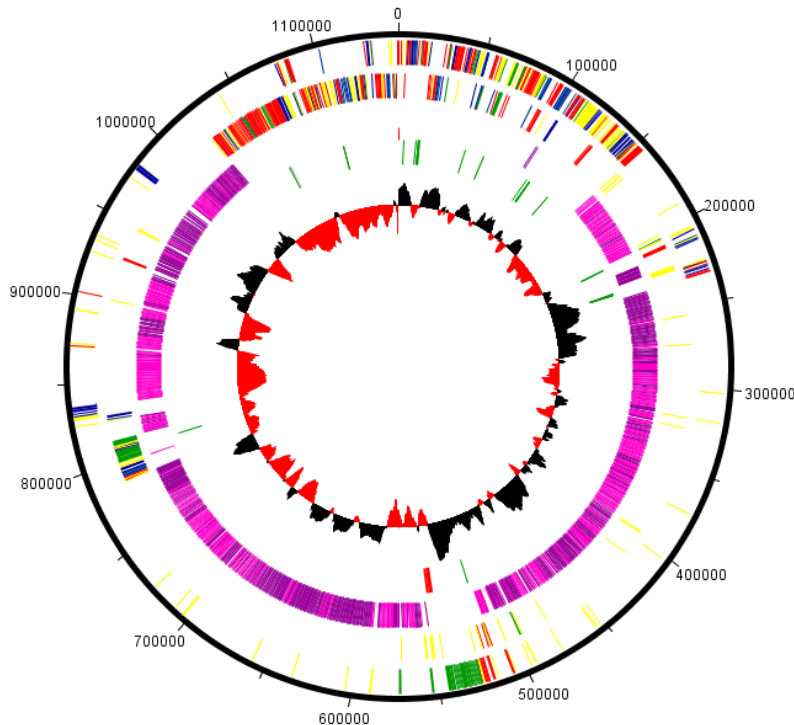


Asymptomatic healthy carriers exist



# 🌟 *Mycoplasma haemofelis* genome results

- 1.15 Mbp circular genome
- 1,580 genes including coding for 1,545 putative proteins

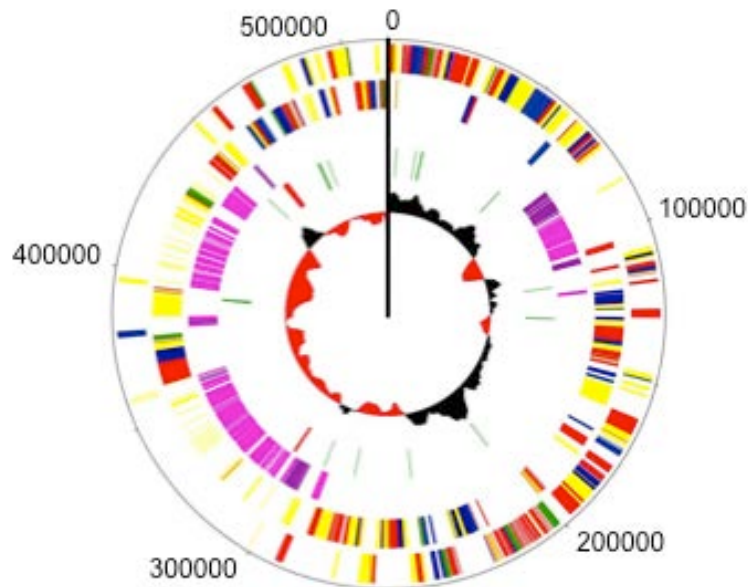


- 21% matched non-haemoplasma proteins
- 73% were repeated genes encoding unmatched hypothetical proteins (**paralogous repeats**)
- 6% were non-paralogous uncharacterised hypothetical proteins



# 🌟 '*Candidatus Mycoplasma haemominutum*' str. Birmingham

- 0.51 Mbp circular genome
- 583 genes including coding for 547 putative proteins



- 47% matched non-haemoplasma proteins
- 33% were repeated genes encoding unmatched hypothetical proteins (**paralogous repeats**)
- 20% were non-paralogous uncharacterised hypothetical proteins



# Applications of whole genome sequencing

- Predict metabolic capabilities to direct *in vitro* culture attempts
  - Carbohydrate metabolism genes limited to glycolytic pathway:  
glucose = sole energy source
  - Range of metabolic pathways identified or missing  
limited synthesis of nucleotides / co-factors (vitamins, folate)
- Compare low and high pathogenicity species
  - Pathogenic determinants
  - Vaccine candidates
  - Targets for novel diagnostic tests
- Provide data to support transcriptomic / proteomic studies







# Publications

- 1<sup>st</sup> haemoplasma genome to be published (*M. haemofelis* Langford 1)
- Reference sequences for *M. haemofelis* and ‘Ca. *M. haemominutum*’

JOURNAL OF BACTERIOLOGY, Apr. 2011, p. 2060–2061  
 0021-9193/11/\$12.00 doi:10.1128/JB.00076-11  
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Vol. 193, No. 8

## Complete Genome Sequence of *Mycoplasma haemofelis*, a Hemotropic Mycoplasma<sup>∇</sup>

Emily N. Barker,<sup>1\*</sup> Chris R. Helps,<sup>1</sup> Iain R. Peters,<sup>1</sup> Alistair C. Darby,<sup>2</sup>  
 Alan D. Radford,<sup>3</sup> and Séverine Tasker<sup>1</sup>

School of Veterinary Sciences, University of Bristol, Langford, United Kingdom<sup>1</sup>; Centre for Genomic Research, Institute of Integrative Biology, University of Liverpool, Liverpool, United Kingdom<sup>2</sup>; and Institute of Infection and Global Health, University of Liverpool, Liverpool, United Kingdom<sup>3</sup>

Barker et al. *Veterinary Research* 2011, **42**:83  
<http://www.veterinaryresearch.org/content/42/1/83>



RESEARCH

Open Access

## Molecular characterization of the uncultivable hemotropic bacterium *Mycoplasma haemofelis*

Emily N Barker<sup>1\*</sup>, Alistair C Darby<sup>2†</sup>, Chris R Helps<sup>1</sup>, Iain R Peters<sup>1</sup>, Kate J Heesom<sup>3</sup>, Christopher J Arthur<sup>4</sup>, Ben Crosssett<sup>5</sup>, Margaret A Hughes<sup>2</sup>, Alan D Radford<sup>6</sup> and Séverine Tasker<sup>1</sup>



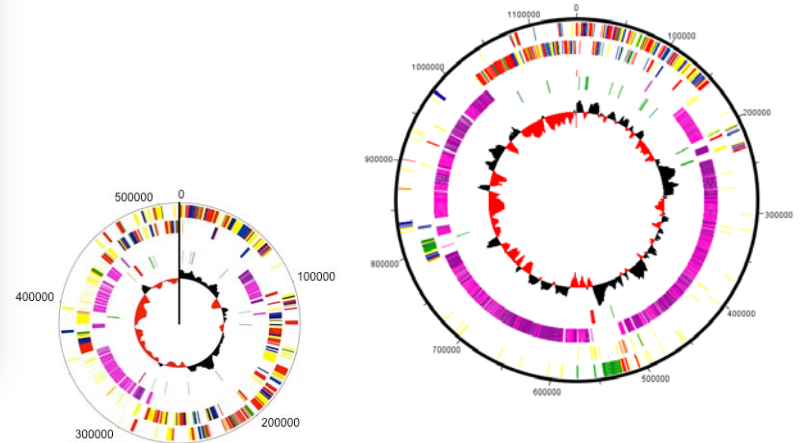
GENOME ANNOUNCEMENT

## Genome Sequence for “*Candidatus Mycoplasma haemominutum*,” a Low-Pathogenicity Hemoplasma Species

Emily N. Barker,<sup>a</sup> Alistair C. Darby,<sup>b</sup> Chris R. Helps,<sup>a</sup> Iain R. Peters,<sup>a</sup> Margaret A. Hughes,<sup>b</sup> Alan D. Radford,<sup>c</sup> Marilisa Novacco,<sup>d</sup> Felicitas S. Boretti,<sup>d</sup> Regina Hofmann-Lehmann,<sup>d</sup> and Séverine Tasker<sup>a</sup>

School of Veterinary Sciences, University of Bristol, Langford, United Kingdom<sup>a</sup>; Centre for Genomic Research, Institute of Integrative Biology, University of Liverpool, Liverpool, United Kingdom<sup>b</sup>; School of Biological Sciences, University of Liverpool, Liverpool, United Kingdom<sup>c</sup>; and Vetsuisse Fakultät, Universität Zürich, Zürich, Switzerland<sup>d</sup>

We present the genome sequence of “*Candidatus Mycoplasma haemominutum*” strain Birmingham 1, a low-pathogenicity feline hemoplasma strain.



# Acknowledgements

## **University of Bristol**

Dr Chris Helps, Dr Iain Peters, Professor Tim Gruffydd-Jones, Professor Michael Day

## **University of Liverpool**

Dr Alistair Darby, Dr Alan Radford

## **University of Zürich**

Prof. Regina Hoffmann-Lehmann, Dr Barbara Willi, Dr Felicitas Boretti, Dr Marilisa Novacco

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Pfizer Animal Health (PhD); University of Bristol (PhD & sequencing); RCVS Trust (sequencing); Wellcome Trust (samples)



# 🌿 Any Questions?



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