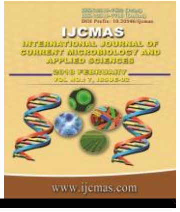
Int.J.Curr.Microbiol.App.Sci (2018) *7*(2): 3166-3173

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 7 Number 02 (2018)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2018.702.381

Genetic Analysis of Green Super Rice (*Oryza sativa* L.) for Yield and Quality Traits

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ABSTRACT

The diversity of rice germplasm is the base of rice improvement programmes. Various agromorphological traits of five randomly selected plans were recorded for the evaluation of 36 green super rice germplasm. Analysis of variance indicated difference among genotypes were highly significant for the entire traits under studied, this indicated that these genotypes have sufficient amount of variation. The high heritability accompanied with high genetic advances show the predominant of additive gene action for the trait-like number of tiller/plant, biological yield/plant, panicle weight/plant, number of spikelet/panicle, fertile spikelet/panicles, spikelet density, grain yield/plant, panicle index, harvest index, head rice recovery and amylose content etc. It indicates that the heritability is most likely due to additive gene action and selection may be effective. Therefore, this character may be given importance during hybridization programmes. In the principal component analysis, it has been found that the PC_1 showed the highest variability among the genotypes of the traits under study, therefore on the basis of it, the genotype from PC_1 has given due importance on the basis of yield attributing and quality traits. The genotype HHZ10-DT8-DT1-DT1 has highest PC value and hence this genotype can be used to develop new variety in plant breeding programmes.

Keywords

Diversity, DUS, Genetic advance, heritability, PCA

Article Info

Accepted:
26 January 2018
Available Online:
10 February 2018

Introduction

The rice belongs to family Bumbusoideae and tribe Oryzaeae. This tribe has 11 genera of which *Oryza* is only one cultivated species. The Oryza have two cultivated species and with twenty two wild species. Among these two cultivated species *Oryza sativa* (Asian rice) is grown worldwide whereas, *Oryza glaberrima* (African rice) is cultivated on a limited scale in West Africa. The subspecies or varietal group of *O. sativa* viz., Indica Japonica and Javanica are the results of centuries of selection by human and nature for desired quality and adaptation to a new niche. Rice is the world's most important staple cereal crop after wheat. It is grown worldwide over an area of 163.24 million hectares with a total production of 740.95 million tons (FAO, 2016). The area under rice in India is 44.14 million hectares with a production of 106.65 million tonnes and productivity of 2416 kg/ha (Agricoop statistics, 2015). It has been found that annual growth of rice is 2.5% from the begging of the green revolution (Riveros and Figures, 2000). Rice occupies 35-60% of the caloric intake of three billion Asians (Guyer *et al.*, 1998). The concept of green super rice (GSR) evolved from an international rice research institute to increase in the rice yield. It is bred to perform excellence during adverse condition. Green super rice is a simple mixture of a large number of varieties and generally, it contains more than 250 rice varieties. In green super rice, the word green indicate environment-friendly because it provides more grain with low input and the word super indicates its better ability to tolerate drought, salt, flood and insect pests. The breeding programme for green super rice is a collaborative project between International rice research institute and Chinese Academy of Agricultural Sciences, which is funded by the Bill and Melinda Gates Foundation. The aim of developing rice varieties that remains their stable sustainable yield potential even when grown with low input or under unfavourable environmental conditions (Ali *et al.*, 2013). Besides the yield the qualitative traits are also important, it may be considerd from milling efficiency, grain appearance, grain shape, grain size, length width ratio of the grains and translucency of the endosperm (Zhang, 2007). The heritability is an index to measure transmissibility of the traits from one generation to another and it has predictive key role in crop improvement programmes (Khan and Naqvi, 2011). The genetic advance for the various traits is depend upon the extent of genetic variability, heritability and selection intensity (Alard, 1960). Principal component analysis (PCA) is a multivariate method that analyse a data table which have observation descrive by several intercorelated quantitative dependent variables. It is a multivariate statistical analysis to reduce the data with large number of correlated variables into substantially smaller set of new variables through linear combination of the variables that accounts most of the variations present in the original variables. The objectives of PCA are to identify minimum number of components which can explain maximum variability out of the total variability (Anderson., 1972 and Morrison., 1982). It is a well-known method of dimension reduction (Massey., 1965 and Jolliffie., 1986) which seeks linear combination of the column with maximum variance or equivalently, high information. The goal of PCA is to extract the important information from the table, to represent it as a set of new orthogonal variables which is known as principal component, and to display the pattern of similarities of the observations and of the variables as pointed in map (Nachimuthu *et al.*, 2014).

Materials and Methods

For evaluation of green super rice, an afield experiment was conducted at seed breeding farm Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.). The experimental material consists of 36 green super rice lines (Table 1) received from the International Rice Research Institute. This line was planted in a randomized complete block design with three replications. The seedling of 21 days old was transplanted in the experimental site with a spacing of 2 cm between plant to plant and 20 cm between the rows by keeping single seedling per hill. The gap filling did within a week after transplanting in order to maintain uniform plant population. Fertilizer was applied with the dose of 100 kg N, 60 kg P_2O_5 and 4 kg K_2O. The entire dose of P2O5 and K2O along with a half dose of N was applied as basal dose at the time of final field preparation, the remaining amount of N was split in two equal doses and was applied at the time of active growth and grain filling stages. The standard agronomic practised were adopted for normal crop growth and observations were recorded for various agro-morphological traits as per the DUS guidelines for rice and on the basis of five random competitive plants. In the present investigation for the parameter of genetic variability mean, range genotypic and phenotypic coefficient of variation were mainly used. The genotypic and phenotypic coefficients of variation were calculated by the method suggested by Burton (1952). Heritability is the ratio of the genetic variance to phenotypic variance.

In this investigation heritability was calculated in broad sense by the formula given by Hanson *et al.*, (1956). Genetic advance is improvement in the mean phenotypic value of selected plants over the parental population. The expected genetic advance was calculated by Johnson *et al.*, (1955). Correlation coefficient was calculated for all quantitative traits combination at phenotypic, genotypic and environmental level by the formula given by Miller *et al.*, (1958). The genotypic, phenotypic and environmental correlation was computed by substituting corresponding variance and covariance. The estimation of covariance between two traits was derived in the same way as for corresponding variance components. Path coefficient analysis is the direct and indirect contribution of various traits to yield was calculated which were suggested by weight (1921) and it was further elaborated by Dewey and Lu (1959). Later path coefficient was rated based on various scales (Lenka and Mishra., 1973). Principal component are generally estimated either from correlation matrix or covariance matrix. When the variables are measures in different unit, scale effect can influence the composition of derived components. In this condition it becomes desirable to standardize the variables. In the present investigation correlation matrix was used to extract the principal components.

Results and Discussion

Morphological characterization

It refers to the characterization of rice on the basis of its morphological character that is appearance viz., leaf sheath colour, stigma colour, awans, height etc. The genotype was characterized for thirty morphological traits viz., coleoptiles colour, basal leaf sheath colour, leaf sheath: anthocyanin coloration, leaf: pubescence of blade surface, leaf: auricles, leaf: anthocyanin colouration of auricles, leaf: collar, leaf: shape of ligule, leaf: colour of ligule, culm: attitude, flag leaf: attitude of blade (early), stem: anthocyanin colour of nodes, panicle: awns, panicle: distribution of awns, panicle: colour of awns, lemma: anthocyanin coloration of keel, lemma: anthocyanin colouration of area below apex, lemma: anthocyanin anthocyanin colouration of apex, spikelet: colour of tip of lemma, lemma and palea colour, panicle: exertion, panicle curvature of main axis, panicle: attitude of branches, panicle: presence of secondary branching and flag leaf attitude of blade. Analysis of variance for quantitative morpho agronomic trait showed significant variability among all traits viz., plant height, panicle length and a total number of tillers/plant.

Genetic variability

Presence of phenotypic differences among the individuals of the population is referred to as variability. The genotypic coefficient of variation (GCV) measures the extent of genetic variability present in a crop species and also enables to quantify the extent of variability present in different traits. The phenotypic coefficient of variation (PCV) of a trait was the manifestation of genotypes, environment and interaction between the genotype and environment. Therefore, the total variance needs to be partitioned into heritable and non-heritable components to assess the true breeding nature of the particular trait. The result obtains from the present investigation are discussed here for yield and quality traits.

Results of analysis of variance indicated that maximum variability was observed for spikelets density and lowest of stem thickness. High phenotypic and genotypic coefficient of variation was observed for harvest index, grain yield/plant and panicle index. Moderate phenotypic and genotypic coefficient of variation were observed for biological yield/plant followed by panicle weight/plant, spikelet density, number of tiller/plant, number of spikelets/panicle, fertile spikelets/panicle, amylase content, number of productive tiller/plant, number of panicle/plant and head rice recovery. Low phenotypic and genotypic coefficient of variation were observed for 1000 grain weight followed by length-breadth ratio, flag leaf length, stem length, stem thickness, decorticated grain breadth, plant height panicle length, spikelet fertility, flag leaf width, decorticated grain length, days to 50% flowering, grain breadth, milling percentage, hulling percentage, plant height, days to 50% flowering, length-breadth ratio and panicle length.

Heritability and genetic advance

Heritability help to the plant breeder in the selection of elite genotype from the diverse genetic population and genetic advance refers to the implement in the genetic value of the selected single plants over the base population. Heritability estimates along with genetic advances are normally more helpful in predicting the genetic gain under selection than heritability estimates alone. The heritability estimates ranged from 99.9%in number of spikelets/panicle to 12.2%iin grain breadth. The range of genetic advances as a percentage of the mean was 10.63% to 49.56%in length-breadth ratio and harvesting index respectively. The pattern of heritability in broad sense coupled genetic advance as a percentage of the mean was observed as follows:

High heritability coupled with high genetic advance was recorded for a number of tiller/plant followed by biological yield/plant, number of spikelet/panicle, fertile spikelet/panicle, spikelet density, grain yield/plant, panicle index, harvest index, head rice recovery and amylase content. A number of tillers/plant and grain yield/plant was recorded as high heritability with high genetic advance. Biological yield/plant was recorded as high heritability coupled with high genetic advance and this was also observed in the case of harvest index. The high heritability along with high genetic advance was observer in the case of number spikelets/panicle. Fertile spikelets/panicle was recorded as high heritability coupled with high genetic advance. In the case of flag leaf length, stem length, length breadth ratio and test weight, high heritability coupled with moderate genetic advance were observed. Flag leaf recorded as high heritability coupled with moderate genetic advance. The high heritability coupled with moderate genetic advance observed for the length-breadth ratio. High heritability accompanied with low genetic advance was observed for days to 50%flowering followed by plant height, panicle length, spikelet fertility, hulling percentage, milling percentage, grain length and decorticated grain length. Plant height was recorded as high heritability coupled with low genetic advance. Milling percentage was recorded as high heritability coupled with low genetic advance. High heritability coupled with low genetic advance was also recorded for grain length.

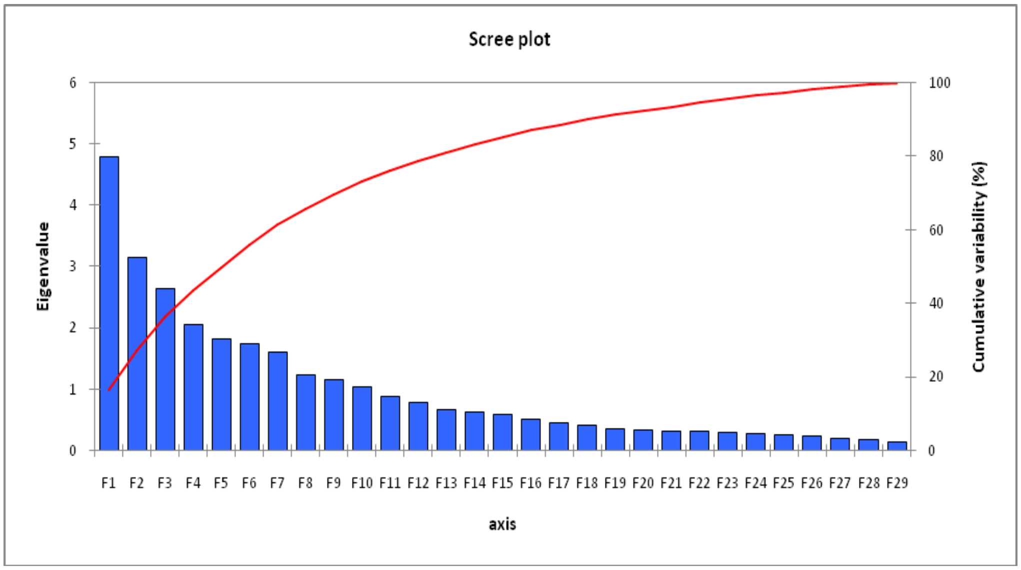
Table.1 List of 36 green super rice lines

Sl.no.	Lines	Sl.no.	Lines	Sl.no.	Lines
1	HHZ 1-DT7-LI2-LI1	13	HHZ 10-DT8-DT1-DT1	25	HHZ 21-DT7-Y1-Y1
2	Sahbhagi (LC)	14	Danteshwari (LC)	26	HHZ 3-SAL13-Y2-DT1
3	HHZ 3-SAL6-Y1-Y1	15	IRRI 104	27	HHZ 14-SAL19-Y1
4	HHZ 4-SAL5-Y2-Y1	16	HHZ 1-DT4-LI1-LI1	28	HHZ 4-DT3-Y1-Y1
5	MTU-1010 (LC)	17	HHZ 22-Y3-DT1-Y1	29	IRRI 154
6	HHZ 18-Y3-Y1-Y1	18	HHZ 26-SAL12-Y1-Y1	30	HHZ 15-DT7-SAL2
7	HHZ 4-SAL5-LI1-LI1	19	HHZ 24-DT11-LI1-LI1	31	HHZ 16-SAL13-LI1-LI1
8	HHZ 21-Y4-Y2-Y1	20	IR64 (LC) Quality	32	HHZ 3-SAL4-Y1-Y1
9	HHZ 21-SAL13-Y1-Y1	21	HHZ 15-SAL13-Y1	33	HHZ 23-DT16-DT1-DT1
10	HHZ 1-DT3-Y1-Y1	22	HHZ 4-DT6-LI2-LI1	34	HHZ 10-DT5-LI1-LI1
11	HHZ 2-SUB2-DT1-DT1	23	HHZ 15-SAL13-Y3	35	IR77186-122-2-2-3
12	HHZ 3-SAL13-Y1-SAL1	24	HHZ 6-DT1-LI1-LI1	36	HHZ 4-SAL12-LI1-LI1

Table.2 The eigen values, % variance and cumulative eigen value of green super rice germplasm and rotated component matrix for the 29 traits of germplasm

Traits	PC	Eigen value	% Variance	Cumulative %	PC_1	PC_2	PC_3	PC_4	PC_5
DFF	PC_1	4.574	15.771	15.771	0.088	-0.246	-0.294	0.016	0.172
NTPP	PC_2	3.229	11.136	26.907	-0.135	0.787	-0.145	0.011	0.083
NPTPP	PC_3	2.585	8.914	35.821	-0.196	0.746	-0.329	0.115	-0.072
FLW(cm)	PC_4	2.064	7.116	42.937	0.462	-0.059	0.029	0.093	0.205
FLL(cm)	PC_5	1.850	6.379	49.316	-0.218	0.228	0.211	0.012	0.599
ST(mm)	PC_6	1.732	5.972	55.288	0.404	-0.045	-0.197	-0.006	-0.061
SL(cm)	PC_7	1.586	5.469	60.756	0.349	0.296	0.516	-0.227	-0.412
PH(cm)	PC_8	1.212	4.181	64.937	0.262	0.286	0.547	-0.191	-0.358
NPPP	PC_9	1.201	4.140	69.077	-0.204	0.771	-0.225	0.031	0.050
PL(cm)	PC_{10}	1.015	3.501	72.578	-0.372	0.163	0.132	0.311	0.157
BYPP(g)	PC_{11}	0.864	2.978	75.556	0.210	0.388	-0.173	0.040	0.353
PWPP(g)	PC_{12}	0.801	2.763	78.319	0.220	0.497	-0.004	0.418	-0.163
NSPP	PC_{13}	0.685	2.363	80.682	0.765	0.226	-0.033	0.265	0.142
FSPP	PC_{14}	0.652	2.247	82.929	0.810	0.115	-0.011	0.085	0.083
SF(%)	PC_{15}	0.588	2.028	84.957	0.170	-0.103	0.121	-0.487	-0.267
SD(%)	PC_{16}	0.516	1.780	86.737	0.797	0.172	-0.086	0.148	0.013
TGW(g)	PC_{17}	0.459	1.584	88.321	-0.478	0.005	0.304	0.113	0.154
GYPP(g)	PC_{18}	0.427	1.473	89.794	0.770	0.066	0.062	0.174	0.281
PI(%)	PC_{19}	0.371	1.278	91.071	0.572	-0.297	0.132	-0.188	0.368
HI(%)	PC_{20}	0.344	1.186	92.258	0.510	-0.190	0.161	0.131	0.044
HULL(%)	PC_{21}	0.334	1.150	93.408	-0.053	-0.025	0.365	0.600	-0.239
MILL(%)	PC_{22}	0.310	1.069	94.477	-0.081	-0.006	0.459	0.587	-0.151
HRR(%)	PC_{23}	0.286	0.987	95.464	0.156	0.265	-0.363	-0.203	-0.317
GL(mm)	PC_{24}	0.276	0.951	96.415	-0.451	-0.072	-0.068	0.376	0.036
GB(mm)	PC_{25}	0.257	0.888	97.303	-0.216	-0.219	0.337	-0.002	0.440
DGL(mm)	PC_{26}	0.243	0.840	98.142	0.066	-0.380	-0.035	0.492	-0.201
DGB(mm)	PC_{27}	0.218	0.753	98.895	-0.011	0.207	0.711	-0.084	0.080
L/B	PC_{28}	0.188	0.647	99.542	0.061	-0.425	-0.597	0.300	-0.144
AC(%)	PC_{29}	0.133	0.458	100.000	0.125	-0.151	-0.046	0.146	-0.381

Fig.1 Screen plot of principal component analysis of green super rice germplasm between eigen value and principal components



Correlation coefficients

Studies of correlation provide a better pathway for yield improvement during selection. Grain yields a polygenic inherited trait and is highly influenced by environmental effects. Knowledge of genetic correlation among the factor contributing to yield leads to the most effective method of selection by use of a favourable combination of traits. Correlation studies revealed the positive and significant association of grain yield/plant with flag leaf width followed by biological yield/plant, panicle weight/plant, number of spikelets/panicle, fertile spikelets/panicle and spikelet density. Correlation of flag leaf width with grain yield/plant was positive and significant.

Path coefficient analysis

If the correlation between yield and the trait which is due to the direct effect of the trait, it reflects true relationship between them, under such condition selection can be predicted for such a trait in order to improve yield. However if the correlation is due to the indirect effect of the trait through another component trait, the breeder has to select for the latter trait through which indirect effect is exerted. Highest positive direct effect towards grain yield/plant was observed for stem length followed by panicle length, panicle index, fertile spikelet/panicle, panicle weight/plant, spikelet density, decorticated grain length, test weight, Number of panicles/plant, Grain breadth and milling percentage.

Principal component analysis

Principal component analysis revealed that out of 36, only 16 principal components (PCs) exhibited more than 0.5 Eigen value and showed about 86.737% of total variability. The PC_1 showed highest variability i.e. 15.771% while PC_2, PC_3, PC_4, PC_5, PC_6, PC_7, PC_8, PC_9, PC_{10}, PC_{11}, PC_{12}, PC_{13}, PC_{14}, PC_{15} and PC_{16} exhibited 11.136%, 8.914%, 7.116%, 6.379%, 5.972%, 5.469%, 4.181%, 4.140%, 3.501%, 2.978%, 2.763%, 2.363%, 20247%, 2.028% and 1.780% variability respectively among the germplasm for the trait under study (Table 2).

Scree plot explains the percentage of variance associated with each principal component obtain by drawing a graph between eigenvalues and principal component numbers. The PC_1 showed 15.771%

variability with eigenvalue 4.574 which then declined gradually. Semi curved line is obtained after ten PC tended to become straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC_1 in comparison to other sixteen PCs. So, the selection of lines from this PC will be useful (Figure 1).

Rotated component matrix revealed that the PC1 which accounted the highest variability (15.771%). A principal component like PC1 and PC2 accounts for yield-related component while PC3 and PC5 account for yields as well as quality traits. PC4 accounts for quality-related traits. The PC_1 account mostly yields related traits like spikelets/panicle, fertile spikelets/panicle, spikelet density, spikelet fertility, grain yield/plant, stem thickness, flag leaf length, panicle index and harvesting index. The PC2 was also dominated by yield-related trait like biological yield/plant, panicle weight, number of panicle/plant, number of tillers/plant, number of reproductive tillers/plant and also quality related like head rice recovery. The PC3 was dominated by yield as well as quality traits like stem length, plant height, 1000 grain weight are yield-related trait and decorticated grain breadth as a quality related trait. The PC4 dominated by quality traits like hulling percentage, milling percentage, grain length, decorticated grain length, length-breadth ratio and amylase content. Similarly, the PC5 was dominated by yield-related traits days to 50% flowering, flag leaf length and quality trait like grain breadth (Table 2). The rice germplasm includes in this investigation for PCA analysis of the 29 yield and quality traits, all the traits were estimated on the basis of principal component scores (PC score) and presented in table2. This score can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of the principal components. High PC score for a particular germplasm in a particular component denotes high values for the variables in the particular germplasm.

Green super rice germplasm included in this research programme for PCA analysis on 36 genotypes, all the genotype were estimated on the basis of principal component scores. On the basis of PC scores, the genotype acquires the highest positive values in all of the five PCs. In the PC1 genotype, 10-DT8-DT1-DT1 acquire maximum value (5.146) followed by HHZ 4-DT6-LI2-LI1 (4.648) and HHZ 1-DT7-LI2-LI1 (3.092). In PC2 genotype HHZ 24-DT11-LI1-LI1 acquires maximum value (4.786) followed by IR64 (LC) quality (3.106) and IRRI 154 (2.746). PC3 ranges its maximum value in the genotype HHZ 3-SAL6-Y1-Y1 (3.49) followed by HHZ 22-Y3-DT-1-Y1 (3.084) and Sahbhagi (LC) sensitive (2.756). Similarly, in PC_4 genotype, IR 77186-122-2-2-3 (NSICRCI58) acquires 2.960 value followed by HHZ 3-SAL13-Y2-DT1 (2.612) and HHZ 1-DT4-LI1-LI1 (2.149). In PC5 genotype HHZ 1-DT7-LI2-LI1 accounted highest value 3.203 followed by HHZ 10-DT5-LI1-LI1 (2.793) and HHZ 10-DT8-DT1-DT1 (2.699).

Characters viz., coleoptile colour, basal leaf sheath colour, leaf pubescence of blade surface, leaf auricle, leaf anthocyanin coloration of auricle, leaf; shape of ligule, leaf ligule colour, stem anthocyanin coloration of nodes, spikelet colour of stigma, leaf colour, leaf sheath anthocyanin colouration and panicle colour of awns showed no variation. While flag leaf attitude of the blade, spikelet density of pubescence, sterile lemma colour, spikelet colour of tip of the lemma, panicle exertion, panicle attitude of branches, panicle awns and distribution of awns over the panicle had sufficient amount of variability. High heritability with high genetic advance was observed for trait viz., number of tillers/plant, biological yield/plant (gm), panicle weight/plant (gm), number of spikelet/panicle, fertile spikelet/panicle, spikelet density (%), grain yield/plant (gm), panicle index (%), harvest index (%), head rice recovery (%) and amylase content (%). It indicates that heritability is most likely due to additive gene effect and selection may be effective. On the basis of yield attributing and quality traits, five genotypes viz., HHZ 10-DT8-DT1-DT1, HHZ4-DT6-LI2-LI1, HHZ1-DT7-LI2-LI1, HHZ24-DT11-LI1-LI1 and HHZ 26-SAL 12-Y1-Y1 were found superior, hence this genotype can be used as a donor for improvement in grain yield/plant.

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How to cite this article:

Megha Singh, Hausila Prasad Singh, Rana Saha, Prabhudutt Samal, Md. Ekram Hussain, Shailja Sharma, S. D. Nitesh and Koutu, G.K. 2018. Genetic Analysis of Green Super Rice (*Oryza sativa* L.) for Yield and Quality Traits. *Int.J.Curr.Microbiol.App.Sci.* 7(02): 3166-3173. doi: https://doi.org/10.20546/ijcmas.2018.702.381