

# Current knowledge on pathogenicity of *Ascochyta rabiei* and implications for disease and risk management

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## Key words

chickpea, *Ascochyta* blight, *Ascochyta rabiei*, pathogenicity, disease and risk management

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## Take home message

- Pathogenicity of *Ascochyta rabiei* isolates has increased significantly over the past 5 years leading to reduced resistance of current chickpea varieties
- Rainfall frequency and total amounts together with numbers of days at specific temperatures during the cropping season are important predictions for the emergence of highly aggressive isolates
- The [Asco Dashboard \(http://bit.ly/asco-dashboard\)](http://bit.ly/asco-dashboard) is an online tool for interrogating the presence and pathogenicity of *A. rabiei* isolates in specific locations and offers a scenario-based risk-prediction tool
- Reporting disease incidence and assisting with sample and metadata collection is crucial for monitoring the populations and improve risk prediction accuracy
- Adhering to disease-free seed and clean equipment practices and biosecurity guidelines is imperative to reduce the risk of introducing highly aggressive isolates between regions.

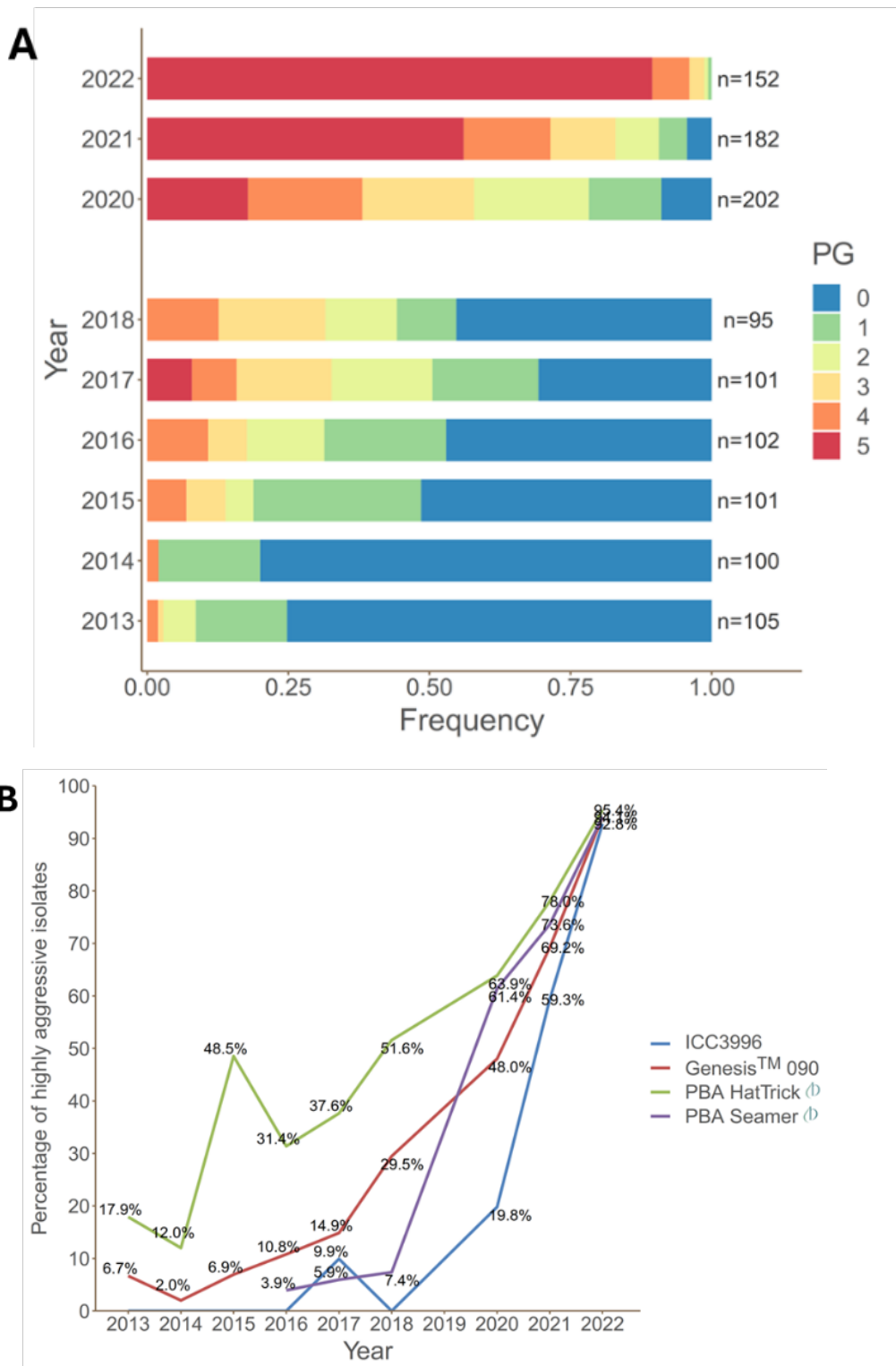
## Background

Research on the Australian *Ascochyta rabiei* population over the past ten years has established a comprehensive isolate database (with 1,450 isolates), provided insights into the population structure and identified trends in adaptation and possible evolution across all chickpea growing regions. Most recently, sequencing-based genotyping technologies have identified and compared SNP loci among isolates collected across years, locations and host genotypes. This has enabled the accurate assessment of the molecular diversity and the population structure of *A. rabiei* in Australia over time<sup>1-4</sup>. However, despite recent advancement in genomic approaches and methods, to date, little is known about avirulence or effector sequences and their role in conferring virulence or pathogenicity in *A. rabiei*.

## Findings

The pathogen in Australia appears to be clonal with a single mating type detected and low genetic diversity. However, sufficient diversity was uncovered to provide a range of pathotypes, some able to overcome the best host resistance sources. This is evidenced by the erosion of more recently released 'resistant' genotypes and the discovery of unique clusters of highly aggressive isolates within specific locations that potentially pose a major and ongoing threat to the Australian chickpea industry (Figure 1). The risk from local micro-evolution of highly

aggressive isolates (PG 4-5) is significant when combined with cross-region gene flow caused by cropping activities.



**Figure 1.** Summary of *Ascochyta rabiei* aggressiveness between 2013 and 2022.

A. Distribution of isolates by Pathogenicity Group (PG) classification (cumulative disease response to the set of host genotypes) in each year. B. Frequency of highly aggressive isolates (PG 4-5) on each chickpea host genotype each year. These figures were retrieved from the Asco Dashboard on June 26, 2024.

The Asco Dashboard, an online comprehensive *A. rabiei* isolate dashboard that stores pathogenicity and dispersal patterns within and between geographical locations was developed to make this information readily accessible to growers. This tool was designed to aid in disease risk management planning by allowing growers and agronomists to interrogate where and when the most highly aggressive isolates are collected, which cultivars they are collected from and if the frequency of highly aggressive isolates is changing in their local region.

Meanwhile, the information hosted on the dashboard, including host genotype, geographical location, climatic and farming practices data was assessed for individual or combined correlation with isolate aggressiveness at the time and location of collection. This provided a better understanding of the major external factors that influence isolate aggressiveness and was used to develop a model and scenario-based risk prediction tool to inform on the potential emergence of highly aggressive isolates and assist in IDM decision making.

Genetic and molecular analysis could not identify clear association between single-point mutations and the increased aggressiveness observed in the Australian *A. rabiei* population. Instead, a transcriptomics approach identified differences in the expression of genes that were highly associated with isolate pathogenicity. The mechanisms that regulate the expression of these genes should be further explored to validate their function and role in the pathogenicity of *A. rabiei* and to develop isolate aggressiveness biomarkers for future population screening. Such tools would enable growers to pre-survey their inherent and local *A. rabiei* populations for presence and frequency of highly aggressive isolates. This would enable decision making about timing and location of planting, as well as timing and type of pre-emptive and within-crop chemical control strategies.

## References

1. Sambasivam, P. *et al.* Evidence of recent increased pathogenicity within the Australian *Ascochyta rabiei* population. *bioRxiv* 2020.06.28.175653 (2020) doi:10.1101/2020.06.28.175653.
2. Mehmood, Y. *et al.* Evidence and Consequence of a Highly Adapted Clonal Haplotype within the Australian *Ascochyta rabiei* Population. *Front Plant Sci* **8**, (2017).
3. Bar, I. *et al.* Current population structure and pathogenicity patterns of *Ascochyta rabiei* in Australia. *Microb. Genom.* **7**, (2021).
4. Vaghefi, N. *et al.* Population-level whole genome sequencing of *Ascochyta rabiei* identifies genomic loci associated with isolate aggressiveness. 2024.04.02.587819 Preprint at <https://doi.org/10.1101/2024.04.02.587819> (2024).

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