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Sirex noctilio is a woodwasp of Eurasian origin that was inadvertently introduced to the southern hemisphere in the 1900s and to North America over a decade ago. It attacks various *Pinus* species and cause significant mortality in pine plantations. *Sirex noctilio* is associated with a symbiotic white rot fungus, *Amylostereum areolatum*, which females inject into trees when they oviposit and which is required for survival of developing larvae. We examined the genetic diversity of *A. areolatum* isolated from *S. noctilio* and other woodwasps collected from Europe in comparison with samples from northeastern North America to determine origin of introduction(s). Multilocus genotyping of nuclear ribosomal regions and protein genes revealed two widespread multilocus genotypes (MLGs) among the European samples, one of which is present in the US. The other US *S. noctilio*-associated *A. areolatum* represented unique MLGs, although variation was primarily due to the laccase gene, with the other loci having conserved sequences. The closest relative to these US strains is a German strain with identical ITS, mtssu and tef sequences. These findings indicate multiple introductions of *S. noctilio* to North America from Europe or from Europe via South America. Our results also showed lack of fidelity between wasp hosts and *Amylostereum* species, and we found a North American woodwasp carrying an *A. amylostereum* MLG likely introduced by *S. noctilio*. These results underscore the need to study North American siricids and their fungal symbionts as *S. noctilio* continues to spread in North America.

Contributed paper. Wednesday, 8:30. **136**

Preliminary analysis of the genome sequence of *Beauveria caledonica*

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Beauveria caledonica is a pathogen of a number of insects, especially Coleoptera. Occurrence has probably been under-reported due to the morphological similarity the ubiquitous entomopathogenic fungus *Beauveria bassiana.* Recent phylogenetic studies have shown that *B. bassiana sensu lato* is really a species complex. The genomic differences between species of *Beauveria* can assist understanding of the importance of selected gene in disease and ecology of these fungi. We report on initial comparisons of the genome of *B. caledonica* strain isolated in New Zealand and *B. bassiana.* The genome was sequenced using 3 lanes of a MiSeq by NZGL (New Zealand). 15,890,840 150-bp read pairs were obtained for the 32-Mb *Beauveria* strain (~149 fold coverage). After assembly using the programme ABySS, a total of 10,951 contigs were obtained over 39 bp and an N50 of 21676, with 2827 over 500 bp. Preliminary comparisons were conducted on a range of phylogenetic, secondary metabolite and mitochondrial gene regions. Assembly of the mitochondrial genome was used to assess completeness of the coverage. The genome sequence of *B. caledonica* shows significant divergence from *B. bassiana*.

Contributed paper. Wednesday, 8:45 **137**

MALDI-TOF Mass Spectrometry: A complement to sequence-based identification technologies for major fungal entomopathogens

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Matrix-Assisted Laser Desorption/Ionization Time of Flight mass spectrometry has been tested and proven to be a rapid and inexpensive approach closely replicating the results of gene sequence-based analyses to identify species in such major entomopathogenic fungal genera as *Metarhizium* and *Beauveria*. While MALDI-TOF cannot replace PCR-based approaches for identifications or phylogenetic studies and cannot demonstrate relationships among fungi, it does appear to be extremely valuable for rapidly detecting anomalous isolates that need further detailed PCR-based study. This mass-spectrometric technique may be extremely valuable for ecological and population biology studies, as well as offering significant support for the efficient curation of large culture collections holding hundreds to thousands of isolates for which verified MALDI-TOF profiles are available. In comparison to the results obtained from the more routine analyses of (still) small numbers of individual genes, MALDI-TOF uses large numbers of cell proteins to group samples and, therefore, monitors much larger proportions of a total organismal genome; evidence will be presented that such a more complete coverage of the total genome suggest the existence of biogeographical groupings that may not be easily detected by PCR-based studies.

Contributed paper. Wednesday, 9:00 **138**

Transcriptomic study reveals *Pandora formicae* expressing pathogenicity related genes in final stages of host infection

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Pandora formicae (*Entomophthorales*, Entomophthoro-mycota) is an obligate pathogen of the common red wood ant, *Formica rufa*. The fungus, similarly to other fungi of this group, enters the host body through cuticle, where it exploits nutritional resources within the haemocoel. When the infected ant is close to death, the fungus triggers a change in host behavior, manipulating it to climb a leaf (e.g. grass) or a twig. The fungus attaches the moribund host with rhizoids, the host legs grasp around the leaf or twig and the mandibles bite to vegetation and lock. Then the host dies and soon after the fungus breaks through the cuticle with conidiophores producing asexual spores. This quick transformation requires activity of several enzymes involved in cuticular breakdown, cell wall formation, and other processes. To study this, we have constructed transcriptome libraries of the last two stages: 1) when the ant is just dead with no fungal growth outside except the rhizoids, and 2) when external conidiophores are present. This first *de novo* transcriptome of an entomophthoralean fungus, in interaction with host, provides accurate insight into the plethora of genes expressed during final stages of infection, crucial for fungus transmission and reproductive success.