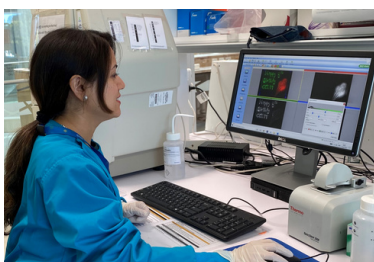


Ascochyta blight of chickpea and lentil

Project description

The rapid emergence of aggressive ascochyta blight (AB) isolates in Australian chickpea and lentil crops requires researchers' urgent attention to limit crop yield reduction for growers.

This project aims to identify novel sources of resistance and integrate these into chickpea and lentil breeding programs where our researchers will use traditional genetic mapping as well as genomic prediction approaches. Furthermore, annual isolate collection of *A. lentis* nationally and *A. rabiei* isolates in WA is undertaken to monitor for changes in pathogenicity/aggressiveness on current lentil and chickpea varieties. The development of a diagnostic in-field toolkit will assist in identifying the levels of the *A. lentis* pathotypes and aid varietal selection for growers. Our researchers will also work to generate a pan-genome for these Ascochyta pathogens and identify novel effectors to assist the industry in developing broad genetic resistance traits in new varieties that are well-understood. For example, the purification of *A. lentis* avirulence effector will generate a tool to screen lentil germplasm, breeding lines and varieties for the presence of the corresponding resistance gene that interacts with this avirulence gene.



Our team

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Key achievements

Using cutting-edge sequencing technologies, complete reference genome assemblies have been generated for Australian *A. rabiei* and *A. lentis* isolates, which can be viewed and interrogated on the [Apollo genome browser](#).

Our team has discovered the first avirulence gene for an Ascochyta pathogen in *AlAvr1* of *A. lentis*. *AlAvr1* triggers a defence response in lentils that carry a corresponding resistance gene that recognises it, leaving certain lentil varieties asymptomatic. Furthermore, in Australia this fungal gene can be one of two forms, and the form type will determine whether it triggers the defence response or not and allows us to distinguish *A. lentis* pathotype 1 from pathotype 2 and we have developed a diagnostic marker.

Our team has generated AB strains with genes knocked out (turned off), which will enable us to determine the role of these genes in pathogenicity. This will be done by inoculating these strains on chickpea/lentil plants and comparing them to the regular (wild-type) strain to see if the knock-out has become less pathogenic.

Our researchers screened a set of germplasm selections, breeding lines and varieties and identified novel sources of AB resistance on par with current resistance sources in chickpeas and lentils. Understanding the genetic control of these resistance sources is focus of current research and will aid chickpea and lentil breeding programs in delivering varieties with improved AB resistance.

