



## PROJECT REVIEW

<b>NAME:</b> Kate Howell		
<b>INSTITUTE:</b> University of Cambridge		<b>FULL TIME</b> Year 3
<b>TITLE:</b> New Approaches to Diagnostics of <i>Haemophilus parasuis</i> related disease		
<b>AIMS &amp; OBJECTIVES:</b>		
<ol style="list-style-type: none"> <li>Investigation of genetic determinants of serotype, as well as possible capsule and lipopolysaccharide modification/variation that would contribute to change of serotype</li> <li>Identification of putative virulence factors comparing whole genome sequence data of disease-associated and non-associated strains</li> <li>Development of molecular tests, e.g. PCR, that rapidly detect <i>H. parasuis</i> in field samples, identify the serotype and virulence type of the isolate, and indicate the likely importance of the isolate for the disease</li> <li>Validation of the newly developed PCR tests using field samples collected from commercial herds</li> </ol>		
<b>KEY MILESTONES:</b>		<b>TARGET DATE:</b>
Sequencing of entire <i>H. parasuis</i> strain collection		07/2012
Determination of separate capsule sequences in the 15 serovars of <i>H. parasuis</i>		09/2012
Publication of Capsule Paper		04/2013
Analysis of the genome sequences for pathotyping methods		12/2013
Submission of the <i>H. parasuis</i> genome paper		12/2013
Choice of potential diagnostics markers		12/2013
Validation of the potential diagnostics		07/2013
<b>PROJECT REVIEW AND COMMENTARY:</b>		
<p>The second year of my project has produced an analysis of the capsule sequences of <i>H. parasuis</i> and a list of further markers of serotype. Serotype information is important for this bacterium as the current vaccines are serotype-specific. We are now working on the draft genome sequences to try to identify putative virulence markers from both single nucleotide polymorphisms (SNPs) from conserved genes, and the presence and absence of genes in the strain collection. These can be validated by finding statistical associations between these potential markers and our clinical data that was collected for these strains. We are considering disease-associated and non-associated strains, as well as splitting these up into more refined categories that are related to the disease caused by this bacterium (e.g. systemic, respiratory and non-clinical). We hope to identify a series of potential disease-associated markers, with the aim of combining these with the serotyping markers to create a multiplex PCR that would predict both likelihood of disease and serotype of a strain. This multiplex PCR which will be validated using our strain collection, and using new samples that will be collected over the course of this year. Once the gene targets have been validated then further platforms can be considered for this diagnostic.</p>		
<b>POTENTIAL BENEFIT TO INDUSTRY:</b>		
<p>This project hopes to provide a new diagnostic with the potential to predict disease causing ability and serotype of a strain of <i>H. parasuis</i> if present. <i>H. parasuis</i> diagnostics are not available in the UK with current serotyping methods being expensive and unreliable. The availability of the information on the strains carried by UK herds would aid in the surveillance of this bacterium and disease, as well as having the potential to inform Vets and farmers on vaccination and treatment to deal with outbreaks and prevent the occurrence of outbreaks.</p>		



**SUPERVISOR:** Dr. Dan Tucker and Prof. Duncan Maskell

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**Notes from Seminar:**