भाकृअनुप
ICAR

ICAR- INDIAN AGRICULTURAL RESEARCH INSTITUTE, REGIONAL STATION, WELLINGTON, THE NILGIRIS, TAMIL NADU

NILGIRI WHEAT NEWS

VOLUME 13 JAN –DEC 2025

ISSUE 13

CONTENTS

Rust Resistance in Solid Stem Trait Introgressed Wheat Lines Carrying Multiple Disease Resistance Genes

ShajithaP[1], Nisha R[1], Sivasamy M[1*], JayaprakashP[1], VikasV.K[1], K. Gajalakshmi [4], Niharikha Mallick[2], Prashant Babu[2], Rajbir Yadav[2], Pramod Prasad[3], Vijaishree S[1], , AkileshwaranK[1], John Peter[1] Geetha M[1], Suganya C[1], Arun Kumar C[1], Balaji V[1], Gokulakrishna M[1], and Sanjeth V[1]

[1]ICAR-Indian Agricultural Research Institute Regional Station, Wellington, Tamil Nadu - 643 231, India
[2]ICAR-Division of Genetics, Indian Agricultural Research Institute, Pusa, New Delhi-12. India
[3] ICAR - Indian Institute of Wheat and Barley Research, Regional Station, Flowerdale, Shimla-171001, India
[4] PSGR Krishnammal College for Women, Peelamedu, Coimbatore, Tamil Nadu, India

***-Corresponding author: iariwheatsiva@gmail.com**

Introduction

Wheat (*Triticum aestivum*) is a staple crop of global significance, covering over 219 million hectares and contributing to 20% of the world's daily caloric intake. Its production, however, is constrained by both biotic and abiotic stresses, including lodging, rust diseases, and emerging foliar pathogens. Lodging can cause up to 80% yield loss when occurring during critical developmental stages, while rust pathogens—stem rust (*Puccinia graminis* f. sp. *tritici*), leaf rust (*P. triticina*), and stripe rust (*P. striiformis* f. sp. *tritici*)—continue to evolve, threatening stable production globally. The highly virulent Ug99 stem rust pathotypes and other evolving races underscore the need for durable resistance.

The solid stem trait, controlled by loci such as *SSt1* and *Qss.msub-3BL*, plays a critical role in reducing lodging, enhancing tolerance to stem-boring pests, and improving drought resilience. Combining this structural trait with multiple rust resistance genes through modern breeding approaches, including gene pyramiding, offers an effective strategy for developing resilient wheat varieties. Genes such as *Lr19+Sr25, Lr37+Sr38+Yr17, Sr31+Lr26+Yr9+Pm8, Yr10, Lr24+Sr24*, and *Sr36+Pm6* have been successfully introgressed from alien and wild wheat relatives, conferring broad-spectrum resistance against leaf, stem, and stripe rusts as well as powdery mildew.

Integrating solid stem with durable rust resistance enhances both agronomic stability and disease resilience. This study evaluates introgressed wheat lines carrying multiple rust resistance genes for seedling and adult plant resistance, solid stem expression, and lodging tolerance, highlighting promising lines for breeding programs aimed at sustainable wheat production under challenging environmental conditions.

Seedling Reaction Test (SRT)

A total of 34 introgressed wheat lines, developed using recurrent parents HD 2967, HD 2733, COW(W)-1, HW 5207, PBW 343, PBW 502, HD 2877, and HD 2687, were evaluated for resistance to leaf rust (*Puccinia triticina*), stem rust (*P. graminis f. sp. tritici*), and stripe rust (*P. striiformis f. sp. tritici*). SRT was conducted at ICAR-Indian Institute of

Wheat and Barley Research (IIWBR), Flowerdale, Shimla under controlled glasshouse conditions. Seedlings at the 2–3 leaf stage were inoculated with prevalent pathotypes of *P. graminis* (*Pgt*) (11, 21A-2, 40A, 117-6, 295), *P.triticina* (*Pt*) (12-5, 77-1, 77-5, 77-9, 104-2), and *P. striiformis* (*Pst*) (46S119, T, 110S84 and 110S119). Disease reactions were scored 12–14 days post-inoculation on a 0–4 scale (0 = immune, 4 = highly susceptible (Stakman et al., 1962). Most lines exhibited strong seedling resistance to leaf rust and moderate to high resistance to stem rust, while stripe rust reactions were low to moderate.

Field Scoring / Adult Plant Response (APR)

Field evaluations were conducted at ICAR-Indian Agricultural Research Institute, Regional Station, Wellington for four seasons during year 2021-22 (winter and summer season)and 2022-23(winter and summer season) under natural infection by mixed pathotypes. Adult plant reactions were recorded for leaf and stem rust using the modified Cobbs scale a 0–100% severity scale, converted into resistant (R), moderately resistant (MR), moderately susceptible (MS), and susceptible (S) categories. (Peterson et al 1948)-. The field scoring largely displayed rust resistance in majority of the lines, demonstrating the use of promising lines such as **HW 5501, HW 5504, HW 5510, HW 5512, HW 5520, HW 5522, and HW 5529** for wheat improvement.

Solid Stem Score and Molecular Confirmation

The solid stem trait in the developed wheat lines was evaluated atICAR- Indian Agricultural Research Institute (IARI) Regional Station, Wellington during the Rabi and Kharif seasons of 2022–23, and at Tamil Nadu Agricultural University (TNAU), Coimbatore during the Rabi seasons of 2021–22 and 2022–23. Solid stem scores ranged from 2 to 5, with lines HW 5510 and HW 5529 showing the highest scores (5). Moderate to high solid stem expression correlated with improved lodging resistance, underscoring the structural and agronomic advantages of this trait. The presence of the solid stem trait was molecularly confirmed using the *SSt1* marker, ensuring precise selection.

Molecular Confirmation of Resistance Genes

Various stem, leaf and stripe rust resistance genes were introgressed, including *Lr19+Sr25, Lr37+Sr38+Yr17, Sr31+, Yr10, Lr24+Sr24, and Sr36+Pm6,* providing effective multiple disease resistance. The combination of these genes with solid stem and lodging resistance makes the shortlisted lines highly valuable for wheat improvement programs.

Lodging Resistance

Lodging scores ranged from 0–1 for the majority of lines, with higher solid stem expression contributing significantly to lodging tolerance. This structural stability is critical for ensuring yield retention, especially in high rainfall or windy conditions.

The study highlights that lines **HW 5501, HW 5504, HW 5510, HW 5512, HW 5520, HW 5522, and HW 5529** are promising, combining durable rust resistance, high solid stem expression, and superior lodging resistance. These lines represent valuable germplasm for the

Indian wheat breeding program mainly in rust-prone areas, supporting the development of high-yielding, disease-resistant, and structurally robust wheat varieties.

References

Peterson, R. F., Campbell, A. B., & Hannah, A. E. (1948). A diagrammatic scale for estimating rust intensity on leaves and stems of cereals. *Canadian Journal of Research*, 26, 496–500.

Stakman, E. C., Stewart, D. M., & Loegering, W. Q. (1962). Identification of physiologic races of *Puccinia graminis* f. sp. *tritici*. *USDA Agricultural Research Service E-617*.

Table 1. Seedling and adult plant reactions to leaf, stem, and stripe rust, along with solid stem expression and lodging resistance

Sl. No.	**Introgressed Lines**	**Recurrent Parent**	**Seedling Reaction Test**														**Adult plant Reaction**								**Solid Stem Score**	**Lodging Resistance Score**
			Stem Rust					**Leaf Rust**					**Stripe Rust**													
			11	**21A-2**	**40A**	**117-6**	**295**	**12-5**	**77-1**	**77-5**	**77-9**	**104-2**	**46S119**	**T**	**110S84**	**110S119**	**Stem rust (2021-22 & 2022-23)**				**Leaf rust (2021-22 & 2022-23)**					
																	W	**S**	**W**	**S**	**W**	**S**	**W**	**S**		
1.	HW 5497	HD 2967	33+	0;	;-	;-	0;	22+	;	;1	33+	;3	;	0;	0;	0;	F	F	F	F	F	F	F	F	2	0
2.	HW 5498	HD 2967	2-	0;	;-	0;	0;	;1	NG	3	NG	NG	3+	NG	3+	3+	F	F	F	F	F	F	F	F	3	1
3.	HW 5499	HD 2967	3+	12	;-	0;	0;	;	;	;1	;3	;1	;	0;	0;	;	F	F	F	F	F	F	F	F	3	1
4.	HW 5500	HD 2967	2-	0;	;	;-	;-	;1	NG	NG	NG	;	;3-	0;	0;	0;	F	F	F	F	F	F	F	F	3	1
5.	HW 5501	HD 2967	;	.;	;	;-	;-	;1	;	;	;1	;	;1-	0;	0;	;	F	F	F	F	F	F	F	F	4	1
6.	HW 5502	HD 2967	NG	;	2-	0;	NG	NG	;	;	;3+	;	;1	NG	NG	0;	F	F	F	F	F	F	F	F	3	1
7.	HW 5503	HD 2733	2-	;-	;	0;	;1	0;	0;	;	NG	0;	3+	0;	3+	;1	F	F	F	F	F	F	F	F	2	0
8.	HW 5504	HD 2733	0;	;-	;	0;	;-	0;	;-	;-	;	0;	;+	;-	0;	;	**F**	**F**	**F**	**F**	**F**	**F**	**F**	**F**	4	1
9.	HW 5505	HD 2733	23	3+	;1	0;	0;	0;	3+	3+	3+	3+	3+	3+	3	3+	5MR	5R	5R	5R	F	F	F	F	3	1
10.	HW 5506	HD 2733	3+	0;	2--	;-	3+	12	;	22+	;	;-	3+	3-	3-	NG	10MR	20MR	20MR	10MR	F	F	F	F	4	1
11.	HW 5507	HD 2733	2-	0;	;-	;-	0;	;1	;	12	23	;	;+	0;	0;	0;	F	F	F	F	F	F	F	F	3	1
12.	HW 5508	COW(W)-1	NG	0;	NG	;-	;-	NG	;-	;-	;	;	3+	0;	0;	0;	F	F	F	F	F	F	F	F	2	0
13.	HW 5509	COW(W)-1	2-	0;	;-	0;	NG	0;	;-	;1	;1	NG	3+	NG	3	NG	F	F	F	F	F	F	F	F	4	1
14.	HW 5510	COW(W)-1	;-	;	;-	0;	;-	;1	0;	;-	;	;	;	0;	0;	0;	F	F	F	F	F	F	F	F	5	1
15.	HW 5511	COW(W)-1	;-	0;	0;	NG	NG	;1	;1	3	NG	NG	3+	0;	0;	0;	F	F	F	F	F	F	F	F	5	1
16.	HW 5512	HW 5207	0;	;1	;-	;-	;	;-	0	;1	0;	;1	;	0;	0;	0;	F	F	F	F	F				4	1
17.	HW 5513	HW 5207	2-	;	;-	;-	NG	;-	0;	;1	3	;	3	3	3	NG			F		F				3	1

18.	HW 5514	HW 5207	12	-	2-	;-	2-	0;	;-	;-	;	;	0;	3-	3	3+	F	F	F	F	F	F	F	F	2	0
19.	HW 5515	HW 5207	2-	;-	NG	;-	NG	0;	;1	2	33+	;	3	;-	NG	3+	F	F	F	F	F	F	F	F	3	1
20.	HW 5516	HW 5207	;-	NG	;-	;-	;-	;-	;-	0;	;	0;	3+	0;	3+	3+	F	F	F	F	F	F	F	F	2	0
21.	HW 5517	HW 5207	2--	0;	;	0;	;1	0;	;-	1;-	;	0;	3+	0;	3+	2-	F	F	F	F	F	F	F	F	4	1
22.	HW 5518	PBW 343	2--	;-	;-	;-	0;	0;	NG	12	NG	;	NG	0;	0;	3+	F	F	F	F	F	F	F	F	2	0
23.	HW 5519	PBW 343	;-	NG	3	0;	;-	;-	NG	NG	NG	;	NG	3+	NG	NG	F	F	F	F	F	F	F	F	3	1
24.	HW 5520	PBW 343	;	0;	0;	0;	0;	;-	;	;1	;-	;1	;	0;	0;	;1	F	F	F	F	F	F	F	F	4	1
25.	HW 5521	PBW 343	2-	0;	2-	0;	3+	;12	;	12	3+	;	;	0;	0;	0;	F	F	F	F	F	F	F	F	3	1
26.	HW 5522	PBW 502	1;	;-	0;	;-	;-	0;	;-	;-	;-	;-	0;	;-	0;	0;	**F**	**F**	**F**	**F**	**F**	**F**	**F**	**F**	**4**	**1**
27.	HW 5523	PBW 502	2-	0;	12	0;	0;	;1	NG	3+	NG	NG	;1	0;	0;	3+	F	F	F	F	F	F	F	F	4	1
28.	HW 5524	PBW 502	3+	0;	0;	;-	3+	;1	NG	2-	NG	NG	;	;	;-	;	F	F	F	F	F	F	F	F	3	1
29.	HW 5525	PBW 502	;-	0;	0;	0;-	;-	;-	NG	12	3+	;	0;	0;	0;	33+	F	F	F	F	F	F	F	F	3	1
30.	HW 5526	HD 2877	2-	;-	;1	0;-	;-	;-	0;	0;	NG	NG	3+	0;	3+	0;	F	F	F	F	F	F	F	F	2	0
31.	HW 5527	HD 2877	12	;1	0;	0;	12	;1	;12	12	3+	;	;	NG	0;	NG	10MR	20MR	10MR	20MR	F	F	F	F	3	1
32.	HW 5528	HD 2877	2--	;1	NG	0;	;-	;1	;-	12	;1	;-	NG	NG	0;	NG	F	F	F	F	F	F	F	F	3	1
33.	HW 5529	HD 2687	-	0;	;1	-	;-	0;	;-	0;	;	0;	;1	0;	0;	0;	F	F	F	F	F	F	F	F	5	1
34.	HW 5530	HD 2687	;1	;-	0;	0;	0;	;-	3+	;-	23	;	3+	0;	0;	;3	F	F	F	F	F	F	F	F	4	1

A Multivariate Analysis of Agronomic and Yield-Related Traits in Indian Released varieties

Sivasamy M*, Nisha.R, P. Shajitha, Vijaishree S, V.K.Vikas, Balaji V, K. Sivan and C. Arun Kumar

ICAR-Indian Agricultural Research Institute Regional Station, Wellington, Tamil Nadu -643 231, India

***Corresponding author:** iariwheatsiva@gmail.com

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops globally, providing a major source of carbohydrates, protein, vitamins, and essential minerals for human nutrition. It is the most widely cultivated crop in the world, playing a critical role in global food security. Global wheat consumption is projected to reach 834.8 million tonnes by 2028 (OECD/FAO, 2019). Despite substantial increases in production over recent decades, meeting future demand remains challenging due to shrinking arable land, depletion of natural resources, declining soil health, increasing biotic stresses, and climate change–induced variability (Yadav et al., 2010, 2017). To sustain global food supply, wheat productivity must increase at an average annual rate of approximately 1.3%, a target that appears increasingly difficult to achieve.

Yield stagnation or slowing genetic gains have been reported in several major wheat-producing regions, including Europe and parts of Australia and North America (Brisson et al., 2010; Fischer and Edmeades, 2010; Matus et al., 2012). While short-term assessments often indicate genetic gains exceeding 1% per year (Waddington et al., 1986; Sayre et al., 1997), long-term evaluations spanning multiple decades typically report more modest gains of around 0.5% annually (Perry and D'Antuono, 1989; Siddique et al., 1989). These trends highlight the need to re-examine breeding strategies and identify the traits that have driven yield improvement historically and those that will underpin future gains.

Green Revolution and wheat productivity in India

India's wheat production landscape was fundamentally transformed during the Green Revolution period of the mid-1960s. The introduction of semi-dwarf, fertilizer-responsive wheat varieties—developed through international collaboration and inspired by Norman E. Borlaug's work in Mexico—led to unprecedented increases in wheat yield. These varieties combined reduced plant height, improved lodging resistance, and higher harvest index with responsiveness to irrigation and fertilizers, enabling rapid gains in productivity.

Simultaneously, wheat research in India underwent major institutional restructuring with the establishment of the All-India Coordinated Wheat Improvement Program (AICWIP) in 1965. This program centralized breeding efforts and organized varietal testing across broad agro-climatic zones. Selection was predominantly conducted under high-input, irrigated conditions, particularly in the northwestern plains of India, encompassing Punjab, Haryana, and western Uttar Pradesh. This region, characterized by fertile soils and assured irrigation, emerged as the primary contributor to national wheat production and currently accounts for nearly half of India’s total wheat output.

Although the Green Revolution ensured national food security and transformed India into a major wheat producer, it also attracted criticism. Scholars highlighted socio-economic disparities arising from the concentration of benefits in irrigated regions and among larger farmers (Cleaver, 1972; Griffin, 1974). Others argued that early high-yielding varieties were poorly adapted to rainfed and low-fertility environments typical of marginal agriculture (Farmer, 1979; Sen, 1974). Nonetheless, the Green Revolution established the foundation for modern wheat breeding in India and continues to influence varietal development strategies.

Wide adaptation and breeding philosophy

A defining feature of post-Green Revolution wheat breeding in India was the adoption of wide adaptation as a guiding principle. Influenced strongly by the Rockefeller Foundation and Borlaug’s breeding philosophy, Indian wheat scientists emphasized the development of varieties capable of producing stable yields across diverse environments. Wide adaptation, also referred to as phenotypic stability or broad adaptation (Finlay and Wilkinson, 1963), was promoted as a means to maximize genetic gain and accelerate varietal dissemination.

Genetic gain and trait-based yield improvement

Genetic gain, defined as the improvement in mean phenotypic performance due to selection across breeding cycles (Crespo-Herrera et al., 2017), provides a quantitative framework to evaluate breeding progress. Numerous studies have assessed genetic gain by evaluating historical series of varieties released over extended periods (Sadras and Lawson, 2011; Sanchez-Garcia et al., 2013; Morgounov et al., 2014). In winter wheat, the most substantial yield gains were realized between 1960 and 2000, coinciding with the widespread adoption of semi-dwarf varieties and improved agronomic practices (Brancourt-Hulmel et al., 2003). However, since the early twenty-first century, yield progress has slowed or plateaued in several regions (Graybosch and Peterson, 2010).

Trait-based analyses reveal that different wheat-growing regions have exploited distinct combinations of yield components. In China, yield gains have been driven by improvements in grain weight, spike weight, biomass, and harvest index (Zhou et al., 2007). In Australia, increased harvest index has played a dominant role (Sadras and Lawson, 2011), while in Spain, gains have primarily resulted from increases in spike number and grains per spike (Sanchez-Garcia et al., 2012). These differences highlight the region-specific nature of yield formation and the importance of identifying context-relevant yield-limiting traits.

In India, particularly in the northwestern plains, yield improvement has resulted from coordinated enhancement of biomass accumulation, canopy architecture, and assimilate partitioning. However, increasing climatic variability—especially terminal heat stress—has led to high year-to-year yield fluctuations across northern states (Yadav et al., 2019). Short-duration, high-yielding varieties often lack sufficient plasticity to compensate for stress during grain filling, emphasizing the need to reassess trait priorities under changing climatic conditions.

Trait plasticity and future breeding challenges

Trait plasticity—the ability of a genotype to modify trait expression in response to environmental variation—has emerged as a critical determinant of yield stability (Sadras and Rebetzke, 2013). Historically, competitive plant types with profuse tillering and large sinks dominated low-input agriculture. In contrast, modern wheat breeding emphasizes communal plant types that maximize yield per unit area while maintaining stability across environments.

Trade-offs among yield components remain a major constraint to further genetic gain. Enhancing one trait often compromises another, necessitating a systems-level understanding of trait interactions. Periodic evaluation of historically important and recently released varieties under disease-free, optimal conditions provides valuable insight into how breeding has reshaped plant architecture, physiology, and yield formation over time.

Objectives of the study

The present study aims to assess genetic gains in Indian wheat over a period of breeding by evaluating historically important and recently released varieties under disease-free, well-managed conditions. The specific objectives were to:(i) quantify genetic gain in grain yield and associated agronomic traits;(ii) identify key traits contributing to yield improvement;
(iii) examine changes in plant type and trait plasticity over breeding periods.

Understanding the trait-based drivers of yield improvement will help refine future wheat breeding strategies for sustaining productivity under increasing climatic and resource constraints.

Materials and Methods

Experimental Site:

The present study was conducted at the ICAR–Indian Agricultural Research Institute (IARI), Regional Station, Wellington, Tamil Nadu, India, over two wheat-growing seasons during the period 2021–2024. The experimental site is located in the Nilgiris district at an elevation of approximately 1,850 m above mean sea level and represents a cool, high-altitude wheat-growing environment.

The climate of the region is characterized by mild temperatures and high humidity. During the cropping season, mean maximum temperatures ranged from 18 to 25 °C, while minimum temperatures ranged from 8 to 14 °C. The site receives an average annual rainfall of about 1,200–1,500 mm, largely from the southwest and northeast monsoons. These conditions are conducive for wheat growth under non-stress environments.

The soil of the experimental field is well-drained loamy soil with good water-holding capacity, moderately acidic to near neutral in reaction, medium in available nitrogen and phosphorus, and adequate in potassium.

Plant Material

A total of 428 wheat genotypes were evaluated, comprising lines of *Triticum aestivum* L., *Triticum durum* Desf., *Triticum dicoccum* Schrank, and triticale (× *Triticosecale* Wittmack). The genotypes represented multiple breeding eras and genetic backgrounds, enabling assessment of long-term genetic gain and trait diversity.

Experimental Design and Crop Establishment

The field experiment was conducted using a non-replicated augmented field design, in which 428 wheat varieties were grown as two-row plots under uniform agronomic management. This layout was adopted to enable large-scale evaluation of agronomic, phenological, and disease-related traits across a broad genetic base of released cultivars.

Genotypic effects were treated as fixed, consistent with the objective of assessing the performance and temporal trends of specific released varieties rather than making inferences to a random genetic population. To reduce environmental noise, the experiment was maintained under non-yield-limiting conditions, and phenotypic observations were restricted to the central portion of each plot, thereby minimizing border effects and inter-plot competition.

As the trial was unreplicated and not arranged in a formal block structure, field heterogeneity was addressed through uniform field management, systematic plot layout, and repeated evaluation across years. Multi-year phenotypic data were integrated, and year of variety release was included as a continuous covariate to estimate genetic trends using regression-based approaches. In addition, linear mixed models incorporating year effects were employed, and best linear unbiased predictions (BLUPs) were generated to improve estimates of genotypic performance by borrowing information across environments. This analytical framework enabled robust assessment of genetic gain and trait–yield relationships despite the absence of within-year replication.

Each genotype was established in double-row plots of uniform length and fixed inter-row spacing, and a uniform seeding rate was applied across all entries to ensure comparable plant density and resource availability. Peripheral plants were excluded from sampling to minimize edge effects.

Soil fertility was maintained at non-limiting levels through the application of recommended doses of macronutrients, with nitrogen supplied in split applications and phosphorus and potassium applied as basal fertilizers. Irrigation was provided at critical growth stages to maintain soil moisture near field capacity throughout the crop growth period. Weed and insect pressures were controlled using standard mechanical and chemical practices. These management interventions ensured a low-stress, yield-potential environment, such that observed phenotypic variation predominantly reflected genetic differences among genotypes.

Trait Quantification and Data Structure

A set of morphological, physiological, and yield-related traits was quantified, including plant height (PH) (cm), productive tiller number per plant (NPT), flag leaf length (FLL) (cm), flag leaf width (FLW) (cm), spike length (SL) (cm), number of spikelets per spike (NSPS), thousand-grain weight (TGW) (g), total above-ground biomass (BM) (g plant^{-1}), seed weight per plant (SW) (g), and harvest index (HI) (dimensionless ratio).

Plant height was measured at physiological maturity as the distance from the soil surface to the tip of the main spike, excluding awns. Spike traits were recorded from randomly sampled representative plants. Thousand-grain weight was estimated from oven-dried grain samples (65 °C, 48 h) and standardized to constant moisture content. Biomass and grain yield were measured after harvest and expressed on a per-plant basis.

Statistical Analysis

Descriptive statistics were used to quantify phenotypic variability among genotypes. Pearson’s correlation coefficients were computed to assess relationships among traits, and statistical significance was determined at appropriate probability levels. Linear regression analysis was performed to assess temporal trends using year of varietal release as the independent variable.

Principal component analysis (PCA) was conducted on standardized trait data to summarize multivariate relationships and identify major components contributing to phenotypic variation. Eigen values, variance explained, and trait loadings were used for interpretation. All statistical analyses were conducted using standard statistical software packages.

Results

Descriptive Statistics and Trait Variability

Substantial phenotypic variation was observed across the 428 Indian wheat varieties for all twelve agronomic, phenological, and yield-related traits (Table 1), indicating a broad genetic base suitable for multivariate analysis and selection. Days to heading ranged from 51 to 123 days (68.09 ± 8.14), while days to maturity varied from 92 to 164 days (108.90 ± 9.91), reflecting moderate diversity in crop duration. Plant height showed wide dispersion (57-140 cm; 100.86 ± 55.50), whereas flag leaf dimensions and spike traits exhibited more constrained distributions. Yield-related traits displayed pronounced variability, particularly plant biomass (12.8–81.6 g), seed weight (4.44–39.42 g), and thousand grain weight (29.0–66.0 g), highlighting their potential contribution to yield differentiation among genotypes.

TABLE -1 SUMMARY STATISTICS

VARIABLE	mean	sd	min	q1	med	q3	max	mad	iqr	cv	skewness	se. skewness	kurtosis	n. valid	pct. valid
AVG.DAYS.TO.HEADING	68.0	8.14	51.0	65.00	68.00	73.00	123	7.41	8.0	0.12	-1.63	0.12	22.07	428	100
AVG.DAYS.TO.MATURITY	108.9	9.91	92.0	106.0	109.0	114.0	164	7.41	8.0	0.09	-5.10	0.12	58.50	428	100
FLAG.LEAF.LENGTH	25.4	4.24	14.0	22.30	25.30	28.30	39	4.45	6.0	0.17	0.26	0.12	-0.02	428	100
FLAG.LEAF.WIDTH	1.89	0.24	1.50	1.70	1.90	1.90	2.5	0.30	0.2	0.13	0.93	0.12	0.27	428	100
HARVEST.INDEX	0.37	0.08	0.20	0.32	0.36	0.42	0.7	0.07	0.1	0.21	0.57	0.12	0.48	428	100
MEAN.TGW	39.8	6.75	29.0	35.00	38.00	42.00	66.0	4.45	7.0	0.17	1.52	0.12	2.09	428	100
NO.OF.SPIKELETS..PER.SPIKE	18.6	2.26	11.0	17.00	19.00	20.00	27.0	1.48	3.0	0.12	0.07	0.12	0.82	428	100
PLANT.BIOMASS	31.8	11.3	12.8	23.80	30.40	37.60	81.6	10.3	13.7	0.36	1.24	0.12	2.30	428	100
PLANT.HEIGHT	100	55.5	57.0	89.00	95.00	103.0	895	10.3	14.0	0.55	13.17	0.12	183.44	428	100
PRODUCTIVE.TILLERS.PER.PLANT	13.4	4.29	4.00	11.00	12.00	16.00	45.0	4.45	5.00	0.32	1.37	0.12	6.35	428	100
SEED.WEIGHT	11.6	4.26	4.44	8.76	10.56	13.89	39.4	3.37	5.12	0.37	1.59	0.12	4.64	428	100
SPIKELET.LENGTH	9.88	1.69	1.50	9.00	10.00	11.00	15.0	1.48	2.00	0.17	-0.34	0.12	0.99	428	100

Table 2: CORRELATION ANALYSIS

	PH	ADH	ADM		FLL	FLW	SL	NSPS	TGW	BM	SW	HI
PH	1	-0.01	-0.012	-0.058	0.031	-0.075	0.003	0	-0.019	-0.033	-0.041	-0.025
ADH	-0.01	1	0.973***	-0.15**	-0.073	-0.032	0.063	0.15**	0.02	0.094	0.072	-0.02
ADM	-0.012	0.973***	1	-0.165***	-0.055	-0.043	0.048	0.116*	0.023	0.091	0.069	-0.022
PTN	-0.058	-0.15**	-0.165***	1	0.061	0.031	0.085	-0.014	0.065	0.021	0.005	-0.016
FLL	0.031	-0.073	-0.055	0.061	1	0.094	0.215***	0.037	-0.057	-0.092	-0.058	0.016
FLW	-0.075	-0.032	-0.043	0.031	0.094	1	0.081	0.106*	-0.101*	-0.072	-0.059	0.013
SL	0.003	0.063	0.048	0.085	0.215***	0.081	1	0.369***	-0.147**	-0.096*	-0.064	0.066
NSPS	0	0.15**	0.116*	-0.014	0.037	0.106*	0.369***	1	0.076	0.023	0.029	0.023
TGW	-0.019	0.02	0.023	0.065	-0.057	-0.101*	-0.147**	0.076	1	0.27***	0.266***	-0.026
BM	-0.033	0.094	0.091	0.021	-0.092	-0.072	-0.096*	0.023	0.27***	1	0.812***	-0.301***
SW	-0.041	0.072	0.069	0.005	-0.058	-0.059	-0.064	0.029	0.266***	0.812***	1	0.277***
HI	-0.025	-0.02	-0.022	-0.016	0.016	0.013	0.066	0.023	-0.026	-0.301***	0.277***	1

`## *** Correlation is significant at 0.001 level (two tailed)`
`## ** Correlation is significant at 0.01 level (two tailed)`
`## * Correlation is significant at 0.05 level (two tailed)`

Correlation analysis revealed distinct association patterns among trait groups (Table 2; Fig. 1). Phenological traits were tightly coupled, with days to heading and days to maturity showing a strong positive correlation (r = 0.973, P < 0.001). Both traits were negatively associated with productive tillers per plant and positively correlated with the number of spikelets per spike, indicating coordinated effects of crop duration on tillering and spike development. Structural traits such as flag leaf length and spikelet length were positively correlated, while yield components were strongly interrelated. Plant biomass showed a strong positive correlation with seed weight (r = 0.812, P < 0.001) and thousand grain weight, whereas harvest index was negatively associated with biomass but positively with seed weight, reflecting variation in assimilate partitioning efficiency.

Figure 1: Correlation Analysis

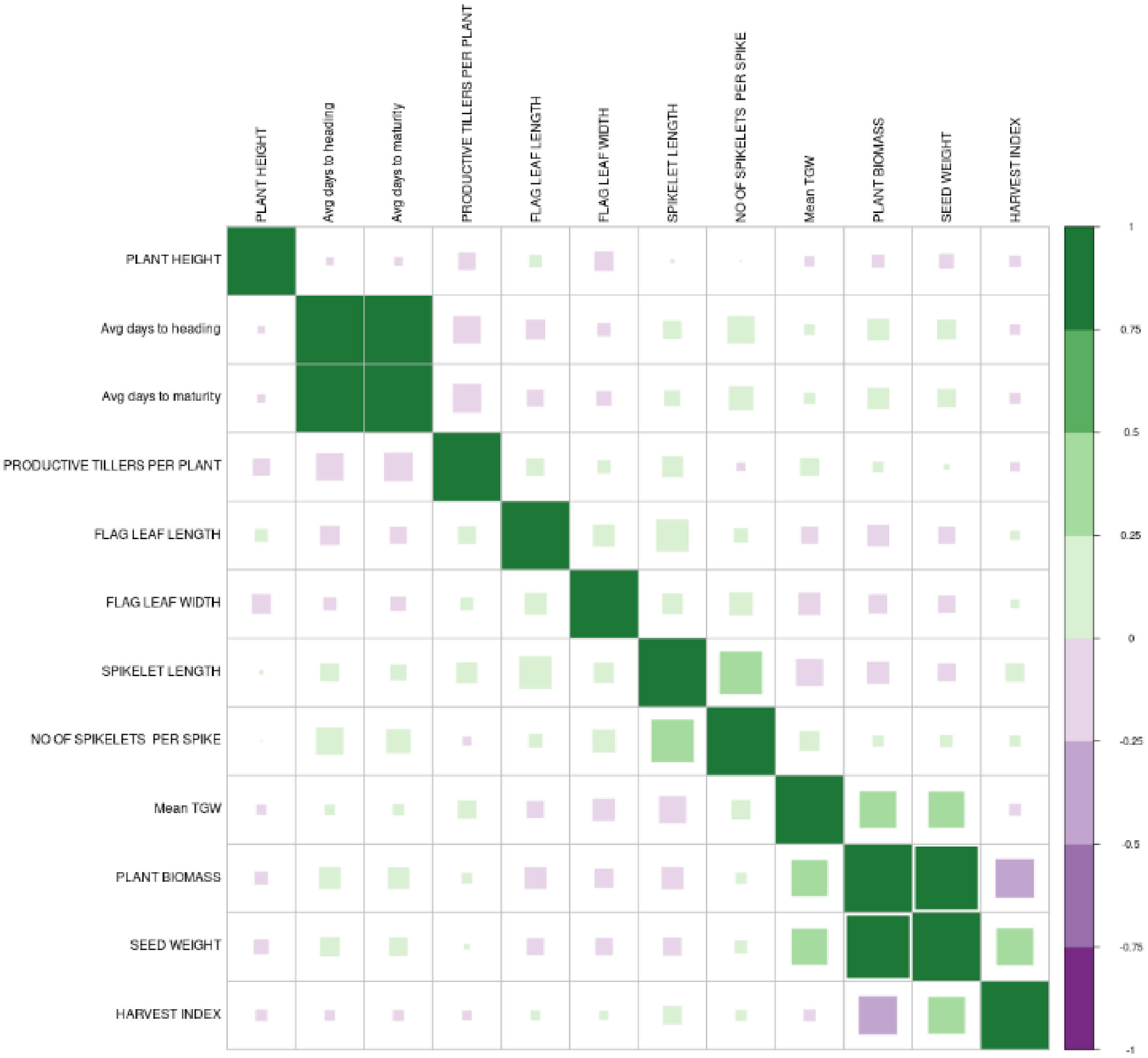
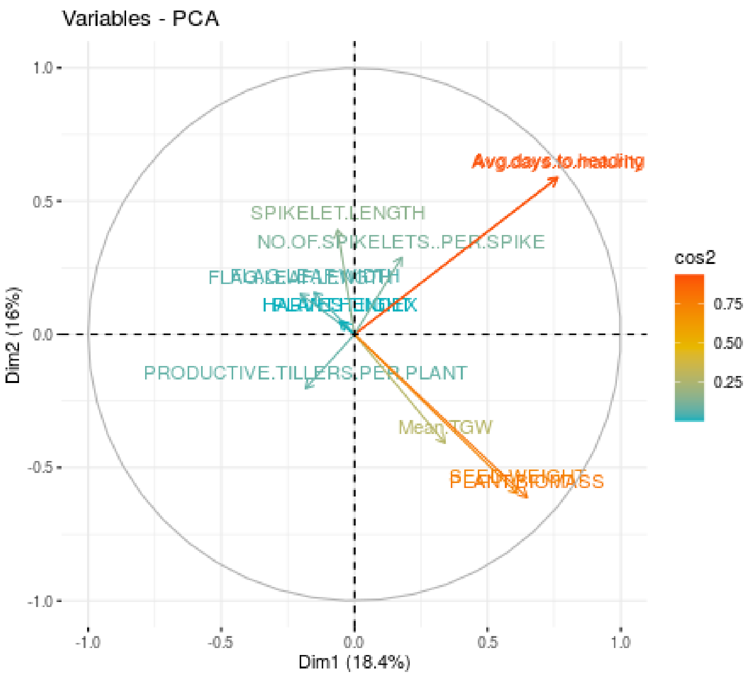


Table 3 Principal Component Analysis and Component Structure

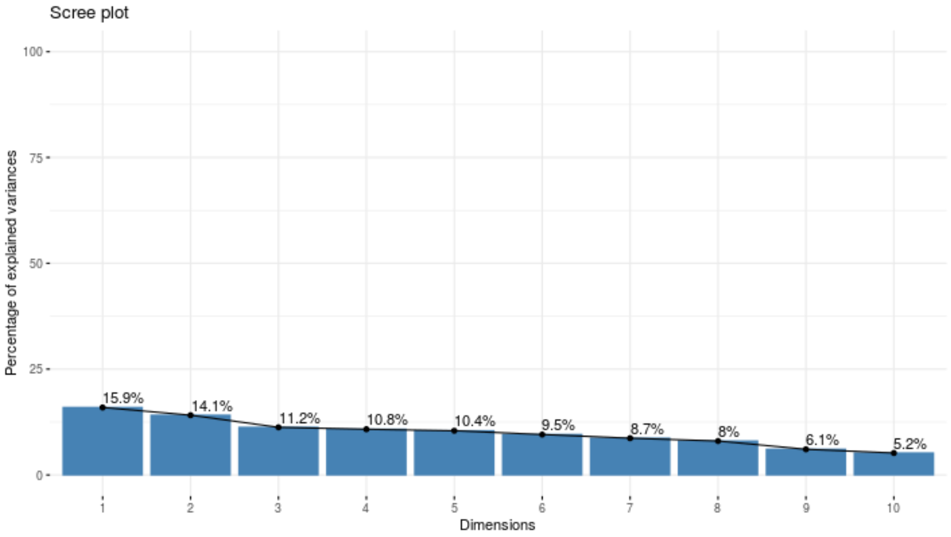
Component	PH	ADH	ADM	PTN	FLL	FLW	SL	NSPS	TGW	BM	SW	HI
X4	0.0296	0.0350	0.0895	0.0735	0.8074	0.1593	0.0341	0.4193	0.3601	0.0225	0.0030	0.0041
X5	-0.5136	0.4260	0.1056	-0.0002	-0.0708	-0.0677	0.1497	0.0823	0.0597	-0.0065	-0.7073	-0.0290
X6	-0.5115	0.4224	0.1248	-0.0042	-0.0683	-0.0566	0.1767	0.0786	0.0340	0.0089	0.7052	0.0228
X7	0.1240	-0.1469	-0.2525	0.1962	-0.2189	-0.5778	0.3932	0.2057	0.5063	-0.1598	0.0126	-0.0062
X8	0.1373	0.1096	-0.3477	0.1061	0.1607	0.2119	0.6692	0.0460	-0.5142	-0.2265	-0.0171	0.0175
X9	0.1020	0.1136	-0.2663	0.0608	-0.4638	0.5350	-0.1149	0.5844	0.1588	0.1440	0.0055	0.0042
X10	0.0426	0.2836	-0.5642	0.0792	0.1612	-0.0806	-0.0413	-0.3279	0.1117	0.6625	0.0038	-0.0044
X11	-0.1195	0.2087	-0.5061	0.1141	0.1301	-0.1350	-0.5390	0.0238	-0.0802	-0.5828	0.0241	-0.0038
X12	-0.2285	-0.2941	-0.0634	0.0629	0.0629	-0.4147	-0.1474	0.5171	-0.5172	0.3474	-0.0055	0.0075
X13	-0.4361	-0.4420	-0.1543	0.2418	0.0114	0.2390	0.0477	-0.1681	0.1214	-0.0131	-0.0226	0.6549
X14	-0.4112	-0.4304	-0.2687	-0.2775	0.0390	0.1939	0.0985	-0.0872	0.1273	-0.0339	0.0252	-0.6496
X15	0.0379	0.0348	-0.1874	-0.8846	0.0328	-0.1021	0.0599	0.1177	0.0474	-0.0350	-0.0129	0.3837

Figure 2



Principal component analysis (PCA) was performed using all twelve traits to summarize multivariate variation among wheat varieties (Fig. 2). The scree plot (Fig. 3) showed a clear inflection at the third component, while eigenvalue analysis indicated that the first five components (eigenvalue > 1) captured the major sources of variation.

Figure 3 Scree Plot



The first principal component (PC1; 15.9% variance) represented a growth and productivity axis, characterized by high loadings for plant biomass, seed weight, thousand grain weight, and related architectural traits. This component reflected coordinated variation in biomass accumulation and grain production and corresponded closely with the strong positive correlations observed among yield-related traits.

The second principal component (PC2; 14.1%) was dominated by phenological traits, with days to heading and days to maturity contributing most strongly. PC2 was largely orthogonal to PC1, indicating that variation in crop duration was largely independent of yield potential.

The third principal component (PC3; 11.22%) captured yield partitioning and tillering variation, with productive tillers per plant, thousand grain weight, seed weight, and harvest index contributing prominently. Subsequent components (PC4–PC5) were associated with harvest index and tillering ability, while later components explained progressively smaller proportions of variance and represented fine-scale, trait-specific variation.

Overall, the PCA structure closely mirrored the correlation matrix, confirming that phenotypic diversity in wheat is structured primarily by yield components (PC1), phenology (PC2), and yield partitioning mechanisms (PC3).

Temporal Trends in Trait Expression

Regression analysis revealed modest but consistent temporal trends. Phenological traits exhibited weak positive trends with year of release, indicating slight shifts toward longer crop duration without loss of variability. Canopy traits showed mixed responses: flag leaf length declined gradually, flag leaf width remained stable, and spikelet length showed no clear trend. In contrast, the number of spikelets per spike increased moderately over time.

Yield-related traits displayed clearer directional change. Thousand grain weight and seed weight increased consistently with year of release, while plant biomass showed a gradual upward trend (Fig.4). Productive tillers per plant declined over time, whereas harvest index remained relatively stable despite wide inter-varietal variation.Trend analysis further indicated that modern varieties are improving grain size and biomass at a faster rate than older varieties, whereas vegetative traits such as leaf dimensions and tiller number show minor declines. Overall, these results highlight the directional changes in wheat morphology and yield components driven by breeding efforts over time.

Temporal Trends and Trait Variation in Wheat

Modern wheat varieties showed higher thousand-grain weight (40.34 g vs 38.41 g), seed weight (12.27 g vs 10.93 g), plant biomass (33.56 g vs 29.68 g) compared with older varieties, reflecting a shift toward larger grains and greater biomass. In contrast, plant height, productive tillers, flag leaf length, and spikelet length were slightly reduced, while flag leaf width and harvest index remained largely stable.

Principal Component Analysis supported these observations: components associated with grain weight, biomass, spike length, and harvest efficiency (X4, X7, X10, X13, X15) dominated variation, whereas components linked to tillering and leaf dimensions (X5, X6, X11, X12) contributed less. Together, these results indicate that modern breeding has prioritized reproductive traits and yield efficiency, favoring grain-focused ideotypes over vegetative growth, highlighting the directional improvement of wheat morphology and productivity over time.

Integrated Interpretation of Multivariate Patterns

Collectively, correlation analysis, PCA, and temporal trends demonstrate that yield improvement in Indian wheat has been driven primarily by traits loading strongly on PC1—biomass accumulation and grain weight—while phenology (PC2) and spike or tiller traits (PC3) have contributed independent and complementary variation. This multivariate structure highlights distinct but exploitable trait complexes underlying yield formation and harvest efficiency.

Discussion

This study integrates univariate, bivariate, and multivariate analyses to elucidate the trait architecture underlying yield formation and harvest efficiency in Indian wheat. By combining descriptive statistics, correlation analysis, principal component analysis, and temporal trends, the results provide a coherent picture of how breeding has shaped phenology, plant architecture, and yield components over time.

Trait Variability as a Basis for Genetic Gain

The substantial phenotypic variation observed across all twelve traits confirms the existence of a broad genetic base within Indian released wheat varieties, despite decades of systematic selection. Pronounced variability in yield-related traits—particularly plant biomass, seed weight, and thousand grain weight—indicates that these traits have remained responsive to selection and continue to contribute strongly to yield differentiation among genotypes. In contrast, the relatively constrained distributions of flag leaf dimensions and spikelet traits suggest stabilizing selection toward optimal canopy and spike architecture. Moderate diversity in phenological traits reflects a balance between adaptation to diverse agro-ecological zones and the need to maintain reliable crop duration for yield stability.

Functional Trait Associations and Yield Formation Strategies

The correlation structure revealed clear functional groupings among traits that reflect distinct biological processes. The very strong association between days to heading and days to maturity confirms tight coordination of developmental timing, a characteristic feature of wheat phenology. Their negative relationship with productive tillers per plant and positive association with spikelet number suggests alternative yield formation strategies, whereby longer-duration genotypes rely more on spike development, while shorter-duration types compensate through increased tillering. Structural traits such as flag leaf length and spikelet length were positively associated, indicating coordinated development of photosynthetic and reproductive structures. However, their weak correlations with yield components suggest that these traits contribute indirectly to productivity, likely through physiological efficiency rather than direct yield determination. In contrast, yield-related traits formed a tightly connected network, with strong positive associations among biomass, seed weight, and thousand grain weight. The negative relationship between biomass and harvest index highlights a classical trade-off between total dry matter production and partitioning efficiency, emphasizing that increased vegetative growth does not always translate into proportional grain yield gains.

Multivariate Organization of Trait Diversity

Principal component analysis provided a clear multivariate framework that integrated and validated the correlation results. The dominance of PC1 as a growth and productivity axis underscores the central role of biomass accumulation and grain weight in structuring phenotypic diversity. Traits loading heavily on this axis—plant biomass, seed weight, and thousand grain weight—represent the primary drivers of yield variation and reflect sustained breeding emphasis on enhancing source capacity and sink strength.

PC2 captured phenological variation that was largely orthogonal to PC1, indicating that crop duration has been modified independently of yield potential. This independence is agronomically significant, as it suggests that breeding programs have maintained flexibility in phenology to suit diverse environments without compromising productivity. PC3, associated with tillering, grain weight, and harvest index, highlights variation in yield partitioning strategies and efficiency, further emphasizing that multiple, partially independent trait complexes contribute to overall performance.

The consistency between PCA structure and correlation patterns confirms that phenotypic diversity in wheat is not random but organized around a few dominant biological axes, with additional components capturing finer-scale and trait-specific variation.

Breeding-Induced Temporal Shifts in Trait Expression

Temporal trend analysis revealed that wheat improvement has involved gradual, targeted trait modifications rather than abrupt directional changes. Slight increases in days to heading and maturity over time suggest cautious optimization of phenology, likely aimed at maximizing yield potential under favorable conditions while retaining adaptability. The decline in flag leaf length alongside stable flag leaf width indicates refinement of canopy architecture toward compact and efficient forms rather than simple enlargement.

Clearer directional gains were evident for yield-related traits. Consistent increases in thousand grain weight, seed weight, and plant biomass demonstrate sustained genetic progress in grain filling and assimilate accumulation. In contrast, the progressive decline in productive tillers per plant reflects a shift away from yield strategies based on high tillering toward developing an ideotype with fewer but more productive tillers, plant erectness with strong culm and heavier ear head accommodating more grains. The stability of harvest index across decades suggests that partitioning efficiency may have approached a physiological optimum, with further yield gains relying primarily on increased biomass and grain sink capacity.

Consolidation of Gains in Modern Varieties

The comparison between older and modern varieties reinforces these temporal patterns. Modern cultivars exhibited higher grain weight and biomass, confirming that yield improvement has been driven mainly by traits aligned with PC1. Reduced tiller number, flag leaf length, and spikelet length in modern varieties indicate greater efficiency in resource allocation and reduced intra-plant competition. The minimal difference in harvest index between varietal groups further supports the view that yield gains have arisen through enhanced assimilate production and utilization rather than changes in partitioning ratios.

Implications for Future Wheat Improvement

Collectively, these findings demonstrate that yield improvement in Indian wheat has been governed primarily by biomass accumulation and grain weight, while phenology and architectural traits have provided adaptive flexibility and stability. The clear separation of these trait complexes in PCA space suggests that future breeding efforts can target underexploited variation in harvest index, spike fertility, and stress-responsive traits without adversely affecting yield potential. The integrated analytical framework used here provides a robust basis for designing multivariate selection strategies aimed at sustaining yield gains and improving harvest efficiency under evolving climatic and management conditions.

References

Brancourt-Hulmel, M., Doussinault, G., Lecomte, C., Berard, P., Le Buanec, B., &Trottet, M. (2003). Genetic improvement of agronomic traits of winter wheat cultivars released in France from 1946 to 1992. *Crop Science*, 43, 37–45.

Brisson, N., Gate, P., Gouache, D., Charmet, G., Oury, F. X., & Huard, F. (2010). Why are wheat yields stagnating in Europe? A comprehensive data analysis for France. *Field Crops Research*, 119, 201–212.

Cleaver, H. (1972). The contradictions of the Green Revolution. *American Economic Review*, 62, 177–186.

Crespo-Herrera, L. A., Crossa, J., Huerta-Espino, J., Autrique, E., Mondal, S., Velu, G., & Singh, R. P. (2017). Genetic yield gains in CIMMYT's international elite spring wheat yield trials by modeling the genotype × environment interaction. *Crop Science*, 57, 789–801.

Farmer, B. H. (1979). *Green Revolution? Technology and change in rice-growing areas of Tamil Nadu*. Macmillan, London.

Finlay, K. W., & Wilkinson, G. N. (1963). The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research*, 14, 742–754.

Fischer, R. A., & Edmeades, G. O. (2010). Breeding and cereal yield progress. *Crop Science*, 50, S85–S98.

Foulkes, M. J., et al. (2011). Physiological drivers of genetic gains in wheat yield and biomass accumulation.

Graybosch, R. A., & Peterson, C. J. (2010). Genetic improvement in winter wheat yields in the Great Plains of North America, 1959–2008. *Crop Science*, 50, 1882–1890.

Griffin, K. (1974). *The political economy of agrarian change: An essay on the Green Revolution*. Harvard University Press, Cambridge.

Matus, I. A., Gonzalez, M. I., Del Pozo, A., & Madariaga, R. (2012). Yield, yield components and grain protein concentration of Chilean bread wheat cultivars released between 1920 and 2000. *Field Crops Research*, 126, 46–56.

Morgounov, A., Zykin, V., Belan, I., Roseeva, L., Zelenskiy, Y., Gomez-Becerra, H. F., & Budak, H. (2014). Genetic gains for grain yield in high latitude spring wheat grown in Western Siberia in 1900–2008. *Field Crops Research*, 159, 101–112.

OECD/FAO. (2019). *OECD–FAO Agricultural Outlook 2019–2028*. OECD Publishing, Paris / FAO, Rome.

Perry, M. W., & D'Antuono, M. F. (1989). Yield improvement and associated characteristics of some Australian spring wheat cultivars between 1860 and 1982. *Australian Journal of Agricultural Research*, 40, 457–472.

Sadras, V. O., & Lawson, C. (2011). Genetic gain in yield and associated changes in phenotype, trait plasticity and competitive ability of South Australian wheat varieties released between 1958 and 2007. *Crop & Pasture Science*, 62, 533–549.

Sadras, V. O., &Rebetzke, G. J. (2013). Plasticity of wheat grain yield is associated with plasticity of ear number. *Crop & Pasture Science*, 64, 234–243.

Sanchez-Garcia, M., Álvaro, F., Peremarti, A., Martín-Sánchez, J. A., & Royo, C. (2013). Changes in bread wheat yield and associated traits in Spain during the 20th century. *Journal of Agricultural Science*, 151, 105–118.

Sanchez-Garcia, M., Royo, C., Aparicio, N., Martín-Sánchez, J. A., & Alvaro, F. (2012). Genetic improvement of bread wheat yield and associated traits in Spain during the 20th century. *Journal of Agricultural Science,* 150, 105–118.

Sayre, K. D., Rajaram, S., & Fischer, R. A. (1997). Yield potential progress in short bread wheats in northwest Mexico. *Crop Science*, 37, 36–42.

Sen, A. K. (1974). *Poverty, inequality and unemployment*. Oxford University Press, Oxford.

Siddique, K. H. M., Kirby, E. J. M., & Perry, M. W. (1989). Ear:stem ratio in old and modern wheat varieties; relationship with improvement in number of grains per ear and yield. *Field Crops Research*, 21, 59–78.

Waddington, S. R., Ransom, J. K., Osmanzai, M., & Saunders, D. A. (1986). Improvement in the yield potential of bread wheat adapted to northwest Mexico. *Crop Science*, 26, 698–703.

Xu, B., et al. (2023). Recent advances in semi-dwarfing gene deployment and yield gains in wheat breeding.

Yadav R, Gupta S, Gaikwad KB, Bainsla NK, Kumar M, Babu P, Ansari R, Dhar N, Dharmateja P, Prasad R. Genetic Gain in Yield and Associated Changes in Agronomic Traits in Wheat Cultivars Developed Between 1900 and 2016 for Irrigated Ecosystems of Northwestern Plain Zone of India. Front Plant Sci. 2021 Sep 23;12:719394. doi: 10.3389/fpls.2021.719394. PMID: 34630466; PMCID: PMC8496457.

Yadav, S. S., McNeil, D., & Redden, R. (2017). Climate change impacts on crop productivity. *Current Agriculture Research Journal*, 5, 1–10.

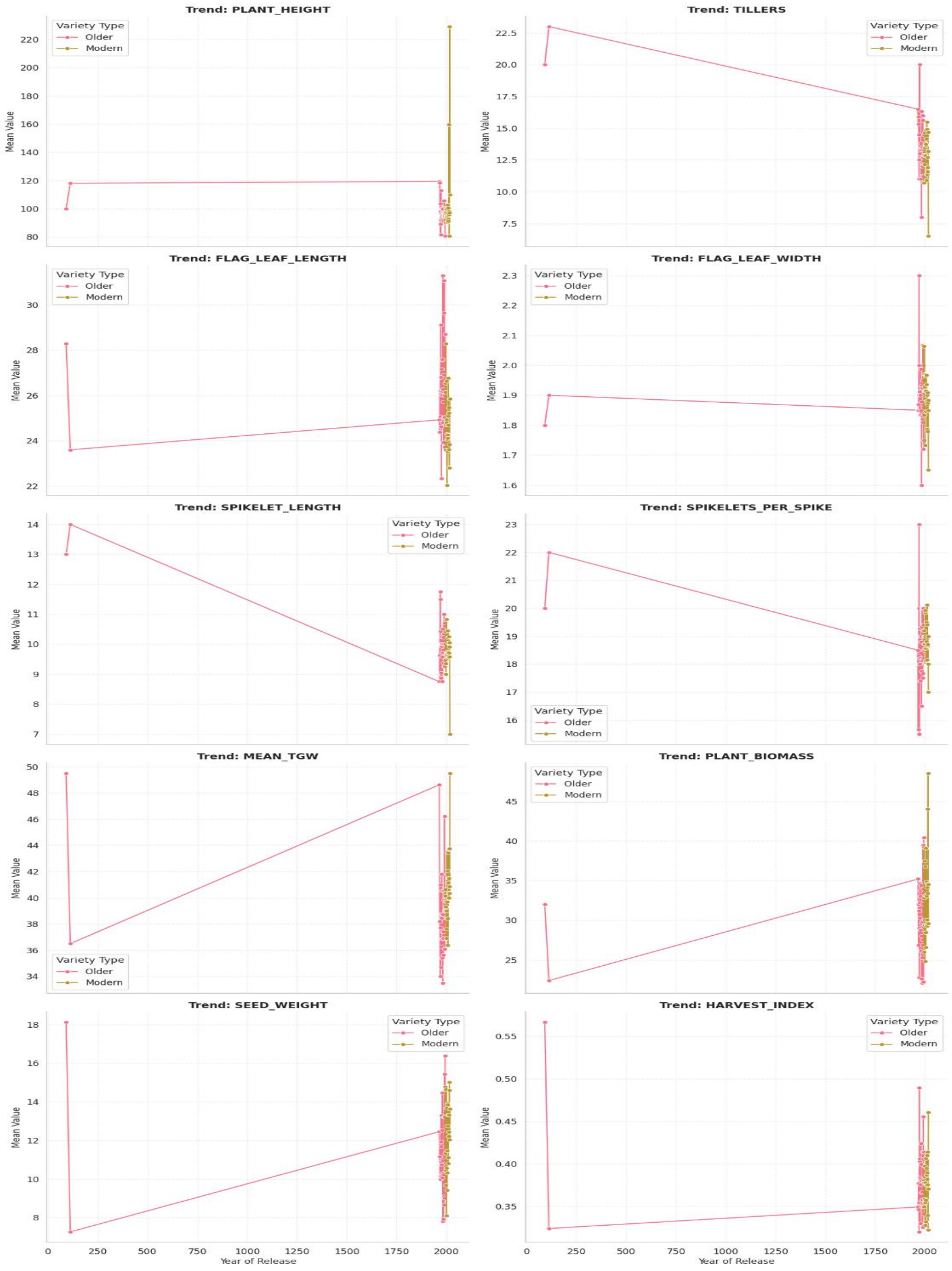
Yadav, S. S., Redden, R., Hatfield, J. L., Lotze-Campen, H., & Hall, A. E. (2010). *Crop adaptation to climate change*. Wiley-Blackwell, Oxford.

Yadav, S., Lobell, D. B., & Kaur, P. (2019). Climate variability and wheat yields in India. *Agricultural Systems*, 168, 1–8.

Yue Xi, Yan-Lei Du, Dong Wang, Jie-Ying Ren, Wen-Yuan Luo, Qiao Peng, Wan-Ying Fang, Feng-Min Li,Wheat genetic progress in biomass allocation and yield components: A global perspective, Field Crops Research,Volume 318,2024,109617,ISSN 0378-4290,https://doi.org/10.1016/j.fcr.2024.109617.

Zhou, Y., He, Z. H., Sui, X. X., Xia, X. C., Zhang, X. K., & Zhang, G. S. (2007). Genetic improvement of grain yield and associated traits in the Northern China winter wheat region from 1960 to 2000. *Crop Science*, 47, 245–253.

Figure 4 Simple linear regression scatter plots with fitted trend lines



Breaking the yield barrier in bread wheat through marker assisted pyramiding of yield enhancing rust resistance genes

Vikas VK, Sivasamy M, Jayaprakash P, Geetha M, John Peter, Suganya C., Vaishali, Nisha R, and Shajitha P.

ICAR-Indian Agricultural Research Institute, Regional Station, Wellington 643 231, The Nilgiris, Tamilnadu.

Wheat is the staple food for more than 2.5 billion people globally. Wheat contributes substantially to food security by providing 20% of dietary calories and protein worldwide. By 2050, human population is expected to grow by 25% and would reach around ten billion (Hickey et al., 2019). To meet the projected demands from increasing population and diet shifts, global crop production need to be doubled (Ray et al., 2013). The current rate of improvement of wheat is @ 0.9% per year which is less than the 2.4% per year rate required to double global production by 2050 (Ray et al., 2013).

Research on yield improvement in wheat in the past two decades in India were mostly based on imparting resistance to biotic stresses (diseases) and tolerance to abiotic stresses (drought and heat) which reduced the losses, thereby increasing the yield indirectly. However, research on yield improvement per se is paltry. Yield improvement in wheat started during the "Green Revolution" period (in the 1960s & 1970s) with the introduction of the dwarfing, *Rht* (Reduced height) genes (*Rht-B1b* and *Rht-D1b*). *Rht* genes reduced the plant height by 15–20%, associated with increased productive tillers, contributing to enhanced yield. *Rht* gene was followed by wheat–rye 1BL/lRS translocation, the short arm of the 1B chromosome of wheat (*Triticum aestivum*) is replaced by the short arm of the 1R chromosome of cereal rye (*Secale cereale*).1BL/lRS translocation not only provided resistance to stem (*Sr31*), leaf (*Lr26*) and stripe rust (*Yr9*) and powdery mildew (*Pm8*) diseases, but also improved bio mass, spikelets/spike, grains/spike and 1000 grain weight contributing to high grain yield (Villareal et al. 1995). Due to diseases resistance and yield enhancing attributes 1BL/lRS translocation had been widely used in bread wheat-breeding program from 1980s till the detection of *Sr31* virulent stem rust pathotype (Ug99) in 1999.

Similar to 1BL/lRS translocation, there are translocations from wild relatives of wheat viz., 7DL.7Ag translocation and 2NS.2AS translocation which provide disease resistance coupled with yield enhancing attributes. The 7DL.7Ag translocation from *Agropyron elongatum,* that carries stem (*Sr25*) and leaf rust (*Lr19*) resistance genes increased the yield by 8.2% compared to lines without the translocation besides providing resistance (Singh et al., 1998). Increased yield is due to the increased partitioning of biomass to spike growth at anthesis, higher grain number per spike and higher flag-leaf photosynthetic rate during grain filling (Reynolds et al., 2001). Genomics studies revealed the yield improving ability of 2NS.2AS translocation from *Aegilops ventricosa* (Juliana et al., 2019), which accommodates leaf (*Lr37*), stem (*Sr38*) and stripe (*Yr17*) rust resistance genes along with resistance to wheat blast. In India, these translocations were not used to improve the yield per se, however few reports on the use of these translocations as a source of resistance to rust diseases is available. With this background information, study had been carried out to improve the wheat yield using the two translocations through marker assisted backcross approach following foreground and background selection.

Plant material comprised of recurrent parents viz., HD3086 and GW322. HD3086 is well-adapted, high yielding variety released for cultivation in North west plain zone (NWPZ) and North east plain zone (NEPZ). GW322 is a well-adapted variety cultivated in Central and Peninsular zone. Donor parents include bread wheat varieties viz., DPW621-50+ and LOK1+ carrying, *Lr37/Yr17/Sr38 + Yr15 &Lr19/Sr25* and *Lr37/Yr17/Sr38 & Lr19/Sr25* separately respectively. Recurrent parents viz., HD3086 and GW322 were crossed with donor parents each separately viz., DPW621-50 and LOK1 carrying, *Lr37/Yr17/Sr38 + Yr15 &Lr19/Sr25* and *Lr37/Yr17/Sr38 & Lr19/Sr25* respectively.

Near isogenic lines (NILs) with leaf rust resistance genes (*Lr37/Yr17/Sr38 & Lr19/Sr25*) and their respective recurrent parents (HD3086 and GW322) with more than 90% recurrent parent genome recovery were evaluated in Randomized Block Design (RBD) for two years (2023-24 and 2024-25) which includes four seasons (winter and summer season of each year). Each genotype was sown in 5m row length of 5 rows each in three replications under unsprayed and sprayed treatments (Fungicide-Propiconazole spray). In unsprayed treatments genotypes were not given Propiconazole spray, while in sprayed treatment, genotypes were provided with Propiconazole spray (200 ml/acre) for rust diseases. Unsprayed and sprayed treatments were necessary to demarcate the contribution of rust resistance gene towards yield. Following agronomic/yield attributing traits viz., plant height, days to flowering, spike length, spikelet number/spike, ear heads/m^2, number of grains/spike, thousand grain weight, days to maturity, economic yield/m^2, biological yield/ m^2 and harvest index were recorded in both the NILs and their respective recurrent parents under unsprayed and sprayed treatments.

Near isogenic lines (NILs) in the background of HD3086+ showed a yield increase of 7.4% compared to the parent, HD3086 under the sprayed treatment which can be attributed to the leaf rust resistance genes (*Lr37/Yr17/Sr38 & Lr19/Sr25*). Yield enhancement is mainly due to the increase in the number of grains/spikes, which got boosted by 20% compared to the parent, HD3086. Moreover, the days to flowering and days to maturity got delayed by 5 days which also contributed to the yield enhancement. Contribution of rest of the traits to the yield increase is not significant. Under unsprayed treatment, yield increase was 17.2%, as the parent HD3086 was moderately susceptible to leaf and stem rust, while NILs (HD3086+) was resistant to both the rusts.

NILs in the background of GW322+ showed a yield increase of 9.8% compared to the parent, GW322 under the sprayed treatment which can be attributed to the leaf rust resistance genes (*Lr37/Yr17/Sr38 & Lr19/Sr25*). Yield enhancement is mainly due to the increase in the number of grains/spikes, which got boosted by 24% compared to the parent, GW322. Moreover, the days to flowering and days to maturity got delayed by 5–6 days which also contributed to the yield enhancement. Contribution of rest of the traits to the yield increase is not significant. Under unsprayed treatment, yield increase was 15.8%, as the parent GW322 was moderately susceptible to leaf and stem rust, while NILs (GW322+) was resistant to both the rusts.

As the wheat is a sink limited crop, increase in the number of grains per spike had contributed to the increase in the yield of the NILs (HD3086+ and GW322+). High efficiency in the translocation of photosynthates from source (leaves and stem) to the sink (spike) made the way for increased yield in the NILs (HD3086+ and GW322+). So, the leaf rust resistance genes ((*Lr37/Yr17/Sr38 & Lr19/Sr25*) had improved the translocation efficiency in the NILs (HD3086+ and GW322+) compared to the recurrent parents (HD3086 and GW322) and increased the yield.

References

Hickey LT, Hafeez AN, Robinson H*et al.* (2019). Breeding crops to feed 10 billion. *Nat Biotechnol.* 37:744-754.

Ray DK, ND Mueller, PC West and JA Foley. 2(013). Yield trends are Insufficient to Double Global Crop Production by 2050. *PLoS ONE*(6): e66428.

Singh RP, Huerta-Espino J, Rajaram S and Crossa. J (1998). Agronomic Effects from Chromosome Translocations 7DL.7Ag and 1BL.1RS in Spring Wheat. *Crop Sci.* 38: 27-33.

Reynolds MP, Calderini DF and Condon AG. (2001). Physiological basis of yield gains in wheat associated with the *Lr19* translocation from *Agropyron elongatum*. *Euphytica* 119: 137-141.

Juliana P, J Poland, J Huerta-Espino, S Shrestha, J Crossa, L Crespo-Herrera, *et al.*(2019). Improving grain yield, stress-resilience, and quality of bread wheat using large-scale genomics. *Nat. Genet.*51:1530-9.

Inauguration of Busts of Dr. Norman Borlaug and Prof. M. S. Swaminathan and Foundation Day Celebrations at ICAR–IARI Regional Station, Wellington

The Foundation Day of ICAR–IARI Regional Station, Wellington, was celebrated on 13th September 2025 with the inauguration of the busts of Dr. Norman Borlaug and Prof. M.S. Swaminathan at the Green Revolution Plot. The event was graced by the Hon'ble Director & Vice-Chancellor, Dr. Ch. Srinivasa Rao, IARI, New Delhi, and the Joint Director (Research), Dr. C. Viswanathan, IARI.

The program began with a formal welcome by Dr. M. Sivasamy, Principal Scientist & Head, in the presence of scientists, staff, and dignitaries from other local institutes — ICAR–IISWC, Ooty and ICAR–CPRI. The guests visited key facilities and reviewed research materials spanning three decades, the Mini Molecular Biology Laboratory, advanced wheat evaluation plots, oats trials, mustard breeding program, Fusarium Head Blight (FHB) screening lines, pathology glasshouses, and wild wheat accessions. The Director commended the Regional Station's impactful contributions and its diversified research supporting resilient and sustainable agriculture.

At the Green Revolution Plot, the busts of Dr. Norman Borlaug and Prof. M.S. Swaminathan were unveiled, followed by floral tributes. In his address, Hon'ble Director & Vice-Chancellor, Dr. Ch. Srinivasa Rao reflected on their transformative role in India's Green Revolution, and emphasized the need to build on their vision through innovation, modern breeding tools, and sustained crop improvement to tackle challenges of disease outbreaks and nutritional security. He added that their legacy continues to inspire scientists to work with dedication for the benefit of farmers and society. The JDR, Dr. C. Viswanathan in his Tamil address, warmly appreciated the contributions of scientists, staff, and field laborers, while urging young researchers to carry forward the station's legacy.

The formal program began with Tamizh Thai Vazhthu, lamp lighting, and a welcome by Dr. M. Sivasamy. In his address, the JDR, Dr. C. Viswanathan, highlighted the need for stronger disease resistance research and farmer-focused innovations. Delivering the Chief Guest Address, the Hon'ble Director & Vice-Chancellor, Dr. Ch. Srinivasa Rao, celebrated the legacy of the Regional Station and outlined a renewed vision for its future role in strengthening national agriculture. The event concluded with memento presentations and the National Anthem.

The dignitaries expressed satisfaction with the progress at Wellington and encouraged the scientists and the staff to continue their dedicated efforts for the betterment of Indian agriculture.


GREEN REVOLUTION PLOT


FOUNDATION DAY
IARI
REGIONAL STATION

Wheat Germplasm Monitoring at ICAR–IARI Regional Station, Wellington

A wheat germplasm monitoring visit was conducted at ICAR–Indian Agricultural Research Institute (IARI), Regional Station, Wellington, from 19th to 21st November 2025 as part of the ongoing evaluation activities under the Consortium Research Platform (CRP) – Agro-Biodiversity, Component III: Trait Discovery and Pre-Breeding in Wheat. The program focused on the systematic assessment of tetraploid durum wheat germplasm for resistance to Fusarium Head Blight (FHB) and major rust diseases.

During the Kharif and Rabi seasons of 2024–25, a total of 5,068 tetraploid durum wheat accessions were under evaluation. In addition, the visiting team reviewed the performance of more than 1,000 wild wheat germplasm accessions obtained from ICAR–NBPGR. The monitoring visit provided an opportunity to assess field performance across this diverse germplasm, and to discuss progress, challenges, and future directions of the pre-breeding program.

The event was attended by eminent scientists, including Dr. Gyanendra Pratap Singh, Director, ICAR–NBPGR, New Delhi; Dr. Arun Gupta, Nodal Scientist, CRP–AB, IIWBR, Karnal; Dr. Sushil Pandey, Principal Scientist and Lead Centre Platform Coordinator, NBPGR, New Delhi; Dr. Kavita Gupta, NBPGR, New Delhi and Dr. Jyoti Kumari, Principal Scientist and Principal Project Investigator, NBPGR, New Delhi.

In his presidential address, Dr. Gyanendra Pratap Singh appreciated the systematic research efforts and field-based evaluations being carried out at ICAR–IARI Regional Station, Wellington, under the CRP–Agro-Biodiversity programme. He emphasized the importance of broadening the genetic base through effective utilization of diverse germplasm in wheat pre-breeding initiatives. The visit further underscored the value of multi-institutional collaboration in identifying novel trait sources for enhancing disease resistance and strengthening future wheat improvement efforts.

Field Exposure- Student Visits

Students from various colleges, including those from Tamil Nadu Agricultural University, Coimbatore and other state universities in Tamil Nadu as well as institutions from other states, frequently visit our station as part of their academic curriculum.


FARMER'S TRAINING HALL.