

some unstable species including small mammals and birds. A fundamental assumption in many of our studies is that the heavily infected individuals are responsible for much of the transmission but we have preliminary evidence that this may not be the case and other factors including secondary infections and host status influence the likelihood of being a shedder and a spreader.

Session

### **Symposium 3b - Host-Parasite Interactions (B)**

Time: Tuesday, 08/Jul/2008: 10:30am - 11:30am

Location: Conference Room 1

Session Chair: Dr. Charles Nunn

S8

**Tasmanian Devil Facial Tumour Disease: a parasitic clonally-reproducing mammal, which threatens to cause extinction of an iconic species**

**Hamish McCallum**

University of Tasmania, Australia

Tasmanian Devil facial tumour disease is an infectious cancer. The tumour cells themselves are the infectious agent, tumours are genetically distinct from their hosts and all tumours are derived from one, long dead individual. The tumour cell line is a parasitic, clonally-reproducing mammal. The tumour, which emerged in the mid-1990s, is transmitted by biting and continues to spread across the range of the devil, causing an overall population decline of 50% (up to 90% in affected areas). Models and current population trends project extinction within 25-30 years, with no disease-free populations remaining within five years. We estimated the rate of disease transmission in natural populations. Prevalence did not differ between male and female devils, although there were strong age-class effects. The rate of increase in prevalence differed between three sites monitored from the time of disease arrival, but was not related to host density. Prevalence remained high despite major decreases in devil density, suggesting little association between host density and transmission. Estimates of transmission rates suggest it may be possible to suppress disease by removing at least 50% of diseased animals every three months. A trial on a semi-isolated peninsula provides evidence that this strategy might be successful.

S9

**Parasitic worms to treat human disease**

**Rick Speare**

JCU, Queensland, Australia

Parasitic nematodes, particularly the pig whipworm, *Trichuris suis*, and the human hookworm, *Necator americanus*, are being used to treat human

autoimmune disease. Currently, these “treatments” are only available through research projects or as unregistered treatments. Eggs of whipworms for the treatment of inflammatory bowel disease were previously available commercially in USA with FDA approval, but not now.

What is the evidence for the hypothesis that intestinal helminths can improve clinical outcomes in autoimmune disease? The initial stimulus was that epidemiological data indicated an inverse association between the prevalence of intestinal helminths and the prevalence of inflammatory bowel disease, asthma, allergic rhinitis and multiple sclerosis between countries and also within countries over time. The next step was prospective studies that demonstrated treating helminths in endemic countries rapidly increased the incidence of allergic responses. One serendipitous case study showed that treatment of enterobiasis caused loss of colonic wall T-reg cells and was followed by the development of ulcerative colitis.

Trials on use of *T. suis* and *N. americanus* in humans with inflammatory bowel disease and allergic rhinitis marked the next intervention phase. Current research now seeks to understand host-parasite mechanisms and to isolate active compounds to bypass the use of live parasites.

Session

#### **Symposium 4 - State-of-the-Art Technologies: Proteomics**

Time: Tuesday, 08/Jul/2008: 10:30am - 12:00pm

Location: Conference Room 2

Session Chair: Prof. John P Dalton

**S10**

#### **Fractionation for proteomics**

##### **Ben Herbert**

Proteomics Technology Centre of Expertise, University of Technology,  
Sydney, Australia

If you can't solubilise, you can't analyse. This simple statement presents a major challenge on two levels, firstly the chemical diversity within even the simplest proteome cannot be captured by any single extraction and separation step, and consequently, the wealth of literature on sample preparation is equally diverse. Secondly, a relatively small number of proteins are present in high concentration, whilst the majority are expressed at less than 50,000 copies per cell. This dynamic range issue, coupled with the chemical diversity has made sample preparation and fractionation key technology development areas of proteomics. In this presentation I will briefly focus on two of the sample preparation and fractionation techniques used in our lab.

1. Enriching low abundance proteins by proteome-wide affinity using a combinatorial hexapeptide library. We have worked with derivatisation of proteins to enable a wider range of insoluble or hydrophobic proteins to be