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Chickpea Ascochyta – is the pathogen changing?

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Ascochyta in 2014 chickpea crops

Ascochyta blight (AB) was first found in the GRDC Northern Region at North Star on 2 July as a small (2–5 plants) focus in a crop of Flipper®. By the end of September, AB had been detected in 62 of 332 crop inspections (18.7%), considerably more than was found in 2013 (5/280 crops, 1.8%) and 2012 (11/213 crops, 5.2%). Most of the 2014 cases were in NSW but four were confirmed in Qld, including one crop of PBA Boundary® at Toobeah, west of Goondiwindi. The NSW cases covered an area from Yallaroi in the east, west to Mungindi, Nevertire and Tullamore and south to Forbes.

Four cases of AB were found in July, with the majority detected in August (25) or September (33) with none in October.

Two cases involved Flipper®, two PBA Boundary®, one PBA Slasher®, one Yorker® (that the grower believed was PBA HatTrick®) and the rest were PBA HatTrick®. This distribution of cases by variety reflects the fact that in 2014, PBA HatTrick® was by far the predominant variety grown in north central NSW, northern NSW and southern Queensland.

Infected crops had typical symptoms of AB including ghosting leaf lesions, mature leaf lesions and stem lesions. In most cases, the disease was limited to isolated areas in the paddock but in several crops the infection was widespread with foci being detected every 10–30 seconds of walking across the paddock. In these crops, stem breakage was common. In spite of the incidence of AB infection and severity of symptoms, all growers were able to manage the disease with judicious use of chlorothalonil fungicides (up to four applications in the worst cases). All growers believed the disease had little if any impact on final yield although it did impact on production costs.

Why was there more Ascochyta in 2014 than in the previous two seasons?

Although total winter crop rainfall was well below average across the region, June and July were above average in southern parts (57.4 mm and 34 mm respectively at Trangie; 57.6 mm and 55.6 mm at Dubbo). At Moree and Goondiwindi, June/July rain was 23.8/5.0 mm and 29.2/15.4 mm, respectively. The AB fungus requires the impact energy of raindrops to disperse its conidia so it has to rain for the disease to establish. That is, dews alone will not produce the initial infection. However, the pathogen only needs 3–6 hours of leaf wetness to infect; a few mm of rain falling late on a winter's day or at night will satisfy that requirement. Although Moree Airport only recorded 23.8/5mm in June/July, the AWS at Kindee (north east of Moree) recorded 44.0/11.4 mm for the same period with 5/2 days >1.0 mm respectively. Kindee is only a few km from a local epidemic of AB in several PBA HatTrick® crops. That the disease did occur over such a broad geographical area is evidence that sufficient rain fell to initiate and spread infections. As well as favourable weather conditions, another explanation for the amount of AB in 2014 is varietal impurity. That is, not every plant in a paddock of PBA HatTrick® was actually a PBA HatTrick® plant. Varietal purity is a concern in the GRDC Northern Region and the presence of plants of susceptible varieties in a crop of PBA HatTrick® would increase disease pressure on bona fide PBA HatTrick® plants.

Key findings

Ascochyta blight occurred in more chickpea crops in the northern region in 2014 than in 2012 and 2013 combined. Most infected crops were PBA HatTrick® but this is also the most commonly grown variety.

Infections in 2014 arose from inoculum in diseased chickpea stubble and infected volunteers.

Research confirmed the fungus varies in its pathogenic ability but there was no evidence it has changed in response to the widespread cultivation of PBA HatTrick®.

In localities where Ascochyta was found in 2014, growers are advised to apply an early season preventative fungicide to all 2015 chickpea crops including PBA HatTrick®.

***Table 1**. Pathogenicity ranking of 35 isolates of Phoma rabiei collected in 2013 (location and variety collected from) on three chickpea genotypes, ICC3996, Genesis™ 090 and PBA HatTrick(ϕ)*

Location	Variety	ICC3996	Genesis™ 090	PBA HatTrick(ϕ)
North Star	Flipper(ϕ)	Low	Low	Low
North Star	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	High
Tooraweenah	HatTrick(ϕ)	Low	Low	High
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Medium
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Medium
Tooraweenah	HatTrick(ϕ)	Low	Low	High
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Medium
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Tooraweenah	HatTrick(ϕ)	Low	Low	Low
Garah	HatTrick(ϕ)	Low	Low	Low
Garah	HatTrick(ϕ)	Low	Low	Low
Garah	HatTrick(ϕ)	Low	Low	Low
Garah	HatTrick(ϕ)	Low	Low	High
Garah	HatTrick(ϕ)	Low	Low	Low
Garah	HatTrick(ϕ)	Low	Low	Low
Garah	HatTrick(ϕ)	Low	Low	Low
Garah	HatTrick(ϕ)	Low	Low	Low
Garah	HatTrick(ϕ)	Low	Low	Low

Where did the inoculum come from?

The AB pathogen, *Phoma rabiei* (previously called *Ascochyta rabiei*) survives on volunteer chickpeas, on chickpea residue and on seed. Volunteers with AB were reported in fallows and nearby wheat crops. We tested some of the seed used to plant the crops in the above-mentioned local epidemic. Five thousand seeds (untreated) were surface sterilised and plated to detect any seed borne infections – none were found. This does not exclude seed as a source of primary inoculum, but together with the absence of any lesions on pods of 2012 and 2013 crops, it presents a robust case against seed as the main source of inoculum for the 2014 infections.

We believe the main source of inoculum was infected chickpea residue from 2012 and 2013 crops. We propose the dry summers of 2012–13 and 2013–14 slowed residue breakdown both *in situ* and in the following year's chickpea paddocks and that this provided inoculum for infection of summer volunteers and the 2014 crop.

Has the Ascochyta pathogen changed?

The short answer is we don't yet know. Why? Because we have limited data on pathogenic variability in the pathogen population. However, as a population of living individuals (isolates), we should expect it to change. The little research that has been done shows that there are differences in pathogenicity among isolates. Table 1 classifies 35 isolates of *Phoma rabiei* collected from northern NSW chickpea crops in 2013. Isolates were rated low, medium or high based on their ability to cause disease on ICC3996 (R), Genesis™ 090 (R) or PBA HatTrick$^{\phi}$ (MR). We conclude that none of the isolates caused severe disease on the two resistant genotypes and that most also did not cause severe disease on PBA HatTrick$^{\phi}$ either. Three caused severe, and three caused moderate, disease on PBA HatTrick$^{\phi}$ (Table 1). This establishes that the pathogen varies in pathogenicity.

Another way of assessing pathogenic variability in the AB pathogen populations is to determine the latent period for individual isolates. The latent period is the time from infection to the development of pycnidia, the small dark fruiting bodies that develop in the leaf and stem lesions. Six isolates representing a sub-set of the pathogen population in eastern Australia were evaluated in a growth cabinet (20 °C/15 °C 12 h day/12 h night) on four chickpea genotypes ICC3996 (rated R, coded ICC), Genesis™ 090 (rated R, coded GEN), PBA HatTrick$^{\phi}$ (rated MR, coded HAT) and Kyabra$^{\phi}$ (rated S, coded KYB). There were eight replicates (pots) for each of the 24 genotype by isolate combinations. The latent period was estimated by survival analysis with the status of a pot being whether pycnidia had or had not developed. For each pot, the data is the latent period or the day of last observation if pycnidia had not developed. Details of the isolates are:

- T12437 – 2010, Darling Downs, QLD, highly pathogenic on PBA HatTrick$^{\phi}$ and ICC3996, moderate on Genesis™ 090 (glasshouse)
- 10TEM005 – 2010, Temora, NSW, highly pathogenic on PBA HatTrick$^{\phi}$ and ICC3996, moderate on Genesis™ 090 (glasshouse)
- 13MUR002 – 2013, Murtoa, VIC, highly pathogenic on Genesis™ 090 (field and glasshouse)
- 13DON002 – 2013, Donald, VIC, highly pathogenic on Genesis™ 090 (field and glasshouse)
- TR6415 – 2014, Yallaroi, NSW, highly pathogenic on PBA HatTrick$^{\phi}$ (field)
- 10MEL001– 2010, Melton, SA, extremely low pathogenicity

Latent period (LP) varied with isolate and genotype (Table 2). All isolates had the shortest LP on the most susceptible entry, Kyabra$^{\phi}$ (KYB) and the longest LP on the most resistant entry, ICC3996 (ICC). The isolate from Yallaroi (TR6415) had

the shortest LPs on all genotypes and we interpret this as meaning that isolate was the most aggressive in the experiment. This LP experiment complements the pathogenicity work and confirms variability does exist in the pathogen population. However, it does not prove that it has changed in response to the widespread cultivation of PBA HatTrick$^{\phi}$.

***Table 2**. Mean latent period (days) of six* Phoma rabiei *isolates on six isolates of* P. rabiei *on four chickpea genotypes, ICC3996 (ICC), Genesis™ 090 (GEN), PBA HatTrick$^{\phi}$ (HAT) and Kyabra$^{\phi}$ (KYB).*

Genotype	Isolate	Latent period	SE (mean)
GEN	T12437	7.1	0.1
HAT	T12437	6.8	0.2
ICC	T12437	7.8	0.2
KYB	T12437	6.0	0.0
GEN	10TEM005	7.3	0.2
HAT	10TEM005	7.0	0.0
ICC	10TEM005	7.9	0.1
KYB	10TEM005	6.0	0.0
GEN	13MUR002	7.4	0.3
HAT	13MUR002	6.9	0.2
ICC	13MUR002	8.0	0.0
KYB	13MUR002	6.0	0.0
GEN	13DON002	6.1	0.1
HAT	13DON002	6.4	0.2
ICC	13DON002	7.3	0.2
KYB	13DON002	6.0	0.0
GEN	TR6415	6.0	0.0
HAT	TR6415	6.0	0.0
ICC	TR6415	7.1	0.1
KYB	TR6415	6.0	0.0
GEN	10MEL001	7.0	0.3
HAT	10MEL001	6.9	0.1
ICC	10MEL001	7.9	0.1
KYB	10MEL001	6.0	0.0

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