

## Is dieback in invasive plants due to a loss of protective microorganisms, or encounters with new pathogens?

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**Summary** *Parkinsonia aculeata* L. (parkinsonia) is a Weed of National Significance. It impacts heavily on biodiversity, livestock and pasture management across northern Australia. Dieback in some parkinsonia populations has resulted in levels of control not previously achieved by other methods, and therefore raises the possibility of biological control of parkinsonia, using dieback. The composition of parkinsonia's microbial endophyte communities, or 'phytobiome', suggests that multiple endophyte species may be responsible for dieback. Since dieback does not occur in the native range, we hypothesized that native-range parkinsonia hosts a different phytobiome that 'protects' its host against dieback-causing agents, whereas introduced parkinsonia does not. Hence, dieback may be caused by pathogens encountered by invasive parkinsonia upon its introduction to Australia.

To test this hypothesis we compare microbial DNA from healthy parkinsonia sampled in the USA, to DNA from healthy and dieback-affected parkinsonia

in Australia. Using Next-Gen Illumina sequencing we identified species of fungal, bacterial and archaeal endophytes that are unique to the country from which they were sampled. We also found evidence that some of these endophytes are vertically transmitted, but others are not, suggesting that parkinsonia may have lost potentially protective endophytes upon introduction to Australia, thereby reducing its capacity to fight generalist pathogens that cause dieback.

This study describes a novel way to analyse multiple microbial taxa using a single high-throughput method. Although many plant diseases are caused by single putative pathogens, we've shown that parkinsonia dieback may be caused by interactions between endophyte communities. These results will lead to further insights into the biological control of dieback-affected weeds in Australia.

**Keywords** Endophytes, fungi, bacteria, Illumina sequencing, native-range, phytobiome.