Breeding For Rust Resistance in Wheat: A Review

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Abstract

Wheat is one the most important staple crop across the world. Contribution of India in wheat production is marked to a point. Majority of people in India specially north cultivates wheat. It is used in many ways. Even in foreign countries wheat is used for preparation of malt, beverages etc… Among all the diseases affecting wheat, Rust is highly dangerous to reduce its yield. So, controlling of rust disease and producing more yield per unit area is the challenging path for all wheat growers. There are 3 types of wheat named Leaf rust, Stripe rust and Stem rust. Out of all Leaf rust damages more to crop than rest all. There are many ways to bring resistance to wheat. But breeding by selection of parents gives better result. Following the traditional practices for getting rid of rust doesn't give good result. The new technologies principles must be implied for that. This paper discusses about management of rust disease in the feasible ways.

Key words: Rust, spores, host, leaf rust, stem rust, stripe rust, avirulence, pathogen, genes, molecular breeding, genetic control, Backcross, Marker Assisted Selection, Marker Assisted Backcrossing, Adult Plant Resistance (APR), seedling resistance and all stage resistance.

Introduction:

Wheat is the food source opted by many people worldwide (Ashraf, Rimsha., 2021). Among all the diseases of wheat, Rust is most devasting in nature (Al – Doss, A.A., et al., 2021). The importance for controlling wheat rust is to make more production out of smaller area with a healthy crop. As the population of world is rising up, feeding them with the same food production is not possible **(**Hanafi, M.M., et.al., 2017**).** Out of many diseases affecting wheat crop, Rust reduces yield to much extent. The first seed race of wheat susceptible to rust is in Uganda i.e., Ug99 and then in Kenya and Ethiopia (Bukhari, A., et.al., 2012). There are three rusts of wheat, namely:

Stripe rust – Puccinia striiformis f.sp. tritici

Stem rust – Puccinia graminis f.sp. tritici

Leaf rust – Puccinia triticina erkinson (Ashraf, Rimsha., 2021)

Wheat is also classified as Winter wheat and Spring wheat. In both of them Spring wheat shows much resistance (Gultyaeva, E., 2020). Rust is highly virulent and damage crop to a greater extent (Chen, X., Line, R.F., 1995). Wheat yield loss due to leaf rust is up to 10% (Akram, U.A., et al.,2021). Out of all rusts, stripe rust is making economic loss up to 40%. (Amanov, A., et al., 2016). If situation is severe, it affects crop specially during grain filling stage thereby reduction in the yield. If situation goes like same it cause 100% yield loss. In India, approximately 28 pathotypes for stripe rust resistant and Himalayan region is the actual place where these pathotypes originated. (Balyan, H.S., et al., 2021). In our country stripe infestation is more in less temperate regions covering North West – India, stem rust at high temperature in Central India and leaf rust is common in entire country (Agarwal, P., et al., 2021). Genetic diversity is most important for the control of rust disease and also to know the behaviour of it (Bansal, UK., et al., 2007).

Rust occurs mostly in

Bread Wheat – *Triticum aestivum*

Durum Wheat – *Triticum turgidum* var *durum*

Triticale – *Secale cereale* (Figlan,S., et al., 2020).

Rust produces uredinospores that are carried by wind for larger distances. Wheat rust fungi is an obligate parasite that completes its entire lifecycle only upon the host organism. It causes damage against specific set of host (Bharadwaj, S.C., et al., 2017). Primary gene pool is the source from where wheat rust resistance is taken from (Bharadwaj, S.C., et al., 2019). First to know whether or not seedlings are showing resistance to rust we have to screen the plants in filed or glasshouse. Glasshouse screening gives best results as it maintains controlled conditions. But most of the people choose of field screening as it is too easy and less costly. Based on the results of incidence of pathogen, select for the best method to breed for rust inheritance **(Chan, X.M., et al., 2014).**

Give scoring to the disease incidence in a way that stands S for Susceptibility, S- for moderately susceptible, R- for resistant and R as highly resistant. The plant which is previously R should continue as R. If not, the variety is not stable. Breed such a way that a crop having such genes shouldn’t lose its ability for expressing its gene (Parker, J.H., et al., 1918).

Wheat Rust:

Wheat leaf rust is a heteroecious rust that may live on two distinct hosts. It grow into teliospores, basidiospores, urediniospores in contact with cereals; pycniospores, and aeciospores with alternative hosts. Because of their dikaryotic nuclear state, urediniospores may reproduce in their cereal hosts indefinitely. Uredinial infections produce teliospores from two dikaryotic nuclei. Teliospores germinate, meiosis, and release 4 haploid basidiospores into the atmosphere. Basidiospores must then adhere and infect the new host (Kolmer, J., 2013).

Leaf rust:

Brown rust shares similar life cycle as Black rust. The fungus has been found on a variety of host plants, including those in the genus *Thalictrum*, the genus *Isopyrum*, the genus *Clematis* and the genus *Anchusa*. Unfortunately, under Indian circumstances, the uredial stage is the only stage of the fungus' life cycle that can survive. Although Thalictrum javanicum in India does not infect wheat, it does harbour an early stage of Puccinia persistens that has been related to *Agropyron semicostatum*. Brown rust, which mostly affects wheat, may also infect other *Aegilops sp* (Bharadwaj, S.C., et al., 2016). It multiplies at fast rate when temperature is 10 – 30^0C (Huerta-Espino, J., et al., 2002).

Stem rust:

Phase – 0 and Phase – 1 stands for Pycnial and aceidial phases that grows on alternative plants of host like Berberis, Mahonoberberis etc.. The rest of the phases – Uredial and telial grows on cereal plant hosts. Telio (Teleuto) spores emerge when exposed to freezing temperatures after a protracted period of hibernation. When the seed has germinated, a four-celled promycelium develops, and from each cell, a sterigma (plural: sterigmata) arises that is infected with basidiospores that induce pycnia in wheat. A pycnia is made up of flask-shaped spermatia (pycniospores) and receptive hyphae. Aecia and aeciospores are created when two distinct species mate in a receptive hyphae or pycniospore. Aeciospores are a problem for wheat (Bharadwaj, S.C., et al., 2016). It occurs in temperatures of 15 – 35^0 C (Huerta-Espino, J., et al., 2002).

Stripe rust:

Infected plant components might include leaves, leaf sheaths, stems, glumes, awns, and even kernels. The pathogen that causes yellow rust is heteroecious. After being infected with aeciospores from naturally infected *Berberis chinensis* and *B. koreana*, grass uredinia resembling those of *P. striiformis* yellow rust is created (Bharadwaj, S.C., et al., 2016). It prefer cool conditions of 2 – 15^0C (Huerta-Espino, J., et al., 2002).

Table 1: Wheat rust with its hosts and symptoms: (Huerta-Espino, J., et al., 2002).

Disease	Pathogen	Primary hosts	Alternate hosts	Symptoms

Leaf rust	Puccinia triticina	Triticale, Durum and Bread wheat	*Isopyrum. Clematis, Thalictrum, Anchusa*	Isolated uredinia on the top surface of the leaves and sometimes on the leaf sheaths.
Stem rust	Puccinia graminis f.sp. tritici	Durum, Bread wheat, Triticale and Barley	*Berberis vulgaris*	Isolated uredinia on the top and bottom surfaces of the leaves, the stem, and the spikes.
Stripe rust	Puccinia striiformis f.sp. tritici	Few barley varieties, Triticale, Durum and Bread wheat	Not known	On leaves, spikes, and sometimes on leaf sheaths, systemic uredinia is present.

Breeding methods for Rust in Wheat:

Fig. 1 (Balyan, H.S., et al., 2021):

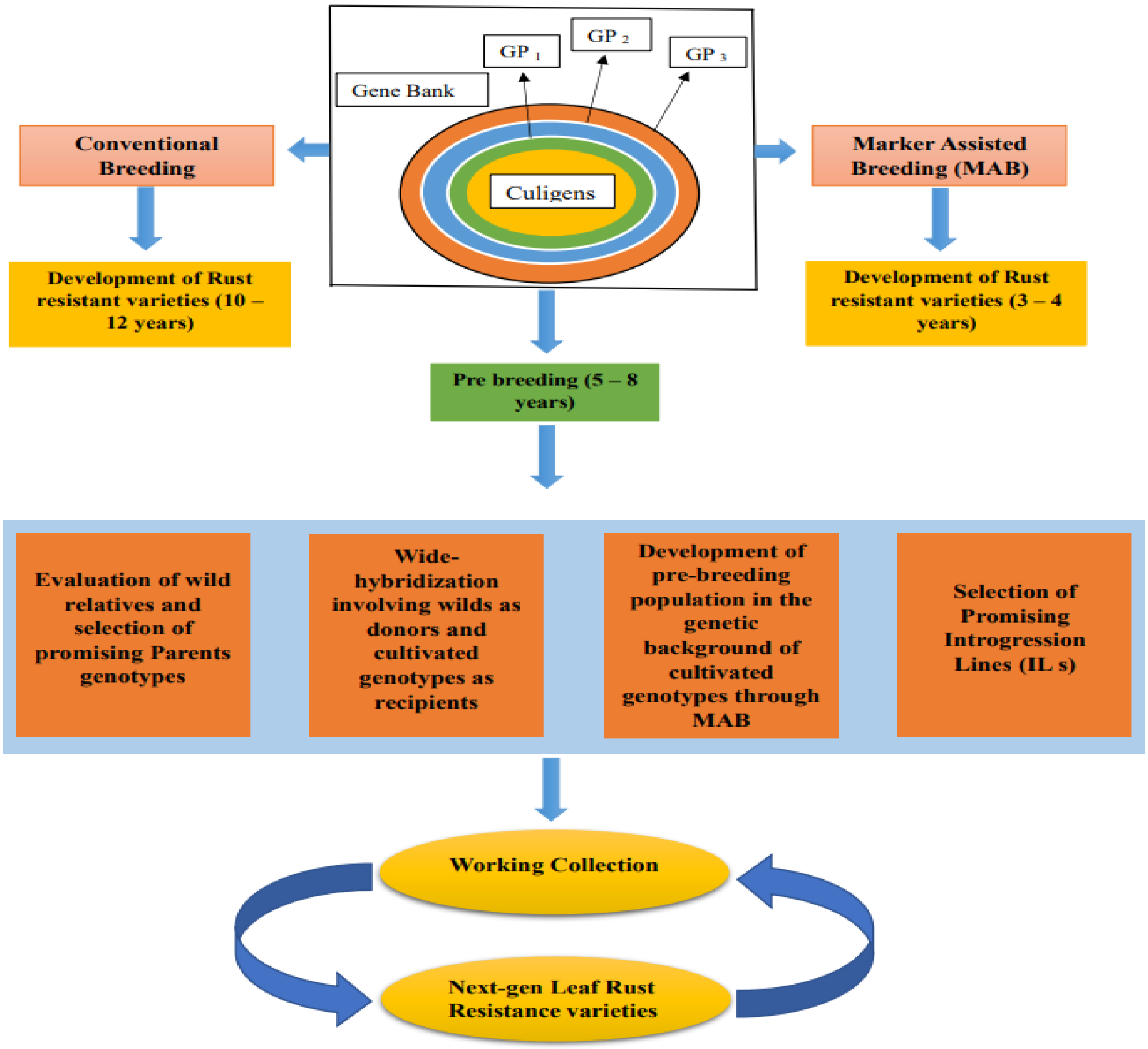

Fig 1 explanation:

The above picture depicts the development of a variety or hybrid having rust resistance in several ways. Mentioned methods are:

1. Conventional breeding
2. Marker Assisted Breeding (MAB).
3. Pre – breeding

Before selecting method, choose parents from which rust resistance is to be transferred. For that purpose, approach gene bank and examine level 1, 2 and 3 of gene pool. Pick up the right gene from gene pool. Next to it, select breeding method based on plant species and breeding objective

If it is conventional breeding – specially Backcross Breeding is used to transfer of desirable resistance trait. But the only major disadvantage associated with it is "Time requirement". It takes at least 10 – 12 years to release a variety. Environmental affects much for expression a phenotype too (Bharadwaj., S.C., et al., 2017).

Marker Assisted Breeding or Marker assisted Selection is one of the precised and best methods to acquire rust resistant varieties. Less time is required i.e., 3 – 4 years.

Pre – breeding has a process. It deals with selection of parents that have resistance genes, crossing between two distant parents with one wild relative donor parent and local variety as recipient, use of Marker Assisted Selection to identify resistance genes in progeny and finally select lines.

To every breeder to produce resistant varieties in resistance to Ug – 99 wheat variety is the breeding objective (Saunders, D.G.O., et al., 2019). in case of Wheat. Generally Wild relatives are major source of resistivity for that (Ashraf., & Rimsha., 2021).

Two methods are used to control rust in Wheat – Genetic control and Chemical control **(**Hanafi, M.M., et.al., 2017**).** But out of all methods to control rust, deployment found environmentally safe to restrict disease to low level (Al – Doss, A.A., et al., 2021).

Chemical control:

There are many chemical formulations available in different regions which are used to control at different rates. There are many Agri industries developing chemicals to cope up the resistance build by a pathogen for the previously existing chemicals. But these are totally unsafe for environment and some may causes illness even in humans **(**Hanafi, M.M., et.al., 2017).

Genetic control:

Before knowing for breeding methods, it is important to know Avirulence factors in host and virulence factors in pathogen (Balyan, H.S., et al., 2022). Introgression of two or more genes called Gene Pyramiding can be employed to maintain varieties with resistance. It helps to introduce resistant genes into a single variety (Al – Doss, A.A., et al., 2021).

Hybrid breeding by gene pyramiding: Gene pyramiding can also be grouped under conventional breeding methods (Beukert,U., et al., 2020). Different genomes play a vital role in conferring transfer of gene that is resistant for rust. For example, D genome of *Aegilops tauschii* provides genes resistance to stripe rust. Sound knowledge of this is must before breeding for disease resistance (Chen, F., et al., 2019).

There are many ways to control rust disease genetically. Specially 2, it includes:

Backcross breeding:

Gene governing for rust is major gene. A donor parent and a recipient parent is selected and both are crossed for transfer of a single resistant trait. Then it is evaluated under greenhouse conditions (Chen, X., et al., 2013). Single backcross is successful in transfer of genes of Adult Plant Resistance (APR). the only disadvantage of Backcross breeding is time requirement is too high. (Bansal, U.K., et al., 2007).

Marker Assisted Selection (MAS):

Marker-assisted selection, or MAS, ushers in a new era of molecular breeding when it is used to enhance crops by enabling the change of genomic regions involved in the target trait of interest using DNA markers. When the desired attribute is paired with a genetic marker, molecular association selection (MAS) is more effective than obvious phenotypic selection (Chandra, K., et al., 2021**).**

MAS – Incorporation of many genes conferring rust resistance (Agarwal,P., et al., 2021). MAS is done using molecular markers. Many markers are used for the identification of our gene of interest. DNA markers results accurate than phenotypic markers (Datta, D., et al., 2004). It uses Quantitative trait loci to map the genes. QTL Technology is also gaining much importance in breeding as Molecular screening takes less time than conventional breeding (Al – Doss, A.A., et al., 2021).

Many genes are responsible for retaining resistance in wheat crop. For example, stem rust is governed by genes *Sr*2, *Sr*10, *Sr*11, *Sr*12, *Sr*17, *Sr*24, *Sr*26, *Sr*30, *Sr*31 and *Sr*36. Leaf rust is governed by *Lr*13, *Lr*34. Similarly stripe rust by *Yr*2, *Yr*7, *Yr*9, *Yr*6 etc… (Bhukari, A., et al., 2013). QTL is majorly used to find genes expressing during Adult Stage. APR genes are found in all 21 chromosomes. Among all genomes – A, B and D, B genome have more resistant genes (Boyd, L.A., 2018).

Wheat lines are evaluated for the presence of resistance genes by marker system in short period of time. It includes usage of SSR, SNP, DArT, STS etc… (Kaldate, R., et al., 2020). Mode of transferring genes is Hypersensitive in nature and Race specificity. But few are Race non – specific namely *Lr*34, *Yr*18 and *Yr*29(Beukert, U., et al., 2020). A good linkage of markers with genes is must to be known before transferring of genes. To that, linked markers for Lr 80 was observed namely KASP – 17425, KASP – 17148 and BARC 124 (Atishova, M., et al., 2021). The major genes that make wheat plant resistance to wheat rust was found in diploid species of wheat namely durum and bread wheat. Example is *Triticum monococcum, Aegilops speltoides* and *Aegilops squarrosa.* (Aung, T., et al., 1999).

Though molecular markers screening is an indirect selection, but it is very much effective as QTL is adopted in it (Al-Doss, AA., 2021). It is much important to find out new genes for resistance. **There are many stem rust genes out of which majority are derived from wild relatives such as *Triticum monococcum* having cultivated *T. monococcum* ssp. *monococcum* and wild species – *T. monococcum* ssp. *aegilopoides* that is related to *T. uratu*. From wild wheat, resistance genes for stem rust are transferred to cultivated ones by *ph1b* mutation in A – genome recombined with chromosomes of *T. monococcum* (**Chen, S., et al., 2022). From ten years, about 140 such genes resistance to Stripe rust were identified by QTL (Espino, J.H., et al., 2013). It found genes like *Sr*7a, *Sr*24, *Sr*31, *Sr*38 and *Sr*57 in bread wheat and Sr 13 in Durum wheat (Bartaula, R., et al., 2022). Even for the first identified race Ug99, stem rust resistance is due to Sr35 gene isolated from *Triticum monococcum.* This is transferred to the rest all generations through QTL (Akhunov, E., et al., 2013). Through rust resistance plants it is possible even to develop transgenic plants that have many genes at a single position (Dodds, P.N., et.al., 2007).

There is an evidence that gene for leaf rust named Lr80 was found during gene pyramiding (Bansal, UK., et al., 2021) as well as 82 stripe rust resistance genes are permanently designed which we can change too (Balyan, H.S., et al., 2021).

There are some tactics of rust resistance genes. Some genes show resistance during late stages i.e., Adult phase while some marketedly expresses during seedling stage. Few gene effects for resistance is shown in all phases. Examples are:

*Lr*19, *Lr*24, *Lr*TrK, *Sr*36, *Yr*5, *Yr*10 and *Yr*15 – Seedling resistance genes

*Lr*34, *Lr*46, *Lr*67, *Lr*68, *Lr*74, *Lr*75, *Lr*77 and *Lr*78 – Adult Plant Resistance (APR) genes (Agarwal, P., et al., 2021). And (Balyan, H.S., et al., 2022).

All stage resistance genes are *Yr*5, *Y*15 (Ashraf., Rimsha., 2021).

Leaf rust resistance genes called as Lr genes are able to confer Seedling Resistance (SR) called as All Stage Resistance (ASR) or Adult Plant Resistance (APR), at adult phase following booting. Using a combination of APR and 4-5 Lr genes results in long-lasting resistance. Also, all phase resistance genes confer to durable resistance i.e., *Lr*34 and *Lr*67. There are Some genes produce resistance to both leaf and stripe – *Lr*34, *Sr*57, *Yr*18, *Pm*38, and *Lr*67, *Sr*55, *Yr*46, *Pm*46 (Balyan, H.S., et al., 2022). Most of the APR genes are pleiotropic such as, *Sr*2, *Yr*30, *Lr*27, *Sr*55, *Yr*46, *Lr*67, *Ltn*3, *Sr*57, *Yr*18, *Lr*34, *Ltn*1, *Sr*58, *Yr*29 and *Lr*46 (Ashraf, Rimsha, 2021).

In nature there are genes that are responsive to temperature. Such as, *Lr*18 gene which provides resistance at 15 – 18^{o}C but doesn't work at >18^{o}C specially at 25^{o}C (Balyan, H.S., et al., 2022). Among all *Lr*80 gene governs to leaf rust that has compatibility with other genes too for introgression (Bansal, U.K., et al., 2021).

Stripe rust fungi in wheat leaves and tissues take up nutrients. This slows photosynthesis, which in turn slows the plant's developmental stage. Up until now, 80 *Yr* genes (*Yr*1–*Yr*80) and more than 100 Pst resistance genes with temporary names have been reported.

As new races have come out, only a few of the older genes have lost some or all of their resistance to stripe rust. These include *Yr*1, *Yr*2, *Yr*3, *Yr*4, *Yr*6, *Yr*7, *Yr*9, *Yr*10, *Yr*17, *Yr*22, *Yr*23, *Yr*26, and *Yr*27. At the moment, only a few *Yr* genes, like *Yr*5 and *Yr*15, have kept their resistance to rust fungi across the whole field (Bai, B., et al., 2022).

In *Triticum dicoccoides*, *Yr*15 gene is present on chromosome that provides resistance in both adult and seedling stage of the plant. So, use of marker assisted selection for transfer of this trait to a plant is much effective and time taken by it is too less (Bariana, H., et al., 2015).

Even in United states, there was a successful story of transfer of *Yr*5 and *Yr*15 genes that show resistance in all the stages of plant was recorded. This is achieved only by mapping populations using Quantitative loci (Campbell, K.G., et al., 2009).

Combinations of genes given best results than transfer of a single gene. For leaf rust resistance scientists combined *Lr*13, *Lr*37 and *Lr*34. with other genes governing to leaf rust resistance. It resulted in *Lr*13 + *Lr*34, *Lr*13 + *Lr*37 and *Lr*34 + *Lr*37(Kloppers, F.J., & Pretorious, Z.A., 2009). Wheat line Tr – 129 is from *Aegilops triuncialis* that acts against rust disease but its origin is unknown (Ghazvini, H., et al., 2022).

Coming to QTLs, Sr have more than 150 QTLs for resistance have been mapped on 21 wheat chromosomes (Bai, B., et.al., 2022). **In case of *Lr* genes, by 2017, about 250 QTLs and 35 meta – QTLs are witnessed. After 2017 till 2022, extra 103 QTLs coding for *Lr* and *Lr*/*Yr* are found** (Balyan, H.S., et al., 2022).

Marker Assisted Backcrossing (MABC):

MABC is the combination of both Marker Assisted Selection and Backcross Breeding. Thus it has benefits of both the methods in effectiveness. It is used for the gene introgression on genome recovery (Mallick, N., et al., 2015)

It involves 3 steps:

1. Foreground selection
2. Reduction of unwanted genes
3. Background selection (Yadav, P.S., et al., 2015).

In the entire process, parents are crossed each other and the obtained progeny is backcrossed with recurrent parent for two times then the resultant is subjected to Marker Assisted Selection. Finally progeny is selfed and tested for the presence of Resistance genes (Chen, X., et al., 2022). **Each backcross generation's plants were selected using foreground and background criteria to determine which ones would be used in subsequent backcrosses or selfing** (Agarwal, P., et al., 2022).

Despite of resistance to biotic stress, MABC is also useful for transfer of combined traits of biotic and abiotic. The resultant progeny is tested for NDUS – Novelty, Distinctiveness, Uniformity and Stability (Bellundagi, A., et al., 2018)

MABC is appropriate to transfer multiple genes at a time. In a study, Near Isogenic Lines having genes for resistance to all types of rust such as *Lr*19, *Sr*26 and *Yr*10 are obtained by backcrossing with a parent later followed Marker assisted Selection (MAS) to screen out plants having all genes. It also aids in quick recovery of recurrent parent's genome (Mallick, N., et al., 2015).

Table 2: Varieties having leaf rust resistance (Bhukari, A., et al., 2013)

Varieties	**Year**	**Country/Region**	**Genes**
Lemma Rojo	1964	Mexico	*Lr*13, *Lr*17
Champingo 53	1953	Mexico	Lr*34*
Penjamo 62	1962	Mexico	*Lr*14*a*, *Lr*34
Pitic 62	1962	Mexico	*Lr*14*a*
Sonora 64	1964	Mexico	*Lr*1
Mexipak 65, Kalyansona	1965	India, Pakistan	*Lr*14*a*
Sonalika, Bluesilver	1967, 1971	India, Pakistan	*Lr13*, *Lr*14*a*
Lyalpur 73	1973	Pakistan	*Lr*1, *Lr*13, *Lr*34
Bluebird, Yecora 70	1970s	Mexico, Pakistan	*Lr*1, *Lr*13, *Lr*34
Ciano 79	1979	Mexico	*Lr*16
Arz	1973	Lebnon	*Lr*17

Pavon F 76, Dollarbird	1983, 1987	Mexico, Australia	*Lr*1, *Lr*10, *Lr*13, *Lr*46+
Parula	1981	CIMMYT	Lr*34*, *Lr*46+
Punjab 81	1981	Pakistan	*Lr*10, *Lr*13, *Lr*34
Era	1970	North America	*Lr*10, *Lr*13, *Lr*34

Table 3: Different hosts of stem rust of wheat with their genes and origin (Dilnesaw, et al., 2014)

Differential hosts	***Sr* genes**	**Pedigree/Origin**
LcSr24Ag	**24**	**Little Club/ Agent (CI 13523)**
W2691SrTt-1	**36**	**CI12632 *Trtiticum timopheevii***
ISr7b-Ra	**7b**	**Hope/ Chinese Spring**
ISr8a-Ra	**8a**	**Rieti/Wilhelmina/Akagomughi**
CnSSrTmp	**Tmp**	**Triumph 64(CI 13679)/ Chinese Spring**
Sr31 (Benno)/6*LMPG	**31**	**Kavkaz**
CS_T_mono_deriv	**21**	**Einkorn CI 2433**
RL6081	**38**	**Spear*4/VPM (P1519303)**
ISr9a-Ra	**9a**	**Red Egyptian/ Chinese Spring**
ISr9d-Ra	**9d**	**Hope/ Chinese Spring**
W2691Sr9b	**9b**	**Kenya 117A**
Vernstein	**9e**	**Little Club/3*Gabo/2***
W2691Sr10	**10**	**Marquis*4/Egypt NA95/2/2*W2691**
BtSr30Wst	**30**	**Festival/Uruguay C10837**
CnsSr9g	**9g**	**Selection from Kubanka (CI1516)**
ISr11-Ra	**11**	**Kenya C6402/Pusa4/Dundee**
McNair 701	**McN**	**CI 15288**

Table 4: Different cultivars for identifying stripe rust resistance genes (Bayles, R.A., et al., 2000).

Differential cultivar	**Gene**
Chinese 166	***Yr* 1**
Kalyansona	***Yr* 2**
Vilmorin 23	***Yr* 3**
Nord Desprez	***Yr* 3**
Hybrid 46	***Yr* 4**
Heines Peko	***Yr* 6, *Yr* 2**
Heines Kolben	***Yr* 6, *Yr* 2**
Lee	***Yr* 7**
Reischersberg 42	***Yr* 7+**

Compare	***Yr* 8**
Kavkaz X 4 Federation	***Yr* 9**
Moro	***Yr* 10**
Yr15/6*AvS	***Yr*15**
VPM 1	***Yr* 17**
Carstens V	**CV**
Avocet 'R'	***Yr* A**
Suwon 92 X Omar	**Su**
Strubes Dickkopf	**SD**
Spaldings Prolific	**SPA**

Future prospects:

There are many countries in the world. India stands in second place for the production of wheat. To maintain future food security to outgrowing populations, it is important to produce good quality and sufficient amount of food grains to feed the communities (Chatrath, R., et al.,2007). Use of more Functional Markers (FM) from polymorphic gene strands for identification of rust resistance genes and also for transfer of it makes easier (Appels, R., et al., 2012). Development of more durable plant resistance in all the stages of the plant is challenging for a breeder. It should get intricated using different technologies (Figlan, S., et al., 2020).

Conclusion:

Rust causing effect on leaf, stem and stripes of leaf is common in all the regions of India and world. It is accounting for major yield losses. To compensate yield loss, use of only chemical method makes no sense. With chemicals genetic control such as selecting resistant varieties developed by plant selection method or biotechnological methods gives fruitful conclusions. Also, to meet the demand of people worldwide the production of wheat which was developed is not sufficient. The solution for all such problems comes when both incidence of disease and production of crop gets manageable. To manage that breeder, have to develop resistant varieties, pathologists have to score the new diseases. Biotechnologists have to develop new technologies and agronomists should study the cultural practices that increases maximum yield per unit area.

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