

Assessing the risk posed by transgenic virus-resistant *Trifolium repens* to native grasslands in Southeast Australia

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Introduction In Australia, comprehensive environmental risk assessments must be performed on transgenic plants (GMOs) prior to their commercial release. A key element is the determination of whether the release of a particular GMO poses any weediness threat to the environment or other agricultural systems, which can occur by means of direct invasion or by introgression of transgenes into wild populations of the same or closely related species. For transgenic pasture plants this question could be of added importance because many of these species have been selected for traits encouraging long-term persistence and competitiveness in complex plant communities (Godfree *et al.*, 2004a). In situations where native vegetation is of high conservation value, such as Australia, the potential for transgenic pasture plants to invade native plant communities must therefore be quantified and analysed within a rigorous risk assessment framework. Over the past three years we have investigated the level of risk posed by transgenic virus-resistant (VR) *Trifolium repens* (white clover) to native grasslands and woodlands in the subalpine and montane regions of southeastern Australia. We have focused on identifying the viruses present in white clover populations in the subalpine zone, on determining the floristic composition of the communities that are most at risk, and on quantifying the likely selective advantage of VR *T. repens* in these environments.

Materials and methods Our assessment of the potential weediness of VR *T. repens* has involved three phases: 1) determination of the prevalence of *Alfalfa mosaic virus* (AMV), *Clover yellow vein virus* (CIYVV) and *White clover mosaic virus* (WCIMV) in 31 wild populations of *T. repens* over a large part of the subalpine region of NSW, Australia, 2) use of surveys and plot-based coverage and biomass collection to identify communities and species that are of highest risk of further invasion by *T. repens*, and the functional significance of *T. repens* in these environments, and 3) initiation of a large-scale glasshouse and field trials comparing the performance of white clover plants both uninfected and infected by CIYVV, which is the dominant virus in the subalpine region. The field trial, which is ongoing, is being conducted at multiple spatial scales and in four distinct grassland and woodland communities.

Results Census results show that *Clover yellow vein virus* is the most abundant virus of white clover in the subalpine zone, being present in 80% of sites investigated in both grassland and woodland environments and infecting on average 18% of plants (range 0% to 59%). AMV and WCIMV were present at only one site, and in lower frequencies (Godfree *et al.*, 2004b). These data suggested that selective pressure would likely be greatest on CIYVV-resistant *T. repens* in the subalpine environment. Ecological survey work conducted on wild *T. repens* populations indicated that moist, high-fertility *Poa* grasslands and *Eucalyptus-Poa* woodlands are the most heavily invaded communities, with *T. repens* comprising up to 25% cover and being more abundant in many plots than the nearest herbaceous native species (Godfree *et al.*, 2004c). Both of these communities contain a range of native species that appear to occupy a similar functional niche to *T. repens*. Finally, preliminary data suggest that the impact of CIYVV on growth, survival and fecundity of *T. repens* can be large in the glasshouse (up to 60% reduction in some parameters), but that these impacts, while detectable, are more transient and of smaller magnitude in native plant communities, primarily a result of the dominant climatic and topo-edaphic impacts on white clover in subalpine environments.

Conclusions Our work to date indicate that *T. repens* is a significant component of subalpine plant communities in south-eastern Australia, and that wild populations contain large amounts of *Clover yellow vein virus*. Given the presence of both host and pathogen in threatened plant communities in this region, development of an understanding of the importance of CIYVV in limiting the size of white clover populations in these environments is an important step in the ecological risk assessment of VR *T. repens* prior to commercial release. It is hoped that with further investigation, this will function as a model system and thereby provide insights into the functioning of host-pathogen relationships for a wider range of transgenic pasture species.

References

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