A review on origin and genetic analysis of Wheat genes conferring resistance to wheat rust in common bread wheat (*Triticum aestivum L.*)

Abstract

Wheat rusts, produced by three species of *Puccinia,* are severe diseases and important biotic impediments in efforts to keep wheat production going around the world.The most commercially significant and prevalent diseases among global wheat varieties includes leaf rust also known as brown rust, caused by *Puccinia graminis triticina Eriks,* stem or black rust caused by *Puccinia graminis f. sp. tritici,* and stripe or yellow rust caused by *Puccinia striiformis f. Tritici.*Currently,more than 200 rust resistance genes (100 leaf rust, 60 stem rust, and 51 stripe rust) have been identified by using various molecular approaches from several wheat crop species and related wild species. This review highlights various aspects of *Lr* (Leaf rust), *Sr* (Stem rust) and *Yr*(yellow rust) resistance genes, their primitive origins, and their prevalence in globally wheat cultivars.

Kewwords: Wheat production, Rust, Resistant genes, Molecular approaches.

Introduction

Wheat is one of the major cereal crops grown worldwide and one of the most important staple food crop for feeding 2.5 billion world population. Wheat cultivation represents approximately 19 % of global major cereal production **(FAOSTAT,2020-21).** It is agronomically and nutritionally most important cereal essential for the food security, poverty alleviation and improved livelihoods. Wheat production is hampered by many biotic and abiotic stresses, resulting in yield disparity. Genetic vulnerability to different biotic and abiotic stresses is increased by the scarcity of genetic diversity on the farmer's land **(Wang *et al*., 2017)**. Biotic stresses, including rust diseases, pose a serious danger to future food security since they reduce cereal crop yields drastically. This disease has the potential to reduce wheat yield by up to 30% and destroy the crop within a month after the initial attack, posing a serious threat to food security (**Shafi *et al*., 2022)**.

Rust fungi are one of the most important diseases for cereals. Rust pathogens are obligatory parasitic organisms that have a macrocyclic and heteroecious life cycle **(Kolmer 2013).**

Controlling of rust infections is very difficult due to the airborne nature of their spores, which can travel large distances and the fast emergence of highly aggressive races of rust pathogens. Rust infections have become more common in recent years, causing epidemics in Austarlia **(Murray *et al*., 2009),** in Europe **(Volkova *et al*., 2009)** and North and South American wheat-growing regions **(Germán *et al*., 2007).**Ug99, a novel strain of stem rust discovered in Uganda in 1999, and its variants are pathogenic on around 80–90% of wheat cultivars and germplasm **(Goyal and Manoharachary 2014)**.

As a result, managing rust diseases is important for increasing world wheat production on a long-term basis. The most efficient and long-term strategies of managing diseases in crop plants are the development and deployment of resistant cultivars.**Biffen 1905**, made the first attempt to implement rust resistance breeding programmes in wheat.Modern breeding procedures, which are based on advanced genetic engineering and molecular biology tools, enable fresh and efficient techniques for developing new improved varieties. Recently, many genes and QTLs governing rust resistance genes have been identified in wheat **(Buerstmayr *et al.*, 2014).** A brief description about different identified rust resistant genes present below.

<u>Leaf rust resistance genes derived from various wheat species</u>

Leaf rusts are the most severe rust disease in global wheat production, with yield losses of more than 50% reported in susceptible cultivars **(Draz *et al.*, 2015).** Over 100 leaf rust resistance genes have been isolated from common wheat, including *Lr* 1 **(Roelfs *et al*., 2000**).*Lr*2,*Lr*2a,*Lr*2b,*Lr*2c,*Lr*3,*Lr*3a,*Lr*3b,*Lr*3c and *Lr*4 to *Lr*6 and also *Lr*9 which was derived from Ae.umbellulata,*Lr*14 gene that confers long term resistance in durams **(McIntosh *et al*.,2003).***Lr*20 **(Neu *et al*., 2002),** *Lr*23 and *Lr*30 **(Nelson *et al*., 1997),** *Lr*49 and *Lr*67**(shahin *et al.*, 2015),** *Lr*68 **(Herrera *et al.*, 2012),** *Lr* 80 **(Kumar *et al.*, 2021),** trp1 and trp2 recessive genes that conferred adult plant resistance in Brazilian wheat cultivar Toropi **(da SILVA *et al*., 2012).**Many resistance genes of major wheat diseases come from wild wheat cultivars like *Aegilops tauschii*, *Aegilops squarrosa*., and *Triticum tauschii*. 3 leaf rust resistance genes *Lr*19,*Lr*24 and *Lr*29 was derived from *Aegilops elongatum*, 4 genes namely *Lr* 28, *Lr*36,*Lr*47 and *Lr*51derived from *Aegilops speltoides* and one single gene from *Aegilops ventricosa* also isolated **(Todorovska *et al*.,2009).** *Lr*41 and *Lr*43 leaf rust resistance genes that transferred to common wheat from a wild species known as *Triticum tauschii***(Cox *et al.*,1994). According to**

gill et al., (2019) at both seedling and adult plant stages, the gene *Lr*42 resistance gene derived from *Aegilops tauschii* (TA2450) confers effective resistance to leaf rust**.** 2 another leaf rust resistance genes *Lr*14a from duram wheat cultivars Hope and Gaza transferred into common wheat**(Aktar *et al.,* 2017).** Recently, a new *LrAp* resistance gene derived from wild wheat species *Aegilops peregrina* genetically mapped by **Narang *et al.,* (2020).**

Identified stem rust resistance genes against Ug99 race

In Uganda, a novel aggressive stem rust strain known as Ug99 was discovered in 1999 **(Pretorius *et al.*, 2000).**It is currently a major danger to global wheat production. Only 25% of India's total wheat-growing region is susceptible to stem rust **(Nandni *et al.*, 2020).**Approximately 60 genes for stem rust resistance (*Sr*) has been discovered so far **(McIntosh*et al.*, 2016).** According to **Singh *et al*. (2011),** 90% of wheat cultivars grown worldwide are susceptible to Ug99**.** Stem rust is expected to affect grain yields by 10% to 50% in susceptible varieties, with heavier losses of up to 90% recorded in rare but severe occurrences **(Beard *et al.,* 2004).** *Sr13* was the first resistance gene identified in the germplasm of *Triticum dicoccom* but it also present in several *Triticum durum* species **(Huerta *et al.,* 1992)**. **Jyoti *et al.*,2022** conducted genetic and phenotypic analysis on F2 and doubled haploid population from the cross between RL6071 (wheat line) and Tr129. Tr129 was also a wheat line which consist stem rust resistance gene derived from *Aegilops triuncialis*. Tr129 has 4 stem rust resistance (*Sr*) genes *Sr*9b , *Sr*7b, *Sr*8a and *Sr*Tr129, according to mapping and phenotyping.*Sr*21 resistance gene derived from *Triticum monococcum* showed resistance against Ug99 race (**Chen *et al.*, 2018).** *Sr*35 is a coiled-coil, nucleotide-binding, leucine-rich repeat gene from *Triticum monococcum* that exhibited resistance against Ug99 race **(Saintenac *et al*., 2013).***Sr*2, *Sr*24, *Sr*25, *Sr*26, *Sr*31, and *Sr*38 resistant genes identified using linked molecular markers **(Lin*et al*., 2021).**Some other resistance genes like *Sr*24,*Sr*36, *Sr*7b and *Sr*9b identified by using gene specific markers in Nebraska bread wheat germplasm conferred resistance against stem rust **(Wu *et al.,* 2014).** *Sr27* resistant gene is also identified effective against TTKSK (Ug99) race **(Upadhyaya, *et al.*,2021).** In recent years, new stem rust races like TKTTF, TTRTF have arisen, triggering a pandemic. As a result, stem rust has resurfaced as a danger to global wheat production **(Olivera *et al.*, 2019).**

stripe rust resistance genes derived from various wheat species

Stripe rust was common in the northwest United States and infection was mainly associated with cool weather **(Johnson 1988).** Approximately 51 genes for stripe rust resistance (*Yr*) have been discovered so far in which *Yr*5 and *Yr*15 are extremely resistant to all races found thus far in the United States **(Mu *et al.*, 2020).***Yr*10 was the first identified seedling resistance gene against stripe rust by using a map-based technique obtained from Moro wheat **(Liu *et al.*,2014).***Yr* 15 resistant gene derived from wild emmer wheat **(Yaniv *et al.*,2015),***Yr*51 and *Yr*57 genes have been recently discovered to be effective in Australia against pre- and post-2002 *Pst* pathotypes **(Randhawa *et al.*, 2019).***Yr*81 from common wheat land race Aus27430 **(Gessese *et al.*,2019),***Yr*82 from Aus27969**(Pakeerathan *et al.*, 2019),***Yr*83 **(Li *et al.*, 2020)**also identified.

MAS and Modern approaches for Gene Pyramiding,mapping and gene Deployment for rust resistance genes

Marker-assisted selection is a time-saving method of selecting desirable characters in an indirect manner.The primary prerequisite for marker assisted selection is the detection of markers releated to the gene of interest. By the use of MAS it can be possible to release resistant variety by gene deployment and gene pyramiding. Molecular markers are important in both genetic analysis of new sources of resistance genes and transferring two or more resistance genes in a single line **(Haile *et al.*,2013).** Molecular markers such as S*SR*(simple sequence repeat), AFLP (amplified fragment length polymorphism) and RAPD (random amplified polymorphic DNA) can be used to detect the resistance gene and compare rust populations. Some modern breeding tools include TILLING-targeting induced local lesions in genomes for resistace gene sequence analysis **(Comai *et al.*, 2006),** incorporation of genes by transgenic technology **(Periyannan *et al.*, 2013),** cisgenesis, reverse breeding,RNA-dependent DNA methylation **(Becker *et al.*,2012),** genome editing technology (GET), and genomic selection **(Desta *et al.*,2014)**, have been added to molecular breeding techniques that already exist**(Savadi *et al.*,2018).**Recentaly,numerous genes and QTLs involving rust resistances have been identified in wheat **(Buerstmayr *et al.*, 2014).**

STS marker was first used for detection of *Lr9* gene derived from *Aegilops umbellulata* **(Schachermayr *et al*., 1994).** STS, SCAR and CAPS markers was used for identification of *Lr*19 **(Prabhu *et al*.,2004).** *Lr*51 **(Helguera *et al*., 2005)** and *Lr*52 **(Hiebert *et al*., 2005),** *Sr*24 and *Sr*26 **(Mago *et al*.,2005).** *Lr*1 **(Cloutier *et al*., 2007)** and *Lr*10 **(Feuillet *et al*., 2003)** have been identified by cloning and gene sequencing. *Lr*36, *Lr*37 and *Lr*38 by PCR assay **(Helguera *et al*.,2003)**. Using two molecular markers, csLV34 and Xwmc44, a multiplex polymerase chain reaction (PCR) assay was developed for detection of two essential wheat slow rust resistance genes, Lr34 and Lr46 **(Skowrońska *et al*.,2019).** Some stem rust resistance genes like *Sr*39 resistant gene was identified by using SCAR marker in Canadian wheat **(Zhang *et al*., 2012)**. *Sr*9a stem rust resistant gene was also identified by Microsatellite markers **(Tsilo *et al*., 2007)**. *Sr*6, *Sr*40 by Microsatellite marker **(Ejaz *et al*., 2012).** Simple sequence repeat S*SR* markers used to identify and map the APR (adult plant resistance) stem rust resistant gene *Sr56* in a winter wheat variety **(Bansal *et al*., 2014).** *Sr*58, *Lr*46 and *Yr*29 by CAPS molecular marker **(Yu *et al*., 2014).** Other relevant markers, EST-STS diagnostic markers, which were used for the resistance gene YrSM139-1B derived from *Triticum dicoccoides* against stripe rust in bread wheat **(Zhang *et al*., 2016).** Therefore, these technologies enable us to modify crop plants more precisely than ever before, accelerating crop enhancement efforts for long-term food production while also approaching safety concerns about food crops.

Conclusion

Knowledge about origin, distribution and deployement of resistance genes is essential for developing new wheat varieties with desirable characters. Gene pyramiding by MAS and the application of other molecular methods are essential for maintaining the long-term or durable resistance against rust disease. Wheat breeders face a significant problems in developing new cultivars or improving existing cultivars using new resistance genes because of regular appearance of novel virulence pathotypes and races, Therefore, continuous strict efforts are required to identify sources for novel genes/QTLs to overcome new emerging pathogen races and gain long-term resistance in the field. Overall, the goal of this review paper is to improve understanding of the present status of wheat research among wheat researchers, students, academics, plant breeders, and pathologists.

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