

# Managing the noogoora burr complex: Biological control and taxonomic advancement

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## Background

Species in the Noogoora burr complex are problematic weeds in primary production, the environment and to the Australian community.

Nationally significant impacts on productivity and profitability are experienced in summer cropping (e.g. cotton, sorghum, maize and pulse industries), in pastures and in rangelands (particularly for wool production). Noogoora burrs are also hosts of insect pests and pathogens such as *Verticillium* wilt (*Verticillium dahliae*), an important crop disease.

They are a serious threat to riverine ecosystems, habitats and native species, impacting 36 vegetation communities, including 11 'Endangered Ecological Communities' in NSW alone. While a range of herbicides control Noogoora burrs in cropping systems, all cause off-target damage and are inappropriate for use in sensitive situations such as the riverine areas.

## What are the species in the complex?

Four species comprising the Noogoora burr complex have been taxonomically described in Australia (*X. cavanillesii*, *X. italicum*, *X. occidentale* and *X. orientale*), while only a single species (*X. strumarium*) is defined in the Americas, the source of the burr. In practice, intra- and inter-specific variation exists, with some plants not readily conforming to any of the published taxonomic descriptions.

## What are you researching?

The NSW Department of Primary Industries (NSW DPI) and Cotton Research and Development Corporation (CRDC), in partnership with Murrumbidgee Irrigation and the University of Queensland, received funding under the Control Tools and Technologies for Established Pest Animals and Weeds competitive grants program.

The two year project (2017-2019) aimed to develop a bioherbicide for species and/or hybrids within the Noogoora burr species complex from an existing, naturally occurring fungal pathogen agent (*Alternaria zinniae*). Sampling and testing also determined if all species in the Noogoora burr complex were hosts of *Verticillium dahlia* – currently a pathogen of great concern to the cotton industry. Bio-herbicide development is currently constrained by taxonomic confusion within the complex. As such, DNA sequencing helped to clarify the current recognised distinctions between the complex and hybrids found in the field to ensure the efficacy of the bioherbicide agent against the species.



### What have you found?

Through DNA barcoding and next generation sequencing the project identified that the Noogoora burr complex consists of two distinct genetic groups and a wide range of hybrids, not the four morphologically distinct species originally thought by scientists (*X. cavanillesii*, *X. italicum*, *X. occidentale* and *X. orientale*). One group consisting of *X. occidentale* and *X. orientale* morpho-species, and the second group consisting of *X. cavanillesii* and *X. italicum* morpho-species. These results have direct implications for how, in future, the taxonomic community treats the Noogoora burr complex in Australia and taxonomic keys used for their identification.

### Why is this important?

The development of a new complex emulsion technique has the potential to deliver an environmentally friendly bioherbicide alternative for the integrated management of Noogoora burr species. The use of the complex emulsions also can be potentially extended to other pathogen/weed combinations to achieve the safe control of other established weeds in primary production and environmental ecosystems.

Determining whether all *Xanthium* species were hosts for the pathogen that causes Verticillium wilt in cotton has resulted in innovation in the techniques developed in this project and should greatly assist with detecting the host status of a range of other weeds. Due to the low infection of Noogoora seeds per plant we had a very low recovery of the pathogen when using traditional isolating techniques therefore it was essential to utilise molecular techniques to detect *Verticillium dahliae*.

NSW DPI molecular specialists Toni Chapman and John Webster from EMAI used a TissueLyser II to assist with molecular tests. All species of Noogoora Burr complex were identified as hosts of a number of *Verticillium dahliae* strains. This raises further questions around the potential for some of these

strains to be present in other weeds, and in cotton. The techniques developed in this project will enable these possibilities to be further explored in future research.

### Where do I go for more information?

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