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Session 1: Invasion Biology and Lessons for Biological Control

**PHYLOGEOGRAPHY AND GENETIC STRUCTURE OF THE  
INVASIVE WHEAT STEM SAWFLY, *CEPHUS CINCTUS* NORTON,  
(HYMENOPTERA: CEPHIDAE) IN NORTH AMERICA: NEW  
INSIGHTS INTO THE BIOLOGICAL CONTROL MANAGEMENT  
OF THIS PEST**

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The wheat stem sawfly, *Cephus cinctus*, which was originally recovered from wild grasses, has become a chronic pest of wheat in the semi-arid steppe region of the North American Great Plains. Traditional pest management practices are not effective, therefore biological control options are being investigated. To provide the background necessary to manage this pest with biological control, it is important to clarify the geographical history and population structure of this species so that source areas for biological control agents can be more accurately located. In addition, such study may settle a current standing debate about the origin of *C. cinctus*: is it synonymous with an Asian species, and introduced from Northeastern Asia during historical times, or is it indigenous to North America?

Due to the lack of Asian specimens, we began our study with North American samples, using cytochrome oxidase subunit I mitochondrial DNA genealogies obtained from 57 North American populations to assess the extent of the phylogeographic structure in this morphologically monotypic insect. Mitochondrial sequences uncovered 25 haplotypes, thirteen of which were present in Montana, five in Canada (Alberta and Saskatchewan), and the remaining ones in Wyoming, Nebraska, North Dakota, and Idaho. The results showed highest nucleotide diversity in Montana and absence of structuring of mtDNA variation within the wheat continuum that is represented by these two provinces of Canada and Montana. The phylogeographic pattern observed did not reflect the population bottleneck that likely would have occurred during a single recent colonization event of new regions. However, the present analysis is providing multiple inferences on the reconstruction of the invasion routes and origin of the pest that will be discussed, and a further refinement of the biological control program proposed.

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## LOCAL ADAPTATION OF A SOUTH AMERICAN PARASITOID FOLLOWING ITS INTRODUCTION TO NEW ZEALAND

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Invasion biologists and classical biological control practitioners share a keen interest in the factors which regulate: (i) the establishment of non native species in new regions; and (ii) the extent of their subsequent impacts on resident communities. The potential of a species to adapt to its new environment is expected to be a key regulatory factor, and intraspecific genetic variation is therefore thought to play a major role in the outcomes of new introductions, both purposeful and unintentional. In classical biological control, efforts to maximise the probability an introduced natural enemy to adapt to its new environment are reflected in common practices such as endeavouring to obtain a large sample of the natural enemy genetic diversity present in the native range, minimising both inbreeding and selection for laboratory fit populations during culturing, and releasing as much genetic variation as possible in the new environment. Another common practice, climate matching, seeks to minimise the evolution required for an introduced species to become locally adapted by sourcing it from locations where it may already possess climatic adaptations appropriate to the intended region of introduction. However, despite widespread acceptance that populations should evolve to become locally adapted following establishment in new regions, there has been little or no supporting evidence. Here, research is described which shows that an asexually reproducing South American insect parasitoid, *Microctonus hyperodae* Loan (Hymenoptera: Braconidae), has undergone rapid, adaptive evolution since its introduction to New Zealand for biological control of an exotic pest, *Listronotus bonariensis* (Kuschel) (Coleoptera: Curculionidae). Morphometric, protein and molecular analyses have all shown the *M. hyperodae* collected from South America and released in New Zealand comprised two genetically differentiated biotypes. Therefore, explicit comparisons were made between the parasitoid genetic variation which was released in New Zealand and that which survived. Of the two biotypes which were released together at each New Zealand site, one exhibited the highest fitness at nearly all release sites, with the other usually becoming rare or absent within two years of the release. There was a highly significant probability this change in the genetic composition of the released populations was due to selection. A population dynamics study at a New Zealand site where both biotypes were relatively common has provided a strong indication of why one has performed well, and the other poorly, at most New Zealand sites. This contribution therefore describes evidence of rapid, adaptive evolution following the introduction of a species to a new region, and demonstrates the importance of intraspecific variation to the outcomes of new introductions.