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Wheat: Biotrophic Fungi and Resistance Genes

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Abstract

Nowadays, biotrophic diseases such as fungi in wheat fear farmers since they cause serious losses of income. Wheat has been adapted to diverse climatic conditions, for instance, grown over a range of altitudes and latitudes under irrigated, dry, and wetter conditions. Expectedly wheat plant cultivation will reach sixty percent to cover human food necessity in coming decades. However, biotrophic fungi, for instance, *Puccinia graminis* f. sp. *tritici*, *Puccinia striiformis* f. sp. *tritici*, *Puccinia triticina,* and *Blumeria graminis* f. sp. which are obligate parasites weaken the plant structured plant framework and out coming in poor plant health and minimized grain fill. Therefore, this review has moved forward to answer the main three research questions as **RQ1:** How genetic resistance affects wheat crop? **RQ2:** What are the damages that cause via biotrophic fungal on the wheat? **RQ3:** What are the diversity and the area distribution of the "Ug99" pathotype. In addition, the result of this observational study will be expected to be beneficial for several areas such as in cultivation, production, education, and moreover in research.

Keywords: Rust resistance, Adult plant resistance (APR), Powdery mildew.

1. Introduction

Recently, agricultural diseases which have affected the majority of food crops diversity were documented as causing 15% pre-harvest yield loss (Cerda, R, 2017; Randhawa et al., 2019). Therefore, based on these crops, barley and wheat are critical staple foods providing 20 percent of calories and 25% of protein consumed by human (Hubbard et al., 2015). Farmers and big producers seek to ensure high-quality products via improving their production conditions such as by fertilization. Likewise, wheat cultivation is a significant group in cereals that could easily be cultivated on a large scale being third in the production area across the world (Gargouri-Kammoun et al., 2014; Abdullah and Atroshi, 2016). Wheat has improved itself to adapt to diverse climatic conditions, for instance, a range of altitudes and latitudes under irrigated, severe drought, and wet conditions. 735 million tons of wheat remained manufactured universally, worth approximately US$ 145 billion in 2015 and 2016. Agricultural Organization of the UN indicates that the existing wheat crop may cover food necessities (Vos and Bellŭ, 2019). Similarly, as declared by Singh et al., (2016) the wheat crop outcomes on a per-hectare percentage basis will be required to increase the region of five tons ha^{-1} from the existing three tons per/hectare (Randhawa et al., 2019). In fact, wheat represents 19% percent of the global major cereal crop production. Consequently, wheat products are heavily dependent on imports to meet their food safety in some countries like East and North African Countries. Therefore, the demand for wheat in the world continues to rapidly enhance the cultivation with increasing population growth development. It is statistically, predicted that the worldwide population will surpass eight billion by 2025 therefore the demand is expected to rise to 760 million tons in 2020 and exceed 880 million metric tons by the 2050, (Dixon et al., 2009), consequently, the required production needs to increase at least by 50% based on the year of 2025 (Yadav et al., 2017). Even though the scale of disease has been impacted which can vary from one period to another; diseases are always active as an important challenge if they attack only by certain plant fragments. Furthermore, all plant parts are prone to diseases, regarding multiple diseases which can occur on the same plant. In addition, multiple diseases can occur in several plant species', depending on environmental conditions and the susceptibility of host cultivars, therefore, crop production throughout the world is reduced via biotic and abiotic stresses. On the other hand, infections were dramatically minimized to around 14% of the agricultural production area. Also, prominent infections of wheat crops that contribute to these losses such as rusts, blotches and head blight / scab. Supplementary, in recent times, emerged unnoticed diseases, for instance, wheat blast and spot blotch, correspondingly, threaten grain production (Figueroal et al., 2018). Mobasser et al., (2012) reported that the genetic diversity enhanced cultivars resistance and pathogen emergence during diseases storms. In the same way, plant pathogens or agents may affect storage, vigor, germination, marketability, yield, seed appearance, and toxins during the storage. When infected seeds are planted, the pathogens are distributed throughout the field and contaminate the land. It is important to know what levels of pathogens are in or on the seed. When levels of disease are high, it may be important to seek a different source of seed for planting. It also may be very helpful to know the present pathogens, to choose a good treatment. Many pathogens can persist in soil or on crop trash and become a problem for many consecutive years.

What's more, as reported by Singh et al. (2016) and Figueroal et al., (2018) wheat is susceptible to numerous pathogens including stem rust (SR) initiated via (*Puccinia graminis* f.sp. *tritici,*) leaf rust (LR) caused via (*P. triticina),* and yellow rust (YR) initiated via (*P. striiformis)* (Martinez et al., 2012). While some pests such as bacteria, viruses, insects, fungi, etc. can persist in seed, stubble in soil in the coming term, others require green plant material to surviving, which is termed as **'green bridge'**. Therefore, the lifestyles, self-sown volunteer of wheat crops **''the green bridge''** important in enabling the survival of the pathogens from one cropping cycle. Consequently, destroying the green bridge is an important component of the integrated control of these pathogens. (Park et al., 2015). Moreover, the utilization of resistant wheat varieties has reduced the damage together with the reduction of green bridge (Park, 2016). This observational research study, in short, has moved forward to answer the main three research questions which are RQ1: How genetic resistance affect wheat crop? RQ2: What's are the damages that cause via biotrophic fungal on the wheat? RQ3: What is the diversity and the area distribution of "Ug99" pathotype.

1.1. The Required Questions in the Research

1.1.1. RQ1: How Genetic Resistance Affect Wheat Crop?

Rational$_1$: The characteristic of the host plant resistance gene(s) that in any way limits damage. Furthermore, various levels of resistance vary amongst the varieties. Moreover, the level of protection from economic damage afforded by durable resistance is the most significant feature of the resistance.

1.1.2. RQ2: What's the Damages that Cause via Biothrophic Fungal on the Wheat?

Rational$_2$: In fact, pathogenic fungi varieties represent a constraint to wheat production. Furthermore, prominent diseases of wheat crops that at present contribute to these losses include the rusts disease and powdery mildew (PM). Moreover, the optimal answer can be observed from the literature review; and also, the answer to this question is presented in Table.1.

1.1.3. RQ3: What is the Diversity and the Area Distribution of "Ug99" Pathotype?

Rational$_3$: In fact, the Worldwide Wheat and Maize Improvement Center (CIMMYT) has drastically minimized and examined against "Ug99" races in Kenya. Furthermore, the progress of virulence against *Sr31* with the emergence of "Ug99" led to susceptibility to SR in wheat crops grown varieties around the world. Especially in Uganda, Ethiopia eastern and southern African nations Yemen, Iran, Egypt, and the Americas, Europe, and Australia.

1.2. Literature Review

1.2.1. Biotrophic Fungi Diseases of Wheat Crop

Biotrophic fungi varieties are obligate parasites which survive on living plants to obtain the nutrients for their survival. Consequently, weakening the plant system and outcome in poor plant health and grain fill (Singh et al., 2016; Randhawa et al., 2019). Among the rust diseases affecting wheat, stripe rust was the most destructive (Hovmoller et al., 2011). The income of the farmers has reduced due to these diseases (Ali et al., 2017). Singh et al., (2016) has announced that the causal pathogens have distinct strains otherwise physiological races, which a strong-minded evaluation reveal diverse resistance genes.

Scientifically, the rust diseases are identified as brown rust, yellow, and leaf rust, which all caused by Basidiomycete order (McIntosh et al., 1995; Figueroa et al., 2018). Among biotrophic disease, rust fungus and powdery mildew (PM) continue to decrease the world's wheat production. In the same way, biotrophic fungi has attacked only living plant crops and affect universal diseases of wide distribution are brown, yellow, and stem rust as well as powdery mildew (Table.1 and Figure. 1.1). Additionally, Singh et al., (2015); Huerta-Espino et al., (2011) have mentioned that wheat rusts and powdery mildew have been a major focus of several experimental studies because of breeding concerns, deployed race-specific resistance genes in a short duration, which in turn cause the phenomenon called as "Boom and Bust". Because their biotrophic lifestyles, self-sown volunteer wheat crops which is termed as green bridge are significant in enabling the survival of these pathogens from one cropping cycle (Park, 2016). In West Asia and North African nations, severe epidemics of septoria leaf blotch have occurred, in a specific condition in some countries such as Morocco, Tunisia, and Turkey (Saari, 1974). In addition, isolates of the pathogen have been identified in diverse regions, along with their specificity for durum and bread wheat.

1.2.2. Powdery Mildew (PM)

Blumeria graminis f. sp. *tritici* is the causal agent of (PM) with wider distribution in dry, warmer and cool climatic conditions (Table.1). Furthermore, (*Blumeria graminis f.* sp. *tritici)* has great significance in some nations, for instance, China, Europe, and South America. Consequently, wheat cultivation varieties which have been cultivated in South Asia is highly prone to (*Blumeria graminis* f. sp. *tritici*) if over-sensitive varieties are grown in a conducive environment. In contrast with rusts wheat, powdery mildew conidia do not disseminate to distant locations, however, do evolve at a fast percentage. Therefore, the outcome losses attributable to powdery mildew (*Blumeria graminis* f. sp. *tritici*) vary with the seasons around locations a record high of 20% in the UK, also, (10 to 15%), below 10% in Western Europe; (5 to 17%) in North Carolina, on the other hand, sometimes reaching (30 to 35%) to in Russia, up to 62% in Brazil, equally, (30 to 40%) in China during heavy epidemics. (PM) has international distribution in regions with dry and cool climates, together with China, Europe, and Southern Cone of South America (Beddow et al., 2015). In the same way, epidemics of (PM) and economic losses of wheat are enhanced via high plant density, heavy usage of nitrogen fertilizers, and irrigation conditions (Cowger et al., 2012; Mehta, 2014; Savary et al., 2019). Largely, yield decreases of higher than 40% are infrequent, on the other hand, early infections might lead to the death of seedlings otherwise tillers that eventually fail to producing seeds infection via (PM) which was documented on the wheat plant after the tenth day of pollination (Aranyi et al., 2014). Symptoms of (PM) have been reported on all the above-ground parts. However, the leaves are the main issues on which symptoms occur. Consequently, fungicides, for instance, triadimefon, are often applied on the above-ground parts to control (PM) when susceptible cultivars are grown, or the host resistance cannot provide sufficient protection from the disease (Johnson et al., 1979; Li et al 2016; Li et al., 2020) However, PM-resistant cultivars are preferred via wheat crop cultivators for the sake of waste in the line process of the production costs and better environment-friendly (Johnson et al., 1979).

1.2.3. Stem Rust (SR)

According to Roelfs et al., (1992) the most damaging fungal diseases of wheat which has been found in warmer, humid wheat-growing regions is (SR) which has been caused via *Puccinia graminis* f. sp. *tritici* (Pgt). (SR) is widely distributed all over the national domain, even though less common than the other two wheat rusts varieties (Singh et al., 2015). Furthermore, Kolmer (2005) has documented that symptoms of stem rust infection on the plant parts, for instance, leaf sheaths, stems, glumes, and awns of susceptible plants are masses of dark red urediniospores (Figueroa et al., 2018). Stem rust causes the outcome of loosening through a reduction of wheatquality. In severe epidemics, producers will lose their total harvest returns if susceptible cultivars are grown in rust hot spot zones. Moreover, in the last century the CIMMYT put serious efforts on Stem Rust (Figueroa et al., 2016). Stem rust has gained significance as new virulence traits have evolved in (SR) populations, and broadly utilized wheat cultivars across the globe (Singh et al., 2015). Similarly, (SR) has turned out to be a significant pathogen, since a highly aggressive (SR) race of *P. graminis* f. sp. *tritici*. Such as the "Ug99" race TTKSK including *Sr31*, *Sr21*, *Sr24*, *Sr36* and *Sr9h* were detected before 22 years in Uganda (Singh et al., 2015; Figueroa et al., 2018). (SR) is the most devastating rust disease which has wide distribution globally in some countries, for instance, Africa, America, Europe, and Australia (Singh et al., 2012; Singh et al., 2016). Archaeologically, it caused losses of (19.3 to 28.4%) in the US from the 1910s to 1950s. Later, however, stem rust has been under satisfactory control condition later by the year (1954). The longer adoption of resistant cultivars is associated with the removal of barberry, the alternative host of the (SR) fungus (Singh et al., 2015). Epidemics remained low internationally for the last 30 years except for major epidemics in Ethiopia; in the period amongst (1993-1994) on Enkoy, which carries resistance gene *Sr36*. In the same way, (SR) rematerialized in the form of the "Ug99" race, which cause economic losses (Singh et al., 2012). Likewise, extra "Ug99" unrelated races have appeared in various parts of the world, decreasing the efficacy of the sources of resistance. Additionally, the 'Digalu' race caused a devastating epidemic in Ethiopia amongst (2013 - 2014) which is similar to race that has been registered in Germany and severe stem rust epidemics in the southern wheat production region and the epidemics continued into the 2014 crop season (Olivera Firpo et al., 2015). Race analyses of samples from the epidemic regions detected race TKTTF to be the causal race behind these epidemics. Race TKTTF is highly virulent to the widely grown 'Digalu' wheat, which possesses resistance gene *SrTmp* that is effective against the "Ug99" race group and ineffective against TKTTF. This race has been known from Turkey since (2005) and it is widely distributed in the Middle East region. It is being increasing detected across a wide geographic distribution area. Currently, it has been confirmed in nine countries such as Turkey, Iran, Lebanon, Egypt, Ethiopia, Georgia, Azerbaijan, Eritrea and Yemen; with two countries such as Germany and Denmark; detecting TKTTF-like variants in 2013. The German and Danish isolates differed by having virulence on four additional: *Sr33, Sr7a*, *SrTt-3*, *Sr45* (Olivere Firpo et al., 2015). By the year 2016, the broadly virulent race that has been detected in recent time, the (SR) subversive 10.000 of hectares in an outbreak in Sicily. What's concerning is that (GRRC) experimental examinations has suggested that fungi can infect dozens of lab-developed strains of wheat crops, containing hardy varieties that remained reported highly resistant to disease (Bhattacharya, 2017).

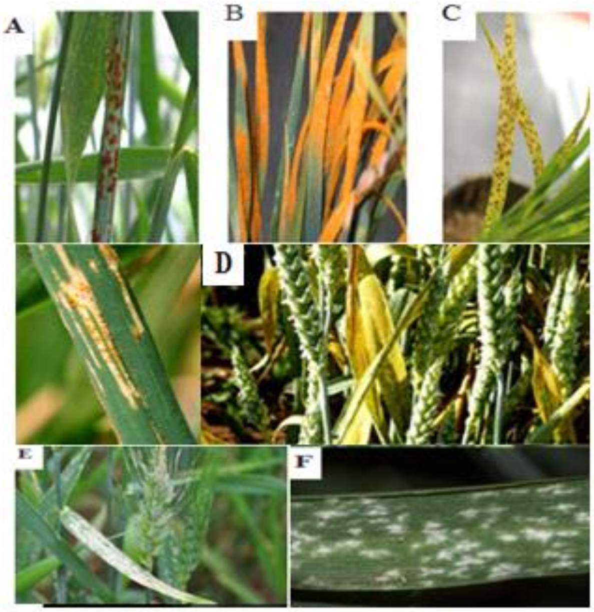

Figure.1.1. The wheat rust diseases symptoms which are affected via *(Puccinia graminis* f. sp. tritici) **(A),** (*Puccinia striiformis* f. sp. *tritici*) **(B)** and (*Puccinia triticina*) **(C)** adapted from (Figueroa et al., 2018) and **(D)** Mature symptoms of stripe rust that has turned out to be brown, dry (Martínez-Espinoza et al., 2009) and symptoms of PM on wheat- flag leaf and head infection via **(***Blumeria graminis* f. sp. *tritici*) **(E, F)** **(**Wicker et al., 2013**).**

Table. 1. Biotrophic fungi pathogen on wheat

Fungial pathogen	**Name patho**	**Type of wheat**	**Climate**	**Pathogen distribution**	**Reference**
Puccinia triticina	wheat leaf rust (also known as brown rust)	(*Triticum turgidum* ssp. *durum),* wild emmer *(Triticum dicoccoides),* domesticated emmer wheat *(Triticum dicoccum*), and *triticale.*	Warmer region	Americas, Europe, South, Central, and North Asia, South and North Africa, and Australia	(McCallum et al., 2012); (Singh et al., 2016)
Puccinia striiformis f. sp. tritici	wheat stripe rust (also known as yellow rust)	On tetraploid durum wheat *Triticum turgidum ssp. Durum* *Triticosecale* *Triticum aestivum L*	Warmer region	United States and Australia represents the introduction of a single lineage and including Asia and Europe	(Khanfri et al., 2018); Singh et al., 2015); (Singh et al., 2016); Sharma et al., 2016)
P. graminis f. sp. tritici	wheat stem rust (now known widely as ‘Ug99)	Durum wheat, emmer wheat,triticale (*Triticosecale)*	Aggressiveness and adaptation to Warmer temperature	Especially in Africa Uganda, Ethiopia eastern and southern African countries Yemen, Iran, Egypt, and the Americas, Europe, and Australia	Rodriguez-Algaba et al., 2014); (Singh et al., 2016); (Singh et al., 2015)
Blumeria graminis f. sp. tritici	wheat powdery mildew	*Triticum* spp.	especially important in regions with dry and cool	including China, Europe, and the Southern Cone of South America	Singh et al., 2016; Mehta, 2014)

1.2.4. Leaf Rust (LR)

Scientifically, leaf rust is widely adapted fungal pathogen based on wheat crops on an international basis. Its main epidemic regions are spread throughout some registered documentation nations such as America, Europe, South Asia, Central North Asia, South, and North Africa, and Australia, affecting various levels of damage (McCallum et al., 2012). In the US, the disposable income of trade and industrial losses of $350 million in total remained attributed to (LR) in the period of (2000-2004). Huerta-Espino et al., (2011) has demonstrated that in China, annual outcome losses because (LR) is estimated at 3 million tons. In the last decades, it remained also a devastating fungal pathogen in Mexico and South Asia, on the other hand, has turned out to be negligible in recent decades for the reason that cultivars protected via low rusting resistance genes (Figueroa et al., 2018).

According to Bolton et al., (2008); Huerta-Espino et al., (2011) the pathogenic (*Puccinia triticina* (Pt) has affected (LR) is widely distributed of the three rust fungal pathogens. Furthermore, environmental conditions such as modest temperatures which is linked with moist has affected wheat-growing areas. Likewise, as an outcome, the main factors that have affected the outcome losses has been decreased in some plant areas, for instance, seed size, seed weight, besides several numbers of grains per spike. Moreover, in the period (2000-2004), the total monetary financial losses in the USA is US$ 350 million in total attributable to (LR) remained estimated (Huerta-Espino et al., 2011). Murray and Brennan, (2009) have presented that, in Australia, yield losses in AU$ was 12 million ascribed to leaf rust. As a final point, leaf rust is a problematic fungal pathogen since the pathogen displays high diversity. (McCallum et al., 2016).

1.2.5. Yellow Rust (Stripe rust)

Stripe or yellow has conventionally occurred on wheat crops besides the fungal pathogen survives in wheat crops as dormant mycelium in cooler climates and wetter regions, regarding the region of Asia and Europe (Martinez et al., 2012). Environmentally, disease development of (YR) is mostly rapid in low temperature which is raged (from 10 to 16 ºC). Therefore, urediniospores are spread via wind to healthy plants where they can initiate new infections. Heavy dew or intermittent rains can accelerate the spread of the disease. Infection tends to cease when temperatures, consistently, exceed 21 - 23ºC (Martinez et al., 2012). However, new aggressive races that have been adapted to warmer climates have spread to other continents and caused severe losses in several countries in the meantime, 2000 (Ali et al., 2014). Furthermore, (YR) commonly causes yield reductions of 5 to 50%, depending on the region, along with the conditional developmental stage of wheat crops. Based on the current valuation, annual yield reductions of 5.47 million tons of wheat crop are attributable to this disease, which is equivalent to annual losses of $979 million (Beddow et al., 2015). In Australi, the damage of stripe rust disease, causing average annual economic losses of AUD$127 million (Beddow et al., 2015). Therefore, the pathogen (*Puccinia striiformis* f. sp. *tritici* (Pst), is prevalent in cooler wet wheat conditions. Moreover, (YR) is considered the most significant pathogen fungal disease because its potential to the effect of total out came losses in susceptible wheat cultivars, because its frequent which is a wide occurrence. Based on the latest estimations, the international annual losses affected via (*Puccinia striiformis* f. sp. *tritici* (Pst) are US$ a billion in total. According to Chen et al., (2014) the genetic diversity has been specified of (*Puccinia striiformis* f. sp. *tritici)* populations in some countries such as Europe, Australia, and North America, although significant levels of diversity prevail within several fungal pathogen populations. As declared by Ali et al., (2014) YR populations in western China, Himalayan, nearby regions and Central Asia are pathogen diversity, where sexual recombination appears to be commonly happened (Hovmøller et al., 2016; Hubbard et al., 2015).

1.3. Resistance Biotrophic Fungal

Scientifically, the resistance has been identified as whichever genetically detected characteristic of a host plant that in whichever way limits damage along with yielded via disease. Furthermore, the term resistance can vary amongst apparent immunity and extreme susceptibility. Consequently, the stage of protection from economic damage afforded besides the time is a significant feature of resistance (Park, 2016). In the same way, in genetic is termed as oligogenic, which is starting controlled via one or few genes of individually small phenotypic effect. Functionality, resistance is recognized centered on epidemiological, for instance, low rusting and rate-reducing (Aktaş and Zencirci, 2016). Basically, Periyannan et al., (2017) has declared that resistance gene to rust infection by fungal pathogen has been recognized as either race-specific which is also identified as a seedling, or qualitative resistance or non-race-specific resistance. Therefore, more than 70 genes are labelled resistance genes of yellow rust which is had been presented to condition reactions to Pst (McIntosh et al., 2014; McIntosh et al., 2017). On the other hand, all over the world, (YR) virulence was documented for all most of these genes. In contrast, most (PM) besides rust resistance genes are expressed during the life of the wheat crops all-stage resistance (ASR), as well termed to seedling, while others stand expressed only at post seedling growth stages termed as adult plant resistance (APR), which is mentioned to as minor gene resistance (Martinez et al., 2012; He et al., 2018; Park, 2016). In the same point, yield loss researches have commonly presented that (APR) will protect against an important yield loss. For instance, several researches in which the protective value of (YR), (APR) gene *Yr18* were assessed utilizing near-isogenic paired lines with and without *Yr18* demonstrated yield losses of seventy-four to ninety-four percent in the line lacking *Yr18*, however, (31 to 52%) in the line carrying *Yr18* (Park, 2016). In fact, (APR) genes has been presented by several researchers and switched on at diverse growth stages, after seedling growth stages in addition to others not until flag leaf emergence. Growth stage resistance genes are expressed which are an important consideration in ensuring adequate protection from diseases. McIntosh et al., (2014); Singh et al., (2016) has declared that wheat germplasm has high genetic diversity for its resistance to several diseases, which is numerous race-specific and a specific durable resistance gene which is has been characterized. Moreover, this diversity has been enriched via methodically transferring several resistance genes from various species and genera related to wheat through cytogenetic interventions. On the other hand, resistance expression initiates at later growth stages. What is more, the magnitude of resistance conferred via these genes varies to a great extent, ranging from immunity to only small reductions in disease symptoms. Even though several race-specific rust and (PM) resistance genes has been recognized by matching virulence's in the fungal pathogen population, opportunities to enhance their longevity exist via pyramiding multiple, undefeated genes through marker-assisted selection (MAS). Furthermore, in Western Australia in the earlier stage of an experimental test domain has been detected a breakdown in (PM) resistance, for instance, (*Pm4b, Pm7, Pm24* and *Pm28*) in less than four years (Golzar et al., 2016).

Thus, Li et al., (2014) and Burdon et al., (2014) have approved that the lifespan of race-specific resistance approaches based on gene stacking with a range of (PM) genes together, regional allocation based on temporal deployment of resistance-gene was recommended for durable breeding. Consequently, durable resistance is conferred via quantitative trait loci (QTLs), which have small to intermediate, however, additive effects, and the accumulation of multiple QTLs can lead to a high level of (APR0 approaching near immunity (Brown et al., 2015; Kang et al., 2020; Singh et al., 2016). Even though several QTLs were recognized to confer resistance to rusts and (PM) (Periyannan et al., 2017), three pleiotropic multi-pathogen resistance genes are identified, of which (*Lr34; Yr18; Sr57; Pm38*) concerned with (*Lr67; Yr46; Sr55; Pm46*) are cloned which is detected to confer resistance through novel mechanisms (Moore et al., 2015; Singh et al., 2016; Li et al., 2014; Yu et al., 2014). Up to the current time, McIntosh et al., (2014); McIntosh et al., (2017) has reported that more than 200 rust resistance-genes which categorized and formally designated in wheat plant otherwise wild families; the majority of these confer race-specific-resistance at least sixty are designated as (SR) resistance-genes (McIntosh et al., 2017). Another example, (*Sr31*) remained one of the major widely utilized race-specific (SR) resistance genes; on the other hand, in Kenya "the International Maize which is associated with Wheat Improvement Center (CIMMYT)" that has been drastically reduced the exanimating against "Ug99" races (Singh et al., 2016; Randhawa et al., 2019). Furthermore, the measurements of virulence against (*Sr31*) with the emergence of "Ug99" led to susceptibility to (SR) in a huge number of the sorts of wheat plant cultivation around the world. What's more, according to Figueroa et al., (2018) and Olivera Firpo et al., (2015), new races in the "Ug99" lineage is related to numerous genes, for instance, (*Sr21*; *Sr24; Sr36; Sr38* and *SrTmp*). At the present time, Singh et al., (2015) has presented that the genes, for instance, (*Sr2; Sr23; Sr25; Sr33; Sr35; Sr45; Sr47and Sr50*) are most valuable ones for protection against newly evolved races. In contrast, numerous (YR) resistance-genes are considered as (seventy-eight) have been categorized which is ceremoniously termed in formal (Anh et al., 2015). On the other hand, in several parts of the world a huge number of these genes have been rendered ineffective with the emergence of virulent races, an effective worldwide except for a few combinations, for instance, (*Yr5* and *Yr15*). Equally, Dakouri et al., (2013) has documented that 70 (LR) resistance-genes have been genetically and frequently deployed in wheat cultivars, for instance, (*Lr1*; *Lr3; Lr10* and *Lr2* 0) (Ellis et al., 2014; Randhawa et al., 2019). In consequence, it has been well acknowledged in the registration section through cloning of eleven race-specific genes in wheat plant, for example, (*Sr22; Sr33; Sr35; Sr45*; *Sr50; Yr5; Yr10; Lr1; Lr10; Lr21;* and *Lr22*) that these genes encode nucleotide-binding site– leucinerich repeat (NBS-LRR) proteins (Steuernagel et al., 2016; Thind et al., 2017; Marchal et al., 2018). Therefore, markers linked to several (SR) resistance-genes such as (*Sr2; Sr22; Sr24* and *Sr26; Sr32; Sr38; Sr43; Sr45; Sr55*) (Moore et al. 2015), (*Sr56*, and *Sr57*) have been reviewed and published. In the same direct, (Randhawa, 2015) has documented that (YR) resistance several genes, for instance, (*Yr1; Yr5; Yr10; Yr15; Yr17; Yr18; Yr26; Yr28; Yr6; Yr50; Yr51; Yr57; Yr59; Yr61; Yr64;* and *Yr65*). Similarly, (LR) resistance gene marker has been reported by Schachermayr et al. (1994; 1997) as (*Lr1; Lr9; Lr10; Lr19; Lr24; Lr26; Lr28; Lr34; Lr35; Lr37; Lr51; Lr67* and Lr68) (Moore et al., 2015). In the same context, these markers can be advantageously used for the selection of desirable gene combinations along with phenotypic assays. Likewise, procedures for recognized markers requirement to being optimized and validated before used in the selection of plants carrying the respective genes. In the same way, the DNA of the donor is included in the PCR reactions of markers to avoiding any error. On the other hand, race non-specific rust resistance-genes offer durable resistance, as the pathogen fungal cannot without difficulty overcome them, termed as adult plant resistance (APR). Furthermore, confers quantitative resistance against wheat plant rusts (Periyannan et al., 2017) has the characteristic partial resistance phenotypes limit inoculum build-up besides the likelihood of the occurrence of epidemics. According to Ellis et al., (2014) examples of this sort of resistance contain (*Sr2; Lr34; Lr46; Lr67; Lr68* and *Yr36*). Similarly, cloning of *Yr36* revealed the role of a cytoplasmic protein kinase in mediating resistance (Figueroa et al., 2018). Besides, *Lr34, Lr67* both are encoding an ATP-binding (Dodds and Lagudah, 2016; Moore et al., 2015). Furthermore, the cloning gene such as (*Pm38; Lr34; Yr18*; *Sr57*) encodes a protein in terms of resembling adenosine triphosphate binding cassette transporters of the pleiotropic drug resistance sub-family. Additionally, the gene is more strongly expressed at later growth stages, consistent with its action as an (APR) gene. Consequently, breeding resistance cultivars International Centre for Wheat and Maize Improvement (CIMMYT), breeding can targeted for smallholder agriculturalists in Asia, Africa, also Latin America, strongly emphasizes selecting high-yielding wheat germ-plasma that possesses high levels of rust resistance based on diverse combinations of multiple pleiotropic resistance genes and other QTLs with significant progress made for all 3 rusts (Singh et al., 2015; Moore et al., 2015). Furthermore, deployment of CIMMYT derived wheat cultivars with (APR) in Mexico, Asia, and Africa have stabilized (LR) fungal populations for more than two decades in contrast to other regions, for instance, South America where race-specific resistance genes remained utilized (Singh et al., 2015; Guo et al., 2015). Similarly, high-yielding cultivars with resistance to the old Chinese cultivar Sumai 3 is a breeding challenge based on progress in breeding has been relatively slow development. Moreover, a combination of numerous minor genes of moderate-to small effects leads to resistance durability. Up to the present time, (89) meta-QTLs have been recognized; on the other hand, specific (QTLs) are mapped at or near identified genes, in a specific condition (Stb6), which remained present in several sources of resistance (Brown et al., 2015). Likewise, new broad-spectrum resistance to (STB) derived from synthetic hexaploid wheat plant remained identified (Brown et al., 2015) also breeding semi-dwarf, high yielding wheat germ-plasma accumulation of both major and minor genes trace to diverse origins. In addition, commonly finding high yield lines that combine high levels of resistance to rusts and (STB) under high disease pressures in several countries, for instance, Mexico, Ethiopia, and other targets environmental worldwide (Singh et al., 2016; Kang et al., 2020).

2. Conclusion

This paper has reviewed the current knowledge of biotrophic pathogens of four fungal diseases, such as (*Blumeria graminis* f. sp *tritici*); (*Puccinia triticina)*; (*P. striiformis* f. sp. *tritici*) and (*P. graminis* f. sp. *tritici*); that affected wheat crops, for instance, (powdery mildew, leaf rust, yellow rust and stem rust); respectively, need resistance genes. Furthermore, wheat improvement has been made by documents and the utilization of new adapted sources of disease resistance and wheat varieties with high yield potential to increase the quality of the manufacturing production sector. In fact, disease resistance which is to increase wheat yields varieties by using molecular methodologies ability in conjunction with broad phenotypic evaluation provides opportunities to harness genetic diversity. This research study has acknowledged that there are various other diseases which will be studied further in the future, these fungal pathogens are labeled as the blotch diseases varieties, that correspondingly threaten wheat production, for instance, *Septoria tritici* blotch, *Septoria nodorum* blotch, Tan spot, scab disease development, wheat blast, take all, eyespot, bare patch and crown rot, etc.

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