



Fusarium head blight of wheat: Pathogenesis and control strategies



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ABSTRACT

Fusarium head blight (FHB) is one of the main fungal diseases of grain crops such as wheat, barley and maize. The FHB species complex produces mycotoxins that cause quality and yield reductions, as well as human and animal health risks. Resistance breeding, integrated with chemical and or cultural control practices has the potential for sustainable control of FHB. However, breeding for FHB resistance has been slow due to limited genetic gains from conventional breeding, requiring complementary genomic tools to explore and manipulate genetic resources. Breeding for FHB resistance in wheat is also hampered by the quantitative nature of the trait, limited understanding of FHB pathogenesis and the large size of the host genome. This paper highlights the state of knowledge on FHB severity, pathogenesis and genetic control strategies. Available genomic technologies used to uncoil the underlying mechanisms of virulence in the dominant FHB species, *F. graminearum*, are further outlined. Interdisciplinary collaboration is required for successful development and deployment of FHB resistant genotypes to wheat growers.

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1. Introduction

Fusarium head blight (FHB) also known as scab, caused by members of the FHB species complex, is one of the most

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devastating fungal diseases of grain crops including wheat, barley and maize. The FHB species complex comprises of more than 16 species (O'Donnell et al., 2004), that infect a range of hosts (van der Lee et al., 2015). These fungal species produce various mycotoxins, notably deoxynivalenol (DON) and zearalenone (ZEA) that are toxic to humans and animals, respectively (Darwish et al., 2014). The predominant species, *F. graminearum* (teleomorph *Gibberella zeae*), is currently ranked fourth among plant fungal pathogens based on its scientific and economic importance (Dean et al., 2012). The infection biology of *F. graminearum* is yet to be fully understood, but some important aspects of the infectious process have been resolved. In addition, signal transduction pathways which promote invasive growth, sexual reproduction and adaptive stress responses contributing to FHB symptoms have been examined (Gu et al., 2015).

The past decade has witnessed major FHB outbreaks causing significant economic losses in cereal crops globally (Kriel and Pretorius, 2008; Lilleboe, 2011; Makandar et al., 2006; McMullen et al., 2012; Salgado et al., 2015). Given the current global warming associated with increased temperatures, major epidemics of FHB are likely to occur in the near future particularly under high humidity conditions (Shah et al., 2014). Global climate indices and models could be used to monitor FHB development. This could assist in determining the distribution of the FHB species complex across the major cereal production agro-ecologies to allow effective monitoring of the occurrence of the disease. Currently, several groups have catalogued the distribution of FHB species complex members and their chemotype composition from various parts of the world (Przemieniecki et al., 2014; van der Lee et al., 2015). Previous studies attempted to reconcile phylogenetic with chemotypic properties to provide distribution trajectories that are linked to possible mycotoxicoses. Combined, these studies have provided a better picture of the epidemiology of FHB across the globe which can be a useful guide when devising disease management strategies.

Effective management of FHB cannot be achieved through the use of a single control strategy because each has its own limitations. Employing different control strategies including cultural, biological, chemical and host plant resistance are all powerful tools for FHB management. Genetic control, involving breeding for resistance, when integrated with other control methods mentioned, has the potential to be a sustainable FHB control solution. To date, breeding efforts that include integration of conventional approaches with genomic tools such as quantitative trait loci (QTL) mapping have revealed about 52 QTL conferring FHB resistance that are distributed on all wheat chromosomes, except 7D (Buerstmayr et al., 2009). Consequently, targeted breeding and deployment of resistance genes in breeding programs has gained momentum. Nonetheless, underlying factors influencing FHB resistance breeding including the pathogen and its virulence mechanisms, environmental factors promoting pathogenesis, as well as the host and its resistance mechanisms should be understood for effective control of the disease. Further, various agronomic traits including plant height and flowering biology during anthesis (anther retention/exclusion) should be evaluated together with FHB sensitivity scores to deduce their association with the development of the disease (Malihpour et al., 2016). For instance, various studies have shown that plant height and anther exclusion are negatively correlated to FHB severity, suggesting that tall genotypes that do not retain their anthers could have some levels of resistance to FHB (Lu et al., 2013; Moidu et al., 2015; Yan et al., 2011). This review highlights FHB pathogenesis, infection mechanisms, chemotypic distribution and control options available for integrated management of FHB. Emphasis is given to resistance breeding as a key pillar to a sustainable control strategy.

2. The impact of *F. graminearum* and its mycotoxins

Fusarium head blight was first described as a major threat to wheat and barley in England in 1884 (Goswami and Kistler, 2004). Since then, numerous epidemics have been reported worldwide, costing millions to billions of US dollars in some parts of the world including the US (McMullen et al., 2012). Natural toxins in grain lots, feed and general food chain are commonly plant secondary metabolites, bacterial toxins, pycotoxins and mycotoxins that require constant monitoring (Berthiller et al., 2013). Likewise, existence of *F. graminearum* toxins in cereal grains and animal feeds have long been of global concern (da Rocha et al., 2014; Pleadin et al., 2013).

Due to mycotoxin production by the FHB species complex, chemotyping is key in monitoring the impact of FHB mycotoxins on human and livestock health. Type B trichothecenes, deoxynivalenol (DON), nivalenol (NIV) and their derivatives particularly 3-acetyl and 15-acetyl deoxynivalenol (3ADON and 15ADON) and 4-acetyl nivalenol (4ANIV) are some of the most important fungal toxins. As such, researchers have set out to understand some of the mechanisms underlying the clinical outcomes of FHB mycotoxins. Table 1 summarizes the geographic regions where some key FHB species dominate as reviewed by van der Lee et al. (2015). The trend shows that 15-DON is the dominant FHB chemotype globally.

The FHB incidence was highly associated with type B trichothecenes including DON (Boutigny et al., 2012). Concentrations of DON were also found to be up to 2356 µg/kg, which is beyond the regulatory limit, of 1000 µg/kg, in commercial compound feed samples supplied by the Animal Feed Manufacturers Association (AFMA) of South Africa between 2010 and 2011 (Njobeh et al., 2012). Evidently, trichothecenes such as DON are the most common mycotoxins of *F. graminearum* found as contaminants in foods and feeds in sub-Saharan Africa (Njobeh et al., 2012; Rodrigues et al., 2011; Stoev et al., 2010; Darwish et al., 2014). It is, therefore, important to study the physical factors promoting FHB pathotypes to allow monitoring of the disease, particularly in developing countries to limit mycotoxin levels in food and feeds.

Recently, a new field studying the plant metabolites of mycotoxins from plants infected by *F. graminearum* also known as masked mycotoxins has gained significant interest. Plants are able to convert the chemical structure of mycotoxins as a defense mechanism to prevent xenobiotic effects (Galaverna et al., 2009). For instance, plants can convert the *Fusarium* toxins DON and ZEA by Glucosyltransferase enzymes into deoxynivalenol-3-glucoside and zearalenone-14-glucoside, respectively, which are not virulent factors (Berthiller et al., 2015). These substances are often not the primary target of researchers when analyzing toxic compounds in plants. However, there is a chance that chemical reactions during food or feed processing or digestion can revert the masked mycotoxins back to their original toxicological states, which can cause significant human and livestock health problems (Berthiller et al., 2013). Alternatively, some of these hidden mycotoxins could pose health hazards in their present forms. More research on the detection and monitoring of these *F. graminearum* masked mycotoxins is becoming just as essential in wheat grain and bi-products as these mycotoxins can accumulate in significant quantities during FHB disease development without notable negative effects on yield or quality.

Global contamination of food and feeds with mycotoxins is an important problem, with trichothecenes and zearalenone being among the mycotoxins of great agro-economic importance (Zain et al., 2012). Limited research has been conducted to assess the economic losses due to FHB, however, there are widespread reports on the health impacts of *Fusarium*-infected food and feed to both humans and livestock. Health impacts due to consumption of

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