Project Title: **Quantitative tissue-specific and species-specific analyses of animal feed**

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CASE partner: Animal Health and Veterinary Laboratories Agency

Introduction:

Since 1994, there has been a European-wide ban on the feeding of mammalian meat and bone meal (MBM) to cattle, sheep and goats, and this ban was extended in 2001 to the use of processed animal proteins (PAP) in feed. In Great Britain, the National Feed Audit monitors for the presence of prohibited ingredients of animal origin in feed with zero tolerance for breaches in the law. In considering the gradual lifting of the feed ban, there has been a suggested risk-based approach taking into account the availability of a reliable test to identify the species of trace ammounts of MBM in feed, and its quantitation, with a view to introducing a tolerance level for feedstuffs. The polymerase chain reaction (PCR) amplification of species-specific DNA in feed is used to detect banned ruminant constituents but the allowed presence of ruminant milk in European animal feed and the poorer performance of PCR against heated samples precludes its use as a one-test screening and quantitation method in the member states of the European Union.

The aims of this studentship are to investigate the potential of a targeted proteomics approach using selected reaction monitoring (SRM), not only for the speciation and quantitation of PAP, but to account for different source tissues and their likely alteration during the rendering processes. This approach will provide quantitative data of the specificity and sensitivity of mass spectrometry for feed contamination with MBM or mammalian PAP in animal feed.

Project Summary:

Current microscopy-based methods of species identification of MBM are limited to only separating terrestrial from non-terrestrial animal sources. DNA-based methods of identification are severely impacted upon by the rendering process and cannot differentiate between different tissues. This project seeks to further investigate proteomics-based analyses, which offer a solution to all of these limitations, with a particular focus on exploring the ability to determine tissue, species, and processing history determination.

In addition to tissue and species information using advanced proteomics methods, including quantitative SRM approaches, protein decay measurements will also be investigated using a wide range of analytical techniques including both LC and GC-MS.

The student working on this cross-disciplinary project will gain a wide breadth of training in appropriate research skills including mass spectrometry, bioinformatics, anatomy and morphological identification methods. They will have access to world-class facilities in the Faculty of Live

Sciences and the Williamson Research Centre for Molecular Environmental Science at the University of Manchester. The techniques will provide a basis for a future career in environmental science, in the industrial, government or academic/educational sectors, in a rapidly expanding research area of international importance.

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References:

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