

Full Length Research Article

Agro-physiological response of different okra (*Abelmoschus esculentus* L.) genotypes and their F₁ crosses under waste water and normal irrigation treatments

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Abstract

Water scarcity is a major threat to agriculture sector that contributes about 21 percent to the Pakistan's gross domestic product (GDP) and to employment about 45 percent of the country's labor force. Pakistan has the largest irrigation system, but water losses from the system are the highest in the world. In order to achieve the maximum genetic gain with minimum resources and in minimum time, the gene action studies are of great importance in executing an efficient breeding program. The present research was performed to estimate the overall performance and the gene action of five okra varieties/genotypes viz., 19228, 19224, 19232, 19225, 15382 and their respective crosses for some morphological, physiological and quality parameters i.e., photosynthetic active radiation, net photosynthesis rate, transpiration rate, fruit yield per plant, No. of fruits per plant and fruit weight, protein contents, dietary fiber contents and carbohydrates percentage in fruit. Highly significant results were observed among genotypes for all the traits. The results of the diallel analysis demonstrated that transpiration rate, fruit yield per plant, no. of fruits per plant, fruit weight, dietary fiber contents and carbohydrate percentage under wastewater irrigation were ruled by over-dominance with non-additive gene action while partial dominance was observed in photosynthetic active radiation, net photosynthesis rate and protein contents under wastewater irrigation. Fruit yield per plant, fruit weight, No. of fruits per plant, dietary fiber contents and carbohydrates under normal irrigation water showed additive gene action which suggested that early selection might lead to the development of desirable okra genotypes. The overall performance of both treatments revealed that the crops performed better under wastewater irrigation with better growth and productivity compared to the normal irrigation.

Keywords: Okra, normal irrigation, waste water irrigation. gene action.

Introduction

Pakistan is an agricultural country and water is life blood of agriculture. About 68% of the land area of the country falls in arid and semiarid regions where evapo-transpiration exceeds precipitation, rainfall is low, uncertain and erratic. Underground water in many areas is unfit for irrigation. Farmers using waste water (WW) in developing countries are often limited in adopting safeguards for human, animal and environmental health control and in improving beneficial use of water and nutrients. Case studies from Ghana, Bolivia, Pakistan, Tunisia and Mexico are used to illustrate the complex factors that influence the use of WW by farmers. Contamination of vegetables with heavy metals present in WW e.g., cadmium (Cd), copper (Cu), nickel (Ni), iron (Fe), lead (Pb), zinc (Zn), cobalt (Co), chromium (Cr), and the human health risks, were determined, where sewage water is used in vegetables farming (Mapanda, 2006). The removal of heavy metals from WW is difficult and unaffordable; hence WW is used without treatment. Many technologies used for abolishing of heavy metals are expensive for a low-income country like Pakistan (Singh *et al.*, 2010).

Therefore, we need to grow such vegetables which can give more yields and gather heavy metals in non-edible portion instead of edible portion.

Okra (*Abelmoschus esculentus* L.) is one of important vegetable crops from Malvaceae family and very popular in Indo-Pak subcontinent. It is one of the oldest cultivated crops and is widely distributed from Africa to Asia, Southern Europe and America (Oyelade *et al.*, 2003). It is a tropical to subtropical crop and is sensitive to frost, low temperature, water logging and drought conditions. In Pakistan, okra is a favorite vegetable cuisine, which resulted in a progressive increase in the area of okra but the last five-year statistics shows that there was a decreasing trend in yield per unit area and production as compared to the last 10 years. A number of factors are considered to cause reduction in yield and production but it is argued that the limiting availability of irrigational water has been a key factor for its reduction.

The breeding programs of many crops use diallel analyses because they offer genetic information on quantitative traits to breeders (Viana *et al.*, 2001).

Knowledge of genetic inheritance of characters and the role of non-allelic interaction is essential to the breeders at the time of decision for the selection method and breeding procedure to follow (Esmail, 2007). From diallel analysis, plant breeders are able to gather information on heterosis, reciprocal and maternal effects, general combining ability (GCA) and the specific combining ability (SCA) of parents in crosses (Glover *et al.*, 2005). Diallel mating systems have provided genetic understanding for a chosen set of parents (Murray *et al.*, 2003) and have been used to study various traits in many crops. The present investigation will be carried out to assess the effectiveness of waste water irrigation in comparison with normal irrigation among various okra genotype and their crosses in full diallel mating design.

MATERIALS & METHODS

Germplasm development:

A field experiment consisting of five genotypes of okra was conducted in the research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during crop season of 2010-2011. The germplasm of okra was collected from Ayub Agricultural Research Institute, Faisalabad. All possible crosses were made to obtain F₁ seed following diallel mating design. The genotypes used as parents are 19228, 19224, 19232, 19225 and 15382. The F₁ seed along with their parents were evaluated. The experiment was laid out following randomized complete block design with three replications. Each replicate possessed 25 genotypes. Parents and crosses evaluation were made by applying two treatments, one was normal irrigation water and another was waste water irrigation to check the effect of waste water on growth and productivity of okra. Plant to plant and row to row distance was 10 cm.

Germplasm Evaluation:

At maturity 10 guarded plants from each genotype were selected at random and data were recorded for some morphological, physiological and quality parameters as follows.

Photosynthetic active radiation (mmol/m²/s):

It designates the spectral range (wave band) of solar radiation from 400 to 700 nm that photosynthetic organisms are able to use in the process of photosynthesis. Five leaves per plant per entry were used. The Photosynthetic active radiation (PAR) was measured by Infrared Radiation Gas Absorption (IRRGA) at maturity of plant.

Net photosynthesis rate (mmol/m²/s):

Net Photosynthesis rate was calculated by the difference between the total amount of photosynthesis and the sum of the rates of respiration (i.e. photorespiration and dark

respiration), by using Infrared Radiation Gas Absorption (IRRGA) at maturity of plant.

Transpiration rate (mmol/m²/s):

No. of samples per entry were tagged and transpiration rate was recorded by the use of IRRGA. All the measurements of above-mentioned parameters were made on colorless clear days between 11:00 and 13:00 solar time.

Protein content: -

The percentage of protein was calculated by the equation $(P / T \times 100)$ where, "P" is the number of calories that come from protein and "T" is the total number of calories in the food.

Other Traits:

No. of fruits per plant, fruit weight (g), fruit yield per plant (g), carbohydrates (%) and dietary fiber contents (%).

Statistical Analysis:

The data thus collected were subjected to analysis of variance technique as outlined by Steel *et al.* (1997) for all characters under study to observe the level of significance among various F₁ hybrids and their parental lines. The data collected for the characters showing significant differences among genotypes were further subjected to combining ability analysis using Method I, developed and illustrated by Griffing (1956). The various formulae applied for calculation of general combining ability, specific combining ability and components of variance are as follows:

General combining ability effects:

General combining ability effects were calculated by using the expression:

$$g_i = 1/2p (X_{i.} + X_{.i}) - 1/p^2 X.$$

Where:

g_i = General combining ability effects of i^{th} parent.

P = Number of parents.

$X_{i.}$ = Total of mean values of F₁s resulting from crossing j^{th} parent with i^{th} parent.

$X_{.i}$ = Total of mean values of F₁s resulting from crossing i^{th} parent with j^{th} parent.

X. = Grand total of all mean values in the table.

Specific combining ability effects:

Specific combining ability effects were computed as follows:

$$S_{ij} = 1/2 (X_{ij} + X_{ji}) - 1/2p (X_{i.} + X_{.i} + X_{j.} + X_{.j}) + 1/p^2 X ..$$

Where:

S_{ij} = Specific combining ability between i^{th} and j^{th} parents.

X_{ij} = Mean value of the F₁ resulting from crossing the i^{th} and j^{th} parents.

X_{ji} = Mean values of the F₁ resulting from crossing the j^{th} and i^{th} parents.

$X_{i.}$ = Total of mean values of F₁s resulting from j^{th} parent with i^{th} parent.

$X_{.i}$ = Reciprocal value of $X_{i.}$

$X_{.i}$ = Total values of F_1 s resulting from crossing i^{th} parent with j^{th} parent.

$X_{.j}$ = Value of reciprocal F_1 s of $X_{.i}$.

X = Grand total of the observations.

Reciprocal effects:

$$r_{ij} = 1/2 (X_{ij} - X_{ji})$$

Where:

r_{ij} = Reciprocal effects of i^{th} parent with j^{th} parent.

X_{ij} = Mean values of F_1 s resulting from crossing the i^{th} parent with j^{th} parent.

X_{ji} = Mean values of F_1 s resulting from crossing the j^{th} parent with i^{th} parent.

RESULTS & DISCUSSION

The combining ability for the diallel crossing technique was done using the diallel technique produced by Griffings, Model I, (1956) for both the treatments. Data being recorded were subjected to analysis of variance (ANOVA) technique prepared by Steel *et al.* (1997). Estimated polygenic characters of okra from both the treatments were presented and discussed below:

Photosynthetic active radiation (PAR) ($\text{mmol/m}^2/\text{s}$):

Analysis of variance indicated highly significant differences among treatments, genotypes and genotype $\times$ treatment interaction for photosynthetic active radiation in both normal and wastewater irrigated treatments (Table 2a). The photosynthetic active radiation (PAR) was higher under waste water irrigated treatment except cross 19232 $\times$ 19228 which showed higher PAR under normal irrigation. On an average, among genotypes, the 19224 had maximum PAR value and 19224 $\times$ 19232 had minimum PAR value (Table 2 a) under waste water irrigation condition. The combining ability analysis of normal irrigated treatment indicated that the photosynthetic active radiation (PAR) was controlled by additive and non-additive gene actions because GCA and SCA both was highly significant (Table 1). Among the parents, 19228 was the best general combiner for PAR. Among the crosses, 19228 $\times$ 19224 was the best specific combination (Table 3). When the combining ability was studied under waste water irrigated treatment, it was determined that the GCA and SCA were highly significant and both types of gene actions (additive and non-additive) were present (Table 1). Among the parents, 19225 was the best general combination for PAR. Among the crosses, 19228 $\times$ 15382 was the best specific combination (Table 3). The significance of GCA and SCA variances indicated the importance of both additive and non-additive gene actions. This is in conformity with the reports of Vijay and Manohar (1986).

Net photosynthesis rate ($\text{mmol/m}^2/\text{s}$):

Analysis of variance indicated highly significant differences among treatments, genotypes and genotype $\times$ treatment interaction for net photosynthesis rate in

both normal and waste water irrigated treatments (Table 2). The mean values of analysis of variance under normal and waste water irrigated treatments indicated that 13 genotypes had higher values of net photosynthesis rate under wastewater irrigation and 12 genotypes had higher values under normal irrigation. Among genotypes, a cross (15382 $\times$ 19224) had maximum net photosynthesis rate and 19228 had minimum photosynthetic rate (Table 2) under waste water irrigation condition. The combining ability studies under normal irrigated treatment showed that the net photosynthesis rate was controlled by both additive and non-additive gene actions as GCA and SCA were highly significant (Table 1). But non-additive gene action was dominant over additive gene action. Among the parents, 19224 was the best general combination. Among the crosses, 19224 $\times$ 19225 was the best specific combination for net photosynthesis rate (Table 3). Under waste water irrigated treatment the net photosynthesis rate was controlled by both additive and non-additive gene actions as GCA and SCA were highly significant (Table 1). But non-additive gene action was dominant. Among the parents, 15382 was the best general combiner. Among the crosses, 19225 $\times$ 15382 was the best specific combiner for net photosynthesis rate (Table 3). The variances due to GCA and SCA were significant indicating the operation of both additive and non-additive types of gene action in the inheritance of net photosynthesis rate. However, the greater magnitude of SCA variance than that of GCA pointed out the predominance of non-additive gene action as was reported by Veeraraghavathatham and Irulappan (1991).

Transpiration rate ($\text{mmol/m}^2/\text{s}$):

Analysis of variance indicated highly significant differences among treatments, genotypes and genotype $\times$ treatment interaction for transpiration rate in both normal and waste water irrigated treatments (Table 2). When the effect of normal and waste water was studied, it was determined that the transpiration rate was increased under waste water irrigated treatment. Among genotypes, a cross (19224 $\times$ 19232) exhibited maximum transpiration rate and 15382 $\times$ 19225 had minimum transpiration rate under both normal and waste water irrigated treatments (Table 2). The combining ability studies under normal irrigated treatment indicated that the transpiration rate was controlled by both additive and non-additive gene actions as indicated by higher values of GCA and SCA but the effect of non-additive gene action was dominant (Table 1). Among the parents, 19225 was somehow best general combination compared to other parents. Among the crosses, 19224 $\times$ 19232 was somehow best specific combination compared to other crosses under normal irrigated treatment (Table 3). Under waste water irrigated treatment, the combining ability analysis indicated that transpiration rate was controlled by non-additive gene

action as SCA was highly significant and additive gene action was absent due to non-significance of GCA (Table 1). Among the parents, 19224 was somehow best general combination compared to others. Among the crosses, 19224 × 19225 was the best specific combination under waste water irrigated treatment (Table 3). So, the transpiration rate was increased under waste water treatment and it was controlled by non-additive gene action under both cases. The variances due to GCA and SCA were significant indicating the operation of both additive and non-additive types of gene action in the inheritance of transpiration rate. However, the greater magnitude of SCA variance than that of GCA pointed out the predominance of non-additive gene action as was reported by Vijay and Manohar (1986).

Fruit yield per plant (g):

Analysis of variance indicated highly significant differences among treatments, genotypes and genotype × treatment interaction for fruit yield per plant in both normal and waste water irrigated treatments (Table 2). The fruit yield per plant was higher under waste water irrigation except cross 19225 × 19232 which gave lower fruit yield under wastewater irrigation. The overall fruit yield of genotype 19225 × 15382 was maximum and of 19232 × 19224 was minimum under both treatments (Table 2). The combining ability analysis of fruit yield under normal irrigated treatment indicated that the specific combining ability (SCA) was highly significant which showed that the non-additive gene action was dominant in fruit yield as compared to additive gene action that indicated significant value of general combining ability (GCA) (Table 1). Among the parents, 19225 was the best general combination in case of fruit yield. Among the crosses, 19224 × 15382 was the best specific combination for fruit yield (Table 3). The fruit yield under waste water irrigated treatment indicated that the specific combining ability (SCA) was highly significant which showed that the fruit yield was controlled by non-additive gene action and additive gene action was absent because general combining ability (GCA) was non-significant under wastewater irrigated treatment (Table 1). The parent 15382 was the best general combination under waste water irrigated treatment. Among the crosses, 19224 × 15382 was the best specific combination for fruit yield (Table 1). When both the treatments were compared it was determined that the fruit yield was controlled by non-additive gene action and the cross 19224 × 15382 was the best specific combination under both treatments. The GCA and SCA variances were significant as was reported by Shukla *et.al.* (1989) and Veeraraghavathatham and Irulappan (1990). The ratio of GCA to SCA variance was less than unity indicating that the non-additive component of genetic variance was more important.

No. of fruits per plant:

Analysis of variance indicated highly significant differences among treatments, genotypes and genotype × treatment interaction for no. of fruits per plant in both normal and waste water irrigated treatments (Table 2). The mean values under both treatments indicated that the no. of fruits per plant was higher under wastewater irrigated treatment except a cross (15382 × 19232) which showed higher no. of fruits under normal irrigation. Among genotypes, a cross (15382 × 19224) had maximum no. of fruits per plant and a cross (19232 × 19225) had minimum no. of fruits per plant under both treatments (Table 2). The combining ability analysis of normal irrigated treatment showed that the no. of fruits per plant was controlled by non-additive gene action as SCA was highly significant and additive gene action was absent as GCA was non-significant (Table 1). Among the parents, 15382 was best general combination compared to other parents. Among the crosses, 19225 × 15382 was the best specific combination for further breeding programmes (Table 3). Under waste water irrigated treatment it was determined that the no. of fruits per plant was controlled by non-additive gene action as SCA was highly significant and additive gene action also present but it was not dominant as showed by significant value of GCA (Table 1). Among the parents, 15382 was the best general combination compared to other parents. Among the crosses, 19228 × 19224 was the best specific combination (Table 3). It was clear that the no. of fruits per plant increased under waste water irrigation and it was controlled by non-additive gene action. The parent 15382 was the best general combiner under both treatments. The GCA and SCA variances were significant as was reported by Shukla *et.al.* (1989). The ratio of GCA to SCA variance was less than unity indicating that the non-additive component of genetic variance was more important.

Fruit weight (g):

Results obtained in analysis of variance indicated highly significant differences among treatments, genotypes and genotype × treatment interaction for fruit weight in both normal and waste water irrigated treatments (Table 2). When both the treatments were compared it was determined that the fruit weight increased under waste water irrigated treatment except crosses, 19228 × 19224, 19224 × 19225 and 15382 × 19225 which showed higher fruit weight under normal irrigated treatment. Among crosses, 19224 × 19228, 19232 × 19228, 19232 × 19224 and 19232 × 19225 showed equal fruit weight under both normal and waste water irrigations. On an average, the cross (19225 × 15382) showed maximum fruit weight and 19232 × 19228 showed minimum fruit weight under both types of treatments (Table 2).

When combining ability analysis was carried out under normal irrigated treatment, it was determined

that the pod weight was controlled by non-additive gene action as SCA was highly significant. The significant value of GCA showed that additive gene action also presents but effect of SCA was dominant (Table 1). Among the parents, 15382 was the best general combination. Among the crosses, 19224 × 15382 was the specific combination for further breeding programs (Table 3). The analysis for waste water irrigated treatment indicated that the pod weight was controlled by non-additive gene action as SCA was highly significant. The significant value of GCA showed additive gene action but its effect was not dominant (Table 1). Among parents, 15382 was the best general combination. Among crosses, 19225 × 15382 was the best specific combination (Table 3). It was concluded that the fruit weight was controlled by non-additive gene action. The parent 15382 showed better potential for GCA and the cross 19224 × 15382 showed good potential for SCA. Significant variances due to GCA and SCA were obtained indicating importance for both additive and non-additive genetic variance. This is in line with the findings of Vijay and Manohar (1986) and Veeraraghavathatham and Irulappan (1990). However, the SCA variance was slightly greater than GCA variance implying a major role of non-additive gene action as was reported by Chaudhari *et. al.* (1991) and Shivagamasundar *et. al.* (1992).

Protein contents (%):

Analysis of variance indicated highly significant differences among treatments, genotypes and genotype × treatment interaction for protein contents in both normal and waste water irrigated treatments (Table 2). The analysis of variance under both treatments indicated that the percentage (%) of proteins was higher under wastewater irrigated treatment and lower under normal irrigation. On an average, among genotypes, 19224 × 19225 showed maximum amount of proteins and 19224 × 15382 showed minimum amount of proteins under normal irrigated treatment, Similarly 15382 × 19225 showed maximum and 19224 showed minimum amount of proteins under waste water irrigated treatment (Table 2). When the combining ability was analyzed for normal irrigated treatment, it was determined that the protein contents was controlled by additive gene action as GCA was highly significant. The non-additive gene action was also present but its effect was not dominant (Table 1). Among parents, 19225 was somehow good combination compared to other parents. Among crosses, 19228 × 19224 was good specific combination (Table 3) as average performance of this cross was highest. Under waste water irrigated treatment the analysis indicated that the protein content was controlled by additive gene action as GCA was highly

Analysis of variance indicated highly significant differences among treatments, genotypes and genotype × treatment interaction for carbohydrates in

significant. The effect of non-additive gene action was not dominant (Table 1). Among the parents, 15382 was a good general combination. Among the crosses, 19225 × 15382 was a good specific combination (Table 3). It was concluded after comparison that the protein content was controlled by additive gene action. The variances due to GCA and SCA were significant but indicating the predominant role of additive gene action. This is in conformity with the reports of Chaudhari *et. al.* (1991), Shivagamasundariet. *al.* (1992) and Wankhadeet. *al.* (1995).

Dietary fiber contents (%):

Results obtained in analysis of variance indicated highly significant differences among treatments, genotypes and genotype × treatment interaction for dietary fiber contents in both normal and waste water irrigated treatments (Table 2). When the comparison was made between both normal and waste water irrigated treatments, it was determined that the effect of waste water was significant on dietary fiber contents of all okra genotypes and the effect of normal irrigation was not advantageous. On an average, among genotypes, a cross (19224 × 15382) showed maximum and 19232 × 19228 showed minimum dietary fiber contents under normal irrigated treatment, similarly 15382 × 19225 showed maximum and 19228 showed minimum dietary fiber contents under waste water irrigated treatment (Table 2). The combining ability studies for normal irrigated treatment indicated that the dietary fiber content was controlled by non-additive gene action as showed by highly significant value of SCA.

The additive gene action was absent as GCA was non-significant (Table 1). Among parents, 19225 was a good general combination compared to others. Among crosses, 19224 × 19225 was a good specific combination and had a potential to be used in further breeding programmes (Table 3). When the combining ability analysis was carried out for waste water irrigated treatment, it was determined that the dietary fiber contents was controlled by non-additive gene action as SCA was highly significant. The GCA was significant and showed additive gene action but its effect was not dominant (Table 1). Among the parents, 15382 was a good general combination for fiber contents. Among the crosses, 19228 × 19224 was a good specific combination (Table 3). It was concluded that the dietary fiber content was controlled by non-additive gene action and 19225 and 15382 were potential parents. The variances due to GCA and SCA were significant but indicating the predominant role of non-additive gene action. This is in conformity with the reports of Chaudhariet. *al.* (1991) and Wankhadeet. *al.* (1995).

Carbohydrates (%):

both normal and waste water irrigated treatments (Table 2). The mean values showed differences among genotypes and also indicated the significant effect of

waste water on carbohydrate contents of all okra genotype. On an average, among genotypes, a cross (19225 × 15382) showed maximum percentage and 19224 × 15382 showed minimum percentage of carbohydrates under normal irrigated treatment. Similarly, 15382 × 19225 showed maximum and 19232 showed minimum percentage of carbohydrates under wastewater irrigated treatment (Table 2). The combining ability analysis indicated that the carbohydrate contents were controlled by non-additive gene action under normal irrigated treatment as SCA was highly significant.

The non-significant value of GCA showed that additive gene action was absent for this trait (Table 1). Among the parents, 19225 was a potential parent and good general combination. Among the crosses, 19224 × 19225 was a good specific combination (Table 3). When

the analysis for waste water treatment was carried out, it was determined that the carbohydrate contents were controlled by non-additive gene action and its effect was dominant as SCA was highly significant and GCA was non-significant that showed absence of additive gene action (Table 1). Among the parents, 15382 was a good general combination and potential parent. Among the crosses, 19224 × 19232 was a good genotype for specific combining ability (SCA) (Table 3). It was concluded that the non-additive gene action was dominant for carbohydrate contents and some parents and some crosses were showed potential for further breeding purposes. The variance due to SCA was significant indicating the predominant role of non-additive gene action. The variance due to GCA was non-significant. This is in conformity with the reports of Chaudhari *et. al.* (1991) and Wankhade *et. al.* (1995).

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Table 1: Mean square analysis of variance, effect of General Combining Ability (GCA) and Specific Combining Ability (SCA) and reciprocal effects (RCA) for the computed parameters in the study

Sources	PAR		NPR		TR		FYP		NFP		FW		PC		DFC		CHO	
	Contr ol	Waste water	Contr ol	Waste water	Contr ol	Waste water	Contr ol	Waste water	Contr ol	Waste water	Contr ol	Waste water	Contr ol	Waste water	Contr ol	Waste water	Contr ol	Waste water
Treat ment	17536.54**	25098.79**	1884.577**	2033.308**	19.416**	15.41821**	80.24778**	56.43**	11.30333**	9.592223**	3.955905**	3.798632**	1.871444**	7.041781*	8.431273*	6.752618**	1.052597*	1.478116**
GCA	8097.674**	5685.801**	622.498*	495.6334**	2.453929*	3.488775N.S	26.42988*	9.995259N.S	1.396161N.S	2.241165*	0.7511495**	0.6887605**	7.566088**	3.960556*	3.120157N.S	4.048822**	8.062479N.S	3.352078N.S
SCA	7652.785**	11288.44**	585.6598**	555.1552**	8.900445**	5.765038**	17.53028**	22.03157**	2.561871**	2.02165**	0.9750026**	0.7573419**	5.417782**	2.801486**	2.899528**	.0352837**	2.970024**	8.143061**
RCA	3138.14**	6514.29**	673.0029**	873.2357**	5.650932**	5.173875**	36.09446**	19.11666**	5.922223**	4.755555**	1.889278**	2.006056**	6.529442**	1.246665**	2.594439**	2.553336**	2.326114**	2.334452**
Error	149.9653	104.8845	0.824293	2.42174	0.1176364	0.1358148	8.739261	6.496388	0.5494443	0.7012963	2.646405	3.776187	1.6693	1.20055	1.57971	6.498287	1.827078	1.798761

PAR = photosynthetic active radiation; NPR = net photosynthesis rate; TR = transpiration rate; FYP = fruit yield per plant; NFP = No. of fruits per plant; FW = fruit weight; PC = protein contents; DFC = dietary fiber contents; CHO = carbohydrate contents

Table 2a: Mean of different okra genotype along with their crosses at normal and waste water treatment for different agronomic parameters in the study

Genotype s	PAR		NPR		TR		FYP		NFP		FW		PC		DFC		CHO	
	Contro l	Waste water	Contr ol	Wast e water	Contr ol	Wast e water	Contr ol	Wast e water	Contr ol	Wast e water	Contr ol	Wast e water	Contr ol	Wast e water	Contr ol	Wast e water	Contr ol	Wast e water
19228	1068.2 0 ± 15.94 d	1170.03 ± 06.91 ab	3.74 ± 0.17 b	15.74 ± 0.34 yz	8.14 ± 0.11 xyz	11.19 ± 0.26 mq	118.00 ± 1.53 en	121.6 7 ± 2.85 ck	17.33 ± 0.88 en	17.00 ± 0.58 ck	4.37 ± 0.35 jp	4.97 ± 0.12 ghi	1.383 ± 0.044 jkl	1.767 ± 0.018 be	3.440 ± 0.032 fg	3.667 ± 0.109 e	7.467 ± 0.017 mno	8.637 ± 0.035 fi
19224	1008.0 3 ± 05.57 fg	1179.53 ± 10.86 a	20.30 ± 0.59 vwx	45.22 ± 0.57 lm	5.70 ± 0.37 a	11.60 ± 0.40 lq	118.67 ± 3.53 dn	118.3 3 ± 2.40 dn	18.33 ± 0.88 dn	19.33 ± 0.33 dn	4.17 ± 0.26 lr	4.63 ± 0.09 hm	1.447 ± 0.029 hk	1.710 ± 0.038 e	3.250 ± 0.045 h	4.217 ± 0.059 d	7.470 ± 0.025 mno	8.587 ± 0.027 hi
19232	1060.4 0 ± 05.56 de	1140.03 ± 02.74 bc	22.68 ± 0.40 tuv	16.33 ± 0.33 yz	7.44 ± 0.25 z	12.10 ± 0.41 in	119.67 ± 2.03 cn	124.6 7 ± 2.03 af	17.33 ± 1.45 cn	19.33 ± 0.33 af	4.83 ± 0.23 gj	5.13 ± 0.12 fgh	1.340 ± 0.064 lm	1.750 ± 0.020 cde	3.417 ± 0.024 fgh	4.320 ± 0.074 ad	7.553 ± 0.029 jn	8.570 ± 0.062 i
19225	1060.1 0 ± 23.01 de	1120.83 ± 01.59 c	32.01 ± 0.54 r	17.04 ± 0.04 xyz	10.85 ± 0.21 or	8.51 ± 0.26 vy	120.00 ± 2.89 cn	126.0 0 ± 2.00 ad	16.00 ± 0.58 cn	22.00 ± 0.58 ad	3.43 ± 0.23 uvw	4.00 ± 0.15 ot	1.433 ± 0.038 il	1.823 ± 0.047 ad	3.473 ± 0.038 fg	4.347 ± 0.095 ad	7.500 ± 0.029 kn	8.587 ± 0.049 hi
15382	1061.1 0 ± 25.10 de	1133.97 ± 15.93 c	54.23 ± 1.03 k	38.16 ± 0.50 op	14.14 ± 0.50 cde	12.01 ± 0.43 in	114.00 ± 1.53 ko	118.6 7 ± 1.86 dn	17.00 ± 0.58 ko	21.00 ± 0.58 dn	3.63 ± 0.22 sv	4.33 ± 0.13 jq	1.543 ± 0.038 fgh	1.773 ± 0.009 be	3.420 ± 0.042 fgh	4.310 ± 0.070 ad	7.487 ± 0.059 lmn	8.647 ± 0.032 ei
19928 × 19924	999.60 ± 02.08 fg	1006.70 ± 03.26 fg	33.14 ± 0.28 qr	22.62 ± 0.20 tuv	12.79 ± 0.40 gk	10.30 ± 0.16 qt	116.33 ± 2.40 gn	118.6 7 ± 2.40 dn	16.67 ± 0.33 gn	20.67 ± 0.88 dn	4.60 ± 0.06 in	4.53 ± 0.20 in	1.540 ± 0.029 fgh	1.833 ± 0.044 ad	3.427 ± 0.048 fgh	4.417 ± 0.064 ab	7.447 ± 0.052 no	8.717 ± 0.045 ag
19228 × 19232	981.47 ± 05.56 gk	998.57 ± 02.60 g	58.93 ± 0.35 hi	44.42 ± 1.12 mn	12.02 ± 0.23 in	13.30 ± 0.24 efg	119.33 ± 2.73 cn	123.6 7 ± 2.73 ah	19.00 ± 0.58 cn	22.33 ± 0.33 ah	5.53 ± 0.09 ef	6.13 ± 0.12 cd	1.397 ± 0.038 jkl	1.830 ± 0.040 ad	3.460 ± 0.015 fg	4.283 ± 0.074 bcd	7.553 ± 0.029 jn	8.633 ± 0.022 fi
19228 × 19225	937.33 ± 10.54 lmn	979.53 ± 00.92 gk	34.09 ± 0.56 qr	37.85 ± 0.93 op	14.39 ± 0.56 cd	15.04 ± 0.43 bc	113.33 ± 2.96 mno	123.0 0 ± 2.65 bi	17.00 ± 0.58 mno	21.67 ± 0.33 bi	4.50 ± 0.17 io	5.33 ± 0.12 efg	1.570 ± 0.055 f	1.787 ± 0.035 be	3.407 ± 0.027 fgh	4.357 ± 0.104 ad	7.547 ± 0.078 jn	8.727 ± 0.022 af

19228 × 15382	1030.7 0 ± 19.35 ef	1121.37 ± 06.96 c	32.05 ± 0.84 r	58.25 ± 0.63 hij	11.12 ± 0.51 nr	12.83 ± 0.42 gj	116.00 ± 4.16 hn	124.0 0 ± 3.21 ag	14.67 ± 0.88 hn	21.33 ± 1.20 ag	4.30 ± 0.12 kq	4.67 ± 0.13 hi	1.427 ± 0.033 il	1.803 ± 0.047 be	3.400 ± 0.050 fgh	4.310 ± 0.083 ad	7.480 ± 0.017 lo	8.687 ± 0.064 bi
19224 × 19228	988.03 ± 03.23 ghi	1003.10 ± 00.60 fg	40.88 ± 1.63 no	48.12 ± 0.50 l	13.12 ± 0.19 fgh	14.16 ± 0.08 cde	116.00 ± 3.51 hn	127.0 0 ± 2.65 abc	15.00 ± 0.58 hn	22.00 ± 1.53 abc	4.50 ± 0.15 io	4.53 ± 0.18 in	1.553 ± 0.026 fg	1.770 ± 0.029 be	3.413 ± 0.052 fgh	4.340 ± 0.052 ad	7.460 ± 0.020 mno	8.763 ± 0.069 ae
19224 × 19232	736.20 ± 08.00 r	825.33 ± 09.70 q	61.59 ± 1.92 gh	56.49 ± 0.19 ijk	15.57 ± 0.35 b	15.60 ± 0.56 b	121.33 ± 3.71 cl	126.0 0 ± 3.51 ad	15.00 ± 1.15 cl	22.00 ± 1.15 ad	4.70 ± 0.06 hk	5.33 ± 0.09 efg	1.450 ± 0.029 gk	1.753 ± 0.023 cde	3.420 ± 0.042 fgh	4.440 ± 0.108 ab	7.490 ± 0.067 kn	8.690 ± 0.025 ai
19224 × 19225	843.37 ± 34.41 q	991.40 ± 01.79 gh	91.37 ± 1.59 c	55.10 ± 1.43 jk	10.95 ± 0.15 or	17.27 ± 0.04 a	121.67 ± 3.53 ck	117.3 3 ± 3.28 fn	15.00 ± 0.58 ck	20.67 ± 0.88 fn	3.63 ± 0.18 sv	3.30 ± 0.12 vwx	1.580 ± 0.029 f	1.740 ± 0.031 de	3.457 ± 0.018 fg	4.347 ± 0.052 ad	7.570 ± 0.030 jm	8.687 ± 0.055 bi
19224 × 15382	884.60 ± 03.55 p	924.67 ± 02.12 mno	26.39 ± 0.59 s	24.56 ± 0.38 st	10.45 ± 0.46 ps	10.50 ± 0.21 ps	120.00 ± 0.58 cn	125.3 3 ± 1.86 ae	13.67 ± 0.88 cn	19.33 ± 0.33 ae	4.30 ± 0.12 kq	5.77 ± 0.26 de	1.250 ± 0.036 m	1.837 ± 0.030 ad	3.493 ± 0.038 ef	4.407 ± 0.041 abc	7.360 ± 0.042 o	8.660 ± 0.067 di
19232 × 19228	961.77 ± 07.16 h1	943.60 ± 09.03 l m	21.12 ± 0.35 tw	20.69 ± 0.41 uvw	8.22 ± 0.14 xyz	8.89 ± 0.43 ux	107.67 ± 3.18 op	125.6 7 ± 2.03 ae	16.00 ± 1.00 op	18.00 ± 0.58 ar	2.80 ± 0.12 xy	2.83 ± 0.20 xy	1.373 ± 0.062 kl	1.833 ± 0.019 ad	3.310 ± 0.030 gh	4.373 ± 0.094 ad	7.530 ± 0.035 jn	8.600 ± 0.029 ghi
19232 × 19224	886.83 ± 02.13 p	1006.93 ± 04.98 fg	14.99 ± 0.17 za	36.47 ± 1.19 pq	9.83 ± 0.29 stu	11.44 ± 0.71 lp	102.00 ± 4.04 p	112.3 3 ± 2.03 no	13.67 ± 0.33 p	19.33 ± 0.88 no	3.50 ± 0.15 tw	3.53 ± 0.15 tw	1.380 ± 0.058 jkl	1.797 ± 0.033 be	3.390 ± 0.052 fgh	4.347 ± 0.082 ad	7.480 ± 0.050 lo	8.810 ± 0.029 a
19232 × 19225	955.60 ± 10.75 jm	1003.97 ± 06.82 fg	16.48 ± 0.22 yz	32.85 ± 0.54 r	7.51 ± 0.46 z	9.42 ± 0.40 tuv	113.67 ± 2.85 lo	119.6 7 ± 1.45 cn	14.67 ± 1.20 lo	16.00 ± 1.00 cn	2.73 ± 0.20 y	2.73 ± 0.35 y	1.460 ± 0.049 gk	1.750 ± 0.046 cde	3.420 ± 0.046 fgh	4.237 ± 0.055 cd	7.570 ± 0.030 jm	8.673 ± 0.028 ci
19232 × 15382	952.13 ± 05.78 klm	1078.30 ± 34.55 d	11.90 ± 0.23 a	66.96 ± 1.54 e	8.93 ± 0.53 ux	8.98 ± 0.39 ux	119.00 ± 4.04 dn	124.0 0 ± 3.61 ag	15.00 ± 0.58 dn	21.33 ± 0.88 ag	2.80 ± 0.06 xy	3.90 ± 0.17 pu	1.457 ± 0.023 gk	1.783 ± 0.049 be	3.447 ± 0.035 fg	4.370 ± 0.089 ad	7.510 ± 0.021 jn	8.723 ± 0.038 af
19225 × 19228	986.13 ± 06.69 gj	1120.63 ± 10.36 c	17.12 ± 0.12 xyz	32.67 ± 0.89 r	12.20 ± 0.51 hl	11.97 ± 0.46 jn	121.33 ± 4.26 cl	121.3 3 ± 1.20 cl	18.00 ± 0.58 cl	18.33 ± 0.33 cl	2.57 ± 0.15 y	4.13 ± 0.18 ms	1.460 ± 0.035 gk	1.800 ± 0.021 be	3.483 ± 0.050 fg	4.383 ± 0.090 ad	7.453 ± 0.026 mno	8.753 ± 0.048 af

19225 × 19224	1001.2 7 ± 03.65 fg	1141.97 ± 16.88 bc	66.04 ± 1.47 ef	44.72 ± 0.50 lm	11.41 ± 0.16 lp	14.33 ± 0.33 cd	123.33 ± 2.73 bh	123.0 0 ± 1.53 bi	17.33 ± 0.33 bh	19.67 ± 1.67 bi	3.67 ± 0.12 rv	4.80 ± 0.23 hk	1.440 ± 0.006 hl	1.813 ± 0.019 be	3.457 ± 0.033 fg	4.373 ± 0.070 ad	7.543 ± 0.020 jn	8.777 ± 0.037 ad
19225 × 19232	1000.1 7 ± 03.21 fg	1150.50 ± 02.10 abc	44.24 ± 1.55 mn	80.10 ± 2.26 d	13.87 ± 0.32 def	12.98 ± 0.27 fi	123.00 ± 1.53 bi	115.0 0 ± 1.73 jo	15.67 ± 0.33 bi	21.00 ± 0.58 jo	3.07 ± 0.09 wxy	4.70 ± 0.21 hk	1.380 ± 0.023 jkl	1.807 ± 0.028 be	3.363 ± 0.049 fgh	4.303 ± 0.058 bcd	7.610 ± 0.053 jk	8.700 ± 0.035 ah
19225 × 15382	978.63 ± 09.98 gk	1003.53 ± 02.98 fg	62.99 ± 1.14 fg	44.49 ± 0.78 m	11.81 ± 0.26 ko	11.70 ± 0.48 lo	125.67 ± 1.45 ae	129.6 7 ± 3.84 ab	20.00 ± 0.58 ae	23.00 ± 0.58 ab	6.57 ± 0.18 abc	6.90 ± 0.15 a	1.520 ± 0.035 fi	1.870 ± 0.025 ab	3.400 ± 0.021 fgh	4.393 ± 0.062 ad	7.623 ± 0.048 j	8.770 ± 0.017 ad
15382 × 19228	959.33 ± 08.94 il	1128.00 ± 11.29 c	79.18 ± 1.20 d	98.82 ± 1.29 b	10.52 ± 0.23 ps	12.14 ± 0.25 hm	115.33 ± 1.76 io	123.3 3 ± 1.33 bh	18.00 ± 0.58 io	19.33 ± 0.33 bh	2.63 ± 0.12 y	3.83 ± 0.33 qu	1.440 ± 0.058 hl	1.853 ± 0.041 abc	3.420 ± 0.040 fgh	4.313 ± 0.070 ad	7.597 ± 0.046 jkl	8.703 ± 0.020 ah
15382 × 19224	910.63 ± 04.35 nop	988.63 ± 05.56 ghi	92.11 ± 0.26 c	120.8 7 ± 6.29 a	9.40 ± 0.22 tw	10.18 ± 0.29 rst	123.67 ± 2.33 ah	131.3 3 ± 2.73 a	20.33 ± 0.88 ah	23.00 ± 0.58 a	6.33 ± 0.12 bc	6.67 ± 0.12 ab	1.540 ± 0.058 fgh	1.860 ± 0.055 ab	3.370 ± 0.031 fgh	4.310 ± 0.074 ad	7.473 ± 0.052 mno	8.793 ± 0.023 abc
15382 × 19232	893.13 ± 03.3 1op	996.50 ± 01.45 g	18.72 ± 0.30 wxy	21.27 ± 0.91 tw	8.31 ± 0.10 xyz	12.07 ± 0.40 in	121.00 ± 3.79 cm	122.0 0 ± 2.00 bj	20.33 ± 0.33 cm	20.00 ± 0.58 bj	6.27 ± 0.09 bcd	6.57 ± 0.20 abc	1.483 ± 0.034 fj	1.847 ± 0.030 abc	3.427 ± 0.050 fgh	4.437 ± 0.093 ab	7.537 ± 0.035 jn	8.750 ± 0.067 af
15382 × 19225	1010.2 3 ± 05.66 fg	1142.80 ± 06.16 bc	24.10 ± 0.11 stu	22.72 ± 0.43 tuv	7.54 ± 0.18 yz	8.40 ± 0.26 wz	119.33 ± 2.40 cn	124.6 7 ± 3.28 af	16.33 ± 0.33 cn	19.67 ± 1.20 af	4.10 ± 0.15 ns	3.77 ± 0.32r v	1.477 ± 0.015 fk	1.927 ± 0.027 a	3.457 ± 0.028 fg	4.487 ± 0.121 a	7.537 ± 0.063 jn	8.797 ± 0.058 ab

PAR = photosynthetic active radiation; NPR = net photosynthesis rate; TR = transpiration rate; FYP = fruit yield per plant; NFP = No. of fruits per plant; FW = fruit weight; PC = protein contents; DFC = dietary fiber contents; CHO = carbohydrate contents

Table 3a: General Combining Ability (GCA) effects of the parents for all the recorded agronomic parameters in the study

	PAR		NPR		TR		FYP		NFP		FW		PC		DFC		CHO	
Parents	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water
19228	31.877	12.139	-6.817	-4.609	0.417	0.223	-1.84	0.347	0.207	-0.527	-0.125	-0.088	0.00001	0.0001	0.003	-0.112	-0.014	-0.012
19224	-39.54	-27.237	7.496	5.838	-0.158	0.821	0.193	-0.887	-0.36	0.24	0.215	0.092	-0.01	0.022	-0.024	0.018	-0.038	0.009
19232	-17.39	-23.641	-9.884	-4.911	-0.736	-0.188	-1.34	-0.887	-0.293	-0.427	-0.035	-0.081	-0.047	0.015	-0.01	0.02	0.025	-0.026
19225	17.093	25.583	2.829	-5.643	0.491	-0.062	2.16	-0.087	-0.093	0.107	-0.371	-0.315	0.022	0.009	0.022	0.02	0.031	0.008
15382	7.96	13.156	6.375	9.326	-0.014	-0.795	0.827	1.513	0.54	0.607	0.315	0.392	0.015	0.028	0.009	0.02	-0.005	0.02

PAR = photosynthetic active radiation; NPR = net photosynthesis rate; TR = transpiration rate; FYP = fruit yield per plant; NFP = No. of fruits per plant;

FW = fruit weight; PC = protein contents; DFC = dietary fiber contents; CHO = carbohydrate contents

Table 3b: Specific Combining Ability (SCA) effects of the crosses for all the recorded agronomic parameters in the study

	PAR		NPR		TR		FYP		NFP		FW		PC		DFC		CHO	
Direct Crosses	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water
19928 × 19924	35.28	-32.019	-2.884	-9.961	2.048	-0.693	-0.16	0.72	-0.707	1.327	0.318	-0.152	0.084	0.02	0.024	0.149	-0.009	0.045
19228 × 19232	-9.07	-69.433	17.508	-2.027	-0.212	-0.815	-1.293	2.553	0.893	0.827	0.185	-0.029	-0.021	0.042	-0.025	0.098	0.017	-0.043
19228 × 19225	-53.437	-39.656	-9.623	1.41	1.742	1.464	-0.96	-0.747	0.693	0.127	-0.112	0.455	0.04	-0.02	0.003	0.125	-0.031	0.046
19228 × 15382	-11.02	47.371	16.837	29.718	-0.232	1.182	-1.293	-0.847	-1.107	-0.04	-0.865	-0.735	-0.034	-0.004	-0.019	0.059	0.043	-0.011
19224 × 19232	-97.754	-85.006	1.46	1.451	2.943	1.01	-5.16	-1.713	-1.707	0.56	-0.222	-0.259	-0.001	0.007	0.022	0.032	-0.016	0.069
19224 × 19225	-21.437	16.321	29.164	5.615	0.198	3.166	2.173	-1.513	-0.073	-0.473	-0.335	0.409	0.025	-0.015	0.042	-0.015	0.049	0.017
19224 × 15382	-37.003	-81.286	6.164	13.451	-0.553	-1.566	2.84	5.053	0.127	0.027	0.645	1.051	-0.083	0.038	0.03	-0.024	-0.055	0
19232 × 19225	11.98	23.274	-1.803	22.926	0.288	-0.423	-0.46	-4.347	-1.14	-1.473	-0.835	-0.569	-0.008	-0.021	-0.038	-0.107	0.02	0.007
19232 × 15382	-34.137	-4.133	-20.394	-4.4	-1.279	-0.37	2.54	-0.28	0.727	0.193	0.111	0.241	0.049	-0.003	0.021	0.019	-0.01	0.045
19225 × 15382	3.18	-17.589	-4.875	-14.179	-1.451	-0.968	1.54	3.087	1.027	0.327	1.248	0.575	0.008	0.056	-0.019	0.041	0.04	0.058

PAR = photosynthetic active radiation; NPR = net photosynthesis rate; TR = transpiration rate; FYP = fruit yield per plant; NFP = No. of fruits per plant; FW = fruit weight; PC = protein contents; DFC = dietary fiber contents; CHO = carbohydrate contents

Table 3c: Reciprocal Combining Ability (RCA) effects of the crosses for all the record agronomic parameters in the study

	PAR		NPR		TR		FYP		NFP		FW		PC		DFC		CHO	
Indirect Crosses	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water	Control	Waste water
19224 × 19228	5.783	1.8	-3.872	-12.753	-0.167	-1.932	0.167	-4.167	0.833	-0.667	0.05	0.0005	-0.007	0.032	0.007	0.038	-0.007	-0.023
19232 × 19228	9.85	27.483	18.903	11.868	1.898	2.203	5.833	-1	1.5	2.167	1.367	1.65	0.012	-0.002	0.075	-0.045	0.012	0.017
19232 × 19224	-75.317	-90.8	23.302	10.013	2.872	2.083	9.667	6.833	0.667	1.333	0.6	0.9	0.035	-0.022	0.015	0.047	0.005	-0.06
19225 × 19228	-24.4	-70.55	8.485	2.593	1.095	1.535	-4	0.833	-0.5	1.667	0.967	0.6	0.055	-0.007	-0.038	-0.013	0.047	-0.013
19225 × 19224	-78.95	-75.55	12.665	5.192	-0.233	1.472	-0.833	-2.833	-1.167	0.5	-0.017	-0.75	0.07	-0.037	0	-0.013	0.013	-0.045
19225 × 19232	-22.983	-73.267	-13.878	-23.623	-3.178	-1.78	-4.467	2.333	-0.5	-2.5	-0.167	-0.983	0.04	-0.028	0.028	-0.033	-0.02	-0.013
15382 × 19228	35.683	-3.317	-23.565	-20.287	0.297	0.343	0.333	0.333	-1.667	1	0.833	0.417	-0.007	-0.025	-0.01	-0.002	-0.058	-0.008
15382 × 19224	-13.017	-31.983	-32.858	-48.153	0.528	0.16	-1.833	-3	-3.333	-1.833	-0.017	-0.45	-0.145	-0.012	0.062	0.048	-0.057	-0.067
15382 × 19232	29.5	40.9	-3.41	22.843	0.31	-1.547	-1	1	-2.667	0.667	-1.733	-1.333	-0.013	-0.032	0.01	-0.033	-0.013	-0.013
15382 × 19225	-15.8	-69.633	19.445	10.888	2.135	1.648	3.167	2.5	1.833	1.667	1.233	1.567	0.022	-0.028	-0.028	-0.047	0.043	-0.013

PAR = photosynthetic active radiation; NPR = net photosynthesis rate; TR = transpiration rate; FYP = fruit yield per plant; NFP = No. of fruits per plant; FW = fruit weight; PC = protein contents; DFC = dietary fiber contents; CHO = carbohydrate content