

Research Article



Genetic Variability, Heritability and Genetic Advance for Morphological Traits in $F_{5:6}$ Rice Lines

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Abstract | This study was conducted to investigate variability, heritability and genetic advance among $F_{5:6}$ lines of rice for various morphological traits. Thirty-eight lines derived from F_5 rice cross combinations along with their 8 parents were planted in a randomized complete block design (RCB) having three replications at The University of Agriculture, Peshawar during 2016 rice crop growing season. Data were taken on some of the morphological traits like number of days to heading (days), number of days to maturity (days), flag leaf area (cm^2), culm length (cm), panicle length (cm), primary branches panicle⁻¹ (no.) and secondary panicle branches (no.). Analysis of variance showed highly significant ($p \leq 0.01$) differences for parents, $F_{5:6}$ lines and parents vs $F_{5:6}$ lines for all the studied traits. Among the $F_{5:6}$ lines, AUP-304 showed minimum days to heading (91 days) while the $F_{5:6}$ line AUP-361 took minimum days to maturity (118 days). $F_{5:6}$ line AUP-311 exhibited maximum flag leaf area (55 cm^2) and maximum culm length (132.3 cm). Maximum panicle length (28.3 cm) among $F_{5:6}$ lines was recorded for AUP-271, whereas, AUP-345 and AUP-322 showed best performance for primary panicle branches (13) and secondary panicle branches (41.3), respectively. High broad-sense heritability estimates were observed for all the studied characters, number of days to maturity (99.6%), culm length (99.4%), flag leaf area (98.9%), days to heading (95.9%), secondary branches panicle⁻¹ (88.3%), panicle length (70.7%) and primary branches panicle⁻¹ (60.6%), respectively. Genetic advance estimation showed that flag leaf area exhibited high genetic advance (40.2%) followed by secondary branches panicle⁻¹ (36.6%) and culm length (31.4%) among studied traits of rice genotypes. On the basis of good performance for early maturity, area of flag leaf and panicle contributing traits like primary and secondary branches panicle⁻¹ $F_{5:6}$ lines AUP-361, AUP-311 and AUP-345, AUP-322 could be advanced further in multi-locations trials to develop new rice genotypes for local cultivation.

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Introduction

Rice (*Oryza sativa* L.) is the chief staple food for one third of the world's population. The genus *Oryza* belongs to the tribe *Oryzaeae* of the family Poaceae. The genus *Oryza* contains 20 wild and two cultivated rice species. *O. sativa* is grown world-wide while *O.*

glaberrima is planted in West African countries. Rice is the primary nutritional source for 17 nations in Asia and the Pacific, nine states in North and South America and 8 states in Africa. Globally rice was cultivated on an area of 161.8 million ha which gives the production of 494.4 million tons having an average yield of 3.05 tons ha^{-1} (FAOSTAT, 2016). The chief

rice producing nations are: China, India, Indonesia, Bangladesh, Japan, United States of America, and Pakistan. China is the leading producer with the production of 142.3 million tons. On nutritional basis cultivated rice delivers 35-60% of their entire calorie intake to around 3.3 billion individuals in the Asia (Naseer et al., 2015). Morphologically rice is a monocot and is planted as an annual crop with round culms, flat leaves and terminal panicle. Roots are fibrous, possessing rootlets and root hairs. Association of arrangement between flower-pattern and the timing of floret receptiveness create *O. sativa* largely auto-gamous and self-pollinated. However, there is still some chances of out-crossing in rice. Pakistan's ranks third among the main crop in positions of the area sown, after wheat and cotton while it ranks second amongst the staple food grain crop. Rice provides 3.2% of the cost adding in agriculture and 0.7% of Gross domesticated products. In Pakistan, rice is cultivated on an area of 2.8 million ha, which gives the production of 6.8 million tons ha (PBS, 2016). In the province of Punjab, rice is cultivated on area of 2.03 million ha which gives the average production of 4.13 million tons. In Khyber-Pakhtunkhwa rice area under cultivation is 0.07 million ha⁻¹ giving the production of 0.15 million tons (FBS, 2015-16).

The presence of genetic variation for morphological characters in segregating generations is important for identification and formation of desirable genotypes. Breeders have the choice of choosing appropriate genotypes in early generations of selection or postponing intense-selection till advanced generations as soon as progenies are become closely homozygous. Better information of the genetic planning of numerous genotypes is therefore essential to articulate an effective breeding procedure.

Heritability is the percentage of genotypic variation to the total (phenotypic) variance, which comprises both genetic and environmental variance. The heritability of the character estimates the extent to which it is expected to transfer next generation and is more valuable tool when used in combination with estimation of expected genetic advance. Genetic advance is the enhancement in the mean phenotypic value of the selected plants over the parental population. Genetic advance gives evidence on expected gain resultant from selection of higher individuals. Estimation of heritability along with genetic advance combination are useful in predicating the gain under selection than

heritability alone (Ogunbayo et al., 2004). Keeping in view the significance of above facts, an experiment was conducted with the following objectives; i) To evaluate genetic variability among the genotypes for morphological traits. ii) To, estimate heritability and genetic advance in $F_{5:6}$ rice lines derived from different cross combinations and iii) To identify the superior $F_{5:6}$ lines for morphological traits for further use in rice breeding programs.

Materials and Methods

This study was conducted to assess genetic variability among $F_{5:6}$ rice lines for morphological traits at Plant Breeding and Genetics Research Farm, The University of Agriculture, Peshawar during 2016 rice crop growing season. Thirty-eight lines derived from F_5 rice cross combinations along with their eight parents were used in this study. Single plant selection has been made from $F_2 - F_5$ generations and the seed of the selected plants have been bulked to raise the next generation (Table 1). Nursery was grown in the May 1st week while the transplantation of seedlings into well-puddled field was done, during the first week of June 2016. Field management of the crop were made through recommended cultural practices. Parental genotypes along with their $F_{5:6}$ populations were planted in a completely randomized block design with three replications. Every genotype of rice was planted in a four-rows/plot, with a row-length of 3 m, whereas row-to-row and plant-to-plant spacing will be retained as 30 and 15 cm respectively.

Data were documented on the some of the following morphological characters, using ten randomly selected plants in each entry as per IRRI descriptor. Number of days to heading was calculated by totaling the days from seeding to the date when 50% tillers of each particular plant in each entry produced panicles. Flag leaf area was measured for every genotype, by multiplying length of leaf and width of leaf with the correction factor (0.75) with the procedure of Francis et al. (1969). Culm length was measured in centimeters starting from earth surface to the base of the panicle near maturity by using meter rod. Number of days to maturity was calculated by including the number of days from date of sowing to the date when most of the 80 percent of the grains on panicles were ripened. Panicle length was calculated in centimeters from the bottom to the tip of the panicle without awns. Primary branches panicle⁻¹ and secondary

panicle branches were counted after complete bloom of panicles on five randomly selected plants for each entry.

Table 1: *The genetic material used in this study.*

Parental genotypes	F _{5,6} Lines	Cross combinations
1. Basmati-2008	1. AUP-262	1. Basmati-6129/
2. Kangni-27	2. AUP-263	Basmati-370
3. TN-1	3. AUP-264	
4. Basmati-370	4. AUP-271	2. Basmati-6129/
5. Basmati-6129	5. AUP-274	Dokri-Basmati
6. Dilrosh	6. AUP-282	3. Basmati-2008/
7. Kashmir-Basmati	7. AUP-285	Kashmir-Basmati
8. Dokri-Basmati	8. AUP-292	4. Basmati-2008/TN-1
	9. AUP-294	
	10. AUP-295	
	11. AUP-302	5. Basmati-2008/Dilrosh
	12. AUP-304	
	13. AUP-305	
	14. AUP-311	6. Dokri-Basmati/
	15. AUP-312	Basmati-6129
	16. AUP-315	
	17. AUP-321	7. Dilrosh/ Kashmir-
	18. AUP-322	Basmati
	19. AUP-325	
	20. AUP-335	8. Kashmir-Basmati/
		Dilrosh
	21. AUP-341	9. Dilrosh/TN-1
	22. AUP-342	
	23. AUP-343	
	24. AUP-345	
	25. AUP-351	10. Kashmir-Basmati/
	26. AUP-352	TN-1
	27. AUP-354	
	28. AUP-355	
	29. AUP-361	11. TN-1/Kashmir-
	30. AUP-362	Basmati
	31. AUP-364	
	32. AUP-365	
	33. AUP-373	12. Kangni/Kashmir-
	34. AUP-374	Basmati
	35. AUP-381	13. Kashmir-Basmati/
	36. AUP-382	Kangni
	37. AUP-383	
	38. AUP-385	

Statistical analysis

Data were analyzed according to analysis of variance procedure as defined by Singh and Chaudhary (1985) for the parents and F_{5,6} lines derived from the parental lines (Table 1). Least-Significant-Difference (LSD) test was estimated for means partition and appropriate association.

Heritability estimation

Genetic and environmental-variances and heritability estimation from the mean squares in ANOVA for each parameter were estimated according to Singh and Chaudhary (1979).

$$\text{Genetic Variance (Vg)} = \frac{\text{Genotypes Mean Square} - \text{Error Mean Square}}{\text{Number of replications}}$$

$$\text{Environmental Variance (Ve)} = \text{Error Mean Square}$$

$$\text{Phenotypic Variance (Vp)} = \text{Vg} + \text{Ve/r}$$

Broad sense heritability (h^2_{bs}) on entry mean basis was calculated as:

$$h^2_{(bs)} = \frac{Vg}{Vp}$$

V_p: Phenotypic variance for a particular trait; (h^2_{bs}): Broad sense heritability for a particular trait; V_g: Genetic variance.

Genetic advance

Genetic advance was computed using the following method of Panse and Sukhatme (1965).

$$GA = k \times \sqrt{\sigma^2 p} \times h^2$$

Where; GA: Genetic advance; K: 1.76 (10 percent selection-intensity).

$$\sqrt{\sigma^2 p} = \text{Phenotypic standard deviation}$$

H²: broad-sense heritability for a particulate trait.

Genetic advance was calculated as percent of mean via the following formula;

$$GA \% = \frac{GA}{\bar{X}} \times 100$$

Where; X: the mean of specific F_{5,6} lines for a particular trait.

Results and Discussion

Days to 50% heading

Inherent enhancement of rice following breeding methods may help to achieve self-sufficiency in rice through the development of high yielding cultivars. Some of the traits like early heading assures the breeder to get sufficient yield and short duration varieties by receiving appropriate duration for grain

development. Analysis of variance displayed highly significant ($p < 0.01$) differences among the parents, $F_{5,6}$ lines and parents vs $F_{5,6}$ lines were observed for days to heading (Table 2). These results are supported by the findings of Bitew (2016) and Tiwari (2015). Bitew (2016) evaluated 22 genotypes for yield attributing traits and detected significant differences for number of days to heading. Among the parents, mean values for days to heading varied from 78-94.6 days. Basmati-2008 took minimum days (78) to heading while maximum days (94.6) were recorded for Kangni-27. Among the $F_{5,6}$ lines, mean values varied from 90.6 to 103 days. AUP-304 showed minimum days to heading (90.6) while maximum days (103) were recorded for AUP-274 (Table 3). Heritability is important for selection-based improvement as it specifies the degree of transmissibility of a character into upcoming generations. Genetic advance provides clear representation and accurate opinion of segregating generations for promising selection. High broad -sense heritability of 95.9% having genetic advance of 8.3% was recorded among the studied traits of rice genotypes (Table 4). Corazon et al. (2015) assessed 48 rice genotypes for yield and yield associated traits and recorded high heritability (91.3%) for days to heading.

Table 2: Mean squares for various morphological traits of rice genotypes at Peshawar during 2016.

Traits	Repli- cations	Gen- otypes	Par- ents	$F_{5,6}$ Lines	P vs $F_{5,6}$	Error
Df	2	45	7	37	1	90
Days to heading	4.24**	61.73**	94.9**	18.6**	1421**	0.85
Days to maturity	1.27**	243.4**	226.4**	101.8**	5598**	0.27
Flag leaf area	4.16**	227.3**	82.5**	258.8**	77.7**	82.8
Culm length	10.8**	1052**	579.8**	1157**	482.5**	1.93
Panicle length	1.78 ^{NS}	13.3**	22.5**	11.6**	10.97**	1.61
Primary branch- es panicle ⁻¹	2.11*	3.81**	4.7**	2.6**	38.69**	0.68
Secondary branches panicle ⁻¹	9.38 ^{NS}	105.9**	67.6**	113.1**	107.9**	6.61

*, ** = Significant at 0.05 and 0.01 levels of probability, ^{NS} = Non significant.

Days to maturity

Early maturing rice genotypes are highly focused throughout the world by plant breeders in current climatic conditions. For the adaptability of rice to different environments and geographical regions, maturity trait is considered as a critical parameter.

Statistical analysis showed highly significant ($p \leq 0.01$) differences among the parents, $F_{5,6}$ lines and parents vs $F_{5,6}$ lines for this trait (Table 2). Similar results have been reported by Corozon et al. (2015) for days to maturity. They assessed 48 rice genotypes for morphological traits and observed significant differences for days to maturity. Among the parents mean values ranges between 99 and 120 days. Basmati-370 took minimum days to maturity (99) while maximum days (120) were recorded for Kangni-27. Among $F_{5,6}$ lines, the mean values range from 118 to 134 days. AUP-361 showed minimum days (118) to maturity while AUP-322 showed maximum days (134) to maturity (Table 3). High broad-sense heritability of 99.6% and genetic advance of 12.8% was observed among studied traits of rice genotypes (Table 4). Results are similar with the findings of Bitew (2016) for the said trait.

Flag leaf area

Flag leaf area contributes major role in determining the yield potential of cereal crops and contribute mainly to the filling of grains, since flag leaf area deliveries photosynthetic foodstuffs primarily to the panicle. The genotypes displayed highly significant ($p \leq 0.01$) differences for parents, $F_{5,6}$ lines and parents vs $F_{5,6}$ were observed for flag leaf area (Table 2). Similar results have been reported by Devi et al. (2016) and Naseem et al. (2014) who also reported highly significant difference for flag leaf area. Among the parental genotypes, mean values ranges from 31 to 46.0 cm². Basmati-2008 exhibited minimum flag leaf area (31) while maximum flag leaf area (46.0) was recorded for Dilrosh. Among the $F_{5,6}$ lines the mean values ranged from 19.8 to 55 cm². AUP-364 showed minimum flag leaf area (19.8 cm²) while maximum flag leaf area (55 cm²) was observed for AUP-311 (Table 3). High broad-sense heritability of 98.9% and genetic advance of 40.2% was recorded for flag leaf area (Table 4). Similar results of high heritability and genetic advance for flag leaf area were described by Devi et al. (2016) and Gangashetty et al. (2013).

Culm length

Culm is the connected stem of rice and is made-up of sequences of nodes and internode which contribute towards numbers of panicles density. Mean squares exhibited highly significant ($p \leq 0.01$) differences among parents, $F_{5,6}$ lines and parents vs F_6 lines for culm length. Highly significant results for culm length are analogous to the outcomes of Lingaiah (2015) and

Table 3: Means for days to heading, days to maturity and flag leaf area, culm length, panicle length, primary branches and secondary branches panicle⁻¹ of rice genotypes at Peshawar during 2016.

Genotypes	Days to heading	Days to maturity	Flag leaf area (cm ²)	Culm length (cm)	Panicle length (cm)	Primary branches panicle ⁻¹	Secondary branches panicle ⁻¹
Parents							
Basmati-2008	78	100	31	99.6	27.7	8.7	21.2
Kangni-27	94	120	33.3	112.7	27.3	9.6	31.1
TN-1	91	120	37.3	115.2	29.9	9.3	20.2
Basmati-370	83	99	43.2	89.5	22.0	6.5	18.9
Basmati-6129	82	106	40.6	103.1	27.4	10.9	28.2
Dilrosh	88	102	46.0	108.5	26.7	9.4	17.3
Kashmiri-Basmati	91	116	43.8	104.5	25.2	9.6	25.0
Dokri-Basmati	88	112	39.9	73	22.4	8.7	24.3
F₆ Lines							
AUP-262	95	131	31.3	104.3	28.1	10.47	25.0
AUP-263	95	131	37.8	110.4	26.8	9.4	19.7
AUP-264	94	132	36.4	111.6	27.5	10.2	31.8
AUP-271	101	132	44.2	122.7	28.3	10.8	30.4
AUP-274	103	133	46.8	120.4	26.9	11.0	39.6
AUP-282	93	123	40.8	109.5	25.5	9.8	22.6
AUP-285	94	123	37.0	121.2	26.6	10.2	23.8
AUP-292	94	127	33.2	109.4	24.3	9.8	20.1
AUP-294	94	126	38.4	112.3	23.7	9.8	26.1
AUP-295	94	126	39.0	121.5	24.3	10.0	30.1
AUP-302	91	122	35.6	112.2	25.4	11.0	32.8
AUP-304	91	122	36.2	102.2	25.3	9.5	23.7
AUP-305	91	121	32.9	116.6	24.0	10.4	26.4
AUP-311	93	133	55.0	132.3	27.2	9.8	24.5
AUP-312	97	133	52.9	128.3	27.6	11.1	24.8
AUP-315	97	133	54.2	127.4	27.0	11.0	32.4
AUP-321	92	133	39.7	120.1	27.0	10.5	29.3
AUP-322	92	134	45.2	118.7	27.2	10.9	41.3
AUP-325	91	132	45.0	119.7	24.5	10.0	29.1
AUP-335	93	121	42.9	113	23.9	9.2	29.3
AUP-341	95	119	24.7	83.4	24.3	11.4	18.1
AUP-342	96	118	23.5	82.6	25.0	11.4	17.1
AUP-343	96	119	25.7	77.3	23.9	11.6	19.4
AUP-345	96	120	28.7	84.4	26.3	13.0	24.8
AUP-351	97	125	37.5	94.8	26.3	12.2	34.8
AUP-352	97	125	34.7	95.2	26.3	10.6	25.4
AUP-354	97	123	29.3	98.7	26.5	11.2	29.8
AUP-355	97	124	30.7	97.8	26.9	11.0	30.9
AUP-361	94	118	25.3	63.6	22.8	11.8	19.6
AUP-362	94	118	23.9	63.8	22.2	10.8	19.2
AUP-364	95	119	19.8	62.2	20.6	10.7	15.7
AUP-365	95	120	23.8	64.6	20.4	11.0	14.1
AUP-373	94	120	43.0	122.6	23.4	9.0	23.9
AUP-374	93	121	41.8	123.6	22.2	8.2	20.7
AUP-381	94	133	49.7	111.4	25.8	9.6	25.4
AUP-382	95	133	52.1	110.4	26.9	10.6	25.6
AUP-383	94	133	40.5	109.0	26.0	9.4	22.3
AUP-385	95	133	43.0	121.4	25.9	9.5	23.6
Genotype Means	93.2	123.3	37.7	104.4	25.5	10.2	25.2
LSD (0.05)	1.4	0.83	1.54	2.2	2.1	1.3	4.1

Parental Means LSD (0.05)	86.2	109.4	39.4	100.3	26.1	9.1	23.3
	1.7	0.99	1.84	2.68	2.4	1.5	4.9
F _{5:6} Line Means LSD (0.05)	94.7	126.2	37.4	105.3	25.3	10.5	25.6
	1.5	0.85	1.57	2.2	2.1	1.3	4.2

and Idris and Mohammad (2013). They also reported highly significant differences for this trait (Table 2). Among the parental genotypes, mean values varied from 73 to 115.2 cm. Dokri-Basmati manifested minimum culm length (73 cm) while maximum culm length (115.2 cm) was recorded for TN-1. Among the F_{5:6} lines mean values ranged from 62.2 to 132.3 cm. Minimum culm length (62.2 cm) was observed for AUP-364 while maximum culm length (132.3 cm) was recorded for AUP-311 (Table 3). Culm length exhibited high broad-sense heritability of 99.4% and genetic advance of 31.4% among studied traits of rice genotypes (Table 4). Das (2015), Lingaiah (2015) and Tiwari (2015) also reported high heritability and genetic-advance for culm length.

Table 4: Broad-sense heritability (h^2) and genetic advance of rice genotypes studied at Peshawar during 2016.

Parameters	Heritability (h^2_{BS})	Genetic advance (%)
Days to heading	95.9	8.3
Days to maturity	99.6	12.8
Flag leaf area	98.8	40.2
Culm length	99.4	31.4
Panicle length	70.7	11.4
Primary branches panicle ⁻¹	60.6	13.6
Secondary branches panicle ⁻¹	88.3	36.6

Panicle length

The terminal component of the rice tiller is an inflorescence called the panicle. Longer panicle will bear increased number of spikelets resulting in enhanced grain yield. Highly significant ($p \leq 0.01$) differences were recorded among parents, F_{5:6} lines and parents vs F_{5:6} for panicle length (Table 2). Similar results for panicle length are supported to the findings of Das (2015) and Jambhukar and Bose (2014). Among the parental geotypes mean values ranges between 22.4 and 29.9 cm. Basmati-370 showed minimum (22.4 cm) panicle length while maximum panicle length (29.9 cm) was recorded for TN-1. Among F_{5:6} lines, mean data ranged from 20.4 to 28.3 cm. AUP-365 showed minimum panicle

length (20.4 cm) while maximum was recorded for AUP-271 (28.3 cm) (Table 3). High broad-sense heritability of 70.7% and genetic advance of 11.4% was recorded for panicle length (Table 4). High heritability estimates for panicle length are supported by the findings of Servan et al. (2012) and Rafi et al. (2014).

Primary branches panicle⁻¹

Number of primary panicle branches are the furthestmost imperative yield attributing components concerning high yield in rice, more the number of primary branches more will be the number of grains. Analysis of variance displayed highly significant ($p < 0.01$) differences among the parents, F_{5:6} lines and parents vs F_{5:6} lines for primary branches panicle⁻¹ (Table 2). Yadav et al. (2014) also reported significant differences for primary branches panicle⁻¹. Among the parental genotypes, mean values ranged from 6.5 to 10.9 primary branches panicle⁻¹. Basmati-370 took minimum number of branches (6.5) while maximum number of primary branches (10.9) were recorded for Basmati-6129. Among the F_{5:6} lines, mean values varied from 8.2 to 13 primary branches panicle⁻¹. AUP-374 exhibited minimum number of primary branches (8.2) while maximum number of primary branches (13) was recorded for AUP-345 (Table 3). High broad-sense heritability of 60.6% and genetic advance of 13.6% was recorded among the studied traits of rice genotypes (Table 4). Similar results have been reported by Ketan and Sarkar (2014). They observed high heritability of 70% among the rice genotypes for primary branches panicle⁻¹.

Secondary branches panicle⁻¹

Secondary branches panicle⁻¹ is important yield contributing trait resulting more number of grains which turn increase the yield in rice crop. Statistical analysis revealed highly significant ($p \leq 0.01$) differences among parents, F_{5:6} lines and parents vs F_{5:6} for secondary branches panicle⁻¹ (Table 2). Ketan and Sarkar (2014) also reported similar results. Among the parental genotypes, mean values ranged from 17.3 to 31.1 branches panicle⁻¹. Minimum number of secondary branches (17.3) was recorded for Dilrosh

while maximum number of secondary branches panicle⁻¹ (31.1) was recorded by Kangni-27. Among F_{5:6} lines, mean values ranged from 14 to 41.3 branches panicle⁻¹. AUP-365 exhibited minimum number of secondary branches panicle⁻¹ (14) while maximum number of secondary branches panicle⁻¹ (41.3) was recorded for AUP-322 (Table 3). High broad-sense heritability of 88.3% and genetic advance of 36.6% was recorded for secondary branches panicle⁻¹ (Table 4) Ketan and Sarkar (2014) and Sanghera et al. (2013) also observed high heritability and genetic advance values for secondary branches panicle⁻¹.

Conclusions and Recommendations

Highly significant differences among the parents, F_{5:6} lines and parents vs F_{5:6} lines were observed for all the studied characters. Among the F_{5:6} lines, early heading and early maturity was recorded for AUP-304 and AUP-361 respectively. AUP-345 showed highest number of primary branches panicle⁻¹ while AUP-322 showed highest number of secondary branches panicle⁻¹. High broad-sense heritability with moderate to high genetic advance was observed for entirely study traits. On the basis of good performance for maturity and yield related traits, F_{5:6} lines AUP-361 and AUP-345 are recommended for further evaluation in replicated yield trials across locations.

Author's Contribution

Arshad Iqbal and Aziz-ur-Rahman: Collected and analysed the data and wrote the manuscript.

Syed Mehar Ali Shah: Provision of the genetic material, wrote the manuscript and guided in research.

Hidayat ur Rahman: Interpreted the data, wrote the manuscript and guided in research

Faiza Aman: Reviewed the literature, analysed the data and wrote the manuscript.

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