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### BREEDING WHEAT FOR RUST RESISTANCE: CONVENTIONAL AND MODERN APPROACHES

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#### ABSTRACT

Three rusts are destructive, diminishing produce and nutritious value significantly, affect food availability and consequently food security through reductions in yield. In agricultural research institutes with mandate of wheat improvement, incorporating genes resistant against rust is matter of routine. The dilemma of rusts in wheat has been addressed the most, leading to discovery of principles of plant breeding for resistance e.g. gene disease genes inherit following Mendelian genetics, concept of genetic diversity and concept of gene for gene theory. Two strategies of breeding wheat for disease resistance are being followed. 1- Conventional and 2- Advanced. Among conventional approaches selection and hybridization are well known. However rust resistance has been found short lived and may also be durable in certain cases. Durability of disease resistance is desired and has been explored widely. Durability of resistance is generally attained through incorporation of genes effective at adult plant stage and combination of quantitative genes. Application of biotechnology to improve productivity of rust resistance breeding is the usage of molecular markers in pyramiding genes and substantiates the existence of genes in, and confirming released cultivars are pure. This involves molecular markers that are precise and pertinent across extensive ranges of breeders' germplasm. This review article encompasses all features of wheat development through application of different techniques of wheat improvement. However, despite development of novel approaches that has accelerated wheat breeding, breeding in pathogen leading to producing more virulent strains. Consequently, wheat breeding is a continuous process.

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#### INTRODUCTION

Wheat (*Triticum aestivum* L.) is the fundamental staple diet for majority of world population and among the crops cultivated during pre-historic era (Khanfri et al., 2018; Waqar et al., 2018). Fifty percent of the calories requirement of the world is accomplished by three




major crops wheat, paddy and corn (Mateen et al., 2015). In wheat crop several factors cause difference in potential yield and yield harvested. Diseases in crops are main constraints in achieving the target of food security (Halstead and Henricot, 2010).

Three rust diseases in wheat (Table 1) are the main

limitations in harvesting abundant crop produced, triggering extensive yield decline in crop and huge damage in several regions, at different times (Badebo et al., 1990; Solh et al., 2012; Afzal et al., 2022). Rusts are the most detrimental diseases of cereals and, ever since ancient times, have an excessive effect on human cultures (McIntosh, 2009). The injury caused by the cereal rusts had been documented by scholars prior the

arrival of Christ (Carefoot and Sprott, 1967). More archaeological relics, a storage jar found in Israel encompassing spores and hyphae of the wheat stem rust fungus indicated the dilemma existed in antiquity documented Late Bronze Age dated to (circa 1,300 BC) (Kislev, 1982). The rusts resulting grains desiccated, results reduced quantity as well as quality of produce (Figure 1).

Table 1: Detail of damage caused by three rusts.

| Sr. No. | Disease  | Losses  | Reference   |
|---------|--|---|---|
| 1       | <p>Stripe Rust (Yellow Rust)</p>  | In 2017, approximately 88% of the wheat was susceptible to the stripe rust caused by <i>Puccinia striiformis</i> f. sp. <i>tritici</i> worldwide, causing yield losses estimated to be 1 billion USD  | (Brandt et al., 2021)                             |
| 2       | <p>Leaf Rust (Brown rust)</p>    | Leaf rust caused by <i>Puccinia triticina</i> damages wheat production severely in temperate zone areas where the composite or generally prevailing weather conditions of a region is characterized by broad difference between extremes of temperature. Losses in yield indicted to range 30-70% | (Kolmer et al., 2005; Huerta-Espino et al., 2011) |
| 3       | <p>Stem rust (Black rust)</p>   | Damages up to 1.12 bln US \$ collectively resulting mostly as a consequence of reduced end-use value of the crop and decrease in yield  | (Pardey et al., 2013).                            |

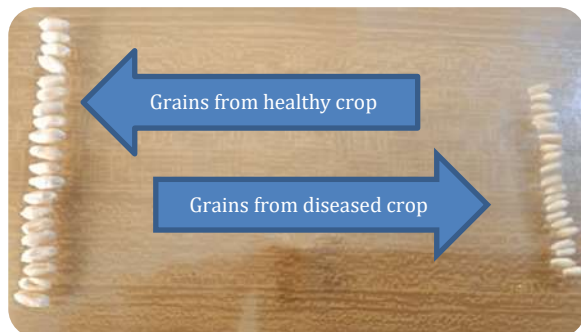


Figure 1: Comparison of rust affected and healthy grains.

### Damages caused by wheat rusts

Rust stress a cause decrease in wheat-grain yield and influences other yield component traits such as the grain size, number of grains per head, grain weight, plant biomass, vigor, and plant growth (Dimmock and Gooding, 2002). Plant progressive stages are affected by rust stress. Tillering early and jointing anthesis stage, curtailed number of kernel per spike, reduced grain weight and quality are the characteristic features in infection caused by rust (Afzal et al., 2008, 2020; Channa et al., 2021). Investigation to assess yield depression caused by wheat rusts was initiated not before the 20<sup>th</sup> century. Improved comprehension of dilemma led to evaluate monetary investment in projects of disease management (McIntosh et al., 1995).

Subsequently, damage in produce and the financial influence of wheat rusts has been evaluated comprehensively and publicized (Afzal et al., 2020; Tariq-Khan et al., 2020). During last century losses attributable to periodic epidemics of rusts resulted in starvation circumstances in many fragments of the world. As a result of successful rust management in numerous wheat creating countries over \$ 200 million annually saving of income in farmers is documented (Brennan and Murray, 1988). Stripe rust prevailed in fairly low temperature and humid situation during previous decades (Zadoks, 1961) but migrating and evolving innovative genetic variants of pathogen with increased capacity to endure warmer temperatures have been recorded in wheat in regions unaffected previously (Milus et al., 2009; Hovmøller et al., 2016).

Among three rusts, stem rust of wheat has been the most detrimental disease (Afzal et al., 2015; 2021). Because of the huge financial injury caused by wheat rusts, wheat scientists have addressed this field seriously.

### Incorporation of resistance through breeding

Although fungicides control rusts effectively and chemotherapy is usual practice in advanced countries for management of these diseases. However, it is uneconomical for the farmers in developing countries attributed to poverty of farming community in these regions. Shortage of fungicides at the proper time and emerging of new race groups reduce fungicide efficacy to prevent losses restrict application of fungicides to control rusts in wheat. These evidences described above highlights the importance of breeding and deployment of resistant germplasm to curtail epidemics. It dedicates a final part to rapidly evolving technologies and their potential to accelerate genetic gains. At present detection for sources of rust resistance in wheat is a foremost activity in wheat improvement programs. Global rust research has led to the evolution and deployment of rust resistant cultivars. Experts engaged in crop improvement cannot overlook the dilemma of rusts and concentrate entirely on the serious problem of yield enhancement through breeding. Wheat development through breeding has caused 27 times improvement in its worth and reimbursements from breeding for resistance against brown rust in spring wheat (Marasas et al., 2004). More than 220 rust resistance genes encompassing, 79 leaf rust resistance genes, 60 stem rust resistance and 83 stripe rust resistance genes have been catalogued (McIntosh et al., 2017). Wheat breeding will continue contributing wheat germplasm characterized by high yielding, possessing improved rust resistance, decreasing the potential hazard of rusts. El-Orabey et al. (2020) categorized genes into three sets based on the infection type. The first class comprised the most effective. Finding of work conducted is summarized in Table 2.

Table 2: List of effective genes against three rusts (El-Orabey et al., 2020).

|   | Stripe Rust  | Leaf Rust                             | Stem Rust   |
|---|--|---------------------------------------|---|
| Most Effective Genotypes                      | Yr 1, Yr 5, Yr 10, Yr 15, Yr SP, Misr 3 and Sakha 95 | Lr 17, Lr 18, Lr 21, Lr 28 and Misr 3 | Sr 2, Sr 24, Sr 32, Sr 33, Sr 36, Sr 38, Sr 39 and Misr 3 |
| Widely adapted and stable in their resistance | Yr 17  | Lr 28, Lr 22a, Lr 14b                 | Sr 20, Sr 25, Sr 31, Sr 9e, Sr 12                         |

Deployment of wheat cultivars resistant to this disease is being concentrated critically for development in breeding wheat and novel technologies are being applied (Ellis et al., 2014). Rusts in wheat are amongst

the most studied diseases of plants owing to the effect that have had on wheat production (Afzal et al., 2015). This research work conducted lead to detections of Principles of plant breeding for disease resistance

(Biffen,1905; Stakman and Levine, 1922; Flor,1956; Van der Plank, 1963). Description is as under:

1- Biffen (1905) established that wheat yellow rust (stripe rust) is inherited following Mendel's laws of inheritance.

2- Stalkman and Piemeisel (1917) confirmed existence of genetic diversity in stem rust pathogen.

3- Flor (1942, 1956) suggested gene for gene concept.

4- Loegering in 1966 developed two important rules parallel to basic Mendelian Principles described as:

a)- Incompatibility is defined the reaction of contact among the products of at least one resistant host and at least one corresponding avirulent pathogen i.e., LIT is low infection type, LIT=LP (low pathogenicity):LR., LR (low reaction).

b) -  $LIT_{1,2} < LIT_1$  where:  $LIT_1 < LIT_2$ . It is explained when more gene pairs are engaged as participants the degree of incompatibility as low as, or lower than, the level produced by the most incompatible interacting gene pair acting single. Development of disease resistant varieties through breeding is carried following the principles mentioned above (Randhawa et al., 2019). Genetic resistance is advantageous for ecological and commercial point of view, predominantly for wheat growers in the developing countries, and as a result of the prospect that rust pathogens develop resistance to chemicals.

### **Wheat breeding for rust resistance (conventional approach)**

#### **Selection**

Wheat improvement initiated in the beginning of 19<sup>th</sup> century. The blend of different genotypes was frequently recognized as landraces, which grew as an outcome of selection and sponsored by growers through individual collection of improved spikes for the kernels of crop for coming year. These landraces were grown during the beginning of previous century (Rehman et al., 2009). Johannsen (1903, 1926) working with a common bean variety Princess developed pure line theory was followed as focal breeding technique utilized by the wheat experts of 19<sup>th</sup> century characterized by segregation of pure entries from local land races.

#### **Hybridization**

Hybridization was begun during last decade of 19<sup>th</sup> century. Crossing was conducted to combine in progeny different traits of genotypes used as parentages. Farrer (1898), from Australia, worked as pioneer for developing wheat genotype with resistance against rust.

He focused on developing varieties ripening early to circumvent rust through hybridization of parentage selected prudently. Farrer imported Indian oriented germplasm characterized early maturing and crossed with local germplasm for incorporation of resistance against rust into local material through using back cross method. In this study selection was conducted using these parameters i.e., stomata smaller in size, existence of wax on leaf, thick cuticle, leaf angle and breadth of leaf. These traits are unusually analogous to those utilized for selection for durable disease resistance. In another experiment conducted during 1896-1901 different species of Triticum were crossed and screened in Indian situation against wheat rusts but results were undesired (Rehman et al., 2013). In sub-continent some genotypes e.g., Nagpur hybrid, Majhi, Pissi, Mundia, Bansi, Bakhshi were not immune but reacted moderately resistant (Howard and Howard, 1909), which showed that they may carry quantitative type of resistance for rust. As the technique applied for the evolution of genotypes in that era was segregating pure lines, hence, it is expected quantitative genes co-evolved with the wheat. In sub-continent, hybridization was initiated in 1926 (Aziz, 1966), by conjugation required traits existing in more than one variety in a genotype. The genotypes such as C-217, C-273, C-250, C-271, C-591 and C-518 and were evolved by crossing exotic and native genetic resources. These genotypes were remarkable to varieties under cultivation already in every respect. The genotype C271 possess Lr34 (Kolmer, 2009). This gene is characterized by leaf tip necrosis and authentic source of a durable rust resistance (McIntosh et al., 1995). This exhibited that this gene has been in use in wheat breeding deliberately or instinctively since many years. So, it is conclusion of the evidences above that, varieties having resistance were selected even during the primary wheat breeding, although scientific community engaged in wheat breeding for rust resistance was ignorant with principles of wheat breeding to improvement of disease resistance.

#### **Green revolution and rusts management**

In the beginning of green revolution, the short statured genotypes evolved at CIMMYT, brought sudden improvement in wheat yield in many fragments of the planet including Pakistan, India, Turkey, Afghanistan. These varieties were not found durable as infected by novel strain of stem rust nevertheless, However, Borlaug, 1968 described some cultivars e.g., the cultivar

Lerma Rojo 64 performed in field 11 year, while others (e.g., Yaqui 50; Chamingo 52 & Chamingo 53) withheld their resistance till they were evacuated from commercial cultivation by varieties yielding higher. The situation is ascribed to genetic background of these varieties (Borlaug, 1958). Wheat breeding program at CIMMYT amalgamated variety of genes during the era 1965-1985. Highest of the genotypes comprise Sr2 and 2 to 4 additional genes for resistance against stem rust spread in this interval. Knott (1988) and Rajaram et al. (1988) have enlisted these supplementary genes. The analogous plan was also executed by numerous projects. The status of gene Lr13 for resistance against leaf rust was identified in the initiation of the decade 70's. The, Lr13 gene does not deliver anticipated resistance if it is single but when combined with other genes it offers

durable resistance. Lr13 complex is characterized as non-race specific and achieved durable in Bluebird series in combination with Lr34. One more illustration of Lr13 combined with Lr34 is, Lyalpur73, which substituted in field by the development of innovative genotypes higher in yield but, it still possess' resistance for brown rust. The varieties Torim 73 and Genero 81, sustained resistant to brown rust for long duration have complex of Lr 34 gene with other genes. Lr 34 is allied with leaf tip necrosis (LTN) (Figure 2) morphological marker (Singh, 1992) mapped on chromosome 7DS was reported first in genotype "Frontona", and wheat cultivars possessing Lr34 have been evolved extensively and more than 25 million ha is under cultivation reduce depression in produce effectively in the years when disease appear in epidemics.

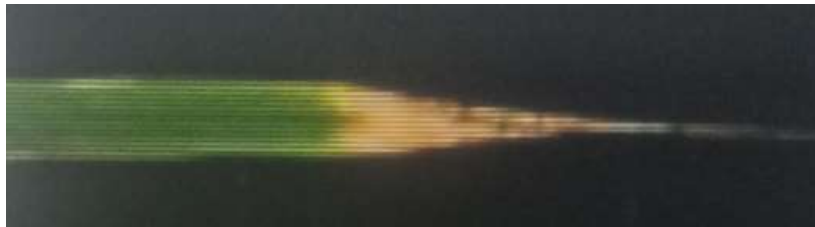


Figure 2: Leaf tip necrosis affiliated with Lr34.

### Genetic basis of durable resistance

Breakdown of Yr9, Yr27 and Sr31 compelled scientific community to change breeding strategy. Additive effect of partial resistant quantitative genes, typically multigenic and effective in adult plant stage deliver long lasting (durable) resistance. Keeping the principle in view test material is screened in seedling stage and those entries are selected that show susceptible response at seedling stage and studied further to observe their response at adult stage. This type of resistance is characterized by the combined effect of slow rusting components i.e., pustule size per mm<sup>2</sup>, pustule density per cm<sup>2</sup>, incubation period and latent period. Disease data is recorded repeatedly. Audpc (Area Under Disease Progress Curve) is the parameter used to distinguish slow rusters and fast rusters. Area Under Disease Progress Curve is calculated using data recorded repeatedly with the help of formula (Wilcoxson et al., 1975). Slow rusters are susceptible as well but are least affected by the disease. Such genotypes are generally durable based on the principle Live and Let Live. Studies have revealed that 10-12 dissimilar genes are associated

in germplasm developed in CIMMYT. Nevertheless, two to three genes in a line offer moderate resistance and level of resistance near to immunity can be attained by collecting four to five quantitative genes (Singh et al., 2005; Channa et al., 2022). Mostly these genes have not been designated. Sr2/Yr30, Lr34/Yr18 and Lr46/Yr29 are the only genes have been designated to definite chromosomes. These genes pairs are firmly associated. The varieties having quantitative gene-based resistance demonstrate practically level of resistance same continuum. E.g. Lyalpur-73, among most important varieties in 1970's still performs as resistant in screening nurseries. While, the genotypes possessing qualitative gene-based is race specific in nature do not survive for judicious period and flop frequently in next 4-5 years. Durable rust resistant varieties react similarly against unlike strains and in different ecological circumstances. The variety Frontana released around fifty years before still possess operative resistance against rust. There are also few examples that some major genes performed for longer duration but this situation is very infrequent. Six autonomous loci,

contribute to slow rust contributing to two rusts in a population were recognized in material originated from cross of Avocet "S," and Pavon. Stripe rust is influenced noteworthy. The loci on 3BS and 6BL chromosome had noteworthy impact on stripe rust. The putative (its role and the protein it codes for has not been completely recognized) loci deploying resistance to yellow and leaf rust recognized on 6AL 1BL and 4BL chromosomes (William et al., 2006). In one more population a locus on the distal location of chromosome 1BL was recognized with exceedingly substantial impacts on resistance against stripe rust (Suenaga et al., 2003). William et al. (2006) claims Avocet S and Morocco have some genomic features that comprise slow rusting resistance which outcomes in substantial pause and it becomes vulnerable completely. Accumulating quantitative genes for achieving favorite degree of resistance in a genotype is an inspiring mission as it involves detection of genotypes possessing quantitative genes, crossing in precise outlines succeeding top cross or back cross method, sustaining necessary size of population and selecting desired lines from material segregating. The crossing plans and assortments approaches used for breeding qualitative genes-based resistance do not generate desired output if applied for breeding quantitative gene resistance and cannot produce any improvement. The material having quantitative gene-based resistance was evolved in CIMMYT near to immunity (<10M) and distributed worldwide in 1990s (Singh et al., 2000). Wheat breeding for development of resistant cultivars using conventional methods is prolonged, complicated and takes adequate time to generate output that is not affordable sometimes. Molecular markers present brilliant substitute in evolution of ameliorated cultivars that carry resistance would lead to enhanced crop production. These tools tag desired genes and bestow useful collaboration in improving screening potency for useful characters.

#### **Sources of durable rust resistance**

Durable resistance may be delivered by a single gene or by amalgamations of several genes (McIntosh and Watson, 1982). The term durable resistance is used recurrently in preference to horizontal resistance or non-race specific to designate resistance effective for long duration. The explanation of durability is not that resistance is effective against all strains of a pathogen but that the resistance was active for a lengthened duration (Johnson and Law, 1975). Sources of

germplasm occupy status of key role to accomplish desired result of breeding for crop development. But instead, sources of pioneering resistance genes can be installed hurriedly to avoid destruction. These sources are held in reserve in freezers. Definitely, numerous derivatives of genes from wild grasses in *Triticum* and related genera such as Rye executed efficiently (Hoisington et al., 1999). *Aegilops* species has been exploited frequently as parent to assign genes resistant against Pgt (Schneider et al., 2007; Olson et al., 2013a,b). An inspiring result of work conducted is that genes originated from bread wheat were not found successful usual (Jin et al., 2007). The worth of preserving plant genetic diversity is realized since many decades ago (Gessese, 2019), and wild relatives of wheat possess colossal source of genetic diversity for numerous commercial traits together with resistance to rusts in wheat (Warburton et al., 2006). This rightfulness offers prospect to experts for relocating desired genes from wild ancestors through inter-specific hybridization to evolve resistant wheat varieties (Bansal et al., 2017). Useful source of genomic diversity is wheat landraces (Warburton et al., 2006). Leading wheat-cultivating region of the planet between 30° and 45°N latitude, is rich in resources of wheat germplasm (Hawkes, 1981). The potential of landraces conserved is identified and characterized to exploit genetic diversity to accomplish target. Diverse resistance sources available to scientists have been maintained in international germplasm banks. This design guarantees comprehensive genetic base in crop. Eighty banks of wheat germplasm all around the globe carry amongst 410,000 ( Tanksley and McCouch, 1997) and 800,000 accessions (Ortiz et al., 2008). Wheat landraces have occupied status of varieties in considerable area. Some fundamental integrities ensue in these circumstances: a)- It is sensible to use valued rich source of resistance of wild wheats. b)- It is not verified that the resistance combined is durable definitely. An illustration of this is Sr31 from rye, which surrendered to critical black rust strain TTKSK after considerable period (30 years) of employment (Afzal et al., 2015; 2021). The vital benefit about revolving to wild or species far related is that resistance genes are accessible sharp. c)- It is not possible predicting prospect success in wide crossing. Therefore, it is rationale to attain complete advantage of the prospects of attainment by increasing and trying hybridization and transmission of chromosome from unfamiliar sources

with assortment of species, accessions, or landraces. Most important topographies leading the application of wild species as a source of desirable traits from agronomic viewpoint are (a) Attaining of a prolific cross breed and (b) Allocation the segment of chromosome holding resistant genes to wheat positively. Effective hybridization, preservation of the F1 generation, and retrieval of likely recombinants may be prejudiced by chance genetic structures besides chromosomal physical heterozygosity. Species with genomes more far interrelated often display reduced proportion of homoeologous combination while closely related to wheat establish higher frequency of pairing (Mujeeb-Kazi et al., 2013). Conventional crop improvement is unhurried and cannot keep step with increasing diet concerns. Biotechnology is being executed to improve crop productivity.

#### **Application of advance techniques in improvement of crop**

Breeding with technologically advanced apparatuses play a key role for the future. Adequate information has been generated in the discipline of Biotechnology during the recent past. Thus, new prospects have unlocked and these procedures will be practiced effectively for improvement of crop. Plant breeding strategies with known molecular markers for resistance and functional genomics enable a breeder for developing resistant cultivars of wheat against different fungal diseases. Improved know how in genetics, molecular biology and knowledge of plant physiology at the end of last century applied for better management of crops. The data generated have made accessible innovative scenarios to diminish the influence of this adverse situation which are challenging in achievement of target (Begum et al., 2014).

Pyramiding of many resistant genes enhances durability of rust resistance in wheat. Incorporation of many genes encoding partial resistance pyramiding in a more practical strategy to attain durable resistance because conventional breeding is not appropriate as process of variety development engages simultaneous experiments of the breeding materials with diverse genetic variants of pathogen. Generally, it is not possible for a program of breeding to carry on all tests needed for rust strains desired for this work (Khan et al., 2013). Hence, Marker Assisted Selection is a proper substitute to smooth fast evolution of rust resistant cultivars (Beukert et al., 2020). In wheat procedures of molecular genetics is not

simple. The hexaploidy along with the small gradation of polymorphism among elite varieties the wheat offers considerable trials for those struggling to evolve molecular markers and practice to explore genetics. Amplified fragment length polymorphism (AFLP) and microsatellite marker systems are being exploited to explore inheritance of traits in wheat. Disease tolerance is inherited potential of genotype under the situation when it is not resistant but damages the produce negligible. Combinations of 'slow rusting' genes provide opportunity to develop of wheat varieties possessing tolerance under disease pressure. Gene pyramiding becomes simple with the assistance of molecular markers (Chukwu et al., 2019). Race specific genes originated from wild relatives are commonly connected to genes conferring characters undesirable. Contravention this relation and install R genes into breeding programs is not easier job but demands aptitude. Problems associated with genes characterization of those are unfamiliar before encompass slight physical resolution of cytogenetic protocol (Lukaszewski et al., 2005) and restricted potential of simple sequence repeats (SSR), simple sequence length polymorphisms (SSLP) and short tandem repeats (STR), fluctuating to the tertiary gene pool. Mullan et al. (2005) recognized as gene pool three (GP3). These problems upset the employment of these valued sources for progress of wheat. A widely deliberated method, though not exploited extensively, is host induced gene silencing abbreviated as (HIGS) of central genes in the pathogen. This path of job includes enunciating small interfering RNAs in the host that may be transferred to the pathogen and persuade silencing of genes authoritative for virulence of pathogen (Nunes and Dean, 2012). Nevertheless, the advancement in genomic strategies as well as accessibility of several genome sequences has allowed the fast contact to genes in wild species. This has enabled the development of gene-specific molecular markers for rapid characterization of gene through Marker Assisted Selection (MAS). Markers contribute in pyramiding of Adult Plant Resistant genes or genes resistant at all stages to develop durable rust resistant wheat cultivars (Singh et al., 2014).

MAB is conceivable for characters, controlled by monogenic as well as multigenic (Francia et al., 2005). The marker systems based on gel are not cost effective. Usually used marker systems for instance Single

Sequence Repeat (SSR) and Single Nucleotide polymorphism (SNP) depend on sequence data. These limitations bound the capacity of breeding programs considerably to accomplish reasonable outputs on benefit to justify the practice marker-assisted selection in breeding for several characters in routine and mainly quantitative traits. Among population single nucleotide polymorphisms, commonly known as SNPs ("snips"), are usual sort of genomic variance among individuals of a particular species takes place due to sexual reproduction and mutation. SNP markers are called 'markers of choice' because of their profusion and circulation in the genomes and the aptitude to categorize populations at rather less expenses (Gut, 2001). Individually SNP designates distention in a single deoxyribonucleic acid building block, named a nucleotide. For instance, in a certain stretch of deoxyribonucleic acid, a SNP may substitute the nucleotide cytosine (C) with the nucleotide thymine (T). SNPs are the key tactic to understand process through which living organisms have developed and hereditary links within/between species, explain of traits of agronomic characters and resistance/susceptibility to pathogenic infections. Predominantly, identifying genomic loci those lead to diverse trait is significant. With the benefits of constancy, lucrative progresses, and huge material assays, SNP has converted gradually important in crop genomic research. The development of genotyping apparatuses has been practiced successfully in biology since long to categorize the crops into model and non-model. Polymorphisms is exposed quickly with the development of subsequent generation sequencing technologies and the modification to the more genotyping assays. Nevertheless, the fault-prone style of Next Generation Sequencing study apparatuses is yet a huge problem which might cause findings not truthful. That requires for the improvement of apparatus for taking out gigantic data, provision for the data investigation, and rational decision. To accomplish need, instead of usage of binary structure of nucleotides mechanization has been done. Combined integrated SNP Mining and Utilization (ISMU) Channel is classified among early trials to advance a machine learning technique to SNP finding. The combined method together with the fresh developments will allow an augmented data and practise of SNPs sooner or later. DArT marker analysis is characterised by sequence-independent and qualifies more than usual multiplexing;

synchronized typing of numerous hundred to numerous thousands of polymorphic loci spread over the genome. DArT executes fair in several polyploid species and not expensive (Sánchez-Sevilla et al., 2015; Hong et al., 2009). This method does not entail any DNA-sequence data. Nucleotide polymorphisms within restriction enzyme (RE) appreciation locations and the high reliability of the RE can present better duplicability. DArT polymorphisms result from as compare to assays based on polymerase chain reaction that are based on lesser reliability selective primer annealing. DArT markers have been industrialized in over forty plant species and have been working widely for building of molecular maps, identifying trait-marker associations, assessment of genetic diversity, association mapping, and routine genotyping in various crops for varietal identification. DArT markers, are converted into precise PCR assays; change needs to take account of marker idleness, at the level of both DNA sequences and segregation patterns. Diversity Arrays Technology (DArT™) is a lucrative hybridization-based marker technique that offers an improved multiplexing level while being autonomous of sequence information. Marker alteration to PCR-based assays is mostly comprises several transitional phases (McNeil et al., 2011). The occurrence of markers those are redundant could be designated by the feature that base of DArT technology is a hybridization line. The provisions of the probes may not be familiar, and the identical probes are exploited with different names. Instead, probes possessing miscellaneous DNA sequences may be associated together. The profusion acknowledged is characteristic of DArTs and might up to 40 %, (Raman et al., 2013). The available sign is that rehabilitated DArTs characteristically carry on the segregation pattern of the innovative DArT marker (Eckstein et al., 2008; Afzal et al., 2021).

#### **Emergence of new rust races**

It has been experienced bitter in past varieties evolved possessing similar genetic background. Example is the germplasm with 1B-1R translocation was incorporated extensively in development of wheat varieties. This created monoculture situation in the last decade of previous century. This accelerated to the evolution of some new devastating rust races resulting a serious threat to global wheat production. A race of *P. striiformis*, virulent against Yr9 was observed very first time in East Africa in 1986 and later travelled to



Northern Africa and Southern Asia. In 1991 it was reported first in Yemen it reached in south Asia in 1995 (Singh and Huerta-Espino, 2000). In the same way, Yr27 emerged and moved following the similar track posed threat to wheat cultivation in subcontinent, where cultivars Inqilab-91 and PBW343 possessed Yr27 gene-based resistance (Fayyaz et al., 2017). Stem rust resistance in wheat cultivars with Sr31 remained effective for more than 30 years. In 1990s, most of the wheat varieties were having 1B-1R translocation which created a monoculture situation in Africa, Asia and other parts of the world. This disease occurred as a threat with the detection of Ug-99, in 1998 in Uganda (Pretorius et al., 2000). Sr31 virulent isolates of pgt were observed first time in Uganda and then disseminated all over East Africa (Pretorius et al., 2000). The innovative race was first branded in Uganda in 1999 (hence the name Ug-99), is nominated as TTKSK (Pretorius et al., 2012) following the North American nomenclature system (Roelfs, 1988). It next dispersed in Ethiopia and Kenya during 2005 (Waynera et al., 2006). The race is virulent on majority wheat varieties in Kenya. Development and spread of Ug-99 race group modelled threat to production of wheat crop extremely all-inclusive (Singh et al., 2011). A new variant of this stem rust race virulent on Sr24 has been originated in Kenya since 2006 (Jin et al., 2007, 2008). It jumped the red sea and its incidence has been recognized in Yemen in 2006 and afterward and was reported in Sudan also in the same time. In 2007, incidence of Ug99 was observed in Iran (Nazari et al., 2009). Original strains of Ug-99 appeared that are further contagious to Sr36 (Jin et al., 2009), Sr24 (Mukoyi et al., 2011) and SrTmp (Newcomb et al., 2016) afterward implanting more varieties susceptible. The prevalence and distribution of Sr31-virulence variants in the Ug99 in East Africa and additional virulent variants instigating local eruptions and epidemics in Ethiopia (Olivera et al., 2015), Central Asia (Shamanin et al., 2018) and Europe (Lewis et al., 2018), entitles that the disease is emerging as a threat to wheat cultivation in wheat production zones. These are the examples the rusts damaged crop in current century. It happened despite breeding for rust resistance is conducted using advanced techniques and new varieties are introduced in shorter duration than during previous era but we have not succeeded to achieve the target of rust-free wheat cultivation. It is because genes become ineffective in the war of existence between wheat and rust.

## CONCLUSION

The three rust diseases occupy challenge in many wheat production regions. Extreme regional rust epidemics have been documented during this century. The most dominant factor is lacking of diversity in host for resistance and continuously evolving rust races and their migration in large zone that cause a threat wherein breeding for this novel aggressive arrival or evolution of new strains. It is well known that to accomplish the target of nourishing increasing population advanced strategies must be applied combined with the conventional breeding strategies to accelerate the process by decreasing net period and expenses. Details regarding how do pathogen perpetuates, reproduces, evolves new strains in the war of survival, spreads and infects is well known. Serious hazard is because of the severe injury these maladies cause to susceptible cultivars. Wild relatives of wheat must be explored to recognize more rust resistance genes. The ever-fluctuating nature of three rusts in wheat poses a serious risk to wheat production in future. Knowledge gained through learning from history of wheat breeding and epidemic losses by wheat rusts, breeders developed the plan of pyramiding APR/quantitative genes. Deployment of APR genes with combinations of race specific genes can be a preferable approach to achieve the target of enhanced durability. The plan of pyramiding APR genes was established by apprehension of rust resistance mechanism predominant in historical wheat varieties like Lerma Rojo-64, Yaqui-50 and Lyalpur-73 which remained resistant for long time attributed to then unfamiliar APR genes. Incorporation of genetic resistance through deployment of major and QTLs used quite widely in breeding programs, combinations of partially effective pleotropic race- nonspecific genes such as Sr2, Lr34, Lr46, Lr67, and Lr68 have been found effective to grant durable resistance. Wheat breeders developed a plan of pyramiding APR genes unaccompanied or in combination with major genes to contest the newly developed races of stem and yellow rust. Wheat varieties e.g., Shafaq-06, Lasani-08 and AARI-11 are strong evidence of potential of APR gene pyramiding strategy to deal with menace of wheat rusts. Development in molecular genetics has opened the opportunity to the researcher to integrate miscellaneous vital characters. It looks as that innovations in breeding methods will be imperative driver to the title role of

Marker Assisted Selection in subsequent era and we are conscious even today advanced breeding schemes usage of molecular markers will be the integral component of crop improvement system. Cloning and development of gene-specific DNA markers of rust genes have ameliorated pyramiding into useful wheat backgrounds with a feasibility to improve wheat accessions with application of cassette of multiple cloned resistance genes. Molecular markers are not affected by atmosphere, used in all plant developing stages for selection of required traits accompanied by target gene(s). Molecular markers should be low-priced and flexible to analyse on gigantic scale to become suitable for selection purposes. Moreover, it is also useful to differentiate between dissimilar phenotypes with certainty. Such circumstances could be skilled by high output genotyping related with new marker systems, and selection tactics. In the molecular breeding programme MARS demonstrate to be one of the most vital styles as this can be exploited for multiple QTLs regulating the expression of a compound trait which is a constraint in the event of Marker Assisted Backcrossing. However, despite sufficient improvement in methods of breeding, scientific community is not in position to claim that we have defeated rust pathogen.

#### AUTHORS' CONTRIBUTIONS

All the authors contributed equally in collecting the literature and information, arranging and compiling the data and proofread the review article.

#### CONFLICT OF INTEREST

The authors declare no conflict of interest.

#### REFERENCES

- Afzal, A., Ali, S.R., Ijaz, M., Saeed, M., 2021. Combating Ug99-Current Scenario. *International Journal of Phytopathology* 10, 57-70.
- Afzal, A., Ijaz, M., Shah, S.R.A., 2020. Determination of suitable growth stage for application of fungicide against stripe rust in wheat. *Pakistan Journal of Agricultural Research* 33, 714-719.
- Afzal, A., Riaz, A., Ashraf, S., Iqbal, J., Ijaz, M., Naz, F., Shah, S.K.N., 2022. Identification of durable resistance against stripe rust. *International Journal of Phytopathology* 11, 97-113.
- Afzal, A., Riaz, A., Mirza, J.I., Shah, K.N., 2015. Status of wheat breeding at global level for combating

Ug99-A Review. *Pakistan Journal of Phytopathology* 27, 211-218.

- Afzal, S.N., Haque, M.I., Ahmedani, M.S., Rauf, A., Munir, M., Firdous, S.S., Rattu, A.R., Ahmad, I., 2008. Impact of stripe rust on kernel weight of wheat varieties sown in rainfed areas of Pakistan. *Pakistan Journal of Botany* 40, 923-929.
- Aziz, M.A., 1966. *Cereals and Pulses, Resume of Fifty Years Research Work at Punjab Agricultural College and Research Institute, Lyallpur.* Department of Agriculture, West Pakistan.
- Badebo, A., Stubbs, R.W., van Ginkel, M., Gebeyehu, G., 1990. Identification of resistance genes to *Puccinia striiformis* in seedlings of Ethiopian and CIMMYT bread wheat varieties and lines. *Netherlands Journal of Plant Pathology* 96, 199-210.
- Bansal, M., Kaur, S., Dhaliwal, H.S., Bains, N.S., Bariana, H.S., Chhuneja, P., Bansal, U.K., 2017. Mapping of *Aegilops umbellulata*-derived leaf rust and stripe rust resistance loci in wheat. *Plant Pathology* 66, 38-44.
- Begum, S., Iqbal, M., Ahmed, I., Fayyaz, M., Shahzad, A., Ali, G.M., 2014. Allelic variation at loci controlling stripe rust resistance in spring wheat. *Journal of Genetics* 93, 579-586.
- Beukert, U., Thorwarth, P., Zhao, Y., Longin, C.F.H., Serfling, A., Ordon, F., Reif, J.C., 2020. Comparing the potential of marker-assisted selection and genomic prediction for improving rust resistance in hybrid wheat. *Frontiers of Plant Science* 11, 594113.
- Biffen, R.H., 1905. Mendel's laws of inheritance and wheat breeding. *The Journal of Agricultural Science* 1, 4-48.
- Borlaug, N.E., 1958. The impact of agricultural research on Mexican wheat production. *Transactions of the New York Academy of Sciences* 20, 278-295.
- Boyd, L.A., 2005. Can Robigus defeat an old enemy?—Yellow rust of wheat. *The Journal of Agricultural Science* 143, 233-243.
- Brandt, K.M., Chen, X., Tabima, J.F., See, D.R., Vining, K.J., Zemetra, R.S., 2021. QTL analysis of adult plant resistance to stripe rust in a winter wheat recombinant inbred population. *Plants* 10, 572.
- Brennan, J.P., Murray, G.M., 1988. Australian wheat diseases—assessing their economic importance. *Agricultural Science* 1, 26-35.
- Carefoot, G.L., Sprott, E.R., 1967. Famine on the wind:

- man's battle against plant disease. Longmans Canada.
- Channa, A.W., Bux, H., Sial, M.A., Jatoi, G.H., Kumar, R., 2021. Virulence phenotyping of leaf rust (*Puccinia triticina*) isolates from southern Pakistan. *International Journal of Phytopathology* 10, 101-123.
- Channa, A.W., Bux, H., Jatoi, G.H., Sial, M.A., Shah, S.M., Figari, I.M., Koondhar, N., 2022. Evaluation of seedling resistance and marker assisted selection for leaf rust (*Puccinia triticina*) resistance in Pakistani wheat landraces, cultivars and advanced Lines. *International Journal of Phytopathology* 11, 155-169.
- Chukwu, S.C., Rafii, M.Y., Ramlee, S.I., Ismail, S.I., Oladosu, Y., Okporie, E., Onyishi, G., Utobo, E., Ekwu, L., Swaray, S., 2019. Marker-assisted selection and gene pyramiding for resistance to bacterial leaf blight disease of rice (*Oryza sativa* L.). *Biotechnology & Biotechnological Equipment* 33, 440-455.
- Dimmock, J.P.R.E., Gooding, M.J., 2002. The influence of foliar diseases, and their control by fungicides, on the protein concentration in wheat grain: a review. *The Journal of Agricultural Science* 138, 349-366.
- Eckstein, P., Rossnagel, B., Scoles, G., 2008. DArTs without the DArT board: the application of individual DArT markers to marker-assisted selection, The 8th International Oat Conference, June 28th-July 2nd.
- Ellis, J.G., Lagudah, E.S., Spielmeyer, W., Dodds, P.N., 2014. The past, present and future of breeding rust resistant wheat. *Frontier Plant Science* 5, 1-13.
- El-Orabey, W.M., Mabrouk, O.I., Gad, M.A., Esmail, S.M., 2020. Inheritance and detection of leaf rust resistance genes in some Egyptian wheat cultivars. *International Journal of Genetics and Genomics* 8, 1-10.
- El-Orabey, W.M., Mabrouk, O.I., Gad, M.A., Esmail, S.M., 2020. Inheritance and detection of leaf rust resistance genes in some Egyptian wheat cultivars. *International Journal of Genetics and Genomics* 8, 1-10.
- Farrer, W., 1898. The making and improvements of wheats for Australian conditions. *Agricultural Gazette of New South Wales* 9, 131-168.
- Fayyaz, M., Shahzad, A., Ali, G.M., Rattu, A.R., Muhammad, F., 2017. Identification of stripe rust (*Puccinia striiformis*) resistant genes among Pakistani spring wheat by using molecular markers. *International Journal of Biosciences* 11, 320-334.
- Flor, H.H., 1942. Inheritance of pathogenicity in *Melampsora lini*. *Phytopathology* 32, 653-669.
- Flor, H.H., 1956. Complementary genetic system in flax of recombination values in heredity. *Advance Genetics* 8, 29-54.
- Francia, E., Tacconi, G., Crosatti, C., Barabaschi, D., Bulgarelli, D., Dall'Aglio, E., Valè, G., 2005. Marker assisted selection in crop plants. *Plant Cell, Tissue and Organ Culture* 82, 317-342.
- Gessese, M.K., 2019. Description of wheat rusts and their virulence variations determined through annual pathotype surveys and controlled multi-pathotype tests. *Advances in Agriculture* 7, 3-4.
- Gut, I.G., 2001. Automation in genotyping of single nucleotide polymorphisms. *Human Mutation* 17, 475-492.
- Halstead, A., Henricot, B., 2010. *Pest and Diseases*. First American Edition DK Publishing. New York.
- Hawkes, J.G., Gerrish, E.E., Rick, C.M., 1981. Germplasm collection, preservation, and use In: *Plant Breeding II* (Frey KJ, ed.). The Iowa State University Press/ Ames.
- Hoisington, D., Khairallah, M., Reeves, T., Ribaut, J.-M., Skovmand, B., Taba, S., Warburton, M., 1999. Plant genetic resources: what can they contribute toward increased crop productivity? *Proceedings of the National Academy of Sciences* 96, 5937-5943.
- Hong, Y.-H., Xiao, N., Zhang, C., Su, Y., Chen, J.-M., 2009. Principle of diversity arrays technology (DArT) and its applications in genetic research of plants. *Yi Chuan= Hereditas* 31, 359-364.
- Hovmøller, M.S., Walter, S., Bayles, R.A., Hubbard, A., Flath, K., Sommerfeldt, N., Leconte, M., Czembor, P., Rodriguez-Algaba, J., Thach, T., 2016. Replacement of the European wheat yellow rust population by new races from the centre of diversity in the near-Himalayan region. *Plant Pathology* 65, 402-411.
- Howard, A., Howard, G.L.C., 1909. *Wheat in India: Its Production, Varieties and Improvement: The Empirical Dept. Agric. India*. Thacker, Spink and Co., Calcutta, India.

- Huerta-Espino, J., Singh, R.P., German, S., McCallum, B.D., Park, R.F., Chen, W.Q., Bhardwaj, S.C., Goyeau, H., 2011. Global status of wheat leaf rust caused by *Puccinia triticina*. *Euphytica* 179, 143-160.
- Jin, Y., Singh, R.P., Ward, R.W., Wanyera, R., Kinyua, M., Njau, P., Fetch, T., Pretorius, Z.A., Yahyaoui, A., 2007. Characterization of seedling infection types and adult plant infection responses of monogenic Sr gene lines to race TTKS of *Puccinia graminis* f. sp. *tritici*. *Plant Disease* 91, 1096-1099.
- Jin, Y., Szabo, L.J., Pretorius, Z.A., Singh, R.P., Ward, R., Fetch Jr, T., 2008. Detection of virulence to resistance gene Sr24 within race TTKS of *Puccinia graminis* f. sp. *tritici*. *Plant Disease* 92, 923-926.
- Jin, Y., Szabo, L.J., Rouse, M.N., Fetch Jr, T., Pretorius, Z.A., Wanyera, R., Njau, P., 2009. Detection of virulence to resistance gene Sr36 within the TTKS race lineage of *Puccinia graminis* f. sp. *tritici*. *Plant Disease* 93, 367-370.
- Johannsen, W., 1903. Ueber Erblichkeit in Populationen und reinen Linien. Eine Beitrag zur Beleuchtung schwebender Selektionsfragen. Jena, Germany: Gustav Fischer.
- Johannsen, W., 1926. Elemente der exakten Erblichkeitslehre. Jena, Germany: Gustav Fischer.
- Johnson, R., Law, C.N., 1975. Genetic control of durable resistance to yellow rust (*Puccinia striiformis*) in the wheat cultivar Hybride de Bersee. *Annals of Applied Biology* 81, 385-391.
- Khan, M.H., Bukhari, A., Dar, Z.A., Rizvi, S.M., 2013. Status and strategies in breeding for rust resistance in wheat. *Agricultural Sciences* 4, 292-301.
- Khanfri, S., Boulif, M., Lahlali, R., 2018. Yellow rust (*Puccinia striiformis*): a serious threat to wheat production worldwide. *Notulae Scientia Biologicae* 10, 410-423.
- Kislev, M.E., 1982. Stem rust of wheat 3300 years old found in Israel. *Science* 216, 993-994.
- Knott, D.R., 1988. Using polygenic resistance to breed for stem rust resistance in wheat. In: Simmonds, N.W. and Rajaram, S., Eds., *Breeding Strategies for Resistance to the Rusts of Wheat*, CIMMYT, Mexico. 39-47.
- Kolmer, J.A., 2009. Postulation of leaf rust resistant genes in selected soft red winter wheats. *Crop Science* 43, 1266-1274.
- Lewis, C.M., Persoons, A., Bebbler, D.P., Kigathi, R.N., Maintz, J., Findlay, K., Bueno-Sancho, V., Corredor-Moreno, P., Harrington, S.A., Kangara, N., 2018. Potential for re-emergence of wheat stem rust in the United Kingdom. *Communications Biology* 1, 1-9.
- Loegering, W.Q., 1966. The relationship between host and pathogen in stem rust of wheat. *Proceedings of the Second International Wheat Genetics Symposium*. (Ed. J Mackey.) Lund, Sweden, 1963. *Hereditas Supplement* 2, 167-177.
- Lukaszewski, A.J., Lapinski, B., Rybka, K., 2005. Limitations of in situ hybridization with total genomic DNA in routine screening for alien introgressions in wheat. *Cytogenetic and Genome Research* 109, 373-377.
- Marasas, C.N., Smale, M., Singh, R.P., 2004. The economic impact in developing countries of leaf rust resistance breeding in CIMMYT-related spring bread wheat. *CIMMYT*.
- Mateen, A., Khan, M.A., Rashid, A., Hussain, M., Rehman, S.U., Ahmed, M., 2015. Identification of leaf rust virulence pattern on wheat germplasm in relation to environmental conditions in Faisalabad. *Academia Journal of Agricultural Research* 3, 137-155.
- McIntosh, R.A., 2009. History and status of the wheat rusts. R.A. McIntosh (Ed.), *Proceedings of 2009 Technical Workshop, Borlaug Global Rust Initiative*, Cd. Obregón, Sonora, Mexico, March 17-20, 2009, Borlaug Global Rust Initiative, Ithaca, New York, USA. 11-23.
- McIntosh, R.A., Watson, I.A., 1982. *Genetics of host-pathogen interactions in rusts*. Academic Press, Oxford.
- McIntosh, R.A., Wellings, C.R., Park, R.F., 1995. *Wheat rusts: an atlas of resistance genes*. CSIRO publishing.
- McNeil, M.D., Hermann, S., Jackson, P.A., Aitken, K.S., 2011. Conversion of AFLP markers to high-throughput markers in a complex polyploid, sugarcane. *Molecular Breeding* 27, 395-407.
- Milus, E.A., Kristensen, K., Hovmøller, M.S., 2009. Evidence for increased aggressiveness in a recent widespread strain of *Puccinia striiformis* f. sp. *tritici* causing stripe rust of wheat.

- Phytopathology 99, 89-94.
- Mujeeb-Kazi, A., Kazi, A.G., Dundas, I., Rasheed, A., Ogonnaya, F., Kishii, M., Bonnett, D., Wang, R.R.-C., Xu, S., Chen, P., 2013. Genetic diversity for wheat improvement as a conduit to food security. *Advances in Agronomy* 122, 179-257.
- Mukoyi, F., Soko, T., Mulima, E., Mutari, B., Hodson, D., Herselman, L., Visser, B., Pretorius, Z.A., 2011. Detection of variants of wheat stem rust race Ug99 (*Puccinia graminis* f. sp. tritici) in Zimbabwe and Mozambique. *Plant Disease* 95, 1188-1188.
- Mullan, D., Platteter, A., Teakle, N., Appels, R., Colmer, T., Anderson, J., Francki, M., 2005. EST-derived SSR markers from defined regions of the wheat genome to identify *Lophopyrum elongatum* specific loci. *Genome / NRC Canada = Génome / Conseil national de recherches Canada*. 48, 811.
- Nazari, K., Mafi, M., Yahyaoui, A., Singh, R.P., Park, R.F., 2009. Detection of wheat stem rust (*Puccinia graminis* f. sp. tritici) race TTKSK (Ug99) in Iran. *Plant Disease* 93, 317-317.
- Newcomb, M., Olivera, P.D., Rouse, M.N., Szabo, L.J., Johnson, J., Gale, S., Luster, D.G., Wanyera, R., Macharia, G., Bhavani, S., 2016. Kenyan isolates of *Puccinia graminis* f. sp. tritici from 2008 to 2014: Virulence to SrTmp in the Ug99 race group and implications for breeding programs. *Phytopathology* 106, 729-736.
- Nunes, C.C., Dean, R.A., 2012. Host-induced gene silencing: a tool for understanding fungal host interaction and for developing novel disease control strategies. *Molecular Plant Pathology* 13, 519-529.
- Olivera Firpo, P.D., Newcomb, M., Flath, K., Sommerfeldt-Impe, N., Szabo, L.J., Carter, M., Luster, D.G., Jin, Y., 2017. Characterization of *Puccinia graminis* f. sp. tritici isolates derived from an unusual wheat stem rust outbreak in Germany in 2013. *Plant Pathology* 66 1258-1266.
- Olson, E.L., Rouse, M.N., Pumphrey, M.O., Bowden, R.L., Gill, B.S., Poland, J.A., 2013a. Introgression of stem rust resistance genes SrTA10187 and SrTA10171 from *Aegilops tauschii* to wheat. *Theoretical and Applied Genetics* 126, 2477-2484.
- Olson, E.L., Rouse, M.N., Pumphrey, M.O., Bowden, R.L., Gill, B.S., Poland, J.A., 2013b. Simultaneous transfer, introgression, and genomic localization of genes for resistance to stem rust race TTKSK (Ug99) from *Aegilops tauschii* to wheat. *Theoretical and Applied Genetics* 126, 1179-1188.
- Ortiz, R., Sayre, K.D., Govaerts, B., Gupta, R., Subbarao, G.V., Ban, T., Hodson, D., Dixon, J., M., Ortiz-Monasterio, J.I., Reynolds, M., 2008. Climate change: can wheat beat the heat? *Agriculture, Ecosystems & Environment* 126, 46-58.
- Pardey, P., Beddow, J., Kriticos, D., Hurley, T., Park, R., Duveiller, E., Sutherst, R., Burdon, J., Hodson, D., 2013. Right-Sizing Stem-Rust Research. *Science* 340, 147-148.
- Pretorius, Z.A., Singh, R.P., Wagoire, W.W., Payne, T.S., 2000. Detection of virulence to wheat stem rust resistance gene Sr31 in *Puccinia graminis* f. sp. tritici in Uganda. *Plant Disease* 84, 203-203.
- Pretorius, Z.A., Szabo, L.J., Boshoff, W.H.P., Herselman, L., Visser, B., 2012. First report of a new TTKSF race of wheat stem rust (*Puccinia graminis* f. sp. tritici) in South Africa and Zimbabwe. *Plant Disease* 96, 590-590.
- Rajaram, S., Singh, R.P., Torres, E., 1988. Current CIMMYT approaches in breeding wheat for rust resistance. Pp. 101-118 in: N.W. Simmonds and S. Rajaram (Eds.) *Breeding strategies for resistance to the rusts of wheat*. CIMMYT. Mexico.
- Raman, H., Raman, R., Kilian, A., Detering, F., Long, Y., Edwards, D., Parkin, I.A.P., Sharpe, A.G., Nelson, M.N., Larkan, N., 2013. A consensus map of rapeseed (*Brassica napus* L.) based on diversity array technology markers: applications in genetic dissection of qualitative and quantitative traits. *BMC Genomics* 14, 1-13.
- Randhawa, M.S., Bains, N.S., Sohu, V.S., Chhuneja, P., Trethowan, R.M., Bariana, H.S., Bansal, U., 2019. Marker assisted transfer of stripe rust and stem rust resistance genes into four wheat cultivars. *Agronomy* 9, 497.
- Rehman, A.U., Khan, M.A., Muhammad, F., Ahmad, N., Hussain, M., 2009. Review of wheat breeding in Punjab-Pakistan. *The Cereal Rusts* 1.
- Rehman, A.U., Sajjad, M., Khan, S.H., Ahmad, N., 2013. Prospects of Wheat Breeding for Durable Resistance against Brown, Yellow and Black Rust Fungi. *International Journal of Agriculture & Biology* 15, 1209-1220.

- Roelfs, A.P., Martens, J.W., 1988. An international system of nomenclature for *Puccinia graminis* f. sp. *tritici*. *Phytopathology* 78, 526-533.
- Sánchez-Sevilla, J.F., Horvath, A., Botella, M.A., Gaston, A., Foltá, K., Kilian, A., Denoyes, B., Amaya, I., 2015. Diversity arrays technology (DArT) marker platforms for diversity analysis and linkage mapping in a complex crop, the octoploid cultivated strawberry (*Fragaria × ananassa*). *PLoS One* 10, e0144960.
- Schneider, A., Molnár, I., Molnár-Láng, M., 2008. Utilisation of *Aegilops* (goatgrass) species to widen the genetic diversity of cultivated wheat. *Euphytica* 163, 1-19.
- Shamanin, V., Salina, E., Zelenskiv, Y., Kokhmetova, A., Patpour, M., Holmoller, M., 2018. Large scale wheat stem rust outbreaks in Western Siberia/Northern Kazakhstan in 2015–2017. In *Proceedings of the BGRI 2018 Technical Workshop*.
- Singh, R.P., 1992. Genetic association of leaf rust resistance gene *Lr34* with adult plant resistance to stripe rust in bread wheat. *Phytopathology (USA)*.
- Singh, R.P., Herrera-Foessel, S., Huerta-Espino, J., Singh, S., Bhavani, S., Lan, C., Basnet, B.R., 2014. Progress towards genetics and breeding for minor genes based resistance to Ug99 and other rusts in CIMMYT high-yielding spring wheat. *Journal of Integrative Agriculture* 13, 255-261.
- Singh, R.P., Hodson, D.P., Huerta-Espino, J., Jin, Y., Bhavani, S., Njau, P., Herrera-Foessel, S., Singh, P.K., Singh, S., Govindan, V., 2011. The emergence of Ug99 races of the stem rust fungus is a threat to world wheat production. *Annual Review of Phytopathology* 49, 465–481.
- Singh, R.P., Huerta-Espino, J., Rajaram, S., 2000. Achieving near-immunity to leaf and stripe rusts in wheat by combining slow rusting resistance genes. *Acta Phytopathologica et Entomologica Hungarica* 35, 133-139.
- Singh, R.P., Huerta-Espino, J., William, H., 2005. Genetics and breeding for durable resistance to leaf and stripe rusts in wheat. *Turkish Journal of Agriculture and Forestry* 29, 121-127.
- Solh, M., Nazari, K., Tadesse, W., R., W.C., 2012. The growing threat of stripe rust worldwide. *Borlaug Global Rust Initiative (BGRI) Conference*. Beijing, China.
- Stakman, E.C., Levine, M.N., 1922. *The Determination of Biologic Forms of Puccinia Graminis on Triticum Spp.* The University of Minnesota Agricultural Experiment Station.
- Stakman, E.C., Piemeisel, F.J., 1917. A new strain of *Puccinia graminis*. *Phytopathology* 7, 73.
- Suenaga, K., Singh, R.P., Huerta-Espino, J., William, H.M., 2003. Microsatellite markers for genes *Lr34/Yr18* and other quantitative trait loci for leaf rust and stripe rust resistance in bread wheat. *Phytopathology* 93, 881-890.
- Tanksley, S.D., McCouch, S.R., 1997. Seed banks and molecular maps: unlocking genetic potential from the wild. *Science* 277, 1063-1066.
- Tariq-Khan, M., Younas, M.T., Mirza, J.I., Awan, S.I., Jameel, M., Saeed, M., Mahmood, B., 2020. Evaluation of major and environmentally driven genes for resistance in Pakistani wheat landraces and their prospected potential against yellow rust. *International Journal of Phytopathology* 9, 145-156.
- Vanderplank, J.E., 1963. *Plant Disease: Epidemics and Control*. Academic Press, New York, . 349.
- Waqar, A., Khattak, S.H., Begum, S., Rehman, T., Rabia, Shehzad, A., Ajmal, W., Zia, S.S., Siddiqi, I., Ali, G.M., 2018. Stripe rust: A review of the disease, *Yr* genes and its molecular markers. *Sarhad Journal of Agriculture* 34, 188-201.
- Warburton, M.L., Crossa, J., Franco, J., Kazi, M., Trethowan, R., Rajaram, S., Pfeiffer, W., Zhang, P., Dreisigacker, S., Ginkel, M.v., 2006. Bringing wild relatives back into the family: recovering genetic diversity in CIMMYT improved wheat germplasm. *Euphytica* 149, 289-301.
- Wilcoxson, R.D., Skovmand, B., Atif, A.H., 1975. Evaluation of wheat cultivars for ability to retard development of stem rust. *Annals of Applied Biology* 80, 275-281.
- William, H.M., Singh, R.P., Huerta-Espino, J., Palacios, G., Suenaga, K., 2006. Characterization of genetic loci conferring adult plant resistance to leaf rust and stripe rust in spring wheat. *Genome* 49, 977-990.
- Zadoks, J.C., 1961. Yellow rust on wheat studies in epidemiology and physiologic specialization. *Tijdschrift over Plantenziekten* 67, 69-256.