



A Review on Origin and Genetic Analysis of Wheat Genes Conferring Resistance to Wheat Rust in Common Bread Wheat (*Triticum aestivum* L.)

Abhishek Dwivedi ^a, Satyam Pathak ^a, Sajan Kumar ^a, Aman Srivastava ^b,
Vinod Singh ^a and Ashim Debnath ^{a*}

^a Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, India.

^b Department of Genetics and Plant Breeding, RPCAU, Pusa, Samastipur, Bihar, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2022/v34i1931105

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/87005>

Mini-review Article

Received 10 March 2022

Accepted 13 May 2022

Published 25 May 2022

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.

Keywords: Wheat production; rust; resistant genes; molecular approaches.

1. 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 [1]. 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 [2]. 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 [3].

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 [4]. 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 Australia [5], in Europe [6] and North and South American wheat-growing regions [7]. 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 [8].

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 [9] 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 [10]. A brief description about different identified rust resistant genes present below.

2. LEAF RUST RESISTANCE GENES DERIVED FROM VARIOUS WHEAT SPECIES

Leaf rusts are the most severe rust disease in global wheat production, with yield losses of more than 50% reported in susceptible cultivars [11]. Over 100 leaf rust resistance genes have been isolated from common wheat, including *Lr1* [12]. *Lr2, Lr2a, Lr2b, Lr2c, Lr3, Lr3a, Lr3b, Lr3c* and *Lr4* to *Lr6* and also *Lr9* which was derived from *Ae.umbellulata, Lr14* gene that confers long term resistance in durams [13]. *Lr20* [14], *Lr23* and *Lr30* [15], *Lr49* and *Lr67* [16], *Lr68* [17], *Lr 80* (Kumar et al., 2021), *trp1* and *trp2* recessive genes that conferred adult plant resistance in Brazilian wheat cultivar Toropi [18]. 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 *Lr19, Lr24* and *Lr29* was derived from *Aegilops elongatum*, 4 genes namely *Lr 28, Lr36, Lr47* and *Lr51* derived from *Aegilops speltoides* and one single gene from *Aegilops ventricosa* also isolated [19]. *Lr41* and *Lr43* leaf rust resistance genes that transferred to common wheat from a wild species known as *Triticum tauschii* [20]. According to Gill et al., [21] at both seedling and adult plant stages, the gene *Lr42* resistance gene derived from *Aegilops tauschii* (TA2450) confers effective resistance to leaf rust. 2 another leaf rust resistance genes *Lr14a* from durum wheat cultivars Hope and Gaza transferred into common wheat [22]. Recently, a new *LrAp* resistance gene derived from wild wheat species *Aegilops peregrina* genetically mapped by Narang et al., [23].

3. IDENTIFIED STEM RUST RESISTANCE GENES AGAINST UG99 RACE

In Uganda, a novel aggressive stem rust strain known as Ug99 was discovered in 1999 [24]. It is currently a major danger to global wheat production. Only 25% of India's total wheat-growing region is susceptible to stem rust [25]. Approximately 60 genes for stem rust resistance (*Sr*) has been discovered so far (McIntosh et al., 2016). According to Singh et al. [26], 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 dicoccum* but it also present in several *Triticum durum* species [27].

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 *Sr9b*, *Sr7b*, *Sr8a* and *SrTr129*, according to mapping and phenotyping. *Sr21* resistance gene derived from *Triticum monococcum* showed resistance against Ug99 race [28]. *Sr35* is a coiled-coil, nucleotide-binding, leucine-rich repeat gene from *Triticum monococcum* that exhibited resistance against Ug99 race [29]. *Sr2*, *Sr24*, *Sr25*, *Sr26*, *Sr31*, and *Sr38* resistant genes identified using linked molecular markers (Lin et al., 2021). Some other resistance genes like *Sr24*, *Sr36*, *Sr7b* and *Sr9b* identified by using gene specific markers in Nebraska bread wheat germplasm conferred resistance against stem rust [30]. *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 [31].

4. 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 [32]. Approximately 51 genes for stripe rust resistance (*Yr*) have been discovered so far in which *Yr5* and *Yr15* are extremely resistant to all races found thus far in the United States [33]. *Yr10* was the first identified seedling resistance gene against stripe rust by using a map-based technique obtained from Moro wheat [34]. *Yr15* resistant gene derived from wild emmer wheat [35], *Yr51* and *Yr57* genes have been recently discovered to be effective in Australia against pre- and post-2002 *Pst* pathotypes [36]. *Yr81* from common wheat land race Aus27430 [37], *Yr82* from Aus 27969 [38], *Yr83* [39] also identified.

5. MAS AND MODERN APPROACHES FOR GENE PYRAMIDING, MAPPING AND GENE

5.1 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 related 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 [40]. Molecular markers such as SSR (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 resistance gene sequence analysis [41], incorporation of genes by transgenic technology [42], cisgenesis, reverse breeding, RNA-dependent DNA methylation [43], genome editing technology (GET), and genomic selection [44], have been added to molecular breeding techniques that already exist [45]. Recently, numerous genes and QTLs involving rust resistances have been identified in wheat [10].

STS marker was first used for detection of *Lr9* gene derived from *Aegilops umbellulata* [46]. STS, SCAR and CAPS markers was used for identification of *Lr19* [47], *Lr51* [48] and *Lr52* [49], *Sr24* and *Sr26* [50]. *Lr1* [51] and *Lr10* [52] have been identified by cloning and gene sequencing. *Lr36*, *Lr37* and *Lr38* by PCR assay [53]. 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* [54]. Some stem rust resistance genes like *Sr39* resistant gene was identified by using SCAR marker in Canadian wheat [55]. *Sr9a* stem rust resistant gene was also identified by Microsatellite markers [56]. *Sr6*, *Sr40* by Microsatellite marker [57]. Simple sequence repeat SSR markers used to identify and map the APR (adult plant resistance) stem rust resistant gene *Sr56* in a winter wheat variety [58]. *Sr58*, *Lr46* and *Yr29* by CAPS molecular marker [59]. 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 [60]. 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.

6. CONCLUSION

Knowledge about origin, distribution and deployment 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.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Food and Agriculture Organization Corporate Statistical Database (FAOSTAT 2020-21) [Internet]. Available: <https://www.fao.org/faostat/en/#home>
2. Wang C, Hu S, Gardner C, Lübberstedt T. Emerging avenues for utilization of exotic germplasm. *Trends in Plant Science*. 2017 Jul 1;22(7):624-37.
3. Shafi U, Mumtaz R, Shafaq Z, Zaidi SM, Kaifi MO, Mahmood Z, Zaidi SA. Wheat rust disease detection techniques: a technical perspective. *Journal of Plant Diseases and Protection*. 2022 Jan 31;1-6.
4. Kolmer J. Leaf rust of wheat: pathogen biology, variation and host resistance. *Forests*. 2013 Mar;4(1):70-84.
5. Murray GM, Brennan JP. Estimating disease losses to the Australian wheat industry. *Australasian Plant Pathology*. 2009 Nov;38(6):558-70.
6. Volkova GV, Alekseeva TP, Anpilogova LK, Dobryanskaya MV, Vaganova OF, Kol'bin DA. Phytopathological characteristics of leaf rust resistance of new winter wheat varieties. *Russian Agricultural Sciences*. 2009 Jun;35(3):168-71.
7. Germán S, Barcellos A, Chaves M, Kohli M, Campos P, de Viedma L. The situation of common wheat rusts in the Southern Cone of America and perspectives for control. *Australian Journal of Agricultural Research*. 2007 Jun 26;58(6):620-30.
8. Goyal A, Manoharachary C, editors. *Future challenges in crop protection against fungal pathogens*. Springer New York; 2014 Sep 6.
9. Biffen RH. Mendel's laws of inheritance and wheat breeding. *The Journal of Agricultural Science*. 1905 Jan;1(1):4-8.
10. Buerstmayr M, Matiasch L, Mascher F, Vida G, Ittu M, Robert O, et al. Mapping of quantitative adult plant field resistance to leaf rust and stripe rust in two European winter wheat populations reveals co-location of three QTL conferring resistance to both rust pathogens. *Theoretical and Applied Genetics*. 2014 Sep;127(9):2011-28.
11. Draz IS, Abou-Elseoud MS, Kamara AE, Alaa-Eldein OA, El-Bebany AF. Screening of wheat genotypes for leaf rust resistance along with grain yield. *Annals of Agricultural sciences*. 2015 Jun 1;60(1):29-39.
12. Roelfs AP, Hughes ME, Long DL. Rust resistance genes in wheat lines and cultivars. *US Dep. Agric. Res. Serv. Cereal Dis. Lab. Online, Publication CDL-EP*. 2000;6.
13. McIntosh RA, Yamazaki Y, Dubcovsky J, Rogers J, Morris C, Appels R. Catalogue of gene symbols for wheat. In *Proceedings of the 12th International Wheat Genetics Symposium*. 2013 Sep 8;8-13). Yokohama Japan.
14. Neu ,C, Stein N, Keller, B. Genetic mapping of the Lr20 genes Pm1 resistance locus reveals suppressed recombination on chromosome arm 7AL in hexaploid wheat. *Genome*. 2002 Aug 1;45(4):737-44.
15. Nelson JC, Singh RP, Autrique JE, Sorrells ME. Mapping genes conferring and suppressing leaf rust resistance in wheat. *Crop science*. 1997 Nov;37(6):1928-35.
16. Shahin SI, El-Orabey WM. Relationship between partial resistance and inheritance of adult plant resistance gene Lr 46 of leaf rust in six bread wheat varieties. *International Journal of Science and Research*. 2015 Feb 28;4(1):1511-7.
17. Herrera-Foessel; SA, Singh RP, Huerta-Espino J, Rosewarne GM, Periyannan SK, Viccars L, et al. Lr68: A new gene

- conferring slow rusting resistance to leaf rust in wheat. *Theoretical and Applied Genetics*. 2012 May;124(8):1475-86.
18. da SILVA PR, Brammer SP, Guerra D, Milach SC, Barcellos AL, Baggio MI. Monosomic and molecular mapping of adult plant leaf rust resistance genes in the Brazilian wheat cultivar Toropi. *Embrapa Trigo-Artigo em periódico indexado (ALICE)*; 2012.
 19. Todorovska, E, Christov, N, Slavov., S, Christova, P, Vassilev D. Biotic stress resistance in wheat breeding and genomic selection implications,. *Biotechnology & Biotechnological Equipment*. 2009 Jan 1;23(4):1417-26.
 20. Cox TS, Raupp WJ, Gill BS. Leaf rust-resistance genes Lr41, Lr42, and Lr43 transferred from *Triticum tauschii* to common wheat. *Crop science*. 1994 Mar; 34(2):339-43.
 21. Gill HS, Li C, Sidhu JS, Liu W, Wilson D, Bai G, Gill BS, Sehgal SK. Fine mapping of the wheat leaf rust resistance gene Lr42. *International Journal of Molecular Sciences*. 2019 Jan;20(10):2445.
 22. Aktar-Uz-Zaman MD, Tuhina-Khatun MS, Hanafi MM, Sahebi M. Genetic analysis of rust resistance genes in global wheat cultivars: An overview. *Biotechnology & Biotechnological Equipment*. 2017 May 4;31(3):431-45.
 23. Narang D, Kaur S, Steuernagel B, Ghosh S, Bansal U, Li J, et al. Discovery and characterisation of a new leaf rust resistance gene introgressed in wheat from wild wheat *Aegilops peregrina*. *Scientific reports*. 2020 May 5;10(1):1-9.
 24. Pretorius ZA, Singh RP, Wagoire WW, Payne TS. Detection of virulence to wheat stem rust resistance gene Sr31 in *Puccinia graminis*. f. sp. tritici in Uganda. *Plant Disease*. 2000 Feb;84(2):203.
 25. Nandni S, Dev D, Singh KP. Ug99: Wheat Stem Rust Race: Exploring the World. In *Diseases of Field Crops: Diagnosis and Management*. Apple Academic Press. 2020 May 16;81-88.
 26. Singh RP, Hodson DP, Huerta-Espino J, Jin Y, Bhavani S, Njau P, Herrera et al. The emergence of Ug99 races of the stem rust fungus is a threat to world wheat production. *Annual Review of Phytopathology*. 2011 Sep 8;49:465-81.
 27. Huerta-Espino J, Roelfs AP. Leaf rust on durum wheats. *Vortraege fuer Pflanzenzuechtung (Germany)*; 1992.
 28. Chen S, Zhang W, Bolus S, Rouse MN, Dubcovsky J. Identification and characterization of wheat stem rust resistance gene Sr21 effective against the Ug99 race group at high temperature. *PLoS genetics*. 2018 Apr 3;14(4): e1007287.
 29. Saintenac C, Zhang W, Salcedo A, Rouse MN, Trick HN, Akhunov E, Dubcovsky J. Identification of wheat gene Sr35 that confers resistance to Ug99 stem rust race group. *Science*. 2013 Aug 16;341(6147): 783-6.
 30. Wu XX, Li TY, Chen S, Wang GQ, Cao YY, Ma SL, Li MJ. Stem rust resistance evaluation and Ug99-resistance gene detection of 139 wheat cultivars. *Scientia Agricultura Sinica*. 2014;47(23): 4618-26.
 31. Olivera PD, Sikharulidze Z, Dumbadze R, Szabo LJ, Newcomb M, Natsarishvili K, et al. Presence of a sexual population of *Puccinia graminis* f. sp. tritici in Georgia provides a hotspot for genotypic and phenotypic diversity. *Phytopathology*. 2019 Dec 20;109(12):2152-60.
 32. Johnson R. Durable resistance to yellow (stripe) rust in wheat and its implications in plant breeding. In *Breeding Strategies for Resistance to the Rusts of Wheat*, El Batan, Mexico (Mexico), 29 Jun-1 Jul 1987 1988. CIMMYT.
 33. Mu J, Liu L, Liu Y, Wang M, See DR, Han D, Chen X. Genome-wide association study and gene specific markers identified 51 genes or QTL for resistance to stripe rust in US winter wheat cultivars and breeding lines. *Frontiers in Plant Science*. 2020;998.
 34. Liu W, Frick M, Huel R, Nykiforuk CL, Wang X, Gaudet DA, et al. The stripe rust resistance gene Yr10 encodes an evolutionary-conserved and unique CC–NBS–LRR sequence in wheat. *Molecular Plant*. 2014 Dec 1;7(12):1740-55.
 35. Yaniv E, Raats D, Ronin Y, Korol AB, Grama A, Bariana H, et al. Evaluation of marker-assisted selection for the stripe rust resistance gene Yr15, introgressed from wild emmer wheat. *Molecular breeding*. 2015 Jan;35(1):1-2.
 36. Randhawa MS, Bains NS, Sohu VS, Chhuneja P, Trethowan RM, Bariana HS, Bansal U. Marker assisted transfer of stripe rust and stem rust resistance genes into four wheat cultivars. *Agronomy*. 2019 Sep;9(9):497.

37. Gessese M, Bariana H, Wong D, Hayden M, Bansal U. Molecular mapping of stripe rust resistance gene Yr81 in a common wheat landrace Aus27430. *Plant disease*. 2019 Jun 16;103(6):1166-71.
38. Pakeerathan K, Bariana H, Qureshi N, Wong D, Hayden M, Bansal U. Identification of a new source of stripe rust resistance Yr82 in wheat. *Theoretical and Applied Genetics*. 2019 Nov;132(11):3169-76.
39. Li J, Dundas I, Dong C, Li G, Trethowan R, Yang Z, Hoxha S, Zhang P. Identification and characterization of a new stripe rust resistance gene Yr83 on rye chromosome 6R in wheat. *Theoretical and Applied Genetics*. 2020 Apr;133(4):1095-107.
40. Haile JK, Rouml MS. Status of genetic research for resistance to Ug99 race of *Puccinia graminis* f. sp. *tritici*: A review of current research and implications. *African Journal of Agricultural Research*. 2013 Dec 18;8(50):6670-80.
41. Comai L, Henikoff S. TILLING: practical single-nucleotide mutation discovery. *The Plant Journal*. 2006 Feb;45(4):684-94.
42. Periyannan S, Moore J, Ayliffe M, Bansal U, Wang X, Huang L, Deal K, Luo M, Kong X, Bariana H, Mago R. The resistance gene Sr33, an ortholog of barley Mla genes, encodes resistance to wheat stem rust race Ug99. *Science*. 2013 Aug 16;341(6147):786-8.
43. Becker C, Weigel D. Epigenetic variation: origin and transgenerational inheritance. *Current Opinion in Plant Biology*. 2012 Nov 1;15(5):562-7.
44. Desta ZA, Ortiz R. Genomic selection: genome-wide prediction in plant improvement. *Trends in plant science*. 2014 Sep 1;19(9):592-601.
45. Savadi S, Prasad P, Kashyap PL, Bhardwaj SC. Molecular breeding technologies and strategies for rust resistance in wheat (*Triticum aestivum*) for sustained food security. *Plant pathology*. 2018 May;67(4):771-91.
46. Schachermayr G, Siedler H, Gale MD, Winzeler H, Winzeler M, Keller B. Identification and localization of molecular markers linked to the Lr9 leaf rust resistance gene of wheat. *Theoretical and applied genetics*. 1994 Apr;88(1):110-5.
47. Prabhu KV, Gupta SK, Charpe A, Koul S. SCAR marker tagged to the alien leaf rust resistance gene Lr19 uniquely marking the *Agropyron elongatum*-derived gene Lr24 in wheat: a revision. *Plant Breeding*. 2004 Oct;123(5):417-20.
48. Helguera; M, Vanzetti L., Soria M, Khan IA, Kolmer J, Dubcovsky J. PCR markers for *T. speltoides* leaf rust resistance gene Lr51 and their use to develop isogenic hard red spring wheat lines. *Crop science*. 2005 Mar;45(2):728-34.
49. Hiebert C, Thomas J, McCallum B. Locating the broad-spectrum wheat leaf rust resistance gene Lr52 (LrW) to chromosome 5B by a new cytogenetic method. *Theoretical and Applied Genetics*. 2005 May;110(8):1453-7.
50. Mago, R, Bariana, H.S, Dundas I.S, Spielmeyer, W, Lawrence G.J, Pryor AJ, Ellis JG. Development of PCR markers for the selection of wheat stem rust resistance genes Sr24 and Sr26 in diverse wheat germplasm. *Theoretical and Applied Genetics*. 2005 Aug;111(3):496-504.
51. Cloutier S, McCallum BD, Loutre C, Banks TW, Wicker T, Feuillet C, Keller B, Jordan MC. Leaf rust resistance gene Lr1, isolated from bread wheat (*Triticum aestivum* L.) is a member of the large psr567 gene family. *Plant molecular biology*. 2007 Sep;65(1): 93-106.
52. Feuillet C, Travella S, Stein N, Albar L, Nublait A, Keller B. Map-based isolation of the leaf rust disease resistance gene Lr10 from the hexaploid wheat (*Triticum aestivum* L.) genome. *Proceedings of the National Academy of Sciences*. 2003 Dec 9;100(25):15253-8.
53. Helguera; M, Khan I.A, Kolmer J, Lijavetzky D, Zhong-Qi L, Dubcovsky J. PCR assays for the Lr37-Yr17-Sr38 cluster of rust resistance genes and their use to develop isogenic hard red spring wheat lines. *Crop science*. 2003 Sep;43(5):1839-47.
54. Skowrońska R, Kwiatek M, Tomkowiak A, Nawracała J. Development of multiplex PCR to detect slow rust resistance genes Lr34 and Lr46 in wheat. *Journal of Applied Genetics*. 2019 Nov;60(3):301-4.
55. Zhang Q, Klindworth DL, Friesen TL, Chao S, Jin Y, Cai X, Xu SS. Development and characterization of wheat lines with Sr37 for stem rust resistance derived from wild Timopheev's wheat. In Meeting Abstract. 2012 Jan 14;316(6).
56. Tsilo TJ, Jin Y, Anderson JA. Microsatellite markers linked to stem rust resistance allele Sr9a in wheat; 2007.

57. Ejaz M, Iqbal M, Shahzad A, Ahmed I, Ali GM. Genetic variation for markers linked to stem rust resistance genes in Pakistani wheat varieties. *Crop Science*. 2012 Nov;52(6): 2638-48.
58. Bansal U, Bariana H, Wong D, Randhawa M, Wicker T, Hayden M, Keller B. Molecular mapping of an adult plant stem rust resistance gene Sr56 in winter wheat cultivar Arina. *Theoretical and applied genetics*. 2014 Jun;127(6): 1441-8.
59. Yu LX, Barbier H, Rouse MN, Singh S, Singh RP, Bhavani S, Huerta-Espino J, Sorrells ME. A consensus map for Ug99 stem rust resistance loci in wheat. *Theoretical and Applied Genetics*. 2014 Jul;127(7):1561-81.
60. Zhang T, Jin, Y, Zhao JH, Gao F, Zhou BJ, Fang YY, Guo HS. Host-induced gene silencing of the target gene in fungal cells confers effective resistance to the cotton wilt disease pathogen *Verticillium dahliae*. *Molecular Plant*. 2016;9(6):939-942.

© 2022 Dwivedi et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/87005>