

Genetic analysis of willow dispersal in Victoria

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Research scope

This project will use high-throughput DNA analysis of adult and seedling willow genotypes to: 1) examine historical patterns of willow movement across Victorian catchments through the analysis of the geographical genetic structure of established populations of these species and; 2) determine current patterns of seed dispersal and pollen movement by using parentage and paternity analysis to ascertain the origin of invading seedlings and thus directly measure dispersal distances.

Objective 1) Genetic structure of willow populations: The study will initially focus on a large-scale analysis of the genetic diversity of two selected species; *Salix cinerea* (pussy willow) and *S. × rubens* (basket willow) across their range in Victoria. These two selected species have differing reproductive strategies with pussy willow spreading mainly by seed (sexual reproduction) which is wind dispersed and therefore has the potential to travel significant distance between river catchments. Basket willow alternatively is thought to spread by vegetative (asexual) reproduction with branches or twigs breaking off and moving downstream with the water flows before being caught and rooting, effectively spreading only downstream along watercourses. These contrasting strategies for reproduction require different control strategies and differing management scales.

Objective 2) Direct analysis of current invasion dynamics: The second phase is a more locally extensive and detailed study of genetic structure for a smaller selected number of key Victorian river systems. It will look at the frequency and pattern of seed and pollen movement within and across catchments by genotyping seedlings and identifying the most likely source populations. This information will again be compared to the breeding systems to identify any correlation between genetic structure along river systems and the reproductive strategies.

As well as identifying the scale of seed and pollen movement between populations using molecular markers, the project will also undertake exclusion experiments to determine if pollen is being exclusively spread by insects or if wind pollination is occurring and if so, to what extent this is occurring.

Results to date

The pilot study undertaken with East Gippsland Catchment Management Authority found a considerable amount of genetic variation between populations. The critical implication of the study was that the strategies for the control of willow populations in south-eastern Australia should be scoped at the landscape level, rather than focusing on specific catchments. Molecular genetic markers can identify the range of catchments that should be included in these regional strategies.

Implications for management / research gaps

The results from this study will provide information on the historical invasion patterns, current reproductive strategies and extant patterns of willow dispersal in terms of the scale of seed and pollen movement and its relationship to landscape structure. These data will directly assist land managers responsible for controlling willows to develop the most effective eradication strategies by: 1) identifying the most efficient geographical scale of control that will minimise the likelihood of reinfestation; 2) providing more quantitative analysis of catchments that are most at risk of invasion in the future.

Related publications

How do invasive willows move across the Australian landscape? Go to:

<http://www.weeds.org.au/WoNS/willows/docs/>

[How do invasive willows move across the Australian landscape.pdf](#)

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