those harbouring a C-terminal extension. We have now generated high-resolution crystal structures of several PR-1 proteins as well Tox3 and are using these dissect the basis and function of this protein interaction.

In this talk I will present our latest findings on dissecting the dual functionality of the Tox3 effector protein. Together with its function in causing cell death through its interaction with Snn3, we demonstrate that Tox3 has an important role in mediating PR-1 defence signalling and is required for disease development. These data have not only significantly advanced our understanding of necrotrophic diseases, but also provided a rare insight into the function and mechanism of the enigmatic plant PR-1 proteins.

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Parasites of land and sea: Comparative genomics of microbial eukaryotes *Perkinsus olseni* and *Theileria orientalis*.

Daniel R Bogema[1], Jerald Yam[2, 1], Melinda L Micallef[1], Sherin Alex[1], Shayne Fell[1], Jeffery Go[1], Cheryl Jenkins[1], Cecile Dang[3]

1. Elizabeth Macarthur Agricultural Institute, NSW Department of Primary Industries, Menangle, New South Wales, Australia

2. The ithree institute, University of Technology Sydney, Ultimo, NSW, Australia

3. Department of Primary Industries and Regional Development, Government of Western Australia, Perth, Western Australia, Australia

Perkinsus spp. are protozoan parasites that cause enormous losses to marine mollusc populations worldwide. In Australia, *P. olseni* has been linked to severe reductions in abalone populations. Significant and devastating reductions of NSW wild abalone populations have been observed since the 1990s, which has been attributed to a *P. olseni* outbreak (Liggins and Upston, 2010). In WA, *P. olseni*has been identified in several farmed and wild mollusc species and is considered a major threat to the state's expanding abalone industry. As part of a larger project targeting this important parasite, we examined five *P. olseni* isolates and one *P. chesapeaki* isolate from local and international sources using Illumina short-read sequencing. We additionally sequenced an Australian isolate of *P. olseni* with an Oxford Nanopore MinION to produce a reference genome. Examination of these sequences has revealed differences in genome size and identity between isolates sourced from the Southern and Northern hemispheres. Notably, analysis of sequence read coverage indicates that regions commonly targeted for diagnostic quantitative PCR assays are potentially subject to substantive gene duplications that vary considerably between isolates.

Theileria orientalis Ikeda genotype is a tick-borne haemoparasite that can cause ill-thrift and anaemia in cattle. The introduction of this pathogenic genotype to naïve cattle in the early 2000s caused significant damage to cattle producers in Australia and the South Pacific (Watts et al, 2016). We previously sequenced an Australian-sourced Ikeda plus two benign genotypes (Chitose and Buffeli) and identified differences that could establish these genotypes as separate *Theileria* species (Bogema et al, 2018). However, the short-read-derived assemblies for these genotypes were severely fragmented. To further explore the genomic diversity of *T. orientalis* in Australia, we sequenced an additional 21 isolates of *T. orientalis* Ikeda variant from diverse locations and time-points. We also used nanopore sequencing technology to greatly improve the contiguity of Ikeda, Chitose and Buffeli genome sequences.

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Potential applications of vinasse as low-cost culture media for fungi

Sandhya K Jayasekara[1], Yoshan Madusanka[2], Charmalie L Abayasekara[3], Renuka R Ratnayake[1], Asiri Weerasinghe[4]

1. Bioenergy & Soil Ecosystems Research Project, National Institute of Fundamental Studies, Kandy, Sri Lanka

2. Department of Agriculture Engineering,Faculty of Agriculture, , University of Ruhuna, Matara, Sri Lanka

3. Department of Botany, Faculty of Science, , University of Peradeniya, Kandy, Sri Lanka

4. Sugarcane Research Institute, Udawalawa, Sri Lanka

Vinasse is a distillery effluent which is produced during sugarcane molasses-based ethanol fermentation. Although numerous researches have been conducted on potential applications of vinasse, it's still underutilized in practice. This study evaluated the potential use of vinasse in preparing growth media for ethanologenic yeast and cellulolytic fungi that are used in ethanol production from sugarcane bagasse. Vinasse agar was prepared with two vinasse concentrations (50% & 100% v/v). Two *Saccharomyces* isolates (Y4 and Ysev) were serially diluted in sterile saline (0.09%) and the 10^{-5} dilution was plated in triplicate, while yeast extract peptone dextrose (YEPD) agar was the positive control. The cultures were aerobically incubated at 37 ˚C for 24 hours. 100 µl of *Trichoderma viridae* spore suspension (1×10^{8}) was inoculated in to a series of vinasse solutions (0% to 100%, 30 ml) containing sugarcane bagasse (1.0 g) as the carbon source. After one week of incubation at 30 ˚C with 120 rpm shaking, the total cellulase activity of crude enzyme extracts were determined. Park's cellulase production medium was the positive control. In vinasse agar, the highest growth of 1.13×10^{4} CFU/ml and 1.00×10^{4} CFU/ml were observed in Ysev-cultured, 100% and 50% vinasse agar media respectively. Its growth in YEPD agar (1.05×10^{4}CFU/ ml) wasn't significantly different from values at 100% and 50% vinasse. However, Y4's growth in vinasse agar was significantly lower than Ysev. In 50 % vinasse agar, 8.33×10^{3}CFU/ml of Y4 was observed which was not significantly different from 8.6×10^{3} CFU/ml growth in YEPD agar. The lowest growth was observed in Y4 as 4.87×10^{3} CFU/ml in 100% vinasse agar. The growth in vinasse was isolate-dependent. The highest total cellulase activity of *T. viridae* was observed at 50% vinasse as 1.46 FPU/ml whereas in Park's medium it was only 0.859

FPU/ml. These results show that vinasse has facilitated the growth of yeast isolates and *T. viridae* which proves the potential application of vinasse in formulating low-cost culture media for fungi.

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Chagas disease in Australia: What are the risks?

Robert L Flower[1], Elvina Viennet[1], Helen Faddy[1]

1. Australian Red Cross Blood Service, KELVIN GROVE, QLD, Australia

Introduction: Chagas disease is a zoonotic tick-transmitted parasitic disease endemic in Latin American countries. In non-endemic countries it is mainly transmitted congenitally or via blood transfusion. There is an increased risk of spread outside South America as a result of migration of asymptomatic parasitemic individuals. A current WHO initiative is to identify strategies to reduce transmission in non-endemic countries to zero. While potential vectors occur in northern Australia only two cases in immigrants from South America have been reported here. The aims of this study were to estimate the risks for congenital and for transfusion transmission of Chagas disease in Australia.

Methods: Census data (2017) on immigration to Australia from South America, births and country of birth of the mother, as well as prevalence in source countries were used to estimate the risk of congenital transmission. The risk of a parasitemic donation was estimated on the basis of reported data from Canada.

Results: Following published methodology it was estimated that 3.37% of South American immigrants were potentially parasitemic, representing 5,971 individuals in Australia, with 2,023 females of childbearing age. For those females, it was estimated that there would be 90 births annually with 4.5 exposed, potentially parasitemic newborns. Based on published data from the Canadian Blood Service, it was estimated that 199 exposed potentially parasitemic individuals are likely to present to donate blood each year, with a risk of 3.6 antibody-positive donations.

Discussion: This study suggests that the risk both of congenital transmission and transfusion transmission is very low in Australia. In addition there is universal leukodepletion of the blood supply in Australia and published data suggests that this filtration step removes the trypanosomes with the result that there is zero risk.

While in Australia identifying Chagas disease in immigrants from endemic regions of South America is an emerging challenge for general practitioners, the risks for secondary congenital or transfusion transmission here are very low.

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Inflammation and the Microbiome:A Dangerous Liaison

Alan Landay[1]

1. Rush University Medical Center, Chicago, IL, United States

The implementation of highly active antiretroviral therapy for HIV disease led to dramatic improvements in patient morbidity and mortality. That said in many HIV patients who had good CD4 T cell recovery and viral suppression there still existed persistent level of immune activation and inflammation. These changes in the immune system have been linked to persistent alterations in gastrointestinal tract permeability and microbial translocation .More recent studies have focused on the cause of these gut abnormalities and found they are linked to alterations in the gut microbiome. This presentation will provide novel data on the changes seen in the gut microbiome in HIV subjects highlighting the alterations in specific bacterial species and how the bacterial metabolic profile leads to persistent systemic inflammation especially with the loss of short chain fatty acid producing bacteria. Further data will focus on the critical changes in the tryptophan catabolic pathway and its pro inflammatory profile that contributes to non HIV co morbidities especially cardiovascular disease diabetes and neurocognitive outcomes. The additional metabolic profiles of the gut bacteria will be discussed including changes in TMAO and ceramides Data will be presented utilizing animal models to demonstrate the critical role of diet in modifying the host microbiome. The talk will conclude with a discussion of the current therapeutic paradigm for modifying the host microbiome with pre or probiotics and the prospective of fecal transplants in HIV The talk will conclude with a detailed description of the inflammatory pathways contributing to non HIV co morbidities and what novel interventional strategies are being utilized as interventional approaches. This will include studies evaluating immune based therapies targeting IL6 or IL1-beta and Jak stat inhibitors and methotrexate. In addition there will be a discussion of repurposing drugs from other therapeutic areas such as diabetes with new trials being pursued with metformin.

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Current and Future Trends in Diagnostic Microbiology

Karen Carroll[1]

1. Johns Hopkins Medicine, Baltimore, MD, United States