

Genetic analysis of quality traits in Okra (*Abelmoschus esculentus*) under waste water irrigation

Najaf Ali, Ali Anwaar*, Muhammad Sheraz, Tayyab Nawaz Khan

Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan.

*Corresponding author: alifatehpur29@gmail.com

Abstract

A field experiment consists of five genotypes of okra (19228, 19224, 19232, 19225 and 15382) 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 (protein content, dietary fiber content and carbohydrates) and morphological traits (pods weight, no. of pods/plant and fruit yield per plant) and physiological traits (transpiration rate, photosynthesis rate and photosynthetic active radiation). 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 the selection in early generations for these traits would be difficult. Photosynthetic active radiation and net photosynthetic rate both was controlled by additive gene action. Transpiration rate, fruit yield, no. of pods per plant and fruit weight was controlled by non-additive gene action. Rate of morphological and physiological traits under waste water irrigation was high.

Keywords: Genetic analysis, genetics, quality, okra, *Abelmoschus esculentus* and waste water

Introduction

Okra (*Abelmoschus esculentus* L.) is one of important vegetable crop in *Malvaceae* family. It is tropical to subtropical crop. It is sensitive to frost, low temperature, water logging and drought conditions. Cultivars from different countries have adapted some traits specific to the country to which they belong (Siemonsma, 1982). The total area under cultivation is 1148.0 ha and total production is 8,900.43 thousand tons in the world (anonymous, 2016). Okra is an important vegetable, mostly grown in India, Nigeria, Mali, Pakistan, Sudan, Egypt, Malaysia, Mexico and Ghana. Though, Okra is not grown in Europe and North America but most of the people of these countries have been started liking this vegetable due to the presence of good amount of vitamin A, folic acid, carbohydrate, phosphorus, magnesium, potassium and other minerals (Camciuc *et. al.*, 1981). The okra seed is a good source of protein and oil. Okra seed oil have unsaturated fatty acid such as linoleic acid (Savello *et. al.*, 1980).

Pakistan is an agricultural country. About 68% of the land areas of the country is in arid and semi-arid region. Rainfall is low and fickle. Underground water is not good for irrigation. Due to the lack of comprehensive waste water management, a major portion of the waste water pollutes natural water bodies. The waste water contains lot of nutrients which may increase the yield of crops 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 waste water in developing countries are often limited in adopting suitable measurements 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 waste water producers, government institutions and farmers (Martijn, 2005).

Contamination of vegetables with heavy metals present in waste water e.g. cadmium, copper, nickel, iron, lead, zinc, cobalt and chromium and the human health risks, were determined, where sewage water is used in vegetables farming (Mapanda, 2006). These heavy metals not only affect the plant growth but also contaminate the soil. Many technologies used to get rid 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. Diallel analysis gives genetic information on quantitative traits to carry out

breeding programs (Viana *et. al.*, 2001). From diallel analysis, plant breeders are able to gather information on reciprocal and maternal effects, heterosis, 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 selection set of parents (Murray *et. al.*, 2003) and have been used to study various traits in many crops.

Much work has been done on various kinds of industrial effluents and municipal sewage waste water to study the effect on various crop plants. In view of above mentioned subject, the present study was carried out to assess the performance of genotypes under urban wastewater and canal water irrigation against different physiological, morphological and quality standards i.e. photosynthetic active radiation, net photosynthesis rate, transpiration rate, fruit yield per plant, no. of pods per plant, pod weight, protein contents, dietary fiber contents and carbohydrate percentage and gene action controlling these traits.

Materials and Methods

Germplasm Development

A field experiment consisted of Okra's five genotypes was conducted in the research area of Department of Plant Breeding and Genetics of University of Agriculture Faisalabad. The germplasm was collected from Ayub Agriculture Research Institute Faisalabad. Genotypes used as parents were 19228, 19224, 19232, 19225 and 15382, while crosses (Direct and Indirect) made were 19228 x 19224, 19232 x 19225, 19228 x 19232, 19232 x 15382, 19228 x 19225, 19225 x 19228, 19228 x 15382, 19225 x 19224, 19224 x 19228, 19225 x 19232, 19224 x 19232, 19225 x 15382, 19224 x 19225, 15382 x 19228, 19224 x 15382, 15382 x 19224, 19232 x 19228, 15382 x 19232, 19232 x 19224 and 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 was possessed 25 genotypes. Parents and crosses evaluation was made by applying two treatments, one was normal irrigation water (NI) and another was waste water (WW) irrigation to check the effect of waste water 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 are given below. Data for Photosynthetic Active Radiation (PAR), Net Photosynthesis Rate (NPR), Transpiration Rate (TR), No of Pods per Plants (gm) (NPPP), Fruit Weight (gm) (FW), Protein Content (%) (PC), Dietary Fiber Contents (%) (DFC), Carbohydrates (%) (C) were collected.

Statistical Analysis

The statistical data were subjected to ANOVA for all characters under study to observe the significance among various F₁ hybrids and their parental lines. The characters showing significant differences among genotypes were further subjected to combining ability analysis using Method 1 developed by Griffing (1956). The various formulae used for calculation of GCA and SCA and Reciprocal effects.

General combining ability effects:

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

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:

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

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 $X_{i.}$

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

$X_{j.}$ = Value of reciprocal F₁s of $X_{.j}$.

$X_{..}$ = 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 F₁s resulting from crossing the i^{th} parent with j^{th} parent.

X_{ji} = Mean values of F₁s resulting from crossing the j^{th} parent with i^{th} parent.

Total genetic variance of ANOVA was partitioned into variances due to general combining ability, specific combining ability and reciprocal effects.

Results and Discussion

The combining ability of diallel crossing technique was done using technique produced by Griffings, Model 1, (1956) for both treatments. Data being recorded was subjected to analysis of variance (ANOVA) technique produced by Steel *et al.* (1997). Estimated polygenic characters of okra from both the treatments were presented and discussed below:

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

Analysis of variance show highly significant differences among treatments, genotypes and interaction PAR in both normal and WW irrigated treatments (Table 3 and 4). The PAR was higher under WW irrigated treatment.

The combining ability analysis of normal irrigated treatment indicated that the PAR was controlled by additive and non-additive gene actions because GCA and SCA were highly significant. 19228 was the best general combiner for PAR among parents and 19228 $\times$ 19224 was the best specific combination among the crosses (Table 1 and 2).

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

Analysis of variance of this character showed the highly significant differences among all the treatments, genotypes and their interaction for net PR in both treatments (Table 3 and 4). The mean value analysis for variance under both treatments showed the 13 genotypes had higher values for net PR under WW irrigation and the other remaining genotypes had higher values under normal irrigation.

The combining ability test under normal irrigation indicated that the net PR was controlled by additive and non-additive gene actions as GCA and SCA were highly significant. Additive gene action was masked by non-additive gene action. 19224 and 19224 $\times$ 19225 was the best combiner among parent and crosses for net PR. The net PR was controlled by both gene actions and GCA and SCA were highly significant but additive gene action was masked. 15382 was good general combiner and 19225 $\times$ 15382 was good specific combiner for net PR (Table 1 and 2).

Higher magnitude of SCA than GCA indicated the predominance of non-additive gene action was reported by Veeraraghavathatham and Irulappan (1991).

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

ANOVA indicated highly significant differences among all genotypes in both treatments. When effects of both treatments were studied it was determined that transpiration rate was increased under WW irrigation (Table 3 and 4).

Combining ability test under normal irrigated treatment that the TR was controlled by additive and non-additive gene action as showed by higher values of GCA and SCA but the effect of additive gene action was masked. 19225 was the best general combiner and 19224 $\times$ 19232 was the good specific combiner among parents and crosses (Table 1 and 2).

Combining ability analysis showed that the transpiration rate was controlled by non-additive gene under WW irrigated treatment. So the TR was increased under WW treatment.

Fruit yield per plant:

The fruit yield was higher under WW irrigation except the genotype 19225 $\times$ 19232 with lower fruit yield. The overall fruit yield of genotypes 19225 $\times$ 15382, 19232 $\times$ 19224 was maximum and minimum under both treatments (Table 3 and 4). The CA analysis of fruit yield under normal irrigated treatment indicated that the SCA was highly significant which showed that the non-additive gene action was stronger in fruit yield as compared to additive gene action that indicated by significant value of GCA. The fruit yield under WW irrigated treatment indicated that SCA was highly significant which showed that the fruit yield was controlled by non-additive gene action and additive gene action was absent because GCA was non-significant. When we compare the both treatments it was concluded that fruit yield was controlled by non-additive gene action the cross 19224 $\times$ 15382 was the best specific combiner under both treatments (Table 1 and 2).

No. of pods per plant:

The mean values of ANOVA for both treatments indicated that the no. of pods per plant was higher under WW irrigated treatment except the genotype 15382 $\times$ 19232 which showed higher no. of pods under normal irrigation. Under both treatments genotype 15382 $\times$ 19224 had maximum and 19232 $\times$ 19225 with minimum no. of pods. The CA analysis showed that in both treatments the no. of pods per plant was controlled by non-additive gene action. SCA in normal irrigated treatment was highly significant and additive gene action was absent as GCA was non-significant (Table 1). Among the crosses 19225 $\times$ 15382 was the best specific combiner for further breeding programs as SCA was highly significant and additive gene action also present but it was not dominant as showed in (Table b). Among the crosses, 19228 $\times$ 19224 was the best specific combiner. It was cleared that the no. of pods per plant was increased under wastewater irrigation and it was controlled by non-additive gene action. The parent 15382 was the best general combiner under both treatments.

Fruit weight (gm):

When both the treatments were compared it was determined that the fruit weight increased under wastewater irrigated treatment except genotypes, 19228 $\times$ 19224, 19224 $\times$ 19225 and 15382 $\times$ 19225 which showed higher fruit weight under normal irrigated treatment. Among genotypes, 19224 $\times$ 19228, 19232 $\times$ 19228, 19232 $\times$ 19224 and 19232 $\times$ 19225 showed equal fruit weight under both irrigations. On an average, the genotype 19225 $\times$ 15382 showed maximum and genotype 19232 $\times$ 19228 showed minimum pod weight under both treatments. When combining ability analysis carried

out it was determined that in the pod weight was controlled by non-additive gene action as SCA was highly significant in both treatments. The significant value of GCA showed that additive gene action is also present but effect of SCA was dominant. Among the parents 15382 was the best general combiner in both treatments. Among the crosses, 19225 x 15382 was the best specific combiner. It was concluded that the pod weight was controlled by non-additive gene action. The parent 15382 showed better potential for GCA and the cross 19224 x 15382 showed good potential for SCA (Table 1 and 2).

Protein contents (%):

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 c and d). On an average, among genotypes, 15382 x 19225 showed maximum amount of proteins and 19224 x 15382 showed minimum amount of proteins under both types of treatments.

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 the parents, 19225 was somewhat good combiner compared to other parents. Among the crosses, 19228 x 19224 was also somewhat good specific combiner (Table 2).

Under wastewater 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 1). Among the parents, 15382 was a good general combiner. Among the crosses, 19225 x 15382 was a good specific combiner.

Dietary fiber contents (%):

Analysis of variance indicated significant differences among replications, treatments and genotypes for dietary fiber contents in both normal and wastewater irrigated treatments (Table 3 and 4). 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. Among the parents, 19225 was a good general combiner compared to others. Among the crosses, G2 x G4 (19224 x 19225) was a good specific combiner and had a potential for further breeding programs (Table 1 and 2).

When the combining ability analysis was carried out for wastewater 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. Among the parents, 15382 was a good general combiner for fiber contents. Among the crosses, 19228 x 19224 was a good specific combiner (Table 1 and 2).

It was concluded that the dietary fiber content was controlled by non-additive gene action and 19225 and 15382 were potential parents.

Carbohydrates

Analysis of variance indicated significant differences among replications, treatments and genotypes for carbohydrates (Table 3 and 4). 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. Among the parents, 19225 was a potential parent and good general combiner. Among the crosses, 19224 x 19225 was a good specific combiner (Table 1 and 2).

When the analysis for wastewater 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. 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 1 and 2).

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.

References

- Camciuc, M., J.M. Bessifre, G. Vilarem and A. Gaset. 1981. Volatile components in okra seed coat. *Phytochem.* 48:311 - 315.
- Chaudhary, D.R., Kumar, J., Vidyasagar and Sharma, S.K. 1991. Line x tester analysis of combining ability in okra (*Abelmoschus esculentus* (L.) Moench). *South Indian Hort.* 39: 337-340.
- Esmail R.M. 2007. Genetic analysis of yield and its contributing traits in two intraspecific cotton crosses. *J. Appl. Sci. Res.*, 3: 2075-2080.
- Glo Glover M.A., Willmot D.B., Darrah L.L., Bruce E.H., Zhu X. 2005. Diallel analyses of agronomic traits using Chinese and US maize germplasm. *Crop Sci* 45:1096-1102.
- Ka Kausar, S. 2011. Effect of wastewater on the growth and productivity of okra. M.phil Thesis, Aligarh Muslim University, Aligarh, India. 13p.
- Ma Mapanda, F., E.N. Mangwayana, K.E. Giller and J. Nyamangara. 2006. Uptake of heavy metals by vegetables irrigated using

- wastewater and the subsequent risks in Harare, Zimbabwe. *Soil Sci.* 147(6): 143-161.
- Ma Martijn, E., M. Redwood. 2005. Wastewater irrigation in developing countries- limitations for farmers to adopt appropriate practices. *Irrig. and drain.* 54(9): 63-70.
- Mu Murray L.W., I.M. Ray, H. Dong and A. Segovia-Lerma. 2003. The Gardner and Eberhart analyses II and III revisited. *Crop. Sci.*, 43: 1930-1937.
- Oy Oyelade, O.J, B.I.O. Ade-Omowaye and V.F. Adeomi. 2003. Influence of variety on protein, fat contents and some physical characteristics of okra seeds. *J. Food Eng.* 57(2):111-114.
- Savello, P., F.W. Martin and J.M. Mill. 1980. Nutritional composition of okra seed meal. *Agri. Food Chem.* 28: 1163-1166.
- Scott, C.A., N.I. Faruqui and L. Raschid-Sally. 2004. Wastewater use in irrigated agriculture: confronting the livelihood and environmental realities. *Int. Water Management Inst.* 3: 1-7.
- Shivagamasundari, S., Irulappan, I., Arumugam, R. and Jayasankar, S. 1992. Combining ability in okra (*Abelmoschus esculentus* (L.) Moench.). *South Indian Hort.* 40: 21-27.
- Siemonsma, J.S. 1982. West African okra - Morphological and cytogenetical indications for the existence of a natural amphidiploid of *Abelmoschus esculentus* (L.) Moench and *A. manihot* (L.) Medikus. *Euphytica* 31(1): 241-252.
- Singh, A., R.K. Sharma, M. Agrawal and F.M. Marshall. 2010. Risk assessment of heavy metal toxicity through contaminated vegetables from waste water irrigated area of Varanasi, In. *J. Tropic. Ecol.* 5(2): 375-387.
- Steel, E.W. and E.J. Beg. 1954. Effect of sewage irrigation upon soil. *Sewage and Industrial waste.* 26(3):13-25.
- Viana JMS, Cruz CD, Cardoso AA. 1999. Theory and analysis of partial diallel crosses. *Genetic. Mol. Biol.*, 22: 591-599.
- Wa Wankhade, R.V., Kale, P.B. and Dod, V.N. 1995. Combining ability in okra. *PKV Res. J.* 19(2): 121-124.

Table 1. GCA Values

	PAR		NPR		TR		FYPP		NFPP		FW		PC		DFC		CBH	
	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW
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	0	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	0.034	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	0.041	-0.005	0.02

Table 2. SCA Values

PAR	NPR		TR		FYPP		NFPP		FW		PC		DFC		CBH			
	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW	Control	WW
Direct Crosses																		
19228×19224	35.28	-32.019	-2.884	-9.96	2.048	-0.69	-0.16	0.72	-0.707	1.327	0.318	-0.152	0.084	0.002	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

Table 3. Analysis of Variance (Mean Square Values)

Source of Variation	PAR	PR	TR	FYPP	NPPP	FW	PC	DFC	C
Replications	163	2.48	0.2892	7.807	1.087	0.0685	0.00067	0.0071	0.0042
Treatments	276173**	895.34**	56.5003**	821.340**	486.000**	10.9350**	4.63936**	30.8267**	52.5459**
Genotypes	38262**	3266.88**	27.0367**	96.393**	12.784**	7.2840**	0.01256**	0.0405**	0.0134**
Treatments × Genotypes	4372**	651.00**	7.7975**	40.284*	8.111**	0.4706**	0.01320**	0.0355**	0.0121**
Error	384	4.79	0.3801	22.847	1.855	0.0968	0.00427	0.0120	0.0055

Table 4: Mean squares for Quality Traits under Wastewater and Normal Irrigation

SOV	PAR		PR		TR		FYPP		NPP		FW		PC		DFC		C	
	NI	WW	NI	WW	NI	WW	NI	WW	NI	WW	NI	WW	NI	WW	NI	WW	NI	WW
Replication	542.5	94.99	0.80	2.62	0.12	0.54	22.77	7.59	1.77	0.17	0.15	3.44	2.68	5.96	5.38	1.51	3.29	0.01
Treatment	17536.54**	25098.79	1884.57**	2033.30**	19.41**	15.41**	80.24**	56.43**	11.30**	9.59**	3.95**	3.79**	1.87**	7.04*	8.43*	6.75**	1.05*	1.47**
Error	449.89	314.65	2.47	7.26	0.35	0.40	26.21	19.48	1.64	2.10	7.93	0.11	5.00	3.6	4.7	1.94	5.4	5.39