What pathogens were detected in central and northern cereal crops in 2018?

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Take home messages

- Disease surveys are important to stay abreast of developing issues within farming systems.
- Fusarium crown rot and common root rot (*Bipolaris*) were widespread in cereal crops in 2018 and are potentially dominating other diseases such as take-all.
- The yellow spot fungus was detected in all 102 wheat crops surveyed and surprisingly also in 43 of the 46 (94%) barley crops. This presumably highlights how effective the yellow spot fungus is as a saprophyte of dead barley tissue.
- Spot form of net-blotch was detected more frequently and at higher DNA concentrations in barley crops than net-form of net blotch in 2018. Saprophytic colonisation of wheat as an alternate host appeared lower with net-blotch compared with the reciprocal situation with yellow spot.
- PREDICTA® B assays appear to be a valuable tool to rapidly quantify a wide range of fungal pathogens, nematode pests and beneficial fungi within wheat and barley crops.

Introduction

Regular crop surveys are important for monitoring changes in disease prevalence, distribution and importance in changing farming systems. Structured survey data can be used to a) guide priorities for continued research, b) inform integrated disease management (IDM) decisions i.e. ensure correct identification, c) ensure breeding efforts are targeted at priority and/or changing pathogen populations, d) determine success of recommended IDM strategies, e) provide a mechanism for proactive surveillance for new e.g. exotic or spread of new pathotypes or sporadic diseases e.g. FHB and viruses and f) maintain industry awareness and preparedness.

What did we do?

In collaboration with a range of locally based agronomists, a total of 150 winter cereal crops were surveyed in 2018 between the start and end of grain filling. The GPS location and background information for each paddock were recorded, but to maintain confidentiality data is presented here based on broad LLS boundaries. A total of 39 paddocks were surveyed in the Central West (32 wheat and 7 barley), 83 paddocks in the North West (47 wheat, 12 durum and 24 barley), 17 in the Northern Tablelands (3 wheat and 14 barley), 9 in Southern Qld (8 wheat and 1 barley) and 2 on the North Coast (1 wheat and 1 barley). In 2018, survey sites and numbers were dictated to some extent by the

availability of crops in a relatively dry season. The two North Coast samples were excluded from this current paper due to limited commercial relevance, and in the North West the bread wheat and durum sample data were combined and treated as wheat.

Within each crop, a diagonal transect (~500 m) was created starting at least 50 m in from a road or fence line and avoiding obvious barriers such as trees or dams. Five consecutive whole plants (roots with adhering soil, stems and heads) were collected along the planting row from ten separate sampling points across the diagonal transect (i.e. total of 50 plants/crop). Samples were transported to Tamworth and stored at 4°C before processing;

- 100 random tillers (i.e. two/plant) were assessed for incidence of basal browning (crown rot), leaf diseases (e.g. yellow spot or net blotch) and head infections (e.g. bunt, smut or FHB).
- Fifty crown and stem bases (one/plant) are currently being rated for the severity of basal browning and scored for root health prior to plating on laboratory media to the determine the incidence of *Fusarium* (crown rot) and *Bipolaris sorokiniaina* (common root rot) infection..

The 100 tillers used for visual assessments were further separated into root and shoot (crown, stem, leaves and heads) samples, dried at 40°C for 48 h and then couriered to SARDI to assess fungal DNA concentrations using a range existing PREDICTA® B assays. The dried shoot samples were put through a fine plant grinder prior to DNA analysis. A 20 g subsample of ground shoot material, and the whole dried root samples were mixed with a set quantity of sterile sand before extraction of total DNA and PREDICTA B analysis. All DNA data, picograms (pg) or 1000 DNA copies (kDNA) were then converted to per gram of dry root or shoot weight. Due to the availability of data at the time of writing the rest of this paper predominantly outlines the DNA results.

What did we find?

PREDICTA B DNA assays are extremely sensitive with specificity to the target fungal pathogen or plant parasitic nematode of interest. Hence, because these organisms are plant pathogens they become concentrated in the tissues they infect.

The approach used in this survey is quite different from traditional PREDICTA B soil testing where calibrations have been developed to determine the relative risk of infection prior to sowing. A soil test detects DNA of the target pathogen in the soil, old plant roots and stubble residues, particularly those added when following the recommended PREDICTA B sampling strategy. This approach defines the risk of infection developing within a season.

In this survey we collected plant samples during grain filling and washed them to remove soil and any old stubble residues. Hence, the DNA tests in this context are determining the level of pathogen burden within the roots or shoots of the plant at a specified growth stage and not residues from previous crops.

The key point being, the DNA values presented in the following tables should ***not*** be compared with current PREDICTA B pre-sowing risk levels or population densities for the different pathogens. Furthermore, the DNA values within roots or shoots have been assigned to a purely arbitrary low, medium or high category based on the spread of data across sites in 2018. They should ***not*** necessarily be interpreted as low, medium or high infection levels.

For example, the 2018 season was generally dry which was not conducive to the development of leaf diseases such as yellow spot in wheat and net blotches in barley. Hence, even though DNA of the causal fungal pathogens was detected in shoots in 2018, these levels are probably considerably lower than what is likely to be detected in a wetter year. However, DNA concentrations did correlate with visual assessments of disease incidence e.g. crops with higher incidence of basal browning had elevated *Fusarium* DNA levels. DNA data at this stage should be considered for comparative purposes only with continued surveys and research, hopefully developing relationships between pathogen burden in roots and shoots and disease severity and yield loss. Enough of the caveats. What was actually interesting using this new approach with PREDICTA B assays?

Fusarium crown rot (_Fusarium_ spp.)

Two DNA assays detect *Fusarium pseudograminearum* with a third detecting *F. culmorum* + *F. graminearum*, but cannot distinguish between these two species. All three *Fusarium* species cause basal infection of cereal stems resulting in crown rot and the expression of whiteheads when heat and/or moisture stress occurs during grain filling. When wet weather occurs during flowering these species, especially *F.* graminearum, can also infect heads causing Fusarium head blight (FHB). DNA data for all three tests were combined for this interpretation. The incidence of crown rot, based on basal browning, was high across the survey area in 2018 (data not shown).

Fusarium DNA was detected in the shoots (crown, stem, leaves and heads) of 99% of the 148 cereal crops surveyed in 2018 (Table 1). The DNA levels were most likely associated with crown rot infection of the crown and lower stem sections. However, FHB was visually recorded in a limited number of crops in the North West region in 2018 (Liverpool Plains) which had proportionally higher levels of *F. culmorum/F. graminearum* DNA in shoot samples (data not shown). *Fusarium* DNA levels tended to be lower in shoots in the Northern Tablelands compared with the other regions.

The 2018 season was quite conducive to the development of Fusarium crown rot with DNA levels in shoots highlighting the continued importance of this disease across the region (Table 1). *Fusarium pseudograminearum* is primarily considered a crown and lower stem pathogen but interestingly high incidence and levels of DNA were also detected in root samples across regions. Only 4% of root samples had no detection of *Fusarium* spp. (Table 1). Voss-Fels et al. (2018), recently investigated genetic variability in 215 international wheat lines to *Fusarium* root rot (FRR) caused by *F. graminearum*. Interestingly they found FRR resistance accumulated in European winter wheat germplasm which also had reduced browning of stem bases. These preliminary DNA results indicate that a similar study may be warranted on the importance and genetic resistance to FRR caused by *F. pseudograminearum*.

Table 1. Proportion of paddocks (%) with varying levels of *Fusarium* spp. (crown rot) DNA detected in wheat and barley roots or shoots in 2018

Fusarium spp. (pg DNA/g)	Roots				Shoots			
Region (no. paddocks)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<1000)	Medium (<10000)	High (>10000)
Central West (39)	0	15	3	82	3	28	33	36
North West (83)	4	13	13	70	1	24	26	49
Northern Tablelands (17)	6	47	12	35	0	76	12	12
Southern Qld (9)	11	22	11	56	0	33	0	67
Total (148)	***4***	***18***	***10***	***68***	***1***	***32***	***24***	***43***

Common root rot (*Bipolaris sorokiniana*)

Bipolaris primarily infects the sub-crown internode causing dark brown to black discolouration of this tissue which would be related to DNA levels in root samples in this survey. Tiller bases and surrounding leaf sheathes can also be brown in common root rot infected tillers which would be reflected in shoot DNA levels.

Bipolaris DNA was detected in 95% of root and shoot samples (Table 2). DNA levels in the roots were relatively consistent across regions but a larger proportion of crops in North West (34%) and Southern Qld (56%) had high DNA levels in the shoot samples compared with the Central West and Northern Tablelands crops which had no crops in the high category (Table 2).

Table 2. Proportion of paddocks (%) with varying levels of *Bipolaris sorokiniana* (common root rot) DNA detected in wheat and barley roots or shoots in 2018

Bipolaris (pg DNA/g)	Roots				Shoots			
Region (no. paddocks)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<1000)	Medium (<10000)	High (>10000)
Central West (39)	3	21	50	26	10	49	41	0
North West (83)	6	12	48	34	2	23	41	34
Northern Tablelands (17)	12	24	41	23	6	41	53	0
Southern Qld (9)	0	11	56	33	0	0	44	56
Total (148)	***5***	***16***	***49***	***30***	***5***	***30***	***43***	***22***

***Gaeumannomyces graminis* var. *tritici* (*Ggt*, take-all)**

Take-all predominantly causes black discolouration of infected roots, but sub-crown internodes and tiller bases can also appear black, especially in seasons with wet conditions during spring causing "black sock" symptoms. The take-all fungus (*Ggt*) hosts on all winter cereal crop species and a range of grass weeds. Take-all is generally not considered a significant pathogen of cereal crops in northern NSW and Qld compared with southern NSW, SA and Victoria. However, DNA *Ggt* was detected in 99% of root samples and 79% of shoot samples, mostly at low concentrations, in 2018. Although the number of paddocks surveyed in Southern Qld in 2018 were relatively small (9), this region had a higher proportion of crops with medium *Ggt* DNA levels in both the roots and stems (Table 3). Given the similar host range of *Ggt* and Fusarium crown rot fungi, plants with medium *Ggt* DNA levels also tended to have medium to high *Fusarium* DNA concentrations (data not shown). This raises the issue as to whether the importance of take-all in this region is potentially going unrecognised due to symptoms being masked by crown rot infection.

Table 3. Proportion of paddocks (%) with varying levels of *Gaeumannomyces graminis* var. *tritici* (*Ggt,* take-all) DNA detected in wheat and barley roots or shoots in 2018

Ggt (pg DNA/g)	Roots				Shoots			
Region (no. paddocks)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<1000)	Medium (<10000)	High (>10000)
Central West (39)	0	77	21	2	28	72	0	0
North West (83)	1	76	23	0	10	86	4	0
Northern Tablelands (17)	6	82	12	0	71	29	0	0
Southern Qld (9)	0	56	44	0	0	89	11	0
Total (148)	***1***	***76***	***22***	***1***	***21***	***76***	***3***	***0***

Root lesion nematodes

Root lesion nematodes (RLN, *Pratylenchus* spp.) are microscopic plant parasites which feed on crop roots. Two important species are known to infect crops in eastern Australia, namely *Pratylenchus thornei* (*Pt*) and *P. neglectus* (*Pn*). *Pt* is known to be the more important species in higher clay content soils in northern NSW and Southern Qld while *Pn* is generally more prevalent in lighter soil types in south-eastern Australia and WA.

Only root samples were assayed for RLNs with a known conversion used to express DNA values as nematode numbers. Sharma et al. (2001) reported for *Pn* that 0-1000 *Pn*/g root caused no yield loss in cereals; 1000-10000 caused up to 15% yield loss whilst >10,000 caused 15-30% yield loss in WA. Similar data on dry root RLN densities was not found for *Pt*. These values were used as a rough guide to set arbitrary densities categories in Table 4.

Pt was detected in roots of a higher proportion (60%) of cereal crops than *Pn* (39%) but did vary by LLS region. *Pn* was detected in 92% of Central West crops but was present at lower incidence in Northern Tablelands (41%), North West (17%) and Southern Qld (11%). RLN densities detected in root systems were generally in the low category with only 18% of crops in the Central West having medium *Pn* densities while 5% of crops in the North West had medium *Pt* densities based on the Sharma et al. (2001) categories (Table 4).

Table 4. Proportion of paddocks (%) with varying densities of the root lesion nematodes *Pratylenchus thornei* or *P. neglectus* in wheat and barley roots in 2018

Root lesion nematodes	*P. thornei* (no./g)				*P. neglectus* (no./g)			
Region (no. paddocks)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<1000)	Medium (<10000)	High (>10000)
Central West (39)	44	56	0	0	8	74	18	0
North West (83)	31	64	5	0	83	17	0	0
Northern Tablelands (17)	65	35	0	0	59	41	0	0
Southern Qld (9)	67	33	0	0	89	11	0	0
Total (148)	***40***	***57***	***3***	***0***	***61***	***34***	***5***	***0***

White grain disorder (*Eutiarosporella* spp.)

White grain disorder (WGD) can be a sporadic issue to cereal production, primarily in Southern Qld, when wet weather occurs during flowering. Infection produces symptoms similar to FHB with premature bleaching of infected sections in heads and, as the name implies, production of white grains. WGD is caused by three different species of the fungus *Eutiarosporella* (formerly thought to be *Botryosphaeria*) in Australia, namely *E. tritici-australis* (*Eta*) and *E. darliae* (*Ed*) or *E. pseudodarliae* (*Ep*). There are two DNA assays to allow detection of these species with one for *Eta* and a second that detects both *Ed*+*Ep,* with combined data presented (Table 5).

Eutiarosporella does not appear to have been a significant pathogen of cereal roots in 2018 with only low DNA levels detected in 14% of crops. The incidence of *Eutiarosporella* DNA was higher in shoot samples being detected in 55% of cereal crops including all nine crops surveyed in Southern Qld (Table 5). Incidence and DNA levels of *Ed*+*Ep* tended to be higher than *Eta* in each region (data not shown).

Table 5. Proportion of paddocks (%) with varying levels of *Eutiarosporella* (white grain disorder) DNA detected in wheat and barley roots or shoots in 2018

Eutiarosporella (kDNA/g)	Roots				Shoots			
Region (no. paddocks)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<1000)	Medium (<10000)	High (>10000)
Central West (39)	90	10	0	0	67	23	10	0
North West (83)	88	12	0	0	41	48	7	4
Northern Tablelands (17)	76	24	0	0	41	59	0	0
Southern Qld (9)	67	33	0	0	0	56	11	33
Total (148)	***86***	***14***	***0***	***0***	***45***	***43***	***8***	***4***

Charcoal rot (*Macrophomina phaseolina*)

Charcoal rot, caused by the fungus *Macrophomina phaseolina*, is primarily a disease of summer crops including sorghum, soybean, mungbean and sunflower in northern NSW and Qld. Infection causes light brown lesions on crowns and roots and results in increased lodging and/or premature plant death when stress occurs late in the growing season. In 2014, charcoal rot was reported to cause premature senescence of lupin crops in WA when they were exposed to high temperatures and moisture stress during pod set. *Macrophomina phaseolina* has a wide host range of more than 500 weed and crop species including winter cereals.

Pathogen DNA was detected at low levels in 84% of cereal root samples and 42% of cereal shoot samples (Table 6). Medium levels of *Macrophomina* DNA was detected in 22% (2 of 9) of shoot samples from crops in Southern Qld. This pathogen has not been recorded as a significant pathogen of winter cereal crops but certainly appears to be hosting on roots and shoots of wheat and barley crops across the survey region.

Table 6. Proportion of paddocks (%) with varying levels of *Macrophomina phaseolina* (charcoal rot) DNA detected in wheat and barley roots or shoots in 2018

Macrophomina (kDNA/g)	Roots				Shoots			
Region (no. paddocks)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<1000)	Medium (<10000)	High (>10000)
Central West (39)	13	84	3	0	59	41	0	0
North West (83)	16	82	2	0	53	43	4	0
Northern Tablelands (17)	12	88	0	0	65	35	0	0
Southern Qld (9)	11	89	0	0	33	45	22	0
Total (148)	***14***	***84***	***2***	***0***	***55***	***42***	***3***	***0***

Yellow spot (*Pyrenophora tritici-repentis*)

Yellow spot is a stubble-borne disease of durum and bread wheat caused by the fungus *Pyrenophora tritici-repentis* (*Ptr*). Wet weather favours infection and production of tan lesions with a yellow margin on the leaves of susceptible wheat varieties. Repeated rainfall events during the season are required for yellow infection to progress up the canopy of a wheat plant. Given the generally dry conditions in 2018, the visual incidence of yellow spot lesions on the top three leaves during grain filling was low. However, in many crops the presence of yellow spot lesions on the lower leaves was noted when the plant samples were collected (data not shown). Although *Ptr* is a leaf pathogen of wheat, it is also an effective saprophyte (feeds on dead tissue) and can colonise dead leaves and stubble of barley late in the season under wet conditions. Hence, both wheat and barley shoot samples were assayed for *Ptr* DNA levels.

Ptr DNA was detected in every wheat crop surveyed and surprisingly also in 94% of barley crops (Table 7). Medium to high *Ptr* DNA levels were measured in wheat crops across all regions, especially Southern Qld and Northern Tablelands; but low sample numbers in these areas limit severity estimates.

The proportion of barley crops with medium to high *Ptr* DNA in shoots was lower compared to wheat except in the Central West (Table 7). Underlying differences in rotation sequences or rainfall patterns in 2018 between these regions, which have not currently been explored. This initial survey however, certainly highlights that barley should not be considered a break crop for yellow spot in wheat. Presumably *Ptr* is growing as a saprophyte on dead barley tissue and requires further investigation.

Table 7. Proportion of paddocks (%) with varying levels of *Pyrenophora tritici-repentis* (yellow spot) DNA detected in wheat and barley shoots in 2018

Yellow spot (kDNA/g)	Wheat				Barley			
Region (no. paddocks W, B)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<1000)	Medium (<10000)	High (>10000)
Central West (32, 7)	0	38	37	25	15	15	42	28
North West (59, 24)	0	38	47	15	0	71	21	8
Northern Tablelands (3, 14)	0	0	0	100	15	71	7	7
Southern Qld (8, 1)	0	0	62	38	0	100	0	0
Total (102, 46)	***0***	***33***	***44***	***23***	***6***	***63***	***20***	***11***

Spot form of net-blotch (*Pyrenophora teres* f. *maculata*)

Spot form of net-blotch (SFNB) is a stubble-borne pathogen of barley crops causing brown circular lesions with a limited yellow margin on infected leaves. Similar to yellow spot in wheat, prolonged wet weather favours initial infection and progress up the canopy of susceptible barley varieties. The SFNB fungus was detected in the shoots of 95% of the barley crops surveyed at generally low to medium DNA concentrations (Table 8). SFNB was detected in 50% of wheat crops surveyed at largely low DNA concentrations. It is not clear if this reflects a lower saprophytic capacity with *P. teres* compared with *Ptr* or varying sequencing of wheat and barley crops within rotations. That is, barley tends to follow wheat within rotations rather than the other way around. This would tend to favour saprophytic colonisation of *Ptr* on barley compared with *P. teres* hosting on wheat as its alternate host.

Table 8. Proportion of paddocks (%) with varying levels of *Pyrenophora teres* f. *maculata* (spot form or net-blotch, SFNB) DNA detected in barley and wheat shoots in 2018

SFNB (kDNA/g)	Barley				Wheat			
Region (no. paddocks B, W)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<1000)	Medium (<10000)	High (>10000)
Central West (7, 32)	0	43	43	14	69	31	0	0
North West (24, 59)	0	54	42	4	37	59	2	2
Northern Tablelands (14, 3)	14	57	29	0	67	33	0	0
Southern Qld (1, 8)	0	100	0	0	63	37	0	0
Total (46, 102)	***5***	***54***	***37***	***4***	***50***	***48***	***1***	***1***

Net form of net-blotch (*Pyrenophora teres* f. *teres*)

Net form of net-blotch (NFNB) is a stubble-borne pathogen of barley crops causing brown elongated lesions with a net-like cross hatch appearance on infected leaves. Similar to yellow spot in wheat and

SFNB in barley, prolonged wet weather favours initial infection and progress up the canopy of susceptible barley varieties.

The NFNB fungus was detected in a lower proportion (69%) of barley crops (Table 9) compared with SFNB (Table 8) in 2018. The concentration of NFNB DNA in barley shoots also tended to be lower than with SFNB. NFNB was also only detected in 8% of wheat crops across the survey area only at low DNA concentrations with all eight wheat crops in the North West region.

Table 9. Proportion of paddocks (%) with varying levels of *Pyrenophora teres* f. *teres* (net form or net-blotch, NFNB) DNA detected in barley and wheat shoots in 2018

NFNB (kDNA/g)	Barley				Wheat			
Region (no. paddocks B, W)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<1000)	Medium (<10000)	High (>10000)
Central West (7, 32)	57	43	0	0	100	0	0	0
North West (24, 59)	17	79	4	0	86	14	0	0
Northern Tablelands (14, 3)	43	50	7	0	100	0	0	0
Southern Qld (1, 8)	0	100	0	0	100	0	0	0
Total (46, 102)	***31***	***65***	***4***	***0***	***92***	***8***	***0***	***0***

Other DNA test results

The cereal cyst nematode, *Heterodera avenae*, was not detected in any of the root samples while DNA of the eyespot fungus (*Oculimacula yallundae*) and septoria tritici blotch fungus (*Zymoseptoria tritici*) were not detected in any of the shoot samples. *Rhizoctonia solani* (AG8) DNA was only detected in the root sample from one surveyed wheat crop near North Star in 2018 at a relatively low concentration (58 pg DNA/g root) and was not detected in any shoot samples.

Low levels of *Pythium* clade f DNA, a pathogen usually associated with seedling blight in wet soils, was detected at low levels in roots from 44% of cereal crops surveyed with higher detection (82%) in Central West crops (Table 10). Medium *Pythium* DNA levels were recorded in one barley crop near Yallaroi in North West NSW; and separate barley and wheat crops near Inverell in the Northern Tablelands.

Arbuscular mycorrhizae fungi (AMF) colonise roots of host plants and develop a hyphal network in soil which reputedly assists the plant to access phosphorus and zinc. Low levels of AMF have been associated with long fallow disorder in dependent summer (cotton, sunflower, mungbean and maize) and winter crops (linseed, chickpea and faba beans). Although wheat and barley are considered to be low and very low AMF dependent crops respectively, they are hosts and are generally recommended to grow to elevate AMF populations prior to sowing more AMF dependent crop species.

There are two DNA assays for AMF with combined results presented. It is important to remember that in contrast to all the other pathogen assays, AMF is a beneficial so nil or low DNA levels are the actual concern. AMF DNA was not detected in 39% of cereal root samples with the highest proportion of nil detection (59%) in Central NSW crops (Table 10). The proportion of cereal crops with higher concentrations of AMF DNA in roots appeared to be greater on the Northern Tablelands, than North West, than the Central West. None of the nine paddocks surveyed in Southern Qld in 2018 had above a low level of AMF DNA in the roots (Table 10). The implication of these levels within cereal roots on AMF populations across a rotation sequence is not clear and cannot be determined from this current survey.

Table 10. Proportion of paddocks (%) with varying levels of *Pythium* or arbuscular mycorrhizae fungi (AMF) DNA detected in wheat and barley roots in 2018

Other	*Pythium* (pg DNA/g)				AMF (kDNA/g)			
Region (no. paddocks)	Nil	Low (<1000)	Medium (<10000)	High (>10000)	Nil	Low (<100)	Medium (<1000)	High (>1000)
Central West (39)	18	82	0	0	59	33	8	0
North West (83)	70	29	1	0	33	41	25	1
Northern Tablelands (17)	53	35	12	0	24	29	41	6
Southern Qld (9)	67	33	0	0	44	56	0	0
Total (148)	***54***	***44***	***2***	***0***	***39***	***39***	***21***	***1***

Conclusion

Molecular testing, such as PREDICTA® B assays used in this survey, are a powerful tool for quantifying levels of fungal pathogens, nematode pests or beneficial fungi (AMF) within crop tissue. Dividing plant samples into root and shoot (crown, stem, leaf and heads) samples prior to DNA testing allows an additional level of interpretation. At present DNA concentrations within root or shoot tissue can only be used for comparative purposes between regions, crops, seasons, rotation sequences, climatic conditions etc. Continuing surveys and associated research is required to understand what the actual impact of different DNA concentrations within root or shoot tissue has on crop production.

References

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