DEVELOPMENT AND PERFORMANCE EVALUATION OF NIFA SARSON-T23: A HIGH YIELDING RAPESEED VARIETY

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ABSTRACT

The development of high-yielding and broadly adaptable rapeseed (*Brassica napus* L.) cultivars is imperative for strengthening domestic edible oil production and reducing import dependency in Pakistan. A promising recombinant line, RR-8-1, was developed through the hybridization of two advanced rapeseed lines, namely NR-2-2/09 and NR-23/09, during Rabi 2010–11 at the Nuclear Institute for Food and Agriculture (NIFA), Peshawar. The F_1 generation was established during the summer of 2011 at the Summer Agricultural Research Station (SARS), Kaghan. Subsequently, the F_2 to F_5 generations were advanced from Rabi 2011–12 to 2014–15 through rigorous single-plant selection based on phenotypic performance to attain genetic uniformity and stability for enhanced grain yield. The recombinant line RR-8-1 was subjected to replicated station yield trials and multi-location evaluations to assess its yield potential, agronomic performance, and environmental adaptability. Across diverse testing environments, the line consistently surpassed the commercial check cultivar, Super Canola, in seed yield and associated agronomic traits. In the National Uniform Rapeseed Yield Trial (NURYT) conducted during 2018–19, RR-8-1 achieved a mean seed yield of 1881 kg ha^{-1}, representing a 16% improvement over the national check (1626 kg ha^{-1}), and secured the second position among 24 candidate genotypes. In the subsequent NURYT evaluation during 2019–20, RR-8-1 maintained its superior performance with a mean yield of 2937 kg ha^{-1}, exceeding the check cultivar (2663 kg ha^{-1}) by 10% and ranking first among 21 candidate entries. The line possesses a high genetic yield potential of 3800–4000 kg ha^{-1} and an oil content ranging from 43–46%, rendering it suitable for cultivation under both irrigated and rain-fed agro-ecological conditions. For varietal authentication and molecular characterization, seeds of NIFA Sarson-T23 (RR-8-1) along with eight commercial canola cultivars, including Super Canola, were subjected to genotyping-by-sequencing (GBS)-based DNA fingerprinting. A total of 501 high-quality single nucleotide polymorphism (SNP) markers were identified across the *Brassica napus* genome. The genotype RR-8-1 exhibited 96% polymorphism and 10.1% heterozygosity, facilitating its precise molecular discrimination from other cultivars. In recognition of its superior yield performance, phenotypic stability, wide adaptability, and desirable agronomic attributes, the genotype was approved by the Khyber Pakhtunkhwa Provincial Seed Council for commercial cultivation under the varietal designation NIFA Sarson-T23.

Keywords: *Brassica napus L., Hybridization, Seed Yield, Oil Content, DNA, Genotype-by-Sequencing, SNPs*

INTRODUCTION

Brassica napus L. is an amphidiploid species (AACC genome, 2n = 38) that originated through interspecific hybridization between the diploid species *Brassica rapa* (AA, 2n = 20) and *Brassica oleracea* (CC, 2n = 18) (Mahmood *et al*., 2019). Belonging to the family Brassicaceae, it is one of the most important oilseed crops cultivated worldwide for vegetable oil production (Nath *et al*., 2016). Rapeseed seeds contain a high oil concentration, typically ranging from 40 to 44%, while the residual meal contains approximately 38–40% protein (Mustafa *et al*., 2022). The protein-rich meal possesses a well-balanced amino acid composition, including essential amino acids such as lysine, methionine, and cystine, making it a valuable source of livestock feed (Iqbal *et al*., 2008).

Pakistan continues to face a substantial deficit between domestic edible oil production and national consumption. Rapid population growth, increasing per capita consumption, and limited local production have collectively intensified the country's dependence on imported edible oils (Mustafa *et al*., 2017). During the financial year 2025, the total availability of edible oil in Pakistan was projected at 3.07 million tons, of which 2.58 million tons, valued at approximately Rs. 765 billion, were expected to be imported, including 0.148 million tons derived from imported oilseeds. In contrast, domestic production was estimated at only 0.486 million tons, meeting just over 21% of the national requirement (PBS, 2025). This widening gap underscores the urgent need to enhance indigenous edible oil production through the development and deployment of high-yielding, climate-resilient oilseed cultivars.

Among the major oilseed crops cultivated in Pakistan, cotton, rapeseed/mustard, and sunflower contribute significantly to domestic vegetable oil production. Rapeseed and mustard rank second only to cottonseed and are

well adapted to diverse agro-ecological conditions across the country (Ahmed and Ahmed, 2022). These crops occupy approximately 0.427 million hectares, producing around 0.47 million tons annually; however, productivity remains considerably below its potential. The national average yield of rapeseed is approximately 1101 kg ha^{-1} (PBS, 2025), whereas the average productivity in Khyber Pakhtunkhwa (KP) is only 575 kg ha^{-1} (Ali *et al*., 2025). Such low productivity is primarily attributed to the limited availability of high-yielding and broadly adapted cultivars capable of maintaining stable performance under diverse macro- and micro-climatic conditions (Ali *et al*., 2013). Therefore, enhancing domestic oilseed production through the development and dissemination of improved cultivars is essential for reducing the country's reliance on costly edible oil imports and improving the livelihoods of farming communities, particularly in KP (Ahmed and Ahmed, 2022).

The oilseed improvement programme at the Nuclear Institute for Food and Agriculture (NIFA), Peshawar, has made significant contributions to national agricultural research and development through the breeding of rapeseed cultivars with enhanced seed yield, elevated oil content, early maturity, and improved quality traits. These objectives are achieved through the application of induced mutagenesis, conventional hybridization involving recombinant and mutant germplasm, or the integration of both approaches. The development and commercialization of such improved cultivars are expected to substantially increase per-hectare productivity, thereby contributing to national edible oil security and sustainable agricultural development.

MATERIALS AND METHODS

The experimental material used in this study was developed through a hybridization programme aimed at generating high-yielding rapeseed germplasm. Two advanced rapeseed breeding lines, designated NR-2-2/09 and NR-23/09, were selected as parental genotypes based on their superior agronomic performance and seed yield potential. A single cross between these parental lines was made during the Rabi season of 2010–11 to produce the initial recombinant population (F_1). The resulting F_1 seeds were grown during the summer season (July–September) of 2011 at the Summer Agricultural Research Station (SARS), Kaghan, following a shuttle-breeding approach to accelerate generation advancement. Standard agronomic and crop management practices were maintained throughout the growing period. The F_2 population was subsequently planted during the Rabi season of 2011–12 at the Nuclear Institute for Food and Agriculture (NIFA), Peshawar. Individual plant selection was conducted based on visual assessment of seed yield and associated morphological characteristics. Selected plants were advanced to the next generation for further evaluation. During the Rabi seasons of 2012–13 and 2013–14, plant-to-progeny rows of the F_3 and F_4 generations were evaluated at NIFA, Peshawar. These generations were screened for uniformity of breeding behavior, genetic stability, and consistency of desirable agronomic traits over successive generations. Selection was performed using standard rapeseed breeding criteria, including plant vigour, maturity, yield-contributing traits, and overall plant performance. During the Rabi season of 2014–15, forty-four F_5 recombinant lines were evaluated in an early-generation, non-replicated yield trial. The experimental lines were assessed for seed yield and related agronomic traits, while the commercial canola cultivar Faisal Canola was included as a standard check. Based on their performance, superior recombinant lines were identified and selected for advancement to subsequent yield evaluation trials. Data generated from replicated experiments were subjected to statistical analysis using Statistix 8.1 software (Analytical Software, 2003).

Station Yield Trials

The newly developed recombinant line RR-8-1 was evaluated in a series of station yield trials, including a Preliminary Yield Trial (PYT) during the Rabi season of 2015–16 and an Advanced Yield Trial (AYT) during 2016–17, at the Nuclear Institute for Food and Agriculture (NIFA), Peshawar. Both experiments were conducted using a randomized complete block design (RCBD) with three replications.

Seeds were sown manually using a hand-operated seed drill, maintaining a row-to-row spacing of 30 cm. Each experimental plot consisted of four rows, each 5 m in length. Recommended agronomic and crop management practices were uniformly applied throughout the growing season to ensure optimal crop establishment and development. Seed yield data were recorded at physiological maturity and used to assess the performance of the experimental line relative to the standard checks.

Multi-location Yield Trial

Multi-location yield trials were conducted during the 2017–18 and 2018–19 cropping seasons across diverse agro-ecological zones of Khyber Pakhtunkhwa (KP) and Punjab to evaluate the seed yield performance and adaptability of eleven advanced rapeseed recombinant/mutant lines, including RR-8-1. Hyola-401 and Faisal Canola were used as standard check varieties during the first and second years, respectively. The trials were established at

five research locations: Nuclear Institute for Food and Agriculture (NIFA), Peshawar; Arid Zone Research Center (AZRC), Dera Ismail Khan (DIK); Regional Agricultural Research Institute (RARI), Bahawalpur; Barani Agricultural Research Station (BARS), Kohat; and Barani Agricultural Research Institute (BARI), Chakwal. During 2017–18, the genotypes were evaluated at all five locations, whereas in 2018–19 the adaptability trials were conducted at four locations. The experiments were conducted using a randomized complete block design (RCBD) with three replications. At all experimental stations, each plot measured 6 m² (04 rows, each 5 m long & row spacing of 0.30 m). Seed yield (kg ha^{-1}) was recorded at each experimental site, and mean yield performance across locations and years was used to assess genotype performance, adaptability, and yield stability. Comparative analyses were performed to identify superior high-yielding lines relative to the respective check varieties and to determine their suitability for cultivation across diverse production environments.

National Uniform Rapeseed Yield Trial

The recombinant rapeseed line RR-8-1 was evaluated for seed yield performance in the National Uniform Rapeseed Yield Trial (NURYT) over two consecutive cropping seasons, 2018–19 and 2019–20. These multi-location trials were conducted across major rapeseed-growing regions to assess the genotype's yield potential, adaptability, and stability under diverse agro-climatic conditions. The commercial cultivar Super Canola was included as the standard check variety. During the 2018–19 season, RR-8-1 was evaluated alongside 24 candidate genotypes, while in 2019–20 it was tested with 21 entries. The trials were conducted using an alpha lattice design with two replications. Standardized agronomic management practices were followed throughout the experimental period. Seed yield (kg ha^{-1}) was recorded at crop maturity, and data from all test locations were pooled to calculate mean yield values. These data were subsequently used to determine genotype rankings and to evaluate the yield advantage of RR-8-1 relative to the check cultivar. The trials were coordinated by the National Oilseed Coordinator at PARC, Islamabad.

Variety-Specific DNA Barcoding

DNA extraction

The genomic DNA was extracted from 3–5 cm long seedling leaves grown in peat moss-filled plastic trays. The extraction was carried out using a Plant Genomic DNA Extraction Kit (TIANGEN, Beijing, China). Following extraction, the DNA was quantified on a 1% agarose gel, and a concentration of 100 ng/µL was maintained for subsequent SNP analysis.

Whole-genome resequencing and SNP calling

The DNA of NIFA Sarson T-23 and eight other cultivars was subjected to next-generation sequencing (NGS) library preparation using a 150 bp insert size paired-end library, following a two-enzyme GBS library preparation protocol (Poland *et al*., 2011). These libraries were sequenced on a T7 MGI-Seq NGS system. The raw data, in the form of FASTA files, was trimmed and subjected to quality control (QC) using the GATK SNP calling pipeline. All sequencing work was conducted at BGI, China, while SNP calling data analysis was carried out at the Department of Plant Sciences, Quaid-i-Azam University. The trimmed reads were aligned to the reference genome sequence of *Brassica napus* cv. AST_PRJEB5043, and SNPs were identified using the GATK pipeline.

DNA Barcoding

Among all the identified SNPs, a strict quality control procedure was applied to filter high-quality SNPs based on their chromosomal distribution and allele frequencies. At the end only, those SNPs were considered with 100% data availability (no missing data) in 9 Brassica cultivars. This resulted in 501 SNPs distributed across all 38 *Brassica* chromosomes, and the allelic states in all nine cultivars are provided as a genome variant calling format (vcf) file at DryAd (https://doi.org/10.5061/dryad.15dv41p4g).

RESULTS AND DISCUSSION

The yield performance of the recombinant line RR-8-1 was assessed in a series of station-based yield trials conducted at the Nuclear Institute for Food and Agriculture (NIFA), Peshawar. During the 2015–16 cropping season, six stable and high-yielding rapeseed mutant/recombinant lines, including RR-8-1, were evaluated in a Preliminary Yield Trial (PYT) along with the commercial cultivar Faisal Canola as the standard check. Among the tested entries, RR-8-1 exhibited the highest seed yield of 4583 kg ha^{-1}, significantly outperforming the check variety Faisal Canola (3000 kg ha^{-1}) by 53% (Table 1). This superior performance demonstrated the line's high yield potential and justified its advancement to subsequent stages of evaluation.

In the following year (2016–17), RR-8-1 was included in an Advanced Yield Trial (AYT) comprising nine superior rapeseed mutant/recombinant lines, with Hyola-401 serving as the commercial check. The recombinant line maintained its superior performance, producing a seed yield of 3778 kg ha^{-1} compared with 3139 kg ha^{-1} for Hyola-401 (Table 1). The consistent yield advantage observed over the commercial check further confirmed the genetic potential and agronomic superiority of RR-8-1.

Across both station trials, RR-8-1 achieved an average seed yield of 4180.5 kg ha^{-1}, substantially exceeding the yields of the respective check cultivars. The sustained high performance of RR-8-1 in both preliminary and advanced evaluations indicates its excellent yield potential, adaptability, and suitability for further multi-location testing and eventual commercial release. These findings also highlight its value as a promising genetic resource for rapeseed improvement program targeting enhanced productivity under the agro-climatic conditions of Peshawar and similar environments.

Table 1. Yield Performance of RR-8-1 in Station Trials at NIFA, Peshawar.

Year	Name of trial	Seed Yield (kg ha^{-1})			*LSD (5%)*
		RR-8-1	**Faisal Canola**	**Hyola-401**	
2015-16	Preliminary Yield Trial	4583*	3000	-	678.2
2016-17	Advanced Yield Trial	3778	-	3139	958.5
Average		4180.5	3000	3139	-

**Significance at 5%; LSD-Least Significant Difference*

Multi-location Yield Trial

The yield performance and adaptability of eleven advanced rapeseed recombinant/mutant lines were evaluated during the 2017–18 cropping season across five diverse agro-ecological locations in Khyber Pakhtunkhwa and Punjab, namely NIFA Peshawar, AZRC Dera Ismail Khan, RARI Bahawalpur, BARS Kohat, and BARI Chakwal. Hyola-401 was included as the commercial check cultivar. Considerable variation in productivity was observed among testing environments, reflecting the diverse climatic and edaphic conditions prevailing across the target production zones.

Among all evaluated entries, the recombinant line RR-8-1 exhibited outstanding performance and demonstrated broad adaptation across locations. It achieved the highest mean seed yield of 2115 kg ha^{-1}, surpassing the commercial check Hyola-401 (1534 kg ha^{-1}) by 27% (Table 2). The superior performance of RR-8-1 was particularly evident at NIFA, Peshawar and RARI, Bahawalpur, where it produced significantly higher yields than the check cultivar. Analysis of location means indicated that AZRC, Dera Ismail Khan and RARI, Bahawalpur were the most favorable environments for rapeseed production, recording average yields of 2922 and 2959 kg ha^{-1}, respectively. These findings highlight the strong yield potential of RR-8-1 under both irrigated and relatively moisture-stressed production environments.

To further validate its adaptability and yield stability, RR-8-1 was evaluated during the 2018–19 cropping season in second-year multi-location adaptability trials conducted at four locations: NIFA, Peshawar, AZRC, Dera Ismail Khan, BARI, Chakwal and RARI, Bahawalpur. Fourteen advanced recombinant / mutant lines were included in the trial, with Faisal Canola serving as the commercial check. Consistent with the previous year's results, RR-8-1 maintained its superior performance, recording a mean seed yield of 2540 kg ha^{-1} compared with 2175 kg ha^{-1} for Faisal Canola, representing a yield advantage of approximately 17% (Table 2).

Table 2. Yield performance of RR-8-1 in Multi-location Yield Trial.

Year	Line/Check	Seed Yield (kg ha^{-1})					Genotypic Means
		NIFA, Peshawar	**AZRI, D.I. Khan**	**RARI, Bahawalpur**	**BARS, Kohat**	**BARI, Chakwal**	
2017-18	RR-8-1	3194*	3139	3038*	914	290	2115
	Hyola-401	2111	3219	1577	519	243	1534
	Loc. Mean	2467	2922	2959	566	261	-
	$LSD_{(0.05)}$	972	806	275	738	59	-
2018-19	RR-8-1	4528*	2430*	-	1612	1528	2540
	Faisal Canola	3597	1953	-	1612	1537	2175
	Loc. Mean	4122	2213	-	1306	1441	
	$LSD_{(0.05)}$	868	283	-	223	176	

**Significance at 5%; LSD-Least Significant Difference; 2018-19 RARI, Bahawalpur was not included*

The superior performance of RR-8-1 across multiple testing environments and over two consecutive years demonstrates its high yield potential, phenotypic stability, and wide adaptability. Notably, the line consistently produced mean seed yields exceeding 2000 kg ha^{-1} under diverse agro-climatic conditions, indicating a favorable genotype × environment response and enhanced yield resilience. The sustained superiority of RR-8-1 over the commercial check cultivars across years and locations confirms its suitability for large-scale cultivation and supports its advancement for varietal release and commercialization.

National Uniform Rapeseed Yield Trial

RR-8-1 was evaluated for the first-year mandatory adaptability testing in the National Uniform Rapeseed Yield Trial (NURYT) 2018-19, along with twenty-four candidate lines including hybrids and the commercial check Super Canola. The recombinant RR-8-1 produced a high genotypic mean of 1881 kg ha^{-1}, exhibiting 16% higher seed yield than Super Canola (1626 kg ha^{-1}) on overall mean basis and secured the second position among all tested entries (Table 3)

For the second-year obligatory adaptability testing in NURYT 2019-20, RR-8-1 again outperformed the check, presenting a 10% increase in seed yield by producing a high genotypic mean of 2937 kg ha^{-1} compared to super canola (2663 kg ha^{-1}). It ranked first among twenty-one evaluated entries, reaffirming its stability and superior genetic potential across environments (Table 4).

Table 3. Yield Performance of RR-8-1 in National Uniform Rapeseed Yield Trial 2018-19.

Entry Name	NARC, Islamabad	BARS, Fateh Jang	ORS, Khan Pur	NIA, Tando Jam	NIFA, Peshawar	RARI, Bahawalpur	BARI, Chakwal	AZRC, D.I. Khan	AARI, Faisalabad	ARI, Tando Jam	AZRI, Bhakkar	Mean
RR-8-1	2845	753	1852	326	2914	1555*	1665	2689*	3204*	1692*	1191	1881
Super Canola	2741	660	1519	282	2781	1222	2052	1802	2667	1117	1045	1626
Location Mean	2619	663	1215	341	2897	1229	1846	2183	2602	1154	974	1611
$LSD_{(0.05)}$	190	144.5	460	260	183	247	354	111	321	262	358.3	
% Incr. over Check	4	14	22	16	5	27	-19	49	20	51	14	16

Table 4. Yield Performance of RR-8-1 in National Uniform Rapeseed Yield Trial 2019-20.

Entry Name	ARI D, D.I. Khan	AZRC, D.I. Khan	BARI, Chakwal	NIFA, Peshawar	ORI Faisalabad	ORI Tando Jam	RARI Bahawalpur	NARC Islamabad	Gen. Mean
RR-8-1	2422	2350	2517*	4178	2274*	5221	2372*	2162*	2937
Super Canola	2337	3047	2189	4255	1655	5097	1692	1032	2663
Location Mean	2299	2138	2342	3888	2057	4839	1826	1857	-
LSD(0.05)	809	262	262	857	176	411	38	204	-
% Incr. over Check	4	-23	15	-2	37	2	40	109	10

Hybridization followed by selection is a fundamental breeding approach in *Brassica napus*, promoting recombination and enabling fixation of favorable alleles for complex quantitative traits. Seed yield improvement is largely achieved through manipulation of major yield components, including siliques per plant, seeds per silique, and thousand seed weight, which are polygenically controlled and highly responsive to selection (Wang *et al*., 2016, Zhu *et al*., 2023; Fu *et al*., 2015). The observed improvement is largely attributed to additive and non-additive gene effects expressed during hybridization and selection. This is in agreement with the principles described by Douglas Scott Falconer (1996), who emphasized the role of genetic variance and selection in improving quantitative traits, and George W. Allard (1960), who highlighted the importance of selection in fixing desirable alleles in crop

improvement. Similar findings in rapeseed have been reported by Wolko *et al.* (2019) and Liu *et al*. (2017), who demonstrated that hybridization enhances yield and its component traits. The recombinant RR-8-1 demonstrated remarkable and consistent yield superiority over Faisal Canola, Hyola-401, and Super Canola across preliminary, multi-location, and national trials, underscoring its exceptional genetic potential and stability in *Brassica napus*. Its sustained high performance across diverse environments and years reflects the presence of favorable allelic combinations governing yield and a robust genotype × environment interaction. Notably, its enhanced productivity in regions such as Dera Ismail Khan and Bahawalpur highlights its responsiveness to favorable agro-ecological conditions. Furthermore, its consistent top rankings in NURYT trials affirm its wide adaptability, resilience, and strong candidacy for varietal release as well as its strategic value in future rapeseed breeding programs (Kang, 2002; Diepenbrock, 2000; Yan and Kang, 2003; Gauch, 2013).

Agronomic, Botanical and Distinguishing Features of NIFA Sarson-T23

NIFA Sarson-T23 (RR-8-1) is an indeterminate variety with a plant height of 175 - 180 cm, low to middle branching, green leaves featuring weak lobing and dark yellow inflorescences. Verified through two years of Distinctness Uniformity Stability (DUS) testing with Federal Seed Certification & Registration Department (FSC&RD), the variety requires 90 - 94 days to reach 50% flowering and 165–170 days to mature. Its semi-erect, anthocyanin-free pods carry 28 - 30 grains, producing bold, rounded, black seeds with a 1000-seed weight of 3.5 - 4.0 g. Showing strong tolerance to aphids and Alternaria blight, it delivers an average yield of 3400 kg ha^{-1} and a maximum potential of 3900 kg ha^{-1}, significantly outperforming its parent line and the national commercial check.

Nutritional Value / Quality Profile of NIFA Sarson-T23 (RR-8-1)

The quality profiling of RR-8-1 was carried out in comparison with the national check (Super Canola) using the non-destructive technique Near Infra-red Reflectance Spectroscopy (NIRS)**.** The average values recorded during evaluation in station trials indicated that RR-8-1 possessed higher oil content (46.9%) and lower glucosinolate level (28.1 µmol/g) than Super Canola (45.2% oil and 30.8 µmol/g GSL)**.** However, its slightly higher erucic acid content (3–5%) places it marginally below the acceptable limit for canola-quality standards (Table 5).

Table 5. Mean Values of Quality Parameters of RR-8-1 done at NIRS (Foss 6500).

Entry	Oil (%)	GSL (µmol/g)	Erucic acid (%)
RR-8-1	46.9	28.1	5-3
Super Canola (Check)	45.2	30.8	1

Source: Oilseed *Brassica Lab., NIFA, Peshawar*

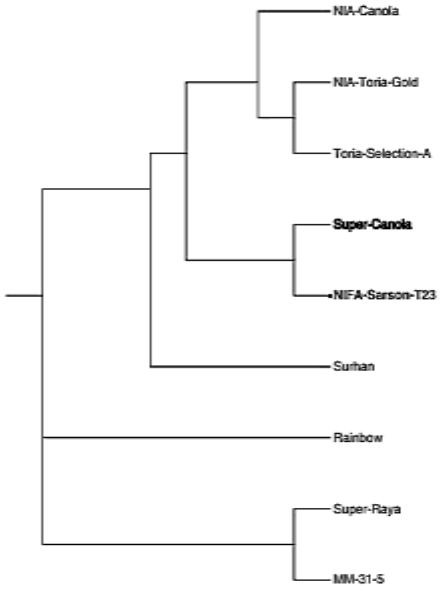

Fig. 1. Phylogenetic tree of seven Brassica cultivars from Pakistan including NIFA Sarson T-23 using 501 high-quality SNP markers using genotyping-by-sequencing (GBS) technology.

Fig.2. 2-D Digital Barcode of the Nucleotides of NIFA Sarson T-23 (https://me-qr.com/BWSMTyPc).

Fig. 3. NIFA Sarson-T23 (RR-8-1).

Genetic Diversity and DNA Barcoding of NIFA Sarson-T23

For genetic identity maintenance and Plant Variety Protection (PVP) compliance in Pakistan, submission of DNA fingerprinting data to the relevant authority is mandatory. Accordingly, DNA barcoding and molecular characterization were performed to confirm the genetic distinctness and identity of the candidate variety. High-quality genomic DNA was successfully extracted from seedling leaves, suitable for next-generation sequencing and SNP analysis. Normalizing DNA concentration ensured consistent library preparation and sequencing efficiency. Although, GBS resulted in more than 20,000 SNPs but we used a very strict quality control procedure to filter low-quality SNPs and only retained those polymorphic SNPs with more than 5% minor allele frequency and 100% data availability in nine cultivars. This resulted in 501 high-quality SNPs distributed over all 19 (2n=38) chromosomes. Of the 501 selected SNPs, cv. NIFA Sarson-T23 was polymorphic at 481 loci (96%) with 10.1% heterozygosity, indicating substantial genetic variability (Fig. **3**). Compared to Super Canola, 46 SNPs (9.1%) differed, reflecting measurable genetic divergence. The genome-wide SNP panel provides a robust tool for DNA barcoding, cultivar discrimination, and breeding applications. Phylogenetic analysis (Fig. **1**) confirmed genetic distinctiveness among cultivars, and the 2-D QR code (Fig. **2**) enables rapid digital identification and traceability. These results demonstrate the effectiveness of SNP-based approaches for precise genomic characterization of Brassica cultivars.

Variety Approval

The rapeseed recombinant RR-8-1 was submitted to the Khyber Pakhtunkhwa Provincial Seed Council for variety evaluation in 2022. Owing to its consistent superiority over the respective commercial checks in preliminary, advanced, multi-location and National Uniform Rapeseed Yield Trials (NURYT), the line was approved as a new rapeseed variety with name NIFA Sarson-T23 for cultivation in both irrigated and rainfed areas across the province.

Conclusion

The rapeseed variety NIFA Sarson-T23 throughout its developmental cycle from preliminary and advanced yield trials to multi-location testing and national uniform evaluation has consistently demonstrated superior performance over the respective commercial checks. Its high and stable seed yield, improved oil content and reliable adaptability across diverse environments highlight its worth as a promising candidate. The stronger and consistent performance of NIFA Sarson-T23 across years and location supports its suitability for cultivation and its potential for formal release. It is expected that the adoption of NIFA Sarson-T23 by farmers will contribute to improve per acre productivity and support rapeseed enhancement efforts under the agro-climatic conditions of Pakistan.

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