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## CONTENTS

# Gene Stewardship in developing improved Indian bread wheat cultivars and genetic stocks with low terminal disease value-*A compendium –Part-III*: Introgression of Stripe rust resistance genes

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## Introduction

Wheat (*Triticum aestivum* L.) is one of the most important staple cereal crops globally, providing nearly 20% of the calories and protein consumed by the world's population and serving as a primary food source for more than 35% of humanity (Juliana et al., 2017). In India, wheat is the second most important cereal crop after rice and plays a crucial role in national food and nutritional security, particularly in the North Western Plains Zone (NWPZ), Northern Hills Zone (NHZ), and North Eastern Plains Zone (NEPZ). Sustaining wheat productivity under increasing biotic and abiotic stresses remains a major challenge for Indian agriculture.

Among biotic stresses, stripe rust or yellow rust is one of the most destructive diseases of wheat worldwide. Stripe rust is caused by the obligate biotrophic fungus *Puccinia striiformis* f. sp. *tritici* (Pst), which infects leaves and leaf sheaths, forming characteristic yellow-orange pustules arranged in stripes along the veins (Chen, 2005). The pathogen is highly adaptable, capable of long-distance dispersal through airborne urediniospores, rapid multiplication, and continuous evolution of new virulent races, allowing it to overcome host resistance genes (Line, 2002; Chen, 2005). Stripe rust thrives under cool and humid conditions, making the Indian wheat-growing regions—particularly the NHZ and NWPZ—highly vulnerable to epidemics.

Stripe rust poses a serious global threat, with epidemics reported across Asia, Europe, Africa, the Americas, and Australasia, and an estimated 80% of the global wheat area exposed to some level of risk (Chen, 2005). Yield losses typically range from 10–70%, but can reach 90–100% when infection occurs at early growth stages on susceptible cultivars under favorable environmental conditions (Chen, 2005). In India, stripe rust epidemics have repeatedly caused significant yield losses and necessitated the withdrawal of once-popular wheat varieties due to resistance breakdown (Singh et al., 2015; Sharma et al., 2021). The continual emergence of new pathotypes has made stripe rust one of the most persistent constraints to stable wheat production in the country.

Genetic resistance is widely recognized as the most economical, environmentally safe, and sustainable strategy for managing stripe rust compared with chemical control

(Chen, 2005). Resistance genes against stripe rust, designated as *Yr* genes, are broadly classified into seedling resistance or all-stage resistance (ASR) genes and adult plant resistance (APR) genes. ASR genes typically provide race-specific, high-level resistance expressed from the seedling stage, whereas APR genes confer partial, race-nonspecific resistance that becomes effective at later growth stages and is generally more durable (Lupton and Macer, 1962; Chen, 2005). To date, more than 80 formally designated *Yr* genes (*Yr1–Yr86*) and over 300 quantitative trait loci (QTLs) for stripe rust resistance have been reported in wheat and its relatives (Li et al., 2020; Klymiuk et al., 2022).

**Table 1 Catalogue of wheat, rye and triticale resistance genes based on the catalogue of gene symbols for wheat (McIntosh et al. 2003). Genes with available DNA markers are marked with asterisks**

| Wheat | Source | Rye | Chromosomal location |
|---|---|---|---|
| *Yr1* | *T.aestivum* | | 2AL |
| *Yr2* | *T.aestivum* | | 7B |
| *Yr a-c* | *T.aestivum* | | 1B |
| *Yr4a-b* | *T.aestivum* | | 6B |
| *Yr5** | *T.spelta album* | | 2BL |
| *Yr6* | *T.aestivum* | | 7BS |
| *Yr7* | *T.aestivum* | | 2BL |
| *Yr8* | *Aegilops comosa* | | 2D=T2DS-2M#1L.2M#1S |
| *Yr9** | *Secale cereale* | *Yr1* | 1RS.1BL |
| *Yr10** | *T.spelta* | | 1BS |
| *Yr11* | *T.aestivum* | | |
| *Yr12* | *T.aestivum* | | |
| *Yr13* | *T.aestivum* | | |
| *Yr14* | *T.aestivum* | | |
| *Yr15** | *T.dicoccoides* | | 1BS |
| *Yr16* | *T.aestivum* | | 2D |
| *Yr17*+Lr37+Sr38* | *Aegilops ventricosa* | | 2AS |
| *Yr18** | *T.aestivum* | | 7DS |
| *Yr19* | *T.aestivum* | | 5B |

| | | | |
|---|---|---|---|
| *Yr20* | *T.aestivum* | | 6D |
| *Yr21* | *T.aestivum* | | 1B |
| *Yr22* | *T.aestivum* | | 4D |
| *Yr23* | *T.aestivum* | | 6D |
| *Yr24* | *T.aestivum* | | 1BS |
| *Yr25* | *T.aestivum* | | 1D |
| *Yr26** | *Haynaldiavillosa* | | 6AS(6AL.6VS) |
| *Yr27+Lr13* | *T.aestivum* | | 2BS |
| *Yr28** | *T.tauschii* | | 4DS |
| *Yr29+Lr46* | *T.aestivum* | | 1BL |
| *Yr30+Sr2+Lr27* | *T.aestivum* | | 3BS |
| *Yr31* | *T.aestivum* | | 2BS |
| *Yr32* | *T.aestivum* | | 2BS |
| *Yr35+Lr53* | *T.turgidum var. Dicocoides* | | 6BS |
| *Yr37+Lr54* | *Ae.kotschyi* | | 2DL |
| *Yr38+Lr56* | *Ae.sharonensis* | | 6A |
| *Yr40+Lr57* | *Ae.geneculata* | | T5DL.5DS-5M$^{g}$S(0.95), |
| *Yr42+Lr62* | *Ae.negleta* | | T6AS-6AL |
| *Yr48* | *Ae.tauchii* | | 5AL |
| *YrH52*+Yr15* | *T.dicoccoides*<br>*Secale cereale*<br>*Secale cereale*<br>*Secale cereale* | <br>*Yr2*<br>*Yr3*<br>*YrBl* | 1BS<br>2RL<br>6R<br>6R |

In the Indian context, several ASR(All Stage Resistance) genes such as *Yr5*, *Yr10*, *Yr15*, *Yr24/Yr26*, *Yr32*, and *YrSp* remain effective against the most prevalent Pst pathotypes, whereas many widely deployed genes including *Yr2*, *Yr9*, *Yr17*, and *Yr18* have lost effectiveness due to pathogen evolution (Singh et al., 2015; Sharma et al., 2021). Among these, *Yr5*, *Yr10*and *Yr15*are particularly valuable as they continue to confer high levels of resistance across diverse environments and against multiple pathotypes, both in India and globally (Zeng et al., 2015; Wang et

al., 2019). APR genes such as *Yr18* (linked with *Lr34*), *Yr29* (*Lr46*), and *Yr46* contribute to slow-rusting resistance and are used in combination with ASR genes to enhance durability (Reynolds et al., 2009).

In India, the current breeding strategy emphasizes pyramiding of multiple resistance genes with diverse modes of action using marker-assisted selection (MAS), supported by genome-wide association studies (GWAS) and QTL mapping to identify novel resistance sources from Indian germplasm, landraces, and exotic donors (Maccaferri et al., 2015; Wu et al., 2020). Despite these systematic efforts, frequent breakdown of resistance in released varieties highlights gaps in resistance gene diversity and incomplete knowledge of the resistance gene composition of Indian wheat cultivars.

**Table 2 Donor parents in the back-cross programme (*Triticum aestivum*) taken at IARI RS Wellington**

| S.No. | Stock | Gene(s) | Reaction to | | | |
|---|---|---|---|---|---|---|
| | | | **Stem rust** | **Leaf rust** | **Stripe rust** | **Powdery mildew** |
| 1. | WH 542 | *Yr9 Lr26 Sr31 Pm8* | 10R MR | 80S | F | 3 |
| 2. | Moro,<br>WH 542+*Yr10*(BGlm) | *Yr 10* | F | F | F | 0-1 |
| *3.* | *T.dicocoides* G-25 | *Yr 15* | F | F | F | 0-1 |
| 4. | Thatcher*8/VPM 1,<br>RL 6081 | *Yr17 Lr37 Sr38* | 20R MR MS | F | 15MS | 4 |
| 5. | EC 463655 | *Yr 17* | F | 90S | F | 4 |

Although numerous *Yr* genes and QTLs for stripe rust resistance have been identified, the rapid evolution of *Puccinia striiformis* f. sp. *tritici* continues to threaten the durability of resistance in Indian wheat varieties. In their breeding program, the authors have primarily utilized a few highly effective genes, incorporating *Yr10* and *Yr15* in the background of nearly 20hexaploid wheat varieties, often in combination with *Lr19, Lr45*, *Lr47*, *Lr57* and other resistance genes, to develop multiple rust resistance lines with enhanced and durable resistance through gene pyramiding.

**Table 3 Effective Rust resistance genes Used in the Back cross Programme at IARI, Wellington**

| S.No. | Gene | Source | Reference stocks used (RIL's) | Chromosomal location |
|---|---|---|---|---|
| 1. | ***Yr9****+Lr26+Sr31+Pm8* | *Secale cereale (Petkus rye)* | WH 542 (Bacanora) | 1BL1RS |
| 2. | ***Yr10*** | *Triticum aestivum/T.spelta* | Moro, Yr10+WH 542 | 1BS |
| 3. | ***Yr15*** | *T.dicocoides* | *T.dicocoides*G-25 V763-2312 | 1BL |
| 4. | ***Yr16*** | Capelle-Desprez | Capelle-Desprez | 2DS |
| 5. | ***Yr17****+ Lr37+Sr38* | *Ae.ventricosa* | Thatcher*8/VPM 1,RL 6081 | 2AS |
| 6. | ***Yr18****+Lr34+BDV1+ Pm 38+ Sr resistance/Ltn* | *T.aestivum* Terenizo | RL 6058 | 7DS |
| 7. | ***Yr30****+Sr2 +Lr27+ (Pseudo Black Chaff)* | *T.aestivum* | Maden | 3BS |
| 8. | ***Yr35****+Lr53* | *T.turgidum-T.dicocoides* | | 6BS |
| 9. | ***Yr37****+Lr54* | *Aegilops kotschyi* | | 2DL. |
| 10. | ***Yr38****+Lr56* | *Aegilops sharonensis* | | 6A |
| 11. | ***Yr40****+Lr57* | *Ae.geniculata* | | T5DL.5DS-5MgS(0.95), |
| 12. | ***Yr42****+Lr62* | *Ae. neglecta* | | |

### *Yr5*

*Yr5* is a highly effective seedling (all-stage) resistance gene originally derived from *Triticum spelta* var. *album* and located on chromosome **2BL**. It confers strong, race-specific resistance to stripe rust and has remained effective against a wide range of *Puccinia striiformis* f. sp. *tritici* (Pst) races globally, including in China, the USA, and parts of Europe (Chen, 2005; Zeng et al., 2015). In India, *Yr5* continues to be effective against all major prevailing pathotypes and is considered one of the most reliable ASR genes currently available (Singh et al., 2015; Sharma et al., 2021). However, virulence to *Yr5* has been reported in limited regions outside India (e.g., the TAS-6 race, China), emphasizing the need for pyramiding with other genes to ensure durability (Zhang et al., 2020).

### *Yr9*

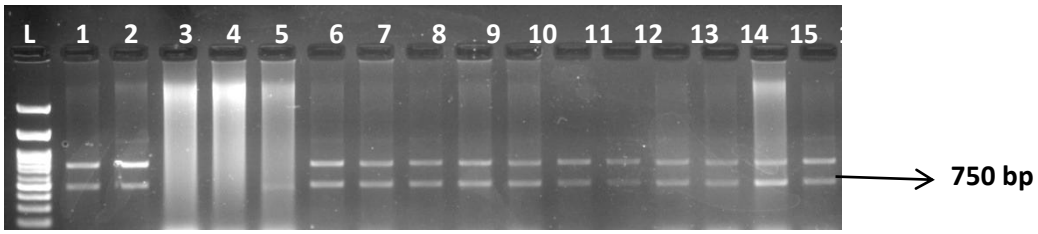
*Yr9* was introgressed into wheat from rye (*Secale cereale*) as part of the 1BL·1RS translocation. It is located on chromosome **1BL** and was widely deployed during the Green Revolution due to its strong seedling resistance (Chen, 2005). However, *Yr9* has been rendered ineffective globally following the emergence of virulent Pst races, since the 1990s (Line, 2002). In India, *Yr9* is completely susceptible to current stripe rust pathotypes(78S84 & other pathotypes

110S119, 238S119, 110S84) and is no longer recommended for resistance breeding (Singh et al., 2015). Its widespread breakdown highlights the risks associated with extensive deployment of single major resistance genes.

### *Yr10*

*Yr10* is a seedling resistance gene derived from bread/Spelt wheat and mapped to chromosome **1BS**. It provides high levels of race-specific resistance at early growth stages and has been widely deployed in breeding programs (Chen, 2005). Globally, *Yr10* remains effective against several Pst races but has been overcome in some regions due to pathogen evolution (Wang et al., 2019). In India, *Yr10* is still effective against most prevalent stripe rust pathotypes and is frequently used in combination with other resistance genes (Singh et al., 2015). The authors successfully introgressed the stripe rust resistance gene *Yr10* into the genetic background of recently released bread wheat varieties, including HD 3086, HD 3090, HD 3059, and WH 1124, which are specifically adapted to the North Western Plains Zone (NWPZ) of India, where stripe rust poses a major threat to wheat production. In addition, *Yr10* was pyramided with other leaf and stem rust resistance genes to develop multiple-rust-resistant genetic stocks. A total of approximately 65 breeding lines carrying *Yr10* in combination with *Lr19+*,*Lr45*, *Lr47*, and *Lr57* were developed, providing valuable resources for enhancing durable rust resistance in Indian wheat breeding programs.

**Molecular Confirmation of *Yr10* gene using *E1* marker**



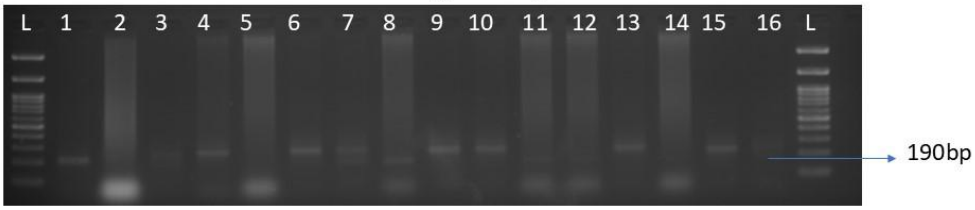

L:100bp ladder, Lane 1:MORO (positive control), , Lane 2:WH 542/*Yr10*(positive control), , 3- COW(W)-1(Negative control), 4-16: HD 3068//*Yr10*introgressed lines

The *E1* molecular marker is a tightly linked, PCR-based marker used for the detection of the stripe rust resistance gene *Yr10* in wheat. The *E1* marker employs primers that amplify a ~750 bp diagnostic fragment in genotypes carrying *Yr10*, while no amplification is observed in susceptible lines (William et al., 2003). Due to its clear banding pattern, strong linkage with *Yr10*, and ease of amplification, the E1 marker has been widely adopted in marker-assisted selection (MAS) and gene pyramiding strategies, including Indian wheat breeding programs targeting durable stripe rust resistance (Prasad et al., 2009; Randhawa et al., 2018).

### *Yr15*

*Yr15* is one of the most important stripe rust resistance genes, originating from wild emmer wheat (*Triticum dicoccoides*) and located on chromosome 1BS. It confers strong, broad-spectrum resistance across all growth stages and has remained effective against nearly all known *Pst*races worldwide (Klymiuk et al., 2022). In India, *Yr15* shows complete resistance to all currently prevalent pathotypes and is considered a cornerstone gene for stripe rust resistance breeding (Singh et al., 2015; Sharma et al., 2021). Its durability and broad effectiveness make it a preferred donor in Indian breeding programs, especially for pyramiding with APR genes.The authors have developed nearly 30 backcross inbred lines (BILs) carrying the stripe rust resistance gene *Yr15*, either alone or in combination with stem rust (*Sr36*) and powdery mildew (*Pm6*) resistance genes, providing valuable multi-disease-resistant germplasm for wheat breeding programs. The presence of *Yr15* in these lines was confirmed using the *Xbarc8* molecular marker, which amplifies a 190 bp fragment in resistant genotypes and a 230 bp fragment in susceptible genotypes, facilitating rapid and reliable selection in breeding populations (Lillemo et al., 2008).

**Molecular marker confirmation of *Yr15* gene using Xbarc8 marker**




L:100bp ladder, Lane 1: COW(W)-1(Negative control), Lane 2- 15: HD 3059//*Yr15* introgressed lines, Lane 16: *Yr15* Donor(positive control),

### *Yr17*

*Yr17* is another rye-derived resistance gene associated with the 2NS/2AS translocation from *Aegilops ventricosa*, located on chromosome **2AS**. It is tightly linked to *Lr37* and *Sr38* genes. It provides seedling resistance and was widely used in European and Asian wheat cultivars (Chen, 2005). Globally, virulence to *Yr17* is now common, leading to loss of effectiveness in many regions (Zeng et al., 2015). In India, *Yr17* has become ineffective against most prevalent Pst pathotypes and is considered susceptible (Sharma et al., 2021). Its breakdown emphasizes the need for diversification of resistance sources.

### *Yr18*

*Yr18* is an adult plant resistance (APR) gene located on chromosome **7DS** and is pleiotropically associated with *Lr34* and *Pm38*. Unlike ASR genes, *Yr18* confers partial, race-nonspecific, slow-rusting resistance that is durable across environments (Reynolds et al., 2009). Globally, *Yr18* has shown long-term effectiveness, although its resistance level is moderate and insufficient alone (Sadras and Lawson, 2013). In India, *Yr18*contributes to durable resistance when

combined with effective ASR genes, but by itself it does not provide adequate protection under high disease pressure (Singh et al., 2015). The authors developed several backcross-derived lines using recurrent parents that already possessed adult plant resistance genes. Notably, cultivars such as HD 2967, HD 2733, HD 2189, PBW 343, and NIAW 34 carry the ***Lr34 + Yr18*** gene complex.

### *Yr24*

*Yr24* and *Yr26* are closely linked or allelic seedling resistance genes located on chromosome **1BL**, derived from common wheat. These genes have been widely deployed in Asian wheat breeding programs due to their strong race-specific resistance at early growth stages (Chen, 2005). Globally, virulence to *Yr24/Yr26* has been reported, particularly in China and neighbouring regions, reducing their effectiveness in some environments (Zeng et al., 2015; Wang et al., 2019). In contrast, in India, *Yr24/Yr26* remain effective against most prevalent Pst pathotypes and continue to be important components of resistance breeding programs, although their race-specific nature necessitates pyramiding with other genes for durability (Singh et al., 2015; Sharma et al., 2021).

### *Yr25*

*Yr25* is an alien introgression derived from *Thinopyrum ponticum* and mapped to chromosome **7DL**. It provides strong seedling resistance and has demonstrated broad effectiveness against diverse Pst races across environments (Chen, 2005; Li et al., 2020). Despite its effectiveness, the utilization of *Yr25* in breeding programs has been limited due to linkage drag and associated agronomic penalties. In the Indian context, *Yr25* remains effective against stripe rust but is primarily exploited as a donor gene in pre-breeding and resistance introgression programs rather than in direct varietal release (Singh et al., 2015).

### *Yr29*

*Yr29* is another APR gene, closely linked with *Lr46*, and mapped to chromosome **1BL**. It provides partial, race-nonspecific resistance and contributes to slow rusting at the adult plant stage (William et al., 2006). Globally, *Yr29* has been shown to enhance resistance durability when pyramided with major genes (Foulkes et al., 2011). In Indian wheat, *Yr29* alone is insufficient for complete protection but plays an important supporting role in resistance gene combinations deployed through ICAR breeding programs (Sharma et al., 2021).Several recurrent parents used in the backcross program carried the adult plant resistance gene *Lr46*, which is genetically linked with *Yr29*. Cultivars such as HD 3086, WH 1105are known sources of this gene complex. The inclusion of *Lr46* in the recurrent parent background was aimed at conferring slow-rusting, race-non-specific resistance, leading to reduced disease progression and enhanced durability of resistance against both leaf rust and stripe rust across environments.

### *Yr30*

*Yr30* is an adult plant resistance gene tightly linked to *Sr2*, located on chromosome **3BS**. It provides partial, race-nonspecific resistance and contributes to slow rusting. Globally, *Yr30* has shown moderate effectiveness and durability

when combined with other resistance genes (Reynolds et al., 2009). In India, *Yr30* is considered a supportive APR gene and is mainly effective as part of multi-gene pyramids rather than as a standalone source of resistance (Sharma et al., 2021).The adult plant resistance gene ***Yr30*** is frequently associated with ***Sr2***, a linked stripe rust resistance gene that together form an important component of durable, race-non-specific resistance. Both older cultivars such as Sonalika, and Kalyansona, and several modern, high-yielding varieties including HD 2967, HD 3086 and PBW 343 are known to carry the *Sr2–Yr30* linkage. In the present backcrossing program, recurrent parents possessing this gene combination were deliberately selected to facilitate the introgression and accumulation of adult plant resistance against both stem rust and stripe rust. The *Sr2–Yr30* complex confers partial but stable resistance, often expressed at later growth stages, and contributes to the well-known "Sr2 complex," which enhances durability and long-term effectiveness when pyramided with other APR genes such as *Lr34/Yr18*, *Lr46/Yr29*, and *Lr67/Yr46* across diverse agro-climatic conditions.

### *Yr35*

*Yr35* is a major seedling resistance gene introgressed from wild emmer wheat (*Triticum dicoccoides*) and mapped to chromosome **6BS**. It confers high levels of race-specific resistance and has shown effectiveness against a wide range of Pst races globally (Klymiuk et al., 2022; Li et al., 2020). In India, *Yr35* is considered effective against prevailing stripe rust pathotypes, although its deployment has been more limited compared to widely used genes such as *Yr5* and *Yr15*. Nevertheless, *Yr35* is increasingly recognized as a valuable source of novel resistance for gene pyramiding strategies aimed at broadening the resistance base (Singh et al., 2015).

### *Yr40*

*Yr40* is a major stripe rust resistance gene linked with *Lr57*, introgressed from *Aegilops geniculata* and located on chromosome 4AL. Unlike typical adult plant resistance genes, *Yr40* confers a high level of race-specific resistance, particularly effective at seedling and early growth stages, though its effectiveness may vary with pathogen virulence. While Yr40 alone may not provide durable protection under high disease pressure, it has shown moderate to stable effectiveness when deployed in combination with adult plant resistance genes, thereby contributing to enhanced resistance durability (Chen, 2005; Reynolds et al., 2009). In the Indian context, reliance on *Yr40* as a single gene is insufficient due to the prevalence of diverse and evolving rust races; however, its inclusion in gene pyramiding strategies, together with APR genes such as *Yr18*, *Yr29*, *Yr30*, and *Yr46*, is considered valuable for strengthening resistance and reducing the risk of resistance breakdown (Sharma et al., 2021).

### *Yr46*

*Yr46* is an APR gene located on chromosome **1BL** and is associated with *Lr67*. It confers partial, non-race-specific resistance to stripe rust and other foliar diseases (Herrera-Foessel et al., 2014). Globally, *Yr46* is valued for its durability and contribution to broad-spectrum

resistance. In India, *Yr46* is increasingly recognized as an important component of resistance pyramids, particularly in combination with strong ASR genes such as *Yr5* and *Yr15* (Singh et al., 2015). The authors employed recurrent parents arbouring the pleiotropic adult plant resistance gene *Lr67*, associated with *Yr46* in the backcrossing program. The strategic use of *Lr67* was intended to impart partial yet durable resistance, contributing to broad-spectrum protection against multiple rust pathogens and improving the long-term stability of resistance when combined with other APR genes.

**Conclusion**

However, the available evidence demonstrates that seedling (all-stage) resistance genes such as ***Yr10*** and ***Yr15***continue to provide high and stable resistance to stripe rust under Indian conditions, whereas formerly widely deployed genes including ***Yr9*** and ***Yr17*** have become largely ineffective due to the emergence of virulent *Puccinia striiformis* f. sp. *Tritici* pathotypes (Singh et al., 2015; Zeng et al., 2015; Sharma et al., 2021). In contrast, adult plant resistance (APR) genes such as ***Yr18, Yr29, Yr30*** **and*Yr46*** confer partial, race-nonspecific resistance that enhances durability but is insufficient when deployed individually. Consequently, the pyramiding of effective ASR genes with complementary APR genes has emerged as a key strategy for achieving stable and long-lasting stripe rust resistance in Indian wheat breeding programs (Reynolds et al., 2009; Foulkes et al., 2011; Sharma et al., 2021).

| **Table 4: List of rust resistant lines developed carrying stripe rust resistance genes- *Yr9+, Yr10, Yr15*and *Yr17*** | | | |
|---|---|---|---|
| **S.No.** | **PEDIGREE** | **Genes introgressed** | **HW Number assigned** |
| | | ***Lr24+Sr24, Sr31+Yr9*** | |
| 1. | HD 2402*2/Tr380-14//WH 542 | *Lr24+Sr24, Sr31+Yr9* | HW 2075 |
| 2. | HD 2402*2/Tr380-14//WH 542 | *Lr24+Sr24, Sr31+Yr9* | HW 2075-1 |
| 3. | PBW 226*2/Tr380-14//*Sr31+* | *Lr24+Sr24, Sr31+Yr9* | HW 2076 |
| | | ***Lr24+Sr24,Sr26,Sr31+,Sr36+,Yr15*** | |
| 4. | HW 3094*4//HW 2436-2 | *Lr24+Sr24,Sr26,Sr31+Yr9,Sr36+,Yr15* | HW 4459 |
| 5. | HW 3094*4//HW 2436-2 | *Lr24+Sr24,Sr26, Sr31+Yr9,Sr36+,Yr15* | HW 4459-1 |
| 6. | HW 3094*4//HW 2436-2 | *Lr24+Sr24,Sr26, Sr31+Yr9,Sr36+,Yr15* | HW 4459-2 |
| 7. | HW 3094*4//HW 2436-2 | *Lr24+Sr24,Sr26, Sr31+Yr9,Sr36+,Yr15* | HW 4459-3 |
| | | ***Lr19+Sr25,Sr36+Pm6,Yr10*** | |
| 8. | HD 2687*4/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1933 |
| 9. | HD 2687*4/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1933-1 |
| 10. | HD 2687*4/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1933-2 |
| 11. | HD 2687*4/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1933-3 |
| 12. | HD 2687*3/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1933-4 |
| 13. | HD 2687*3/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1933-5 |
| 14. | *Yr10*2/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1934 |
| 15. | HD 2967*3/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1935 |
| 16. | HD 2967*3/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1935-1 |
| 17. | DBW 39*3/Wheatear//HW 4444 | *Lr19+Sr25,Sr36+Pm6,Yr10* | HW 1936 |
| 18. | *Yr10*2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931 |
| 19. | *Yr10*2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-1 |
| 20. | *Yr10*2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-2 |
| 21. | *Yr10*2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-3 |
| 22. | *Yr10*2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-4 |
| 23. | *Yr10*2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-5 |
| 24. | *Yr10*2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-6 |

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| 25. | *Yr10**2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-7 |
| 26. | *Yr10**2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-8 |
| 27. | *Yr10**2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-9 |
| 28. | *Yr10**2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-10 |
| 29. | *Yr10**2//Wheatear | *Yr10,Lr19+Sr25* | HW 1931-11 |
| ***Lr19+Sr25,Yr10,Sr36+Pm6*** | | | |
| 30. | HD 2687*3/Wheatear//HW 4444 | *Lr19+Sr25,Yr10,Sr36+Pm6* | HW 1933-6 |
| 31. | HD 2687*3/Wheatear//HW 4444 | *Lr19+Sr25,Yr10,Sr36+Pm6* | HW 1933-7 |
| 32. | HD 2687*3/Wheatear//HW 4444 | *Lr19+Sr25,Yr10,Sr36+Pm6* | HW 1933-8 |
| 33. | HD 3059* 4/*Yr10*// HD 2687/*WLr19*/HW 4444 | *Lr19+Sr25,Yr10,Sr36+Pm6* | HW 1939 |
| 34. | HD 3059* 4/*Yr10*// HD 2687/*WLr19*/HW 4444 | *Lr19+Sr25,Yr10,Sr36+Pm6* | HW 1939-1 |
| 35. | HD 3059* 4/*Yr10*// HD 2687/*WLr19*/HW 4444 | *Lr19+Sr25,Yr10,Sr36+Pm6* | HW 1939-2 |
| 36. | HD 3086*4/*Yr10*// HD 2687/*WLr19,Sr36,Yr10* | *Lr19+Sr25,Yr10,Sr36+Pm6* | HW 1939-3 |
| 37. | *HD 3086*4/Yr10// HD 2687/WLr19,Sr36, Yr10* | *Lr19+Sr25,Yr10,Sr36+Pm6* | HW 1939-4 |
| 38. | HUW 234*2/CLr19//*Yr10* | *Yr10* | **HW 4444*** |
| 39. | HD 3086*3//*Yr10* | *Yr10* | HW6001 |
| 40. | HD 3059*3//*Yr10* | *Yr10* | HW 6002 |
| 41. | HD 3090*3//*Yr10* | *Yr10* | HW 6003 |
| 42. | WH 1124*3//*Yr10* | *Yr10* | HW 6004 |
| 43. | HD 3086*3//*Yr15* | *Yr15* | HW 6005 |
| 44. | HD 3059*3//*Yr15* | *Yr15* | HW 6006 |
| 45. | HD 3090*3//*Yr15* | *Yr15* | HW 6007 |
| ***Lr19+Sr25,Sr36+Pm6,Sr31+Yr9,Yr10*** | | | |
| 46. | HD 2285*3/HW 3619/HW 4444//HW 5555 | *Lr19+Sr25,Sr36+Pm6, Sr31+Yr9,Yr10* | HW 1943 |
| 47. | HD 2285*3/HW 3619/HW 4444//HW 5555 | *Lr19+Sr25,Sr36+Pm6, Sr31+Yr9,Yr10* | HW 1943-1 |
| 48. | HD 2285*3/HW 3619/HW 4444//HW 5555 | *Lr19+Sr25,Sr36+Pm6, Sr31+Yr9,Yr10* | HW 1943-2 |
| 49. | HD 2285*3/HW 3619/HW 4444//HW 5555 | *Lr19+Sr25,Sr36+Pm6, Sr31+Yr9,Yr10* | HW 1943-3 |
| 50. | HD 2285*3/HW 3619/HW 4444//HW 5555 | *Lr19+Sr25,Sr36+Pm6, Sr31+Yr9,Yr10* | HW 1943-4 |
| 51. | HD 2285*3/HW 3619/HW 4444//HW 5555 | *Lr19+Sr25,Sr36+Pm6, Sr31+Yr9,Yr10* | HW 1943-5 |

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| 52. | HD 2285*3/HW 3619/HW 4444//HW 5555 | *Lr19+Sr25,Sr36+Pm6, Sr31+Yr9,Yr10* | HW 1943-6 |
| | | ***Yr15,Lr19/Sr25, Sr36/Pm6*** | |
| 53. | *Yr15**2/Wheatear//COOK | *Yr15,Lr19/Sr25, Sr36/Pm6* | HW 1944 |
| 54. | *Yr15**2/Wheatear//COOK | *Yr15,Lr19/Sr25, Sr36/Pm6* | HW 1944-1 |
| 55. | *Yr15**2/Wheatear//COOK | *Yr15,Lr19/Sr25, Sr36/Pm6* | HW 1944-2 |
| 56. | *Yr15**2/Wheatear//COOK | *Yr15,Lr19/Sr25, Sr36/Pm6* | HW 1944-3 |
| 57. | *Yr15**2/Wheatear//COOK | *Yr15,Lr19/Sr25, Sr36/Pm6* | HW 1944-4 |
| 58. | HD 3086*4/*Yr15//Lr19,Sr36, Pm6* | *Yr15, Lr19/Sr25, Sr36/Pm6* | HW 1945 |
| 59. | HD 3086*4/*Yr15//Lr19,Sr36, Pm6* | *Yr15, Lr19/Sr25, Sr36/Pm6* | HW 1945-1 |
| 60. | HD 3086*4/*Yr15//Lr19,Sr36, Pm6* | *Yr15, Lr19/Sr25, Sr36/Pm6* | HW 1945-2 |
| 61. | HD 3086*4/*Yr15//Lr19,Sr36, Pm6* | *Yr15, Lr19/Sr25, Sr36/Pm6* | HW 1945-3 |
| 62. | HD 3086*4/*Yr15//Lr19,Sr36, Pm6* | *Yr15, Lr19/Sr25, Sr36/Pm6* | HW 1945-4 |
| 63. | HD 3086*4/*Yr15//Lr19,Sr36, Pm6* | *Yr15, Lr19/Sr25, Sr36/Pm6* | HW 1945-5 |
| 64. | HD 3086*4/*Yr15//Lr19,Sr36, Pm6* | *Yr15, Lr19/Sr25, Sr36/Pm6* | HW 1945-6 |
| | | ***Lr37+Yr17*** | |
| 65. | HD 2285*2// RL 6081 | *Lr37+Yr17* | HW 4022 |
| 66. | HD 2687*2//RL 6081 (VPML) | *Lr37+Yr17* | HW 4033 |
| 67. | LOK-1*3/VPML | *Lr37+Yr17* | HW 4026 |
| 68. | LOK-1*3/VPML | *Lr37+Yr17* | HW 4026-1 |
| 69. | PBN 51*2//RL 6081 | *Lr37+Yr17* | HW 4035 |
| 70. | PBW 226*2//RL 6081 | *Lr37+Yr17* | HW 4028 |
| 71. | SONALIKA*2//RL 6081 | *Lr37+Yr17* | HW 4029 |
| 72. | WH 147*2// VPML | *Lr37+Yr17* | HW 4030 |
| 73. | WH 542*2//RL 6081 | *Lr37+Yr17* | HW 4031 |
| 74. | PBW 343*3//HW 4031 | *Lr37+Yr17* | HW 4038 |
| 75. | DBW 39*3//HW 4031 | *Lr37+Yr17* | HW 4039 |
| 76. | HD 2733*3//HW 4031 | *Lr37+Yr17* | HW 4040 |
| 77. | HW 2045*3//HW 4031 | *Lr37+Yr17* | HW 4041 |
| 78. | HD 2967*3//HW 4031 | *Lr37+Yr17* | HW 4042 |

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| | | ***Lr37+, Sr31+*** | |
| 79. | PBW 343*4//HD 2733/*Lr37* | *Lr37+Yr17, Sr31+Yr9+* | HW 4067 |
| 80. | PBW 343*4//HD 2733/*Lr37* | *Lr37+Yr17 ,Sr31+Yr9+* | HW 4067-1 |
| | | ***Lr37+ Sr31+, Sr24+Lr24, Sr36+Pm6,Yr10*** | |
| 81. | DBW 39*3/WH 542/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24+Lr24, Sr36+Pm6,Yr10* | HW 4068 |
| 82. | DBW 39*3/WH 542/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24+Lr24, Sr36+Pm6,Yr10* | HW 4068-1 |
| 83. | DBW 39*3/WH 542/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr0* | HW 4068-2 |
| 84. | HD 2733*2/WH 542/*Lr37*//HD 2733/*Sr36* | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr0* | HW 4069 |
| 85. | HD 2733*2/WH 542/*Lr37*//HD 2733/*Sr36* | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4069-1 |
| 86. | HD 2733*2/WH 542/*Lr37*//HD 2733/*Sr36* | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4069-2 |
| 87. | HW 2045*4/PBW 226/*Lr37*// HW 2436-2 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4070 |
| 88. | HW 2045*4/PBW 226/*Lr37*// HW 2436-2 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4070-1 |
| 89. | HW 2045*4/PBW 226/*Lr37*// HW 2436-2 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4070-2 |
| 90. | HW 2045*4/PBW 226/*Lr37*// HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4071 |
| 91. | HW 2045*4/PBW 226/*Lr37*// HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4071-1 |
| 92. | HW 2045*4/PBW 226/*Lr37*// HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4071-2 |
| 93. | PBW 343*4//HD 2733/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4072 |
| 94. | PBW 343*4//HD 2733/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4072-1 |
| 95. | PBW 343*4//HD 2733/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4072-2 |
| 96. | PBW 343*4//HD 2733/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4072-3 |
| 97. | HD 2967*4/WH 542/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4073 |
| 98. | HD 2967*4/WH 542/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24/Lr24, Sr36/Pm6,Yr10* | HW 4073-1 |
| 99. | HD 2967*4/WH 542/*Lr37*//HW 2436-4 | *Lr37+Yr17, Sr31+Yr9+, Sr24+Lr24, Sr36+Pm6,Yr10* | HW 4073-2 |
| | | *Lr45, Sr36+Pm6,Yr10* | |
| 100. | HD 2329*/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3641 |
| 101. | HD 2329*/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3641-1 |
| 102. | HD 2329*/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3641-2 |
| 103. | HD 2329*/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3641-3 |

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| 104. | HD2402*2/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3642 |
| 105. | HD2402*2/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3642-1 |
| 106. | HD2402*2/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3642-2 |
| 107. | HD 2687*3/RL6144///HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3643 |
| 108. | HD 2877*2/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3645 |
| 109. | HD 2877*2/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3645-1 |
| 110. | KALYANSONA*2/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3652 |
| 111. | KALYANSONA*2/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3652-1 |
| 112. | KALYANSONA*2/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3652-2 |
| 113. | KALYANSONA*2/RL 6144//HW 4444 | *Lr45, Sr36+Pm6,Yr10* | HW 3652-3 |
| 114. | LOK-1*3/RL 6144//HW 4444 | *Lr45,Yr10,Sr36+Pm6* | HW 3654 |
| 115. | LOK-1*3/RL 6144//HW 4444 | *Lr45,Yr10,Sr36+Pm6* | HW 3654-1 |
| 116. | MACS 2496*2/RL 6144//HW 4444 | *Lr45,Sr36+Pm6,Yr10* | HW 3655 |
| 117. | MACS 2496*2/RL 6144//HW 4444 | *Lr45,Sr36+Pm6,Yr10* | HW 3655-1 |
| 118. | NIAW 34*2/RL 6144//HW 4444 | *Lr45,Sr36+Pm6, Yr10* | HW 3657 |
| 119. | PBN 51*3/RL 6144//HW 4444 | *Lr45, Sr36+Pm6, Yr10* | HW 3658 |
| 120. | PBN 51*3/RL 6144//HW 4444 | *Lr45, Sr36+Pm6, Yr10* | HW 3658-1 |
| 121. | PBN 51*3/RL 6144//HW 4444 | *Lr45, Sr36+Pm6, Yr10* | HW 3658-2 |
| 122. | PBN 51*3/RL 6144//HW 4444 | *Lr45, Sr36+Pm6, Yr10* | HW 3658-3 |
| 123. | PBW 226*2/RL 6144//HW 4444 | *Lr45,Sr36+Pm6, Yr10* | HW 3659 |
| 124. | PBW 502*2/RL 6144//HW 4444 | *Lr45,Sr36+Pm6, Yr10* | HW 3661 |
| 125. | PBW 343*3/RL 6144//HW 4444 | *Lr45,Sr36+Pm6,Yr10* | HW 3660 |
| 126. | PBW 343*3/RL 6144//HW 4444 | *Lr45,Sr36+Pm6,Yr10* | HW 3661 |
| 127. | PBW 343*3/RL 6144/COOK//Yr10 | *Lr45,Sr36+Pm6,Yr10* | HW 3662 |
| 128. | RAJ 3077*3/RL 6144//HW 4444 | *Lr45,Sr36+Pm6, Yr10* | HW 3662 |
| 129. | UP 2338*2/RL 6144//HW 4444 | *Lr45,Sr36+Pm6,Yr10* | HW 3663 |
| 130. | HD 2967*2/RL 6144//HW 4444 | *Lr45,Sr36+Pm6,Yr10* | HW 3702 |
| 131. | HD 2877*3/RL 6144//HW 4444 | *Lr45,Sr36+Pm6,Yr10* | HW 3645 |
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| | | ***Lr45,Yr10*** | |
| 132. | LOK-1*2/RL6144//Yr10 | *Lr45,Yr10* | HW 3705 |
| 133. | LOK-1*2/RL6144//Yr10 | *Lr45,Yr10* | HW 3705-1 |
| 134. | PBW 343*2/Pavon7S 3//HW 4444 | *Lr47,Sr36+Pm6,Yr10* | HW 4735 |
| 135. | PBW 343*2/Pavon7S 3//HW 4444 | *Lr47,Sr36+Pm6,Yr10* | HW 4735-1 |
| 136. | HD 2967*2/Pavon 7S 3//HW 4444 | *Lr47,Sr36+Pm6,Yr10* | HW 4736 |
| 137. | HD 3086*4//Yr10, Lr47, Sr36 | *Lr47,Sr36+Pm6,Yr10* | HW 4737 |
| | | ***Lr47,Yr10*** | |
| 138. | HD 3090*4/Yr10// HD 2687/Lr47 | *Lr47,Yr10* | HW 4738 |
| 139. | HD 3086*4//Yr10, Lr47 | *Lr47,Yr10* | HW 4739 |
| 140. | HD 3086*4//Yr10, Lr47 | *Lr47,Yr10* | HW 4739-1 |
| | | ***Lr47,Yr15,Sr36+Pm6*** | |
| 141. | WH 1124*4/Yr15//HD 2687/*Lr47, Sr 36* | *Lr47,Yr15,Sr36+Pm6* | HW 4740 |
| 142. | WH 1124*4/Yr15//HD 2687/*Lr47, Sr 36* | *Lr47,Yr15,Sr36+Pm6* | HW 4740-1 |
| 143. | WH 1124*4/Yr15//HD 2687/*Lr47, Sr 36* | *Lr47,Yr15,Sr36+Pm6* | HW 4740-2 |
| 144. | WH 1124*4/Yr15//HD 2687/*Lr47, Sr 36* | *Lr47,Yr15,Sr36+Pm6* | HW 4741 |
| 145. | WH 1124*4/Yr15//HD 2687/*Lr47, Sr 36* | *Lr47,Yr15,Sr36+Pm6* | HW 4741-1 |
| 146. | WH 1124*4/Yr15//HD 2687/*Lr47, Sr 36* | *Lr47,Yr15,Sr36+Pm6* | HW 4741-2 |
| | | ***Lr57/Yr40,Sr36+Pm6,Yr10*** | |
| 147. | HD 3086*4/Lr57//HW 2436-2 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5734 |
| 148. | HD 3086*4/Lr57//HW 2436-2 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5734-1 |
| 149. | HD 3086*4/*Lr57*//HW 2436-2 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5734-2 |
| 150. | HD 3086*4/*Lr57*//HW 2436-2 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5734-3 |
| 151. | HD 3086*4/*Lr57*//HW 2436-2 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5734 -4 |
| 152. | HD 3086*4/*Lr57*//HW 2436-2 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5734 -5 |
| 153. | HD 3086*4/*Lr57*//HW 2436-2 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5734-6 |
| 154. | HD 3086*4/*Lr57*//HW 2436-2 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5734 -7 |
| 155. | HD 2687*4/*Lr57*//HW 2436-4 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5735 |
| 156. | HD 2687*4/*Lr57*//HW 2436-4 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5735 -1 |

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| 157. | HD 2687*4/*Lr57*//HW 2436-4 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5735 -2 |
| 158. | HD 2687*4/*Lr57*//HW 2436-4 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5735 -3 |
| 159. | HD 2967*3/*Lr57*//HW 2436-4 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5736 |
| 160. | HD 2967*3/*Lr57*//HW 2436-4 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5736-1 |
| 161. | HD 2967*3/*Lr57*//HW 2436-4 | *Lr57/Yr40,Sr36+Pm6,Yr10* | HW 5736-2 |
| | | ***Sr36+Pm6, Yr15*** | |
| 162. | MACS 2496*2/COOK//*Yr15* | *Sr36+Pm6, Yr15* | HW 4455 |
| 163. | NI 5439*2/COOK//*Yr15* | *Sr36+Pm6,Yr15* | HW 4456 |
| 164. | NI 5439*2/COOK//*Yr15* | *Sr36+Pm6,Yr15* | HW 4456-1 |
| 165. | NI 5439*2/COOK//*Yr15* | *Sr36+Pm6,Yr15* | HW 4456-2 |
| 166. | NI 5439*2/COOK//*Yr15* | *Sr36+Pm6,Yr15* | HW 4456-3 |
| 167. | *Yr15**2//COOK | *Sr36+Pm6,Yr15* | HW 3634 |
| 168. | *Yr15**2//COOK | *Sr36+Pm6,Yr15* | HW 3634-1 |
| 169. | *Yr15**2//COOK | *Sr36+Pm6,Yr15* | HW 3634-2 |
| 170. | *Yr15**2//COOK | *Sr36+Pm6,Yr15* | HW 3634-3 |
| | | ***Sr36+Pm6,Yr10*** | |
| 171. | HD 2967*2/*Yr10*//HW 4444 | *Sr36+Pm6,Yr10* | HW 4457 |
| 172. | HD 2967*2/*Yr10*//HW 4444 | *Sr36+Pm6,Yr10* | HW 4457-1 |
| | | ***Yr15,Yr10, Sr36/Pm6*** | |
| 173. | HD 3086*4/*Yr15*//HW 2436-4 | *Yr15,Yr10, Sr36/Pm6* | HW 4458 |
| 174. | HD 3086*4/*Yr15*//HW 2436-4 | *Yr15,Yr10, Sr36/Pm6* | HW 4458-1 |

***HW4444 used as donor**

# DUS Characterization of Indian Released Varieties Using Agro-Morphological Descriptors

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**Abstract**

This study evaluated the extent of agro-morphological diversity among released Indian wheat varieties and elucidated phenotypic relationships using multivariate graphical analyses. A total of 428 wheat cultivars released between 1961 and 2018 for six major agro-climatic wheat-growing regions of India were characterized for Distinctness, Uniformity, and Stability (DUS) traits using 35 standardized descriptors encompassing seedling, vegetative, stem and reproductive stages. Considerable phenotypic(qualitative) variation was observed across most traits, confirming the effectiveness of morphological descriptors as the primary basis for DUS testing and varietal discrimination worldwide (UPOV, 2019). Traits such as waxiness of plant parts, plant height, and growth habit emerged as major contributors to phenotypic differentiation and genetic diversity. The comprehensive dataset generated through this study provides a robust reference for varietal identification and protection under the PPV&FRA framework and offers valuable insights for agro-morphological evaluation, core collection development, and the effective utilization of Indian wheat germplasm in breeding programmes.

Keywords: DUS characterization, morphological descriptors, Indian released varieties, PPV&FRA, varietal identification

**Introduction**

India remains the world's second-largest wheat producer and consumer, trailing only China, thanks to steady gains in yield and cultivation area. Wheat, as a nutritional powerhouse, emerged as a key driver of this transformation, ensuring caloric adequacy while addressing broader nutritional needs across the region (Kashyap, 2024).According to the Second Advance Estimates for 2024–25 released by the Ministry of Agriculture and Farmers' Welfare, the country's wheat output is projected to reach around 115 million metric tons, marking a new record and an increase over the previous year's production levels. The government is also targeting higher output for the 2025–26 Rabi season, with aims of around 119 million metric tons to meet rising demand. Despite these achievements, enhancing and sustaining productivity is vital to meet the nutritional needs of India's burgeoning population. By 2050, the country's wheat requirement is expected to exceed 140 million metric tons to feed an estimated 1.64 billion people. (Bhardwaj et al., 2019; Mottaleb et al., 2023).

Wheat (*Triticum aestivum* L.) is a principal staple crop in India and a critical component of national food and nutritional security. India ranks second globally in wheat production, supported by sustained varietal improvement and expansion across diverse agro-climatic regions. The country's wheat cultivation spans five major agro-climatic zones namely the North Western Plains Zone, North Eastern Plains Zone, Central Zone, Peninsular Zone, and Northern Hills Zone each characterized by distinct temperature regimes abiotic and biotic stress pressures. These diverse environments have strongly influenced breeding objectives

and driven the development of region-specific wheat varieties with tailored adaptation (Bhardwaj et al., 2019; IIWBR, 2023).

The evolution of Indian wheat varieties can be broadly categorized into pre-Green Revolution, post-Green Revolution, and modern breeding phases. Prior to the Green Revolution, wheat cultivation relied largely on tall indigenous landraces and traditional cultivars, which possessed valuable adaptive traits but were limited by low yield potential and susceptibility to diseases and lodging. The introduction of semi-dwarf, high-yielding varieties during the Green Revolution period in the late 1960s marked a paradigm shift, leading to dramatic increase in productivity through improved plant architecture, fertilizer responsiveness and synchronized maturity. Subsequent post-Green Revolution breeding focused on yield stabilization, wide adaptability, and resistance to major diseases such as rusts, resulting in the release of a large number of improved varieties suited to different agro-ecological zones (Joshi et al., 2007; Singh et al., 2011).

In recent decades, the advent of molecular marker technologies has further strengthened Indian wheat improvement programs. Marker-assisted selection has enabled the precise introgression and pyramiding of genes governing disease resistance, quality traits and abiotic stress tolerance into elite genetic backgrounds. Comparative molecular studies have highlighted clear genetic differentiation between pre- and post-Green Revolution cultivars, while also emphasizing the need to maintain phenotypic and genetic diversity within modern breeding pools (Mottaleb et al., 2023; Sharma et al., 2021). Nevertheless, despite advances in genomics, morphological traits continue to serve as the primary and legally recognized basis for varietal identification and protection.

Distinctness, Uniformity, and Stability (DUS) characterization using standardized morphological descriptors remains fundamental for the registration, protection, and maintenance of wheat varieties under national and international frameworks such as the PPV&FR Act and UPOV guidelines. Morphological descriptors are stable, visually assessable, and reflect the cumulative effects of selection across agro-climatic zones and breeding eras. Comprehensive DUS characterization of Indian released wheat varieties therefore provides critical insights into phenotypic diversity, facilitates effective varietal identification, and supports sustainable utilization of wheat genetic resources in future breeding programs.

## Materials and Methods

### Plant Material

The study comprised of 428 Indian released varieties, representing nearly six decades of varietal development (1961–2018)and released in last fifty years under AICW&BIP, were used to estimate the genetic variability (Table 1).Observations were recorded during 2021-23(winter & summer- 4 seasons at ICAR–Indian Agricultural Research Institute (IARI), Regional Station, Wellington, Tamil Nadu, India (11°22′47.5″N; 76°46′26.1″E; 1850 m AMSL) at appropriate growth stages as recommended for DUS testing. These varieties encompass a wide range of genetic backgrounds and adaptation to various wheat cultivating zones across India. Varieties were evaluated with 35 morphological descriptors covering seedling, vegetative, stem, and reproductive stages.

The descriptors and corresponding states of expression followed standard DUS guidelines prescribed by PPV&FRA and UPOV (PPV&FRA, 2007; UPOV, 2019). Each trait was scored using predefined numerical codes to ensure uniformity and reproducibility. Qualitative traits such as pigmentation, waxiness, hairiness and for presence/absence of awns were visually assessed, while quantitative traits such asplant height, leaf length, leaf breadth, peduncle length and

phenological traits were classified into discrete state categories, as practiced in earlier DUS characterization studies.

**Results**

The qualitative/quantitative attributes among 35 DUS descriptors and their respective states were scored as numeric values for 428 wheat varieties as given in Table 2. The consolidated DUS data (Table 2) reveal substantial agro-morphological diversity among 428 Indian wheat varieties released over the past five decades, reflecting intensive selection under diverse agro-climatic conditions. Coleoptile anthocyanin pigmentation was largely absent (409 varieties), indicating limited use of this trait in varietal differentiation, whereas its presence in only 17 varieties suggests niche adaptation or specific genetic background. Growth habit in Indian wheat varieties was predominantly semi-erect (303) and erect (118), highlighting breeder preference for plant architectures that confer lodging resistance and suitability for high-input cultivation systems. Leaf attitude followed a similar trend, with semi-erect leaves (288) being most common, which is advantageous for optimal light interception and canopy aeration. Leaf hairiness was absent in the majority (379), while mimic traits showed considerable variation, suggesting their limited but specific utility in varietal identification. A striking observation was the dominance of early to very early heading (414 varieties combined) and maturity classes (418 varieties), underscoring strong selection for earliness to escape terminal heat stress prevalent in Indian wheat-growing regions and adapted to short winter conditions where as late maturing types were rare, reflecting reduced adaptation or preference under changing climatic scenarios. High levels of waxiness were recorded across multiple plant organs. Strong to very strong waxiness was most frequent in flag leaf (246), leaf sheath (397), peduncle (332), and ear (184). This widespread expression of waxy bloom suggests intentional or indirect selection for traits associated with drought tolerance, reduced transpiration and improved performance under heat and moisture stress conditions. Correspondingly, waxy bloom presence on stems (400 varieties) further supports this adaptive significance. Most varieties possessed hollow stems (306), while semi-solid (77) and solid stems (43) were less frequent, indicating that solid stem traits—often associated with lodging resistance and pest tolerance—have been incorporated in a limited subset of varieties knowingly or unknowingly. Peduncle length was mainly medium (286), balancing assimilate transport efficiency. Peduncle shape and curvature exhibited wide variation, enhancing the discriminatory power of these traits in DUS characterization. Spike traits displayed pronounced diversity. Dense ears (203) were most common, likely reflecting selection for higher grain number per spike. Tapering ear shape predominated (274), followed by fusiform and strap types. Ear pubescence was largely absent (365), while awnedness showed extreme skewness towards awned types (424), confirming the dominance of awns in Indian wheat for their role in photosynthesis, stress adaptation and relatively less damage from wild animals and birds(at maturity). Variation in awn attitude and color further contributed to varietal distinctness. Glume pigmentation was absent in most varieties (366), whereas glume shoulder width and shape showed moderate variability, with medium width and sloping to round shoulders being most frequent. Beak shape was primarily straight (199) or moderately curved (185), indicating stabilizing selection for these traits. Almost similar distribution was observed for DUS descriptors across six wheat sowing regions of India with minor exception like waxiness on peduncle in varieties developed for southern hilly regions of India.

**Other Associated Traits Contributing to Durable Disease Resistance:** Several other morphological and physiological traits

associated with durable rust resistance were also recorded among the evaluated varieties. The presence of pseudo-black chaff (PBC), a well-known morphological marker linked to the *Sr2* complex, was observed in several classical and modern cultivars such as Hope derivatives, Sonalika, Kalyansona, HD 2967, HD 3086, PBW 343, and DBW 17, indicating the deployment of adult plant stem rust resistance. Similarly, leaf tip necrosis (Ltn)—a phenotypic marker closely associated with the pleiotropic adult plant resistance genes *Lr34/Yr18, Lr46/Yr29,* and *Lr67/Yr46*—was recorded in varieties including HD 2967, HD 3086, PBW 343, DBW 71, MACS 6478, WH 1105, and HI 1500 (Amrita). These traits are indicative of slow-rusting, race-non-specific resistance mechanisms that reduce disease development and enhance resistance durability. The concurrent expression of PBC and Ltn, particularly in genotypes carrying multiple APR genes, underscores their value as field-level indicators of durable, multi-disease resistance and supports their strategic use in resistance breeding and gene pyramiding programs.

## Discussion

The consolidated DUS characterization of 428 Indian wheat varieties revealed substantial agro-morphological diversity, reflecting decades of targeted breeding for wide agro-climatic adaptation across Indian wheat-growing regions. The predominance of semi-erect growth habit, green to waxy green plant colour, and semi-erect leaf attitude suggests strong selection for plant types that balance lodging resistance with efficient light interception, traits widely associated with improved yield stability in modern wheat cultivars (Singh et al., 2011; Reynolds et al., 2012).A high frequency of waxy bloom on flag leaf, leaf sheath, ear, and peduncle was observed, with strong to very strong waxiness dominating most categories. Epicuticular wax is a well-documented adaptive trait conferring tolerance to heat and drought stress by reducing transpiration losses and canopy temperature, particularly under terminal heat stress conditions prevalent in Indian wheat environments (Mondal et al., 2015; Sharma et al., 2021). The widespread presence of this trait highlights its importance in Indian breeding programs targeting climate resilience. Phenological traits showed a clear skew towards very early to early heading and maturity, indicating deliberate selection for short-duration varieties to escape terminal heat stress and fit within multiple cropping systems (Joshi et al., 2007; Kumar et al., 2019). Such adaptation has been central to sustaining wheat productivity in the Indo-Gangetic Plains, where rising temperatures increasingly threaten grain filling duration. Leaf morphological traits such as leaf length, breadth, curliness, and hairiness exhibited marked variation, suggesting their potential utility in varietal identification and distinctness testing. Leaf pubescence, though less frequent, is reported to contribute to abiotic stress tolerance and pest deterrence, indicating its selective retention in specific breeding backgrounds (Blum, 2011). Stem-related traits revealed a predominance of hollow stems, while a smaller proportion of varieties exhibited semi-solid and solid stems. Stem solidness is a valuable trait linked to resistance against lodging and stem-boring insects such as wheat stem sawfly, as well as improved assimilate storage under stress conditions (Cook et al., 2019). The limited frequency of solid stems suggests scope for further introgression of this trait into elite backgrounds.Spike architecture traits, including ear density, shape, awnedness, awn attitude, and ear curvature, showed wide variability. The overwhelming presence of awned spikes reflects their recognized role in enhancing photosynthetic contribution to grain filling, particularly under water-limited and heat-stressed environments (Tambussi et al., 2007). Variations in awn colour, ear shape,

and density further contribute to phenotypic distinctness and reflect diverse genetic origins and selection histories. Glume-related traits such as pigmentation, shoulder width and shape, and beak shape also exhibited considerable diversity. These characters are highly stable across environments and are therefore considered reliable descriptors for varietal identification and protection under DUS testing systems (UPOV, 2012; PPV&FRA, 2007).

Overall, the wide range of agro-morphological variation captured in this study underscores the rich phenotypic diversity present in Indian wheat germplasm. Such diversity not only facilitates effective DUS testing but also provides a valuable resource for breeders aiming to enhance stress resilience, adaptability, and yield stability under changing climatic conditions.

**Figure 1. Expression of Pseudo black chaff linked to the APR stem rust resistance gene *Sr2*+on the glume and internodes**

**Figure 2. Variation inthe expression of leaf tip necrosis (Ltn) associated with APR genes *Lr34/Yr18, Lr46/Yr29,* and *Lr67/Yr46* in wheat**

**Table 1. Morphological characteristics used to evaluate the 428 Indian released varieties (1961-2018)**

| Character code | DUS Characteristics | States of Expression |
|---|---|---|
| 1 | Coleoptile anthocyanin (CP) | 1 Absent, 9 Present |
| 2 | Growth habit (GH) | 1 Erect, 3 Semi-erect, 5 Intermediate, 9 Spreading |
| 3 | Plant colour (PC) | 1 Erect, 3 Semi-erect, 5 Intermediate, 9 Spreading |
| 4 | Leaf attitude (LA) | 1 Erect, 3 Semi-erect, 5 Droopy |
| 5 | Leaf hairiness (LH) | 1 Absent, 9 Present |
| 6 | Mimic (MM) | 1 Absent, 9 Present |
| 7 | Leaf length (LL) | 1 Short < 20 cm, 5 Medium 20–30 cm, 9 Long > 30 cm |
| 8 | Leaf breadth (LB) | 1 Narrow < 1.5 cm, 5 Medium 1.5–2.0 cm, 9 Broad > 2.0 cm |
| 9 | Curly at (CA) | 3 At middle, 5 At base |
| 10 | Average days to heading (ADH) | 1 Very early, 3 Early, 5 Medium, 7 Late, 9 Very late |
| 11 | Average days to maturity (DM) | 1 Very early < 110 days, 3 Early, 5 Medium, 7 Late, 9 Very late |
| 12 | Flag leaf waxiness (FLW) | 1 Absent, 3 Weak, 5 Medium, 7 Strong, 9 Very strong |
| 13 | Leaf sheath waxiness (LSW) | 1 Absent, 3 Weak, 5 Medium, 7 Strong, 9 Very strong |
| 14 | Ear waxiness (EW) | 1 Absent, 3 Weak, 5 Medium, 7 Strong, 9 Very strong |
| 15 | Peduncle waxiness (PW) | 1 Absent, 3 Weak, 5 Medium, 7 Strong, 9 Very strong |
| 16 | Peduncle length (PL) | 1 Short, 5 Medium, 9 Long |
| 17 | Auricle colour (AC) | 1 Absent, 5 Medium, 9 Strong |
| 18 | Auricle hairiness (AH) | 1 Absent, 5 Medium, 9 Strong |
| 19 | Stem anthocyanin (SA) | 1 Absent, 9 Present |
| 20 | Waxy bloom (WB) | 1 Absent, 9 Present |
| 21 | Stem hairiness (SH) | 1 Absent, 9 Present |
| 22 | Stem solidness (SS) | 1 Hollow, 3 Semi-solid, 5 Solid |
| 23 | Colour of nodes (CN) | 1 Absent, 9 Present |
| 24 | Peduncle shape (PS) | 1 Erect, 3 Semi-erect, 5 Recurved, 7 Semi-crooked, 9 Crooked neck |
| 25 | Ear density (ED) | 1 Very lax, 3 Lax, 5 Medium, 7 Dense, 9 Very dense |
| 26 | Ear shape (ES) | 1 Tapering, 2 Strap-shaped, 3 Oblong, 4 Clavate, 5 Fusiform |
| 27 | Ear pubescence (EP) | 3 Absent, 5 Medium, 7 Very strong |
| 28 | Ear awnedness (EA) | 1 Awns absent, 2 Awnletted, 3 Awned |
| 29 | Awn attitude (AA) | 1 Appressed, 2 Semi-spreading, 3 Spreading |
| 30 | Awn colour (ACOL) | 1 White, 2 Brown, 3 Dark brown, 4 Pink/Black |
| 31 | Ear curvature at maturity (CV) | 3 Erect, 5 Semi-erect, 7 Droopy) |
| 32 | Glume pigmentation (GP) | 1 Absent, 9 Present |
| 33 | Lower glume shoulder width (LGSW) | 1 Absent, 3 Narrow, 5 Medium, 7 Broad, 9 Very broad |

**Table 2 . Distribution of agro-morphological characters in Indian wheat varieties (indicated in numbers).**

| Agro-Morphological Character | | Descriptor state and number of varieties in parenthesis | | | | |
|---|---|---|---|---|---|---|
| | | 1 | 3 | 5 | 7 | 9 |
| 1 | Coleoptile anthocyanin | Absent (409) | - | - | - | Present (17) |
| 2 | Growth habit | Erect (118) | Semi Erect (303) | Intermediate (4) | Semi spreading (0) | Spready (1) |
| 3 | Plant colour | Light Green (17) | Waxy green (144) | Green (176) | Dark Green (89) | |
| 4 | Leaf attitude | Erect (85) | Semi Erect (288) | Droopy (53) | | |
| 5 | Leaf hairiness | Absent (379) | | | | Present (47) |
| 6 | Mimic | Absent (253) | | | | Present (173) |
| 7 | Leaf length | Short (190) | - | Medium (0) | - | Long (236) |
| 8 | Leaf breadth | Narrow (191) | | Medium (0 ) | | Broad (235) |
| 9 | curly at | Absent (66) | at Middle (289) | at base (71) | | |
| 10 | Avg days to heading | Very early (238) | Early (176) | Medium (9) | Late (2) | Very late (1) |
| 11 | Avg days to maturity | Very early (317) | Early (101) | Medium (7) | Late (0) | Very late (1) |
| 12 | Flag leaf waxiness | Absent (40) | Weak (68) | Medium (72) | Strong (198) | V.strong (48) |
| 13 | Leaf sheath waxiness | Absent (2) | Weak (9) | Medium (18) | Strong (293) | V.strong (104) |
| 14 | Ear waxiness | Absent (21) | Weak (65) | Medium (156) | Strong (149) | V.strong (35) |
| 15 | Peduncle waxiness | Absent (10) | Weak (32) | Medium (52) | Strong (264) | V.strong (68) |
| 16 | Peduncle Length | Short (35) | | Medium (286) | | Long (105) |
| 17 | Auricle colour | Absent (304) | | Medium (73) | | Strong (49) |
| 18 | Auricle hair | Absent (128) | | Medium (166) | | Strong (132) |
| 19 | Stem Anthocyanin | Absent (28) | | | | Present (398) |
| 20 | Waxy bloom | Absent (26) | | | | Present (400) |
| 21 | Stem Hariness | Absent (403) | | | | Present (23) |
| 22 | Stem solidness | Hollow (306) | Semisolid (77) | Solid (43) | | |
| 23 | Colour of nodes | Absent (425) | | | | Present (1) |
| 24 | Peduncle shape | Erect (108) | Semi Erect (138) | Recurved (123) | Semi crooked (4) | crooked Neck (53) |
| 25 | Ear Density | Very lax (3) | Lax (61) | Medium (154) | Dense (203) | Very dense (5) |
| 26 | Ear shape | Tapering (274) | Strap (48) | Oblong (1) | Clavate (42) | Fusiform (61) |
| 27 | Ear pubescence | Absent (365) | | Medium (37) | V. strong (24) | |

| | | | | | | |
|---|---|---|---|---|---|---|
| 28 | Ear awnedness | Awns absent (1) 0 | Awnletted (2) 2 | Awned (3) 424 | | |
| 29 | Awn attitude | Appresed (141) | Medium (78) | Spreading (207) | | |
| 30 | Awn colour | White (264) | Brown (5) | Dark brown (26) | pink/black (131) | |
| 31 | Ear Curvature at maturity | | Erect (182) | Semi erect (178) | Droopy (66) | |
| 32 | Glume pigmentation | Absent (366) | | | | Present (60) |
| 33 | Lower glume shoulder width | Absent (87) | Narrow (131) | Medium (179) | Broad (29) | Very broad (0) |
| 34 | Lower glume shoulder shape | Sloping (183) | Round (119) | Straight (104) | Elevated (20) | strongly elevated (0) |
| 35 | Glume beak shape | Straight (1) 199 | Mod.curved (2) 185 | Strongly curved (3)25 | Geniculate (4) 16 | |
| 36 | Grain Colour | Amber | Red | | | |

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**Characterization of Indian released varieties for its genetic basis of resistance and stem solidness**

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## Abstract

The present study elucidates the genetic basis of resistance to stem, leaf rust and powdery mildew, along with the climate-resilient solid stem traits, in 428 Indian wheat varieties released between 1961 and 2018. These varieties were evaluated across two contrasting field environments under optimal and heat-stressed conditions. Molecular marker analysis was employed to detect major ASR rust resistance genes, including *Sr24/Lr24*, *Sr25/Lr19*, *Sr26*, *Sr38/Lr37/Yr17*, and *Sr31/Lr26/Yr9*, and to assess their association with stem solidness. Among the screened genotypes, 64 carried *Sr24*, 18 harbored*Sr25/Lr19*, 33 possessed *Sr31*, and 36 contained *Sr38/Lr37*. Phenotypic assessment identified 108 varieties (25%) consistently expressing the solid stem trait, which was genetically associated with the 175-bp allele of the SSR marker *Xgwm247*. Notably, none of the evaluated cultivars carried the Ug99-race specific effective resistance genes *Sr26* or *Sr36*. The results highlight substantial variability in the deployment of rust resistance genes in Indian wheat germplasm and emphasize the potential of integrating stem solidness with effective resistance genes to enhance yield stability, disease resistance and climate resilience. These findings provide a robust molecular foundation for targeted wheat improvement programs.

## Introduction

Wheat (*Triticum aestivum* L.) is the most extensively cultivated cereal crop worldwide and constitutes a primary source of dietary calories and protein for a significant proportion of the global population (FAO, 2021; Jalal et al., 2026). Its allohexaploid genome and long evolutionary history have enabled adaptation to a wide range of agro-climatic conditions (Mansour et al., 2018). However, the sustainability of wheat production is increasingly threatened by climate change, rising temperatures, and an anticipated 60% increase in global demand by 2050 (Pachauri and Reisinger, 2007). These challenges are compounded by intensified biotic and abiotic stresses, including heat stress, lodging, drought, and the resurgence of major diseases (Porter and Semenov, 2005).

Among biotic constraints, rust diseases caused by *Puccinia* species—stem rust (*P. graminis* f. sp. *tritici*), leaf rust (*P. triticina*), and stripe rust (*P. striiformis* f. sp. *tritici*)—remain the most devastating threats to wheat production globally. The emergence and rapid spread of highly virulent races, particularly the Ug99 lineage, have rendered several widely deployed resistance genes ineffective (Pretorius et al., 2000; Singh et al., 2011; Chai et al., 2022). In addition, powdery mildew caused by *Blumeria graminis* f. sp. *tritici* (Bgt) continues to cause significant

yield losses under favorable environmental conditions (Li et al., 2025). These diseases pose a persistent threat to wheat-growing regions of South Asia, including India (Prasad et al., 2022).

In India, stem rust is predominantly prevalent in the Central and Peninsular zones, which together cover nearly seven million hectares of wheat cultivation (Bhardwaj et al., 2019). The pathogen survives year-round in the southern hill regions, such as the Nilgiris, due to favorable climatic conditions (Joshi et al., 1985; Nagarajan and Joshi, 1985). Leaf rust, in contrast, is ubiquitous and occurs across all wheat-growing zones of the country (Bhardwaj et al., 2019). Several rust resistance genes introgressed from wild relatives, including *Sr24/Lr24*, *Sr25/Lr19*, and *Sr26*all from *Thinopyrum ponticum*, and *Lr37/Sr38/Yr17* from *Aegilops ventricosa* as well as the durable adult plant resistance gene *Sr2 (T. aestivum)*, have historically contributed to mitigating rust epidemics (Sharma and Knott, 1966; Sears, 1973; Ellis et al., 2014).

Contemporary wheat improvement strategies emphasize the deployment of durable resistance through gene pyramiding and alien introgressions. Resistance loci such as *Lr24/Sr24*, *Lr19/Sr25*, *Lr37/Sr38/Yr17*, and *Sr31+* carried on the 1BL.1RS rye translocation have played a significant role in enhancing disease resistance and agronomic performance (Bariana and McIntosh, 1993; Cox et al., 1995; Sibikeev et al., 2018). Alongside disease resistance, stem solidness—controlled primarily by loci such as *SSt1* and *Qss.msub-3BL* on chromosome 3B has gained importance as a climate-adaptive trait conferring resistance to lodging, insect pests, and drought stress (Cook et al., 2004; Liu et al., 2023).

Advances in molecular marker technology have enabled precise identification and deployment of resistance genes through marker-assisted selection, thereby improving the durability and efficiency of wheat breeding programs. In this context, the present study aims to characterize major rust and powdery mildew resistance genes in Indian released wheat varieties and to examine their association with the solid stem trait under diverse environmental conditions.

## Materials and Methods

### Plant Material and Field Evaluation

A total of 428 wheat cultivars comprising *T. dicoccum* (8), *T. durum* (60), triticale (5), and *T. aestivum* (353), released between 1965 and 2018, were evaluated for resistance to rusts, powdery mildew, and for the solid stem trait. Field experiments were conducted at the ICAR–Indian Agricultural Research Institute (IARI), Regional Station, Wellington, Tamil Nadu, India (11°22′47.5″N; 76°46′26.1″E; 1850 m AMSL) from 2023-2025. To accelerate generation turnover, two parallel evaluations were undertaken: one at Wellington for rust resistance and stem solidness, and another at Tamil Nadu Agricultural University (TNAU), Coimbatore, for thermo-tolerance and stem solidness assessment.

### Assessment of Solid Stem Trait

For evaluating stem solidness, ten representative plants per plot were sampled. Five consecutive internodes from

each stem were cut transversely and scored using a five-grade scale: grade 1 (0% pith), grade 2 (25%), grade 3 (50%), grade 4 (75%), and grade 5 (100% pith-filled) Figure1. The cumulative score across internodes represented the degree of stem solidness.

**DNA Isolation and PCR Analysis**

Genomic DNA was extracted from 3–4-week-old seedling leaf tissue using the CTAB method (Doyle and Doyle, 1990) and standardized to 25 ng $\mu L^{-1}$. PCR amplification was carried out using gene-linked **SSR** and **STS** markers targeting rust resistance genes and the solid stem trait (Table 1). Amplified products were resolved on 1.5–3.0% agarose or Metaphor agarose gels, stained with ethidium bromide, and visualized under UV illumination.

**Table 1: Molecular markers used in this study**

| S.No | Target gene | Linked marker | Size of fragment (bp) | Reference |
|---|---|---|---|---|
| 1. | *SSt (Solid stem trait)* | *GWM 247* | 175bp | Cook et al., (2004) |
| 2. | *Lr19/Sr25* | *Gb* | 130bp | Prins et al., (2001) |
| 3. | *Lr24/Sr24* | *Sr24#12* | 500bp | Mago et al. (2011) |
| 4. | *Lr37/Sr38/Yr17* | *Ventriup /LN2* | 262 bp | Helguera et al., (2003) |
| 5. | *Sr31/Lr26/Yr9/Pm8* | *Iag95* | 1100 bp | Mago et al. (2005) |
| 6. | *Sr26* | *Sr26#43* | 207bp | Mago et al. (2011) |
| 7. | *Sr36* | *Stm 773* | 155bp | Tsilo et al.(2008) |
| 8. | *Sr2+* | *Gwm533* | 120bp | Spielmeyer et al. (2003) |
| 9. | *Lr34+* | *csLV34* | 150bp | Spielmeyer et al. (2008) |
| 10. | *Lr46+* | *Wmc44* | 242bp | William et al. 2003 |
| 11. | *Lr67+* | *cfd 71* | 214bp | Hiebert et al., 2010 |

**Results**

**Detection of Rust Resistance Genes Using Molecular Markers**

**ALL STAGE RESISTANCE GENES**

***Lr19/Sr25 (Marker: Gb)***

Marker-assisted screening using the diagnostic marker Gb confirmed the presence of the *Lr19/Sr25* gene complex in 18 of the 428 released wheat varieties (4.21%)**,** as evidenced by the amplification of the expected 130 bp fragment. *Lr19/Sr25* confers strong all-stage resistance to both leaf rust and stem rust and is derived from *Thinopyrum ponticum*. Despite its effectiveness, the relatively low frequency of this gene complex among released varieties suggests cautious deployment, likely due to historical concerns regarding linkage drag affecting yield and quality traits. Nevertheless, its confirmed presence in elite backgrounds highlights its continued relevance as a

valuable resistance source when judiciously deployed.

***Sr24/Lr24 (Marker: Sr24#12)***

The *Sr24/Lr24* gene complex was detected in 64 varieties (14.95%) using the marker *Sr24#12*, which produced the characteristic 500 bp PCR product. *Sr24* provides strong resistance to stem rust, including protection against several virulent races, while *Lr24* contributes to leaf rust resistance. The moderate frequency observed indicates that *Sr24/Lr24* has been more widely adopted in Indian breeding programs than other alien introgressions, reflecting its stable performance and minimal negative agronomic effects. Its presence across multiple released varieties underscores its importance as a reliable ASR gene under Indian conditions.

***Sr31/Lr26/Yr9 (Marker: Iag95)***

The rye-derived 1BL.1RS translocation, carrying the *Sr31/Lr26/Yr9* gene complex, was identified in 33 out of the 250 wheat varieties tested (13.20%) using the *Iag95*marker, which yielded the expected 1100 bp amplification product. Historically, *Sr31* has been one of the most widely deployed stem rust resistance genes worldwide due to its broad-spectrum effectiveness and associated yield advantages. The assessment of *Sr31* in a subset of released varieties reflects the phased nature of marker screening, with the remaining lines yet to be evaluated. Despite reports of virulence against *Sr31* in other wheat-growing regions, the continued presence of the *Sr31/Lr26/Yr9* translocation in Indian released varieties indicates its sustained agronomic value and effectiveness under Indian conditions, where virulence remains limited.

***Lr37/Sr38/Yr17 (Marker: VENTRIUP–LN2)***

The *Lr37/Sr38/Yr17* gene cluster was detected in 36 varieties (8.41%) using the *VENTRIUP–LN2* marker, producing a diagnostic 262 bp amplicon. This gene cluster, derived from *Aegilops ventricosa*, confers resistance to leaf rust, stem rust, and stripe rust. Its moderate frequency suggests selective deployment, often in combination with other resistance genes, to broaden the resistance spectrum. The continued presence of this cluster among released varieties reflects its utility in multi-disease resistance breeding, particularly in environments with complex rust pressure.

***Sr26 (Marker: Sr26#43)***

None of the 428 released wheat varieties amplified the diagnostic 207 bp fragment corresponding to *Sr26* when screened with the *Sr26#43* marker. *Sr26* is a highly effective stem rust resistance gene, including effectiveness against Ug99 lineage races. Its complete absence in Indian released germplasm suggests that *Sr26* has not yet been incorporated into commercial cultivars, possibly due to limited availability, breeding challenges, or prioritization of other resistance sources. This highlights *Sr26* as a potential candidate for future introgression and diversification of stem rust resistance in India.

***Sr36/Pm6 (Marker: Xgwm773-2)***

Similarly, screening with the *Xgwm773-2*marker revealed no amplification of the expected 155 bp fragment associated with

the *Sr36/Pm6* gene complex in any of the evaluated varieties. *Sr36*, derived from *Triticum timopheevii*, confers resistance tostem rust and powdery mildew. Its absence from released Indian varieties indicates that this gene has not been utilized in national breeding programs, likely due to concerns over durability or linkage drag, reinforcing the need for careful evaluation before deployment.

## ADULT PLANT RESISTANCE GENES

### *Lr34/Yr18 (Marker: csLV34)*

The pleiotropic adult plant resistance (APR) gene *Lr34/Yr18* was detected in 21 out of 130 recent released varieties (16.15%) using the gene-based functional marker *csLV34*. *Lr34* is well known for conferring durable, race-non-specific resistance against multiple pathogens, including leaf rust, stripe rust, and powdery mildew, and is phenotypically associated with leaf tip necrosis (Ltn). Although its frequency among recently released varieties is moderate, the continued presence of *Lr34* underscores its high breeding value and sustained preference in resistance breeding programs that prioritize durability over complete immunity.

### *Lr46/Yr29 (Marker: Xwmc44)*

The APR gene *Lr46/Yr29* was identified in 22 of the 130 varieties (16.92%) using the linked SSR marker *Xwmc44*. *Lr46* confers partial, slow-rusting resistance and is considered functionally analogous to Lr34, though typically with a milder phenotypic expression. Its comparable frequency to *Lr34* suggests targeted deployment, often in combination with other APR genes. The presence of *Lr46/Yr29* reflects the increasing emphasis on pyramiding multiple minor-effect genes to enhance resistance durability in modern Indian wheat breeding.

### *Lr67/Yr46 (Marker: cfd71)*

The adult plant resistance gene *Lr67/Yr46* was detected in 94 out of 130 varieties (72.31%) using the gene-based marker *cfd71*, making it one of the most prevalent APR genes among recent Indian wheat releases. *Lr67* encodes a modified hexose transporter that confers broad-spectrum, partial resistance to multiple rust pathogens. Its high frequency highlights its central role in contemporary breeding strategies, reflecting a clear shift toward molecularly guided incorporation of durable, race-non-specific resistance.

### *Sr2+ (Marker: Xgwm533)*

The cornerstone stem rust APR gene Sr2 was identified in 104 of the 130 varieties (80.00%) using the SSR marker *Xgwm533*, making it the most frequently detected resistance gene in the study. *Sr2*, often associated with the *Sr2* complex and the morphological marker pseudo-black chaff (PBC), provides durable, partial resistance to stem rust. Its exceptionally high frequency among recent releases highlights its long-standing and continued importance in Indian wheat improvement programs. The persistence of *Sr2* across modern cultivars underscores its unparalleled contribution to long-term stem rust resistance and breeding stability.

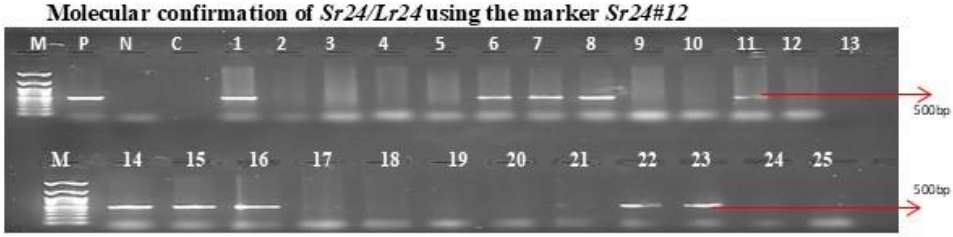
**Molecular Analysis of the Solid Stem Trait**

Assessment of stem solidness revealed substantial variation among the evaluated varieties. Based on phenotypic scoring of internode pith development, 108 varieties (25%) consistently expressed the solid stem trait, while the remaining genotypes exhibited hollow or semi-solid stems.Molecular screening using the SSR marker *Xgwm247* revealed clear allelic differentiation between solid and hollow stem types. Solid-stemmed genotypes consistently amplified a 175 bp fragment, whereas hollow-stemmed varieties showed bands ranging from 180 to 190 bp. A subset of genotypes exhibited intermediate bands (~160 bp), which corresponded to semi-solid stem phenotypes with pith development scores between 2 and 3. Further marker validation confirmed the association of these genotypes with the solid stem allele.

**Assessment of the stem-solidness (DePauw and Read 1982)**

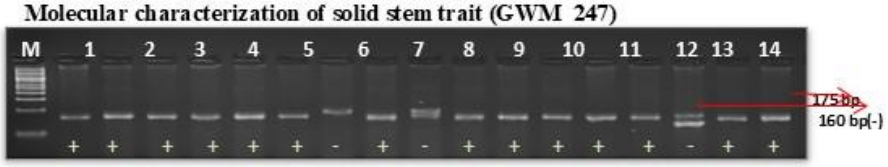

1—hollow pith (0% filled), 2—25% filled, 3—50% filled, 4—75% filled, 5—solid stem (100% filled)

**Molecular confirmation of *Sr24/Lr24* using the marker *Sr24#12***



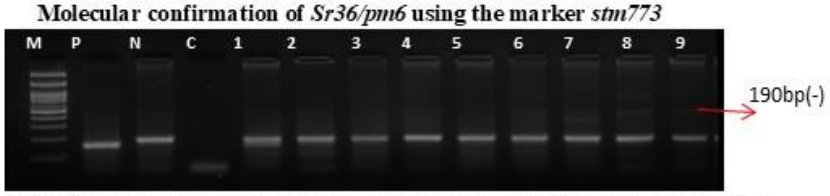

M-Marker, P-Positive control- AKAW 4627, N-Negative- HW 971; C- Non template control ; 3-C306, 4-NI 5439, 5-LOK-1,, 6-HW 1085, 7- HW 2045, 8-HW 5207 9-MACS 2496, 10- PBN 51,11-RAJ 4037, 12-HW 1098, 13-DBW 39,14-KHARCHIA 65, 15-MP 1142, 16-NI 5463, 17-DT 46, 18-HD 3171, 19-UP 2003, 20-TL 2969, 21-UP 215, 22-HW 5216,. 23- SONAK, 24-HD 2967, 25-PBW

**Molecular characterization of solid stem trait (GWM 247)**



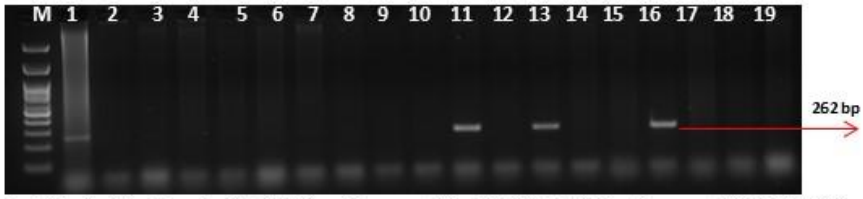

L:100bp ladder, Lane 1:DBW 39 (positive control), , 2- COW(W)-1(positive control), AKAW4627, 4-DL 153-2, 5- HD 2204, 6- HD 2327, 7-DDK 1025, 8-HD 2985, 9-HD 3090, 10- VAISHALI,11- HUW 510 , 12- HW 1085, 13- KSML 3, 14- MP1142, 15- MP1202, 16-MP 3288, 17- NIAW 1415

**Molecular confirmation of *Sr36/pm6* using the marker *stm773***



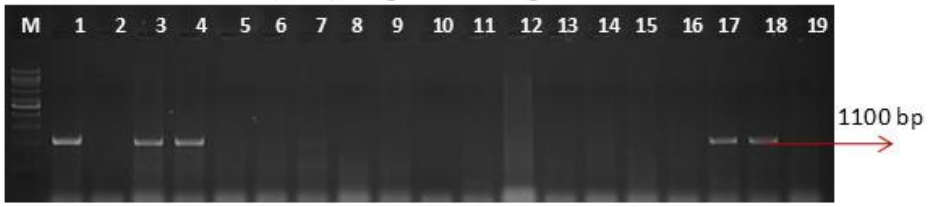

M-Marker, P-Positive control- HW 2436-2, N-Negative- COW(W)-1; C- Non template control ; 1-9- Indian released wheat varieties

**Molecular confirmation *of Lr37/Sr38/Yr17* using the marker *(VENTRIUP/LN2)***




L:100bp ladder, Lane 1-HD 2967(positive control), , 2- WH 147(Negative control), 3-COW(w)-1, 4-HPW 42, 5-C306, 6-HW 5207, 7-PBW 550, 8-Lok-1, 9-Sonalika, 10- Chotti lerma, 11-PBW 723 , 12- PBN 51, 13- HD 3171, 14- DDK 1005, 15- , 16- HW 1098, 17- WH 1105, 18-HPW 184, 19- HD 3090

**Molecular confirmation of *(Sr31+)* using the marker *Iag95***




L:100bp ladder, Lane 1-MACS 2496(positive control), , 2- WH 147(Negative control), 3-COW(W)-1, 4-HPW 42, 5-C306, 6-HW 5207, 7-PBW 550, 8-Lok-1, 9-Sonalika, 10- Chotti lerma, 11- NI5439 , 12-PBN 51, 13- AKAW 4627, 14- DDK 1005, 15- , 16- HW 1098, 17- DT 46, 18- HPW 184, 19- TL1210

## Discussion

The comprehensive molecular and phenotypic characterization of 428 Indian released wheat varieties revealed substantial variability in the deployment of rust resistance genes and the solid stem trait, reflecting historical breeding priorities and evolving disease pressures. The uneven distribution of resistance loci observed in this study underscores both the achievements and limitations of past wheat improvement programs in India.

The relatively higher frequency of *Sr24/Lr24* among the evaluated varieties confirms its long-standing importance in Indian wheat breeding. This gene complex, introgressed from *Thinopyrum ponticum*, has been widely adopted due to its broad-spectrum effectiveness against stem rust and its continued efficacy against several Ug99 variants (Spielmeyer et al., 2003; Bhardwaj et al., 2019). However, the moderate presence of *Lr19/Sr25* indicates a more conservative utilization, likely influenced by earlier concerns regarding linkage drag affecting flour color and yield stability, despite its proven durability against stem rust (Sharma and Knott, 1966; Prins et al., 2001). The coexistence of these alien introgressions in a limited number of genotypes suggests that opportunities remain for combining complementary resistance genes to enhance durability.

The detection of the *Lr37/Sr38/Yr17* gene cluster in a moderate proportion of released varieties highlights the strategic incorporation of the 2NS/2AS translocation in Indian germplasm. This translocation confers resistance to multiple rust pathogens and wheat blast, making it particularly valuable under changing disease scenarios (Helguera et al., 2003; McIntosh et al., 2017). Nevertheless, reports of reduced effectiveness of *Yr17* in certain regions emphasize the need for pyramiding this gene with additional resistance sources to prevent resistance erosion.

Although virulence to *Sr31* has been reported globally, particularly against the Ug99 race group (*Puccinia graminis* f. sp. *tritici*), *Sr31* remains effective under Indian conditions, as Ug99-lineage races have not established widespread virulence in India (Pretorius et al., 2000; Singh et al., 2011; Nagarajan et al., 2014). Consequently, the continued presence of the 1BL.1RS translocation in Indian cultivars reflects its ongoing contribution to stem rust resistance, in addition to its well-documented agronomic advantages such as yield stability and adaptation. Nevertheless, the global breakdown of *Sr31* underscores the importance of reducing reliance on single major genes and adopting gene diversification and pyramiding strategies to ensure long-term resistance durability (Singh et al., 2015; Ellis et al., 2014).Of particular concern is the complete absence of *Sr26* and *Sr36* in the studied germplasm. Both genes are recognized for their high level of resistance to Ug99 and related races and have been successfully deployed in international breeding programs (Liu et al., 2010; Singh et al., 2015). Their absence in Indian released varieties represents a significant vulnerability and highlights an urgent need for their strategic introgression through pre-breeding and marker-assisted selection.

The ASR genes screened in this study were selected based on their documented

effectiveness against prevalent rust races in India and their historical and current deployment in Indian wheat breeding programs. Genes such as *Sr24*, *Sr31*, and *Lr37* continue to provide effective resistance in several agro-ecological zones, while *Lr19* remains valuable due to its associated yield benefits. The objective was to assess the "floating" or persistence of these effective ASR genes in released varieties, rather than screening genes that are either ineffective under Indian conditions or have not been widely deployed.

Only recently released wheat varieties (post-2010) were screened for APR genes in this study because older Indian varieties have already been extensively characterized and reported for APR gene content, and the present analysis aimed to assess the current deployment, accumulation, and shifting trends of durable resistance genes in modern breeding pipelines.

The phenotypic and molecular evaluation of the solid stem trait revealed a strong association between stem solidness and the 175 bp allele of the SSR marker *Xgwm247*, corroborating earlier studies that identified *SSt1* as a major locus governing stem pith development (Cook et al., 2004; Nilsen et al., 2017). Approximately one-quarter of the evaluated varieties consistently expressed solid stems, indicating that this trait has been inadvertently selected in certain breeding backgrounds, possibly due to its association with lodging resistance and improved assimilate partitioning. The identification of semi-solid stems in some genotypes suggests quantitative modulation of pith development, which may offer flexibility in balancing stem strength and biomass allocation.

Beyond its role in lodging resistance, stem solidness has gained importance as a climate-resilient trait. Solid-stemmed wheat lines have been reported to exhibit enhanced tolerance to drought and heat stress, improved stem carbohydrate storage, and resistance to stem-boring insects such as wheat stem sawfly (Cook et al., 2004; Liu et al., 2023). The coupling of solid stem alleles with rust resistance genes observed in certain genotypes presents an opportunity to develop cultivars with combined resistance to biotic and abiotic stresses. Such trait combinations are particularly relevant under Indian agro-climatic conditions, where terminal heat stress and disease pressure frequently co-occur.

The integration of molecular marker data with multi-environment phenotypic screening in this study enhances confidence in the identified resistance sources and their practical breeding value. Marker-assisted selection enables precise tracking of resistance genes and adaptive traits, reducing reliance on phenotypic screening alone, which can be confounded by environmental variability and pathogen diversity. The findings of this study provide actionable insights for wheat breeders, emphasizing the need to broaden the genetic base of rust resistance while simultaneously incorporating climate-adaptive traits such as stem solidness.

In conclusion, the study highlights critical gaps in the current resistance landscape of Indian wheat varieties, particularly the absence of key Ug99-effective genes, while also revealing underutilized opportunities for enhancing resilience through stem solidness. Strategic gene pyramiding, supported by molecular

markers and informed by pathogen surveillance, will be essential for developing durable, high-yielding wheat cultivars capable of withstanding future disease outbreaks and climatic challenges.

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**Table 2 Molecular characterization of released varieties for ASR and APR genes**

| S.NO | Name of the gene | Number of lines tested | Number of Polymorphic Lines | Name of the Varieties |
|---|---|---|---|---|
| 1 | *Lr24/Sr24* | 428 | 69 | AKAW 4627,COW(W)1,DL 784-3 (VAISHALI),DL 788-2 (VIDISHA),DL 803 -3 (KANCHAN),DWR 195 (ANURADHA),DWR 225,GW 11,GW 366,HD 2204,HD 2781 (ADITYA),HD 2833 (TRIPTI),HD 2851 (PUSA VISHESH),HD 2864 (URJA),HD 2888,HD 2932,HD 3043,HDR 77,HI 1418 (NAVEEN CHANDOUSI),HI 1454 (ABHA),HI 1500,HI 1531,HI 1563,HPW 89 (SURABHI),HUW 37 (MALVIYA 37),HUW 468,HUW 510,HW 1085 (BHAVANI),HW 2045,HW 5207 (COW3),K 9533 (NAINA),KHARCHIA 65,MP 1142,MP 1202,MP 3288,NI 5643,NIAW 1415,RAJ 1114,RAJ 1972,RAJ 4037,RAJ 4238,RW 346,SAFED LERMA,SAGARIKA,SKAML 1,SONAK,SWL 8 (SINGCHEN),UAS 304,UP 1109,UP 2121,UP 2338,UP 2382,UP 2565,UP 2572,VL 404,VL 719,VL 738,VL 804,WG 357,WH 1021,WH 1080,WH 157,WH 283,WH 291,WH 533,WH 542,WL 410,WL 711,HW 5216 |
| 2 | *Lr37+* | 428 | 35 | GW1139,PDW 291,PDW 314,TL 1210,UAS 415,DBW 39,DBW 88,DPW 621-50,DWR 225,HD 2285 (GOBIND),HD 2967,HDR 77,HI 617 (SUJATA),HS 507,HS 542,HW 517,MACS 6273,MACS 6478,MP 3173,MP 4106,PBN 51,PBW 660,RW 346,UP 2003,UP 215,UP 2425,UP 262,UTKALIKA,VL 802,WH 1105,HDCSW 18,HD 3171,PBW 677,PBW 723,PBW 725 |
| 3 | *Lr19/Sr25* | 428 | 19 | DT46,TL1210,TL2969,UAS415,WHD912,HW 1098 (NILGIRI KHAPLI),MPO1255,HD3090,K 9644 (ATAL),PBW 527, PBW 533,PBW644,RAJ1482,VL832,DH |

| | | | | |
|---|---|---|---|---|
| | | | | 114(HIMPRATHAM), HD 3117, HD 3118 (PUSA VATSALA), HD 3171 |
| 4 | *Sr31+* | 250 | 33 | DT46,MACS 2496,COW(W)1,CPAN 3004 (SANGAM),DBW 39,DL 803 -3 (KANCHAN),DWR 16 (KEERTHI),DWR 162,GW 89,HD 2643 (GANGA),HD 2687 (SHRESTH),HD 2967,HPW 184 CHANDRIKA,HPW 42 (ARADHANA),NIAW 1415,NW 1067,PBW 533,PBW 550,PBW 644,PBW 660,RAJ 1482,RAJ 4037,RAJ 4079,RATAN (CG 5016),SKW 196 (SHALIMAR WHEAT),UP 2565,UP 301,VL 802,VL 907,WH 157,WH 291,WH 533,WL 711,DBW 107,WH 1142,HW 5216 (PUSA THENMALAI),DH 114(HIMPRATHAM),PBW 723,VL 953 |
| 5 | *Lr34+* | 130 | 21 | DBW 14, DBW 71, HD 2967, HD 3043, HI 1500 (AMRITA), HI 1563, HPW 155, HPW 251, HW 5207 (COW3), KRL 213, MACS 6478, MP 3211, PBW 509, PBW 596, PBW 644, RAJ 4037, RAJ 4083, SKW 196, (SHALIMAR WHEAT), VL 802, VL 829, WH 1080 |
| 6 | *Lr46+* | 130 | 22 | AKAW 3722, AKAW 4627, ARPA (CG 5011), HD 2888, HD 2932, HI 1479 , (SWARNA), HS 420 (SHIVALIK), S 490, K 9644 (ATAL), MACS 6478, MP 1142, MP 1202, MP 3211, PBW 396, RAJ 4120,UP 2526, WH 1021, WH 1025, WR 544 (PUSA GOLD), PBW 658, HIMPRATHAM (DH 114) |
| 7 | *Lr67+* | 130 | 94 | AKAW 3722, CBW 38, COW(W)1, DBW 14,DBW 16, DBW 17 (DWR 17), DBW 39, DBW 71, DBW 88, DBW 90, DBW 93, DPW 621-50, GW 366, HD 2781 (ADITYA), HD 2824 (POORVA), HD 2851 (PUSA VISHESH), HD 2888, HD 2894, HD 2932, HD 2967, HD 2985, HD 2987, HD 3059, HD 3086, HD 3090, HI 1500 (AMRITA), HI 1531 (HARSHITA), HPW 155, HPW 184 (CHANDRIKA), HPW 251, HPW 349 |

| | | | | |
|---|---|---|---|---|
| | | | | HS 420 (SHIVALIK), HS 490, HS 542, HUW 510, K 1006, K 9351 (MANDAKINI), K 9423 (UNNAT HALNA), K 9533 (NAINA), K 9644 (ATAL), KRL 210, KRL 213, KRL 19, MACS 6222, MACS 6478, MP 1142, MP 1201, MP 1202, MP 1203, MP 3173, MP 3211, MP 3288, MP 4010, MP 4106, NIAW 1415, NIAW 301 (TRIMBAK), NIAW 917 (TAPOVAN), NW 5054,PBW 343, PBW 396, PBW 443, PBW 502, PBW 509, PBW 533, PBW 550, PBW 590, PBW 596, PBW 644, RAJ MOLYA RODHAK 01 (CCNRV01), RATAN (CG 5016), SKW 196 (SHALIMAR WHEAT), UAS 304, UP 2526, UP 2565, UP 2584, VL 802, VL 804, VL 907, WH 1021, WH 1080, WH 1105, WH 1124, WH 711, WR 544 (PUSA GOLD) , DBW 107, DBW 110, WH 1142, PDKV WASHIM (WSM 1472), HIMPRATHAM (DH 114), HD 3117, HD 3118 (PUSA VATSALA), HDCSW 18, MP 3382 |
| 8 | *Sr2+* | 130 | 104 | HW 1095 ( COW 2), AKAW 3722, AKAW 4627, ARPA (CG 5011), CBW 38, COW(W)1, DBW 14, DBW 16, DBW 17 (DWR 17), DBW 39, DBW 71, DBW 88, DBW 90, DBW 93, DPW 621-50, GW 322, GW 366, HD 2733 (VSM), HD 2781 (ADITYA), HD 2833 (TRIPTI), HD 2851 (PUSA VISHESH), HD 2864 (URJA), HD 2894, HD 2932, HD 2967, HD 3043, HD 3059, HD 3086, HD 3090, HI 1479 (SWARNA), HI 1544 (PURNA), HI 1563, HPW 251, HPW 349, HS 420 (SHIVALIK), HS 490, HS 507 (PUSA SUKETI), HUW 510,HW 2044, HW 2045 (KAUSHAMBI), HW 5207 (COW3), K 9351 (MANDAKINI), K 9423 (UNNAT HALNA), K 9533 (NAINA), KRL 210, KRL 213, MACS 6222, MACS 6478, MP 1142, MP 1201, MP 1203, MP 3173, MP 3211, MP 3288, MP 4010,MP 4106, NIAW 1415, NIAW 917 (TAPOVAN), NW 1067,NW 2036, PBW 343, PBW 443, PBW 502, PBW 533, PBW 550 |

| | | | | |
|---|---|---|---|---|
| | | | | PBW 596, PBW 644, RAJ 3777, RAJ 4037, RAJ 4079, RAJ 4083, RAJ 4120, RAJ 4238, RAJ MOLYA RODHAK 01 (CCNRV01), RATAN (CG 5016), SKW 196 (SHALIMAR WHEAT), UAS 304, UP 2526, UP 2554, UP 2565, UP 2572, UP 2584, VL 802, VL 804, VL 832, VL 892, WH 1021, WH 1025, WH 1080, WH 1105, WH 1124, WH 711, WR 544 , PUSA GOLD), DBW 107, DBW 110, WH 1142, PDKV WASHIM (WSM 1472), HW 5216 (PUSA THENMALAI), PBW 658, HIMPRATHAM (DH 114), HD 3117, HD 3118 (PUSA VATSALA), HDCSW 18, MP 3382 |
| 9 | *SST-1* | 428 | 108 | HD 4672(MALAV RATNA),HI 8627 (MALAV KIRTI),HI 8713 ( PUSA MANGAL),JNK -4W-184,MACS 1967,MACS 2496,MACS 2971, MACS 9,MPO 1106, WH 943 , AKAW 4627,CHHOTI LERMA, COW(W)1,CPAN 1796, CPAN 3004 (SANGAM),D 134,DBW 17 (DWR 17),DBW 39,DBW 88,DBW 90,DBW 93,DL 153-2 (KUNDAN),DL 784-3 VAISHALI),DL 788-2 (VIDISHA),DL 803 -3 (KANCHAN),DPW 621-50,DURGAPURA 65,DWR 16 (KEERTHI),DWR 162,DWR 195 (ANURADHA),DWR 225,GW 89,HB 208,HD 1925 (SHERA),HD 1941 (HIRA),HD 1949 (MOTI),HD 1981 (PRATAP),HD 2204,HD 2270,HD 2278 (PARVATI),HD 2281,HD 2285 (GOBIND),HD 2307,HD 2329,HD 2428,HD 2501,HD 2643 (GANGA),HD 2687 (SHRESTH),HD 2824 (POORVA),HD 2864 (URJA),HD 2894,HD 2967,HD 3086,HI 617 (SUJATA),HPW 184 (CHANDRIKA),HPW 42 (ARADHANA),HUW 510,HW 1085 (BHAVANI),HW 5207 (COW3),K 88 (K8804),K 9107 (DEWA),K 9644 (ATAL),KSML 3,MP 1142,MP 1202,MP 3288,NIAW 1415,NW1067,NW 2036 ,NW 5054,PBW 527,PBW 533,PBW 550,PBW 644,PBW 660,RAJ 1482,RAJ 4037,RAJ 4079,RAJ 4083,RAJ 4238,RAJ MOLYA |

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| | | | | RODHAK 01 (CCNRV01),RATAN (CG 5016),SKW 196 (SHALIMAR WHEAT),SONALIKA,TAWA 267,UP 2526,UP 2565,UP 301,VL 802,VL 832,VL 892,VL 907,WH 1105,WH 1124,WH 711,WH 1142,HW 5216 (PUSA THENMALAI) , PBW 658, HIMPRATHAM (DH 114), HD 3117, HD 3118 (PUSA VATSALA), HDCSW 18, HD 3171, PBW 677,PBW 723, PBW 725, MP 3382, VL 953, HW 971 |

**Wheat Field Day Report –**

A **Wheat Field Day** was organized at ICAR-IARI Regional Station, Wellington, on **9th October 2024**, as part of the ongoing evaluation program under the **CRP – Agro-Biodiversity Component-III: Trait Discovery and Pre-Breeding in Wheat.** A total of **5068 tetraploid durum wheat accessions** were being evaluated during Kharif 2024 against **Fusarium Head Blight (FHB)** and rusts, and this event provided a platform for reviewing the field performance of these accessions in the presence of eminent scientists and stakeholders.

The event was graced by several eminent personalities including:

**Dr. Gyanendra Pratap Singh**, Director, ICAR-NBPGR, New Delhi

**Dr. Ratan Tiwari**, Director, ICAR-IIWBR, Karnal

**Dr. Arun Gupta**, Nodal Scientist, CRP-AB, IIWBR, Karnal

**Dr. Sushil Pandey**, Principal Scientist, NBPGR, New Delhi - **Lead Centre Platform Coordinator**

**Dr. Jyoti Kumari**, Principal Scientist, NBPGR, New Delhi–**Principal Project Investigator**

**Dr. Sandeep Kumar**, Principal Scientist, NBPGR, New Delhi

**Dr. Ragiba Makendar**, Professor, University of Hyderabad

**Dr. Yashwanthakumar** and **Dr. Sudhir Navathe**, Scientists from ARI, Pune

**Dr. Sunil M. Umate**, Wheat/Maize Breeder, VNMKV, Parbhani

Delegates from UAS, Dharwad

**Dr. Manish Vishwakarma**, Breeder, BISA along with **Dr.M.Sivasamy**, PI & **Dr. V.K.Vikas**, Co-PI of the project and team.

The **Presidential Address** was delivered by **Dr. Gyanendra Pratap Singh**, who appreciated the coordinated efforts under CRP-AB and stressed the need for broader genetic base utilization in pre-breeding programs.