

Genetics of fruit quality in okra (*Abelmoschus esculentus*) under waste water

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Abstract: A field experiment consists 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 2010-2011. All possible crosses were made to obtain F₁ seed following diallel analysis design. The F₁ seed along with their parents was evaluated. The experiment was laid out in randomized complete block design. Data was collected for some quality traits as protein content, dietary fiber content and carbohydrates. The numerical approaches demonstrated that dietary fiber contents and carbohydrate contents under wastewater irrigation were ruled by over-dominance with non-additive type of gene action while partial dominance was observed in protein contents under wastewater irrigation, dietary fiber contents and carbohydrates under normal irrigation water which suggested that early selection might end up in improving these genotypes. Non-allelic interaction or epistasis was absent for all the traits studied. It indicated that selection in early generations for these traits would be difficult.

Keywords: Gene Action, Okra, Diallel, Fruit Quality

1. Introduction

Okra (*Abelmoschus esculentus*) is one of important vegetable crop in the Malvaceae family and very popular in the world. It is a tropical to subtropical crop and is sensitive to frost, low temperature, water logging and drought conditions. Cultivars from different countries have certain adapted distinguishing characteristics specific to the country to which they belong (Siemonsma, 1982). Its fruits are rich in vitamins, calcium, potassium and other mineral matters (Camciuc *et al.*, 1981). The mature okra seed is a good source of oil and protein (Oyelade *et al.*, 2003) and has been known to have superior nutritional quality. Okra seed oil is rich in unsaturated fatty acids such as linoleic acid (Savello *et al.*, 1980), which is essential for human nutrition.

Pakistan is an agricultural country and agriculture is the main stay and lynchpin of its food security and economic stability. Water is life blood of agriculture. About 68% of

the land area of the country falls in arid and semiarid regions where evapotranspiration exceeds precipitation. Rainfall is low, uncertain and erratic. Underground water is unfit for irrigation. In developing countries, fast-growing urban populations are demanding more fresh water and food, while generating greater volumes of wastewater (WW). Due to the lack of comprehensive WW management, a major portion of the WW pollutes natural water bodies. For sustainable crop production, adequate level of inputs like inorganic fertilizers, manure and irrigation water finds great significance and their improper management has been the cause of land degradation and environmental pollution. The WW contains a lot of nutrients which may increase the yield of crop and at the same time may substitute or lower the fertilizer requirement of the crop and simultaneously serve as the source of water as well (Saima Kausar, 2011).

Farmers using 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. Limitations are identified as:

nutrient management, choice of crops, irrigation methods, health risk regulation and land and water rights. In some cases the most viable approach is to acknowledge irrigation as a land-based treatment method, which requires sharing of costs and responsibilities between WW producers, government institutions and farmers (Martijn, 2005).

Due to rapid urbanization and growing WW volumes, WW is widely used as a low-cost alternative to conventional irrigation water; it supports livelihoods and generates considerable value in urban and peri-urban agriculture despite the health and environmental risks associated with this practice. Though pervasive, this practice is largely unregulated in low-income countries, and the costs and benefits are poorly understood (Scott *et al.*, 2004).

Contamination of vegetables with heavy metals present in WW e.g, cadmium (Cd), copper (Cu), nickel (Ni), iron, lead (Pb), zinc (Zn), cobalt and chromium (Cr), and the human health risks, were determined, where sewage water is used in vegetables farming (Mapanda, 2006). These heavy metals not only effects plant growth but also contaminate the soils. 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.

The breeding programmes 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 use of municipal and industrial wastewater for irrigation is well recognized (Steel and Beg, 1954) and has become an important part of industrial and sewage wastewater disposal programmes. Such controlled use of waste water can provide substantial benefits and the development of low cost processes coupled with this reuse of effluent in agriculture offers one of the most suitable options for managing wastewaters.

2. Materials & Methods

2.1. Germplasm Development

A field experiment consisted 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 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 analysis design (Table 1).

Genotypes used as parents

1) 19228, 2) 19224, 3) 19232, 4) 19225, 5) 15382

Table 1: List of crosses (Direct and indirect) made.

1	19228 x 19224	11	19232 x 19225
2	19228 x 19232	12	19232 x 15382
3	19228 x 19225	13	19225 x 19228
4	19228 x 15382	14	19225 x 19224
5	19224 x 19228	15	19225 x 19232
6	19224 x 19232	16	19225 x 15382
7	19224 x 19225	17	15382 x 19228
8	19224 x 15382	18	15382 x 19224
9	19232 x 19228	19	15382 x 19232
10	19232 x 19224	20	15382 x 19225

The F₁ seed along with their parents was evaluated. The experiment was laid out following randomized complete block design with three replications. Each replicate possessed 25 genotypes. Parents and crosses evaluation was made by applying two treatments, one was normal irrigation water and another was wastewater irrigation to check the effect of wastewater on growth and productivity of okra. Standard plant to plant and row to row distance was maintained. At maturity 10 guarded plants from each genotype were selected at random and data was recorded for some physiological, morphological, and quality parameters as follows. All the measurements of above mentioned parameters were made on colorless clear days between 11:00 and 13:00 solar time.

2.2. Quality Traits

1. Protein contents (%)
2. Dietary fiber contents (%)
3. Carbohydrates (%)

3. Results and 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 was recorded 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:

3.1. Protein Contents (%)

Analysis of variance indicated highly significant differences among treatments, genotypes and genotype x treatment interaction for protein contents in both normal

and wastewater irrigated treatments (Table 2.1). The analysis of variance under both treatments indicated that the percentage (%) of proteins was higher under wastewater irrigated treatment and lower under normal irrigation (Table 2.2).

Table 2.1: Analysis of variance for Protein contents (%).

Source of variation	Degrees of freedom	Sum of squares	Mean squares
Replication	2	0.00135	0.00067
Treatment	1	4.63936	4.63936**
Genotype	24	0.30148	0.01256**
Treatment×Genotype	24	0.31674	0.01320**
Error	98	0.41845	0.00427
Total	149	5.67738	

* = Significant ($P > 0.05$); ** = Highly significant ($P > 0.01$)

Table 2.2: Mean squares for protein contents under normal and waste water irrigated treatments.

Source of variation	Degree of freedom	Mean squares	
		Control	Waste water
Replication	2	2.68464	5.963399
Treatment	24	1.871444**	7.041781*
Error	48	5.007888	3.601658
Total	74		

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 2.3). Among parents, 19225 was somehow good combiner compared to other parents. Among crosses, 19228 x 19224 was good specific combiner 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 significant. The effect of non-additive gene action was not dominant (Table 2.3). Among the parents, 15382 was a good general combiner. Among the crosses, 19225 x 15382 was a good specific combiner.

Table 2.3: Mean squares for combining ability for Protein contents.

Source of variation	Degree of freedom	Mean squares	
		Control	Waste water
GCA	4	7.566088**	3.960556*
SCA	10	5.417782**	2.801486**
RCA	10	6.529442**	1.246665**
Error	48	1.669296	1.200553

GCA = General combining ability
SCA = Specific combining ability
RCA = Reciprocal combining ability

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), Shivagamasundari *et al.* (1992) and Wankhade *et al.* (1995).

3.2. Dietary Fiber Contents (%)

Results obtained in analysis of variance indicated highly significant differences among treatments, genotypes and genotype x treatment interaction for dietary fiber contents in both normal and wastewater irrigated treatments (Table 3.1). 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 (Table 3.2).

Table 3.1: Analysis of variance for dietary fibre contents (%).

Source of variation	Degrees of freedom	Sum of squares	Mean squares
Replication	2	0.0142	0.0071
Treatment	1	30.8267	30.8267**
Genotype	24	0.9709	0.0405**
Treatment×Genotype	24	0.8522	0.0355**
Error	98	1.1805	0.0120
Total	149	33.8444	

* = Significant ($P > 0.05$); ** = Highly significant ($P > 0.01$)

Table 3.2: Mean squares for dietary fiber contents under normal and waste water irrigated treatments.

Source of variation	Degree of freedom	Mean squares	
		Control	Waste water
Replication	2	5.388828	1.513524
Treatment	24	8.431273*	6.752618**
Error	48	4.739136	1.949486
Total	74		

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 3.3). Among parents, 19225 was a good general combiner compared to others. Among crosses, 19224 x 19225 was a good specific combiner and had a potential to be used in further breeding programmes.

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 3.3). Among the parents, 15382 was a good general combiner for fiber contents. Among the crosses, 19228 x 19224 was a good specific combiner.

Table 3.3: Mean squares for combining ability for dietary fibre contents.

Source of variation	Degree of freedom	Mean squares	
		Control	Waste water
GCA	4	3.120157 N.S	4.048822**
SCA	10	2.899528**	.0352837**
RCA	10	2.594439**	2.553336**
Error	48	1.579712	6.498287

GCA = General combining ability
 SCA = Specific combining ability
 RCA = Reciprocal combining ability

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 Chaudhari *et al.* (1991) and Wankhade *et al.* (1995).

3.3. Carbohydrates (%)

Analysis of variance indicated highly significant differences among treatments, genotypes and genotype x treatment interaction for carbohydrates in both normal and wastewater irrigated treatments (Table 4.1). The mean values showed differences among genotypes and also indicated the significant effect of waste water on carbohydrate contents of all okra genotypes (Table 4.2).

Table 4.1: Analysis of variance for Carbohydrates (%).

Source of variation	Degrees of freedom	Sum of squares	Mean squares
Replication	2	0.0083	0.0042
Treatment	1	52.5459	52.5459**
Genotype	24	0.3210	0.0134**
Treatment×Genotype	24	0.2894	0.0121**
Error	98	0.5437	0.0055
Total	149	53.7083	

* = Significant (P>0.05); ** = Highly significant (P>0.01)

Table 4.2: Mean squares for carbohydrates under normal and waste water irrigated treatments.

Source of variation	Degree of freedom	Mean squares	
		Control	Waste water
Replication	2	3.297353	.0110328
Treatment	24	1.052597*	1.478116**
Error	48	5.481235	5.396284
Total	74		

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 4.3).

Among the parents, 19225 was a potential parent and good general combiner. Among the crosses, 19224 x 19225 was a good specific combiner.

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 4.3). Among the parents, 15382 was a good general combiner and potential parent. Among the crosses, 19224 x 19232 was a good genotype for specific combining ability (SCA).

Table 4.3: Mean squares for combining ability for Carbohydrates.

Source of variation	Degree of freedom	Mean squares	
		Control	Waste water
GCA	4	8.062479 N.S	3.352078 N.S
SCA	10	2.970024**	8.143061**
RCA	10	2.326114**	2.334452**
Error	48	1.827078	1.798761

GCA = General combining ability
 SCA = Specific combining ability
 RCA = Reciprocal combining ability

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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