Disease dynamics in a changing farm environment

Dr Rohan Kimber and Dr Jenny Davidson, SARDI

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Key Findings:

- A combination of old and new technology is being used to detect and analyse airborne fungal spore patterns affecting cereal and pulse grain crops.
- Intense spore showers were detected for blackspot of field pea and NFNB of barley, but negligible for YLS of wheat, at the experimental site at Hart during the 2013 season.
- Spore dispersal patterns of blackspot of field pea fitted with Blackspot Manager predictions.

Why do the trial?

To understand growth patterns of yellow leaf spot (YLS) (*Pyrenophora tritici-repentis*) on wheat and net form net blotch (NFNB) (*Pyrenophora teres f teres*) on barley in relation to a changing farming environment. The timing of release, dispersal patterns and environmental triggers for dispersal of spores from primary and secondary inoculum sources will form the basis for disease modelling and forecasting, potentially assisting in the development of improved strategies for fungicide application as well as managing inoculum sources. The development of molecular tests for detection of species-specific fungal spores is enabling us to combine simple spore trapping devices with new diagnostic techniques. This allows detailed examination of disease dynamics over the growing season and analysis of the relationship between spore release and climate drivers.

How was it done?

The timing and intensity of spore release for YLS and NFNB were monitored from infested wheat and barley stubble, respectively. A model pathogen, blackspot (*Didymella pinodes*) of field pea, was included for comparative purposes. Monitoring was conducted in the field at five geographical locations as part of an environmental transect for climate: **Urrbrae** (Waite Campus), **Belair** (Adelaide Hills), **Hart** (FD site), **Port Germein** and **Orroroo**. These locations were selected to reflect differences in growing season climates. At each site, infested stubble of each host/pathogen was set out within a 3 x 3 m grid array; the layout was identical at each site. A Burkard volumetric spore trap was placed within the centre of the grid, to capture air- and splash-borne spores. The trap captured air-borne particles over a total 30 week monitoring period from April 11th to November 6th, 2013. Samples were collected in 30-36 day cycles and returned to the laboratory, desiccated and stored at 22^{o}C.

Analyses of the 2013 data are in progress. At the end of the season, a daily segment of tape (9.5 x 9.5 mm) was excised for every 3 trapping days throughout the 30 week period to allow a dot-point analysis of spore release over time. The quantity of spores deposited on these selected samples were detected using molecular assays specific to *P. tritici-repentis, P. teres f teres* and the blackspot complex developed by SARDI's Root Disease Testing Service (RDTS). These results will be validated with trap plant data collected at the Waite Campus and correlated to climate variables (eg. temperature and rainfall).

Results and Discussion

Tapes have been processed and molecular assays performed on samples from the Hart spore trap in 2013. Preliminary results from the molecular assays showed a high correlation (R^2=0.97) between the quantitative controls and detection levels of the model blackspot pathogen, confirming the sensitivity and accuracy of the technique. The assay was able to detect very low levels of spores on trap samples. Some interesting trends can be observed at this preliminary stage of data analysis:

- Airborne spores of YLS were very low, or undetected, throughout the 2013 season at Hart (Fig 1.). This may reflect the short dispersal distances by the pathogen or low level of inoculum on the infested stubble collected in 2012.
- A peak of NFNB spores was detected in the first two weeks of October. Few NFNB spores were detected in the remainder of the growing season. Early season spore dispersal patterns (from February) will be examined in 2014.
- The highest peaks for airborne spores of the model pathogen, Blackspot of field pea, occurred mid May to early June (primary ascospore release from infested stubble) and again in early October (spring ascospore release from infected crops). The result in May – June correlated with predictions of the Blackspot Manager for the Hart district in 2013.

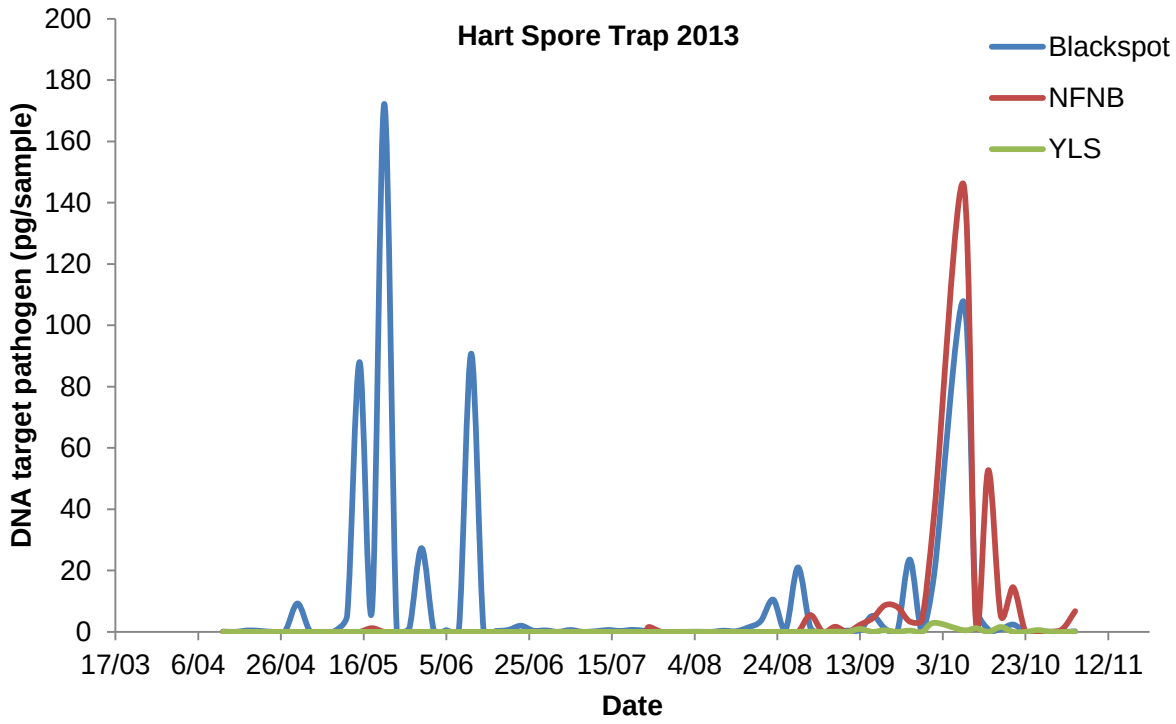

Figure 1. Quantified DNA (pg/sample) extracted of YLS, NFNB and blackspot pathogens captured over time by a volumetric spore trap located at the Hart field site in 2013.

Control standards are currently being completed for YLS and NFNB so spore numbers can be derived from quantified DNA data (pg/sample) on spore tapes. Other trapping sites for 2013 are being processed for comparative analysis. This study aims to establish relationships between fungal spore release patterns and climate triggers to provide valuable information on disease dynamics in a changing farming environment. The data generated could allow improved strategies in disease management and forecasting.