Essay

Resistance to *Fusarium* causing rots in wheat: topicality and prospects for its use in Mexico

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Abstract

Root rot, crown and stem rot in wheat are considered a serious threat to this cereal in various parts of the world since the losses that cause grain yield and quality reach up to 89% and can be comparable to those caused by rust, in addition to the fungi associated with these rotting synthesize mycotoxins that can contaminate food products. This problem in Mexico has been little studied; however, in recent years, these diseases in irrigation and temporary wheats have been more incidents which is causing concern in the producers of this cereal in the country. This review summarizes current aspects of the disease, the sources of resistance available worldwide, as well as how this resistance operates in the *Fusarium*-wheat patosystem. The genetic basis of resistance to root, stem and crown rot of hexaploid wheats has been examined; through the mapping of Quantitative Trait Loci (QTL). To date, 44 QTL have been identified on 14 chromosomes with alleles that induce resistance to this disease and that are derived from hexaploid wheats and close relatives. Genetic improvement for this disease through introgression of alleles with these QTL is the most feasible strategy and the pyramidation of these QTL seems to be the most viable strategy in genetic improvement programs. Important step for the management of the problem in the wheat producing areas in Mexico

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Globally, wheat cultivation is affected by different microorganisms that decrease their yield, of these, the fungi of the genus *Puccinia* that cause different rusts are considered the most harmful; however, another group of fungi causing root, stem and crown rot (PRC) belonging to a complex of the genus *Fusarium* (Mariscal *et al*., 2018) has been identified for soil pathogens in this cereal.

In the field, PRC can cause brown lesions in seedlings that appear in the root, crown, in the leaf sheaths and in the lower stem and in adult stage, a copper wilt of the spikes of the diseased plants is observed, different from the hue white caused by spike gnaw or the usual golden bream of healthy ripe spikes (Mariscal *et al*., 2018). This problem has a greater impact when there is a period of water stress during the development of the seedling and after the anthesis until maturity (Moya, 2013; Liu *et al*., 2015).

The importance of these fungi, in addition to the yield losses they cause and can reach up to 89% (in monetary value, losses of up to 68 million dollars) (Klein *et al*., 1991; Smiley *et al*., 2005; Liu *et al*., 2015), is that, due to their biology, they can develop persistent survival structures (clamidospores) that can remain viable in the soil for several years.

They can synthesize mycotoxins: zearalenone, nivalenol, deoxinivalenol, 3-acetyldeoxynivalenol, 15-acetyldeoxynivalenol, diacetoxyscirpenol, neosolaniol, fusarenone X and fumonisins that contaminate the grain and other tissues (Ferreira *et al*., 2006; Mudge *et al*., 2006; Pinto *et al*., 2008; Orantes *et al*., 2011; Martínez *et al*., 2014; Rebib *et al*., 2014) and may even contaminate food products such as flour and buckwheat (Bertecheni *et al*., 2012).

Different species of *Fusarium* that cause PRC have been identified. Globally, the most frequent species and with which the majority of genetic studies have been done are: *F. graminearum* and *F. pseudograminearum* (Kazan and Gardiner, 2018), but *F. culmorum* has also been identified (Scherm *et al*., 2013), *F. avenaceum*, *F. acuminatum*, *F. crookwellense*, *F. poae* (Cook, 2010), *F. equiseti*, *F. hostae* and *F. redolens* (Shikur *et al*., 2018) causing such diseases. In Mexico, in irrigation and temporary wheat, the species *F. proliferatum*, *F. poae*, *F. verticillioides*, *F. subglutinans*, *F. oxysporum*, *F. thapsinum*, *F. andiyazi*, *F. graminearum*, *F. avenaceum*, *F. equiseti* and *Microdochium nivale* (Gilchrist *et al*., 2005; Limón *et al*., 2016; Leyva *et al*., 2017; Rangel *et al*., 2017). PRC in wheat can occur in all the producing areas of this cereal and are considered more aggressive in humid climates (Gilchrist *et al*., 2005).

In areas where the humidity is low, the infection is almost exclusively caused by the inoculum present in crop residues (Gilchrist *et al*., 2005). It has been observed that the incidence of the different species of the genus *Fusarium* associated with PRC varies year by year and depends largely on the climatic conditions and geography of the wheat regions, with some species being more frequent in low humidity regions relative low while others affect more in high regions with moderate to high relative humidity (Gilchrist *et al*., 2005).

This indicates their high level of adaptation as members of a complex of pathogens that respond to changes in temperature, humidity and edaphic factors (Moya, 2013). It is also mentioned that warm temperatures in the months of February, March, April and May, as well as early sowing, water stress, soil with high temperatures, soil cracking induced by rains, and even the lack of microelements such as Zinc (usable by the plant) in the soil, lead to a higher incidence of the disease (Singh *et al*., 1996; Smiley *et al*., 2005; Saremi *et al*., 2007; Khoshgoftarmanesh *et al*., 2010; Poole *et al*., 2013).

Several authors report that sowing under minimum or conservation tillage, rotation schemes (mainly with corn and barley) and the increase in the dose of nitrogen are the main agronomic factors that increase the incidence of *Fusarium* species that cause PRC (Lamprecht *et al*., 2006; Chakraborty *et al*., 2006; Liu *et al*., 2015; Limón *et al*., 2016; Chekali *et al*., 2016; Zheng *et al*., 2017). It has been observed that plants with excess of N deplete the water supply of the soil more quickly so that they suffer from premature water stress which leads to a higher incidence of the disease (Davis *et al*., 2009).

On the other hand, several species of this genus of fungi, which cause leaf spots and blight on the spike and rot on the spike (stem of the spike), remain as contaminants of the same grain that serves as a source of primary inoculum from where the PRC from seedling (Stenglein *et al*., 2012). According to several authors, control strategies that decrease the incidence of *Fusarium* species that cause PRC in wheat include: 1) crop rotation with crucifers or legumes that help break the fungus's biological cycle (Lamprecht *et al*., 2006; Chekali *et al*., 2016); and 2) threshing at optimal dates that allows less grain contamination; 3) adequate and fractional fertilization that avoids the application of excessive doses of N; 4) the incorporation of zinc in soils lacking this element; 5) crop waste management; 6) Seed treatment with fungicides; and 7) the use of varieties resistant to disease, with tolerance to water stress, or efficient in the use of zinc (Sing h *et al*., 1996; Burgess *et al*., 2001; Edwards, 2004; Burgess, 2005; Lozano *et al*., 2006; Davis *et al*., 2009; Khoshgoftarmanesh *et al*., 2010; Zheng *et al*., 2017).

Globally and in Mexico, the genetic improvement of wheat for resistance or tolerance to this disease should be a constant activity, as well as the identification of sources of resistance and studies that allow understanding the genetic basis of resistance to PRC in this cereal. This review aimed to summarize the advances of genetic improvement for PRC, as well as the genetic basis of resistance to this disease in flour wheats.

Root and stem rot resistance components

The genetics of PRC resistance has been reported in some wheat genotypes and the available results suggest that this resistance, as well as the resistance to spike rust (RE) caused by *F. graminearum* or *F. pseudograminearum*, is also of a polygenic nature, of minor or quantitative genes; although, due to the magnitude of the reduction in the severity of crown rot that may be conferred by a single QTL, some authors suggest that this resistance may be due to larger genes (Ma *et al*., 2010).

The common etiology between RE and PRC raises the possibility that resistance to these two diseases is given by the same genes (Bing *et al*., 2010). However, these authors when evaluating the same wheat genotypes for both resistance to RE and PRC, found that the QTL associated with both resistances are found on different chromosomes.

Similarly, it has been reported that QTL associated exclusively with resistance to PRC are also found in different chromosomes. The above suggests that the genetic mechanism for PRC resistance is multigenetic and different from that of RE resistance (Ma *et al*., 2010; Bing *et al*., 2010). Ma *et al.* (2014) mention that the `Sumai 3' genotype, the source of the best resistance known for RE, has a QTL on the short arm of chromosome 3B, considered as a major locus that provides resistance to this disease.

The 3BS locus contains a glycosyltransferase gene with the potential to detoxify mycotoxin deoxinivalenol which is a virulence factor; however, the QTL 3BS does not confer any significant level of resistance to PRC (Ma *et al*., 2014). In another study Ma *et al*. (2010) confronted the species *F. graminearum* and *F. pseudograminearum* against a population of plants of the cross between 'CSCR6'/'Lang'. With these two species, the same two QTL were detected in the population, which suggested that resistance to PRC in wheat is not specific to the species of the fungus.

It is important to mention that in resistance studies with hard wheats it has been observed that tetraploid wheats are more susceptible to PRC than hexaploids (Ma *et al*., 2012). It has also been observed that resistance to this disease may be influenced by morphological characteristics of the plant since Liu *et al*. (2010) when studying the relationship between plant height and crown rot, they found that dwarf wheat lines were more resistant to crown rot than high lines, due to physiological and structural characteristics such as cell density in the dwarf lines.

Genetic sources for wheat resistance improvement

In countries such as the United States of America, Australia, India and Canada, PRC have been a problem known for several years, so efforts to find sources of resistance have been greater. Different authors have evaluated, in common, some hexaploid wheat genotypes confronted against *F. pseudograminearum*, observing that some materials such as '2-49', 'IRN497' and 'Sunco'.

They have been the most tolerant to PRC with percentages of disease severity ranging from 4.2-32% in seedlings and 24-67.1% in adult plants (Bovill *et al*., 2010; Martin *et al*., 2015). Bing *et al*. (2010) when evaluating 32 wheat genotypes confronted against *F. graminearum* and *F. pseudograminearum*, they observed that the seedling genotypes that were more tolerant to these two species in the greenhouse were '2-49', 'Abura komugi', 'Aso zairai', 'Aso zairai 11', 'Chile' and 'Ernie' with values on the visual scale used from 0= no symptoms to 1= obvious necrotic lesions in the beetle or in the sheath of the first leaf.

The tolerance of flour wheat materials has also been evaluated based on the percentage of withered spikes, reflecting root damage, and in this case, the materials that were classified as tolerant, to these two fungi, with <20% spikes in this condition were '2-49', 'L2-120', 'Frontana', 'Janz', 'Lang', 'EGA Wiley', 'Magenta', 'Drysdale', 'Hartog', 'Wyalkatchem' and 'E34' (Klein *et al*., 1985; Wildermuth and McNamara, 1994; Li *et al*., 2008). Ma *et al.* (2010) when evaluating different wheat genotypes confronted against *F. graminearum* and *F. pseudograminearum* found that the 'CSCR6' genotype was the most tolerant of the disease.

In another similar study, *et al*. (2006), when evaluating different wheat genotypes in a greenhouse trial, against these two species of the fungus, determined that the genotypes 'Sunco', 'Lang', '22397', 'Rowan', 'Sunstate', 'Baxer', 'Sunbri' and 'Sunvale' were the ones with the lowest severity index of the illness. Wildermuth *et al*. (2001); Wallwork *et al*. (2004) evaluated different lines of flour wheats, synthetic wheats and hard wheats confronted against *F. pseudograminearum*.

According to these authors, the most tolerant genotypes in adult plants were the flour wheats '2-49', 'Gluyas Early', 'Kukri' and 'Sunco', the synthetic wheats 'CIMMYT elite synthetic 62', 'CIMMYT elite synthetic 97', 'CIMMYT scab synthetic 92', 'CIMMYT scab synthetic , 'CIMMYT scab synthetic 101' and 'CIMMYT scab synthetic 104' and wheats 'AUS 11434' (*T. dicoccum*), 'AUS 18694' (*T. zhukovskyi*), 'AUS 18743' (*T. dicoccum*) and 'T96-5317' (*T. dicoccum*), all these lines presented a severity of the disease from 0% to 50%.

When assessing necrosis due to greenhouse seedlings, Leyva *et al*. (2017) used the combination of *F. proliferatum* and *F. graminearum* against different wheat genotypes, observing the Mexican varieties Galvez M87', 'Castrejon F97', 'Tlaxcala F2000', `Salamanca S86' and 'Maya S2007' as tolerant. Ma *et al*. (2010) evaluated a backcross between the parents `Bellori'/'CSCR6', the first a durum wheat (*Triticum durum*) highly susceptible to PRC and the second a genotype of the disease-resistant *T. spelta* species, obtained a population they confronted against *F. pseudograminearum*. These authors observed that some segments of a large section of chromosome 6B of the donor resistant parent significantly increased resistance to PRC in durum wheat.

QTL mapping for resistance to root and crown rot in wheat

Table 1 shows the list of significant QTL identified in hexaploid wheats and close relatives in different studies worldwide. Wheat materials are presented where the QTL were identified, the denomination of the QTL (although in many cases these are mentioned without denomination), the chromosome where they were identified, either in their long arm (L) or short arm (S), the or markers used for identification, phenotypic variance in percentage contributed by each QTL, the species of the fungus used in the study, the evaluated character, the stage of the plant where the resistance given by the QTL was observed and the references.

Table 1. List of QTL that confer resistance to root, crown and stem rot in wheat.

GEN	QTL	LOC	MA	VF%	EH	CA	TR	REF
EGA Wylie	Qcrs.cpi-5D Qcrs.cpi-2D Qcrs.cpi-4B.1 Qcrs.cpi-4B.2	5DS 2DL 4BS 4BS	1215315|F|0-1237596|F|0 1131013|F|0-1246993|F|0 100004319|F|0-2324159|F|0 1108472|F|0-1093616|F|0	31.1 20.2 16.9 18.8	Fp	SE	PL PL PL PL	Zheng *et al*. (2014)
Ernie	SD	3BL	wPt-1151-wPt-1834	18.7-34.6	Fp	SE	PL	Bing *et al*. (2010)

GEN	QTL	LOC	MA	VF%	EH	CA	TR	REF
2-49 W21MMT70 2-49 2-49 Sunco	QCr.usq-1D.1 QCr.usq-3B.1 SD QCr.usq-4B.1 QCr.usq-2B.2	1D 3B 7A 4B 2B	wPt-3738-cfd19 wPt-7301-wPt-0365 wPt-4748-wPt-8418 wPt-4535-gwm251 wPt-5374-wPt-0434	10.4 20.4-40.5 3.8 1.2-19.1 3.3-8.4	Fp	SE	PL PL PL PL PL	Bovill *et al.* (2010) Collard *et al.* (2005)
Thinopyrum elongatum	7EL QTL	7EL	Xpsr129-Xgwm282	-	Fp, Fc	ES, EN	PL	Ceoloni *et al.* (2017)
CSCR6 Lang	Qcrs.cpi-3B Qcrs.cpi-4B	3BL 4B	wPt10505-wPt2277 wPt7569-wPt4918	29.7-48.8 14.6-44	Fp, Fg	SE	PL PL	Ma *et al.* (2010) Zheng *et al.* (2015)
Macon Sunco Otis	Qcrs.wsu-3BL SD SD SD SD SD SD Qcrs.wsu-3BL Qcrs.wsu-3BL SD	3BL 4D 4D 7A 3BS 4B 2B 3BL 3BL 3BS	Xgwm299-Xgwm247 - - wPt-3702 wPt-5261-wPt-0021 wPt-667746 - Xwmc471 Xwmc471 Xgwm299-Xgwm247	2-36 9-11 7 20 3-11 7-28 8 7-12 2-22 3	Fp	SE	PL PA PL PA PA PA PA PL PL PA PL PA PA	Poole *et al.* (2012)
2-49 Sunco IRN497	SD SD SD SD SD SD SD SD SD SD SD	1AS 1BS 1DL 3BS 4BS 2BS 2DS 3BL 2AL 4BS 6DL	barc148-gwm164 gwm11-cfd65 cfd19-wmc216 gwm131-wPt-9310PCR wpt-7569PCR-wmc467 gwm630-cfa2278 gwm484-gwm102 wmc236-wPt-0365PCR gwm95-cfa2043 wpt-7569PCR-wmc467 cfd188-cfd47	3.3-16.4 4.4-12.6 6.6-17.4 6.1 4-20.4 6.1-12.2 6-12.1 18.8 19.7 7.5-20.4 7.1-7.8	Fp	SE	PL PA PA PL PL PA PL PA PL PA PA PL PA PA PL PA	Martin *et al.* (2015) Collard *et al.* (2005)
Kukri	SD	4B	Xwmc048c-Xgwm149	48	Fp, Fc	SE	PA	Wallwork *et al.* (2004)

GEN	QTL	LOC	MA	VF%	EH	CA	TR	REF
W21MMT70	SD	2D	cfd11a-wmc190	10.2	Fp	SE	PL	Bovill *et al*. (2006)
		5D	gwm190-cfd8	4.8-28.1			PL	
Mendos	SD	2B	gdm086-barc200	13.2-19.9			PL	
2-49	SD	1AL	Xwmc24-	10	Fp	SE	PL	Collard *et al*. (2005)
	SD	1DL	Xbarc148	21			PL	
	SD	2AS	Xcfd19-	6			PL	
	SD	7BS	Xwmc216	8			PL	
Janz	SD	2BS	Xgwm339-	5			PL	
			Xgwm425					
			Xgwm400-					
			Xwmc476					
			Xgwm388-					
			Xbarc349.1					
Gluyas Early	QCr.usq-1D1	1DL	Xcfd19-	19	Fp	SE	PL	Collard *et al.* (2006)
Janz	QCr.usq-2B1	2BS	Xgwm337	5			PL	
			Xgwm337-					
			Xwmc216					

GEN= genotype; QTL= QTL denomination; SD= no denomination; LOC= chromosome where it is located; MA= markers and/or interval; VF%= phenotypic variation in percentage; EH= fungus used; Fp= *Fusarium pseudograminearum*; Fc= *F. culmorum*; Fg= *F. graminearum*; CA= character evaluated; SE= severity of the disease; ES= symptom extension; EN= extent of necrosis; PL= seedling; PA= adult plant; REF= reference.

Resistance genes associated with root and crown rot

Ma *et al*. (2014) when studying and identifying linked genes and transcriptional changes of the QTL called Qcrs-3B, of the 3BL chromosome, in isogenic wheat lines, observed the induction of 1809 genes after inoculation of seedlings with *F. pseudograminearum*. 638 highly regulated genes contained 46 pathogen-related coding proteins, 42 encoding kinase-like receptors, 21 encoding P450 cytochromes, 17 encoding glutathione transferase and 10 encoding detoxification-related proteins.

These genes also contained proteins involved in the pathogen-host interaction: 14 for proteins related to disease resistance, 6 for proteins related to cell wall, 4 for WIR1 proteins (wheat-induced type 1 resistance), 7 for factors of WRKY transcription, 3 for ascorbate peroxidases; 6 for phenylalanine-ammonium liases and 14 for germin-like proteins (GLP).

As well as, genes for the biosynthesis of phytohormones involved in the wheat-*Fusarium* interaction: jasmonic acid, ethylene and salicylic acid. On the other hand, 22 low regulation genes studied were related to the encoding of RGA1 resistance proteins, calcium-bound proteins with the EF-hand domain and a senescence-associated protein (Ma *et al*., 2014). Motallebi *et al*. (2015) after inoculating plants of the resistant genotype 'Sumai3' with *F. culmorum*.

They observed the synthesis of defense-related enzymes: superoxide dismutase (SOD), catalase (CAT), peroxidases (POX), polyphenol oxidase (PPO), lipoxygenase (LOX) and phenylalanine ammonium lyase (PAL). Zheng *et al*. (2015) when mapping the QTL Qcrs.cpi-3B in nearby isogenic wheat lines, they found that in the locus interval where this QTL was found, genes encoding different disease resistance proteins were identified as rga2, rpm1, rga4, of synthesis of metallothionein, NBS-LRR of partial resistance, and those such as proteins 2 and 3 similar to rpp13, similar to those of the AP3 complex of the beta-A subunit and similar to those of gibberellin-2-beta-dioxygenase 8.

Desmond *et al*. (2006) studied the expression of 26 wheat genes related to resistance to *F. pseudograminearum*. The expression of these genes was evaluated in the susceptible genotype 'Kennedy' and in the partially resistant genotype 'Sunco'. The induction of eight defense genes was observed: PR1.1, PR2 (β, 1-3 glucanase), PR3 (chitinase), PR4 'wheatwin' - ribonuclease activity), PR5 (thaumatine-like protein), TaPERO (peroxidase), PR10 and TaGLP2a (germin-like protein).

The TaPERO gene encodes a peroxidase enzyme that has frequently been implicated in cell wall modifications and in the metabolism of reactive oxygen species. The TaGLP2a gene encodes a protein with superoxide dismutase activity. The PR1, PR2, PR3, PR4 and PR5 genes encode homologs of plant PR proteins. Wang *et al*. (2018) when evaluating wheat materials `Florence-Aurore' (resistant), 'Sumai 3' (susceptible), 'Frontana' (susceptible) and 'Ning 7840' (highly susceptible) against *F. graminearum* observed the expression of the genes TaUGT12887, TaUGT3, CYP709C1, WZF1, WFhb1-c1 and TaMDR1 in root tissue cells from day 1 to 21 after inoculation.

These genes are mainly associated with the ability of the plant to detoxify DON mycotoxins, the trichothecene family and jasmonate signaling. Earlier, it is mentioned that wheat plants show more severe symptoms of PRC under water stress, both in greenhouse and field studies. One of the possible reasons for the interaction between drought and resistance to PRC, is that drought can affect some morphological characteristics of the plant such as height and days to spike.

Characters that have been reported to have a strong influence on PRC resistance in wheat and barley. Another possibility is that the same genes could be associated in both drought tolerance and resistance to PRC. In this regard, Ma *et al*. (2015) studying malondialdehyde, a product of lipid peroxidation, frequently used as a parameter to assess the cellular damage of plants due to water stress, mapped the QTL called Qheb.mda-3B on chromosome 3B. This QTL controls the malondialdehyde content in both plants with and without water stress.

The QTL Qheb.mda-3B was located in the same genetic range as the QTL Qcrs.cpi-3B that controls the resistance to PRC. The results of these authors again suggest that the same set of genes is probably involved in both drought tolerance and resistance to PRC.

Strength improvement for root and crown rot in wheat

Genetic pyramidation has been used as an effective approach that allows multiple and durable resistance to be achieved, and has been effective for resistance to PRC in barley, rice scalding, sunflower mildew and yellow linear rust in wheat (Chen *et al*., 2015; Zheng *et al*., 2017). Zheng *et al*. (2017) evaluated the QTLs called Qcrs.cpi-3B, Qcrs.cpi-5D and Qcrs.cpi-2D, of two segregating populations from the PRC resistant progenitors, ‘CSCR6’ (accession of *Triticum spelta*) with locus 3BL, ‘EGA Wylie’ (Australian commercial variety) with the two 5DS and 2DL loci and the Australian and Chinese susceptible commercial varieties ‘Lang’ and ‘Sumai3’, respectively.

Both populations clashed against *F. pseudograminearum*. The results of this study showed a significant variation in the values of the disease index (IE) in the lines with the same alleles of the QTL evaluated. Comparing with the lines without any resistant allele, those with a resistance allele reduced the IE values between 21 and 33%. Lines with a combination of two resistance alleles reduced IE values between 36 and 38% and lines with all three alleles reduced IE values, 60% on average.

Bovill *et al*. (2010) compared the resistance levels of individuals with different combinations of QTL from each of the donor parents. In the ‘2-49’/‘W21MMT70’ population, the lines with the presence of the three QTL, QCr.usq-1D.1, QCr.usq-3B.1 and one with no denomination located on chromosome 7A, were significantly more resistant to PRC than those without any QTL. The lines with the combination QCr.usq-1D.1 and QCr.usq-3B.1 showed a reduction in the severity of the crown rot of 51.2%, compared to those without any QTL.

The lines without the two QTL mentioned above, but with the QTL of chromosome 7A, showed a severity of 15% lower than those lines without any of them. In the ‘2-49’/‘Sunco’ population it was observed that the lines with three QTL were significantly more resistant to crown rot with 28% less severity than those without any resistance allele. Bovill *et al*. (2006) identified three QTL located on chromosomes 2D, 5D and 2B, the first two inherited from the hexaploid wheat line ‘W21MMT70’ and the third inherited from ‘Mendos’.

A population of 95 double haploid lines from the cross between these two parents was evaluated. The population was confronted against *F. pseudograminearum*. The results of this study showed that those lines with only one of the three alleles showed percentages of disease severity >50 <60%, the lines with the combination of two alleles had percentages of the disease >45 <50%, and those with the three alleles they presented percentages of >40 <45%. The lines without any allele presented percentages of the average disease of 97.6%.

Conclusions

Root, crown and stem rot in wheat flour is a serious problem worldwide. In Mexico this problem, called the wheat dryer or fusariosis, has been increasingly incident and the losses it causes could be compared to those caused by rust. Given this scenario, it is urgent that genetic improvement programs develop a greater number of varieties resistant to this disease.

For this, the constant evaluation of advanced varieties and lines of wheat is necessary for their resistance or tolerance to the disease to have a range of materials that can be used as parents for future crossing plans along with genetic pyramidation. Several QTLs have been detected in wheat materials from different parts of the world, but the identification of resistance QTL in wheat materials adapted to the different wheat regions of the country has been null, so it is necessary to start with this type of study.

Cited literature

Bertecheni, F. C.; Almeida, F. G. C.; Bertecheni, G. K.; Albuquerque, A. T. C.; Tessmann, D. J.; Machinski, J. M. and Barbosa, T. I. P. 2012. Use of the polymerase chain reaction for detection of *Fusarium graminearum* in bulgur wheat. Ciéncia e Tecnologia de Alimentos 32(1):201-208. Doi: dx.doi.org/10.1590/S0101-20612012005000027.

Bing, L. H.; Qiang, X. G.; Ma, J.; Ru, L. G.; Min, W. S.; Ban, T.; Chakraborty, S. and Ji, L. C. 2010. Genetic relationships between resistences to *Fusarium* head blight and crown rot in bread wheat (*Triticum aestivum* L.). Theor. Appl. Genet. 121:941-950. Doi: 10.1007/s00122-010-1363-0.

Bovill. W. D.; Ma, W., Ritter, K.; Collard, B. C. Y.; Davis, M.; Wildermuth, G. B. and Sutherland, M. W. 2006. Identification of novel QTL for resistance to crown rot in the doubled haploid wheat population ‘W21MMT70’ x ‘Mendos’. Plant Breed. 125:538-543. Doi: 10.1111/j.1439-0523.2006.01251.x.

Bovill, W. D.; Horne, M.; Herde, D.; Davis. M.; Wildermuth, G. B. and Sutherland. M. W. 2010. Pyramiding QTL increases seedling resistance to crown rot (*Fusarium pseudograminearum*) of wheat (*Triticum aestivum*). Theor Appl Genet 121:127-136. Doi:10.1007/s00122-010-1296-7.

Burgess, L. W.; Blackhouse, D.; Summerell. B. A. and Swan. L. J. 2001. Crown rot of wheat. *In*: Fusarium: Nelson, P. E. memorial Symposium. Summerell, B. A.; Leslie, J. F.; Blackhouse, D.; Bryden, W. L. and Burgess, L. W. (Eds.). St. Paul, MN. 271-294 pp.

Burgess. L. W. 2005. Intermediate hosts and the management of crown rot and head blight. Final Report Project Code US216. Grains Research & Development Corporation. Kingston. www.grdc.com.au.

Ceoloni, C.; Forte, P.; Kuzmanovic, L.; Tundo, S.; Moscetti, I.; De, Vita, P.; Virili, M. and D’Ovidio, R. 2017. Cytogenetic mapping of a major locus for resistance to Fusarium head blight and crown rot of wheat on *Thinopyrum elongatum* 7EL and its pyramiding with valuable genes from *Th. ponticum* homoeologous arm onto bread wheat 7DL. Theor Appl. Genet. 130(6):2005-2024. DOI 10.1007/s00122-017-2939-8.

Chakraborty, S.; Liu, C. J.; Mitter, V.; Scott, J. B.; Akinsanmi, O. A.; Ali, S.; Dill-Macky, R.; Nicol, J.; Backhouse, D. and Simpfendorfer, S. 2006. Pathogen population structure and epidemiology are keys to wheat crown rot and Fusarium head blight management. Australasian Plant Pathol. 35(6):643-655. Doi: 10.1071/AP06068.

Chekali, S.; Gargouri, S.; Rezgui, M.; Paulitz, T. and Nasraoui, B. 2016. Impacts of previous crops on Fusarium foot and root rot, and on yields of durum wheat in North West Tunisia. Phytopathology Mediterranea. 55(2):253-261. Doi: 10.14601/Phytopathol_Mediterr-17933.

Chen, G.; Habib, A.; Wei, Y.; Zheng, L. Y.; Shabala, S.; Zhou, M. and Liu, C. 2015. Enhancing Fusarium crown rot resistance by pyramiding large-effect QTL in barley. Mol Breed. 35(1):26-33. Doi: 10.1007/s11032-015-0255-z.

Collard, B. C. Y.; Grams, R. A.; Bovill, W. D.; Percy, C. D.; Jolley, R.; Lehmensiek, A.; Wildermuth, G. and Sutherland, M. W. 2005. Development of molecular markers for crown rot resistance in wheat: mapping of QTLs for seedling resistance in a ‘2-49’ x ‘Janz’ population. Plant Breed. 124:532-537. DOI: 10.1111/j.1439-0523.2005.01163.x.

Collard, B. C. Y.; Jolley, R.; Bovill, W. D.; Grams, R. A.; Wildermuth, G. B. and Sutherland, M. W. 2006. Confirmation of QTL mapping and marker validation for partial seedling resistance to crown rot in wheat line '2-49'. Australian J. Agric. Res. 57(9):967-973. Doi: dx.doi.org/10.1071/AR05419.

Cook, R. J. 2010. Fusarium root, crown and foot roots and associated seedling diseases. *In*: Bockus, W. W.; Bowden, R. L.; Hunger, R. M.; Morrill, W. L. and Smiley, R. W. (Eds.). Compendium of wheat diseases and pests. 3rd. (Ed.). APS Press, St. Paul, Minnesota, USA. 37-39 p.

Davis, A. R.; Huggins, R. D.; Cook, R. J. and Paulitz, C. T. 2009. Nitrogen and crop rotation effects on fusarium crown rot in no-till spring wheat. Can J. Plant Pathol 31(4):456-467. Doi: 10.1080/07060660909507620.

Desmond, O. J.; Edgar, C. I.; Manners, J. M.; Maclean, D. J.; Schenk, P. M. and Kazan, K. 2006. Methyl jasmonate induced gene expresion in wheat delays symptom development by the crown rot pathogen *Fusarium pseudograminearum*. Physiol. Mol. Plant Pathol. 67(3-5):171-179. Doi: https://doi.org/10.1016/j.pmpp.2005.12.007.

Edwards, S. G. 2004. Influence of agriculture practices on *Fusarium* infection of cereals and subsequent contamination of grain by trichothecene mycotoxins. Toxicol. Lett. 153(1):29-35. Doi: https://doi.org/10.1016/j.toxlet.2004.04.022.

Ferreira, G. M. R.; Tessmann, D. J. and Kemmelmeier, C. 2006. Production of mycotoxins by Fusarium graminearum isolated from small cereals (wheat, triticale and barley) affected with scab disease in Southern Brazil. Brazilian J. Microbiol. 37(1):58-63. Doi: 10.1590/S1517-83822006000100011.

Gilchrist, S. L.; Fuentes, D. G.; Martínez, C. C.; López, A. R. M.; Duveiller, E. y Singh, R. P. 2005. Guía práctica para la identificación de algunas enfermedades de trigo y cebada. 2ª. (Ed.). CIMMYT, México, DF. 68 p.

Kazan, K. and Gardiner, D. M. 2018. *Fusarium* crown rot caused by *Fusarium pseudograminearum* in cereal crops: recent progress and future prospect. Mol. Plant Pathol. 19(7):1547-1562. Doi: 10.1111/mpp.12639.

Khoshgoftarmanesh, H. A.; Kabiri, S.; Shariatmadari, H.; Sharifnabi, B. and Schulin, Rainer. 2010. Zinc nutrition effect on the tolerance of wheat genotypes to *Fusarium* root-rot disease in a solution culture experiment. Soil science and plant nutrition. 56(2):234-243. Doi: 10.1111/j.1747-0765.2009.00441.x.

Klein, T. A.; Liddell, C. M.; Burgess, L. W. and Ellison, F. W. 1985. Glasshouse testing for tolerance of wheat to crown rot caused by *Fusarium graminearum* Group 1. *In*: Parker, C. A.; Rovira, A. D.; Moore, J. K. and Wong, P. T. W. (Eds.). Ecology and Management of Soil-borne Plant Pathogens. APS Press, St. Paul. 167-168 pp.

Klein, T. A.; Burgess, L. W. and Ellison, F. W. 1991. The incidence and spatial patterns of wheat plants infected by *Fusarium graminearum* Group I and the effect of crown rot on yield. Australian J. Agric. Res. 42(3):399-407. Doi: 10.1071/AR9910399.

Lamprecht, S. C.; Marasas, W. F. O.; Hardy, M. B. and Calitz, F. J. 2006. Effect of crop rotation on crown rot and the incidence of *Fusarium pseudograminearum* in wheat in the Western Cape, South Africa. Australasian Plant Pathol. 35(4):419-426. Doi: 10.1071/AP06040.

Leyva, M. S. G.; Vega, P. H. E.; Villaseñor, M. H. E.; Tlapal, B. B.; Vargas, H. M.; Camacho, T. M. y Tovar, P. J. M. 2017. Caracterización de especies de *Fusarium* causantes de pudrición de raíz del trigo en El Bajío, México. Chilean. J. Agric. Anim. Sci. 33(2):142-151. Doi: 10.4067/S0719-38902017005000404.

Li, X.; Liu, C; Chakraborty, S.; Manners, J. M. and Kazan, K. 2008. A simple method for the assessment of crown rot disease severity in wheat seedlings inoculated with *Fusarium pseudograminearum*. J. Phytopathol. 156(11-12):751-754. Doi: 10.1111/j.1439-0434.2008.01425. x.

Limón, O. A.; Peláez, C. D.; Leyva, M. S. G. y Espinosa, B. C. 2016. Efecto de la dosis de N en la incidencia de *Fusarium* spp., en raíces de trigo bajo camas permanentes. Rev. Mex. Cienc. Agríc. 7(5):1155-1165. Doi: 10.29312/remexca. v7i5.239.

Liu, C. and Ogbonnaya, C. F. 2015. Resistance to Fusarium crown rot in wheat and barley: a review. Plant Breeding 134(4):365-372. DOI: 10.1111/pbr.12274.

Liu, Y. X.; Yang, X. M.; Ma, J.; Wei, Y. M.; Zheng, Y. L.; Ma, H. X.; Yao, J. B.; Yan, G. J.; Wang, Y. G.; Manners, J. M. and Liu, C. J. 2010. Plant heigth affects Fusarium crown rot severity in wheat. Phytopathology 100(12):1276-1281. Doi: 10.1094/PHYTO-05-10-0142.

Lozano, R. N.; Mezzalama, M.; Carballo, C. A. y Hernández, L. A. 2006. Efectos de fungicidas en la calidad fisiológica de la semilla de trigo harinero (*Triticum aestivum* L.) y su eficacia en el control de *Fusarium graminearum* Schwabe [*Gibberella zeae* (Schwein.) Petch] y *Bipolaris sorokiniana* (Sacc.) Shoemaker [*Cochliobolus sativus* S. Ito y Kurib.]. Rev. Mex. Fitopatol. 24(2):115-121. http://www.redalyc.org/articulo.oa?id=61224205.

Ma, J.; Du, G.; Li, X.; Zhang, C. and Guo, J. 2015. A major locus controlling malondialdehyde content under water stress is associated with *Fusarium* crown rot resistance in wheat. Mol Genet Genomics. 290(5):1955-1962. Doi: 10.1007/s00438-015-1053-3.

Ma, J.; Li, H. B.; Zhang, C. Y.; Yang, X. M.; Liu, Y. X.; Yan, G. J. and Liu, C. J. 2010. Identification and validation of a major QTL conferring crown rot resistance in hexaploid wheat. Theor. Appl. Genet. 120(6):1119-1128. Doi: 10.1007/s00122-009-1239-3.

Ma, J.; Zhang, C. Y.; Liu, Y. X.; Yan, G. J. and Liu, C. J. 2012. Enhancing *Fusarium* crown rot resistance of durum wheat by introgressing chromosome segments from hexaploid wheat. Euphytica 186(1):67-73. Doi: 10.1007/s10681-011-0492-0.

Ma, J.; Stiller, J.; Zhao, Q.; Feng, Q.; Cavanagh, C.; Wang, P.; Gardiner, D.; Choulet, F.; Feuillet, C.; Zheng, Y.; Wei, Y.; Yan, G.; Han, B.; Manners, J. M. and Liu, C. 2014. Transcriptome and allele specificity associated with a 3BL locus for Fusarium crown rot resistance in bread wheat. Plos One 9(11): e113309. Doi: 10.1371/journal.pone.0113309.

Mariscal, A. L. A.; Solís, M. E.; Villaseñor, M. H. E.; Ramírez, R. A. y Moreno, G. B. 2018. Manejo integrado de la secadera del trigo en El Bajío. Folleto técnico núm. 11. INIFAP-CIRCE-CEBAJ. Celaya, Guanajuato. 40 p.

Martin, A.; Bovill, W. D.; Percy, C. D.; Herde, D.; Fletcher, S.; Kelly, A.; Neate, S. M. and Sutherland, M. W. 2015. Markers for seedlings and adult plant crown rot resistance in four partially resistant bread wheat sources. Theor. Appl. Genet. 128(3):377-385. Doi:10.1007/s00122-014-2437-1.

Martínez, M.; Castañares, E.; Dinolfo, M. I.; Pacheco, W. G.; Moreno, M. V. and Stenglein, S. A. 2014. Presencia de *Fusarium graminearum* en muestras de trigo destinado al consumo humano. Rev. Argentina de Microbiología. 46(1):41-44. Doi: 10.1016/S0325-7541(14)70046-X.

Mitter, V.; Zhang, M. C.; Liu, C. J.; Ghosh, R.; Ghosh, M. and Chakraborty, S. 2006. A high throughput glasshouse bioassay to detect crown rot resistance in wheat germplasm. Plant Pathol. 55(3):433-441. Doi: 10.1111/j.1365-3059.2006.01384.x.

Motallebi, P.; Niknam, V.; Ebrahimzadeh, H.; Tahmasebi, E. S. and Hashemi, M. 2015. The effect of methyl jasmonate on enzime activities in wheat genotypes infected by the crown and root rot pathogen *Fusarium culmorum*. Acta Physiol Plant. 37(11):237-247. Doi:10.1007/s11738-015-1988-3.

Moya, E. E. A. 2013. *Fusarium* crown rot disease: biologý, interactions, management and function as a posible sensor of global climate change. Ciencia e Investigación Agríc. 40(2):235-252. https://pdfs.semanticscholar.org/febd/af22b6fa8e939e3c6262772be60aede2a736.pdf?_ga=2.141230642.186342093.1566582535-1414126086.1566582535.

Mudge, A. M.; Dill-Macky, R.; Dong, Y. H.; Gardiner, D. M.; White, R. G. and Manners, J. M. 2006 A role for the mycotoxin deoxynivalenol in stem colonisation during crown rot disease of wheat caused by *Fusarium graminearum* and *Fusarium pseudograminearum*. Physiol. Mol. Plant Pathol. 69(1):73-85. Doi: 10.1016/j.pmpp.2007.01.003.

Orantes, G. C.; Garrido, R. E. R.; Espinoza, P. N. y Quiroga, M. R. 2011. Resistencia de varios genotipos de trigo (*Triticum aestivum* L.) a *Fusarium graminearum* Schwabe cultivados en Chiapas, México. Tropical Subtrop. Agroecosys. 14(1):209-220. http://www.redalyc.org/articulo.oa?id=93915703020.

Pinto, F. V. E.; Terminiello, L. A.; Basilico, J. C. and Ritieni, A. 2008. Natural occurrence of nivalenol and mycotoxigenic potential of *Fusarium graminearum* strains in wheat affected by head blight in argentina. Brazilian J. Microbiol. 39(1):157-162. Doi:10.1590/S1517-83822008000100031.

Poole, G. J.; Smiley, R. W.; Paulitz, T. C.; Walker, C. A.; Carter, A. H.; See, D. R. and Campbell, G. K. 2012. Identification of cuantitative trait loci (QTL) for resistance to Fusarium crown rot (*Fusarium pseudograminearum*) in multiple assay environments in the Pacific Nothwestern US. Theor. Appl. Genet. 125(1):91-170. Doi: 10.1007/s00122-012-1818-6.

Poole, G. J.; Smiley, W. R.; Walker, C.; Huggins, D.; Rupp, R.; Abatzoglou, J.; Campbell, G. K. and Paulitz, C. T. 2013. Effect of climate on the distribution of *Fusarium* spp., causing crown roto f wheat in the Pacific Northwest of the United States. Phytopathology. 103(11):1130-1140. Doi: 10.1094/PHYTO-07-12-0181-R.

Rangel, C. A. E.; Valadez, M. E. y Lozoya, S. H. 2017. Caracterización molecular y patogénesis de *Fusarium* asociado al amarillamiento del trigo. Rev. Fitotec. Mex. 40(4):439-450. https://www.revistafitotecniamexicana.org/documentos/40-4/8a.pdf.

Rebib, H.; Bouraoui, H.; Rouaissi, M.; Brygoo, Y.; Boudabbous, A.; Hajlaoui, M. R. and Zouaoui, S. N. 2014. Genetic diversity assessed by SSR markers and chemotyping of *Fusarium culmorum* causal agent of foot and root rot of wheat collected from two different fields in Tunisia. Eur. J. Plant Pathol. 139(3):481-495. Doi: 10.1007/s10658-014-0405-x.

Saremi, H.; Ammarellou, A. and Jafary, H. 2007. Incidence of crown rot disease of wheat caused by *Fusarium pseudograminearum* as a new soil born fungal species in north west Iran. Pak. J. Biol. Sci. 10(20):3606-3612. Doi: 10.3923/pjbs.2007.3606.3612.

Scherm, B.; Balmas, V.; Spanu, F.; Pani, G.; Delogu, G., Pasquali, M. and Migheli, Q. 2013. *Fusarium culmorum*: causal agent of foot and root rot and head blight on wheat. Molecular Plant Pathol. 14(4):323-341. Doi: 10.1111/mpp.12011.

Shikur, G. E.; Sharma, P. D.; Paulitz, T.C.; Erginbas, O. G.; Karakaya, A. and Dababat, A. A. 2018. Identidy and pathogenicity of *Fusarium* species associated with crown rot on wheat (*Triticum* spp.) in Turkey. Eur. J. Plant Pathol. 150(2):387-399. Doi:10.1007/s10658-017-1285-7.

Singh, G. H.; Graham, D. R. and Rengel, Z. 1996. Genotypic variation in zinc efficiency and resistance to crown rot disease (*Fusarium graminearum* Schw. Group 1) in wheat. Plant Soil. 186(2):219-226. Doi: 10.1007/BF02415517.

Smiley, W. R.; Gourlie, A. J.; Easley, A. S.; Patterson, L. M. and Whittaker, G. R. 2005. Crop damage estimates for crown rot of wheat and barley in the Pacific Nothwest. Plant Dis. 89(6):595-604. Doi: 10.1094/PD-89-0595.

Stenglein, S. A.; Dinolfo, M. I.; Bongiorno, F. and Moreno, M. V. 2012. Response of wheat (*Triticum* spp.) and barley (*Hordeum vulgare*) to *Fusarium poae*. Agrociencia. 46(3):299-306. https://www.redalyc.org/articulo.oa?id=30223119009.

Wallwork, H.; Butt, M.; Cheong, J. P. E. and Williams, K. J. 2004. Resistance to crown rot in wheat identified through an improvement method for screening adult plants. Australasian Plant Pathol. 33(1):1-7. Doi: 10.1071/AP03073.

Wang, Q.; Shao, B.; Shaikh, I. F. and Gottwald, S. 2018. Wheat resistances to Fusarium root rot and head blight are both associated with deoxynivalenol- and jasmonate-related gene expression. Phytopathology. 108(5):602-616. https://doi.org/10.1094/PHYTO-05-17-0172-R.

Wildermuth, G. B. and McNamara, G. B. 1994. Testing wheat seedlings for resistance to crown rot caused by *F. graminearum* group 1. Plant Dis. 78:949-953. https://www.apsnet.org/publications/PlantDisease/BackIssues/Documents/1994Articles/PlantDisease78n10_949.PDF.

Wildermuth, G. B.; McNamara, R. B. and Quick, J. S. 2001. Crown depth and susceptibility to crown rot in wheat. Euphytica 122:397-405. Doi: 10.1023/A:1012947516161.

Zheng, Z.; Gao, S.; Zhou, M.; Yan, G. and Liu, C. 2017. Enhancing *Fusarium* crown rot resistance by pyramiding large-effect QTL in common wheat (*Triticum aestivum* L.). Mol Breed. 37(9):107-114. Doi: 10.1007/s11032-017-0708-7.

Zheng, Z.; Kilian, A.; Yan, G. and Liu, C. 2014. QTL conferring Fusarium crown rot resistance in the elite wheat variety EGA Wylie. PLoS One 9(4): e9601. Doi: 10.1371/journal.pone.0096011.

Zheng, Z.; Ma, J.; Stiller, J.; Zhao, Q.; Feng, Q.; Choulet, F.; Feuillet, C.; Zheng, Y. L.; Wei, Y.; Han, B.; Yan, G.; Manners, M. J. and Liu, C. 2015. Fine mapping of a large-effect QTL conferring *Fusarium* crown rot resistance on the long arm of chromosome 3B in hexaploid wheat. BMC Genomics. 16(1):850-857. Doi: 10.1186/s12864-015-2105-0.