CISBIC Project Meeting 5
Sub-project 4 - Mycobacteria

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Overview – Sub-project 4

• Coordinate the work done on mycobacteria as part of CISBIC
  • Reference to original application
  • New areas of work that mesh with ongoing work
    CISBIC collaborators
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- Modelling the glycome – use ONDEX to accelerate generation of background knowledge database in ProLog for use in Machine Learning
  - In original application as part of Sub-project 1
  - Progress to date
  - Potential for future project
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- Veterinary Laboratories Agency (VLA) key collaborator for *M. bovis*

- Model immune response in cattle infected with *M. bovis*, then drug treated and re-challenged with a different strain

- Investigate treatment strategies - determine factors that improve outcome
  - El-Khairi, Ingram (CISBIC), Hewinson, Vordermeier (VLA)
  - ODE model of T cell population dynamics during infection extended to include innate immunity, some cytokines and drug treatment
  - Will be tested using data on levels of drug detected
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- Metabolomics analysis of impact of *M. bovis* on metabonomic profiles of infected cows – biomarkers of disease?
  - Barton (CISBIC), Vordermeier (VLA)
- Original NMR and MS analysis on small set of urine samples
  - Outcome?
- Sample set extended to include further samples of urine and serum
  - Laboratory Infected, Naturally Infected, Immunized, “clear” (control) animals
  - NMR acquisition complete end September 2009.
  - Possibility to add this data to that for the immune modeling
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• **Possible future projects**

  • Modelling the response of *M. bovis* infected cattle to PE/PPE peptide antigens (time course cytokine data available)
    - El-Khairi & Sampson (CISBIC), Hewinson, Vordermoier (VLA)

  • “Integrated Functional Characterization of PPE-MPTR proteins of Mycobacterium tuberculosis.” Project grant submitted to BBSRC

  • Robertson, Sampson (Department of Microbiology), and Moon (CISBIC)

  • Includes modeling the complex temporal pattern of the immune response to a large group of TB genes