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A review of *Fusarium* head blight disease, pathogenicity and immuno-identification

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ABSTRACT

Cereals are the primary staple foods for the human. There is an increased severity in *Fusarium* head blight disease among crops leading to losing a huge amount of economic crops such as wheat, maize, rice and barley throughout the planet. Meanwhile, this disease has a significant impact on the plant quality and products. The prominent pathogens are related to the genus of *Fusarium* that can cause plant and human infectious diseases through having contaminated plant products with fungal mycotoxins that effect directly on immune cell activation and activity in particular in immunocompromised individuals. This review focus on the biology of *Fusarium* head blight, the most common pathogenic agent, the risk of having infected plant products of this disease and the most recent techniques used for fungal identification either by molecular markers or by detection the antigenic structure of pathogens via specific monoclonal antibodies.

Key words: *Fusarium graminearum, Head blight, Mycotoxins, Antigens, A monoclonal antibody.*

Introduction

Fungi are a diverse component of soil microbial communities including decomposers, mycorrhizal, and pathogens that distribute world widely. Fungi have modified strategies to infect a range of hosts. It has been estimated that the variation of fungi ranges from 3.5 to 5.1 million species on this planet (Blackwell, 2011). The most common pathogenic fungal species are primarily located in Ascomycota and Basidiomycota phylum (Heitman, 2011). Among ascomycetes, the genus *Fusarium* includes fungal pathogens that consider significant threat causing infections to humans, animals and devastating diseases to plants such economically vegetables, fruits, grains and seeds resulting in crop yield losses of up to 100 percent (Leslie and Summerell, 2006). Plant disease due to the *Fusarium* infections can lead not just to a reduction in yield of crops, it can affect the quality of the plant products (Lamprecht *et al*., 2011). *Fusarium* Head Blight (FHB) is the best-known *Fusarium* disease in plants, a disease affecting cereal crops, rice and wheat. Other *Fusarium* diseases include sudden death syndrome (SDS), Fusarium wilt, root, stem and seed rots and cankers of many fruits and vegetables including tomato, potato, cotton, cabbage, cucumbers, melons, date palms, peas, and soybeans (Ahmet, 2011; Ajilogba and Babalola, 2013; Gupta *et al*., 2009; Moretti *et al*., 2002; Pérez Vicente *et al*., 2014; Pilotti, Ponzio and Motta, 2002; Schroers *et al*., 2009). Some *Fusarium* species, for example, *F. solani* and *F. oxysporum*, are capable of infecting both plants and humans (Moore *et al*., 2011). In this review the FHB disease and the its impact on human health will be highlighted.

What is the *Fusarium* Head Blight?

Fusarium head blight is considered to be one of the most devastating diseases of grains such as wheat and barley (cereals) (Nielsen *et al*., 2011). This dis-

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ease can infect various parts of a plant such as stems, leaves, roots, fruits and flowers (Osborne and Stein, 2007). This disease is also called Scab or Ear Blight (McMullen *et al*., 2012) and worldwide distribution leading to yield loss, low weights and affect seed germination. *Fusarium* species can produce a wide range of mycotoxins that can contaminate plant products, seeds and grains (Gorczyca *et al*., 2018). Such of these mycotoxins deoxynivalenol (DON), which is also called vomitoxin that has harmful effects on also human, animal health and consequences in the ecosystem, also, FHB is associated with the presence of pathogenic *Fusarium* species mycotoxins (Sobrova *et al*., 2010). This disease has a global geographical distribution range among grains such as wheat in the North and South of America, Europe, Africa, Australia and Asia (Figueroa *et al*., 2018). The losses of the wheat crop in the US was estimated to be approximately $3 billion (Shah *et al*., 2018).

Fungal pathogens

Many *Fusarium* pathogens are causing devastating FHB. Generally, *Fusarium* species are ubiquitous soil-borne pathogens *Fusarium graminearum* (sexual stage is called *Gibberellazeae*) is the most dominant *Fusarium* species causing FHB (Lu and Edwards, 2018). Besides, *F. oxysporum, F. avenaceum, F. culmorum, F. pseudograminearum, F. proliferatum* and *F. poae* are also associated with FHB (Balmas *et al*., 2015; Champeil *et al*., 2004; O'Donnell *et al*., 2010; Yli-Mattila *et al*., 2004). In this review we are focusing on *F.graminearum* as the primary causative for FHB disease. This fungal pathogen has unique characteristic features. In general, *Fusarium* genus has two distinctive kind of conidia microconidia and macroconidia which is very unique shape as banana or fuse-form. This phytopathogen is often had one type of conidia which is macroconidia with thick wall and 5 – 6 septate. Microconidia are absent. On potato dextrose agar media (PDA), *F. graminearum* colony grows relatively quick with dense amounts of conidia and mycelia that vary from light orange, yellow to white in colour (Leslie and Summerell, 2006; Summerell *et al*., 2003). Conidia of this phytopathogen are varied in size (21 - 9 3.5 mm) (Trail *et al*., 2005). Spores of *F. graminearum* have aerial transport capabilities through winds and airwaves to distribute and cover a very wide range of geographical areas and fields resulting in the first step of new infections via adherence and then penetration host cells (Keller *et al*., 2014; Ma *et al*., 2013).At this stage, fungal pathogen invades the outer parts of the leaf to the base of the leaf along with colonisation and mycotoxin production (Stephens *et al*., 2008).

Disease symptoms

FHB disease by *F. graminearum* can generally infect cereals including wheat, maize and barley. Symptoms of this infection typically occur as bleaching of some or all of the florets in the spike or head while healthy heads are still green. However, close examination of the infected plant can appear vast biomass of fungal spores which tend to be pinkish to orange in colour particularly among humid weather (Gorczyca *et al*., 2018). As a result of fungal penetration and colonisation in the host affected plant suffering from slow in germination along with accumulation fungal biomass and mycotoxins (Wilson *et al*., 2018).

Impact on Human Health

The *Fusarium* species can produce toxic secondary metabolites called mycotoxins. These mycotoxins are synthesized via genetic codes responsible for coding of these mycotoxins. Trichothecene, Deoxynivalenol (DON), Zearalenone and fumonisins are the common mycotoxins produced by *Fusarium* species (Bakker *et al*., 2018). Most of *Fusarium* pathogens are releasing one or more mycotoxins. *F. graminearum, F. culmorum*, and *F. oxysporum* are commonly producing high toxic mycotoxins through plant infections such as cereals including wheat, rice, oats, corn and barely (Yazar and Omurtag, 2008). Deoxynivalenol (DON) is one of the major mycotoxins that produced during FHB (Gorczyca *et al*., 2018; Nielsen *et al*., 2011). After harvesting infected plant crops such cereals via *F. graminearum*, DON is accumulated in grains particularly during late harvesting in the season then transfer to animal and human (Shah *et al*., 2018). The risk of human consumption of mycotoxins either directly by having contaminated cereals, grains and bread or indirectly via having animal productions such as milk and animal foods such as eggs. Since DON has associated with FHB, it has serious human health consequences. This mycotoxin causing abdominal pain, diarrhoea, headache along with fever and nausea (Sobrova *et al*., 2010). Besides, *Fusarium* mycotoxins have a direct effect on human immunity through suppression of immune cells proliferation and differentiation resulting in impair antibody pro-

duction via plasma cells and then decrease the rate of phagocytosis process by macrophages and neutrophils which has a serious impact on human health and infections (Gorczyca *et al*., 2018; Khlangwiset *et al*., 2011; Pierron *et al*., 2016).

Pathogen Identification

Molecular Marker

Generally, identification fungal pathogens at the species level are problematic particularly *Fusarium* species due to extreme similarities among conidia and mycelia. For this reason, the *Fusarium* genus has species complex level. Molecular identification through analysis DNA sequences is commonly used for identification of *Fusarium* species (van Diepeningen *et al*., 2014). Most of these techniques depend on isolation of the rDNA Internal Transcribed Spacer (ITS) region which is multi-copies among genomic DNA (Knoll *et al*., 2002). The result of ITS sequencing goes through BLAST on NCBI website for alignment and the check for closer species for molecular identification. However, ITS analysis is not a sufficient tool for *Fusarium* identification because of insufficient nucleotide differences (Balajee *et al*., 2009). Therefore, identification of *Fusarium* requires extra molecular characterisation such design and amplify specific genes of mycotoxins that are unique for *Fusarium* (Kelly *et al*., 2015; Kelly *et al*., 2016) or using an enzyme such as galactose oxidase (GO) (de Biazio *et al*., 2008). Extra specific molecular identification of *Fusarium* relay on protein-encoding genes such as Translation Elongation Factor (TEF-1α) gene (Al-Maqtoofi and Thornton, 2016; Harrow *et al*., 2010), or â-tubulin gene (Yli-Mattila *et al*., 2004).

Antigenic Marker

Detection a specific antigenic structure of fungi is became distributed for identification at the genus or species level. However, for *Fusarium* pathogens identification there is a very few studies have mentioned using monoclonal antibody (MAb) for identification via hybridoma technology to get a specific MAb for detection *Fusarium* antigens.

Al-Maqtoofi and Thornton (2016) developed MAb called ED7 specific for identification of *Fusarium* through binding with a specific antigenic epitope with glycoprotein chemical in nature and with no cross-reaction with closely related fungal species. Specific MAb IF8 using Enzyme-Linked Immunosorbent Assay (ELISA) was developed to *Fusarium* species identification by Hill and his group (Hill *et al*., 2006).

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