

including beet, Swiss chard, *Chenopodium album*, *Halimione portulacoides*, and Russian thistle. We wondered whether this nominal weevil species had cryptic host-specific populations that would be useful as biological control agents. A previous phylogeography study revealed a strong geographic structure of the mitochondrial CO1 genetic diversity with two divergent lineages in the native range, with one being restricted to Sicily and potentially associated only with *S. tragus* ssp. *kali*. The high CO1 divergence between the two lineages allowed defining lineages-specific amplification of the CO1 region. This approach revealed three morphocryptic sublineages of Sicilian origin. Two-way choice oviposition experiments conducted in 2011 confirmed the clear preference of one Sicilian sublineage for *S. tragus* ssp. *kali*, with occasional oviposition on *Bassia hyssopifolia*, *Chenopodium album* and *Suaeda taxifolia* (all Chenopodiaceae). This affordable molecular approach has provided an effective method to reveal cryptic diversity in this little explored taxon and to investigate accurately the specificity of this Sicilian sublineage. The next steps in this project are to characterize the lineage boundaries, which will require complementary insights from nuclear genes, and to examine further factors associated with pre- and postzygotic barriers.

Genetic variation in the invasive pompom weed, *Campuloclinium macrocephalum*, in South Africa

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Campuloclinium macrocephalum (Asteraceae) is native to South and Central America but is a highly invasive weed in South Africa where it is commonly known as the pompom weed. It is a target for biological control and success will depend on host specificity and biotype compatibility with the full genetic diversity of pompom weed in South Africa. We investigated the Amplified Fragment Length Polymorphisms (AFLP) marker diversity in 54 South African, 25 Argentinean and three Brazilian specimens. AFLP analyses showed a close relationship between South African and South American populations, and greatest similarity between the Argentinean population and the South African Gauteng one. All specimens showed different proportions of genetic admixture between two genetic entities but with a low net nucleotide distance of 0.115. Although there was a significant genetic variation among the populations, genetic differentiation and mean heterozygosity were low indicating low genetic diversity between the populations. These results suggest some clonal reproduction has occurred, and at least 23 clones (16 in South Africa) were present among the populations, indicating that clones were introduced to South Africa more than once. A population-assignment analysis revealed that all the South African populations studied contained at least one individual that may have migrated from the Gauteng population. The original point of entry is therefore very likely Gauteng, with Argentina as the most probable source of the South Africa invasion. Long-distance dispersal appears to have played a major role in the spread of the weed across South Africa, as indicated by a weak positive non-significant genetic versus geographic structure. The AFLP results contrast with those of our previous studies based on ribosomal DNA Internal Transcribed Spacer (ITS) regions of 52 specimens from across South Africa, 14 Argentinean and three from Brazil which suggested that all specimens might be a single clone. Nonetheless, both ITS and AFLP markers confirm the close relationship between Argentinean and South African specimens and low genetic diversity among the various populations. Candidate Argentinean biological control agents may therefore be effective on South African populations of *C. macrocephalum*, and testing of the biological control agents should include populations from all invaded provinces.

Mesquite (*Prosopis* species) biological control in Australia

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Mesquite, *Prosopis* species (Fabaceae), is an extremely hardy, long-lived, thorny weed of arid systems. Native to the Americas, it now forms extensive monocultures in Australia, Africa, the Middle East and the Asian subcontinent. In 1987, a mesquite biocontrol program was initiated in South Africa, eventually resulting in the establishment of two seed-feeding bruchid species. Biological control in Australia commenced in the early 1990s with the testing of these two seed-feeders. Four species of biological control agents have now been released in Australia, the two seed-feeders, a leaf-tying moth and a psyllid, of which only one seed-feeder and the moth appear to have become permanently established. The seed-feeder, *Algarobius prosopis* (Coleoptera: Bruchidae), was released from 1996 and is now ubiquitous. Mesquite pods are highly palatable, so are quickly consumed by vertebrate herbivores resulting in seeds being widely dispersed in dung. As a result, seed-predation rates are typically low in pods. However, seed predation continues in seeds on and in the soil and in dung, resulting in up to 80% of the remaining seed bank near mesquite trees being consumed by mid-winter. This is expected to greatly reduce seed bank longevity.