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Application of Genomics Tools in Wheat Breeding to Attain Durable Rust Resistance

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Wheat is an important source of dietary protein and calories for the majority of the world's population. It is one of the largest grown cereal in the world occupying over 215 M ha. Wheat production globally is challenged by biotic stresses such as pests and diseases. Of the 50 diseases of wheat that are of economic importance, the three rust diseases are the most ubiquitous causing significant yield losses in the majority of wheat production environments. Under severe epidemics they can lead to food insecurity threats amid the continuous evolution of new races of the pathogens, shifts in population dynamics and their virulence patterns, thereby rendering several effective resistance genes deployed in wheat breeding programs vulnerable. This emphasizes the need to identify, characterize, and deploy effective rust-resistant genes from diverse sources into pre-breeding lines and future wheat varieties. The use of genetic resistance has been marked as eco-friendly and to curb the further evolution of rust pathogens. Deployment of multiple rust resistance genes including major and minor genes in wheat lines could enhance the durability of resistance thereby reducing pathogen evolution. Advances in next-generation sequencing (NGS) platforms and associated bioinformatics tools have revolutionized wheat genomics. The sequence alignment of the wheat genome is the most important landmark which will enable genomics to identify marker-trait associations, candidate genes and enhanced breeding values in genomic selection (GS) studies. High throughput genotyping platforms have demonstrated their role in the estimation of genetic diversity, construction of the high-density genetic maps, dissecting polygenic traits, and better understanding their interactions through GWAS (genome-wide association studies) and QTL mapping, and isolation of R genes. Application of breeder's friendly KASP assays in the wheat breeding program has expedited the identification and pyramiding of rust resistance alleles/genes in elite lines. The present review covers the evolutionary trends of the rust pathogen and contemporary wheat varieties, and how these

research strategies galvanized to control the wheat killer genus *Puccinia*. It will also highlight the outcome and research impact of cost-effective NGS technologies and cloning of rust resistance genes amid the public availability of common and tetraploid wheat reference genomes.

Keywords: wheat, rust, resistance, discovery, deployment, genomics, Kompetitive allele-specific PCR assay

INTRODUCTION

During the evolution of agriculture, intense changes in the biology of a wider range of traits of cereals have been documented (Preece et al., 2017). These changes assisted in the domestication of wheat and its cultivation in the Fertile Crescent, 10,000 years ago (Nevo et al., 2013). Wheat is a segmental allohexaploid (2n = AABBDD = 42) accommodating three inter-related diploid genomes (Marcussen et al., 2014). Around seven million years ago, diploid progenitors of the AA genome (*Triticum urartu*) and BB genome (closely related to *Aegilops speltoides*) diverged from a common ancestor (Marcussen et al., 2014), and during evolution, both of these genomes combined through a polyploidization event which led to the evolution of emmer wheat (*T. turgidum*), an allotetraploid (AABB) around half a million years ago (El Baidouri et al., 2017). Around five million years ago, DD genome (*Ae. tauschii*) evolved from these two diploid progenitors through homoploid speciation (Sandve et al., 2015; El Baidouri et al., 2017; Pont and Salse, 2017). Common wheat (AABBDD) evolved 8,000 to 10,000 years ago through hybridization between *T. turgidum* and *Ae. tauschii*. Further, domestication, cultivation, and selection by mankind have refined the agronomical features of common wheat (Kihara, 1944; McFadden and Sears, 1946). Wheat is an extensively cultivated cereal across the globe covering a wide range of altitudes except for lowland tropical regions (Feldman, 1995). As per global grain production statistics, around 734 million tonnes of wheat was produced in the crop year 2018 at 215 million ha around the world which puts wheat second to maize (*Zea mays* L.) in production among the cereal crops (FAOSTAT, 2020). Common wheat covers around 95% of the total wheat acreage, whereas durum wheat and others occupy the remaining 5% (Shewry, 2009). The world population is projected to reach 9.7 billion by 2050 (Elferink and Schierhorn, 2016), and around 70% in additional production is needed to fulfil the global wheat demand.

Among many biotic stresses which hinder wheat production, rust pathogens are considered as most pressing threats with large economical losses worldwide (Ellis et al., 2014). Stem rust and stripe rust can cause 100% loss, whereas leaf rust can result in 50% loss under severe rust epidemics (Bhardwaj et al., 2019). To minimize the loss incurred by the rust pathogens, there are two effective approaches: 1. chemical control *via* fungicidal spray and 2. genetic control *via* breeding for rust resistance (Asad et al., 2012). The International Maize and Wheat Improvement Centre (CIMMYT), Mexico has been rigorously engaged in improving wheat for rust resistance since its inception in the 1940s, and rich dividends up to 27:1 benefit-to-cost ratio have been attributed to the development of resistant cultivars through genetic approach (Kolmer et al., 2009). The worldwide estimated losses caused by wheat rusts were as high as USD 170 million for stripe (Pakistan) (Hussain et al., 1980), AUD 100–200 million for stem (Australia) (McIntosh et al., 1995) 83 and USD 100 million for leaf rust (Pakistan) (Duveiller et al., 2007), and hence the economic value of rust diseases has been a driving factor for research funding. Breeding for rust resistance is an environmentally safe approach adapted by wheat breeders permitting a reduction in the use of pesticides and greater yield stability (Bariana et al., 2013).

Diverse accessions including diploid progenitors, landraces, old cultivars, and synthetic wheat have an inherent ability to restrict the infection induced by the rust pathogens. Such class of resistance is termed as host resistance, and it can be classified into two broad categories, All Stage Resistance (ASR) and Adult Plant Resistance (APR). ASR is active from the seedling to adult plant stages and generally is only effective against specific races of the pathogen. APR is controlled by non-race specific genes with exceptions where some genes provide race-specific resistance such as *Lr13* (Ellis et al., 2014), while *Lr48* confers hypersensitive response (Bansal et al., 2008). These genes express resistance at post seedling stages when adult plants are close to flag leaf or leaf emergence at boot stage. The effect of each APR gene is partial, not enough to cope up high disease pressure; however, combining APR genes provides high levels of resistance (Singh, 1992). The resistance effect of ASR is neutralized due to selection pressure on the pathogen to evolve or mutate to acquire virulence against resistance genes. Such genes when deployed alone result in boom and bust cycles. The successful breeding for rust resistance requires a deep understanding of evolutionary nature of the pathogen, identification of diverse resistance sources, and judicious deployment of resistance genes in combinations (McIntosh et al., 2001).

Development of gene-specific DNA markers is desirable to expedite pyramiding of rust resistance genes in future wheat varieties. Enormous genome size, complexity, repetitive sequences, and extreme level of similarity between homoeologous genome sequences (95–99% in coding regions), and a higher proportion of repetitive elements (over 80%) have posed a challenge to develop robust DNA markers and draft wheat genome sequences (Borrill et al., 2015). In the last decade, polymerase chain reaction-based markers, including Simple Sequence Repeat (SSR), Sequence Tagged Site (STS), and Cleaved Amplified Polymorphic Sequences (CAPS) were largely explored as promising tools for wheat improvement (Somers et al., 2004; Rosewarne et al., 2013). Wheat genomics has been a witness to the advancement in Next-Generation Sequencing technologies (NGS) from whole-Genome

Shotgun (WGS) approach (Brenchley et al., 2012), flow-sorting technology (Vrána et al., 2012), chromosome arm-specific sequencing (IWGSC, 2014; Mayer et al., 2014), long-range sequencing *via* the WGS approach (Chapman et al., 2015), and *de novo* whole-genome assembly (Appels et al., 2018). Development of SNP-based breeder-friendly KASP (Kompetitive Allele-Specific PCR) markers is the outcome of these technologies. These cost-effective technologies have been utilized to isolate rust resistance genes *via* positional cloning and consequently the development of perfect markers for effective ASR and APR genes (Nsabiyera et al., 2020). In this review, we attempt to revisit the nature of rust pathogen resistance sources and available genomic tools useful in gene-specific marker development.

WHEAT RUST DISEASES AND THEIR IMPACT ON PRODUCTIVITY

Three rust diseases namely leaf rust caused by *Puccinia triticina* Eriks (Pt), stem rust caused by *P. graminis* Pers. f. sp. *tritici* Eriks. & Henn. (Pgt), and stripe rust caused by *P. striiformis* Westend. f. sp. *tritici (*Pst) afflict wheat. Rust fungi are obligate plant parasites which include over 7,000 species having agricultural and economic importance (Aime et al., 2018). The genus *Puccinia* belongs to the Pucciniale order. The genus evolved around 235 million years ago and is characterized by vast genome size ~380Mb (Tavares et al., 2014). Since the evidence of rust spores dating back to 700BC, rust diseases have been a formidable challenge to wheat cultivation. Roman farmers offered dogs, sheep, incense, and wine to the rust god "Robigus" to be propitious (Zadoks, 1985). Individual species of *Puccinia* require a conducive environment regimes for the proliferation of rust inoculum followed by their dispersal *via* wind (Singh and Rajaram, 1993). Stem rust is usually favored under warm and humid (≤30°C) conditions. Leaf rust pathogen also prefers humidity but comparatively lower temperatures (20–24°C) Stripe rust proliferates under cooler temperatures (12–20°C) (Singh et al., 2011).

The *Puccinia* spp. inciting rusts on wheat are obligate parasites having five spore stages *viz.*, spermatia, aeciospores, urediniospores, teliospores, and basidiospores in its complex life cycle (Money, 2016). Wheat is a primary host for rust fungi. *Berberis* species and *Mahonia* species are alternate/secondary hosts of Pgt and Pst, while *Thalictrum*, *Anchusa*, *Isopyrum*, and *Clematis* are the alternate hosts of Pt (Jin et al., 2010; Wang et al., 2015). Teliosori containing teliospores/teleutospores replace urediniosori as wheat crop matures. The thick-walled, bicelled teliospores can resist overwintering on stubbles. During the onset of spring, the teliospores produce a promycelium which bear four uninucleate haploid basidiospores from each cell. These basidiospores infect the *Berberis* leaves to form pycnial cups/spermagonia containing spermatia/pycniospores and receptive hyphae. Transfer of spermatia (sexual gametes) to receptive hyphae between oppositely charged (+ or −) spermatia and receptive hyphae on barberry leaves with the help of insects completes the sexual reproduction. The resultant dikaryotic spores (aeciospores) are formed on the lower side of the *Berberis* leaves. Aeciospores are dispersed through the wind to fall on wheat leaves to penetrate the stomata by the formation of an appressorium (Money, 2016). Further, infectious mycelia transform into haustorium that initiates further infection and spread in wheat without affecting its plasma membrane. After a week of infection on wheat, urediniospores are produced in millions on a susceptible variety. During the crop season, rust pathogens can produce numerous cycles of urediniospore production, its dispersal takes place through wind, and lead to build-up of epidemic over a vast region (Aime et al., 2018). In countries like India, alternate hosts are not functional and urediniospores act as repeating spores. The rusts survive on off-season wheat crop or grasses and become active in the season to cause infection on wheat through urediniospores (Bhardwaj et al., 2019).

Among rust diseases, leaf rust is the most common wheat disease worldwide (Huerta-Espino et al., 2011). Due to its wide adaptation, leaf rust fungi can initiate their infection and spread under mild temperatures and moist conditions. Although, yield losses caused by this disease display temporal and geographical variation; the economic significance of the disease is substantial (Figueroa et al., 2016). Devastating nature of the rust pathogen became more apparent after the susceptible response of a North American wheat variety "Thatcher" against leaf rust pathotypes (Pt; Anderson, 1963). This epidemic devastated wheat crop on a large area and forced researchers and policymakers to consider Pt as an alarming pathogen in the USA, former USSR, and China. Higher rate of reproduction, the ability to travel long-distance, the potential to survive on various host species and diverse environments increased aggressiveness and genetic diversity of the pathogen (Watson, 1981; Walter et al., 2016). In India, severe leaf rust epidemics occurred due to susceptibility of green revolution wheat varieties "Kalyansona" and "Sonalika" and, contemporary cultivars K68 and Pbc 306 in the Northwest region of the country during 1971–73. Over one-million-ton yield losses were estimated (Joshi et al., 1975). Similarly, another leaf rust epidemic was evident due to susceptibility of Mexican mega-wheat variety "Jupateco 73" in Northwestern Mexico. It occupied 75 per cent of the wheat acreage in the southern Sonora region within four years of its release (Dubin and Torres, 1981). Another leaf rust epidemic was reported in the eastern Prairies due to gained additional virulence against *Lr13* and *Lr21* in 1999 (Aboukhaddour et al., 2020).

Significant yield losses in areas with cool and high-altitude climates are commonly inflicted by stripe rust (Roelfs et al., 1992; Singh et al., 2000). In the majority of wheat-growing areas stripe rust have shown regular regional crop losses of up to 0.1–5% and in few exceptions, the losses extend up to 5–25% (Wellings, 2011) besides, severe epidemics due to the breakdown of genes in larger areas may inflict up to 70% yield losses. One-billion USD annual loss is estimated due to the severity and around ninety per cent of the world's wheat crop is vulnerable to stripe rust (Schwessinger, 2017). Stripe rust infection at early growth stages can cause complete yield losses through a reduction in

grain quality, seed vigor and poor germination in susceptible cultivars (Chen, 2005). In Asia, around 46% of yield losses have been due to stripe rust epidemics (Singh et al., 2004a). Tajikistan and Uzbekistan also witnessed widespread epidemics of stripe rust in 2010 (Sobhy Draz, 2019). In India, stripe rust is a serious threat in over ten million hectares of Northern India. Restriction on the cultivation of a mega wheat variety of this region namely PBW343 was imposed due to acquired virulence of *Yr9* during 2008–09. The disease pressure was recorded up to 80%, which necessitated the cultivation of stripe rust-resistant wheat varieties (Aggarwal et al., 2018; Bhardwaj et al., 2019).

Stem rust can cause greater damage when susceptible wheat cultivars are grown over wide geographical regions and early infections may lead to large scale epidemics in a short period (Bhavani et al., 2019). Severe stem rust pressure can affect tillering (Rowell and Roelfs, 1976), plant growth by reducing the photosynthetic area, nutrients and water supply, and their transportation in the plant system (Roelfs, 1985). The two most severe epidemics of Europe occurred in Scandinavia (1951) and central Europe (1932) causing nationwide yield losses up to 20–33% (Zadoks and Bouwman, 1985). During, 1948–56 a few severe epidemics were evident in China due to higher than average temperatures and frequent rains which created a conducive environment for the infections. Other historical events of wheat losses due to this disease occurred in Australia during 1973 (AUD 100–200 million loss, McIntosh et al., 1995), United States (North Dakota) during 1919–1923 (1.95 million tons loss, Roelfs, 1978) and 1950–1955 (3.74 million tons, Roelfs, 1978), New Zealand in 1980 (Beresford, 1982), continental Europe, and the Indian subcontinent (Chaves et al., 2013; Singh et al., 2015). The last major stem rust epidemics occurred in Ethiopia in 1993 and 1994 (Shank, 1994). In a major outbreak in 1998, a new race (Ug99) of stem rust pathogen virulent to *Sr31* was first reported in Uganda (Pretorius et al., 2000), and its lineages (TKTTF) have caused 100% yield losses on susceptible wheat cultivars during 2013–14 in Ethiopia (Singh et al., 2015). It is still considered to be a potential threat for Kenya, Ethiopia, Yemen, the Middle East, and South Asia. The overall global crop losses associated with Pgt alone were estimated to be approximately USD 53.7 billion per annum (Pardey et al., 2013).

IDENTIFICATION AND MAPPING OF RUST RESISTANCE GENES

Breeding for genetic resistance assists in developing rust-resistant wheat varieties. Genetic resistance can be categorized in three groups: 1. monogenic resistance (resistance governed by a single gene), 2. oligogenic resistance (resistance governed by few genes) and 3. polygenic resistance (resistance governed by many genes with additive effects) (Russel, 1978). Based on the resistance exhibited, individual rust resistance genes have been named as major genes and minor genes (Russel, 1978). In pathological terms, rust resistance could be distinguished as horizontal resistance and vertical resistance. Horizontal resistance is race non-specific resistance and effective against genetic variants of a rust pathogen. Vertical resistance is effective against certain pathogen races, so it is also called race-specific resistance (Van der Plank, 1963). The term durable resistance is frequently used instead of non-race specific or horizontal resistance to describe long-lasting resistance. The durability does not mean that resistance is active against all genetic variants of a pathogen but simply that the resistance was effective for a long time (Johnson and Law, 1975). Durable resistance may be conferred by a single gene or by combinations of many genes (McIntosh and Watson, 1982). The theory of gene-for-gene relationship implies that for each resistance gene in the host, there is a corresponding and specific avirulence gene in the pathogen (Flor, 1956). This relationship shows two reactions: 1. Incompatible reaction and 2. Compatible reaction. The incompatible reaction can be evident when a pathogen carries avirulence alleles corresponding to the host's resistant alleles which results in a resistance response. Compatible reaction reveals a susceptible response when a pathogen carries virulence alleles to a susceptible host. The pathogen could carry many avirulence genes; each one corresponding to a resistance gene of a cultivar (Person, 1959). The gene-for-gene hypothesis defines existing diversity in physiological races of a pathogen and resistant genes among the relevant host species.

Wild progenitor and related species of wheat constitute an immense reservoir of genetic variation important for several economic traits including resistance to biotic stresses. This had resulted in an opportunity to breeders for transferring resistance genes from wild species to modern wheat cultivars through inter-specific hybridization (Bansal et al., 2017). Over two-hundred twenty rust resistance genes comprising 60 stem rust resistance, 79 leaf rust resistance genes and 83 stripe rust resistance genes have been formally named and catalogued using bi-parental populations in wheat (McIntosh et al., 2017; Li et al., 2020a). During the last decade, discovery and precise mapping of rust resistance genes expedited, and robust breeder-friendly linked-markers have been reported for several genes (**Tables 1A, B**). This was largely possible due to the availability of high throughput genotyping platforms including DArTSeq (www.diversityarrays.com), i-select 90K SNP Infinium array (Wang et al., 2014) and genotyping-by-sequencing approaches (Poland and Rife, 2012).

Pleiotropic Adult Plant Resistances

Four APRs *Lr27/Yr30/Sr2, Lr34/Yr18/Sr57, Lr46/Yr29/Sr58*, and *Lr67/Yr46/Sr55* harboring multiple pathogen resistance have been identified (McIntosh et al., 1995; **Table 1B**). These genes resist devastation incurred by three rusts and powdery mildew caused by *Blumeria graminis f.* sp. *tritici*. The response of *Lr34, Lr46*, and *Lr67* is well characterized by their partial resistance to each of these pathogens and a phenotypic marker, leaf tip necrosis (Ltn) (Lillemo et al., 2008; Herrera-Foessel et al., 2014b). The pleiotropic APR *Lr34* has a comparatively higher level of rust resistance than other APRs (Lillemo et al., 2008; Yang et al., 2013). The APRs *Lr34/Yr18/Sr57/Pm38/Ltn1* and *Lr46/Yr29/Sr58/Pm39/Ltn2* have expressed additive gene

TABLE 1A | Seedling rust-resistant genes and their linked markers.

Seedling rust-resistant genes	Location	Donor	Linked Marker(s)	References
Yr15	1BS	A WEW accession G25	*uhw264* and *uhw259*	Klymiuk et al., 2018
Yr51	4AL	A wheat landrace AUS27858	*owm45F3R3* and *sun104*	Randhawa et al., 2014
Yr53	2BL	A durum wheat accession PI 480148	*wmc441* and *LRRrev/ NLRRrev350*	Xu et al., 2013
Yr60	4AL	A wheat line Almop	*wmc219* and *wmc313*	Herrera-Foessel et al., 2014a
Yr61	7AS	A Chinese cultivar Pindong34	*STS5467* and *STS5765b*	Zhou et al., 2014a
Yr63	7BS	A wheat landrace AUS 27955	*IWB33120* and *IWB52844*	McIntosh et al., 2017
Yr70/Lr76	5DS	An introgressed line IL393-4 carrying gene from *Ae. umbellulata*	*gwm190*	Bansal et al., 2017
Yr73	3DL	An AUS cv. Avocet R (*YrA* resistance was inherited by two complementary dominant genes *Yr73* and *Yr74*)	*DArT markers 116719[F]0*	Dracatos et al., 2016
Yr74	5BL	An AUS cv. Avocet R (*YrA* resistance was inherited by two complementary dominant genes *Yr73* and *Yr74*)	*DArT markers 1091695[F]0*	Dracatos et al., 2016
Yr81	6AS	Wheat landrace AUS27430	*KASP_3077* and *gwm459*	Gessese et al., 2019
Yr82	3BL	Wheat landrace AUS27969	*sun KASP_300* and *sunKASP_8775*	Pakeerathan et al., 2019
Lr16/Sr23	2BS	A Canadian spring wheat line BW278 (AC Domain*2/Sumai3)	*2BS_5175914_kwm847*	Kassa et al., 2017
Lr23	2BS	A common wheat genotype BT-Schomburgk selection and durum wheat cultivar Tamaroi	*sunKASP_16* and *sunKASP_47*	Chhetri et al., 2017
Lr24/Sr24	3DL	A wheat variety Agent carrying a translocation from *Agropyron elongatum*.	*Sr24#12-F* and *Sr24#12-R*	Mago et al., 2005
Lr37/Sr38/Yr17	2AS#2NS	*T. ventricosum* accession #10	*VENTRIUP* and *LN2*	Helguera et al., 2003
Lr52/Yr47	5BS	A wheat landrace Aus28183	*sun180*	Qureshi et al., 2016
Lr65	2AS	A swiss spelt wheat 'Altgold Rotkorn'	*gwm614* and *barc124*	Mohler et al., 2012
Lr71	1B	A swiss spelt wheat cv. Altgold Rotkorn	*gwm18* and *barc187*	Singh et al., 2001
Lr72	7BS	A Mexican durum wheat cultivar Atil C2000	*wmc606*	Herrera-Foessel et al., 2013
Lr73	2BS	A wheat genotype Morocco	*wPt-4453* and *wPt-8235*	Park et al., 2014
Lr79	3BL	A durum wheat landrace Aus26582	*sun786*	Qureshi et al., 2018c
Sr13	6AL	An emmer wheat Khapli and Ethiopian accession ST464	*EX24785*	Zhang et al., 2017
Sr26	6AL	A wheat genotype Avocet 'S' carrying an alien segment 6Ae#1L from *Ag. elongatum*	*sunKASP_224* and *sunKASP_225*	Qureshi et al., 2018b
Sr52	T6AS·6V#3L	A wheat-*Dasypyrum villosum* disomic addition line DA6V#3	*BF201083* and *BE490365*	Qi et al., 2011
Sr53	5DL	TA5599 (T5DL-5MgL·5MgS) carrying an alien segment from *Aegilops geniculata*	*BE443021/MboI* and *BE442814/HaeIII*,	Liu et al., 2011
Sr54	2D	A winter wheat cultivar Norin40	*barc228* and *wmc181*	Ghazvini et al., 2012
Sr60	5A	*T.monococcum* accession PI 306540	*ucw530* and *ucw540*	Chen S. et al., 2020

interaction in combination and is frequently used in CIMMYT breeding programs (Lillemo et al., 2008; Lillemo et al., 2013). Unlike ASRs, the class of APR does not rely on a gene-for-gene hypothesis and partial resistance against a range of pathotypes (Dodds et al., 2010). Cloning of *Lr34/Yr18/Sr57/Pm38/Ltn1* and *Lr67/Yr46/Sr55/Pm46/Ltn3* (Krattinger et al., 2009; Krattinger et al., 2011; Moore et al., 2015) has demonstrated their role in conferring disease resistance in cereals like Sorghum (Schnippenkoetter et al., 2017), Durum wheat (Rinaldo et al., 2017), Rice (Krattinger et al., 2016) and Barley (Risk et al., 2013; Milne et al., 2019). It is also indicated that the resistance response of *Lr34res* and *Lr67res* occurs due to gain of resistance function through alteration in two amino acids in each of ATP-Binding Cassette (ABC) transporter and Hexose (sugar) Transporter Protein (STP), respectively (Krattinger et al., 2011; Moore et al., 2015). The molecular mechanism of few of these genes is not well understood as compared to NLR genes, and the mode of action of Lr34 transporter and molecules it transports is completely unknown (Rinaldo et al., 2017). There are three possible scenarios which may explain the mode of action of Lr67res; First, is altered carbon partitioning caused by Lr67res to limit nutrients to the pathogen, secondly, altered hexose/sucrose ratio triggering defense response and thirdly reduced pathogen growth due to unknown mechanism triggered by altered function of Lr67res (Milne et al., 2019).

Bi-Parental Mapping *vs* Genome-Wide Association Studies (GWAS)

Gene postulation is a classical approach to identify new genes phenotypically, using rust infection type response, multi pathotype test for gene postulation and differential sets. There are two alternative approaches to identify new rust resistance genes. The first approach includes the identification of donor parents expressing a high level of rust resistance and developing bi-parental mapping populations by crossing donor lines with susceptible lines. Genetic studies at F_2 and F_3 generations help us to estimate the number of genetic factors controlling the trait and their interactions in controlling resistance. Selective genotyping at the early segregating generations and/or advanced stages like F_5 and F_6 generations assists in identifying genomic region(s)

TABLE 1B | Adult plant rust-resistant genes in wheat and their linked markers.

Adult plant rust resistance genes	Location	Donor	Linked Marker(s)	References
Yr48	5AL	Synthetic wheat PI610750	*wmc727* and *cfa2149*	Lowe et al., 2011
Yr52	7BL	A wheat germplasm PI 183527 carrying HTAP resistance	*barc182* and *wgp5258*	Ren et al., 2012
Yr54	2DL	A wheat line Quaiu3	*wpt-667162, wpt-667054* and *gwm301*	Basnet et al., 2014
Yr56	2AS	A landrace AUS 91575 and Wollaroi (AUS 99174)	*sun167* and *sun168*	McIntosh et al., 2017
Yr59	7BL	Iraqi germplasm PI 178759	*wgp5175* and *barc32*	Zhou et al., 2014b
Yr62	4BL	Spring wheat germplasm PI 192252	*gwm192* and *gwm251*	Lu et al., 2014
Yr68	4BL	Undesignated International Nursery ex New Zealand 03.25 (AGG91587WHEA)	*IWB74301* and *IWA4640*	McIntosh et al., 2017
Yr71	3DL	An Australian wheat variety Sunco	*gwm114b, KASP_16434, KASP_17207* and *KASP_20836*	Bariana et al., 2016
Yr75	7AL	An Australian wheat variety Axe	*IWB34640* and *cfa2040*	McIntosh et al., 2017
Yr77	6DS	A common wheat PI322118	*IWA167* and *barc54*	McIntosh et al., 2017
Yr78	6BS	A common wheat PI519805	*IWA7257* and *IWA4408*	Dong et al., 2017
Yr79	7BL	A common wheat PI182103 carrying HTAP resistance	*barc72* and *wmc335*	Feng et al., 2018
Yr80	3BL	A wheat landrace AUS27284	*sunKASP_65624* and *sunKASP_53113*	Nsabiyera et al., 2018
Lr68	7BL	A common wheat cultivar Parula	*cs7BLNLRR-F/cs7BLNLRR-R*	Herrera-Foessel et al., 2012
Lr74	3BL	A common wheat genotype BT-Schomburgk selection	*GBS2256311* and *IWB69699*	McIntosh et al., 2017
Lr75	1BL	A Swiss winter wheat cultivar 'Forno'	*B2g38480* and *B2g38640*	Singla et al., 2017
Sr56	5BL	A Swiss winter wheat Arina	*sun209* and *sun320*	Bansal et al., 2014
Sr55/Lr67/Yr46	4DL	A PAK landrace PI 250413	*TM 4* and *TM10*	Moore et al., 2015
Sr57/Lr34/Yr18	7DS	A wheat genotype Parula (PI58548)	*csLV34*	Lagudah et al., 2009
Sr58/Lr46/Yr29	1BL	A wheat cultivar Pavon76	*SNP1_Lr46G22*	Lagudah, personnel communication
Sr2/Lr27/Yr30	3BS	A wheat cultivar Hope	*csSr2*	Mago et al., 2011

underpinning rust resistance in the population (Bansal and Bariana, 2017). Bulk segregant analysis (BSA) is the most commonly used, efficient, and rapid method to identify markers closely linked to a specific gene or any genomic regions (Michelmore et al., 1991) by genotyping a pool of DNA from selected individuals with two extreme phenotypes and the contrasting parents. Then the allelic frequency differences between the bulks will be analyzed and compared with the phenotype to ascertain the possible linkage between the markers and trait of interest (Kthiri et al., 2018). Earlier, in the decade, SSR markers evenly spanning the wheat chromosomes were very frequently used to screen for polymorphic markers but, it was time-consuming and laborious as it was done manually. In recent times, the integration of next-generation sequencing-based 90K SNP arrays with BSA approach has quickened the identification of polymorphic markers and chromosomal location of major genes or the QTLs (Abe et al., 2012; Ramirez-Gonzalez et al., 2015; Qureshi et al., 2016; Kthiri et al., 2018; Wu et al., 2018; Pakeerathan et al., 2019). The BSA approach has also been combined with RNA-Seq to identify gene associated SNPs, NLR exome capture and sequencing (also called as MapRenSeq) to define NLRs associated with resistant genes (Narang et al., 2020) and NGS-based SLAF-seq to locate the gene of interest/QTL (Yin et al., 2018). However, the mapping of disease resistance genes and quantitative trait loci (QTL) through traditional bi-parental mapping approaches is restricted only to the limited diversity present in the parents and the less number of recombination events which results in low map resolution.

Alternatively, the second approach, Genome-wide association studies (GWAS) is primarily focused on quickly screening germplasm collection for genes of interest and to capture historical recombinations to achieve high-resolution mapping at a specific locus. As an advantage over mapping in bi-parental populations, this approach makes use of already existing natural populations, accounts for greater allelic diversity among the diverse individuals at a given locus and uses the recombination events that occur throughout the evolutionary process of germplasm (Yao et al., 2019). To excel in GWAS analysis, as a prerequisite, this approach would need a diversity panel constituting accessions and/or elite lines with similar photoperiod requirements and adaptation (Yu and Buckler, 2006). It has played a remarkable role in dissecting various complex traits in cereals (Yu et al., 2011; Juliana et al., 2015), and several of major and minor quantitative trait loci (QTL) relying on significant marker-trait associations (MTAs) for rust resistance have been identified through this approach (Rosewarne et al., 2012; Li et al., 2014; Zhang et al., 2014; Maccaferri et al., 2015; Juliana et al., 2018) but, none of the named rust genes has been identified through this approach until now. Moreover, several of these novel QTLs have not been validated and functionally characterized which have limited their use in breeding programs (Juliana et al., 2018). Though advances in statistical analysis and genotyping platforms have facilitated in ruling out the false-positive MTAs and rapid discovery of candidate genes using genome references (Bradbury et al., 2007; Zhang et al., 2010; Tang et al., 2016), population structure is still a critical concern and can be overcome by using mixed models to integrate genetic relatedness.

APPLICATION OF GENOMICS TOOLS IN MINING AND ISOLATION OF RUST RESISTANCE GENES

DNA Marker Technology in Wheat

DNA markers reveal allelic variations among individual organisms or species. In wheat research, DNA marker technology has been used in tracing targeted genes. This technique is consistent, mostly neutral/free from environmental variations and does not affect the developmental stage of the plant as it is based on variations in DNA sequences (Collard et al., 2005). Some morphological and biochemical markers are also being used to identify lines carrying durable genes, for instance, pseudo-black chaff and high-temperature-induced seedling chlorosis linked with *Sr2* (Slinkard and McIntosh, 1998), red-glume gene (Rg1) linked with *Yr10* and leaf-tip necrosis (*Ltn*) linked with *Lr34, Lr46, Lr67*, and *Lr68* (Lagudah et al., 2006; Herrera-Foessel et al., 2012; Herrera-Foessel et al., 2014b). The DNA marker technology offers a major advantage in plant breeding by exploring modern genomics tools. The Polymerase chain reaction (PCR)-based markers have been designed and applied to detect marker-trait association across seven groups of wheat chromosomes. The DNA markers namely Restriction fragment length polymorphism (RFLP), Sequence Characterized Amplified Region (SCAR), Sequence Tagged Site (STS), Simple Sequence Repeat (SSR), and Cleaved Amplified Polymorphic Sequences (CAPS) were widely explored as valuable tools for wheat improvement. Gene mapping in wheat was initiated using conventional genetic markers RFLPs (Anderson et al., 1992) and SSRs (Röder et al., 1998). Later, additional PCR-based markers like RGAP, CAPS, EST, STS, AFLP, and RAPD have been implemented in the mapping of disease resistance genes (Bariana et al., 2001). The consensus map of 2004 SSRs has been used to integrate conventional markers to some extent for drafting an integrated map of the identified gene/loci using cMap (Somers et al., 2004; Rosewarne et al., 2013). Sanger sequencing accelerated the identification of the single base pair variations (Wang et al., 1998) and helped to replace gel-based marker systems with robust and bi-allelic single nucleotide polymorphisms (SNPs). This SNP-based DNA marker has enhanced its implementation to detect allelic variation in targeted DNA fragments. The advantage of MAS (Marker Assisted Selection) is not only rapid detection assays for the presence of the gene but also enables gene pyramiding strategies wherein it is difficult to detect gene combinations due to epistatic/masking effect if race-specific genes.

Next-Generation Sequencing (NGS) Platforms

The NGS platforms have revolutionized genetics and genomics studies in crop plants. Several NGS-based approaches played a significant role in allele discovery and genotype-by-sequencing (GBS) through thousands of markers simultaneously to precisely cover the entire crop genome (Davey et al., 2011; Liu H. et al., 2014). In wheat, NGS technology enables detecting the abundance of DNA markers within a short period. The size of the wheat genome is huge (~16GB—around five times bigger than the human genome), more complex, and contains a high percentage of repetitive elements. Several marker development methods have been reported, including RRLs (reduced-representation libraries), CRoPS (complexity reduction of polymorphic sequences), RAD-seq (restriction-site associated DNA sequencing), SBP (sequence-based polymorphic marker technology), MSG (low coverage multiplexed shotgun genotyping), and GBS (genotyping-by-sequencing) to reduce the complexity (Yang et al., 2012). Additionally, GBS pipeline was also developed to reduce the complexity of the wheat genome. The RAD-seq and GBS were explored to target cutting sites after restriction digestion to avoid further redundancy in the genome (Poland et al., 2012). High throughput genotyping platforms including DArT-Seq, SNPs, GBS markers, and population-specific tGBS (targeted genotyping-by-sequencing) have expedited the precise mapping of genomic regions underpinning rust resistance (Qureshi et al., 2018b; Nsabiyera et al., 2020).

Discovery of SNPs Using a Genotyping Array

Discovery of single nucleotide polymorphisms (SNPs) in wheat has been expedited through the advances in genomics resources. Cavanagh et al. (2013) developed a high-throughput SNP genotyping array called i-select 9K SNP Infinium Bead chip Assay using 2,994 worldwide wheat accessions. Later, a high-density SNP map was developed after incorporating the first map and customized as i-select 90K SNP Infinium array covering seven groups of wheat chromosomes (Wang et al., 2014). These linked SNPs would facilitate to overcome, a major bottleneck associated with the application of DNA markers to characterize a wide range of germplasm (Yang et al., 2012). This high-density SNP map comprises nearly 90,000 gene-linked SNPs to characterize genetic variability in tetraploid and hexaploid wheat (Wang et al., 2014). Similarly, the GBS approach was utilized to characterize over 40,000 CIMMYT wheat germplasms as part of Seeds of Discovery (SeeD) initiative (Li et al., 2015). A consensus map of GBS markers was constructed to detect potentially new APR linked with stripe rust, leaf rust, and stem rust resistance and validate known genes/QTL through aligning them on wheat genome reference (IWGSC Refseq v 1.0; Appels et al., 2018). Identified trait-linked SNPs can be converted into Kompetitive allele-specific PCR assay (KASP) using PolyMarker, an automated bioinformatics pipeline (http://www.polymarker.info). The same SNPs are available in different wheat chromosomes at various positions due to its evolutionary nature and diploidization phenomenon. PolyMarker can design SNP-based KASP of the known genome-specificity using IWGSC RefSeq v1.0 (Ramirez-Gonzalez et al., 2015). Developing KASP markers cannot be guaranteed their utility in marker-assisted selection. Mendelian inheritance of individual KASP in a bi-parental mapping population and linkage with phenotypic data can ensure their application in the wheat breeding program.

Challenges to Draft Consensus Maps of Rust Resistance Genes

Several new resistance loci and robust markers of reported genes were developed and explored in gene pyramiding

(Bariana et al., 2007; Wessels and Botes, 2014; Randhawa et al., 2019). High level of redundancy in these identified loci and common MTAs was evident among different mapping studies. A consensus map using public database was drafted for stripe rust resistance on wheat chromosomes with the help of flanking markers to highlight around 140 stripe rust resistance loci and project redundant loci identified in over 30 bi-parental studies (Rosewarne et al., 2013). This study reduced the number of genomic regions conferring stripe rust resistance and laid a platform for further works. Later, Maccaferri et al. (2015) developed an integrated map of stripe rust resistance regions after incorporating significant QTLs identified in ten experiment-wise GWAS studies, 56 *YR* genes and 169 mapped QTLs. An "iterative maps compilation" tool in Biomercator v4.2 was explored to integrate the consensus map of SSRs (Somers et al., 2004), Synthetic × Opata ITMI BARC SSR map (Song et al., 2005), i-select 90K SNP Infinium array, Synthetic × Opata DH GBS map (Saintenac et al., 2013a) and Diversity Array Technology (DArT) map (http://www.diversityarrays.com) to create an integrated map (Maccaferri et al., 2015). This consensus map facilitated in the integration of different marker systems like RFLP, DArT, SSR along with flanking robust SNPs and align them together using published genetic map. This information is available on the GrainGenes webpage (https://wheat.pw.usda.gov/GG3/). Similar approaches have been adapted to develop stem rust resistance loci consensus map of detected in 24 bi-parental mapping populations, three association panels, two backcross populations (Yu et al., 2014), and QTL conferring leaf rust and powdery mildew resistance in wheat (Li et al., 2014).

Several genomic loci are well known to harbor more than one gene, but these integrated maps did not allow further delineation of these regions. For instance, wheat chromosome 5A carries two genes *Yr34* and *Yr48* which were later confirmed as allelic or the same (Qureshi et al., 2018a). Gao et al. (2015) attempted to enrich region of SrCad (source- Canadian wheat cultivar AC Cadillac) and *Sr42* (Norin 40) using GBS and 90K SNP array approach which placed both these genes at the same locus on chromosome 6DS. Moreover, both genes shared a common donor, BW553 and resistance to TTKSK isolate which also suggested that both genes are the same or allelic. Differential expression of AC Cadillac to non-TTKSK Pgt races compared to Norin 40 is due to the existence of background genes like *Lr34*. Cloning of *Rph15* in barley confirmed that *Rph15* and *Rph16* are allelic or the same (Chen C. et al., 2020).

Integrating wheat genome reference (IWGSC RefSeq v 1.0) with the previously published genetic map of rust resistance loci was a major challenge; however, the new genetic map viewing software, Pretzel, was designed to fix the issues. This software is currently being explored to align trait-linked SNPs, DArTseq, and GBS markers with multiple SNP platforms of available wheat and related genomic resources like *Triticum dicoccoides*, *T. turgidum*, *Aegilops tauschii*, *T. urartu*, *Brachypodium_distachyon*, *Hordeum vulgare*, and *Oryza sativa* (Keeble-Gagnere et al., 2019; http://plantinformatics.io/mapview). It assists in the positioning of various genomic regions of the different populations using IWGSC RefSeq v1.0. It would be a milestone achievement in differentiating rust resistance genes/MTAs underlying in similar genomic regions.

Rapid Rust Resistance Gene Cloning Methods

In plants, most of the disease resistance genes are race-specific and contain the Nucleotide-binding site (NBS) and LRR (Leucine-rich repeat) domains. These genes are believed to be regulated by NBS domains through signal transduction, and specific sites of corresponding pathogen virulence genes are recognized by LRR domains (Gill et al., 2015). Six stripe rust resistance genes, *Yr5/YrSP, Yr7, Yr10, Yr15, Yr36*, and *YrAS2388R* (Fu et al., 2009; Liu H. et al., 2014; Klymiuk et al., 2018; Marchal et al., 2018; Zhang et al., 2019), four-leaf rust resistance genes *Lr1, Lr10*, *Lr21*, and *Lr22a* (Feuillet et al., 2003; Huang et al., 2003; Cloutier et al., 2007; Thind et al., 2017), and nine major stem rust resistance genes, *Sr33, Sr35, Sr50, Sr22, Sr45, Sr13, Sr46, Sr21*, and *Sr60* (Periyannan et al., 2013; Saintenac et al., 2013b; Mago et al., 2015; Steuernagel et al., 2016; Zhang et al., 2017; Arora et al., 2018; Chen et al., 2018; Chen S. et al., 2020), and two pleiotropic APR (*Lr34/Yr18/Sr57* and *Lr67/Yr46/Sr55*) (Krattinger et al., 2009; Moore et al., 2015) have been cloned (**Table 2**).

Map-based cloning includes fine mapping of an individual gene, discovery of candidate genes followed by validation of these genes using mutants and available genomics resources (Jander et al., 2002; Thind et al., 2017; Zhang et al., 2019). The first study towards the map-based cloning of Rpg1 and Rpg4 using rice as an inter-genomic mapping vehicle was reported in Barley (Kilian et al., 1997). Many genes of economic importance in cereal crops, most notably, *chloronerva*, a gene involved in the uptake of iron in higher plants encoding *Nicotianamine synthase* (Ling et al., 1999), beta and old-gold (og) color mutations in tomato (Ronen et al., 2000), *Rf-1* in rice (Komori et al., 2004), Soybean *Maturity Locus E3* (Watanabe et al., 2009), *TTG1* homolog in Brassica (Zhang et al., 2009), and *AvrLm6* avirulence gene in *Leptosphaeria maculans* (Fudal et al., 2007), *Lr10* (Feuillet et al., 2003), *Lr21* (Huang et al., 2003), and *Lr1* (Ling et al., 2003) were isolated using this strategy. The main problem associated with map-based cloning is lack of sufficient DNA markers to create a fine map in different crops (Drenkard et al., 2002). Besides, it was essential to construct a physical map, identify markers, and reach close to the gene through chromosome walking. It was then followed by isolation, transformation, complementation, and determination of the sequence of the entire region of interest in the absence of any reference sequence of the wild-type DNA (Jander et al., 2002).

In crops with large genomes like wheat, complexity reduction is very important to clone target genes more quickly and efficiently. A recently developed molecular tool, MutChromSeq (Mutgenesis Chromosome flow sorting and short-read Sequencing), works based on mutagenesis followed by flow sorting of chromosomes and their sequencing to identify the possible induced mutations. This approach does not require a similar gene in bait library and hence enables reference-free forward genetics to open up the pan-genome to functional genomics (Sanchez-Martin et al., 2016;

TABLE 2 | List of cloned rust resistance genes in wheat.

Gene/Locus	Chromosome	Approach	Major/Minor gene	Protein encoded	References
Yr5/YrSP	2B	MutRenSeq	Major	NBS-LRR	Marchal et al., 2018
Yr7	2B	MutRenSeq	Major	NBS-LRR	Marchal et al., 2018
Yr10	1BS	Map-based cloning	Major	NBS-LRR	Liu W. et al., 2014
Yr15	1BS	Map-based cloning	Major	A wheat tandem kinase 1	Klymiuk et al., 2018
YrAS2388R	*4DS*	Map-based cloning	Major	CC-NBS-LRR	Zhang et al., 2019
Lr1	5DL	Map-based cloning	Major	CC-NBS-LRR	Cloutier et al., 2007
Lr10	1AS	Map-based cloning	Major	CC-NBS-LRR	Feuillet et al., 2003
Lr21	1DS	Map-based cloning	Major	CC-NBS-LRR	Huang et al., 2003
Sr13	6AL	map-based cloning	Major	CC-NBS-LRR	Zhang et al. (2017)
Sr21	$2A^{m}L$	map-based cloning	Major	CC-NBS-LRR	Chen et al. (2018)
Sr22	7A	MutRenSeq	Major	CC-NBS-LRR	Steuernagel et al., 2016
Sr33	1D	Map-based cloning	Major	CC-NBS-LRR	Periyannan et al., 2013
Sr35	3AL	Map-based cloning	Major	CC-NBS-LRR	Saintenac et al. (2013b)
Sr45	1D	MutRenSeq	Major	CC-NBS-LRR	Steuernagel et al., 2016
Sr 46	2DS	AgRenSeq	Major	coiled-coil NLR protein	Arora et al., 2018
Sr50	1RS	physical mapping, mutation and complementation	Major	CC-NBS-LRR	Mago et al. (2015)
Sr60	5AmS of T. monococcum	Map-based cloning	Major	A wheat tandem kinase 2	Chen S. et al., 2020
Yr36	*6BS*	Map-based cloning	Minor	Kinase-START gene	Fu et al., 2009
Lr22a	2DS	TACCA	Minor	CC-NBS-LRR	Thind et al., 2017
Lr34/Yr18/Sr57	7DS	Map-based cloning	Minor	ABC transporter	Krattinger et al., 2009
Lr67/Yr46/Sr55	4DL	Map-based cloning	Minor	Hexose transporter	Moore et al., 2015

Zhang et al., 2020). This rapid cloning approach which would need 18–24 months for mutagenesis and screening, approximately one month for chromosome flow sorting, sequencing and bioinformatics were successfully described for cloning of barley *Eceriferum-q* gene and wheat *Pm2* gene (Sanchez-Martin et al., 2016). The first leaf rust resistance gene *Rph1* (*Rph1.a*) on chromosome 2H from cultivated barley (*Hordeum vulgare*) cv Sudan was also rapidly cloned by combining this approach with genetic mapping. The successful application of this approach would need prior information on, chromosome location of the target gene (Dracatos et al., 2019; Zhang et al., 2020), large mutant populations to identify the target genes among five to six mutants (Mago et al., 2017; Dinh et al., 2020) and isolation of individual chromosomes (Periyannan, 2018).

As an alternate approach to MutChromSeq, TACCA makes use of flow sorting of chromosomes, next-generation sequencing, and cultivar specific *de-novo* chromosome assembly. Using this approach a broad-spectrum leaf-rust resistance locus *Lr22a* (encodes an intracellular immune receptor homologous to the Arabidopsis thaliana RPM1 protein) was cloned with molecular marker information and ethyl methanesulfonate (EMS) mutants (Thind et al., 2017).

There are other cloning strategies like MutMap (mutational mapping) which involve mutagenesis, sequencing, and mapping to identify SNPs between wild-type and homozygous mutants and then to narrow down to the region having gene of interest (Li et al., 2020b). Until recently, this approach was considered to be applicable only in crops with small genomes like rice (Abe et al., 2012), but it was demonstrated to successfully map and clone *Ms1* from allohexaploid bread wheat using F_2 plants derived from the progeny of heterozygous *ms1e* mutants (Wang et al., 2017). Still, this is a better choice when the genome is small, and high-quality reference genome is available.

A three-step pipeline including chemical mutagenesis (Mut), exome capture and sequencing (RenSeq) techniques was developed for the rapid isolation of genes (Steuernagel et al., 2016). Here, 'Mut' confers mutagenesis that is a technique to produce random mutations or nucleotide substitutions in the DNA sequence by treating the parent material with mutagens like EMS (Ethyl Methane Sulfonate $CH_3SO_3C_2H_5$) or Sodium Azide (NaN_3). This substitution results in GC to AT transition and can cause loss of function of the resistance gene. An initial kill-curve analysis is used to decide the optimum dose of mutagen to render 50% mortality and reduced growth (Periyannan et al., 2013). The 'RenSeq' technique relies on the sequence information of known resistance genes and uses as bait to capture similar gene fragments in closely related crops and species (Jupe et al., 2013; Steuernagel et al., 2016). In plants, most of the known disease resistance genes belong to NLRs, kinases (receptor-like kinase, receptor-like proteins, wall-associated kinase *etc*) and/or transporters families (Klymiuk et al., 2018). Two stem rust resistance genes (*Sr22* and *Sr45)* were cloned using this technique. In MutRenSeq, NLR gene families are targeted, as it is the major class of R gene family conferring disease resistance in plants. The procedure includes: (1) Bait library construction containing RNA probes with more sequence identity with predicted NLR genes, (2) Preparation of template DNA from the accessions or germplasm conferring disease resistance, (3) Gene capture/hybridization using bait library in PCR based hybridization reaction, (4) Next-generation sequencing of captured and enriched fragments to predict NLR gene structures, (5) Assembly of NBS-LRR reads and their comparison and (6) Validation of candidate genes. MutRenSeq is a rapid and accessible to several organisms including wheat (Steuernagel et al., 2016). The major limitations of this technique are its restriction to discover only the NLR gene, a

reference pan-genome and vital changes due to mutagenesis (Dinh et al., 2020).

AgRenSeq (Association genetics with R-gene enrichment sequencing) or speed cloning has been developed to align GWAS platform (to utilize diverse genome-wide natural variation) and the RenSeq. Unlike map-based cloning and MutRenSeq, this approach does not rely on bi-parental mapping populations or mutagenesis. For instance, AgRenSeq approach was successfully demonstrated to clone R gene, *Sr46* and to identify the candidate gene sequence for *SrTA1662* using a diverse panel of *Ae. tauschii ssp.strangulata* (Arora et al., 2018). It explores a pool of diverse wild relatives carrying many resistance genes as a result enabling the cloning of multiple genes at the same time (Dinh et al., 2020).

BREEDING STRATEGIES TO DEVELOP RUST-RESISTANT WHEAT VARIETIES

Relentless efforts to enhance modern wheat cultivars for rust resistance is of primary importance to many breeding programs which come with a challenge of, not to compromise with yield and quality traits. A rust-resistant hard wheat variety, "Marquillo" developed in 1918 (Hayes et al., 1920) had considerable resistance to rust, but it lacked the flour quality, so it could not become popular in North Dakota (Stoa, 1945). Similarly, a highly rust-resistant line named, "Hope" (McFadden, 1930) which had poor yield potential under drought and heat stress conditions. However, the popular rust-resistant wheat cultivar, "Thatcher" released in 1934 (Hayes et al., 1936) carried multiple stem rust resistance genes and provided useful resistance against stem rust in North America (Singh et al., 2004b) occupying 60% of the area during that period under hard red spring wheat in North Dakota. Being a most preferred strategy of rust control, systematic breeding for genetic resistance in wheat started when the inheritance of yellow rust resistance was demonstrated following Mendelian principles of heredity (Biffen, 1905). The resistance controlled by a single locus was considered to be sufficient for complete control of the rust pathogens, until the discoveries of Flor (1956), when the incompatibility of host and pathogens was entirely said to be based on corresponding gene present in the organism and the resistance governed by a single gene need not be always durable. In the 20th century, though, breeders were aware of possible single mutations in pathogens' Avr genes, could result in new virulent pathotypes, still most of the breeding programs adopted single gene pyramiding into cultivars as major "breeding strategy". This could be due to ease in the screening of breeding materials at the seedling stage and high heritability and clear phenotype of the resistance expressed by major genes (Pink and Hand, 2002).

There are multiple approaches, conventional and/or molecular, singly or in combination, being considered to develop wheat varieties with durable rust resistance around the globe. Traditionally, using conventional approaches, the available germplasm and breeding materials are screened at seedling and adult plant stage, to phenotypically identify resistant wheat lines and then to involve them in hybridization programs as one of the parents. Till today, there are several breeding teams with no access to advanced MAS tools have successfully adopted this approach to breeding future rust-resistant wheat varieties. This makes the best use of shuttle breeding, wherein, the breeding lines are grown in one or more off-season locations with congenial environments for all the three individual rust diseases. Due to the cultivation of host crops throughout the year, these offseason environments become the evolution hubs for the new races, which helps them to prolifer and multiply continuously. Besides, these environments will also assist breeder to carefully select wheat lines which show consistent resistance across the years and locations with a large number of naturally occurring pathotype mixtures in the environment.

Breeding strategies to improve wheat for seedling and adult plant resistance may vary usually due to their mode of inheritance which is either qualitative and/or quantitative. Among the many breeding methodologies available to improve a particular trait in crop plants, pureline selection, modified pedigree method, bulk breeding, recurrent selection, backcross breeding, mutation and single seed descent methods of breeding are applied to breed wheat for rusts resistance. Pureline selection improved the agronomical feature of several landraces resulting into popular wheat varieties namely Sharbati, White Pissi, Chandausi and Lal Kanak in India. The wheat variety Marquis was developed as a selection from hybridization between an early ripening Indian wheat "Hard Red Calcutta" and "Common Fife" in 1909. Due to early ripening, it escaped the injury caused by heat and rust to become a prominent variety for several years in Western North Dakota (Stoa, 1945). Breeding through a modified pedigree method would be more successful when resistance is governed by a major gene, while it does not give much improvements in combining minor genes in the population. While, single back cross-selected bulk breeding approach (Singh and Trethowan, 2007) can be used to transfer multiple minor resistance genes into a well-adapted and higher-yielding backgrounds (Singh et al., 2014). We have enlisted a few of popular Indian wheat varieties developed through conventional introgression of resistance genes for all three kinds of rusts (**Table 3**).

Genomics Assisted Improvement of Rust Resistance

Most of the breeding programs with rust resistance as a major focus, work on identification, mapping, isolation, and introgression of diverse resistant genes into agronomically potential but, rust susceptible wheat lines. Though conventional breeding methods are effective, they are very time consuming, need laborious efforts to develop improved versions of crop plants for any target trait/s. In the last two decades, several genomic interventions have become possible which provide tremendous capabilities to characterize and manipulate wheat genome and to accelerate breeding. Though rust resistance has clear-cut phenotype to select for, the advent of molecular marker systems like SNPs and high-throughput

TABLE 3 | List of popular Indian wheat varieties and their known rust resistant source.

Variety	Pedigree	Gene combination (s)		
		Leaf rust *(Lr)*	Stripe rust *(Yr)*	Stem rust *(Sr)*
LOK 1	S308/S331	*Lr13*	*Yr2ks*	*Sr2+Sr9b+Sr11*
PBW502	WH485/PBW343//RAJ1482	*Lr26+*	*Yr9+*	*Sr2+ Sr5+Sr31*
PBW343	ND/VG9144//KAL/BB/3/YCO"S"/4/VEE#S "S"	*Lr26+*	*Yr9+Yr27*	*Sr2+ Sr5+Sr31*
GW273	CPAN2084/VW205	*Lr13+Lr10*	-	*Sr8b+Sr11*
GW322	PBW173/GW196	*Lr13*	-	*Sr2+Sr11*
RAJ3765	HD2402/VL639	*Lr13+Lr10*	*Yr2ks+*	*Sr2+*
WH711	ALD'S'HUAC//HD2285/3/HFW-17	*Lr13*	*Yr2ks*	*Sr2+Sr7b*
DBW17	CMH79A.95/3*CNO79//RAJ3777	*Lr26+Lr23*	*Yr9+*	*Sr31*
PBW550	WH 594/RAJ 3856//W 485	*Lr26+R*	*Yr9+Yr18*	*Sr31*
PBW373	ND/VG9144//KAL/BB/3/YCO"S"/4/VEE#S "S"	*Lr26+*	*Yr9+Yr27*	*Sr2+ Sr5+Sr31*
RAJ4037	DL788-2/RAJ3717	*Lr24*	-	*Sr2+Sr24*
HD2189	HD2963/HD1931	*Lr13+Lr34*	*Sr2+Sr11*	*Yr2+Yr18*
WH147	E4870/C303//S339/PV18	*Lr13+Lr34*	*Yr2ks+Yr18*	*Sr7a+Sr11*
UP2338	UP368/VL421//UP262	*Lr26+Lr34*	*Yr9+Yr18*	*Sr2+Sr31*
WH542	JUPATECO/BLUE JAY//URES	*Lr26+Lr23*	*Yr9+Yr18*	*Sr31*
HUW234	HUW12*2/CPAN1666//HUW12	*Lr14a*	*Yr2ks+*	*Sr9b+Sr11*
HD2329	HD1962/E4870/3/K65/3/HD1553/UP262	*Lr13+Lr10+Lr34*	*Yr2+Yr18*	*Sr8b+Sr9b+Sr11*
C306	REGENT1974/3*CHZ//*2C591/3/C217/N14/C281	*Lr34*	*Yr2ks+Yr18*	-
HD2285	HD1912/HD1592//HD1962/E4870/3/K65/4/HD2160/HD2186	*Lr23*	*Yr2+*	*Sr9b+Sr11*
SONALIKA	II53.388/AN//YT54/N10B/3/LR/4/B4946.A.4.18.2IY/Y53//3*Y50	*Lr13*	*Yr2+*	*Sr2+Sr11*
UP262	S308/BJ66	*Lr23+Lr34*	*Yr2+Yr18*	*Sr2+Sr11*
PBW226	WG138/JUSTIN//CHIRS/HD1941	*Lr23*	*Yr2+*	*Sr2+*
MACS2496	A selection from SERI 'S'	*Lr26+Lr23+Lr1+*	*Yr9+*	*Sr2+Sr31*
WH283	HD1981/RAJ821	*Lr10+*	*Yr2+*	*Sr8b+*
GW190	VEE/3/BB 'S'/SKA//ARJUN	*Lr26+Lr23+Lr1+*	*Yr9+*	*Sr2+Sr31*
HS 295	CQT/AZ//IAS55/ALD/3/ALD/NAFN/4/PJN/PEL SL 1276.69	*Lr23+Lr34*	*Yr2ks+Yr18*	*Sr2+Sr8b+Sr11*
HD2967	ALD/CUC//URES/HD2160M/HD2278	*Lr23+*	*Yr2+*	*Sr8a+Sr11+Sr2*
HD3086	DBW14/HD2733//HUW468	*Lr13+Lr10+*	*Yr2+*	*Sr7b+Sr2*
WH1105	MILAN/S87230//BABAX	*Lr13+*	*Yr2+*	*R+*

Nayar et al. (2001); Bhardwaj (2011); Singh et al. (2011).

genotyping platforms like SNP arrays have enabled precise estimation of marker-trait associations and hence, to select for the trait of interest without the greater involvement of environmental effects and to combine multiple genes at the same time.

To identify and map novel rust resistance genes, the biparental and genome-wide association based mapping are most widely followed, with the latter having the ability to localize multiple genes and/or QTLs. Rust resistance based on a single dominant gene is generally considered to be leading to genetic changes in pathogen virulence (Wilcoxon, 1981) and when incorporated singly into cultivars, it may become ineffective within a few years of cultivation. Hence, it is always recommended to use combinations of major and minor genes (Roelfs et al., 1992) which could confer broad-spectrum resistance. Here, MAS may be incorporated into backcross breeding to simultaneously introgress several rust resistant genes against a wider range of pathogens. Rapid generation advance protocols like doubled haploids (DH) and Speed breeding combined with marker-assisted breeding, would also assist in developing resistant cultivars in a very short period. Although MAS is a very efficient breeding strategy, its implementation is limited due to unavailability of tightly liked markers and can only identify few large effect QTLs.

In recent years, GS, an advanced version of MAS, is being largely used to increase the selection efficiency and to dissect complex polygenic traits with lower heritability. GS has the power to capture small individual effects of thousands of genes through whole genome prediction models, to estimate breeding values for the complex traits and hence overcome the problems associated with the MAS. Breeding for race nonspecific minor gene resistance is one way to minimize genotype and environment interaction of resistance, which in turn leads to stability in resistance and yield (Bekele et al., 2019). Breeders have already preferred to go for many minor gene based resistance instead of major genes, where GS is considered to be the best molecular breeding approach in place of MAS. The integration of GS with selected bulk, recurrent selection, and back cross breeding is being explored to maximize the genetic gain for quantitative traits like APR through selection. Transgene-free genetic engineering through genome editing with sequence specific nucleases has paved a way for manipulating any specific genomic sequence superseding random mutagenesis (Wang et al., 2018). Among the four types of nucleases used in genome editing, CRISPR/Cas9 has a higher success rate in gene modification and requires less know-how. The application of genome editing for disease resistance would be much feasible; due to the better understanding of the molecular mechanisms underlying resistance, modification of a single gene may lead to resistance phenotype, and targeted mutagenesis is well applicable to knockout susceptible genes (Borrelli et al., 2018).

Deployment of Adult Plant Genes Delaying the Evolution of Pathotypes

Race-specific APRs which can be screened at the greenhouse level at two or third-leaf stage like *Lr13* and *Yr49* (McIntosh et al., 1995) are more vulnerable to succumb matching virulence in rust pathogens. Race-specific APR *Lr13* expresses at the seedling stage (two-leaf stage) in a greenhouse as well as at field conditions against avirulent pathotypes. Due to their expression at an early stage, some researchers have cited these genes as seedling resistance genes (Chen and Kang, 2017). APR *Lr22a* confers leaf rust resistance under field conditions and rendered resistance against 22 leaf rust pathotypes at flag leaf stage (Sawhney et al., 1982). *Lr34* was reported to be partially effective against leaf rust pathotypes in India (Sawhney and Sharma, 1990) and it expresses enhanced resistance along with other resistance genes (German and Kolmer, 1992). APR *Lr34* carrying genotype reduced the yield losses up to 18% and genotype lacking *Lr34* revealed 60 to 84% of losses (Singh et al., 1994). Slow rusting characters of *Lr34* and its interaction with other genes have made it useful for rust resistance (Nayar et al., 1999). Similarly, *Lr46/Yr29/Pm39* gene complex was identified in "Pavon76" and conferred a slow rusting to leaf rust, stripe rusts, and powdery mildew in wheat (William et al., 2003; Lillemo et al., 2008; Singh et al., 2013). The leaf rust resistance genes *Lr48* and *Lr49* were reported in wheat cultivars CSP44 and VL404, respectively as hypersensitive adult plant resistance genes (Saini et al., 2002). Another gene *Lr67/Yr46/Sr55* also confers slow rusting to leaf and stripe rusts (Hiebert et al., 2010; Herrera-Foessel et al., 2011). An Australian Pst pathotype 239 E237 A- 17 + 33+ has changed the rust rating of Australian cultivar "Axe" carrying *Yr75* (Cuddy and Hollway, 2018). Previous studies showed the susceptible nature of *Yr49* against Chinese Pst races (Ellis et al., 2014). Several stripe rust APRs have been overcome by newly detected Pst races in Europe and North America, so those APRs were tentatively classified as race-specific APRs (Hao et al., 2011; Sthapit et al., 2012; Sørensen et al., 2014). An accession HS628 expressed broad-spectrum resistance to Pt, Pst, and Pgt pathotypes in India (Pal et al., 2018). Developing wheat varieties possessing these diverse gene combinations could be a feasible approach to delay the evolution of pathotypes with matching virulence genes.

CONCLUDING REMARKS

Breeding for rust resistance is an integral part of wheat improvement. APRs *Sr2*, *Lr34*, *Lr46*, *Lr67*, and *Lr68* have been found durable and non-race specific. These APRs can offer only partial resistance which is insufficient to address food insecurity threat. Deployment of both durable rust resistance genes along with major R genes has been reported as a sound breeding strategy to avoid rust epidemics worldwide. Development of gene-specific DNA markers is essential to introgress the rust resistance gene in the desired wheat background and avoid linkage drag. Positional-cloning and MutRenSeq approach along with available genomics resources were explored to develop gene-specific marker of around twenty rust resistance genes including four APRs (*Lr34*, *Lr67*, *Yr36* and *Lr22a*). Stacking of five cloned resistance genes in modern wheat variety is underway *via* cis-genic approach. In future, this approach will be fruitful to develop resistant wheat against three rusts. Rust pathogen has been continuously evolving to shrink the number of effective rust resistance genes. The high-quality reference genome of over ten wheat varieties (10+ genome project) will assist in the cloning of additional major genes and APR. The major future challenge would be to identify effective resistance genes and their deployment to attain durable rust resistance.

AUTHOR CONTRIBUTIONS

PB, DB, DW, HB, and AS wrote the manuscript. All authors contributed to the article edits and approved the submitted version.

REFERENCES

Abe, A., Kosugi, S., Yoshida, K., Natsume, S., Takagi, H., Kanzaki, H., et al. (2012). Genome sequencing reveals agronomically important loci in rice using MutMap. *Nat. Biotechnol.* 30, 174. doi: 10.1038/nbt.2095

Aboukhaddour, R., Fetch, T., McCallum, B. D., Harding, M. W., Beres, B. L., and Graf, R. J. (2020). Wheat diseases on the prairies: A Canadian story. *Plant Pathol.* 69 (3), 418–432. doi: 10.1111/ppa.13147

Aggarwal, R., Kulshreshtha, D., Sharma, S., Singh, V. K., Manjunatha, C., Bhardwaj, S. C., et al. (2018). Molecular characterization of Indian pathotypes of *Puccinia striiformis* f. sp. *tritici* and multigene phylogenetic analysis to establish inter- and intraspecific relationships. *Genet. Mol. Biol.* 41 (4), 834–842. doi: 10.1590/1678-4685-GMB-2017-0171

Aime, M. C., Bell, C. D., and Wilson, A. W. (2018). Deconstructing the evolutionary complexity between rust fungi (Pucciniales) and their plant hosts. *Stud. Mycol.* 89, 143–152. doi: 10.1016/j.simyco.2018.02.002

Anderson, J., Ogihara, Y., Sorrells, M., and Tanksley, S. (1992). Development of a chromosomal arm map for wheat based on RFLP markers. *Theor. Appl. Genet.* 83 (8), 1035–1043. doi: 10.1007/BF00232969

Anderson, R. G. (1963). Studies on the inheritance of resistance to leaf rust of wheat. *Proc. 2nd Int. Wheat Genet. Symp. Lund*, 144–155.

Appels, R., Eversole, K., Stein, N., Feuillet, C., Keller, B., Rogers, J., et al. (2018). Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science* 361 (6403), eaar7191. doi: 10.1126/science.aar7191

Arora, S., Steuernagel, B., Chandramohan, S., Long, Y., Matny, O., Johnson, R., et al. (2018). Resistance gene discovery and cloning by sequence capture and association genetics. *bioRxiv* 248146. doi: 10.1038/s41587-018-0007-9

Asad, M. A., Xia, X., Wang, C., and He, Z. (2012). Molecular mapping of stripe rust resistance gene *YrSN104* in Chinese wheat line Shaannong 104. *Hereditas* 149 (4), 146–152. doi: 10.1111/j.1601-5223.2012.02261.x

Bansal, U., and Bariana, H. (2017). ""Advances in Identification and Mapping of Rust Resistance Genes in Wheat"," in *Wheat Rust Diseases: Methods in Molecular Biology*. Ed. S. Periyannan (New York, NY: Humana Press), 1659.

Bansal, U., Hayden, M. J., Venkata, B. P., Khanna, R., Saini, R. G., and Bariana, H. S. (2008). Genetic mapping of adult plant leaf rust resistance genes *Lr48* and *Lr49* in common wheat. *Theor. Appl. Genet.* 17, 307–312. doi: 10.1007/s00122-008-0775-6

Bansal, U., Bariana, H., Wong, D., Randhawa, M., Wicker, T., Hayden, M., et al. (2014). Molecular mapping of an adult plant stem rust resistance gene Sr56 in

winter wheat cultivar Arina. *Theor. Appl. Genet.* 127 (6), 1441–1448. doi: 10.1007/s00122-014-2311-1

Bansal, M., Kaur, S., Dhaliwal, H. S., Bains, N. S., Bariana, H. S., Chhuneja, P., et al. (2017). Mapping of *Aegilops umbellulata*-derived leaf rust and stripe rust resistance loci in wheat. *Plant Pathol.* 66 (1), 38–44. doi: 10.1111/ppa.12549

Bariana, H. S., Hayden, M. J., Ahmed, N., Bell, J., Sharp, P., and McIntosh, R. (2001). Mapping of durable adult plant and seedling resistances to stripe rust and stem rust diseases in wheat. *Crop Pasture Sci.* 52 (12), 1247–1255. doi: 10.1071/AR01040

Bariana, H. S., Brown, G. N., Bansal, U. K., Miah, H., Standen, G. E., and Lu, M. (2007). Breeding triple rust resistant wheat cultivars for Australia using conventional and marker assisted selection technologies. *Aust. J. Agric. Res.* 58 (6), 576. doi: 10.1071/ar07124

Bariana, H. S., Bansal, U. K., Basandrai, D., and Chhetri, M. (2013). "Disease Resistance," in *Genomics and Breeding for Climate-Resilient Crops, vol 2 Target Traits*. Ed. C. Kole (Berlin: Springer-Verlag Berlin Heidelberg), 291–314.

Bariana, H., Forrest, K., Qureshi, N., Miah, H., Hayden, M., and Bansal, U. (2016). Adult plant stripe rust resistance gene *Yr71* maps close to *Lr24 in* chromosome 3D of common wheat. *Mol. Breed.* 36 (7), 1–10. doi: 10.1007/s11032-016-0528-1

Basnet, B. R., Singh, R. P., Ibrahim, A. M. H., Herrera-Foessel, S. A., Huerta-Espino, J., Lan, C., et al. (2014). Characterization of *Yr54* and other genes associated with adult plant resistance to yellow rust and leaf rust in common wheat Quaiu 3. *Mol. Breed.* 33 (2), 385–399. doi: 10.1007/s11032-013-9957-2

Bekele, D., Tesfaye, K., and Fikre, A. (2019). Recent Developments in Genomic Selection for Minor Gene Quantitative Disease Resistance Plant Breeding. *J. Plant Pathol. Microbiol.* 10 (478), 1–8. doi: 10.35248/2157-7471.10.478

Beresford, R. M. (1982). Stripe rust (*Puccinia striiformis*), a new disease of wheat in New Zealand. *Cer. Rusts Bull.* 10, 35–41.

Bhardwaj, S. C. (2011). "Resistance genes and adult plant rust resistance of released wheat varieties of India", in *Research Bulletin 5*. (Flowerdale, Shimla, India: Directorate of Wheat Research, Regional Station), 31.

Bhardwaj, S. C., Singh, G. P., Gangwar, O. P., Prasad, P., and Kumar, S. (2019). Status of Wheat Rust Research and Progress in Rust Management-Indian Context. *Agronomy* 9 (12) 1–14. doi: 10.3390/agronomy9120892

Bhavani, S., Hodson, D. P., Huerta-espino, J., Randhawa, M. S., and Singh, R. P. (2019). Progress in breeding for resistance to Ug99 and other races of the stem rust fungus in CIMMYT wheat germplasm. *Front. Agr. Sci. Eng.* 6 (3), 210–224. doi: 10.15302/J-FASE-2019268

Biffen, R. H. (1905). Mendel's laws of inheritance and wheat breeding. *J. Agric. Sci.* 1, 14–48. doi: 10.1017/S0021859600000137

Borrelli, V. M. G., Brambilla, V., Rogowsky, P., Marocco, A., and Lanubile, A. (2018). The Enhancement of Plant Disease Resistance Using CRISPR/Cas9 Technology. *Front. Plant Sci.* 9, 1245. doi: 10.3389/fpls.2018.01245

Borrill, P., Adamski, N., and Uauy, C. (2015). Genomics as the key to unlocking the polyploid potential of wheat. *New Phytol.* 208, 1008– 1022. doi: 10.1111/nph.13533

Bradbury, P. J., Zhang, Z., Kroon, D. E., Casstevens, T. M., Ramdoss, Y., and Buckler, E. S. (2007). TASSEL: software for association mapping of complex traits in diverse samples. *Bioinformatics* 23 (19), 2633–2635. doi: 10.1093/bioinformatics/btm308

Brenchley, R., Spannagl, M., Pfeifer, M., Barker, G. L., D'Amore, R., Allen, A. M., et al. (2012). Analysis of the bread wheat genome using whole-genome shotgun sequencing. *Nature* 491, 705–710. doi: 10.1038/nature11650

Cavanagh, C. R., Chao, S., Wang, S., Huang, B. E., Stephen, S., Kiani, S., et al. (2013). Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. *Proc. Natl. Acad. Sci. U. S. A.* 110 (20), 8057–8062. doi: 10.1073/pnas.1217133110

Chapman, J. A., Mascher, M., Buluç, A., Barry, K., Georganas, E., and Session, A. (2015). A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. *Genome Biol.* 16 (26), 1–17. doi: 10.1186/s13059-015-0582-8

Chaves, M. S., Martinelli, J. A., Wesp-Guterres, C., Graichen, F. A. S., Brammer, S., Scagliusi, S. M., et al. (2013). The importance for food security of maintaining rust resistance in wheat. *Food Secur.* 5 (2), 157–176. doi: 10.1007/s12571-013-0248-x

Chen, X., and Kang, Z. (2017). *"Introduction: history of research, symptoms, taxonomy of the pathogen, host range, distribution, and impact of stripe rust," in Stripe Rust*. Eds. X. Chen and Z. Kang (Dordrect, Netherlands: Springer Science), 1–33.

Chen, S., Zhang, W., Bolus, S., Rouse, M. N., and Dubcovsky, J. (2018). Identification and characterization of wheat stem rust resistance gene *Sr21* effective against the Ug99 race group at high temperature. *PloS Genet.* 14, e1007287. doi: 10.1371/journal.pgen.1007287

Chen, C., Clark, B., Martin, M. J., Matny, O. N., Steffenson, B. J., Franckowiak, J. D., et al. (2020). Ancient BED-domain-containing immune receptor from wild barley confers widely effective resistance to leaf rust. *bioRxiv*. doi: 10.1101/2020.01.19.911446

Chen, S., Rouse, M. N., Zhang, W., Zhang, X., Guo, Y., Briggs, J., et al. (2020). Wheat gene *Sr60* encodes a protein with two putative kinase domains that confers resistance to stem rust. *New Phytol.* 225 (2), 948–959. doi: 10.1111/nph.16169

Chen, X. (2005). Epidemiology and control of stripe rust [*Puccinia striiformis* f. sp. *tritici*] on wheat. *Can. J. Plant Pathol.* 27 (3), 314–337. doi: 10.1080/07060660509507230

Chhetri, M., Bariana, H., Wong, D., Sohail, Y., Hayden, M., and Bansal, U. (2017). Development of robust molecular markers for marker-assisted selection of leaf rust resistance gene *Lr23 in* common and durum wheat breeding programs. *Mol. Breed.* 37 (3), 21. doi: 10.1007/s11032-017-0628-6

Cloutier, S., McCallum, B. D., Loutre, C., Banks, T. W., Wicker, T., Feuillet, C., et al. (2007). Leaf rust resistance gene *Lr1*, isolated from bread wheat (*Triticum aestivum* L.) is a member of the large psr567 gene family. *Plant Mol. Biol.* 65 (1), 93–106. doi: 10.1007/s11103-007-9201-8

Collard, B. C. Y., Jahufer, M. Z. Z., Brouwer, J. B., and Pang, E. C. K. (2005). An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts. *Euphytica* 142 (1-2), 169–196. doi: 10.1007/s10681-005-1681-5

Cuddy, W., and Hollway, G. (2018). Detection of a new wheat stripe rust pathotype in Victoria. *Cereal Rust Rep.* 16 (1), 1.

Davey, J. W., Hohenlohe, P. A., Etter, P. D., Boone, J. Q., Catchen, J. M., and Blaxter, M. L. (2011). Genome-wide genetic marker discovery and genotyping using next-generation sequencing. *Nat. Rev. Genet.* 12 (7), 499–510. doi: 10.1038/nrg3012

Dinh, H. X., Singh, D., Periyannan, S., Park, R. F., and Pourkheirandish, M. (2020). Molecular genetics of leaf rust resistance in wheat and barley. *Theor. Appl. Genet.* 133, 2035–2050. doi: 10.1007/s00122-020-03570-8

Dodds, P., Lawrence, G., Mago, R., Ayliffe, M., Narayana, U., Szabo, L., et al. (2010). "Advances in host-pathogen molecular interactions: rust effectors as targets for recognition," in *Oral papers 2009 Technical Workshop (Full Papers and Abstracts for the Presented Talks)*, (Obregón, Sonora, Mexico: Borlaug Global Rust Initiative, Cd.) 49–54.

Dong, Z., Hegarty, J. M., Zhang, J., Zhang, W., Chao, S., Chen, X., et al. (2017). Validation and characterization of a QTL for adult plant resistance to stripe rust on wheat chromosome arm 6BS (*Yr78*). *Theor. Appl. Genet.* 130 (10), 2127–2137. doi: 10.1007/s00122-017-2946-9

Dracatos, P. M., Zhang, P., Park, R. F., McIntosh, R. A., Wellings, C. R. , et al (2016). Complementary resistance genes in wheat selection 'Avocet R' confer resistance to stripe rust. *Theor. Appl. Genet.* 129 (1), 65–76. doi: 10.1007/s00122-015-2609-7

Dracatos, P. M., Bartos, J., Elmansour, H., Singh, D., Karafiatova, M., and Zhang, P (2019). The coiled-coil NLR *Rph1*, confers leaf rust resistance in barley cultivar Sudan. *Plant Physiol.* 179, 1362. doi: 10.1104/pp.18.01052

Drenkard, E., Richter, B. G., Rozen, S., Stutius, L. M., Angell,N. A., Mindrinos, M., et al (2000). A simple procedure for the analysis of single nucleotide polymorphisms facilitates map-based cloning in Arabidopsis. *Plant Physiol.* 124 (4), 1483–1492. doi: 10.1104/pp.124.4.1483

Dubin, H. J., and Torres, E. (1981). Causes and consequences of the 1976-1977 wheat leaf rust epidemic in northwest Mexico. *Annu. Rev. Phytopathol.* 19, 41–49. doi: 10.1146/annurev.py.19.090181.000353

Duveiller, E., Singh, R. P., and Nicol, J. M. (2007). The challenges of maintaining wheat productivity: pests, diseases, and potential epidemics. *Euphytica* 157, 417–430. doi: 10.1007/s10681-007-9380-z

El Baidouri, M., Murat, F., Veyssiere, M., Molinier, M., Flores, R., Burlot, L., et al. (2017). Reconciling the evolutionary origin of bread wheat (*Triticum aestivum*). *New Phytol.* 213 (3), 1477–1486. doi: 10.1111/nph.14113

Eliana, D., Brent, G. R., Steve, R., Lisa, M. S., Nathaniel, A. A., Michael, M., et al. (2002). A Simple Procedure for the Analysis of Single Nucleotide Polymorphisms Facilitates Map-Based Cloning in Arabidopsis1. *Plant Physiol.* 124 (4), 1483–1492. doi: 10.1104/pp.124.4.1483

Ellis, J. G., Lagudah, E. S., Spielmeyer, W., and Dodds, P. N. (2014). The past, present and future of breeding rust resistant wheat. *Front. Plant Sci.* 5, 641. doi: 10.3389/fpls.2014.00641

FAOSTAT (2020). *Statistical databases. Food and Agriculture Organization of the United Nations*. Available at: http://www.fao.org/faostat/en/#home (Accessed on 31 March 2020).

Feldman, M. (1995). "Wheats," in *Evolution of crop plants*. Eds. J. Smartt and N. W. Simmonds (Harlow, UK: Longman Scientific and Technical), 185–192.

Feng, J., Wang, M., See, D. R., Chao, S., Zheng, Y., and Chen, X. (2018). Characterization of novel gene *Yr79* and four additional quantitative trait loci for all-stage and high-temperature adult-plant resistance to stripe rust in spring wheat PI 182103. *Phytopathology* 108 (6), 737–747. doi: 10.1094/Phyto-11-17-0375-r

Feuillet, C., Travella, S., Stein, N., Albar, L., Nublat, A., and Keller, B. (2003). Map-based isolation of the leaf rust disease resistance gene *Lr10* from the hexaploid wheat (*Triticum aestivum* L.) genome. *Proc. Natl. Acad. Sci. U. S. A.* 100 (25), 15253–15258. doi: 10.1073/pnas.2435133100

Figueroa, M., Upadhyaya, N. M., Sperschneider, J., Park, R. F., Szabo, L. J., Steffenson, B., et al. (2016). Changing the game: using integrative genomics to probe virulence mechanisms of the stem rust pathogen Puccinia graminis f. sp. tritici. *Front. Plant Sci.* 7, 205. doi: 10.3389/fpls.2016.00205

Flor, H. H. (1956). The complementary genic system in flax and flax rust. *Adv. Genet.* 8, 29–54. doi: 10.1016/S0065-2660(08)60498-8

Fu, D., Uauy, C., Distelfeld, A., Blechl, A., Epstein, L., Chen, X., et al. (2009). A kinase-START gene confers temperature-dependent resistance to wheat stripe rust. *Science* 323 (5919), 1357–1360. doi: 10.1126/science.1166289

Fudal, I., Ross, S., Gout, L., Blaise, F., Kuhn, M. L., Eckert, M. R., et al. (2007). Heterochromatin-like regions as ecological niches for avirulence genes in the leptosphaeria maculans genome: map-based cloning of AvrLm6. *Mol. Plant Microbe Interact.* 20 (4), 459–470. doi: 10.1094/MPMI-20-4-0459

Gao, L., Kielsmeier-Cook, J., Bajgain, P., Zhang, X., Chao, S., Rouse, M. N., et al. (2015). Development of genotyping by sequencing (GBS)-and array-derived SNP markers for stem rust resistance gene Sr42. *Mol. Breed.* 35 (207), 2–13. doi: 10.1007/s11032-015-0404-4

German, S. E., and Kolmer, J. A. (1992). Effect of gene *Lr34* in the enhancement of resistance to leaf rust of wheat. *Theor. Appl. Genet.* 84 (1), 97–105. doi: 10.1007/bf00223987

Gessese, M., Bariana, H., Wong, D., Hayden, M., and Bansal, U. (2019). Molecular mapping of stripe rust resistance gene *Yr81* in a common wheat landrace Aus27430. *Plant Dis.* 103, 1166–1171. doi: 10.1094/PDIS-06-18-1055-RE

Ghazvini, H., Hiebert, C. W., Thomas, J. B., and Fetch, T. (2012). Development of a multiple bulked segregant analysis (MBSA) method used to locate a new stem rust resistance gene (*Sr54*) in the winter wheat cultivar Norin 40. *Theor. Appl. Genet.* 126 (2), 443–449. doi: 10.1007/s00122-012-1992-6

Gill, U. S., Lee, S., and Mysore, K. S. (2015). Host versus non-host resistance: distinct wars with similar arsenals. *Phytopathology* 105580, 587. doi: 10.1094/phyto-11-14-0298-rvw

Hao, Y., Chen, Z., Wang, Y., Bland, D., Buck, J., Brown-Guedira, G., et al. (2011). Characterization of a major QTL for adult plant resistance to stripe rust in US soft red winter wheat. *Theor. Appl. Genet.* 123 (8), 1401–1411. doi: 10.1007/s00122-011-1675-8

Hayes, H. K., Pafker, J. H., and Kurtzweil, C. (1920). Genetics of rust resistance in crosses of varieties of *Triticum vulgare* with varieties of *T. durum* and *T dicoccum*. *J. Agric. Res.* 19, 523–542.

Hayes, H. K., Ausemus, E. R., Stakman, E. C., Bailey, C. H., Wilson, H. K., Bamberg, R. H., et al. (1936). Thatcher wheat. *S. Bull. Minn. Agric. Exp. Stn.* 325, 39.

Helguera, M., Khan, I. A., Kolmer, J., Lijavetzky, D., Zhong-qi, L., and Dubcovsky, J. (2003). PCR assays for the *Lr37-Yr17-Sr38* cluster of rust resistance genes and their use to develop isogenic hard red spring wheat lines. *Crop Sci.* 43 (5) 1839–1847. doi: 10.2135/cropsci2003.1839

Herrera-Foessel, S. A., Lagudah, E. S., Huerta-Espino, J., Hayden, M. J., Bariana, H. S., Singh, D., et al. (2011). New slow-rusting leaf rust and stripe rust resistance genes *Lr67* and *Yr46* in wheat are pleiotropic or closely linked. *Theor. Appl. Genet.* 122 (1), 239–249. doi: 10.1007/s00122-010-1439-x

Herrera-Foessel, S. A., Singh, R. P., Huerta-Espino, J., Rosewarne, G. M., Periyannan, S. K., Viccars, L., et al. (2012). *Lr68*: a new gene conferring slow rusting resistance to leafrust in wheat. *Theor. Appl. Genet.* 124, 1475–1486. doi: 10.1007/s00122-012-1802-1

Herrera-Foessel, S. A., Huerta-Espino, J., Calvo-Salazar, V., Lan, C. X., and Singh, R. P. (2013). *Lr72* confers resistance to leaf rust in durum wheat cultivar Atil C2000. *Plant Dis.* 98 (5), 631–635. doi: 10.1094/PDIS-07-13-0741-RE

Herrera-Foessel, S. A., Singh, R. P., Lan, C. X., Huerta-Espino, J., Calvo-Salazar, V., Bansal, U. K., et al. (2014a). *Yr60*, a gene conferring moderate resistance to stripe rust in wheat. *Plant Dis.* 99 (4), 508–511. doi: 10.1094/PDIS-08-14-0796-RE

Herrera-Foessel, S. A., Singh, R. P., Lillemo, M., Huerta-Espino, J., Bhavani, S., Singh, S., et al. (2014b). *Lr67/Yr46* confers adult plant resistance to stem rust and powdery mildew in wheat. *Theor. Appl. Genet.* 127 (4), 781–789. doi: 10.1007/s00122-013-2256-9

Hiebert, C. W., Thomas, J. B., McCallum, B. D., Humphreys, D. G., DePauw, R. M., Hayden, M. J., et al. (2010). An introgression on wheat chromosome 4DL in RL6077 (Thatcher*6/PI 250413) confers adult plant resistance to stripe rust and leaf rust (*Lr67*). *Theor. Appl. Genet.* 121, 1083–1091. doi: 10.1007/s00122-010-1373-y

Huang, L., Brooks, S. A., Li, W., Fellers, J. P., Trick, H. N., and Gill, B. S. (2003). Map-based cloning of leaf rust resistance gene *Lr21* from the large and polyploid genome of bread wheat. *Genetics* 164 (2), 655–664.

Huerta-Espino, J., Singh, R., Germán, S., McCallum, B., Park, R., Chen, W., et al. (2011). Global status of wheat leaf rust caused by *Puccinia triticina*. *Euphytica* 179 (1), 143–160. doi: 10.1007/s10681-011-0361-x

Hussain, M., Hassan, S. F., and Kirmani, M. A. S. (1980). "Virulence in Puccinia recondita Rob. ex. Desm. f. sp. tritici in Pakistan during 1978 and 1979," in *Proceedings of 5th European and Mediterranean cereal rust conference*(Bari, Italy), 179–184.

International Wheat Genome Sequencing, C (2014). A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome. *Science* 345 (6194), 1251788. doi: 10.1126/science.1251788

Jander, G., Norris, S. R., Rounsley, S. D., Bush, D. F., Levin, I. M., and Last, R. L. (2002). Arabidopsis map-based cloning in the post-genome era. *Plant Physiol.* 129 (2), 440–450. doi: 10.1104/pp.003533

Jin, Y., Szabo, L. J., and Carson, M. (2010). Century - old mystery of *Puccinia striiformis* life history solved with the identification of *Berberis* as an alternate host. *Phytopathology* 100, 432–435. doi: 10.1094/PHYTO-100-5-0432

Johnson, R., and Law, C. N. (1975). Genetic control of durable resistance to yellow rust (*Puccinia striiformis*) in the wheat cultivar Hybrid de Bersee. *Ann. Appl. Biol.* 81, 385. doi: 10.1111/j.1744-7348.1975.tb01654.x

Joshi, L. M., Srivastava, K. D., and Nagarajan, S. (1975). An analysis of brown rust epidemics of 1971-72 and 1972-73. *Indian Phytopathol.* 28, 138.

Juliana, P., Rutkoski, J. E., Poland, J. A., Singh, R. P., Murugasamy, S., Natesan, S., et al. (2015). Genome-Wide Association Mapping for Leaf Tip Necrosis and Pseudo-black Chaff in Relation to Durable Rust Resistance in Wheat. *Plant Genome* 8 (2), 1–12. doi: 10.3835/plantgenome2015.01.0002

Juliana, P., Singh, R. P., Singh, P. K., Poland, J. A., Bergstrom, G. C., Huerta-Espino, J., et al. (2018). Genome-wide association mapping for resistance to leaf rust, stripe rust and tan spot in wheat reveals potential candidate genes. *Theor. Appl. Genet.* 131 (7), 1405–1422. doi: 10.1007/s00122-018-3086-6

Jupe, F., Witek, K., Verweij, W., Sliwka, J., Pritchard, L., Etherington, G. J., et al. (2013). Resistance gene enrichment sequencing (RenSeq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. *Plant J.* 76 (3), 530–544. doi: 10.1111/tpj.12307

Kassa, M. T., You, F. M., Hiebert, C. W., Pozniak, C. J., Fobert, P. R., Sharpe, A. G., et al. (2017). Highly predictive SNP markers for efficient selection of the wheat leaf rust resistance gene *Lr16*. *BMC Plant Biol.* 17 (1), 45. doi: 10.1186/s12870-017-0993-7

Keeble-Gagnère, G., Isdale, D., Suchecki, R., Kruger, A., Lomas, K., Carroll, D., et al. (2019). Integrating past, present and future wheat research with Pretzel. *bioRxiv* 4 1–4. doi: 10.1101/517953

Kihara, H. (1944). Discovery of the DD analyser, one of the ancestors of T. vulgare. *Agric. Hortic.* 19, 13–14.

Kilian, A., Chen, J., Han, F., Steffenson, B., and Kleinhofs, A. (1997). Towards map-based cloning of the barley stem rust resistance genes *Rpg1* and *Rpg4* using rice as an intergenomic cloning vehicle. *Plant Mol. Biol.* 35 (1/2), 187–195. doi: 10.1023/a:1005768222615

Klymiuk, V., Yaniv, E., Huang, L., Raats, D., Fatiukha, A., Chen, S., et al. (2018). Cloning of the wheat *Yr15* resistance gene sheds light on the plant tandem kinase-pseudokinase family. *Nat. Commun.* 9 (1), 3735. doi: 10.1038/s41467-018-06138-9

Kolmer, J., Chen, X., and Jin, Y. (2009). "Diseases which challenge global wheat production-The wheat rusts," in *Wheat Science and Trade*. Ed. B. F. Carver (USA: Wiley-Blackwell), 89–124.

Komori, T., Ohta, S., Murai, N., Takakura, Y., Kuraya, Y., Suzuki, S., et al. (2004). Map-based cloning of a fertility restorer gene, *Rf-1*, in rice (*Oryza sativa* L.). *Plant J.* 37 (3), 315–325. doi: 10.1046/j.1365-313x.2003.01961.x

Krattinger, S. G., Lagudah, E. S., Spielmeyer, W., Singh, R. P., Huerta-Espino, J., McFadden, H., et al. (2009). A putative ABC transporter confers durable resistance to multiple fungal pathogens in wheat. *Science* 323 (5919), 1360–1363.

Krattinger, S. G., Lagudah, E. S., Wicker, T., Risk, J. M., Ashton, A. R., Selter, L. L., et al. (2011). *Lr34* multi-pathogen resistance ABC transporter: molecular analysis of homoeologous and orthologous genes in hexaploid wheat and other grass species. *Plant J.* 65 (3), 392–403. doi: 10.1111/j.1365-313X.2010.04430.x

Krattinger, S. G., Sucher, J., Selter, L. L., Chauhan, H., Zhou, B., Tang, M., et al. (2016). The wheat durable, multipathogen resistance gene *Lr34* confers partial blast resistance in rice. *Plant Biotechnol. J.* 14 (5), 1261–1268. doi: 10.1111/pbi.12491

Kthiri, D., Loladze, A., MacLachlan, P. R., N'Diaye, A., Walkowiak, S., Nilsen, K., et al. (2018). Characterization and mapping of leaf rust resistance in four durum wheat cultivars. *PloS One* 13 (5), e0197317. doi: 10.1371/journal.pone.0197317

Lagudah, E. S., McFadden, H., Singh, R. P., Huerta-Espino, J., Bariana, H. S., and Spielmeyer, W. (2006). Molecular genetic characterization of the *Lr34/Yr18* slow rusting resistance gene region in wheat. *Theor. Appl. Genet.* 114 (1), 21–30. doi: 10.1007/s00122-006-0406-z

Lagudah, E. S., Krattinger, S. G., Herrera-Foessel, S., Singh, R. P., Huerta-Espino, J., Spielmeyer, W., et al. (2009). Gene-specific markers for the wheat gene *Lr34/Yr18/Pm38* which confers resistance to multiple fungal pathogens. *Theor. Appl. Genet.* 119 (5), 889–898. doi: 10.1007/s00122-009-1097-z

Li, Z., Lan, C., He, Z., Singh, R. P., Rosewarne, G. M., Chen, X., et al. (2014). Overview and application of QTL for adult plant resistance to leaf rust and powdery mildew in wheat. *Crop Sci.* 54 (5), 1907–1925. doi: 10.2135/cropsci2014.02.0162

Li, H., Vikram, P., Singh, R. P., Kilian, A., Carling, J., Song, J., et al. (2015). A high density GBS map of bread wheat and its application for dissecting complex disease resistance traits. *BMC Genomics* 16 (1), 216. doi: 10.1186/s12864-015-1424-5

Li, J., Yang, J., Li, Y., and Ma, L. (2020b). Current strategies and advances in wheat biology. *Crop J.* doi: 10.1016/j.cj.2020.03.004

Li, J., Dundas, I., Dong, C., Li, G., Trethowan, R., Yang, Z., et al. (2020a). Identification and characterization of a new stripe rust resistance gene *Yr83* on rye chromosome 6R in wheat. *Theor. Appl. Genet.* 133 (4), 1095–1107. doi: 10.1007/s00122-020-03534-y

Lillemo, M., Asalf, B., Singh, R. P., Huerta-Espino, J., Chen, X. M., He, Z. H., et al. (2008). The adult plant rust resistance loci *Lr34/Yr18* and *Lr46/Yr29* are important determinants of partial resistance to powdery mildew in bread wheat line Saar. *Theor. Appl. Genet.* 116, 1155–1166. doi: 10.1007/s00122-008-0743-1

Lillemo, M., Joshi, A. K., Prasad, R., Chand, R., and Singh, R. P. (2013). QTL for spot blotch resistance in bread wheat line Saar co-locate to the biotrophic disease resistance loci *Lr34* and *Lr46*. *Theor. Appl. Genet.* 126 (3), 711–719. doi: 10.1007/s00122-012-2012-6

Ling, H. Q., Koch, G., Baumlein, H., and Ganal, M. W. (1999). Map-based cloning of chloronerva, a gene involved in iron uptake of higher plants encoding nicotianamine synthase. *Proc. Natl. Acad. Sci. U. S. A.* 96 (12), 7098–7103. doi: 10.1073/pnas.96.12.7098

Ling, H. Q., Zhu, Y., and Keller, B. (2003). High-resolution mapping of the leaf rust disease resistance gene *Lr1* in wheat and characterization of BAC clones from the *Lr1* locus. *Theor. Appl. Genet.* 106 (5), 875–882. doi: 10.1007/s00122-002-1139-2

Liu, W., Rouse, M., Friebe, B., Jin, Y., Gill, B., and Pumphrey, M. O. (2011). Discovery and molecular mapping of a new gene conferring resistance to stem rust, *Sr53*, derived from *Aegilops geniculata* and characterization of spontaneous translocation stocks with reduced alien chromatin. *Chromosome Res.* 19 (5), 669–682. doi: 10.1007/s10577-011-9226-3

Liu, H., Bayer, M., Druka, A., Russell, J. R., Hackett, C. A., Poland, J., et al. (2014). An evaluation of genotyping by sequencing (GBS) to map the *Breviaristatum-e* (*ari-e*) locus in cultivated barley. *BMC Genomics* 15 (1), 1–11. doi: 10.1186/1471-2164-15-104

Liu, W., Frick, M., Huel, R., Nykiforuk, C. L., Wang, X., Gaudet, D. A., et al. (2014). The stripe rust resistance gene *Yr10* encodes an evolutionary-conserved and unique CC-NBS-LRR sequence in wheat. *Mol. Plant* 7 (12), 1740–1755. doi: 10.1093/mp/ssu112

Lowe, I., Jankuloski, L., Chao, S., Chen, X., See, D., and Dubcovsky, J. (2011). Mapping and validation of QTL which confer partial resistance to broadly virulent post-2000 North American races of stripe rust in hexaploid wheat. *Theor. Appl. Genet.* 123 (1), 143–157. doi: 10.1007/s00122-011-1573-0

Lu, Y., Wang, M., Chen, X., See, D., Chao, S., and Jing, J. (2014). Mapping of *Yr62* and a small-effect QTL for high-temperature adult-plant resistance to stripe rust in spring wheat PI 192252. *Theor. Appl. Genet.* 127 (6), 1449–1459. doi: 10.1007/s00122-014-2312-0

Maccaferri, M., Zhang, J., Bulli, P., Abate, Z., Chao, S., Cantu, D., et al. (2015). A genome-wide association study of resistance to stripe rust (*Puccinia striiformis* f. sp. *tritici*) in a worldwide collection of hexaploid spring wheat (*Triticum aestivum* L.). *G3: Genes Genom. Genet.* 5 (3), 449–465. doi: 10.1534/g3.114.014563

Mago, R., Bariana, H. S., Dundas, I. S., Spielmeyer, W., Lawrence, G. J., Pryor, A. J., et al. (2005). Development of PCR markers for the selection of wheat stem rust resistance genes *Sr24* and *Sr26* in diverse wheat germplasm. *Theor. Appl. Genet.* 111 (3), 496–504. doi: 10.1007/s00122-005-2039-z

Mago, R., Brown-Guedira, G., Dreisigacker, S., Breen, J., Jin, Y., Singh, R., et al. (2011). An accurate DNA marker assay for stem rust resistance gene *Sr2* in wheat. *Theor. Appl. Genet.* 122 (4), 735–744. doi: 10.1007/s00122-010-1482-7

Mago, R., Zhang, P., Vautrin, S., Simkova, H., Bansal, U., Luo, M. C., et al. (2015). The wheat *Sr50* gene reveals rich diversity at a cereal disease resistance locus. *Nat. Plants* 1, 15186. doi: 10.1038/nplants.2015.186

Mago, R., Till, B., Periyannan, S., Yu, G., Wulff, B. B. H., and Lagudah, E. (2017). "Generation of loss-of-function mutants for wheat rust disease resistance gene cloning," in *Wheat rust diseases: methods and protocols*. Ed. S. Periyannan (New York: Springer), 199–205.

Marchal, C., Zhang, J., Zhang, P., Fenwick, P., Steuernagel, B., Adamski, N. M., et al. (2018). BED-domain-containing immune receptors confer diverse resistance spectra to yellow rust. *Nat. Plants* 4 (9), 662–668. doi: 10.1101/299651

Marcussen, T., Sandve, S. R., Heier, L., Spannagl, M., Pfeifer, M., International Wheat Genome Sequencing, C., et al. (2014). Ancient hybridizations among the ancestral genomes of bread wheat. *Science* 345 (6194):1250092. doi: 10.1126/science.1250092

Mayer, K. F., Rogers, J., Doležel, J., Pozniak, C., Eversole, K., Feuillet, C., et al. (2014). A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome. *Science* 345, 6194. doi: 10.1126/science.1251788

McFadden, E., and Sears, E. (1946). The origin of *Triticum spelta* and its free-threshing hexaploid relatives. *J. Hered.* 37, 81–89. doi: 10.1093/oxfordjournals.jhered.a105590

McFadden, E. S. (1930). Successful transfer of emmer characteristics to vulgare wheat. *J. Amer. Soc Agron.* 22, 1020–1034. doi: 10.2134/agronj1930.00021962002200120005x

McIntosh, R. A., and Watson, I. A. (1982). "Genetics of host-pathogen interactions in rusts," in *The rust fungi*. Eds. K. J. Scott and A. K. Chakravorty (New York: Academic Press), 121–149.

McIntosh, R. A., Wellings, C. R., and Park, R. F. (1995). *Wheat rusts: an atlas of resistance genes* (Australia: CSIRO), 1–204, ISBN: .

McIntosh, R. A., Bariana, H. S., Park, R. F., and Wellings, C. R. (2001). Aspects of wheat rust research in Australia. *Euphytica* 119, 115–120. doi: 10.1023/A:1017546506246

McIntosh, R. A., Dubcovsky, J., Rogers, W. J., Morris, C., and Xia, X. C. (2017). *Catalogue of gene symbols for wheat: 2017 supplement*. (Yokohama, Japan

Komugi Wheat Genetic Resources Database). Available at: https://shigen.nig.ac.jp/wheat/komugi/genes/symbolClassList.jsp.

Michelmore, R. W., Paran, I., and Kesseli, R. V. (1991). Identification of markers linked to disease-resistance genes by bulked segregant analysis: a rapid method to detect markers in specific genomic regions by using segregating populations. *Proc. Natl. Acad. Sci*. 88 (21), 9828–9832. doi: 10.1073/pnas.88.21.9828

Milne, R. J., Dibley, K. E., Schnippenkoetter, W., Mascher, M., Lui, A. C. W., Wang, L., et al. (2019). The Wheat *Lr67* Gene from the Sugar Transport Protein 13 Family Confers Multipathogen Resistance in Barley. *Plant Physiol.* 179 (4), 1285–1297. doi: 10.1104/pp.18.00945

Mohler, V., Singh, D., Singrün, C., and Park, R. F. (2012). Characterization and mapping of *Lr65 in* spelt wheat 'Altgold Rotkorn'. *Plant Breed.* 131 (2), 252–257. doi: 10.1111/j.1439-0523.2011.01934.x

Money, N. P. (2016). "Fungal Diversity," in *The Fungi (Third edition)*. Ed. S. C. Watkinson, L. Boddy and N. P. Money (USA: Academic Press), 1–36. doi: 10.1016/B978-0-12-382034-1.00001-3

Moore, J. W., Herrera-Foessel, S., Lan, C., Schnippenkoetter, W., Ayliffe, M., Huerta-Espino, J., et al. (2015). A recently evolved hexose transporter variant confers resistance to multiple pathogens in wheat. *Nat. Genet.* 47 (12), 1494–1498. doi: 10.1038/ng.3439

Narang, D., Kaur, S., Steuernagel, B., Ghosh, S., Bansal, U., Li, J., et al. (2020). Discovery and characterisation of a new leaf rust resistance gene introgressed in wheat from wild wheat *Aegilops peregrina*. *Sci. Rep.* 10, 7573. doi: 10.1038/s41598-020-64166-2

Nayar, S. K., Bhardwaj, S. C., and Prashar, M. (1999). Characterization of *Lr34* and *Sr2 in* Indian wheat (*Triticum aestivum*) germplasm. *Indian J. Agric. Sci.* 69, 718–721.

Nayar, S. K., Nagarajan, S., Prashar, M., Bhardwaj, S. C., Jain, S. K., and Datta, D. (2001). *Revised catalogue of genes that accord resistance to Puccinia species in wheat*. (Flowerdale, Shimla: Directorate of Wheat Research, Regional Station), 1–48.

Nevo, E., Korol, A. B., Beiles, A., and Tzion, F. (2013). "Evolution of wild emmer and wheat improvement: population genetics, genetic resources, and genome organization of wheat's progenitor," in *Triticum dicoccoides* (Berlin: Springer Science and Business Media).

Nsabiyera, V., Bariana, H. S., Qureshi, N., Wong, D., Hayden, M. J., and Bansal, U. K. (2018). Characterisation and mapping of adult plant stripe rust resistance in wheat accession Aus27284. *Theor. Appl. Genet.* 131 (7), 1459–67. doi: 10.1007/s00122-018-3090-x

Nsabiyera, V., Baranwal, D., Qureshi, N., Kay, P., Forrest, K., Valárik, M., et al. (2020). Fine mapping of Lr49 using 90K SNP chip array and flow sorted chromosome sequencing in wheat. *Front. Plant Sci.* 10:1787:1787. doi: 10.3389/fpls.2019.01787

Pakeerathan, K., Bariana, H., Qureshi, N., Wong, D., Hayden, M., and Bansal, U. (2019). Identification of a new source of stripe rust resistance Yr82 in wheat. *Theor. Appl. Genet.* 132, 3169–3176. doi: 10.1007/s00122-019-03416-y

Pal, D., Bhardwaj, S. C., Khan, H., and Patial, M. (2018). HS628: A potential genetic stock for resistance to new virulent pathotypes of black, brown and yellow rusts of wheat (*Triticum aestivum* L.). *Wheat Barley Res.* 10, 61–63. doi: 10.25174/2249-4065/2018/76849

Pardey, P. G., Beddow, J. M., Kriticos, D. J., Hurley, T. M., Park, R. F., Duveiller, E., et al. (2013). Right-sizing stem-rust research. *Science* 340, 147–148. doi: 10.1126/science.122970

Park, R., Mohler, V., Nazari, K., and Singh, D. (2014). Characterisation and mapping of gene *Lr73* conferring seedling resistance to *Puccinia triticina* in common wheat. *Theor. Appl. Genet.* 127 (9), 2041–2049. doi: 10.1007/s00122-014-2359-y

Periyannan, S., Moore, J., Ayliffe, M., Bansal, U., Wang, X., Huang, L., et al. (2013). The gene *Sr33*, an ortholog of barley Mla genes, encodes resistance to wheat stem rust race *Ug99*. *Science* 341 (6147), 786–788. doi: 10.1126/science.1239028

Periyannan, S. (2018). Sustaining global agriculture through rapid detection and deployment of genetic resistance to deadly crop diseases. *New Pathol.* 219, 45–51. doi: 10.1111/nph.14928

Person, C. O. (1959). Gene-for-gene relationships in host parasite systems. *Can. J. Bot.* 37 (1), 101–130. doi: 10.1139/b59-087

Pink, D., and Hand, P. (2002). Plant resistance and strategies for breeding resistant varieties. *Plant Protection Sci.* 38 (1), 9–14. doi: 10.17221/10310-PPS

Poland, J. A., and Rife, T. W. (2012). Genotyping-by-sequencing for plant breeding and genetics. *Plant Genome* 5 (3), 92–102. doi: 10.3835/plantgenome2012.05.0005

Poland, J. A., Brown, P. J., Sorrells, M. E., and Jannink, J. L. (2012). Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach. *PloS One* 7, 1–8. doi: 10.1371/journal.pone.0032253

Pont, C., and Salse, J. (2017). Wheat paleohistory created asymmetrical genomic evolution. *Curr. Opin. Plant Biol.* 36, 29–37. doi: 10.1016/j.pbi.2017.01.001

Preece, C., Livarda, A., Christin, P. A., Wallace, M., Martin, G., Charles, M., et al. (2017). How did the domestication of Fertile Crescent grain crops increase their yields? *Funct. Ecol.* 31 (2), 387–397. doi: 10.1111/1365-2435.12760

Pretorius, Z. A., Singh, R. P., Wagoire, W. W., and Payne, T. S. (2000). Detection of virulence to wheat stem rust resistance gene Sr31 in *Puccinia graminis*. f. sp. *tritici* in Uganda. *Plant Dis.* 84, 203–203. doi: 10.1094/PDIS.2000.84.2.203B

Qi, L., Pumphrey, M., Friebe, B., Zhang, P., Qian, C., Bowden, R., et al. (2011). A novel Robertsonian translocation event leads to transfer of a stem rust resistance gene (*Sr52*) effective against race *Ug99* from *Dasypyrum villosum* into bread wheat. *Theor. Appl. Genet.* 123 (1), 159–167. doi: 10.1007/s00122-011-1574-z

Qureshi, N., Bariana, H., Forrest, K., Hayden, M., Keller, B., Wicker, T., et al. (2016). Fine mapping of the chromosome 5B region carrying closely linked rust resistance genes *Yr47* and *Lr52 in* wheat. *Theor. Appl. Genet.* 130, 495–504. doi: 10.1007/s00122-016-2829-5

Qureshi, N., Bariana, H., Zhang, P., McIntosh, R., Bansal, U., Wong, D., et al. (2018a). Genetic relationship of stripe rust resistance genes *Yr34* and *Yr48* in wheat and identification of linked KASP markers. *Plant Dis.* 102 (2), 413–420. doi: 10.1094/PDIS-08-17-1144-RE

Qureshi, N., Kandiah, P., Gessese, M. K., Nsabiyera, V., Wells, V., Babu, P., et al. (2018b). Development of co-dominant KASP markers co-segregating with Ug99 effective stem rust resistance gene *Sr26* in wheat. *Mol. Breed.* 38 (8), 97. doi: 10.1007/s11032-018-0854-6

Qureshi, N., Bariana, H., Kumran, V. V., Muruga, S., Forrest, K. L., Hayden, M. J., et al. (2018c). A new leaf rust resistance gene *Lr79* mapped in chromosome 3BL from the durum wheat landrace Aus26582. *Theor. Appl. Genet.* 131 (5), 1091–1098. doi: 10.1007/s00122-018-3060-3

Ramirez-Gonzalez, R. H., Uauy, C., and Caccamo, M. (2015). PolyMarker: a fast polyploid primer design pipeline. *Bioinformatics* 31 (12), 2038–2039. doi: 10.1093/bioinformatics/btv069

Randhawa, M., Bansal, U., Valarik, M., Klocova, B., Dolezel, J., and Bariana, H. (2014). Molecular mapping of stripe rust resistance gene *Yr51* in chromosome 4AL of wheat. *Theor. Appl. Genet.* 127 (2), 317–324. doi: 10.1007/s00122-013-2220-8

Randhawa, M. S., Bains, N. S., Sohu, V. S., Chhuneja, P., Trethowan, R. M., Bariana, H. S., et al. (2019). Marker Assisted Transfer of Stripe Rust and Stem Rust Resistance Genes into Four Wheat Cultivars. *Agronomy* 9 (9), 1–10. doi: 10.3390/agronomy9090497

Ren, R. S., Wang, M. N., Chen, X. M., and Zhang, Z. J. (2012). Characterization and molecular mapping of *Yr52* for high-temperature adult-plant resistance to stripe rust in spring wheat germplasm PI 183527. *Theor. Appl. Genet.* 125 (5), 847–857. doi: 10.1007/s00122-012-1877-8

Rinaldo, A., Gilbert, B., Boni, R., Krattinger, S. G., Singh, D., Park, R. F., et al. (2017). The *Lr34* adult plant rust resistance gene provides seedling resistance in durum wheat without senescence. *Plant Biotechnol. J.* 15 (7), 894–905. doi: 10.1111/pbi.12684

Risk, J. M., Selter, L. L., Chauhan, H., Krattinger, S. G., Kumlehn, J., Hensel, G., et al. (2013). The wheat *Lr34* gene provides resistance against multiple fungal pathogens in barley. *Plant Biotechnol. J.* 11 (7), 847–854. doi: 10.1111/pbi.12077

Röder, M. S., Korzun, V., Wendehake, K., Plaschke, J., Tixier, M. H., Leroy, P., et al. (1998). A microsatellite map of wheat. *Genetics* 149 (4), 2007–2023.

Roelfs, A. P., Singh, R. P., and Saari, E. E. (1992). *Rust diseases of wheat: concepts and methods of disease management* (Mexico: CIMMYT).

Roelfs, A. P. (1978). *Estimated losses caused by rust in small grains cereals in the United States* (United States: United States Department of Agriculture: Agricultural Research Service. 89), 1918–1976.

Roelfs, A. P. (1985). Wheat and Rye Stem Rust, in *The cereal rusts: diseases, distribution, epidemiology, and control*. Eds. A. P. Roelfs and W. R. Bushnell (Orlando, FL, USA: Academic Press), 3–37.

Ronen, G., Carmel-Goren, L., Zamir, D., and Hirschberg, J. (2000). An alternative pathway to beta -carotene formation in plant chromoplasts discovered by map-based cloning of beta and old-gold color mutations in tomato. *Proc. Natl. Acad. Sci. U. S. A.* 97 (20), 11102–11107. doi: 10.1073/pnas.190177497

Rosewarne, G. M., Singh, R. P., Huerta-Espino, J., Herrera-Foessel, S. A., Forrest, K. L., Hayden, M. J., et al. (2012). Analysis of leaf and stripe rust severities reveals pathotype changes and multiple minor QTLs associated with resistance in an Avocet × Pastor wheat population. *Theor. Appl. Genet.* 124 (7), 1283–1294. doi: 10.1007/s00122-012-1786-x

Rosewarne, G., Herrera-Foessel, S., Singh, R., Huerta-Espino, J., Lan, C., and He, Z. (2013). Quantitative trait loci of stripe rust resistance in wheat. *Theor. Appl. Genet.* 126 (10), 2427–2449. doi: 10.1007/s00122-013-2159-9

Rowell, J. B., and Roelfs, A. P. (1976). "Wheat stem rust In Modeling for Pest Management, Concepts, Techniques, and Applications U.S.A./U.S.S.R," in *2nd U.S./U.S.S.R. Symp*. Eds. R. L. Tummala, D. L. Haynes and B. A. Croft (East Lansing: Michigan State University), 69–79.

Russel, G. E. (1978). *Plant breeding for pest and disease resistance* (London: Butterworth and Co. (Publisher) Ltd), pp 16–pp 25.

Saini, R. G., Kaur, M., Singh, B., Sharma, S., Nanda, G. S., Nayar, S. K., et al. (2002). Genes *Lr48* and *Lr49* for hypersensitive adult plant leaf rust resistance in wheat (*Triticum aestivum* L.). *Euphytica* 124 (3), 365–370. doi: 10.1023/a:1015762812907

Saintenac, C., Jiang, D., Wang, S., and Akhunov, E. (2013a). Sequence-based mapping of the polyploid wheat genome. *G3 (Bethesda)* 3 (7), 1105–1114. doi: 10.1534/g3.113.005819

Saintenac, C., Zhang, W., Salcedo, A., Rouse, M. N., Trick, H. N., Akhunov, E., et al. (2013b). Identification of wheat gene *Sr35* that confers resistance to Ug99 stem rust race group. *Science* 341, 783–786. doi: 10.1126/science.1239022

Sanchez-Martin, J., Steuernagel, B., Ghosh, S., Herren, G., Hurni, S., Adamski, N., et al. (2016). Rapid gene isolation in barley and wheat by mutant chromosome sequencing. *Genome Biol.* 17, 221. doi: 10.1186/s13059-016-1082-1

Sandve, S. R., Marcussen, T., Mayer, K., Jakobsen, K. S., Heier, L., Steuernagel, B., et al. (2015). Chloroplast phylogeny of Triticum/Aegilops species is not incongruent with an ancient homoploid hybrid origin of the ancestor of the bread wheat D-genome. *New Phytol.* 208, 9–10. doi: 10.1111/nph.13487

Sawhney, R. N., and Sharma, D. V. (1990). Identification of sources for rust resistance and for durability to Leaf rust in common wheat. *SABRAO J.* 22, 51–55.

Sawhney, R. N., Goel, L. B., and Mathur, H. C. (1982). Adult plant responses of specific genes resistant to leaf rust against Indian population of leaf rust pathogen. *Z. Pflanzenzuchtg* 89, 222–228.

Schnippenkoetter, W., Lo, C., Liu, G., Dibley, K., Chan, W. L., White, J., et al. (2017). The wheat *Lr34* multipathogen resistance gene confers resistance to anthracnose and rust in sorghum. *Plant Biotechnol. J.* 15 (11), 1387–1396. doi: 10.1111/pbi.12723

Schwessinger, B. (2017). Fundamental wheat stripe rust research in the 21(st) century. *New Phytol.* 213, 1625–1631. doi: 10.1111/nph.14159

Shank, R. (1994). "Wheat stem rust and drought effects on bale agricultural production and future prospects. Report on February 17–28 assessment," in *In United Nations Emergencies Unit for Ethiopia* (Ethiopia: Addis Ababa).

Shewry, P. R. (2009). Wheat. *J. Exp. Bot.* 60 (6), 1537–1553. doi: 10.1093/jxb/erp058

Singh, R. P., and Rajaram, S. (1993). Genetics of adult plant resistance to stripe rust in ten spring bread wheats. *Euphytica* 72, 1–7. doi: 10.1007/BF00023766

Singh, R. P., and Trethowan, R. (2007). "Breeding spring bread wheat for irrigated and rainfed production system of developing world," in *a book "Breeding major food staples"*, vol. pp . Eds. M. Kang and P. M. Priyadarshan (Iowa, USA: Blackwell Publishing), 109–140. doi: 10.1002/9780470376447.ch5

Singh, R. P., Hong, M., and Huerta-Espino, J. (1994). "Rust diseases of wheat. In a book "Guide to the CIMMYT Wheat Crop Protection Sub-Program"," in *Wheat special report number 24*. Eds. E. E. Saari and G. P. Hettel (Mexico: CIMMYT), 19–33.

Singh, R. P., Huerta-Espino, J., and Rajaram, S. (2000). Achieving near-immunity to leaf and stripe rusts in wheat by combining slow rusting resistance genes. *Acta Phytopathol. Entomol. Hung.* 35 (1/4), 133–139.

Singh, D., Park, R. F., and McIntosh, R. A. (2001). Postulation of leaf (brown) rust resistance genes in 70 wheat cultivars grown in the United Kingdom. *Euphytica* 120, 205–218. doi: 10.1023/A:1017578217829

Singh, R. P., Rajaram, S., Saini, R. G., Huerta-Espino, J., and William, M. (2004a). "Genetics of host-pathogen interaction and breeding for durable resistance," in *In a book "Plant Breeding- Mendelian to molecular approaches"*. Eds. H. K. Jain and M. C. Kharkwal (New Delhi, India: Narosa Publishing House), 145–166. doi: 10.1007/978-94-007-1040-5_7

Singh, R. P., Huerta-Espino, J., Pfeiffer, W., and Figueroa-Lopez, P. (2004b). Occurrence and impact of a new leaf rust race on durum wheat in Northwestern Mexico from 2001 to 2003. *Plant Dis.* 88 (7), 703–708. doi: 10.1094/PDIS.2004.88.7.703

Singh, S. S., Sharma, R. K., Singh, G., Tyagi, B. S., and Saharan, M. S. (2011). *100 Years of wheat research in India- A saga of distinguished achievements*. (Karnal, India: Directorate of Wheat Research), 281.

Singh, D., Mohler, V., and Park, R. (2013). Discovery, characterisation and mapping of wheat leaf rust resistance gene *Lr71*. *Euphytica* 190 (1), 131–136. doi: 10.1007/s10681-012-0786-x

Singh, R. P., Herrera-Foessel, S., Huerta-Espino, J., Lan, C., Basnet, B., Bhavani, S., et al. (2013). "Pleiotropic gene Lr46/Yr29/Pm39/Ltn2 confers slow rusting, adult plant resistance to wheat stem rust fungus," in *Proceedings Paper presented at the Borlaug Global Rust Initiative* (New Delhi India: Technical Workshop).

Singh, R. P., Herrera-Foessel, S., Huerta-Espino, J., Singh, S., Bhawani, S., Lan, C., et al. (2014). Progress towards Genetics and Breeding for Minor Genes based Resistance to Ug99 and other Rusts in CIMMYT High Yielding Spring Wheat. *J. Integr. Agric.* 13, 255–261. doi: 10.1016/S2095-3119(13)60649-8

Singh, R. P., Hodson, D. P., Jin, Y., Lagudah, E. S., Ayliffe, M. A., Bhavani, S., et al. (2015). Emergence and spread of new races of wheat stem rust fungus: continued threat to food security and prospects of genetic control. *Phytopathology* 105 (7), 872–884. doi: 10.1094/PHYTO-01-15-0030-FI

Singh, R. P. (1992). Genetic association of leaf rust resistance gene *Lr34* with adult plant resistance to stripe rust in bread wheat. *Phytopath* 82, 835–838. doi: 10.1094/Phyto-82-835

Singla, J., Lüthi, L., Wicker, T., Bansal, U., Krattinger, S. G., and Keller, B. (2017). Characterization of *Lr75*: a partial, broad-spectrum leaf rust resistance gene in wheat. *Theor. Appl. Genet.* 130, 1–12. doi: 10.1007/s00122-016-2784-1

Slinkard, A. E., and McIntosh, R. A. (1998). "Proceedings of the 9th international wheat genetics symposium," in *International wheat genetics symposium* (University of Saskatchewan: University Extension Press).

Sobhy Draz, I. (2019). Common Ancestry of Egyptian *Puccinia striiformis* Population Along with Effective and Ineffective Resistance Genes. *Asian J. Biol. Sci.* 12 (2), 217–221. doi: 10.3923/ajbs.2019.217.221

Somers, D. J., Isaac, P., and Edwards, K. (2004). A high-density microsatellite consensus map for bread wheat (*Triticum aestivum* L.). *Theor. Appl. Genet.* 109, 1105–1114. doi: 10.1007/s00122-0041740-7

Song, Q., Shi, J., Singh, S., Fickus, E., Costa, J., Lewis, J., et al. (2005). Development and mapping of microsatellite (SSR) markers in wheat. *Theor. Appl. Genet.* 110 (3), 550–560. doi: 10.1007/s00122-004-1871-x

Sørensen, C. K., Hovmøller, M. S., Leconte, M., Dedryver, F., and de Vallavieille-Pope, C. (2014). New races of *Puccinia striiformis* found in Europe reveal race specificity of long-term effective adult plant resistance in wheat. *Phytopathology* 104 (10), 1042–1051. doi: 10.1094/PHYTO-12-13-0337-R

Steuernagel, B., Periyannan, S. K., Hernandez-Pinzon, I., Witek, K., Rouse, M. N., Yu, G., et al. (2016). Rapid cloning of disease-resistance genes in plants using mutagenesis and sequence capture. *Nat. Biotechnol.* 34 (6), 652–655. doi: 10.1038/nbt.3543

Sthapit, J., Gbur, E. E., Brown-Guedira, G., Marshall, D. S., and Milus, E. A. (2012). Characterization of resistance to stripe rust in contemporary cultivars and lines of winter wheat from the eastern United States. *Plant Dis.* 96 (5), 737–745. doi: 10.1094/PDIS-07-11-0612

Stoa, T. E. (1945). A brief history of wheat variety changes on farms in North Dacota. *Bi-monthly Bull.* 7 (6), 21–26.

Tang, Y., Liu, X., Wang, J., Li, M., Wang, Q., Tian, F., et al. (2016). GAPIT version 2: an enhanced integrated tool for genomic association and prediction. *Plant Genome* 9 (2), 1–9. doi: 10.3835/plantgenome2015.11.0120

Tavares, S., Ramos, A. P., Pires, A. S., Azinheira, H. G., Caldeirinha, P., Link, T., et al. (2014). Genome size analyses of Pucciniales reveal the largest fungal genomes. *Front. Plant Sci.* 5, 422. doi: 10.3389/fpls.2014.00422

Thind, A., Wicker, T., Šimková, H., Fossati, D., Moullet, O., Brabant, C., et al. (2017). Rapid cloning of genes in hexaploid wheat using cultivar-specific long-range chromosome assembly. *Nat. Biotechnol.* 35, 793–796. doi: 10.1038/nbt.3877

Van der Plank, J. E. (1963). Plant diseases: epidemics and control. *Acad. Press New Y.* p, 349.

Vrána, J., Šimková, H., Kubaláková, M., Číhalíková, J., and Doležel, J. (2012). Flow cytometric chromosome sorting in plants: the next generation. *Methods* 57, 331–337. doi: 10.1016/j.ymeth.2012.03.006

Walter, S., Ali, S., Kemen, E., Nazari, K., Bahri, B. A., Enjalbert, J., et al. (2016). Molecular markers for tracking the origin and worldwide distribution of invasive strains of *Puccinia striiformis*. *Ecol. Evol.* 62790, 2804. doi: 10.1002/ece3.2069

Wang, D. G., Fan, J. B., Siao, C. J., Berno, A., Young, P., Sapolsky, R., et al. (1998). Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome. *Science* 280 (5366), 1077–1082. doi: 10.1126/science.280.5366.1077

Wang, S., Wong, D., Forrest, K., Allen, A., Chao, S., Huang, B. E., et al. (2014). Characterization of polyploid wheat genomic diversity using a high-density 90000 single nucleotide polymorphism array. *Plant Biotechnol. J.* 12 (6), 787–796. doi: 10.1111/pbi.12183

Wang, M. N., Wan, A. M., and Chen, X. M. (2015). Barberry as alternate host is important for *Puccinia graminis* f. sp. *tritici* but not for *Puccinia striiformis* f. sp. *tritici* in the U.S. Pacific Northwest. *Plant Dis.* 99, 1507–1516. doi: 10.1094/PDIS-12-14-1279-RE

Wang, Z., Li, J., Chen, S., Heng, Y., Chen, Z., Yang, J., et al. (2017). Poaceae specific *MS1* encodes a phospholipid-binding protein for male fertility in bread wheat. *Proc. Natl. Acad. Sci. U. S. A.* 114, 12614–12619. doi: 10.1073/pnas.1715570114

Wang, K., Riaz, B., and Ye, X. (2018). Wheat genome editing expedited by efficient transformation techniques: progress and perspectives. *Crop J.* 6 (1), 22–31. doi: 10.1016/j.cj.2017.09.009

Watanabe, S., Hideshima, R., Xia, Z., Tsubokura, Y., Sato, S., Nakamoto, Y., et al. (2009). Map-based cloning of the gene associated with the soybean maturity locus E3. *Genetics* 182 (4), 1251–1262. doi: 10.1534/genetics.108.098772

Watson, I. A. (1981). "Wheat and its rust parasites in Australia," in *In a book "Wheat Science Today and Tomorrow"*, Eds. L. T. Evans and W. J. Peacock (Cambridge: Cambridge University Press), 129–147.

Wellings, C. R. (2011). Global status of stripe rust: a review of historical and current threats. *Euphytica* 179 (1), 129–141. doi: 10.1007/s10681-011-0360-y

Wessels, E., and Botes, W. C. (2014). Accelerating resistance breeding in wheat by integrating marker-assisted selection and doubled haploid technology. *S. Afr. J. Plant Soil* 31 (1), 35–43. doi: 10.1080/02571862.2014.903434

Wilcoxon, R. D. (1981). Genetics of Slow Rusting in Cereals. *Phytopathology* 71, 989–993. doi: 10.1094/Phyto-71-989

William, M., Singh, R. P., Huerta-Espino, J., Ortiz Islas, S., and Hoisington, D. (2003). Molecular marker mapping of leaf rust resistance gene *Lr46* and its association with stripe rust resistance gene *Yr29 in* Wheat. *Phytopathology* 93 (2), 153–159. doi: 10.1094/PHYTO.2003.93.2.153

Wu, J., Wang, Q., Xu, L., Chen, X., Li, B., Mu, J., et al. (2018). Combining SNP genotyping array with bulked segregant analysis to map a gene controlling adult-plant resistance to stripe rust in wheat line 03031-1-5 H62. *Phytopathology* 108 (1), 103–113. doi: 10.1094/PHYTO-04-17-0153-R

Xu, L. S., Wang, M. N., Cheng, P., Kang, Z., Hulbert, S., and Chen, X. (2013). Molecular mapping of *Yr53*, a new gene for stripe rust resistance in durum wheat accession PI 480148 and its transfer to common wheat. *Theor. Appl. Genet.* 126 (2), 523–533. doi: 10.1007/s00122-012-1998-0

Yang, H., Tao, Y., Zheng, Z., Li, C., Sweetingham, M. W., and Howieson, J. G. (2012). Application of next-generation sequencing for rapid marker development in molecular plant breeding: a case study on anthracnose disease resistance in *Lupinus angustifolius* L. *BMC Genomics* 13 1–12. doi: 10.1186/1471-2164-13-318

Yang, E. N., Rosewarne, G. M., Herrera-Foessel, S. A., Huerta-Espino, J., Tang, Z. X., Sun, C. F., et al. (2013). QTL analysis of the spring wheat "Chapio" identifies stable stripe rust resistance despite inter-continental genotype × environment interactions. *Theor. Appl. Genet.* 126 (7), 1721–1732. doi: 10.1007/s00122-013-2087-8

Yao, F., Zhang, X., Ye, X., Li, J., Long, L., Yu, C., et al. (2019). Characterization of molecular diversity and genome-wide association study of stripe rust resistance at the adult plant stage in Northern Chinese wheat landraces. *BMC Genet.* 20, 38. doi: 10.1186/s12863-019-0736-x

Yin, J. L., Fang, Z. W., Sun, C., Zhang, P., Zhang, X., Lu, C., et al. (2018). Rapid identification of a stripe rust resistant gene in a space-induced wheat mutant using specific locus amplified fragment (SLAF) sequencing. *Sci. Rep.* 8, 3086. doi: 10.1038/s41598-018-21489-5

Yu, J., and Buckler, E. S. (2006). Genetic association mapping and genome organization of maize. *Curr. Opin. Biotechnol.* 17 (2), 155–160. doi: 10.1016/j.copbio.2006.02.003

Yu, L. X., Lorenz, A., Rutkoski, J., Singh, R. P., Bhavani, S., Huerta-Espino, J., et al. (2011). Association mapping and gene–gene interaction for stem rust resistance in CIMMYT spring wheat germplasm. *Theor. Appl. Genet.* 3 (8), 1257–1268. doi: 10.1007/s00122-011-1664-y

Yu, L. X., Barbier, H., Rouse, M. N., Singh, S., Singh, R. P., Bhavani, S., et al. (2014). A consensus map for *Ug99* stem rust resistance loci in wheat. *Theor. Appl. Genet.* 127 (7), 1561–1581. doi: 10.1007/s00122-014-2326-7

Zadoks, J. C., and Bouwman, J. J. (1985). "Epidemiology in Europe," in *The Cereal Rusts*, vol. Vol. 2 . Eds. A. P. Roelfs and W. R. Bushnell (Orlando, FL: Academic Press), 329–369.

Zadoks, J. C. (1985). On the conceptual basis of crop loss assessment: the threshold theory. A. *Rev. Phytopathol.* 23, 455–473. doi: 10.1146/annurev.py.23.090185.002323

Zhang, J., Lu, Y., Yuan, Y., Zhang, X., Geng, J., Chen, Y., et al. (2009). Map-based cloning and characterization of a gene controlling hairiness and seed coat color traits in Brassica rapa. *Plant Mol. Biol.* 69 (5), 553–563. doi: 10.1007/s11103-008-9437-y

Zhang, Z., Ersoz, E., Lai, C. Q., Todhunter, R. J., Tiwari, H. K., Gore, M. A., et al. (2010). Mixed linear model approach adapted for genome-wide association studies. *Nat. Gen.* 42 (4), 355. doi: 10.1038/ng.546

Zhang, D., Bowden, R. L., Yu, J., Carver, B. F., and Bai, G. (2014). Association analysis of stem rust resistance in US winter wheat. *PloS One* 9 (7), e103747. doi: 10.1371/journal.pone.0103747

Zhang, W., Chen, S., Abate, Z., Nirmala, J., Rouse, M. N., and Dubcovsky, J. (2017). Identification and characterization of *Sr13*, a tetraploid wheat gene that confers resistance to the *Ug99* stem rust race group. *Proc. Natl. Acad. Sci. U. S. A.* 114 (45), E9483–E9492. doi: 10.1073/pnas.1706277114

Zhang, C., Huang, L., Zhang, H., Hao, Q., Lyu, B., Wang, M., et al. (2019). An ancestral NB-LRR with duplicated 3′ UTRs confers stripe rust resistance in wheat and barley. *Nat. Commun.* 10, 1–12. doi: 10.1038/s41467-019-11872-9

Zhang, J., Zhang, P., Dodds, P., and Lagudah, E. (2020). How Target-Sequence Enrichment and Sequencing (TEnSeq) Pipelines Have Catalyzed Resistance Gene Cloning in the Wheat-Rust Pathosystem. *Front. Plant Sci.* 11, 678. doi: 10.3389/fpls.2020.00678

Zhou, X., Wang, M., Chen, X., Lu, Y., Kang, Z., and Jing, J. (2014). Identification of *Yr59* conferring high-temperature adult-plant resistance to stripe rust in wheat germplasm PI 178759. *Theor. Appl. Genet.* 127 (4), 935–945. doi: 10.1007/s00122-014-2269-z

Zhou, X. L., Han, D. J., Chen, X. M., Gou, H. L., Guo, S. J., Rong, L., et al. (2014a). Characterization and molecular mapping of stripe rust resistance gene *Yr61* in winter wheat cultivar Pindong 34. *Theor. Appl. Genet.* 127 (11), 2349–2358. doi: 10.1007/s00122-014-2381-0

Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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