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RESEARCH PAPER

TITLE

EXPLORING FIELD VARIABILITY: CROP DURATION, RICE BLAST RESISTANCE, AND YIELD IN RICE BREEDING LINES

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EXPLORING FIELD VARIABILITY: CROP DURATION, RICE BLAST RESISTANCE, AND YIELD IN RICE BREEDING LINES

ABSTRACT

Rice, a staple food for over half of the world's population, is a critical crop that requires ongoing improvement in disease resistance, crop duration, and yield to ensure food security and sustainability. Field variability plays a crucial role in determining the success of rice breeding programs, especially in relation to these factors. This study, conducted at ARS Baffa Mansehra, evaluated 20 rice breeding lines, developed by National Agriculture Research Centre (NARC), including the local check (Fakhre Malakand), for diversity in disease infestation, crop duration, and yield parameters. Data were collected on rice blast incidence and severity, days to panicle emergence, anthesis, grain filling, maturity, plant height, grain weight, and grain yield. The highest rice blast incidence was recorded for NARC-8 (66.7%), followed by NARC-4 (50.0%), with the lowest incidence in Fakhre Malakand (0%) and breeding lines NARC-12 and NARC-1 (14.3%). Rice blast severity increased from 28.9 to 36.4 on average. Panicle emergence days ranged from 83 (NARC-3 and NARC-6) to 119 (NARC-18). Plant height varied, with NARC-17 being the tallest (87 cm) and NARC-14 and NARC-15 the shortest (64 cm). The maximum thousand-grain weight was observed in NARC-6, NARC-10, and NARC-11 (34 g), while NARC-19 had the lowest (27 g). NARC-12 had the highest grain yield (193 g), followed by NARC-13 (182 g) and NARC-14 (162 g), with the lowest yields in NARC-10 (107 g), NARC-17, and NARC-6 (112 g). The overall variability observed among the advanced breeding lines of rice could be used for subsequent genetic improvement of rice, with particular emphasis on Hazara Division.

Keywords: Rice, blast infestation, variability, crop duration, yield.

1. INTRODUCTION

Rice (Oryza sativa L.) is one of the most crucial crops globally, supplying 35-60% of the caloric intake for approximately three billion people (Fageria et al., 2003; Ullah et al., 2024). To satisfy the food demands of the growing global population by 2050, rice production must increase by about 60% from current levels (Fageria et al., 2007; Ullah et al., 2020). Furthermore, rice is the most water-intensive crop, consuming approximately 80% of the freshwater used for irrigation in Asia (Bouman and Tuong, 2001; Maclean et al., 2002). Globally, rice is significant cereal crop, extensively a cultivated and vital to subsistence economies, where it serves as a primary source of income for many families (Thon et al., 2006; Couch et al., 2002).

Although rice is one of the most indemand food crops globally, its consumption varies regionally (Haq et al., 2002; Sharma et al., 2002). Its critical role in global food security has been widely acknowledged, making it a key crop on the United Nations' agenda (Silva et al., 2009; Kari, 2013). The demand for rice is expected to rise even higher in the near future (IIRR et al., 2005; Chauhan et al., 2017; Ali et al., 2016). Continuous efforts will be required to increase rice output, including enhancing its genetic potential, to meet this growing demand (Sasaki et al., 2000). While the cultivation of rice varies by region, it remains one of the world's most widely grown cereal crops. Various factors, both biotic and abiotic, contribute to low yields. These challenges can be addressed through the genetic improvement of rice, necessitating continuous evaluation of genetic variability in the germplasm (Ullah et al., 2022).

Rice is susceptible to many harmful species and diseases, with rice blast being one of the most serious and devastating (Dean et al., 2005; Wilson et al., 2005; Ou et al., 2005; Pennisi et al., 2010). This disease is caused by the fungus Magnaporthe grisea (Anamorph Pyricularia grisea Sacc. synonym Pyricularia oryzae Cav.). The disease is most evident when the pathogen affects the collar, leaf blades, necks, and panicles of the plant (Bonman et al., 1989). It initially manifests as lesions or brown specks on leaf tissue, which develop into spindleshaped growths over time (Hossain et al., 2017). The lesions have brown edges with greyish centers, and if they spread, the leaf may eventually die completely. The host range and variety specificity of M. grisea exhibit significant pathogenic diversity.

Based on the pattern of infection on a sample of rice differential genotypes, rice blast disease can be further categorized into several pathotypes (Couch et al., 2005; Bonman et al., 2004; Hamer, 1988; Dagdas, 2012). Molecular techniques, such as polymerase chain reaction (PCR), can be used to identify pathogen diversity (Silva et al., 2009). Genome fingerprinting is essential for further characterizing the structure of fungal species and investigating their heterogeneity (Yang et al., 2011; Giraldo et al., 2013).

Assessment genetic of variability is fundamentally important for plant breeding, as variation in different lines can be beneficial for future breeding efforts (Ali et al., 2009; Ali et al., 2016). The diversity among different morphological materials is assessed through field testing and the use of molecular markers (Ismail et al., 2021; Iqbal et al., 2020). Data on crop duration parameters, as morphological factors, enable the identification of lines at different stages, such as early and late lines (Iftikhar et al., 2021). Yield-related parameters include grain weight, grain yield, and biological yield. Understanding the relationship among these parameters is essential to determine how diseases affect various factors. Although several studies have assessed variability in rice germplasm in Pakistan, very few have been conducted under the agroclimatic conditions of District Mansehra.

The current study aims to assess variability in parameters related to disease, crop duration, and yield in rice breeding lines at District Mansehra, comparing them with a local check. The rice material sourced from the National Agriculture Research Centre (NARC), Islamabad, facilitated experiments conducted at the Agriculture Research Station (ARS), Baffa Mansehra. With objectives focused on evaluating crop duration variability, identifying blast disease resistance levels among rice lines, and exploring correlations between disease incidence and morphological parameters, this research seeks to enhance understanding for future rice breeding strategies in the region.

2. MATERIALS AND METHODS

The experiment was designed to assess variability in a set of 20 rice breeding lines along with local check (Fakhre Malakand) at Agriculture Research Station Baffa, Mansehra during the cropping season 2021 (Table. 1). The rice material was provided by the National Agriculture Research Centre (NARC), Islamabad, under a systematic research design.

2.1 Field sowing layout and crop husbandry

The field for the 20 rice breeding lines was consisted of 1m row and the distance among rows was 25 cm. The recommended crop production strategy was followed according to crop recommendations for District Mansehra.

 Table. 1. The set of 20 Rice Breeding Lines along with local check variety for testing rice blast disease.

S. No.	Genotype	Detail	S. No.	Genotype	Detail
1	NARC-1	Breeding Line	12	NARC-12	Breeding Line
2	NARC-2	Breeding Line	13	NARC-13	Breeding Line
3	NARC-3	Breeding Line	14	NARC-14	Breeding Line
4	NARC-4	Breeding Line	15	NARC-15	Breeding Line
5	NARC-5	Breeding Line	16	NARC-16	Breeding Line
6	NARC-6	Breeding Line	17	NARC-17	Breeding Line
7	NARC-7	Breeding Line	18	NARC-18	Breeding Line
8	NARC-8	Breeding Line	19	NARC-19	Breeding Line
9	NARC-9	Breeding Line	20	NARC-20	Breeding Line
10	NARC-10	Breeding Line	21	Fakhre_Malakand	Local Check Variety
11	NARC-11	Breeding Line			

2.2 Disease Incidence (%)

The data for disease incidence (%) was recorded on a set of 20 rice breeding lines along with local check variety (Fakhre Malakand) tested at Baffa, Mansehra considering disease incidence, disease severity recorded in terms of percentage.

2.3 Parameters on crop duration

Data on crop duration parameters was taken on days to panicle emergence, anthesis, grain filling, and maturity. Days to panicle was recording on counting the number of days from date of sowing to the date of emergence. Days to anthesis was recorded on counting the number of days from date of sowing to the date of anthesis. Days to grain filling was recorded on counting the number of days from date of sowing to the date of grain filling. Days to maturity was recorded on counting number of days from date of seeding to the date when more than 80% of the grains on panicle ripen.

2.4 Morphological and yield parameters

Plant height was measured from the base of the ground to the tip of panicle. Grain weight was recorded for 1000 grains from each rice line. At maturity each plot was separately harvested and fresh grain weight was measured with a balance.

2.5 Data Analyses

The data was compiled in MS excel where mean tables, graphs and association was estimated. Analyses of variance techniques were employed using R software to assess the significance of the data collected from the three experimental replications. Cluster analysis was also performed using R software to assess the overall grouping of the lines (Ali *et al.*, 2009).

3. RESULTS

3.1 Variability in rice blast incidence and severity

The data on rice blast incidence for the 20 rice breeding lines tested at district Mansehra is given in Table 1. The maximum rice blast incidence was recorded for NARC-8 (66.7%) during the first scoring, followed by NARC-4(50.0%), while the minimum was recorded for the local check Fakhre Malakand (0%). Among the breeding lines, the minimum was recorded for NARC-12 and NARC-1 (14.3). The mean of rice blast severity increased from 28.9 to 36.4. An overall increase was observed for most of the lines. The line NARC-8 had the maximum of 66.7% rice blast severity at both of the scoring date. The local check Fakhre Malakand had no incidence and severity (0%) during the first score, while it had also a low score of 1% incidence and 3.7% severity during the second scoring.

	1st Re	ading	2nd Reading	
Conotyno	Disease	Disease	Disease	Disease
Genotype	incidence	Severity	incidence	Severity
NARC-1	14.3	1.6	28.6	3.2
NARC-2	25.0	2.8	50.0	5.6
NARC-3	28.6	3.2	42.9	4.8
NARC-4	50.0	5.6	50.0	5.6
NARC-5	16.7	1.9	42.9	4.8
NARC-6	33.3	3.7	33.3	3.7
NARC-7	16.7	1.9	16.7	1.9
NARC-8	66.7	11.1	66.7	11.1
NARC-9	57.1	6.3	42.9	4.8
NARC-10	40.0	4.4	40.0	13.3
NARC-11	42.9	4.8	42.9	7.9

Table 2. Rice blast incidence (%) and severity (%) on 20 rice breeding lines along with the local check tested at ARS, Baffa, Mansehra during 2021.

Overall Mean	28.9	5.6	36.4	5.4
Fakhre Malakand	0.0	0.0	1	3.7
NARC-20	28.6	3.2	42.9	6.3
NARC-19	28.6	3.2	28.6	3.2
NARC-18	25.0	2.8	50.0	5.6
NARC-17	33.3	3.7	50.0	7.4
NARC-16	20.0	2.2	40.0	4.4
NARC-15	33.3	5.0	5.6	5.6
NARC-14	16.7	1.9	16.7	1.9
NARC-13	16.7	1.9	16.7	1.9
NARC-12	14.3	1.6	57.1	7.9

3.2 Variability in crop duration parameters

The data on days to panicle emergence for a set of 20 rice breeding lines along with local check (Fakhre Malakand) is shown in Table 3. The maximum days of panicle emergence was recorded for NARC-18 (119 days), followed by NARC-19 (117) and NARC-5 (114 days), When compared to local check (Fakhre Malakand) for which days to panicle recorded was 92. The overall mean days to panicle emergence in 20 rice breeding lines along with check Fakhre Malakand was 99, while the minimum days were recorded for NARC-3 and NARC-6 (83) followed byNARC-15 (85) and NARC-8 (89) which was less than the local check (Fakhre Malakand) i.e., 92 days.

Table 3. Data on different crop duration parameters as recorded for 20 rice breeding lines
along with the local checks tested at ARS, Baffa, Mansehra during 2021.

Genotype	Days to penicle emergence	Days to anthesis	Days to grain filling	Days to maturity
NARC-1	103	106	111	140
NARC-2	101	105	110	140
NARC-3	83	101	106	135
NARC-4	114	118	123	133
NARC-5	114	120	125	132
NARC-6	83	102	113	134
NARC-7	114	118	124	133
NARC-8	89	92	98	140
NARC-9	102	106	110	140
NARC-10	102	106	111	140
NARC-11	97	102	106	138
NARC-12	96	102	107	138
NARC-13	98	104	108	135
NARC-14	97	106	111	135

Overall Mean	99	107	113	135
Fakhre_Malakand	92	96	99	135
NARC-20	96	100	104	135
NARC-19	117	130	134	138
NARC-18	119	132	136	140
NARC-17	92	126	132	138
NARC-16	92	95	102	107
NARC-15	85	90	96	134

The maximum days to anthesis was recorded for NARC-18 (132) followed by NARC-19 (130) and NARC-17 (126) whereas for the local check (Fakhre Malakand) the data recorded was more than the tested breeding lines i.e., 96 days. The minimum days to anthesis was recorded for NARC-15 (90) followed by NARC-8 (92) and NARC-16 (95), which were less than Fakhre Malakand (96) the local check variety. The overall mean days to anthesis was 107 days. The Maximum days to grain filling was recorded for NARC-18 (136) followed by NARC-19 (134), NARC-17 (132) when compared to Fakhre Malakand is (99) that was very less than NARC -17, NARC-18. NARC-19. The minimum days to grain filling was recorded NARC-15 (96), NARC-8 (98), NARC-16 (102) compare to Fakhre Malakand has (99). The Overall mean of days to grain filling was 113.Data of days to maturity was maximum for NARC-1 (140), NARC-11 (138), NARC-13 (134) while minimum was recorded to NARC-16 (107). Overall mean was days to maturity was recorded (135).

The observed variability in crop duration parameters could be useful for future breeding to generate novel variation for subsequent selection (Ismail *et al.*, 2021; Iqbal *et al.*, 2020). The data on crop duration parameters enables to identify lines with variable maturity, like early and late lines (Iftikhar *et al.*, 2021).

3.3 Variability in morphological and yield parameters

The maximum plant height was recorded for NARC-17 (87 cm) and check variety Fakhre Malakand (82 cm) followed by NARC-1 (78 cm). The minimum plant height was recorded for NARC-14 and NARC-15 (64 cm), followed by NARC-3 (65 cm), which was less then check Fakhre Malakand (82 cm). The overall mean of plant height was recorded (71 cm

The maximum thousand grain weight was recorded for NARC-6, NARC-10 and NARC- (34 g) and the minimum was recorded for NARC-19 (27 g), followed by NARC-18 and NARC-5 (28 g). The overall mean of 1000 grain weight was 30 g.

Maximum grain yield was recorded for NARC-12 (193 g), followed by NARC-13 (182 g) and NARC-14 (162 g). Minimum grain yield was recorded for NARC-10 (107 g), NARC-17 and NARC-6 (112 g). The overall mean of grain yield recorded among the tested lines was 134 g.

		1000 grain weight	Grain yield
Genotype	Plant height (cm)	(g)	(g/plot)
NARC-1	78	30	132
NARC-2	76	29	116
NARC-3	65	31	118
NARC-4	67	32	118
NARC-5	72	28	162
NARC-6	68	34	112
NARC-7	65	31	130
NARC-8	69	32	122
NARC-9	73	29	117
NARC-10	70	34	107
NARC-11	69	31	128
NARC-12	69	30	193
NARC-13	67	30	182
NARC-14	64	34	162
NARC-15	64	31	121
NARC-16	72	30	133
NARC-17	87	29	112
NARC-18	70	28	148
NARC-19	73	27	130
NARC-20	70	29	147
Fakhre-Malakand	82	29	113
Overall Mean	71	30	134

Table 4. Data on plant height (cm), 1000-grain weight (g) and grain yield (g/plot) as recorded for 20 rice breeding lines along with the local checks tested at ARS, Baffa, Mansehra during 2021.

3.4 Association among various field parameters

The association among grain yield (g per plot), plant height (cm) and thousand grain weight (g) as observed for 20 rice breeding lines along with the local check (Fakhre Malakand) tested at ARS, Baffa Mansehra during 2021 is shown in Fig. 1. The association among grain yield (g per plot) and plant height (cm) was negative which means that when height of genotypes increased the grain yield is slightly decreased however with a very weak strength R^2 value (0.0925). The association among grain yield (g per plot) and thousand grain weight also showed weak negative with an R^2 value (0.038). The association between thousand grain weight and plant height was noted negative because the 1000 grain yield decreased as the height of the plant is increased and vice versa

whereas the R^2 value (0.251) shows the strength of the association. This low strength of all associations could be attributed to the variability in the germplasm as suggested earlier in other crops (Ali *et al.*, 2009; Iqbal *et al.*, 2020).

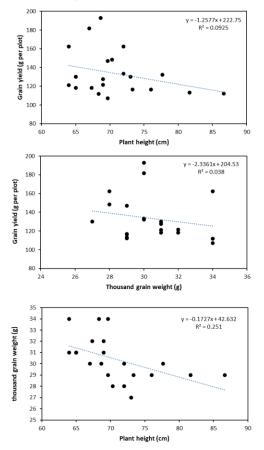


Fig. 1. Association among grain yield (g per plot), plant height (cm) and thousand grain weight (g) as observed for 20 rice breeding lines along with the local checks tested at ARS, Baffa, Mansehra during 2021.

3.5 Association of rice blast severity with field parameters

Association of rice blast severity with field parameters (Plant height, 1000 grains weight and grain yield (g/plot) is shown in Fig. 2. This association among plant height (cm) and rice blast severity was slightly positive which means rice blast severity was increased with the plant height (cm), whereas the value of R^2 is (0.0053) is shown the strength of association was weak. The association of the rice blast severity (%) was increase with the 1000 grain weight was interesting as it increased with the disease increase, tough with a weak R^2 value (0.0568). Grain yield and rice blast infection had a negative association with an R^2 value of 0.065. The variability in the germplasm could be at the background of this weak association, as suggested previously (Ali *et al.*, 2009; Ismail *et al.*, 2020).

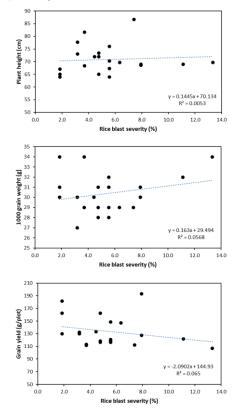


Fig. 2. Association of rice blast severity with grain yield (g per plot), plant height (cm) and thousand grain weight (g) as observed for 20 rice breeding lines along with the local checks tested at ARS, Baffa, Mansehra during 2021.

3.6 Association of crop duration parameters with grain yield

The association among grain yield (g per plot) and days to penicle emergence was weakly positive while the value of R^2 was 0.0016%. The association among of grain yield (g per plot) and days to grain filling was weakly positive while the R^2 value was (0.0016%). The association among grain yield (g per plot) and days to anthesis was weak positive while the value of R^2 was 0.0052%. The association of grain yield (g per

plot) and days to maturity is weakly negative whereas the value of R^2 was 0.0042%.

The consideration of crop duration parameter is of great importance in case of annual crops (Iftikhar *et al.*, 2021), particularly in the intensive agricultural systems, where rice crop needs to be harvest well time to allow cultivation of the subsequent crop. This may have also a role on rice blast infestation, as sowing and harvesting times have been suggested to be modified to encourage escape of the disease (Ali *et al.*, 2009).

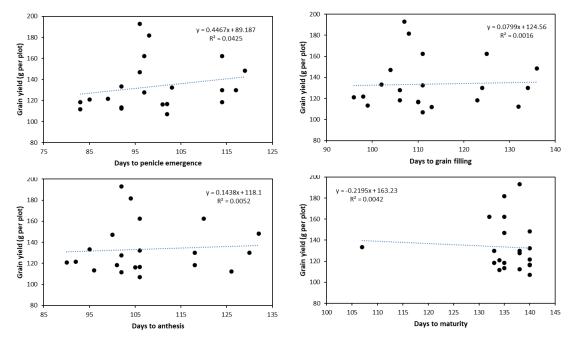


Fig. 3. Association of crop duration parameters with grain yield (g per plot) as observed for 20 rice breeding lines along with the local checks tested at ARS, Baffa, Mansehra during 2021.

3.7 Clustering of rice breeding lines

Clustering of 20 rice breeding lines along with the local check (Fakhre Malakand) based on rice blast disease, morphological, yield and crop duration parameters, tested at ARS, Baffa, Mansehra during 2021 resulted in the grouping into eight clusters. The 1st cluster consisted of NARC-15 and Fakhre Malakand. The 2nd cluster contained NARC-12, NARC-13 and NARC-14. The 3rd cluster consisted of only one breeding line (NARC-8) whereas the fourth cluster further divided in to two sub clusters in which total of four breeding lines (NARC-7, NARC-19, NARC- 5 and NARC-18) were present. The fifth cluster further divided in to 2 sub clusters in which the first cluster contained (NARC-16, NARC-1 and NARC-20), the second cluster was further divided in to 3 sub clusters in which the first cluster contained NARC-4, NARC- 9 and NARC-1. The second sub cluster contained only one breeding line (NARC-17) whereas the third sub cluster

consisted of NARC-3, NARC-6, NARC-2 and NARC-10 rice breeding lines.

There is evidence that cluster analyses identify various genetic clusters in different crops. Ali *et al.* (2009) used such analysis to identify different genetic clusters in different crops. Hussain *et al.*, in 2022, referred to its use in the identification of clusters to be used as heterotic groups.

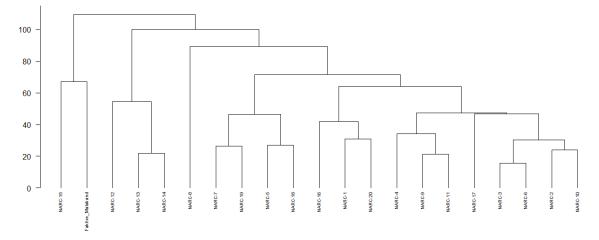


Fig. 5. Clustering of 20 rice breeding lines along with the local checks based on rice blast disease, morphological and yield and crop duration parameters, as tested at ARS, Baffa, Mansehra during 2021.

4. DISCUSSION

The environmental conditions of Mansehra provides a favorable condition for blast infection, with its overall humid and warm climate during the rice crop season (Hossain *et al.*, 2017). This could be further explained by the conducive environment of the ARS, Baffa located at the bank of river Siran, providing an overall conducive environment for the diseases (Barnwal *et al.*, 2012; Che *et al.*, 2001). The variability in rice blast infestation among different rice lines could be attributed to the genetic variability among these lines. Previous work has shown variable response of different crop host lines to different diseases at the same location, as

revealed for wheat yellow rust (Ali et al., 2009). The maximum days to anthesis was recorded for NARC-18 (132) followed by NARC-19 (130) and NARC-17 (126) whereas for the local check (Fakhre Malakand) the data recorded was more than the tested breeding lines i.e., 96 days. The above-mentioned Table 3 displays the information on days to panicle emergence for a group of 20 rice breeding lines and a nearby control (Fakhre Malakand). NARC-18 had the most days of panicle emergence (119), followed by NARC-19 (117) and NARC-5 (114), relative to the local check (Fakhre Malakand), where the number of days to panicle was 92. While the minimum days

were reported for NARC-3 and NARC-6 (83) followed by NARC-15 (85) and NARC-8 (89), which were less than the local check (Fakhre Malakand), i.e., 92 days, the total mean days to panicle emergence in 20 rice breeding lines and check Fakhre Malakand was 99. Information on the genetic variability of these morphological and yield parameters is of utmost important for plant breeding, which serves as a background material for future breeding (Ali et al., 2009). Such studies based on field testing must be accompanied by molecular markers to further validate these results (Ismail et al., 2021; Iqbal et al., 2020). Nevertheless, the information is useful to initiate a preliminary assessment of variability and perform selection (Iftikhar et al., 2021). Because the 1000 grain yield fell as plant height climbed and vice versa, the relationship between thousand grain weight and plant height was noticed to be negative. However, the R2 value (0.251) indicates how strong the relationship is. According to past research on other crops (Ali et al., 2009; Iqbal et al., 2020), the heterogeneity in the germplasm may be to blame for the low strength of all correlations.

5. CONCLUSION:

conclusion, our study In highlights significant variability among the evaluated rice breeding lines in Mansehra district. High incidences of rice blast in varieties like NARC-8 and NARC-4 suggest caution in development their further locally. Conversely, NARC-12 and NARC-1 show promising resistance to rice blast. recommending them for future breeding efforts aimed at enhancing disease resistance. Variability was also observed in plant height, thousand grain weight, and grain yield across different lines. While associations among these parameters were complex and often weak, the diversity present among advanced breeding lines offers opportunities for genetic improvement of rice in the Hazara Division. Future research should aim to capitalize on this variability to develop resilient and highyielding rice varieties suited to local agricultural conditions.

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7. CONFLICT OF INTEREST:

The authors declare no conflicts of interest.

8. AUTHOR'S CONTRIBUTION:

Mazhar Attique: Conceptualization, methodology, and original draft preparation. Sajid Ali: Supervision, and methodology. Project administration. Hamid Ali: methodology, and data analysis. Umar Saeed: data curation. and software. Raja Sheraz Rafique: Methodology, resources, validation, and visualization. Irfan Ullah: Conceptualization, writing, reviewing, and editing. Muhammad Haris: Investigation, writing, reviewing, and editing. Israr Ahmed: Methodology and resource provision. All authors contributed to writing, editing, and have approved the manuscript for publication.

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