Abstracts: Theme 6 – Evolutionary Processes

Population genetics of invasive North American diffuse and spotted knapweed (Centaurea diffusa and C. stoebe)

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Knowing the possible origins of invasive weeds, whether multiple introductions have occurred, and levels of genetic variation relative to the native range is vital to conducting rigorous tests of several hypotheses that underlie classical biological control. We explore the population genetics of two Eurasian species that are invasive in North America, Centaurea diffusa and Centaurea stoebe, using variable chloroplast DNA (cpDNA) sequences and microsatellite loci. C. diffusa has lower haplotype diversity and cpDNA allelic richness in the introduced range relative to the native range, suggesting that the introduction imposed a bottleneck in population size. However, variation at microsatellite loci does not differ, and the data suggest a minimum of two introductions of C. diffusa. Three of the haplotypes of C. stoebe found in North America match haplotypes in species other than C. stoebe from the native range, suggesting the possibility of cryptic invasions. Additionally, C. diffusa and C. stoebe share several cpDNA haplotypes, including their most common haplotype, and they share most microsatellite alleles. This suggests ongoing hybridization between the species or incomplete segregation of alleles. These data can guide further exploration for the origins of these species and point out locations within the introduced range with unique and diverse genetic makeup.

Morphological and genetic methods to differentiate and track strains of Phoma clematidina on Clematis in New Zealand


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A highly pathogenic strain of the leaf pathogen, Phoma clematidina (Thüm.) Boerema, has been deliberately introduced to New Zealand from North America for biocontrol of old man’s beard, Clematis vitalba L. However, the disease levels of this biocontrol agent have been inconsistent, and it is sometimes present as a symptomless endophyte. Local strains of P. clematidina that are mildly or non-pathogenic on C. vitalba were present in New Zealand on C. vitalba and native Clematis species before initiation of the biological control programme. An understanding of how the introduced virulent biocontrol strain is interacting with the avirulent endemic strains, and how this interaction is impacting on the pathogenicity and disease expression on C. vitalba is critical to fully evaluate biocontrol efficacy of the disease. We are using morphological and genetic methods to differentiate local strains of P. clematidina from the exotic biocontrol strain. These are also being used to determine the distribution, pathogenicity and host specificity of the different pathogenic strains present in New Zealand. 'Marked' P. clematidina strains are being developed to track the fungus in the field to further understand the epidemiology of P. clematidina leaf disease on Clematis.