Fusarium head blight of wheat in Alberta: species complex and related trichothecene genotypes

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Abstract

In this study wheat stem and grain samples were collected from three field plots in Alberta (Lethbridge, Lacombe and Beaverlodge) to characterize the major *Fusarium* species associated with FHB in Alberta. A *Fusarium*-selective medium was used to isolate *Fusarium* species from infected stem and grain samples and the elongation factor 1 alpha (EF1α) gene sequence was used for molecular identification of the isolates. The results showed that, *F. graminearum* was recovered at very low rates from Lethbridge (both stem and grain samples) and was not detected in Lacombe or Beaverlodge. *F. avenaceum* was the most dominant species in stem samples, while *F. poae* was the most frequently isolated species from grain samples. Trichothecene genotyping using two multiplex PCR assays based on the *Tri*12 gene showed that, the 3ADON trichothecene is the most dominant genotype in all type B trichothecene producing *Fusarium* species tested during this study. On the other hand, isolates of *F. graminearum* form Lethbridge were found to produce either 15ADON or 3ADON trichothecene genotypes. Application of fungicide showed significant reduction in frequency and diversity of *Fusarium* species isolated from grain samples in comparison to stem samples.

Materials and Methods

Sampling and isolation of *Fusarium* pathogens:
A total of 96 samples were collected from each of the surveyed location (48 stem and 48 grain samples). Collected samples were surface-sterilized in 1% NaOCl for 3 minutes and washed twice with sterile distilled water. Samples were air dried and plated in 9-cm petri plate containing PCNB medium (5 seeds or 3 nodes /plate). From each location, 240 seeds and 144 nodes were examined for the presence of *Fusarium*. Plates incubated at 24 ^{o}C under 12-hours photoperiods for 5 days and growing cultures were purified on PDA medium for DNA extraction and molecular characterization.

DNA extraction and PCR amplification:
DNA was extracted from *Fusarium* isolates using DNeasy Plant Mini Kit (Qiagen), the primers EF1/EF2 (O'Donnell et al 1998) were used to amplify the EF1α gene for sequencing and molecular characterization of *Fusarium* isolates. Trichothecene genotype was determined by multiplex PCR based on the *Tri12* gene according to Ward et al 2007.

Results

Figure 1: *Fusarium* species diversity in wheat stem and grain samples collected from Alberta. The frequency of isolation of each *Fusarium* species (represented as percentage: %) is shown in both grain and stem samples collected from Lethbridge (1), Lacombe (2) and Beaverlodge (3). Number of isolates (N) is shown in each location for stem and grain samples that didn't treated with fungicides (No fungicide) and samples in which fungicide was applied (Fungicide).

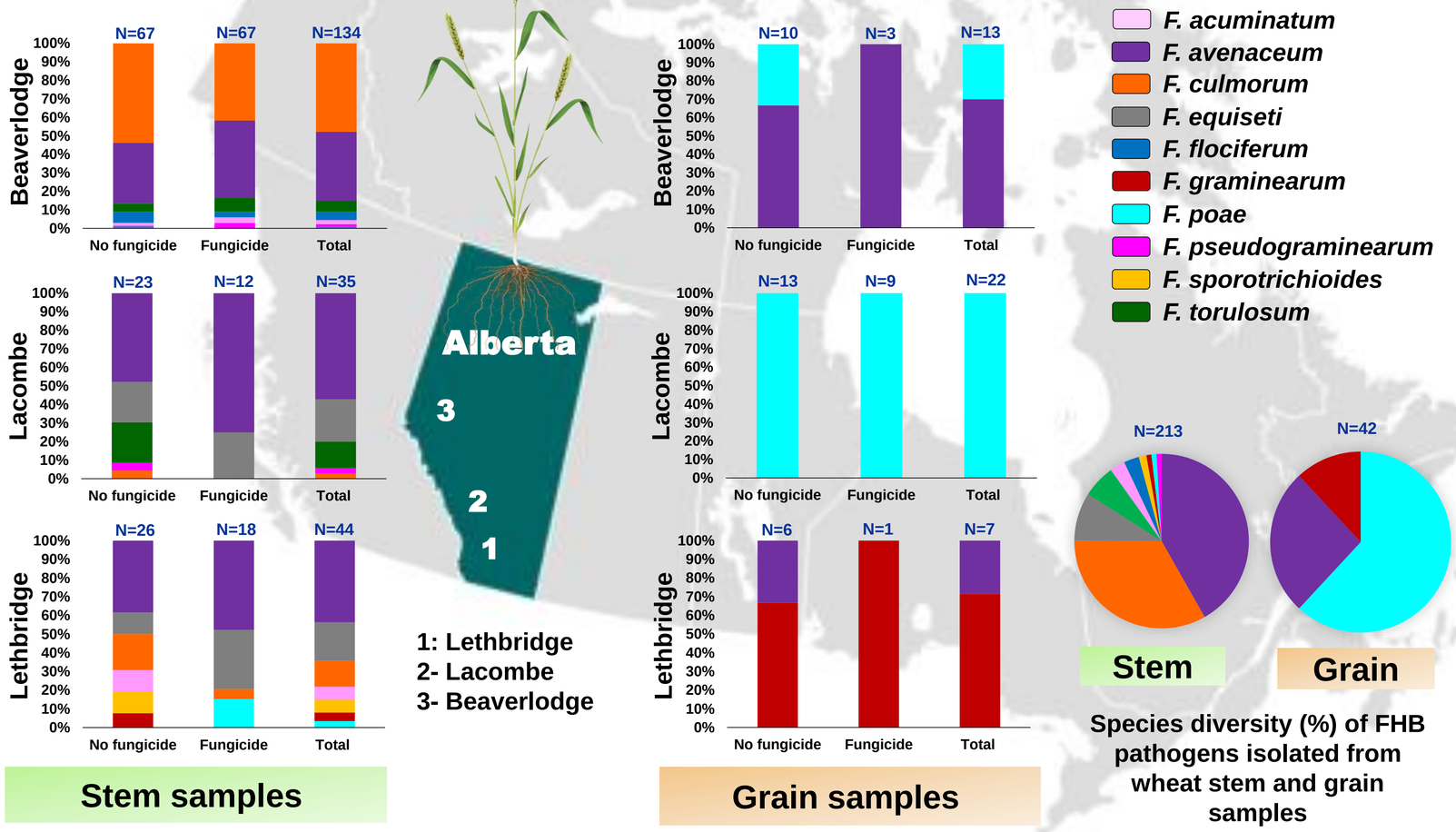


Figure 2: *Tri12* multiplex PCR for trichothecene genotyping. *Tri12* gene was amplified by multiplex PCR in order to determine the type B trichothecene genotype in Fusarium isolates recovered from stem and grain samples. Three different genotypes are found: NIV (840 bp), 15ADON (670 bp) and 3ADON (410bp).

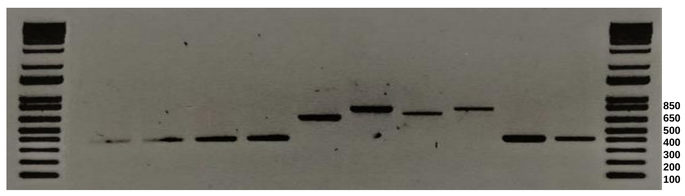
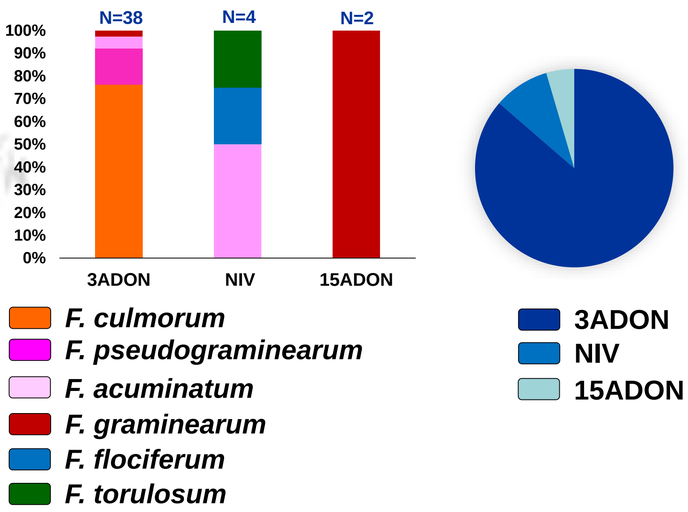


Figure 3: Trichothecene genotype frequencies (%) among the tested *Fusarium* species.



Benefits to farmers and industry

A large number of predominant mycotoxins are produced by the *Fusarium* species, probably constituting the most prevalent toxin-producing fungi found on cereals. Because mycotoxins (like Trichothecene) can harm human and farm animals, undermining productivity and health, a mycological and toxigenic screening will provide Alberta farmers and industry with valuable information about the type of mycotoxins produced by *Fusarium* species in wheat. Such information is highly important for risk mitigation and disease control specially when mycotoxins are considered. So, it is important to detect and monitor the population structure of FHB-species complex frequently to prevent disease spread and follow the appropriate control method.

Conclusion

The results showed that *F. graminearum* is not the main causal agent for FHB in Alberta, and more concern should be given to the other *Fusarium* species involved in FHB complex (e.g. *F. culmorum* and *F. avenaceum*). Fusarium species associated with FHB are variable in different locations, and 3ADON genotype is the most dominant genotype in Fusarium species isolated from Alberta. Applying fungicide could help in reducing FHB symptoms.

References

O'Donnell et al. (1998). *Proceedings of the National Academy of Sciences*, *95*(5), 2044-2049.
Ward et al. (2008). *Fungal Genetics and Biology*, *45*(4), 473-484.

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