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Distribution and genetic chemotyping of *Fusarium graminearum* and *Fusarium culmorum* populations in wheat fields in the eastern Mediterranean region of Turkey

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ABSTRACT

Fusarium graminearum and *Fusarium culmorum* are among the major causal agents of Fusarium head blight, which reduces both crop yield and grain quality in wheat worldwide. The present study was conducted with 57 isolates collected from 23 different locations across four provinces in the 2011/2012 growing season. Out of the 57 *Fusarium* isolates, 32 isolates were identified as *F. graminearum* and 25 isolates were identified as *F. culmorum*. Both pathogens are of particular importance, since they produce several mycotoxins. Among these, deoxynivalenol (DON) and nivalenol (NIV) are well known for their toxicity towards human and animal health. Genetic chemotyping of *F. graminearum* and *F. culmorum* species indicated that both DON and NIV chemotypes were present in the surveyed area. Of the 32 *F. graminearum* isolates, the primer sets Tri13DON and Tri13NIV identified 87.5% as DON chemotypes and 12.5% as NIV chemotypes. Similarly, the 25 *F. culmorum* isolates displayed 88% DON and 12% NIV chemotypes. In addition, DON acetylated derivatives, 3-acetyldeoxynivalenol (3-AcDON) and 15-AcDON, were identified by polymerase chain reaction based methods. It was determined that 15-AcDON sub-chemotype was dominant in *F. graminearum* populations, whereas 3-AcDON was dominant in *F. culmorum* populations. This is the first report demonstrating the presence of *F. graminearum* and *F. culmorum* isolates and the distribution of 3-AcDON and 15-AcDON chemotypes in both *Fusarium* species in wheat fields of eastern Mediterranean region of Turkey.

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Fusarium graminearum; *Fusarium culmorum*; Fusarium head blight; genetic chemotyping; mycotoxin; nivalenol; deoxynivalenol

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops of the world in terms of both areas cultivated and amount of grain produced. Approximately one quarter of the total arable land is cultivated with wheat. The area under wheat cultivation during 2013/14 was 218.5 million hectares with a production of 713.2 million tons.[1] Compared with other cultivated crops, it ranks first in terms of both growing area and production share.

A number of different *Fusarium* spp., *F. graminearum*, *F. culmorum*, *F. avenaceum*, *F. poae*, *Microdochium nivale* and *Microdochium majus*, are commonly associated with Fusarium head blight (FHB) of wheat crops. Of these, *F. graminearum* and *F. culmorum* are potentially the most destructive species in terms of yield loss and mycotoxin production.[2–4] These *Fusarium* species are widely found in nature and are well known as pathogenic for plants and as producers of mycotoxins, which can have an adverse effect on human and animal health. The FHB disease in wheat inhibits the formation of grains by degrading starch granules in the kernels and producing wrinkled, hollow and coarse grains, which results in seed yield reduction.[5] In addition to yield reduction, the disease also reduces the quality of the grain by contaminating it with harmful mycotoxins, such as trichothecenes.[6] These mycotoxins are secondary metabolites produced by several genera of fungi, including *Fusarium*, causing great concern for animal and human health.[6] The incidences of B trichothecene chemotypes and their acetylated derivatives have been reported by different authors.[7] B trichothecene chemotypes, deoxynivalenol (DON) and nivalenol (NIV) differ only in their C-4 position; NIV has a hydroxyl group at this position and DON does not have a hydroxyl group.[8] These changes can affect greatly the toxicity.[9] NIV was reported as more toxic than DON.[10] The NIV chemotype was reported in some of the African, Asian, European and South American

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countries,[11–14] but not in the North American countries. Therefore, the NIV chemotype is restricted to specific regions of the world, as opposed to the DON chemotype, which is common all over the world.[13]

Because of the global importance of FHB, *F. graminearum* and *F. culmorum* have been intensively studied. The mycotoxin, produced by related *Fusarium* ssp. in cereal grains, is of increasing concern in the world, especially in EU and USA, where regulatory limits for mycotoxins permitted in grains and food are set by a range of directives and commission regulations.[15–17]

Both DON and NIV mycotoxins can be observed in the same geographical regions and usually one of the chemotypes is predominant. Thus, it is important to obtain information about the relationship between chemotype and geographical distribution, and to determine the dominant chemotype in the population in order to reduce the contamination risk of food or feed.

Diagnosis and genetic chemotyping of *Fusarium* isolates are very important. The most common methods used for genetic chemotyping are high performance liquid chromatography coupled with mass spectroscopy (HPLC/MS) or gas chromatography–mass spectrometry (GC/MS) analyses of extracts from cultures inoculated onto substrates, such as wheat, maize or rice.[18–20] HPLC comprises several methods with different normal-phase or reversed-phase columns, distinctive elution mixtures and gradients, detection methods, sample preparation and purification procedures. The mycotoxins are categorized by the retention time. In the case of GC/MS analyses, volatile mycotoxins at the column temperature are converted into volatile derivatives and MS sorts them according to their mass-to-charge ratio. Chemical analyses and chemical chemotyping by HPLC/MS and GC/MS are laborious and time-consuming processes.[21] However, various methods for molecular identification have been applied, such as conventional polymerase chain reaction (PCR), real–time PCR, multiplex PCR, DNA microarray and sequencing, in order to study the molecular characterization of trichothecene. However, the mycotoxin biosynthesis pathway via PCR is a useful method, as opposed to the conventional chemical methods, because of its sensitivity and potential specificity.[14,22–24] The genetic chemotyping in *Fusarium* is based on the sequences of the Tri7 and Tri3 highly conserved genes in *F. graminearum*.[25,26] Several PCR assays have been developed for these genes in order to enable the detection of fungi with potential to produce trichothecenes.[27–29]

The purposes of the present study were to investigate the distribution of *F. graminearum* and *F. culmorum* species' complex chemotypes in wheat fields grown in the eastern Mediterranean part of Turkey, to evaluate the possible mycotoxin contamination risks by focusing on species and mycotoxin composition, and to advise the industry of seasonal and regional risks of disease incidence and mycotoxin contamination.

Materials and methods

Collected isolates

The naturally infected mature wheat heads were collected during the 2011–2012 growing season covering 57 isolates in 4 provinces, including Adana (Kadirli, Yüreğir, Ceyhan, Karataş, Yumurtalık, İmamoğlu, Kozan and Feke), Osmaniye (Merkez, Toprakkale and Düziçi), Hatay (Antakya, Reyhanlı, Serinyol, Kırıkhan, İskenderun, Samandag and Altınözü) and Mersin (Silifke, Tarsus, Tuzla, Merkez and Erdemli) locations. Kernels were surface disinfected in 3% (v/v) sodium hypochlorite (NaOCl) for 3 min, rinsed with sterile distilled water and placed on potato dextrose agar (PDA, Merck, Darmstadt, Germany) plates. The plates were incubated at 25 °C under alternating light and dark periods (12 h photoperiod) for 6 d to induce sporulation. All *Fusarium* isolates were purified and the shape and size of macroconidia, nature of conidiogeneous cells, septations, absence of microconidia and chlamidospores on PDA were identified according to the morphological criteria.[30] *Fusarium* isolates were further identified using an optical microscope (Olympus, USA) at 400×–500× magnification, according to the morphological criteria on PDA.[31,32]

DNA extraction

Total genomic DNA was extracted from the mycelia of 6-day-old culture of each isolate grown on the PDA medium. The mycelia were freeze-dried (Edwards Modulyo freeze dryer) and grounded to a fine powder in liquid N_2. Fifty milligram of the powder was transferred to a 1.5-mL Eppendorf tube and mixed with 700 μL 2× cetyltrimethylammonium bromide, hexadecyltrimethylammonium bromide (CTAB) buffer (pH 8.0). The Eppendorf tubes were incubated at 65 °C for 30 min. After the incubation, an equal volume of phenol:chloroform:isoamyl alcohol (25:24:1; v:v:v) was added into the mixture and centrifuged (Heraeus Biofuge centrifuge, Germany) at 13,000*g* for 15 min. The supernatant was transferred into a new tube, mixed with 600 μL isopropanol and chilled to −20 °C, followed by another centrifugation step for 5 min at 15,000*g* at 4 °C. After drying at room temperature for 30 min, the DNA was dissolved in 100 μL of 10 mmol/L Tris, 1 mmol/L ethylenediaminetetraacetic acid (EDTA) (TE, pH 7.5) buffer.

PCR amplification

The PCR amplification was carried out by using 2.5 μL Fg16 F/R and Fc01 F/R specific fungal primers for *F. graminearum* and *F. culmorum*, respectively.[33] The primers and their properties, used to identify *F. graminearum* and *F. culmorum*, are listed in Table 1. The PCR was performed in a 50-μL reaction mixture containing 25 μL of 2× PCR master mix (0.05 U/μL *Taq* DNA Polymerase in reaction buffer (20 mmol/L Tris-HCl, 10 mmol/L $(NH_4)_2SO_4$, 10 mmol/L KCl, 2 mmol/L $MgSO_4$, 0.1% Triton X-100, pH 8.8), 0.4 mmol/L of each dNTPs, Fermentas, Lithuania), 8 μL (25−50 ng) fungal DNA, 2.5 μL (300 nmol/L) of each of the primers and 12 μL nuclease-free water.

The PCR conditions used for *F. culmorum* and *F. graminearum* detection were as follows: 95 °C for 5 min, followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 60 °C for 30 s and extension at 72 °C for 40 s, followed by a final extension at 72 °C for 5 min.

The genetic chemotyping of the collected isolates was done by PCR assays using five specific primer sets, Tri13F/Tri13DONR, Tri7F/Tri7R, Tri315F/Tri315R, Tri303F/Tri303R and Tri13NIVF/Tri13R (Table 1). The same as the above mentioned PCR conditions were applied to these specific primers with the exception that the denaturation temperature was 94 °C. The PCR conditions for the five primer sets was 94 °C for 4 min, followed by 35 cycles of 94 °C for 1 min, 60 °C for 40 s, 72 °C for 40 s and a final extension at 72 °C for 6 min.

The PCR products were electrophoresed on 2% agarose gels (1 × 40 mmol/L Tris base, 1 mmol/L EDTA, 20 mmol/L acetic acid (TAE) buffer adjusted to pH 8.0), stained with ethidium bromide (0.05 mg per 100 mL TAE buffer) and photographed under UV light with a Bio-Imaging System (Bio-RAD, Hercules, USA). All assays were repeated at least twice.

Results and discussion

F. graminearum and *F. culmorum* are causal agents of FHB disease of wheat. A total of 32 isolates from 20 different locations, belonging to Adana, Hatay, Mersin and Osmaniye provinces, were identified as *F. graminearum* and 25 isolates from 14 different locations, belonging to Adana, Hatay and Mersin, were identified as *F. culmorum* by using traditional identification techniques (Table 2). Both *F. graminearum* and *F. culmorum* were confirmed by traditional identification techniques and by species-specific PCR analyses. Based on morphological characteristics, the isolates produced canoe-shaped macroconidia at the initial stages of growth. At later stages, they developed macroconidia. The colonies of *F. culmorum* developed yellow aerial mycelia with red base on PDA. However, microconidia did not have short thick macroconidia with flattened apical cells. Based on the growth rate and colours of the colonies, *F. graminearum* and *F. culmorum* were identified from the samples. The conformation of 32 isolates as *F. graminearum* and 25 isolates as *F. culmorum* was made by using two sets of primers − Fg16F/Fg16R (producing 450 bp) and Fc01F/Fc01R (producing 570 bp), respectively. The samples that produced a common band, ranging from 450 bp, confirmed that the studied isolates were *F. graminearum*. The isolates that produced a 570 bp product were *F. culmorum*.

Both *F. graminearum* and *F. culmorum* produce different types of trichothecene mycotoxins, principally including nivalenol, deoxynivalenol, 3-acetyldeoxynivalenol (3-AcDON) and 15-acetyldeoxynivalenol (15-AcDON).[34] Those mycotoxins are harmful for people and livestock. Tri13DON and Tri13NIV primer sets were used to determine the DON and NIV chemotypes, respectively, of *F. graminearum* and *F. culmorum* isolates. Of the 32 analyzed *F. graminearum* isolates, the primer sets Tri13DON and Tri13NIV identified 87.5% (28/32) as

Table 1. Species- and chemotype-specific primers and the sizes of the expected PCR products.

Primer	Nucleotide sequence (5′−3′)	Product size (bp)	References
Fg16F	CTCCGGATATGTTGCGTCAA	450	Nicholson et al. [33]
Fg16R	GGTAGGTATCCGACATGGCAA		
Fc01F	ATGGTGAACTCGTCGTGGC	570	Nicholson et al. [33]
Fc01R	CCCTTCTTACGCCAATCTCG		
Tri13DONF	CATCATGAGACTTGTKCRAGTTTGGG	282	Chandler et al. [22]
Tri13R	GCTAGATCGATTGTTGCATTGAG		
Tri7F	TGCGTGGCAATATCTTCTTCTA	436, 458, 535	Chandler et al. [22]
Tri7R	TGTGGAAGCCGCAGA		
Tri315F	CTCGCTGAAGTTGGACGTAA	863	Wang et al. [25]
Tri315R	GTCTATGCTCTCAACGGACAAC		
Tri303F	GATGGCCGCAAGTGGA	583	Wang et al. [25]
Tri303R	GCCGGACTGCCCTATTG		
Tri13NIVF	CCAAATCCGAAAACCGCAG	312	Chandler et al. [22]
Tri13R	TTGAAAGCTCCAATGTCGTG		
Tri13F	CATCATGAGACTTGTKCRAGTTTGGG	282	Chandler et al. [22]
Tri13DONR	GCTAGATCGATTGTTGCATTGAG		

Note: Forward (F); reverse (R).

Table 2. Code, origin, identification and chemotyping of *F. graminearum* and *F. culmorum* isolates obtained from infected wheat tissues in the eastern Mediterranean provinces of Turkey.

Isolate	Location	Province	Species	NIV	DON	3-AcDON	15-AcDON
Fg1	Antakya	Hatay	*F. graminearum*	−	+	+	−
Fg2	Reyhanlı	Hatay	*F. graminearum*	−	+	−	+
Fg3	Reyhanlı	Hatay	*F. graminearum*	+	−	−	−
Fg4	Serinyol	Hatay	*F. graminearum*	−	+	−	+
Fg5	Kırıkhan	Hatay	*F. graminearum*	−	+	+	−
Fg6	Serinyol	Hatay	*F. graminearum*	−	+	−	+
Fg7	İskenderun	Hatay	*F. graminearum*	−	+	−	+
Fg8	İskenderun	Hatay	*F. graminearum*	−	+	+	−
Fg9	Samandag	Hatay	*F. graminearum*	−	+	−	+
Fg10	Altınözü	Hatay	*F. graminearum*	−	+	−	+
Fg11	Merkez	Osmaniye	*F. graminearum*	−	+	−	+
Fg12	Merkez	Osmaniye	*F. graminearum*	−	+	−	+
Fg13	Toprakkale	Osmaniye	*F. graminearum*	−	+	−	+
Fg14	Toprakkale	Osmaniye	*F. graminearum*	−	+	+	−
Fg15	Düziçi	Osmaniye	*F. graminearum*	−	+	−	+
Fg16	Kadirli	Osmaniye	*F. graminearum*	−	+	−	+
Fg17	Yüreğir	Adana	*F. graminearum*	−	+	−	+
Fg18	Ceyhan	Adana	*F. graminearum*	+	−	−	−
Fg19	Karataş	Adana	*F. graminearum*	−	+	−	+
Fg20	Yumurtalık	Adana	*F. graminearum*	−	+	−	+
Fg21	İmamoğlu	Adana	*F. graminearum*	−	+	−	+
Fg22	Kozan	Adana	*F. graminearum*	−	+	−	+
Fg23	Kozan	Adana	*F. graminearum*	−	+	−	+
Fg24	Feke	Adana	*F. graminearum*	−	+	−	+
Fg25	Silifke	Mersin	*F. graminearum*	−	+	−	+
Fg26	Tarsus	Mersin	*F. graminearum*	−	+	−	+
Fg27	Tuzla	Mersin	*F. graminearum*	−	+	+	−
Fg28	Merkez	Mersin	*F. graminearum*	−	+	−	+
Fg29	Antakya	Hatay	*F. graminearum*	−	+	−	+
Fg30	Antakya	Hatay	*F. graminearum*	−	+	+	−
Fg31	Reyhanlı	Hatay	*F. graminearum*	+	−	−	−
Fg32	Reyhanlı	Hatay	*F. graminearum*	+	−	−	−
Fg33	Kırıkhan	Hatay	*F. culmorum*	−	+	+	−
Fg34	Serinyol	Hatay	*F. culmorum*	−	+	+	−
Fg35	Merkez	Hatay	*F. culmorum*	−	+	+	−
Fg36	Merkez	Hatay	*F. culmorum*	−	+	−	+
Fg37	Merkez	Hatay	*F. culmorum*	−	+	+	−
Fg38	Reyhanlı	Hatay	*F. culmorum*	−	+	+	−
Fg39	Reyhanlı	Hatay	*F. culmorum*	+	−	−	−
Fg40	Kırıkhan	Hatay	*F. culmorum*	−	+	+	−
Fg41	Kırıkhan	Hatay	*F. culmorum*	−	+	+	−
Fg42	Yumurtalık	Adana	*F. culmorum*	−	+	−	+
Fg43	Karataş	Adana	*F. culmorum*	−	+	+	−
Fg44	Kozan	Adana	*F. culmorum*	−	+	−	+
Fg45	İmamoğlu	Adana	*F. culmorum*	−	+	+	−
Fg46	Ceyhan	Adana	*F. culmorum*	−	+	+	−
Fg47	Ceyhan	Adana	*F. culmorum*	−	+	+	−
Fg48	Ceyhan	Adana	*F. culmorum*	−	+	+	−
Fg49	Feke	Adana	*F. culmorum*	−	+	+	−
Fg50	Feke	Adana	*F. culmorum*	−	+	+	−
Fg51	Merkez	Mersin	*F. culmorum*	−	+	+	−
Fg52	Erdemli	Mersin	*F. culmorum*	−	+	+	−
Fg53	Erdemli	Mersin	*F. culmorum*	−	+	+	−
Fg54	Tarsus	Mersin	*F. culmorum*	−	+	+	−
Fg55	Tarsus	Mersin	*F. culmorum*	−	+	+	−
Fg56	Silifke	Mersin	*F. culmorum*	+	−	−	−
Fg57	Silifke	Mersin	*F. culmorum*	+	−	−	−

Note: Nivalenol (NIV); deoxynivalenol (DON); 3-acetyl-deoxynivalenol (3-AcDON); 15-acetyl-deoxynivalenol (15-AcDON).

DON chemotypes and 12.5% (4/32) as NIV chemotypes. Similar DON/NIV rate was obtained among the 25 isolates of *F. culmorum* – 88% (22/25) were DON chemotypes and 12% (3/25) were NIV chemotypes (Table 2). In both *F. graminearum* and *F. culmorum* populations, the most frequently isolated chemotype was DON and the less isolated chemotype was NIV. Of the 32 locations of *F. graminearum*, the NIV chemotype was found in 1 location in Adana and 3 locations in Hatay, however, DON chemotype was found in 7 locations in Adana, 11 locations in Hatay, 4 locations in Mersin and 6 locations in Osmaniye (Table 3). DON chemotype was further divided into 15-AcDON and 3-AcDON sub-chemotypes. In DON chemotypes of *F. graminearum* and *F. culmorum*,

Table 3. *F. graminearum* and *F. culmorum* chemotype occurrence in the surveyed regions.

	F. graminearum					*F. culmorum*				
Province	Total	NIV	DON	3-AcDON	15-AcDON	Total	NIV	DON	3-AcDON	15-AcDON
Adana	8	1	7	0	7	9	0	9	7	2
Hatay	14	3	11	4	7	9	1	8	7	1
Mersin	4	0	4	1	3	7	2	5	5	0
Osmaniye	6	0	6	1	5	0	0	0	0	0
Total	32	4	28	6	22	25	3	22	19	3

Note: Nivalenol (NIV); deoxynivalenol (DON); 3-acetyl-deoxynivalenol (3-AcDON); 15-acetyl-deoxynivalenol (15-AcDON).

15-AcDON producing isolates were dominant in *F. graminearum* population, whereas 3-AcDON producing isolates were dominant in *F. culmorum* (Figure 1). The 3-AcDON sub-chemotype in *F. graminearum* was found in four locations in Hatay, one location in Mersin and one location in Osmaniye provinces. The 15-AcDON sub-chemotype was found in seven locations in Adana and Hatay, three locations in Mersin and five locations in Osmaniye (Table 3). Within the *F. culmorum* locations evaluated, however, NIV chemotype was found in one location in Hatay and two locations in Mersin, however, DON chemotype was found in nine locations in Adana, eight locations in Hatay and five locations in Mersin. The 3-AcDON sub-chemotype in *F. culmorum* was found in seven locations in Adana, seven locations in Hatay and five locations in Mersin provinces. The 15-AcDON sub-chemotype was found in two locations in Adana and one location in Hatay provinces (Table 3).

The genetic chemotyping of the 57 *F. graminearum* and *F. culmorum* isolates from 23 different locations in four provinces, showed that both DON and NIV chemotypes were present in the eastern Mediterranean region of Turkey. This is consistent with earlier studies of mycotoxin screenings, carried out in the western part of Turkey, which obtained results that both DON and NIV chemotypes were present in wheat fields and the DON chemotype of *F. graminearum* and *F. culmorum* were more frequently isolated than the NIV chemotype.[35,36] However, Mert-Türk and Gencer [24] did not detect 3-AcDON and NIV chemotypes in three western provinces of Turkey. DON and NIV chemotypes of *F. graminearum* and *F. culmorum* have also been identified in many countries in Europe, North and South America, Africa and Asia.[14,23,37–42] It was reported that the NIV chemotype was more toxic than DON.[10] Therefore, NIV is a serious threat for both people and animals and it is necessary to reduce the toxin production by using resistant cultivars and applying cultural methods.

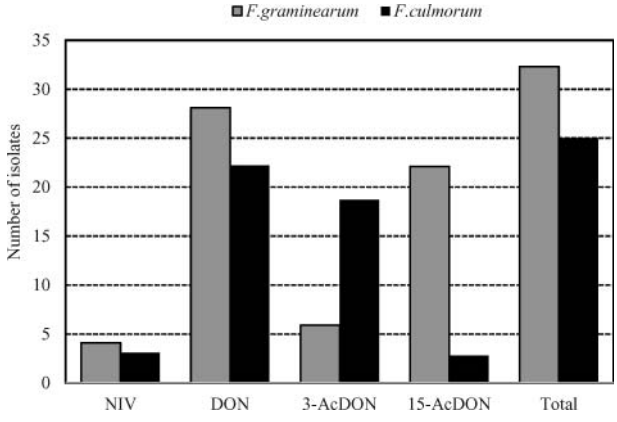

Figure 1. Trichothecene chemotypes of *F. graminearum* and *F. culmorum* isolates collected from four provinces in Turkey.
Note: Nivalenol (NIV); deoxynivalenol (DON); 3-acetyldeoxynivalenol (3-AcDON); 15-acetyldeoxynivalenol (15-AcDON).

The analysis of *F. graminearum* showed that NIV and DON chemotypes coexist in Adana and Hatay provinces, whereas the NIV chemotype was not detected in Osmaniye and Mersin provinces (Table 3). When *F. culmorum* isolates were in consideration, mixed populations of NIV and DON chemotypes were detected in Hatay and Mersin provinces. However, NIV chemotype was not detected in Adana province and neither NIV nor DON chemotypes were detected in Osmaniye province. Similarly, in previous studies, mixed NIV and DON chemotypes have been reported in *F. graminearum* [14,43] and *F. culmorum* [44] populations.

Sub-chemotyping analysis indicated that the majority of *F. graminearum* isolates displayed more of the 15-AcDON sub-chemotype, whereas *F. culmorum* isolates displayed more of the 3-AcDON sub-chemotype. Similar results were reported by Quarta et al. [45] and Stêpieñ et al. [46] that the 3-AcDON sub-chemotype was the most frequent chemotype among the *F. culmorum* isolates, whereas the 15-AcDON sub-chemotype was the most frequent chemotype among *F. graminearum* isolates. Our finding for *F. graminearum* was consistent with the finding of Alvarez et al. [42] that the 15-AcDON chemotype had higher frequency than the 3-AcDON. On the other hand, the opposite results were reported by Quarta et al., [47] whose study reported that the 3-AcDON chemotype was the most dominant chemotype in some parts of Asia and China, Australia, New Zealand and northern Europe. Earlier studies showed that the 3-AcDON chemotype of *F. graminearum* was more aggressive than the 15-AcDON

chemotype in resistant and susceptible wheat cultivars. [12,48] The increase in the incidence of *F. graminearum* and *F. culmorum* populations in the eastern Mediterranean region of Turkey could potentially have resulted in increased levels of DON and reduced levels of NIV contamination in wheat grains, depending on the toxin profile of both *Fusarium* species. However, the high proportion of DON chemotype, found within the *F. graminearum* and *F. culmorum* populations, as reported here, indicated that DON contamination was high and NIV contamination was low in wheat grains in the eastern Mediterranean region of Turkey.

Conclusions

The fungal pathogens, *F. graminearum* and *F. culmorum*, are among the most common causal agents of FHB disease worldwide. Among the 57 isolates collected from four provinces in the eastern Mediterranean region of Turkey, 32 isolates were identified as *F. graminearum* and 25 isolates were identified as *F. culmorum* by traditional identification techniques and PCR assay. Both species produce trichothecenes, most frequently DON and less frequently NIV. DON-producing isolates were further distinguished on the basis of the predominant acetyl DON derivative that they produce – 3-AcDON and 15-AcDON sub-chemotypes. The majority of *F. graminearum* isolates displayed the 15-AcDON sub-chemotype, whereas *F. culmorum* isolates displayed the 3-AcDON sub-chemotype. The information of *Fusarium* chemotypes and their distribution in the wheat cultivation areas could be critical for the projection of disease development, integrated disease control programmes and mycotoxin contamination.

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Disclosure statement

No potential conflict of interest was reported by the authors.

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