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Mehtaensis

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ICAR-Indian Institute of Wheat and Barley Research, Regional Station, Flowerdale, Shimla 171 002 H.P. India

Compiled and Edited by

Jayanth Kallugudi, OP Gangwar, Subodh Kumar, Charu Lata and Pramod Prasad

Email: pramod.prasad@icar.org.in
Tel.: +91 177 2621978
Fax: +91 177 2620108

Prof. K.C. Mehta (1892-1950)
Founder of the Flowerdale station

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सारांश /Summary

फसल वर्ष 2024–25 के दौरान, भारत के कई राज्यों में गेहूँ में रतुआ रोगों का प्रकोप देखा गया, जिसमें पत्ती रतुआ की अधिकता और व्यापकता तना रतुआ और पीला रतुआ की तुलना में कहीं अधिक रही। गेहूँ में पीला रतुआ की पहली प्राकृतिक उपस्थिति जनवरी 2025 के अंत में हरियाणा और पंजाब में दर्ज की गई, जिसके बाद उत्तर भारत के अन्य क्षेत्रों से भी इसकी पुष्टि की गई। भूरा रतुआ सबसे पहले जनवरी के दूसरे सप्ताह में पंजाब से दर्ज किया गया। इसके बाद महाराष्ट्र, मध्य प्रदेश और अन्य राज्यों से भूरा रतुआ की उपस्थिति दर्ज की गई। काला रतुआ पहली बार फरवरी में मुख्यतः महाराष्ट्र और कर्नाटक में देखा गया, जिसमें विभिन्न राज्यों और गेहूँ की किस्मों में विभिन्न स्तर की अधिकता दर्ज की गई। इन फील्ड ऑब्जर्वेशन के आधार पर भाकृअनुप–भारतीय गेहूँ एवं जौ अनुसंधान संस्थान और राज्य व राष्ट्रीय कृषि विभागों के सहयोग से रोग प्रबंधन प्रक्रिया को तेजी से अपनाया गया, जिसमें प्रगतिशील किसानों को रीयल–

शेष पेज 1 पर..........

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कार्यकारी सारांश/Executive summary

टाइम अलर्ट और सलाह जारी की गई। इस फसल वर्ष के दौरान भारत के 14 राज्यों और नेपाल से विश्लेषण के लिए कुल 1,293 रतुआ नमूने एकत्र किए गए। इसमें 155 पीला रतुआ, 261 काला रतुआ और 877 भूरा रतुआ के नमूने लिए गए। जिनमें पीले रतुए के 155 नमूनों में गेहूँ के ग्यारह प्रभेद और जौ के पीला रतुआ का एक प्रभेद पहचाने गए। पीला रतुआ में प्रभेद 46S119 सबसे व्यापक रूप से पाया गया, साथ ही साथ इसमें 47S103 और 110S119 भी उपस्थित थे। इस दौरान जौ की पीला रतुआ के केवल तीन नमूने ही प्राप्त हुए इनका विश्लेषण करने के पश्चात इनमें प्रभेद 57 (0S0) की पहचान की गई। इस सीजन के दौरान विश्लेषण किए गए गेहूँ के 261 काला रतुआ नमूनों में सात प्रभेदों की पुष्टि की गई जिनमें से प्रभेद 11 की अधिकता पायी गई। विशेष रूप से 106G5 और 127G13 जैसे नए प्रभेद कर्नाटक और तमिलनाडु में पाए गए हैं, जो यह दर्शाते हैं कि काला रतुआ (Pgt) के विरुलेंस पैटर्न में बदलाव हो रहा है। गेहूँ की भूरा रतुआ रोगजनक (Pt) के 31 प्रभेदों को 877 नमूनों में पहचाना गया। इनमें प्रभेद 77–9 (121R60–1) सबसे प्रमुख था क्योंकि यह 42% नमूनों में पाया गया, साथ ही साथ इसमें 52–4 (24.65%) भी उपस्थित था जो इनकी व्यापकता को दर्शाता है। राजस्थान के दौसा जिले से एकत्र किए गए नमूनों में से भूरा रतुआ का एक नया प्रभेद 77–13 की पहचाना गया। इसका विरुलेंस पैटर्न 104–2 प्रभेद से मिलता–जुलता है, इसमें अतिरिक्त विरुलेंस जीन *Lr2a, Lr2b, Lr2c, Lr10* और Raj1555 पाया गया।

फसल वर्ष 2024–25 के दौरान नियंत्रित परिस्थितियों में स्क्रीनिंग और प्रतिरोध प्रोफाइलिंग के लिए लगभग 5,000 गेहूँ और जौ की पंक्तियों पर पौध अवस्था पर काला रतुआ (Pgt), भूरा रतुआ (Pt) और पीला रतुआ (Pst) के विभिन्न प्रभेदों की जांच की गई। AVT प्रविष्टि MACS4147 सभी तीन रतुआ रोगजनकों के प्रभेदों के लिए प्रतिरोधी पाई गई। DBW426 ने काला और भूरा रतुआ दोनों के लिए प्रतिरोधकता दिखाई। कई अन्य AVT प्रविष्टियों ने काला और पीला रतुआ के सभी परीक्षण किए गए प्रभेदों के विरुद्ध प्रतिरोध दिखाया। हालांकि, दो प्रविष्टियों NIDW1542 और PBW938 ने भूरा और पीला रतुआ दोनों के विरुद्ध प्रतिरोध दिखाया। ग्यारह प्रविष्टियों (*Sr31* और *Sr24* उपस्थिति वाले जीन को छोड़कर) ने काला रतुआ प्रभेदों के विरुद्ध प्रतिरोध दर्शाया।

204 AVT लाइनों में से 4 Yr जीन (*Yr2, Yr9, YrA*, और *Yr18*) की उपस्थिति दर्ज की गई, जिनमें से *Yr2* सबसे अधिक बार (114 लाइनों में) दर्ज किया गया। इसी तरह 148 पंक्तियों में 8 Lr जीनों (*Lr1*, *Lr3*, *Lr10*, *Lr13*, *Lr23*, *Lr24*, *Lr26*, और *Lr34*) की पहचान की गई, जिनमें *Lr1* और *Lr23* की अधिकता थी। 165 AVT पंक्तियों में 12 काला रतुआ प्रतिरोधी जीनों (*Sr2, Sr5, Sr7b, Sr8a, Sr9b, Sr9e, Sr11, Sr13, Sr24, Sr28, Sr30,* और *Sr31*) की पहचान की गई, जिनमें Sr7b और Sr2 की अधिकता थी।

AVT प्रविष्टियों की एडल्ट प्लांट स्टेज पर Pt, Pst और Pgt के प्रमुख और उग्र प्रभेदों पक्सिनिया ट्रिटिसिना के तीन प्रभेदों (77–5, 77–9 और 104–2), पक्सिनिया स्ट्राइफॉर्मिस के तीन प्रभेदों (46S119, 110S119 और 238S119), और पक्सिनिया ग्रैमिनिस एफ. एसपी. ट्रिटिसी के तीन प्रभेदों (11, 40A और 117–6) को स्क्रीनिंग के लिए उपयोग किया गया। तीन प्रविष्टियाँ (DBW426, DBW390, और DBW369) में सभी Pt प्रभेदों के

विरुद्ध APR (एडल्ट प्लांट रेसिस्टेंस) दर्ज की गई। AVT की 75 प्रविष्टियों में पक्सिनिआ ट्रिटिसिना के एक या अधिक प्रभेदों के लिए APR दर्शाया। इसी तरह, 73 प्रविष्टियों का परीक्षण किए जाने पर विभिन्न प्रभेदों में पीला रतुआ रोगजनक के लिए APR देख गया व 18 प्रविष्टियों में काला रतुआ प्रभेदों के लिए APR दर्ज किया गया।

246 NBDSN और 8 EBDSN प्रविष्टियों को जौ के विभिन्न प्रभेदों में तीनों प्रकार के रतुआ रोगों के प्रतिरोध स्क्रीनिंग के लिए अंकुर अवस्था पर परखा गया। कोई भी NBDSN या EBDSN प्रविष्टि तीनों रतुआ रोगजनकों पक्सिनिया स्ट्राइफॉर्मिस होर्डेई (पीला रतुआ), पक्सिनिया-होर्डेइ (पत्ती रतुआ), और पक्सिनिआ ग्रैमिनिस ट्रिटिसी (काला रतुआ) के सभी प्रभेदो के लिए प्रतिरोधी नहीं पाई गई। NBDSN की 11 प्रविष्टियां (BHS498, BHS503, BHS504, HBL890, RD3137, RD3138, RD3139, RD3141, RD3142, RD3143, और RD3145) भूरा और काला रतुआ दोनों के के लिए प्रतिरोधी पाई गई। EBDSN की तीन प्रविष्टियों (DWRB238, DWRB2309, और DWRB137) में पीला रतुआ के सभी प्रभेदों के विरुद्ध प्रतिरोध देखा गया। 34 NBDSN और 3 EBDSN प्रविष्टियों में जौ भूरा रतुआ प्रतिरोधी जीन (Rph3 और Rph19) की पहचान की गई।

आणविक मार्कर्स का उपयोग करते हुए *Yr9/Lr26/Sr31* मिश्रण को 8 AVT लाइनों में सत्यापित किया गया। 24 AVT प्रविष्टियों में Sr24#12 मार्कर से *Lr24/Sr24* जीन कॉम्प्लेक्स की पुष्टि की गई। इसी तरह 25 पंक्तियों में *Yr15*, 55 पंक्तियों में *Lr68*, 56 पंक्तियों में *Yr17/Lr37/Sr38*, 9 पंक्तियों में *Yr18/Lr34/Sr55*, 43 पंक्तियों में *Yr29/Lr46* और 3 पंक्तियों में *Yr24* जीनों को पहचाना गया।

कई जर्मप्लाज्म पंक्तियों और स्थानीय किस्मों को ज्ञात Lr जीन (*Lr10, Lr67, Lr23, Lr46, Lr13, Lr26*) के साथ संकरित किया गया ताकि F1 हाइब्रिड बनाए जा सकें। इसके बाद इस सीजन में F2 और F3 की 15 पीढ़ियों को Lr जीन पिरामिड को संचित करने के लिए उगाया गया। ब्राउन रस्ट रेसिस्टेंट लाइन हैंगो–2 (जिसमें जीन *Lr80* है) को पीला रतुआ प्रतिरोधी FLW लाइनों के साथ क्रॉस किया गया। जौ जीन Rph5, Rph7, और Rph12 की उपस्थिति वाली F2 पॉपुलेशन को श्रेष्ठ पृष्ठभूमियों में विकसित किया गया। जौ की F2 पॉपुलेशन को पीला रतुआ प्रतिरोधकता अध्ययन के लिए विकसित किया गया है।

रोग की निगरानी, उसकी उपस्थिति और प्रसार का पता लगाने के लिए गेहूँ रोग निगरानी नर्सरी (WDMN) और सार्क गेहूँ रोग निगरानी नर्सरी (SAARC-WDMN) लगाई गई और इन्हें क्रमशः भारत के 38 स्थानों और 6 सार्क देशों सहित भारत के 27 स्थानों पर संचालित किया गया। 150 विभिन्न रतुआ रोगजनकों के प्रभेदों का संग्रह पौधों के ऊपर और शीत–संरक्षित (क्रायो–प्रिजर्व्ड) रूप में पोषित किया गया। गेहूँ और जौ के विभिन्न रतुआ रोगजनकों के न्यूक्लियस/बल्क इनोकुलम को भारत के विभिन्न राज्यों में 50 से अधिक वैज्ञानिकों/रतुआ अनुसंधान केन्द्रों में भेजा गया।

During the 2024–25 crop season, wheat rusts appeared across multiple Indian states, with leaf rust exhibiting significantly higher intensity and prevalence compared to stem rust and yellow rusts. The first natural incidence of stripe rust in wheat was reported during late January 2025 from Haryana and Punjab, followed by confirmations from other regions in North India. The earliest report of wheat leaf rust was from Punjab during the second week of January. The subsequent reports on the occurrence of wheat leaf rust were from Maharashtra, Madhya Pradesh, and other states. Stem rust first appeared in February, primarily in Maharashtra and Karnataka, with variable severity levels recorded across states and wheat varieties. These field observations prompted a swift disease management response, including real-time alerts and advisories issued by ICAR-IIWBR in coordination with progressive farmers, state and national agriculture departments.

During the season, a total of 1,293 rust samples were collected and analyzed from 14 Indian states as well as Nepal. It includes 155 stripe rust, 261 stem rust and 877 leaf rust samples. Eleven pathotypes of stripe rust (*Pst*) and one of barley stripe rust (*Psh*) have been identified in 155 samples of stripe rust. In stripe rust, pathotype 46S119 was most prevalent, followed by 47S103 and 110S119. Only three samples of barley stripe rust were received and analyzed during the season, all of which produced pathotype 57 (0S0). Seven pathotypes of wheat stem rust pathogen have been confirmed in 261 stem rust samples analyzed during the season, of which the pathotype 11 was the most prevalent. Notably, new pathotypes like 106G5 and 127G13 have appeared in Karnataka and Tamil Nadu, indicating that virulence patterns *Pgt* is shifting. Thirty-one pathotypes of wheat leaf rust pathogen (*Pt*) were identified in 877 samples. The pathotype 77-9 (121R60-1) was the most predominant as it was detected in 42% of the samples followed by 52-4 (24.65 %), indicating their widespread presence. A new pathotype of leaf rust 77-13 was identified from samples collected from Dausa district, Rajasthan. Its virulence pattern is similar to pathotype 104-2 with additional virulence on *Lr2a, Lr2b, Lr2c, Lr10* and Raj1555.

For screening and resistance profiling approximately 5,000 wheat and barley lines were screened during 2024-25 at seedling stage under controlled conditions using an array of pathotypes of stem (*Pgt*), leaf (*Pt*) and stripe rust (*Pst*) possessing different avirulence/virulence structures. AVT entry MACS4147 exhibited resistance to all the pathotypes of three rust pathogens. The wheat line DBW426 exhibited resistance to both black and brown rusts. None of the AVT entries showed resistance against all tested pathotypes both of black and yellow rust pathogens. However, two entries (NIDW1542 and PBW938) conferred resistance to both brown and yellow rusts. Eleven entries (excluding those carrying the *Sr31* and *Sr24* genes) conferred resistance to black rust pathotypes.

Among the 204 AVT lines 4 *Yr* genes (*Yr2, Yr9, YrA,* and *Yr18*) were postulated in 114 lines, with *Yr2* being the most frequent. Likewise, 8 *Lr* genes (*Lr1, Lr3, Lr10, Lr13, Lr23, Lr24, Lr26, Lr34)* were characterized in 148 lines. Among these *Lr13* and *Lr1* were the most frequent. Twelve stem rust resistance genes (*Sr*2*, Sr5, Sr7b, Sr8a, Sr9b, Sr9e, Sr11, Sr13, Sr24, Sr28, Sr30* and *Sr31)* were characterized in 165 AVT lines with *Sr7b* and *Sr2* being most frequent.

The AVT entries were screened against the most predominant and virulent pathotypes of *Pt*, *Pst* and *Pgt* at adult plant stage. Three pathotypes each of *P. triticina* (77-5, 77-9 and 104-2) and *P. striiformis* f. sp. *tritici* (46S119, 110S119 and 238S119), and *P. graminis* f. sp. *tritici* (11, 40A and 117-6) were used for screening. Three entries (DBW426, DBW390, and DBW369) conferred APR for all Pt pathotypes. Seventy-five entries of AVT showed APR to one or the other pathotypes of *P. triticina.* Likewise, seventy-three entries showed APR to different tested pathotypes of stripe rust pathogen. Eighteen entries exhibited APR to different stem rust pathotypes.

Two hundred forty-six NBDSN and eight EBDSN entries were screened for rust resistance at seedling stage against different pathotypes of three rusts of barley. None of the NBDSN or EBDSN entries conferred resistance to all the pathotypes of three rust pathogens *P. striiformis hordei* (stripe rust), *P. hordei* (leaf rust) and *P. graminis tritici* (stem rust). Eleven entries of NBDSN (BHS498, BHS503, BHS504, HBL890, RD3137, RD3138, RD3139, RD3141, RD3142, RD3143, and RD3145) were resistant to both leaf and stripe rusts. Resistance to all the pathotypes of stripe rust pathogen was observed in three

(DWRB238, DWRB2309, and DWRB137) entries of EBDSN. The barley leaf rust resistance genes (Rph3 and Rph19) were postulated in 34 NBDSN and 3 EBDSN lines.

Using molecular markers, the *Yr9/Lr26/Sr31* complex was validated in 8 AVT lines. 24 AVT lines carrying the *Lr24/Sr24* gene complex was confirmed using *Sr24*#12 marker. Likewise, *Yr15* was identified in 25 lines, *Lr68* in 55, *Yr17/Lr37/Sr38* in 56, *Yr18/Lr34/Sr55* in 9, *Yr29/Lr46* in 43, and *Yr24* was identified in 3 lines.

Numerous germplasm lines and landraces with known *Lr* genes (*Lr10, Lr67, Lr23, Lr46, Lr13, Lr26*) were crossed to develop F1 hybrids. Fifteen F2 and F3 families were raised during the season to accumulate *Lr* gene pyramids. Brown rust-resistant Hango-2 (with *Lr80*) was crossed with FLW lines for resistance to all three rusts. In barley, F3 populations with Rph5, Rph7, and Rph12 were developed in elite backgrounds. F2 populations of barley has been developed for resistance studies against stripe rust.

To monitor, the occurrence and spread of disease, wheat disease monitoring nursery (WDMN/TPN) and SAARC wheat disease monitoring nursery were organized and conducted at 38 locations in India and 27 locations across the six SAARC countries, respectively. A collection of 150 pathotypes of different rust pathogens was maintained in live culture as well as cryo-preserved. Nucleus/bulk inoculum of different pathotypes of rust pathogen was supplied to more than 50 Scientists/centers for conducting wheat and barley rust research elsewhere in India.

1. Incidence of wheat and barley rusts in India

The systematic surveillance of wheat and barley crops for rust diseases was carried out by multiple monitoring teams during the crop season 2024–25. Based on field observations and disease forecasts, timely advisories were issued by the ICAR-Indian Institute of Wheat and Barley Research (ICAR-IIWBR), Karnal, along with the State Departments of Agriculture and the Department of Agriculture, Cooperation and Farmers' Welfare (Government of India), to effectively manage and curb the spread of rust diseases and insect pests affecting the crop. During this season, wheat rusts were observed across multiple states in India. Disease intensity of leaf rust was more compared to stem and yellow rust. The first incidence of stripe rust (yellow rust) was detected late in January 2025 in a small patch of a farmer's field sown with wheat cultivar DBW303 at Nuhiyawali village, Sirsa district, Haryana. Subsequently, stripe rust was also found on PBW826 in Chhadauri village, Balachaur block, Nawanshahr district, Punjab. A crop health survey conducted on January 28, 2025, confirmed further presence of stripe rust in wheat fields across SBS Nagar, Ropar, and Gharshanker in Punjab. In addition, Jandla village reported stripe rust (80S severity) on barley of unknown variety. Likewise, leaf rust (leaf rust) emerged with its first occurrence in the second week of January in a wheat field (cv. SW23) at Jandla village, Shri Anandpur Sahib block, Ropar district, Punjab. By January 15, leaf rust was also observed on PBW826 in Chhadauri village, Punjab, and later reported from the KVK Ropar nursery on January 31, on HD2204. During the second and fourth weeks of January, leaf rust symptoms were also recorded with 5MS to 20S severity at research farms of Agharkar Research Institute (ARI), Hol and Baramati on off-types and private varieties. In Madhya Pradesh, isolated infection appeared on tall mixture plants in Deep Gaon, Dewas district, on January 24 and 29. A roving survey on January 27 in Nashik and Ahilyanagar districts of Maharashtra showed leaf rust in traces. However, by February, the disease had spread widely, with 20S to 40S severity recorded in Pune, Satara, Ahilyanagar, Ch. Sambhaji Nagar, and Jalna districts, and later reaching 20–60% severity in Nashik district by March 24. The was stem rust was first observed on February 1st week in Pune, Satara, and Sangli districts, with severity ranging from 20S to 60S. A survey on February 21 at ARI Niphad confirmed stem rust (MS type) on older varieties such as Lok-1, Kalyansona, and private lines. By March 24, stem rust (MS type) was also recorded in Dindori, Surgana, and Kalvan tahsils of Nashik, affecting cultivars like Puna Shrabati, Gujarat Sivhor, and off-type mixtures.

The wheat and barley rusts were kept under check with the help of cooperators, through exhaustive rust surveillance in different wheat growing areas of India and neighboring countries. Besides the staff of the station, 28 wheat researchers (Table 1) from different institution/State/Countries helped in effective monitoring of wheat and barley rust diseases and sending wheat and barley rust samples. Wheat monitoring teams of different zones also reported the occurrence of wheat rusts in the areas visited by them.

Table 1. List of actively involved co-operators in monitoring wheat and barley rusts during 2024-25.

Cooperators	Organization/State
Indian States	
AM Patel	WRS, Vijapur, Gujarat
B.M. Mhaske	ARS, Niphad, Maharashtra
Deepshikha	GBPUAT, Pantnagar, US Nagar, Uttarakhand
Dharam Pal	RS, ICAR-IARI, Shimla, Himachal Pradesh
Divya Bhandhari	PAU, Ludhiana, Punjab
Sushil	MPKV, RWRRS, Mahabaleshwar
FA Mohiddin	SKUAST-K, Khudwani
GM Hegde	UAS, Dharwad, Karnataka
Hanif Khan	ICAR-IIWBR, Karnal, Haryana
IB Kapadiya	Wheat Research Station, JAU, Junagadh
Jaspal Kaur	PAU, Ludhiana, Punjab
KK Mishra	ICAR- VPKAS Almora
KK Mishra	JNKVV, Powarkheda, MP
M. Sivasamy	IARI-RS Wellington, T. N.
Pooja Yadav	HAU, Hisar, Haryana
P Nallathambi	IARI-RS Wellington, T. N.
PL Kashyap	ICAR-IIWBR, Karnal
Pradeep Shekhawat	RARI, Durgapura, Jaipur, Rajasthan
Prakash, T L	RS, ICAR-IARI, Indore, Madhya Pradesh
R.V. Thakkar	ARS, Vijapur, Gujarat
Rajendra Singh	HAU, Hisar, Haryana
Shailendra Jha	ICAR-IARI, New Delhi
Satyajeet Hembram	UBKV, Coochbehar, WB
Sawant Shradha Bhaskar	BAU, Sabour, Bihar
Sudhir Navathe	Agharkar Research Institute, Pune, Maharashtra
Uma Maheshwari	IARI-RS Wellington, T. N.
V.K. Yadav	CSAUAT, Kanpur, UP
Nepal	
Suraj Vaidya	NARC, Kathmandu, Nepal

2. Monitoring pathotype distribution of *Puccinia* species on wheat and barley

A total of 1293 samples of three rusts of wheat, stripe and stem rusts of barley collected from fourteen Indian states, and Nepal were analyzed during 2024-25.

i. Stripe (yellow) rust of Wheat and Barley (*Puccinia striiformis* f. sp. tritici, *Pst* and *Puccinia striiformis* f. sp. *hordei, Psh*)

During current season, 155 stripe rust samples of wheat were analyzed from five states and two UTs (Himachal Pradesh, Punjab, Haryana, Uttarakhand, Rajasthan, Delhi and Ladakh) of India and Nepal. Eleven pathotypes of *Puccinia striiformis* f. sp. *trititci* (*Pst*, yellow rust of wheat) {238S119, 110S119, 46S119, T (47S103), P (46S103), 78S84, 6S0, 7S0, 14S64, 15S64 and 78S64} and one pathotype 0S0 (57) of *Puccinia striiformis* f. sp. *hordei* (*Psh*, yellow rust of barley) were identified (Table 2). *Pst* populations were avirulent to *Yr5*, *Yr10*, *Yr15*, *Yr16*, *Yr32*, and *YrSP*. Most of the stripe rust samples were collected from Punjab (49) followed by Rajasthan (33). During this cropping season, the frequency of pathotype 46S119 was maximum (28.3%) followed by 47S103 (20.8%) and 110S119 (20.1%). In Ladakh, pathotypes 14S64, 15S64 and 78S64 were confirmed, these races are endemic to Ladakh region and not occurring elsewhere in India. Pathotype 0S0 (57) was identified in 3 samples of barley. Other pathotypes were identified in low frequency (<6%, Table 2).

ii. Stem (black) rust of Wheat (*Puccinia graminis* f.sp. *tritici,* Pgt)

A total of two hundred sixty-one samples of wheat and barley stem (black) rust were received from five Indian states (Gujarat, Madhya Pradesh, Maharashtra, Karnataka and Tamil Nadu) during the crop season. Seven pathotypes of *P. graminis tritici* were identified from the analysis of 261 samples. Population analyzed during the year had avirulence to *Sr24, Sr26, Sr27, Sr31, Sr32, Sr35, Sr39, Sr40, Sr43, SrTt3* and *SrTmp*. Pathotype 11 (79G31=RRTSF), virulent on *Sr2, Sr5, Sr6, Sr7b Sr9a, Sr9b, Sr9c, Sr9d, Sr9f, Sr9g, Sr10, Sr13, Sr14, Sr15, Sr16, Sr17, Sr18, Sr19, Sr20, Sr21, Sr28, Sr29, Sr30, Sr34, Sr36, Sr38,* and *SrMcN* was recorded in more than 45% of the samples analyzed during the season, which was followed by 40A (23.75%) and 40-3 (19.15%) (Table 3). Pathotypes 40-

2 and 15-1 were identified in twelve and eleven samples, respectively. Diversity of black rust pathogen was maximum in Karnataka as maximum number of pathotypes were identified from this state.

New pathotype of black rust pathogen

Seven new pathotypes of black rust pathogen were suspected from the samples received from Dharwad, Karnataka and Wellington, Tamil Nadu. Detailed studies on these probable newly emerging pathotypes are in progress. One isolate collected from Dharwad, Karnataka during 2018–19 was found to produce a unique infection profile on standard differentials, leading to the identification of a new pathotype 106G5, characterized by virulence corresponding to 21-1 along with additional virulence on *Sr30*. Another pathotype, 63G29, also emerged from the same region and year, showing virulence matching 40A with added virulence to *Sr13*. In the subsequent year 2019–20, pathotype 127G13 was detected in Dharwad, differing by its avirulence on the Charter differential (*Sr11*+), corresponding to 40-3. Shifting focus to Wellington, Tamil Nadu, the year 2021–22 saw the appearance of pathotype 255G31, expressing virulence to 40-3, with added virulence to *Sr37*, while 123G29, close to 40-3, also from Wellington in the same year, exhibited avirulence to *Sr11*. In 2022–23, two new pathotypes 111G29 and 126G29 were identified in Wellington; the former lacked virulence to *Sr8b* from 40A, and the latter demonstrated a complex profile with virulence to 40A and additional virulence on *Sr30* and *Sr25*.

iii. Leaf (brown) rust of Wheat (*Puccinia triticina*, Pt)

A total of 877 samples of wheat leaf rust pathogen were analyzed from 14 states of India and neighboring country Nepal. Thirty-one pathotypes were identified in these samples. Pathotype 77-9 (121R60-1) was the most widely distributed and occurred in 42.30% of the samples followed by 52-4 (121R60-1,7) in 24.28% samples (Table 4). Pathotype 77-5 (121R63-1), which remained most predominant for more than 20 years was observed in 17.33% samples only. The remaining 28 pathotypes were identified in 16% samples only. The *P. triticina* population from Karnataka was highly diverse as highest number of pathotypes (23) was detected in the samples collected from Karnataka (Table 4). From Nepal 13 pathotypes were detected in 98 samples. Like Indian scenario pathotype 77-9 followed by 52-4, from Nepal, were the most predominant pathotypes and detected in 41 and 29 samples, respectively.

New pathotype of brown rust pathogen

77-13 (93R57-1,7)

A brown rust of wheat sample collected from Dausa district of Rajasthan during the cropping season 2022-23 produced different infection types on brown rust differentials in comparison to previously known pathotypes and designated as 77-13 (93R57-1,7). It is similar to pathotype 104-2 (21R55) except additional virulence on *Lr2a*, *Lr2b*, Lr2c, *Lr10* and Raj1555. Raj1555 is a durum wheat is on 7th position of 0-set differential of brown rust of wheat. Earlier only four pathotypes 16 (0R0-7), 16-1 (5R9-7), 52-4(121R61-1,7) and 52-5 (125R28-1,7) were virulent on Raj1555. This pathotype is more virulent on advance wheat lines of wheat in comparison to Pathotype 104-2 (21R55). Detailed studies of this new pathotype are on progress.

Table 2. Pathotype distribution of yellow rust of wheat (*Puccinia striiformis* f. sp. *tritici*) in India and neighboring countries during 2024-25.

S. No.	State/UT/Country	No. of isolates Analyzed	Pathotype											Psh Pathotype
			238S119	110S119	46S119	T (47S103)	P (46S103)	78S84	6S0	7S0	CI (14S64)	**CII (15S64)**	**CIII (78S64)**	57
1.	Himachal Pradesh	23	5	5	12	-	1	-	-	-	-	-	-	-
2.	Punjab	49	8	12	20	3	2	-	3	-	-	-	-	1
3.	Haryana	14	4	8	2	-	-	-	-	-	-	-	-	-
4.	Uttarakhand	2	-	-	-	-	1	-	1	-	-	-	-	-
5.	Rajasthan	33	1	3	4	22	3	-	-	-	-	-	-	-
6.	Delhi	2	2	-	-	-	-	-	-	-	-	-	-	-
7.	Ladakh	12	-	-	-	-	-	-	-	-	6	2	2	2
Other country														
1	Nepal	20	-	1	6	5	1	1	5	1	-	-	-	-
Total		**155**	**29**	**29**	**44**	**30**	**8**	**1**	**9**	**1**	**6**	**2**	**2**	**3**

NB: Yellow rust of wheat (*Puccinia striiformis* f. sp. *trititci, Pst*); Yellow rust of barley (*Puccinia striiformis* f. sp. *hordei, Psh*)

Table 3. Pathotype distribution of black rust (*Puccinia graminis* f. sp. *tritici*) in India and neighboring countries during 2024-25.

S. No.	States/Countries	Number of isolates analyzed	Pathotypes identified*¥						
			11	**15-1**	**21**	**21-1**	**40A**	**40-2**	**40-3**
1	Gujarat	121	95	01	-	-	20	-	05
2	Madhya Pradesh	20	14	-	-	-	04	-	02
3	Maharashtra	06	01	-	-	-	03	-	02
4	Karnataka	30	11	02	03	01	02	03	08
5	Tamil Nadu	84	01	08	-	-	33	09	33
Total		**261**	**122**	**11**	**3**	**1**	**62**	**12**	**50**
Indian binomial names ¥North American equivalents 11 (79G31; RRTSF¥), 15-1 (123G15; TKTSF), 21 (9G5; CHMSC), 21-1 (24G5; CKMSC), 40A (62G29; PTHSC), 40-2 (58G13-3; PKRSC), 40-3 (127G29; PTTSF) based on Jin *et al*., *Plant Dis.* 2008, 92: 923-6.									

Table 4. Pathotype distribution of brown rust (*Puccinia triticina*) in India and neighboring countries during 2024-25.

S. No.	State/Country	No. of isolates Analyzed	Pathotypes																														
			12(5R5)	12-1 (5R37	12-2 (1R5)	12-3 (49R37)	12-4 (69R13)	12-5 (29R45)	12-6 (5R45)	12-7 (93R45)	12-8 (49R45)	12A (5R13)	20-1 (93R57-1)	77-1 (109R63)	77-3 (125R55)	77-5 (121R63-1)	77-6 (121R55-1)	77-9 (121R60-1)	77-11 (125R28)	77-12 (1R31)	77A (109R31)	104A (21R31)	104B (29R23)	104-1 (21R31-1)	104-2 (21R55)	104-3 (21R63)	108-1 (57R27)	162 (93R7)	162A (93R15)	52-4 (121R60-1,7)	52-5 (125R28-1,7)	143 (61R47)	24R44
1.	Himachal Pradesh	15	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	5	-	-	-	-	-	-	4	-	-	-	-	4	-	-	-
2.	Laddakh	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
3.	Punjab	87	-	-	-	-	-	-	1	-	-	-	-	-	-	3	-	47	-	-	-	-	-	-	1	-	-	-	-	35	-	-	-
4.	Haryana	58	1	-	-	-	1	-	-	-	-	-	-	-	-	3	-	33	1					1	1	1				16	-	-	-
5.	Uttar Pradesh	39	-	1	-	-	-	-	1	-	-	-	-	-	-	2	-	20	-	-	-	-	-	-	-	-	-	-	-	15	-	-	-
6.	Uttarakhand	28	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	16	-	-	-	-	-	-	-	-	-	-	-	11	1	-	-
7.	Bihar	22	-	-	-	-	-	-	1	-	-	-	-	1		2	-	12	-	-	-	-	-	-	-	-	-	-	-	4	2	-	-
8.	Jharkhand	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9.	West Bengal	2	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
10.	Madhya Pradesh	70	4	-	-	4	-	-	-	1	-	-	-	-	-	6	1	29	3	-	1	1	3	1	3	3	-	4	-	6	-	-	-
11.	Gujarat	11	-	-	-	-	-	-	-	-	-	-	-	1		3	-	4	-	-	-	-	-	-	-	-	-	-	-	2	1	-	-
12.	Rajasthan	27	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	8	-	-	-	1	-	-	-	-	-	-	1	14	-	-	1
13.	Maharashtra	79	-	-	4	-	-	-	-	-	-	-	-	-	2	8	1	34	2	-	1	1	-	2	3	1	-	-	-	18	2	-	
14.	Karnataka	134	2	1	-	1	1	2	5	-	1	1	-	2	-	4	-	41	2	2	1	2		3	8	2	1	2	-	39	2	-	9
15.	Tamil Nadu	204	-	-	-	-	-	1	-	1	-	-	-	-	-	101	-	78	1	-	-	-	-	-	1	-	-	-	-	20	-	1	-
Other country																																	
1.	Nepal	98	1	_	_	_	1	1	1	1	_	1	1	1	2	17		41	_	_	_	_	_	_	1	_	_	_	_	29	_	_	_
Total		**877**	**9**	**2**	**4**	**5**	**3**	**4**	**9**	**3**	**1**	**2**	**1**	**5**	**4**	**152**	**3**	**371**	**9**	**2**	**3**	**6**	**3**	**7**	**22**	**7**	**1**	**6**	**1**	**213**	**8**	**1**	**10**

3. Seedling resistance test (SRT) in wheat against virulent pathotypes of rust pathogens and characterization of rust resistance genes

To identify sources of rust resistance, over 2,400 wheat and barley lines were evaluated at the seedling stage during the 2024–25. Among these, 458 lines including 204 from the AVT and 254 from NBDSN/EBDSN were subjected to rigorous screening against multiple pathotypes under controlled conditions of light and temperature (Table 5). The 204 advanced wheat lines were screened against 62 pathotypes belonging to three *Puccinia* species known to cause rust diseases in wheat. These included 15 pathotypes of *Puccinia striiformis* f. sp. *tritici* (stripe rust), 23 of *P. graminis* f. sp. *tritici* (stem rust), and 24 of *P. triticina* (leaf rust). The pathotypes selected for evaluation were those that are currently most virulent and predominant in wheat-growing regions of India. The inoculated seedlings were incubated in saturated humid chambers for 48 hours at optimum temperature and light for each of the rust. Subsequently these plants were transferred on to the greenhouse benches where sufficient day light (more than 15,000 Lux) and temperature of 16±2^{0}C (stripe rust), 22±2^{0}C (leaf rust) 24±2^{0}C (stem rust) and relative humidity of 80-100% were maintained. The comprehensive screening helps in identifying lines with broad-spectrum resistance, which are vital for breeding rust-resistant cultivars.

Table 5. Details of wheat and barley materials used for Seedling Resistance Test during 2024-25

S. No.	Description	No of Lines	Pathotypes		
			Black rust	Brown rust	Yellow rust
1.	Barley Lines (NBDSN and EBDSN)	289	11, 21A-2, 40A, 117-6, 122	Multiple	Multiple
2.	Wheat Lines (Mr Amit)	44	-	77-5, 77-9, 104-2	46S119, 78S84, 238S119
3.	Wheat Lines (Dr. Suma)	19	11, 40A, 21A-2, 117-6, 122	Multiple	238S119, 110S119, 78S84, 110S84, T
4.	Wheat Lines (Dr Hanif Khan)	55	Multiple	Multiple	238S119, 110S119, 46S119, 110S84, T, P, 6SO

5.	NBPGR (CRP Project)	298	11, 40A, 40-3, 117-6	12-5, 77-5, 77-9, 104-2	-
6.	Wheat Lines (Dr. Walia)	32	-	77-5 77-9 77-8	T, 238S119, 110S84, P
7.	Wheat Varieties (Dr. Sindhu Sarin)	87	-	12-5, 77-1, 77-5, 77-9, 104-2	110S119, 238S119, T, K
8.	Wheat Lines (H.S. Balyan))	23	11, 40A, 21A-2, 117-6, 122	12-5, 77-2, 77-5, 77-9, 104-2	238S119, 46S119, T, 110S119, 110S84
9.	Wheat Lines (Dr. Deepak)	54	-	77-5, 77-9	110S119, P, 238S119
11.	Wheat Lines (Shailendra Jha)	1	-	Multiple	238S119
12.	Wheat Cross Population (Dr. Madhu Patiyal)	249	-	Multiple	Multiple
13.	Wheat Varieties (Dr. Sindhu Sarin)	6	-	Multiple	238S119, 46S119, T, 110S119, 110S84, PS
14.	Wheat Lines (HAU Hisar)	51	-	-	110S119, 238S119, P, T, 110S84
15.	Wheat Germplasm (Dr. Wani)	400	-	-	238S119, T, 110S119, 110S84
16.	Synthetic Wheat Lines (IIWBR Karnal, Lalit)	88	-	-	Multiple
17.	Barley Germplasm, NBPGR, Dr.V. Kaur	261	-	-	24, 57, 6SO, Q, 24, 57
18.	Wheat Lines (Dr. S. Jha)	2	-	Multiple	Multiple
19.	Wheat Lines (AVT, 2024-25)	204	Multiple	Multiple	Multiple
20.	Wheat Lines (Dr. C.N. Mishra)	09	-	-	238S119, 46S119, T, 110S119, 110S84
21	Wheat Lines (Dr. P. Babu)	262	-	12-5, 77-2, 77-5, 77-9, 104-2	-
Barley					
1.	Barley Lines (NBDSN and EBDSN)	289	11, 21A-2, 40A, 117-6, 122	Multiple	Multiple
Total		**2457**			

Rust resistance in AVT lines

MACS4147 was the only AVT entry exhibiting resistance to all pathotypes of the three rust pathogens. Other wheat lines showing resistance to individual rusts or in combinations are presented in Table 6. The wheat line DBW426 exhibited resistance to both black and brown rusts. None of the AVT entries showed resistance against all tested pathotypes both of black and yellow rust pathogens. However, two entries

(NIDW1542 and PBW938) conferred resistance to both brown and yellow rusts. Additionally, 42 lines were found resistant to leaf rust, and eight showed resistance to yellow rust. Eleven entries (excluding those carrying the *Sr31* and *Sr24* genes) conferred resistance to black rust pathotypes (Table 6).

Table 6. Rust resistance in advanced wheat material (AVT: 2024-25)

Rusts	No. of lines	Variety/line
Brown, Black and Yellow	01	MACS4147(d)
Brown and Black	01	DBW426
Brown and Yellow	02	NIDW1542, PBW938
Black and Yellow	-	None
Brown only	42	BRW3959, CG1029, DDW65, GW554, GW555, GW556, GW561, GW563, GW1029, HD3090, HD3463, HD3515, HI1563, HI1633, HI1683, HI1687, HI1696, HI1697, HI1699, MACS4125, MACS4131, MACS4135, MACS4146, MACS6222, MACS6768, MACS6829, MACS6830, MACS6854, MACS6851, MPO1398, NIAW4267, NIAW4533, NIAW4581, NIDW1557, NIDW1561, NW8089, PBW833, RAJ4083*, UAS484, UBW22, WH1338, WSM138
Black only	11	DBW110, DBW303, DBW377, DBW462, HD3486, HP1983, K1317, MACS6837, MACS6844, MP4010, UP3145
Yellow only	08	DBW477M, HD3467, PBW915, PBW921, PBW942, PBW951, PBW953, SVPWL22-02

Rust resistance genes in AVT lines (Gene postulation)

Wheat rust resistance genes (*Lr, Sr, Yr*) were characterized using gene matching technique. Rust resistance genes were characterized in those lines where differential host-pathogen interaction was present. In addition, linked characters, morphological markers, characteristic infection types and pedigree also formed the basis for postulating rust resistance genes in absence of host-pathogen differential reactions.

Yr-genes

Among the 204 lines of AVT, *Yr* genes were characterized in 114 lines. *Yr* genes were postulated in lines where differential interactions were observed and some cases tight linkage of *Yr* genes to other *Lr* and *Sr* genes also implicated the presence of a resistance gene. Three *Yr* genes viz. *Yr2*, *Yr9*, and *YrA* contributed to yellow rust resistance in Indian wheat material. Among the postulated *Yr* genes, the frequency of *Yr2* was maximum and it was characterized in 98 lines. *Yr9* was postulated in 08 entries (Table 7).

Table 7. *Yr*-genes postulated in AVT entries during 2024-25

Yr-gene	No. of lines	Variety/ line
Yr2+	98	BCW32, BW20R105, CG1029, CG1040, CG1045, CG1052, DBW107, DBW110, DBW187, DBW252, DBW296, DBW303, DBW327, DBW371, DBW372, DBW377, DBW422, DBW426, DBW445, DBW446, DBW455, DBW457, DBW458, DBW459, DBW460, DBW462, DBW466, DBW467, DBW469, DBW509, DDK1068, GW555, HD3059, HD3086, HD3118, HD3171, HD3249, HD3293, HD3386, HD3388, HD3463, HD3468, HD3471, HD3478, HD3482, HD3486, HD3488, HI1563, HI1605, HI1612, HI1621, HI1653, HI1696, HI1697, HI1700, HI8850(d), HI8851(d), HI8856(d), HI8857(d), HW1098, JKW261, K1317, KRL210, MACS4131(d), MACS4135(d), MACS5064, MACS5065, MACS6222, MACS6837, MACS6844, MACS6862, MACS6868 MP1399, MP1401, MP3570, MP3601, MPO1403, NIAW4621, NIAW4624, NIDW1149(d), PBN2115, PBW644, PBW826, PBW833, PBW872, PBW906, PBW929, PBW943, PBW944, PDW291, PDW314, RAJ4083, UAS3034, UBW21, WH1329, WH1337, WH1339, WHD969
Yr9+	08	GW563, HD3090, HI1633, HI1634, HI1699, HI1702, MACS6854, PBW771
YrA+	08	DBW425, DBW432, DBW448, DBW452, DBW465, DBW470, PBW935, UAS3033
Total	**114**	

Lr-genes

Eight *Lr* genes *Lr1*, *Lr3*, *Lr10*, *Lr13*, *Lr23*, *Lr24*, *Lr26,* and *Lr28* were characterized in 148 entries. *Lr13* was the most commonly postulated leaf rust resistance gene that was characterized, alone or in combination, in maximum number of lines (69) followed by *Lr1* (53 lines) and *Lr23* (50 lines). The *Lr24* that is linked with *Sr24* was postulated in 24 entries. *Lr26,* tightly linked with *Yr9* and *Sr31*, was characterized in 8 lines. Other *Lr* genes i.e. *Lr3* and *Lr28* were postulated seven and two entries, respectively. Resistance to leaf rust in five entries was based on a combination of three different genes (Table 8).

Table 8. *Lr*-genes postulated in AVT entries during 2024-25

Lr-Gene	No. of lines	Lines/Varieties
Lr3+	3	DBW425, HI8850, HP1983
Lr13+	15	CG1040, CG1047, DBW222, DBW303, HD2932, HD3249, HD3488, HI1605, HI1621, KRL19, KRL2203, MACS6844, NIAW4621, UAS3034, WH1329
Lr13+1+	26	BW20R105, CG1045, CG1052, DBW422, DBW432, DBW452, DBW457, DBW462, DBW465, DBW509, GW322, HD3482, HD3486, K1317, KRL2301, MP1399, MP1401, MP3601, PBN2115, PBW644, PBW906, PBW934, PBW935, PBW943, UAS3033, UBW21
Lr13+3+	1	HD3059
Lr13+10+	21	DBW88, DBW252, DBW446, DBW448, DBW455, DBW469, DBW470, DBW477, HD3293, HD3386, HD3468, HD3471, HD3495, K2304, MP3570, HD3595, PBW921, PBW939, PBW951, SVPWL22-02, PBW942
Lr13+10+1+	1	NIAW3170
Lr13+10+3+	2	HD3086, HI1653
Lr23+	17	DDK1068, HI1612, HI8851, HI8855, HI8856, HW5306, KRL210, MACS5064, MACS5065, MP3598, MPO1395, NIDW1149, PDW314, PDW367, UAS478, UAS487, WHD969
Lr23+1+	23	BCW32, DBW327, DBW371, DBW372, DBW377, DBW445, DBW458, DBW459, DBW460, DBW466, DBW467, HD3288, HD3467, HD3478, MACS6837, MACS6862, MACS6868, NIAW4624, PBW826, PBW929, UP3145, WH1337, WH1339
Lr23+3+	1	UAS485
Lr23+10+	3	DBW173, PBW872, PBW944
Lr23+10+1+	1	DBW187
Lr23+13+	1	JKW261
Lr23+13+10+	2	DBW296, HD3171
Lr24+	21	CG1029, GW554, GW555, GW556, GW561, GW1029, HI1563, HI1683, HI1687, HI1696, HI1697, HI1700, MACS6222, MACS6829, MACS6830, MACS6851, NIAW4267, NIAW4533, NIAW4581, RAJ4083[@], WSM138
Lr24+26+	3	GW563, HI1699, MACS6854
Lr26+	2	HD3090, HI1633
Lr26+10+	1	HI1702
Lr26+23+1+	2	HI1634, PBW771
Lr28+	2	PBW915, PBW953
Total	**148**	
[@]: Different seed lot to that of previous cropping season		

Sr-genes

Twelve stem rust resistance genes (*Sr*2, *Sr5, Sr7b, Sr8a, Sr9b, Sr9e, Sr11, Sr13, Sr24, Sr28, Sr30* and *Sr31*) were characterized in 165 AVT lines (Table 9). The frequency of *Sr7b* and *Sr2* was maximum as they were postulated in 49 and 48 AVT entries, respectively, followed by *Sr11* and *Sr13*, which were characterized in 46 and 45 entries, respectively. *Sr31* linked with *Lr26* and *Yr9* and conferring resistance to all the known

Pgt pathotypes in Indian subcontinent was postulated in eight AVT entries, while *Sr24* linked to *Lr24* was characterized in 24 entries. Other *Sr* genes i.e. *Sr9b, Sr30, Sr5, Sr9e, Sr8a,* and *Sr28,* were postulated in 24, 19, 16, 11, 6 and 1 entries, respectively. The *Sr* genes were characterized singly or in combination of up to four gens. DBW252 and KRL19 had combination of four *Sr* genes i.e. *Sr8a+5+11+2+* and *Sr8a+9b+11+2+*, respectively (Table 9).

Table 9. *Sr*-genes postulated in AVT entries during 2024-25

Sr genes	No. of Lines	Details of Lines
Sr31+24+	03	GW563, HI1699, MACS6854
Sr31+2+	04	HD3090, HI1633, HI1702, PBW771
Sr31+	01	HI1634
Sr24+	16	GW554, GW555, GW556, GW561, GW1029B, HI1683, HI1696, HI1697, HI1700, MACS6829, MACS6830, MACS6851, NIAW4267, NIAW4533, RAJ4083, WSM138
Sr24+2+	05	CG1029, HI1563, HI1687, MACS6222, NIAW4581
Sr30+8a+2+	01	PBW826
Sr30+5+2+	01	HD3386
Sr30+5+	08	DBW445Q, DBW446, DBW457, DBW509B, HD3086, MP1399, UAS3034, WH1339
Sr30+2+	06	BCW32, BRW3959, CG1045, DBW455, MP3598, PBW935
Sr30+	03	KRL2301, PBW944, PBW951
Sr28+	02	DBW372, HI1621
Sr8a+5+11+2+	01	DBW252
Sr8a+5+	01	DBW371
Sr8a+9b+11+2+	01	KRL19
Sr8a+9b +	01	UBW22
Sr8a+2+	01	NIAW3170
Sr5+9b+13+	01	DBW425
Sr5+9b+11+	01	MACS6868
Sr5+13+	01	DBW327
Sr5+11+	02	DBW187, HI1605
Sr9e+11+	01	PBW921
Sr9e+13+	01	HD3495M
Sr9e+2+	05	HI8627(d), HI8713(d), HI8737(d), PDW291, PDW314
Sr9e+	04	DDW66, HI8854, HI8855(d), MPO1395(d),
Sr9b+13+11+	06	DBW422, DBW432, DBW466, HD3463, PBN2115, SVPWL22-02
Sr9b+13+7b+	03	PBW942, UBW21, WH1329
Sr9b+13+	01	MP3570
Sr9b+11+	04	CG1052, DBW459, HD3118, PBW953
Sr9b+7b+	05	BW20R105, DBW448, HD3488, HD3515M, WH1337

Sr9b+	02	CG1047, DBW467
Sr13+11+	06	DBW458, DBW470, DBW477M, DDK1069, PBW915, PBW934
Sr13+7b+2+	01	WHD969
Sr13+7b+	19	DBW296, GW1369(d), HD3388, HD3471M, HD3482, HI8851(d), HI8858(d), HI8864B, HW5306, K2304, MACS5064, MACS5065, MACS5066, MACS5067, PBW906, PBW938, PDW367, UAS3033, UAS487(d)
Sr13+2+	02	HD3293, HI8853
Sr13+	04	DDK1067, DDK1068, NIDW1561(d), UAS485(d)
Sr11+7b+2+	01	HD3171
Sr11+7b+	04	HD3467, HD3468, HD3478, KRL2203
Sr11+2+	10	DBW88, DDK1029, DDW65, GW322, HD3059, HD3249, HI8823(d), HW1098, NIDW1149(d), PBW644
Sr11+	09	AKAW5441, HD2932, JKW261, MACS4125(d), MACS4135(d), MACS4146, MP3601, MPO1403, NIAW4624
Sr7b+2+	08	AKDW5520(d), HI1612, KRL210, MACS3949(d), MACS6862, PBW833, UAS478(d), UAS484(d)
Sr7b+	08	GW1370(d), HI1653, HI8849(d), HI8850(d), Kharchia 65, MACS4131(d), MPO1398(d), WHD943
Sr2+	01	DBW452
Total	**165**	

4. Race specific Adult Plant Resistance (APR) in AVT entries (2024-25)

For identifying race specific adult plant resistance (APR), 204 AVT lines of wheat were screened against the most predominant and virulent pathotypes of *Puccinia triticina, P. striiformis* f. sp. *tritici* and *P. graminis* f. sp. *tritici* during 2024-25. Three pathotypes each of *P. triticina* (77-5, 77-9 and 104-2) and *P. striiformis* f. sp. *tritici* (46S119, 110S119 and 238S119), and *P. graminis* f. sp. *tritici* (11, 40A and 117-6) were used in present study. The experiments were conducted under controlled conditions in polyhouse. The lines which showed susceptibility at seedling and resistance at adult plant stage were considered to have APR.

The detailed information of wheat lines showing race specific APR to nine pathotypes of three wheat rust pathogens is presented in Table 10, 11 and 12.

Leaf rust

Seventy-five entries of AVT showed APR to one or the other pathotypes of *P. triticina.* APR to all the pathotypes (77-5, 77-9 and 104-2) of leaf rust pathogen was not observed in any of the entries. Fifteen entries had combined APR to 77-5 and 77-9 while combined APR to 77-5 and 104-2 was recorded only in SVPWL22-02. APR to individual pathotypes 77-5, 77-9 and 104-2 was observed in 13, 36 and 07 entries, respectively (Table 10).

Table 10. Race specific adult plant resistance (APR) response in AVT lines to virulent pathotypes of *Puccinia triticina* during 2024-25

Pathotypes	No. of lines	Wheat Lines
All three pathotypes	None	-
Both 77-5 and 77-9	15	CG1040, DBW88, DBW296, DBW448, DBW452, DBW455, DBW458, DBW459, DBW509, K1317, MACS6844, MACS6868, MP3598, NIAW4621, PBW921
Both 77-9 and 104-2	3	HP1983, PBW644, UAS485
Both77-5 and 104-2	1	SVPWL22-02
77-5	13	CG1045, CG1047, DBW110, DBW425, DBW469, HD3468, KRL2203, NIAW4624, PBN2115, PBW951, PBW826, UAS3033, UAS3034
77-9	36	BCW32, DBW173, DBW187, DBW222, DBW327, DBW371, DBW372, DBW445, DBW446, DBW457, DBW462, DBW467, DBW470, HD3059, HD3249, HD3386, HD3467, HD3478, HD3486, HD3488, HI1653, HI1702, HI8857, JKW261, MACS6837, MP1401, MP3570, MP3601, NIAW3170, PBW872, PBW929, PBW934, PBW939, PBW944, WH1337, WH1340
104-2	7	HD2932, HI1621, HI8627, HI8713, HI8853, KRL210, PDW368
Total	**75**	

Stripe rust

Seventy-three lines showed APR to different tested pathotypes of stripe rust pathogen. Among these, 24 lines DBW432, DDW67, HD3118, HD3293, HD3463, HD3495, HI1621, HI8737, HI8851 (D), HI8854, HI8864, MACS3949 (D), MACS4131 (D), MACS4146, MPO1395 (D), MPO1398 (D), NIAW4621, NIDW1149 (D), PBW929, PBW939, UAS484 (D), UAS485 (D), WH1339, and WHD969 possessed APR to three major pathotypes of *P. striiformis* f. sp. *tritici* individually. Eleven lines had APR to 110S119 and 238S119. Five entries DBW296, DBW445, HI1612, HI8823 (D), UAS478 (D) possessed APR to both 110S119 and 46S119 (Table 11). Eighteen entries showed APR to 238S119.

Table 11. Race specific adult plant resistance (APR) response in AVT lines to virulent pathotypes of *Puccinia striiformis* f. sp. *tritici* during 2024-25

APR to pathotype	No. of lines	Detail
238S119, 110S119 and 46S119	24	DBW432, DDW67, HD3118, HD3293, HD3463, HD3495, HI1621, HI8737, HI8851 (D), HI8854, HI8864, MACS3949 (D), MACS4131 (D), MACS4146, MPO1395 (D), MPO1398 (D), NIAW4621, NIDW1149 (D), PBW929, PBW939, UAS484 (D), UAS485 (D), WH1339, WHD969
238S119 and 110S119	11	AKDW5520 (D), DBW222, DBW448, DBW455, HD3471, HI8850 (D), MACS6862, MACS6868, MPO1403, UBW21, WH1338
110S119 and 46S119	05	DBW296, DBW445, HI1612, HI8823 (D), UAS478 (D)
238S119 and 46S119	03	HI8855 (D), HI8849 (D), PDW368
238S119	18	BCW32, DBW422, DBW426, DBW446, DBW458, DBW460, DBW509, GW1369 (D), GW1370 (D), HD3388, HI8856 (D), HW1098, K2304, KRL2301, MACS5066, MACS5067, NIDW1557, PDW367
110S119	07	CG1045, DBW470, HD3249, MP1401, MP3598, NW8089, PBW906
46S119	05	CG1047, HI1633, HI8857 (D), JKW261, MACS4125 (D)
Total	**73**	

Stem rust

Combined APR to *Pgt* pathotypes 11 & 40A was recorded in two AVT entries (MP3570 and PBW915). Likewise, HI8856(d) exhibited APR to both 40A and 117-6. Seven entries (CG1052, DBW327, HD3293, KRL2203, MP3598, PBW942, and PBW943) had APR to pathotype 11. While APR to pathotype 40A and 117-6 was observed in five (HD3086, HD3478, HI1605, HI1621, and KRL210) and three (DBW470, HI8849, and UAS485) entries, respectively (Table 12).

Table 12. Race specific adult plant resistance to the predominant and virulent pathotypes *Puccinia graminis* f. sp. *tritici* (*Pgt*) in wheat lines of AVT during 2024-25

Pathotypes	No. of Lines	Varieties/lines
11 & 40A	02	MP3570, PBW915
40A & 117-6	01	HI8856(d)
11	07	CG1052, DBW327, HD3293, KRL2203, MP3598, PBW942, PBW943
40A	05	HD3086, HD3478, HI1605, HI1621, KRL210
117-6	03	DBW470, HI8849(d), UAS485(d)
Total	**18**	

5. Pathotype distribution in barley rusts and rust resistance in NBDSN and EBDSN (2024-25)

Rust situation and physiologic variation in barley rusts

During the 2024–25 cropping season, no major outbreaks of barley rusts were observed across India. Only a few isolated cases of barley stripe rust were reported from Punjab and Ladakh, indicating a low level of disease occurrence. Notably, there were no reports of stem rust or leaf rust infections in barley fields, suggesting effective resistance or unfavourable environmental conditions. In the case of barley yellow rust caused by *Puccinia striiformis* f. sp. *hordei*, only three infected samples were collected; one from Punjab and two from Ladakh. All three samples were subjected to pathotype analysis, and Pathotype 57 (0S0) was identified in all. The limited distribution and incidence of barley rusts during this period reflect continued surveillance efforts and potentially resistant barley cultivars under cultivation.

Rust resistance in barley NBDSN and EBDSN lines during 2024-25

Two hundred forty-six NBDSN and eight EBDSN entries were screened against different pathotypes of three rusts of barley under precise conditions of temperature and light. Wherever needed, confirmatory and selected testing was also undertaken. These lines were evaluated against six pathotypes of *P. striiformis hordei* (24, 57, M, G, Q and 6S0), five pathotypes of *P. graminis tritici* (11, 21A-2, 40A, 117-6 and 122), and 11 pathotypes of *P. hordei* (H1 to H11). None of the NBDSN or EBDSN entries conferred resistance to all the pathotypes of three rust pathogens *P. striiformis hordei* (stripe rust), *P. hordei* (leaf rust) and *P. graminis tritici* (stem rust). The detailed report is presented below.

Rust resistance in NBDSN lines

A total 246 entries of NBDSN were evaluated against the different pathotypes of *Puccinia* spp on barley. None of the entries were resistant to all three rusts of barley. Eleven entries (BHS498, BHS503, BHS504, HBL890, RD3137, RD3138, RD3139, RD3141, RD3142, RD3143, and RD3145) were resistant to both leaf and stripe rusts. Two entries (DWRB2422 and HUB290) were resistant to all the pathotypes of stripe and stem rust pathogens while DWRB2435 conferred resistance to leaf and stem rusts. Additionally, 10 and 54 NBDSN lines were resistant individually to leaf and stripe rust, respectively. Resistance to all the pathotypes of *P. graminis tritici* was observed in nine entries (DWRB219, DWRB2401, PL958, PL959, PL969, PL971, RD2849, RD3112, and UPB1134) (Table 13).

Table 13. Seedling resistance in NBDSN entries to the pathotype of three rusts of barley during 2024-25.

Resistant to rusts	No. of lines	Lines
Leaf and Stripe	11	BHS498, BHS503, BHS504, HBL890, RD3137, RD3138, RD3139, RD3141, RD3142, RD3143, RD3145
Leaf and stem	01	DWRB2435
Stripe and stem	02	DWRB2422, HUB290
Leaf	10	BHS505, DWRB2411, DWRB2429, HBL113, PL983, UPB1121, UPB1135, VLB118, VLB187, VLB191
Stripe	54	BH1058, BH1059, BH1063, BH1067, BH1071, BH1072, BH1073, DWRB137, DWRB182, DWRB238, DWRB2416, DWRB2418, DWRB2421, DWRB2430, DWRB2432, HBL891, HUB113, HUB303, JHSBB19, JHSBD11, JHSBD22, JHSBF21, JHSBF28, KB2301, NDB1841, PL890, PL955, PL982, RD2552, RD2715, RD2794, RD2899, RD2907, RD3088, RD3089, RD3090, RD3095, RD3102, RD3119, RD3120, RD3126, RD3128, RD3129, RD3130, RD3131, RD3133, RD3134, RD3140, RD3144, RD3146, RD3148, UPB1122, UPB1123, UPB1128

Rust resistance in EBDSN lines

Eight EBDSN entries were evaluated for resistance to three rusts by using six pathotypes of *P. striiformis hordei*, five of *P. graminis tritici*, and 11 of *P. hordei*. Resistance to all three rusts was not recorded in any EBDSN entry. However, DWRB182 was resistant to all the pathotypes of stem and stripe rust pathogens. Resistance to all the pathotypes of stripe rust pathogen was observed in three (DWRB238, DWRB2309, and DWRB137) entries of EBDSN (Table 14). None of the entries conferred resistance to all the pathotypes of *P. hordei*; however, entry DWRB2312 was resistant to all the pathotypes of *P. hordei* except H3 (55H7).

Table 14. Seedling resistance in EBDSN entries to the pathotype of three rusts of barley during 2024-25.

Resistant to rusts	No. of lines	Lines
All	None	
Stripe and stem	01	DWRB182
Stripe	03	DWRB238, DWRB2309, DWRB137
Leaf	None	
Stem	None	

Gene postulation (barley leaf rust) in NBDSN and EBDSN lines

The barley leaf rust resistance genes (specifically *Rph* genes) were postulated following the development of barley leaf rust differentials during 2023-24. The detailed results of gene postulation studies conducted during 2024–25 for NBDSN and EBDSN lines screened against barley leaf rust, caused by *Puccinia hordei* is listed in Table 15 & 16.

NBDSN

Two genes (*Rph3* and *Rph19*) were postulated in 34 NBDSN lines. *Rph3* gene was postulated in 12 lines, including DWRB2312, HBL893, KB2364, RD3140, and UPB1129. These lines likely exhibit moderate to good resistance against brown rust due to the presence of this gene. Similarly, *Rph19* gene was postulated in 22 lines, such as BH1070, DWRB238, PL966, RD3098, and UPB1131. Rph19 is often associated with durable resistance and has broader effectiveness across multiple pathotypes (Table 15).

Table 15. Postulated *Rpg*-gene in NBDSN lines during 2024-25

S. No.	Rph gene	No. of lines	NBDSN Lines
1.	*Rph3*	12	DWRB2312, DWRB2428, DWRB2436, DWRB2437, HBL893, KB2339, KB2364, NBD1847, RD3134, RD3140, SKUAWN101, UPB1129,
2.	*Rph19*	22	BH1070, DWRB238, DWRB244, DWRB2316, DWRB2412, HBL895, HBL896, KB2301, KB2321, KB2358 PL961, PL966, PL979, RD2715, RD3086, RD3088, RD3090, RD3092, RD3098, RD3127, UPB1131, VLB192
Total		**34**	

EBDSN

Like NBDSN, only two genes (*Rph3* and *Rph19*) were postulated in EBDSN entries. One entry (DWRB2312) carried *Rph3*, while two lines (DWRB238 and DWRB2304) had Rph19, indicating the potential use of these elite lines in breeding programs for enhanced rust resistance (Table 16).

Table 16. Postulated *Rpg*-gene in EBDSN lines during 2024-25

S. No.	Rph gene	No. of lines	EBDSN Lines
1.	*Rph3*	1	DWRB2312
2	*Rph19*	2	DWRB238, DWRB2304
Total		**3**	

6. Genetics of rust resistance and developing rust resistant genetic stocks

Development of rust resistant genetic stocks

Barley

14 crosses of Cebada Capa (Rph7), Trumph (Rph12) and Magnif104 (Rph5), made with RD3028, BH1035, VL173, KB1926, RD3089, RD3013, RD3016, and PL908, were advanced to F3 generations.

Wheat

For the development of genetic stocks for resistance to all three rusts (brown, black and yellow rust) one population was screened and advanced to F6 generation, population of six crosses was screened and advanced to F5 generations, and one population was advanced to F4 generation, one to F3 generations and four to F2 generations.

Pyramiding multiple rust resistance and generation advancement

Several germplasm lines and landraces harboring different leaf rust resistance genes such as *Lr10, Lr67, Lr23, Lr46, Lr13* and *Lr26* were crossed to develop F_1 lines with more than two leaf rust resistance genes. A total of 31 crosses from the previous season were sown in rows in 2024-25 cropping season. Among them 14 crosses were selected based on their resistance and other traits. The selected lines were screened using molecular markers for confirmation of desired *Lr* genes to identify the lines having 4 *Lr* gene combinations. Few desirable lines among them were harvested separately to advance to next generation.

List of the crosses selected and forwarded to next generation

S. No.	Cross combination
1.	*(Lr34, Lr13) x (Lr67, Lr23)*
2.	*(Lr67, Lr23) x (Lr34, Lr13)*
3.	*(Lr67, Lr23) x (Lr26, Lr34)*
4.	*(Lr10, Lr46) x (Lr67, Lr23)*
5.	*(Lr26, Lr34) x (Lr67, Lr23)*
6.	*(Lr26, Lr34) x (Lr67, Lr13)*
7.	*(Lr26, Lr34) x (Lr67, Lr23)*
8.	*(Lr10, Lr46) x (Lr34, Lr23)*
9.	*(Lr67, Lr110) x (Lr34, Lr23)*
10.	*(Lr10, Lr34) x (Lr67, Lr13)*
11.	*(Lr67, Lr13) x (Lr10, Lr34)*
12.	*(Lr10, Lr46) x (Lr67, Lr13)*
13.	*(Lr67, Lr10) x (Lr26, Lr34)*
14.	*(Lr67, Lr13) x (Lr10, Lr46)*

Development of durable rust resistance

The brown rust resistance line Hango-2 harboring *Lr80* gene was crossed with FLW lines that carry yellow rust resistance. A total of 8 direct and reciprocal crosses were made in 2023-24. Among them 6 crosses seeds were obtained and were evaluated for rust resistance and gene postulation in cropping season 2024-25. The lines were harvested for advancement

S. No	Cross combination
1.	FLW13 x Hango-2
2.	FLW12 x Hango-2
3.	Hango-2 x FLW10
4.	FLW4 x *Yr10*
5.	FLW6 x *Yr15*
6.	*Yr15* x FLW8

Introgression of yellow rust resistance to elite varieties of wheat

3 popular wheat varieties (HS562, HI1563 and DBW222) which are susceptible to yellow rust were selected to introgress multiple yellow and brown rust resistance genes from donors, which are resistance to yellow rust and bio-fortified with Fe and Zn. The lines were sown in 2024-25 crosses season and crosses among them were made. The F1 seeds were harvested for further advancement.

Rust resistance studies in Barley

Three different F2 families derived from crosses between resistant and susceptible parents were screened at seedling stage using most virulent pathotype of yellow rust and brown rust to deduce the number of genes governing the resistance and their inheritance pattern. The 3:1 resistance: susceptible ratio indicated the rust resistance is governed by single major gene (for yellow rust). The F2 plants along with parents were transplanted in cropping season 2024-25. Individual plants were harvested separately. The DNA was isolated from 20 resistant and 20 susceptible F2 plants along with parents for analysis of BSA to find marker trait association.

7. Molecular profiling of AVT lines using molecular markers

Wheat rust resistance genes (*Lr, Sr, Yr*) were identified using molecular markers in AVT material of 2024-25. DNA from all 204 AVT entries was isolated by following the method of Murray and Thompson (1980) after some basic modifications. DNA quality was checked on 1% agarose gel electrophoresis and quantified on nanodrop. Robust molecular markers were applied on isolated DNA lines to ascertain additional rust resistance in these wheat lines. Eight previously validated molecular markers (*Sr24#12*, *SCSS30.2*, *CsGsSTS*, *VENTRIUP*, *csLV34*, *WMC44*, *GWM11*, *PSY1-E1* and *GWM533*) were used for identification of race specific and race nonspecific rust resistance genes in these lines. Details of molecular markers, linked genes, and the AVT lines consisting resistant gene are given in Table 17.

Table 17. Detail of molecular markers, associated genes, and AVT lines containing these resistant genes.

S. No.	Molecular Marker	Linked Genes	No. of lines	AVT lines
1.	*SCSS30.2*	*Yr9/Lr26/Sr31*	8	GW563, HD3090, HI1633, HI1634, HI1699, HI1702, MACS6854, PBW771
2.	*GWM11*	*Yr15*	8	HD3467, DBW477M, PBW938, PBW921, PBW951, PBW953, PBW915, PBW942
3.	*Sr24#12*	*Sr24/Lr24*	24	CG1029, GW554, GW555, GW556, GW561, GW563, GW1029B, HI1563, HI1683, HI1687, HI1696, HI1697, HI1699, HI1700, MACS6222, MACS6829, MACS6830, MACS6851, MACS6854, NIAW4267, NIAW4533, NIAW4581, RAJ4083, WSM138

4.	*CsGsSTS*	*Lr68*	55	HD3467, HD3478, HP1983, DBW458, MACS6837, MP3570, MP1401, MP3598, WH1338, NIAW4533, HI1700, HI1702, PBW938, WH1329, NW8089, BW20R105, UBW22, HD3515M, DBW422, WH1337, SVPWL22-02, HD3468, HD3486, DBW467, WH1340, KRL2203, PBW915, NIAW4581, HI1687, NIAW4624, UAS3033, PBW929, HD3463, HD2932, PBW826, HD3386, HD3086, DBW173, PBW644, NIAW3170, HD3388, K1317, HD3171, HD3293, DBW252, HD2932, DBW110, CG1040, HI1605, DBW327, PBW872, DBW377, HW1098, KRL210, KRL19
5.	*VENTRIUP*	*Yr17/Lr37/Sr38*	56	PBW944, HD3467, HD3478, K2304, DBW452, BCW32, DBW458, UP3145, MACS6837, GW1369(d), GW554, MP3570, DBW457, DBW509B, WH1338, NIAW4621, UAS484(d), UAS3034, HI8856(d), PBN2115, DBW446, DBW448, DBW455, DBW477M, PBW938, PBW939, PBW943#, WH1329, NW8089, BW20R105, DBW422, DBW460, WH1337, UBW21, HD3468, HD3486, HD3488, DBW466, PBW953, WH1339, KRL2203, PBW915, DBW432, DBW469, DBW470, HI1696, NIAW4624, PBW935, PBW906, PBW934, HI1621, HI1605, DBW327, DBW371, PBW872, DBW303
6.	*csLV34*	*Yr18/Lr34/Sr55*	9	WSM138, HI1697, GW563, PBW644, HI1563, DBW107, HI1634, RAJ4083, HI1633
7.	*WMC44*	*Yr29/Lr46*	43	HD3478, MACS4135(d), HI8849(d), HI8850(d), HI8858(d), MPO1395(d), AKDW5520(d), DBW457, UAS487(d), MACS4131(d), HI8851(d), HI8857(d), NW8089, UBW22, DDW67, WHD969, PDW367, NIDW1542, DBW459, DBW460, DBW466, MACS4125(d), MACS4147(d), HI8855(d), GW1370(d), CG1047, GW563, PBW935, PBW906, DBW445Q, MP1399, DDK1069, DBW222, WHD943, HI1621, HD2932, MACS3949(d), HI8737(d), NIDW1149(d), UAS478(d), DBW377, Kharchia 65, KRL19
8.	*GWM533*	*Sr2*	48	HD3090, HI1633, HI1702, PBW771, CG1029, HI1563, HI1687, MACS6222, NIAW4581, PBW826, HD3386, BCW32, BRW3959, CG1045, DBW455, MP3598, PBW935, DBW252, KRL19, NIAW3170, HI8627(d), HI8713(d), HI8737(d), PDW291, PDW314, WHD969, HD3293, HI8853, HD3171, DBW88, DDK1029, DDW65, GW322, HD3059, HD3249, HI8823(d), HW1098, NIDW1149(d), PBW644, AKDW5520(d), HI1612, KRL210, MACS3949(d), MACS6862, PBW833, UAS478(d), UAS484(d), DBW452
9.	*PSY1-E1*	*Lr19*	0	-

Amplification of *Yr9/Lr26/Sr31*

In AVT material *Yr9/Lr26/Sr31* gene complex was validated by SCSS30.2 marker which gives a sharp band of 550bp in eight AVT lines (GW563, HD3090, HI1633, HI1634, HI1699, HI1702, MACS6854, PBW771).

Amplification of *Lr24/Sr24*

In AVT material 500bp amplicon produced by dominant marker *Sr24#12* indicated the presence of *Lr24/Sr24* gene complex in twenty-four wheat lines.

Amplification of *Yr18/Lr34/Sr55*

Amplification of 150 bp band by molecular marker *csLV34* shows the presence of race nonspecific *Yr18/Lr34/Sr55* gene complex in nine AVT lines.

Amplification of *Sr2*

Amplification of ~120 bp band by molecular marker *Sr2* specific marker (GWM533) showed the presence of *Sr2* gene in maximum of forty-eight AVT entries.

Amplification of *Yr17/Lr37/Sr38*

Amplification of 259bp band by molecular marker *VENTRIUP* showed the presence of race nonspecific *Yr17/Lr37/Sr38* gene complex in maximum of fifty-six AVT entries.

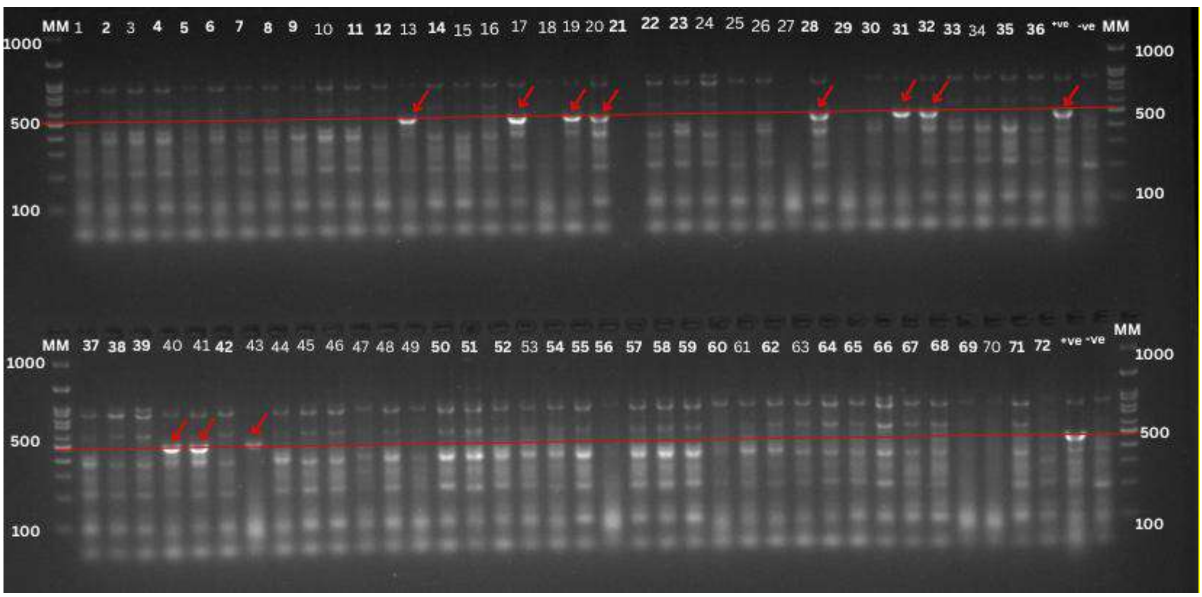

Figure 3. Electrophoresis on 2.5 % agarose gel showing amplification profile of marker SR24 #12 indicated the presence of *Sr24/Lr24* gene complex. Upper row, Lane 1(MM)- Gene Ruler 100 bp DNA ladder; Lane 38(+ve), lane 39 (-ve), lane 40 (MM) - Gene Ruler 100 bp DNA ladder.

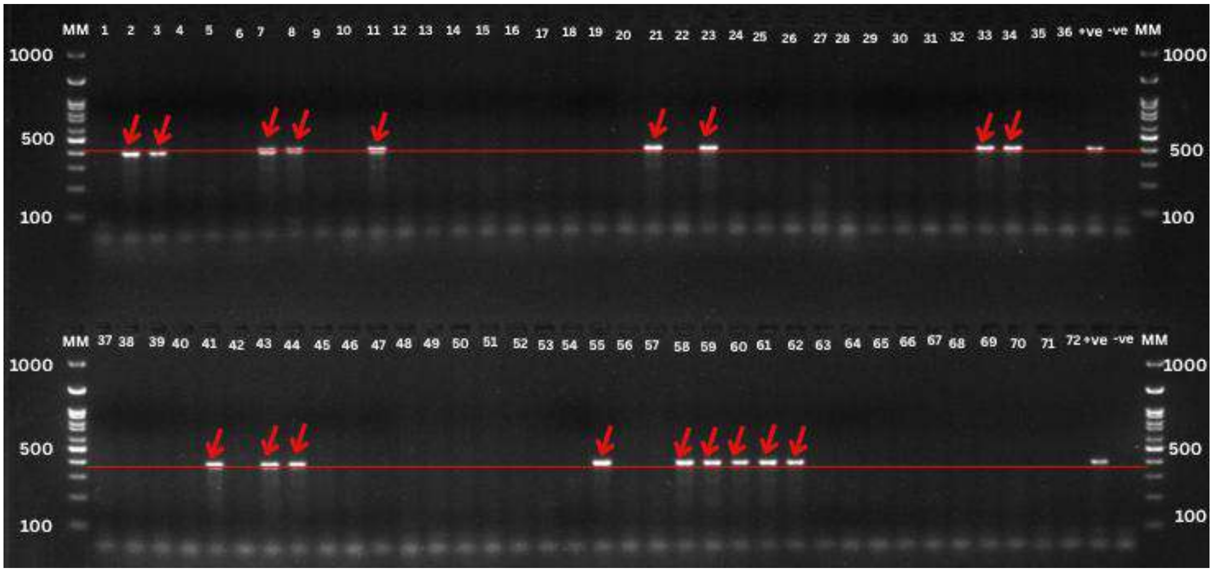

Figure 4. Electrophoresis on 2.5 % agarose gel showing amplification profile of marker CsGsSTS indicated the presence of *Lr68* gene complex. Upper row, Lane 1(MM)- Gene Ruler 100 bp DNA ladder; Lane 38(+ve), lane 39 (-ve), lane 40 (MM) - Gene Ruler 100 bp DNA ladder.

8. Maintenance and supply of nucleus inoculum of pathotypes of wheat and barley rust pathogens

A collection of more than 150 pathotypes of different rust pathogens of wheat, barley, oat and linseed were maintained on host as well as cryo-preserved. For the smooth conduct of wheat and barley rust research, nucleus/bulk inocula of different pathotypes of wheat and barley rust pathogens was supplied to more than 50 scientists/research centers across India (Table 18).

Table 18. Details of rust inocula and seed supplied during the period.

Name	Affiliation
Ajay Aggarwal	IGKV, Raipur, Chhattisgarh
Amit Kumar Singh	ICAR-NBAIR, New Delhi
Anil Kumar	GBPUAT, Pantnagar, Uttarakhand
BC Game	ARS, Niphad, Maharashtra
CN Mishra	IIWBR, Karnal, Haryana
Deepak Varanwal	Bihar Agriculture University Bhagalpur, Bihar
Deepshikha	GBPUAT, Pantnagar, Uttarakhand
Dharam Pal	ICAR-IARI, Tutikandi, HP
G Vishwakarma	BARC, Mumbai, Maharashtra
GM Hegde	UAS, Dharwad, Karnataka

Hanif Khan	ICAR-IIWBR, Karnal, Haryana
Harikrishna	IARI, Pusa, New Delhi
IB Kapadia	JAU, Junagarh, Gujarat
Jaspal Kaur	PAU, Ludhiana, Punjab
Jitendra Kumar	CSAUK, Kanpur, UP
Joginder Pal	Rice and Wheat Research Station, CSKHPKV Palampur HP
KP Singh	GBPUAT, Pantnagar, Uttarakhand
KK Mishra	ICAR-VPKAS, Almora, Uttarakhand
KK Mishra	ARS, JNKVV, Powarkheda, Madhya Pradesh
Madhu Patiyal	ICAR-IARI Shimla
Manoj	RWRS, Mahabaleshwar, Maharashtra
MK Pandey	SKUAST, Jammu, J&K
Muskan Bhullar	Khalsa College, Amritsar, Punjab
Neeraj Kulshrestha	ICAR-CSSRI Karnal Haryana
PL Kashyap	ICAR-IIWBR, Karnal, Haryana
Pradeep Bhati	BISA, PAU, Seed Farm Ladhowal (Ludhiana),Punjab
Pradeep Sharma	ICAR-IIWBR, Karnal, Haryana
Prakasha TL	ICAR-IARI, RS, Indore, MP
Prashant Babu	ICAR-IARI Delhi
Priya Mankotiya	Khalsa College Amritsar Punjab
PS Shekhawat	RARI, Durgapura, Jaipur, Rajasthan
Rajbir Yadav	IARI, PUSA New Delhi
Ravinder Kumar	ICAR-IIWBR, Karnal, Haryana
Reyazul Rouf Mir	SKUAST-K Wadura, Sopore
Ronak Thakkar	ARS, Vijapur, Gujarat
RS Beniwal	CCS HAU, Hissar, Haryana
Santosh Kumar Singh	SKUAST, Chatha, Jammu, J&K
Satinder Kaur	PAU, Ludhiana, Punjab
Satish Kumar	ICAR-IIWBR, Karnal Haryana
Shailendra Jha	IARI, Pusa New Delhi
Shivali Dhimaan	Krishi Vigyan Kendra, Dhaulakuan, Sirmaur
SP Singh	ANDAU, Kumarganj, Ayodhya, UP
SS Vaish	BHU, Banaras, UP
Subhash Chandra	ANDUAT, Kumarganj, Ayodhya
Sudhir Navathe	Agharkar Research Institute, Pune, Maharashtra
Suman Berthin	Rice-Wheat Research Station, Malan HP
Vaibhav Singh	ICAR-IARI, New Delhi
Vijay Rana	CSKHPKV, Malan, HP
Vikas Gupta	ICAR-IIWBR, Karnal, Haryana
Vishnu Kumar	ICAR-IIWBR, Karnal, Haryana
Vishnu Goyal	ICAR-NBPGR Delhi
VP Chaudhary	ANDUAT, Kumarganj, Ayodhya

9. Wheat Disease Monitoring Nurseries

The 57th wheat disease monitoring nursery was planted at 40 strategic locations evenly distributed throughout India. Data were received from 30 locations. Rust diseases were not recorded on any of the entries of WDMN planted at IIWBR, RS Shimla, Kalyani, Junagarh, Akola and Niphad. The yellow rust was noticed at all the locations of NHZ and NWPZ except at IIWBR, RS, Shimla and IARI, RS, Tutikandi, Shimla, where all the WDMN entries were yellow rust free. All the entries of WDMN in other zones were free from yellow rust. Yellow rust was very severe at many locations at NWPZ and NHZ, where severity of more than 60S was reported on many entries. Brown rust was reported from Almora in NHZ; and Rajouri, Kathua, Jammu, Hisar, Durgapura, Abohar, Gurdaspur, Ludhiana, Ropar, Langroya and Pantnagar in NWPZ.

Brown rust appeared at all the locations of NEPZ except Kalyani. It was observed at all the locations of CZ except Junagarh. Brown rust also appeared at all the locations in PZ, and Wellington in SHZ.

Of the 30 locations of WDMNs black rust was observed only at Powarkheda and Vijapur in CZ and Wellington in SHZ and all the entries were black rust free in all other zones. Leaf blight was reported from WDMN planted at Jammu, Kathua, and Rajouri in NWPZ; Sabaur, Pusa, Kanpur, Kalyani, and Ayodhya in NEPZ; and Dharwad in PZ. Kathua, Rajouri, Dhaulakuan, Jammu, Almora, and Wellington were the only locations where powdery mildew was observed on WDMN entries.

SAARC wheat disease monitoring nursery was planted at 33 locations in India, Bangladesh, Bhutan, Nepal and Pakistan. Data were received from all the locations in India, Nepal and Bangladesh whereas; it is still awaited from other SAARC countries.

10. Visitors and News

a. Visitors

- The QRT team visited the station on March 9, 2025 to assess the progress of the work and provide suggestions for further improvements.
- Dr. Sharat Kumar Pradhan, Assistant Director General (Food & Fodder Crops), Indian Council of Agricultural Research (ICAR), visited the station on February 25, 2025.
- Students from university
- Winter school trainee from ICAR-CPRI visited the station on February 28, 2025.
- A group of 46 students from Punyashlok Ahilyadevi Holkar Government College of Agriculture, Halgaon, Mahatma Phule Krishi Vidyapeeth, Rahuri, Maharashtra visited the station on June 7, 2025.

b. Training/conferences/Workshop/Meeting/Lectures etc. organized/attended

- Dr Pramod Prasad participated in international seminar on "*Novel insights on the genetics of susceptibility to necrotrophic fungal pathogens of durum and bread wheat*" organized by International Wheat Genome Sequencing Consortium (IWGSC) on July 17, 2025.

c. Joining/transfer/superannuation

- Dr. Pramod Prasad assumed the charge as Officer-in-Charge of the station with effect from 13th June 2025.
- Dr. Charu Lata was transferred to ICAR-IIWBR Karnal on 13th June 2025.
- Superannuation of Mr. Khem Chand on 28 Feb 2025.

d. Awards

- Dr. Pramod Prasad was conferred with the best worker award-2024 of the ICAR-IIWBR under scientific category.

e. Extension Activities

- Drs. O P Gangwar, Pramod Prasad, Charu Lata and Mr. Jayanth Kallugudi were team member for conducting Viksit Krishi Sankalp Abhiyaan from May 29 – June 12 at Jubbal and Bilaspur blocks, District Shimla and Bilaspur.

f. Activities under Swachh Bharat Abhiyan

- As part of the Swachh Bharat Abhiyan, swachata Abhiyaan was organized at the station. All the staff of the station including research fellows and contractual staff contributed in the Abhiyaan and collected plastics and litter around the office and campus.

Annexure I

Updated Constitution of differential sets- 0, A and B for the binomial designation of pathotypes of wheat rust pathogens

Set-0	Set-A	Set- B
leaf rust (*Puccinia triticina*)		
IWP 94	*Lr14a*	Loros (*Lr2c*)
Kharchia Mutant	*Lr24*	Webster (*Lr2a*)
Raj 3765	*Lr18*	Democrat (*Lr3*)
PBW 343	*Lr13*	Thew (*Lr20*)
UP 2338	*Lr17*	Malakoff (*Lr1*)
K 8804	*Lr15*	Benno (*Lr26*)
Raj 1555	*Lr10*	HP 1633 (*Lr9*+)
HD 2189	*Lr19*	
Agra Local	*Lr28*	
Stem rust (*Puccinia graminis tritici*)		
Sr24	*Sr13*	Marquis (*Sr7b*+)
NI 5439	*Sr9b*	Einkorn (*Sr21*)
Sr25	*Sr11*	Kota (*Sr28*+)
DWR 195	*Sr28*	Reliance (*Sr5*+)
HD 2189	*Sr8b*	Charter (*Sr11*+)
Lok 1	*Sr9e*	Khapli (*Sr7a, Sr13, Sr14*)
HI 1077	*Sr30*	Tc*6/*Sr31/Lr26*(*Yr9*)
Barley Local	*Sr37*	
Agra Local		
Stripe rust (*Puccinia striiformis*)		
WH147	Chinese 166 (*Yr1*)	Hybrid 46 (*Yr4*)
HS507	Lee (*Yr7*)	Heines VII (*Yr2*+)
Hobbit	Heines Kolben (*Yr6*)	Compair (*Yr8*)
PBW752	Vilmorin 23(*Yr3*)	*T. spelta album* (*Yr5*)
PBW757	Moro (*Yr10*)	Tc*6/*Lr26* (*Yr9*)
PBW343	StrubesDickkopf	Sonalika (*Yr2+)*
HS240	Suwon92 X Omar	Kalyansona*Yr2*(KS)
Anza	Riebesel47/51(*Yr9*+)	*Yr24/3**AvS (*Yr24*)
A-9-30-1	Cappelle-Desprez (*Yr16*)	*Yr15/6**AvS (*Yr15*)
Bilara-2 (Barley)	Carsten V (*Yr32*)	*YrSP/6**AvS (*YrSP*)