

Genomics, lineages and phenotypes: Investigations into the stability of the *Puccinia chondrillina*–*Chondrilla juncea* pathosystem in Australia

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Summary *Puccinia chondrillina* (Skeleton weed rust) was the first deliberate release of a fungal pathogen for biological control of an invasive weed. Over three decades four strains of *P. chondrillina* were released in Australia targeting the narrow and intermediate leaf forms of the agricultural weed *Chondrilla juncea* (Skeleton weed). Strain IT32, released in 1971 showed exceptional impact against the narrow-leaf form while strains TU21, IT36 and TU788 released in the 1980s and 1990s against the intermediate leaf-form exhibited poor to moderate impact. Unfortunately no strains of *P. chondrillina* have been identified which are pathogenic and specific to the broad-leaf form of *C. juncea* in the field. It is unknown which strains of *P. chondrillina* have persisted in Australia since their release or the possible effect that evolutionary forces may have exerted on their genotype to shape

their populations or affect their pathogenicity. In this study we employ whole genome sequencing of *P. chondrillina* isolates collected in 2007 and 2016, and of stored urediniospores representing the original released strains, to determine the lineage of contemporary isolates and identify genetic changes that may have occurred over time. In addition, the pathogenicity phenotype of each contemporary isolate is determined through inoculations on the three forms of *C. juncea*. The hypothesis of little genetic change of *P. chondrillina* in Australia will be tested. These results will provide valuable information on the stability of the *C. juncea* – *P. chondrillina* pathosystem and possibly shed additional light on the lifecycle of skeleton weed rust in Australia.

Keywords Skeleton weed, Pucciniales, fungal genomics, pathogenicity phenotype.