ASSESSMENT OF GENETIC DIVERSITY OF RICE (Oryza *sativa* L.)UNDERPRAYAGRAJAGRO-CLIMATICCONDITIONS

Abstract

The goal of the current study was to assess the genetic variability parameters andcorrelationgenetic diversityin 40 rice genotypes for 13 quantitative traits in the *Kharif*, 2022 Season at the fieldexperimentationcenter,DepartmentofGeneticsandPlantBreeding,NainiAgriculturalInstitute, SamHigginbottomUniversityofAgricultureTechnologyandSciences, UttarPradesh. Analysisof varianceindicatedhighlysignificantdifferencesamongthe genotypesforallthetraits.Considerable variability existed inamongthe genotypes for all the characters studied. These were thegenotypes with high mean values in desirable direction i.e., From the present investigationIt isconcluded that among 40 genotypes of rice, Nellore Dhanyarasi showed early flowering (77days), IR-64 had characters like early maturity (108 days), high grain yield per plant is seen inShuats Dhan-6 (62.1 g), JHARA SEL showed high plant height (185 cm) and high biomass isseen in Shuats Dhan-6 (123.6 g), Swathi showed high panicle length (43.7 cm). Highest GCVand PCV were depicted for grain yield per plant, biological yield, harvest index and numberofspikeletsperpanicle.Thehighestheritabilitywasobservedforgrainyieldperplantfollowedb y harvest index, flag leaf length, biological yield and number of spikelets per panicle. TheGeneticAdvance (GA)inpercentofmeanishighforgrainyieldperplant,biologicalyield,harvest index and number of spikelets per panicle. Based on D^2 values, 40 genotypes grouped into 7clusters. Among 67clusters, cluster I had a greater number of genotypes (26) followed by clusterII (8), III (2), IV, V, VI andVII (1) genotype each. Cluster VI and cluster III (365.72) followedbyclusterVIIandclusterV(363.6),weremostdiversefromeachotherandthegenotypespresen tincluded intheseclustersprovideabroadspectrumofvariabilityinsegregationandmaybeusedasparentsinthefut urehybridizationprogrammetodevelopdesirablegenotypesforgrainyieldimprovementinricegenoty pes.Thetraitgrainyieldperhillhadmaximumcontributiontowardsto genetic divergence followed by biological yield, harvest index, test weight. Therefore, allthesecharactersshouldbegivendueconsiderationduringselectionforcropimprovement.

Keywords: GeneticVariability,Heritability,GeneticAdvance,Diversity,Rice

Introduction

Rice(*Oryza sativa* L.)belongstothegenus*Oryza* of*Poaceae*family*Graminae*andisatruediploidwithchromosomenumber2n=24.Ricehasbeencultivated bymankindformorethan10,000years. The cultivated varieties of *Orzya sativa* grouped into three sub-species, *indica, japonica* and*javanica.*Where*indica*aregrownthroughthetropicalandsub-tropicalregionand*japonica*varietiesaregrownthroughoutthetemperate zoneand*javanica*aregrownmainlyinthepart ofIndonesia.

Riceimportantrolein India economy being astaplefood for two third of the overallpopulation.Thenutrientcontentofriceare80%carbohydrates,7-8%protein(Theaminoacidprofileshows that it is rich in glutamic acid and Aspartic acid, highest quality cereal protein being rich inlysine (3.8%), 3%, fiber, iron 1mg and zinc 0.5 mg **(Juliano *et al*. 1985).** Rice isa short-dayautogamouscrop.

Rice is a crop that self-pollinates and has short days. The crop needs a hot, humid climatewith average temperatures between 2 and 370 C for the entirety of its life cycle. In India, rice ispredominantly a Kharif crop and is widely grown in regions with abundant yearly precipitation.
Inareaswithlittlerainfall,itisalsogrownunderirrigation.IntheeasternandsouthernpartsofIndia,riceis acommoningredientinfood.

The direct and indirect impacts of numerous independent variables on dependent variablesare measured using path analysis. Selection becomes more successful when the cause-and-effectrelationship is understood. The path coefficient, which measures the direct effect of a predictorvariable on its response variable, is one component of path analysis; the indirect effect(s) of apredictorvariableontheresponsevariablethroughanotherpredictorvariableisthesecondcomponent **(Dewey and Lu, 1959)**. Path analysis has been used in plantbreeding to help findfeaturesthat canbeused asselectioncriteriatoboostcropoutput.**(SurekandBeser,2003).**

Objectives

1. Toestimategeneticvariability,heritabilityandgeneticadvanceforgrainyieldcomponentcharactersofric e
2. Toassessgeneticdiversityindifferentaccessionsofricefordifferentquantitativecharacters
3. Toidentifydivergentparentsforfuturehybridizationprogramme.

MaterialsandMethods

ThepresentinvestigationwascarriedoutattheFieldExperimentationCenterofDepartmentof Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University ofAgriculture,Technology andSciences,Prayagraj (Allahabad), U.P. during *Kharif*, 2022. Theuniversity is situated on the left side of Allahabad Rewa National Highway, about 5km fromPrayagraj city. All types of facilities necessary for cultivation of successful crop including fieldpreparation inputs, irrigation facilities were provided from the Department of Genetics and PlantBreeding,SamHigginbottomUniversity of Agriculture,Technology andSciences,Prayagraj(Allahabad),U.P.

~~Prayagraj (Allahabad) is located in South Eastern part of Uttar Pradeshstate of India. The site ofexperiment is located at 25.57^{0}N latitude, 81.56^{0}N longitude and 98 meters above mean sea level.Thisregionhassubtropicalclimatewithextremeofsummerandwinter.Thetemperaturefallsdownto as low as 1°C-2°C during Rabi season especially in the month of December and January. Themercury rises up to 46°C-48°C during Zaid. The average rainfallin this area is around 1013.4 mmannually with maximum concentration in kharif during Julyto September with few showers anddrizzles during winter alsoshows the meteorological data recorded for the experimental period.Experimentalmaterial:~~

TheexperimentalmaterialforpresentstudyisobtainedfromtheDepartmentofGeneticsandPlantBreeding,SHUATS,Prayagraj(Allahabad).Thedetailsofexperimentalmaterialare asfollows:

Table1: List shows the name of genotypes

S.NO	NAMEOFGENOTYPES	S.NO	NAMEOFGENOTYPES
1	AGNISAL	21	SWATHI
2	BOICHI	22	NELLOREMAHSURI
3	JHARASEL	23	C.SEL-3
4	PULE	24	NELLURESUGANDHA
5	LALBHUNA	25	BHARINI
6	JALDHAYAPA-3	26	IR -64
7	KHAYAMDHAN	27	RDR-1140
8	TALMUNFAR	28	RNR-15459
9	BALAM	29	RNR-29325
10	LALMALA	30	RNR-15098
11	UBL-4	31	PUSHYAMI
12	LAGEDHAN	32	VARMA
13	KAUKASEL	33	MTU-1280
14	BINNI	34	MTU-1212
15	SITALKUCHI-6	35	MTU-1281
16	PAHARIBOICHI	36	SHUATSDHAN2
17	CHAPKACHAKLAO	37	SHUATSDHAN 3
18	NELLUREDHANYARASI	38	SHUATSDHAN4
19	B.D.O.NAGRA	39	SHUATSDHAN6
20	NELLORESONA	40	NDR-359(CHECK)

STATISTICAL ANALYSISGive in the form of statement

- Analysis of variance (**Fisher, 1918)**
- Genetic Variability (**Burton, 1952**)
- Coefficient of variation (**Burton and De vane, 1953**

  a. Genotypic coefficient of variation **(GCV**

  b. Phenotypic coefficient of variation **(PCV)**
- Heritability broad sense **(Burton and Devane, 1953)**
- Genetic advance **(Johnson *et .al*, 1955)**
- D^2 analysis **(Mahalanobis, 1928)**

ResultsandDiscussion

Analysis of varience

The analysis of variance for ~~seed~~grainyield and its contributing traits has beenpresentedin Tabe-1. The mean squares due to genotypes were highly significantfor all thecharacters indicating the presence of considerable amount of genetic variability in thematerial.This study attempted to assess the mean values, range, coefficient of variation and criticaldifference of 40 rice genotypes for all 13 quantitative characters that are presented in which hadrevealedarange ofvariationforallthe charactersstudied.

Grainyieldperplantrangedfrom 8.1to62.1 gper plant,with agrandmeanof23.2g. SHAUTS DHAN-6 (62.1 g) had the highest grain yield per plant per plant, followed bySHAUTS DHAN-2 (51.5 g) and SHAUTS DHAN-3 (45.3 g). RNR-15459 (8.1 g) had thelowestminimumgrainyieldperplant,followedbyC.SEL(10 g)and Lalmala(10.2 g).

HighestPCVweredepictedforgrainyieldperplant(53.4%)followedbybiologicalyield (41.3 %). Among the 13 quantitative characters, ~~high~~ estimates of GCV ~~and~~ wererecorded highest for grain yield per plant (52.2 %) followed by biological yield (39.8 %)andharvestindex(29.8%).ModerateestimatesofPCVwererecordedfornumberofspikeletsper panicle (27.9%), followed by number of tillers per hill (26.9%) and number of panicles perhill(25.9%).LowestimationofPCVwererecordedfordaystomaturity(8.7%)anddaysto50%flowerin g(12.2%).~~HighestGCVweredepictedforGrainyieldperplant(52.2%)followedbybiologicalyield(39.8 %).~~

Table2: AnalysisofVarianceofthirteentraitsin 40promisingricelinesforagronomictraitsevaluatedunderfieldconditionin*Khari*f2022, at SHUATS,Prayagraj

Sr.No.	Trait	Meansumofsquares		
		Replications	Treatments	Error
	Degrees offreedom	2	39	78
1	Daysto50%flowering	10.008	540.83**	47.17
2	Daystomaturity	5.70	478.20**	61.22
3	Plantheight(cm)	113.967	1798.89**	121.96
4	Panicle length(cm)	10.398	54.43**	5.21
5	Flagleaflength	14.124	256.45**	6.08
6	Flagleafwidth	0.01	0.13**	0.006
7	Numberoftillersperhill	1.79	17.64**	0.79
8	Numberofpaniclesperhill	1.86	15.15**	0.81
9	NumberofSpikeletsperpanicle	863.349	10216.7**	376.34
10	Biologicalyieldperplant(g)	125.58	1624.53**	41.79
11	Test weight(g)	8.933	69.24**	3.98
12	HarvestIndex (%)	3.311	446.12**	8.40
13	Grainyieldperplant(g)	17.22	445.81**	7.05

****indicatessignificanceat1%levelofsignificance**

Table 3: Genetic parameters of grainyield and yield components of 40 promisingrice lines for agronomic traits evaluated underfield condition in Kharif 2022,atSHUATS,Prayagraj

SR. NO	Trait	GCV (%)	PCV (%)	h^2 (Broadsense) (%)	GA(5 %)	GA%(5%)
1	Days to 50%flowering	12.2	13.8	77.7	23.3	22.1
2	Daystomaturity	8.7	10.5	69.4	20.2	15.0
3	Plantheight(cm)	16.1	17.7	82.1	44.1	30.0
4	Panicle length(cm)	15.1	17.4	75.9	7.3	27.2
5	Flagleaflength	22.1	22.9	93.2	18.2	44.0
6	Flagleafwidth	16.9	18.0	88.2	0.4	32.8
7	Numberoftillersperhill	26.9	28.7	87.6	4.6	51.9
8	Numberofpaniclesperhill	25.9	28.0	85.5	4.2	49.3
9	Spikeletsperpanicle	27.9	29.4	89.7	111.7	54.4
10	Biologicalyieldperplant(g)	39.8	41.3	92.7	45.5	78.9
11	Test weight(g)	22.7	24.7	84.5	8.8	43.1
12	HarvestIndex	29.8	30.7	94.6	24.2	59.7
13	Grainyieldperplant	52.2	53.4	95.4	24.3	104.9

GCV: Genotypic CoefficientofVariation,**PCV:**PhenotypicCoefficientof Variation,**h^2:**Heritability,

GA: GeneticAdvance,**GA%ofMean:**GeneticAdvanceatpercentofmean

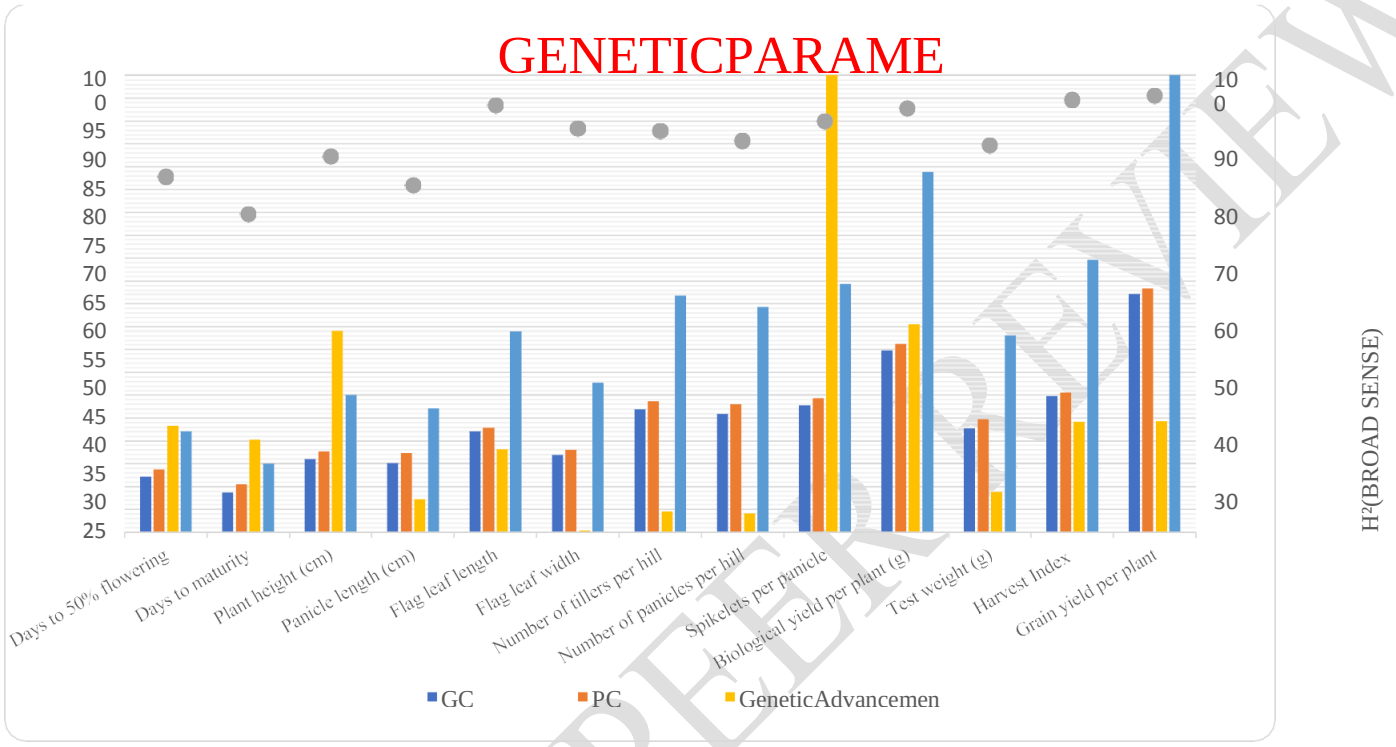


Fig.1 BardiagramdepictingGCV,PCV,heritabilityandgeneticadvancefor13 quantitativecharactersofrice.

Heritability

Thetraitswithhighheritabilityestimatesshowedthatvariationinthesetraitspredominantly governed by heritable factors, whereas both genetics and environment playedequivalent roles in the expression of traits with moderately high heritability indicated that theexpressionofthetraitwasmostlyinfluencedbyenvironmentratherthangenetic.Traitswithhighherit ability estimates in broad sense can be utilized for genetic improvement as they are leastinfluencedbytheenvironmentaleffectsandthushavingapotentialforlargegeneticdetermination. The estimates of heritability from present investigation are presented in (Table 3). Inthe presentstudy, heritability (broad sense) ranged from 95.4% to 69.4%. The highest heritability (above 60%isseeninallparameters) wasobservedfor grainyieldper plant(95.4%)harvestindex(94.6%),flagleaflength(93.2%),biologicalyield(92.7%).

Genetic advance

In the present study a perusal of genetic advance (Table 3) showed that it was highfor number of spikelets per panicle (111.7) followed by biological yield (45.5), plant height(44.1)andgrainyieldperplant(24.3).~~respectively~~.Geneticadvanceshowedthatitwaslowforflag leaf width (0.4), number of panicles per hill (4.2), number of tillers per hill (4.6).

Geneticadvanceas percentmean

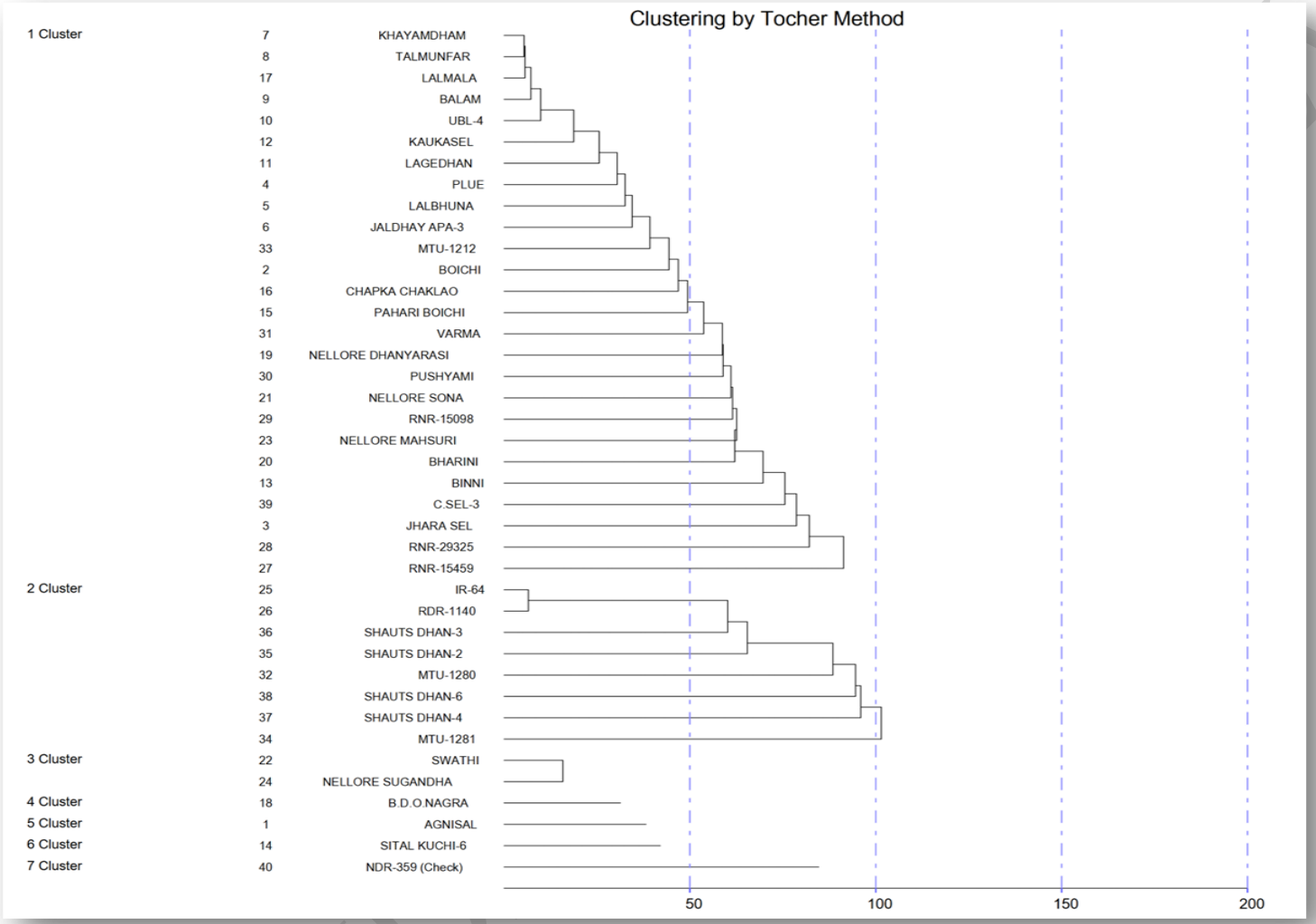
Heritability does not alone does not provide any indication of the amount of geneticimprovement that would result from the selection of individual genotypes. Thus, to arriveatmorereliable conclusion high heritability should be accompanied by high genetic advance**(Johnson *et al.* 1955).** Thus, knowledge of heritability and genetic advance of the characterindicate the scope for the improvement through selection. In the present investigation, highgenetic gain was recorded for grain yield per plant (104.9 %), biological yield (78.9 %),harvestindex(59.7%),numberofspikeletsperpanicle(54.4%),numberoftillersperhill(51.9%),number ofpaniclesperhill(49.3%),flagleaflength(44%),test weight(43.1%),flagleafwidth(32.8%),plantheight(30%),paniclelength(27.2%),daysto50%flowerin g(22.1%)anddaystomaturity(12%).

Table4:Groupingof40ricegenotypesin todifferentclusters

ClusterGroup	No.of Genotypes	List ofGenotypes
Cluster-I	**26**	Khayamdham, Talmunfar, Lalmala, Balam, Ubl-4, Kaukasel, Lagedhan, Plue, Lalbhuna, Jaldhay Apa-3, Mtu-1212,Boichi,ChapkaChaklao,PahariBoichi,Varma,NelloreDhanyarasi,Pushyami,NelloreSona,RNR-15098,NelloreMahsuri,Bharini,Binni,C.Sel-3,JharaSel,RNR-29325&RNR-15459
Cluster-II	**8**	Ir-64,Rdr-1140,ShautsDhan-3,ShautsDhan-2,Mtu-1280,ShautsDhan-6,ShautsDhan-4&Mtu-1281
Cluster-III	**2**	Swathi,NelloreSugandha
Cluster-IV	**1**	B.D.O.NAGRA
Cluster-V	**1**	Agnisal
Cluster-VI	**1**	SitalKuchi-6
Cluster-VII	**1**	NDR-359(Check)

Table5 :Interandintraclusterdistanceof40 genotypesofrice

Clusters	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI	Cluster-VII
Cluster-I	**63.67**	120.80	108.49	117.92	130.94	176.48	160.36
Cluster-II		**105.07**	136.13	186.38	167.26	254.63	199.62
Cluster-III			**15.84**	254.19	202.34	365.72	192.72
Cluster-IV				**0.00**	211.40	42.05	123.10
Cluster-V					**0.00**	246.31	363.60
Cluster-VI						**0.00**	221.70
Cluster-VII							**0.00**



~~Fig.2Dendrogramfor13biometricaltraitsof40genotypesofricetowardsgeneticdivergence~~

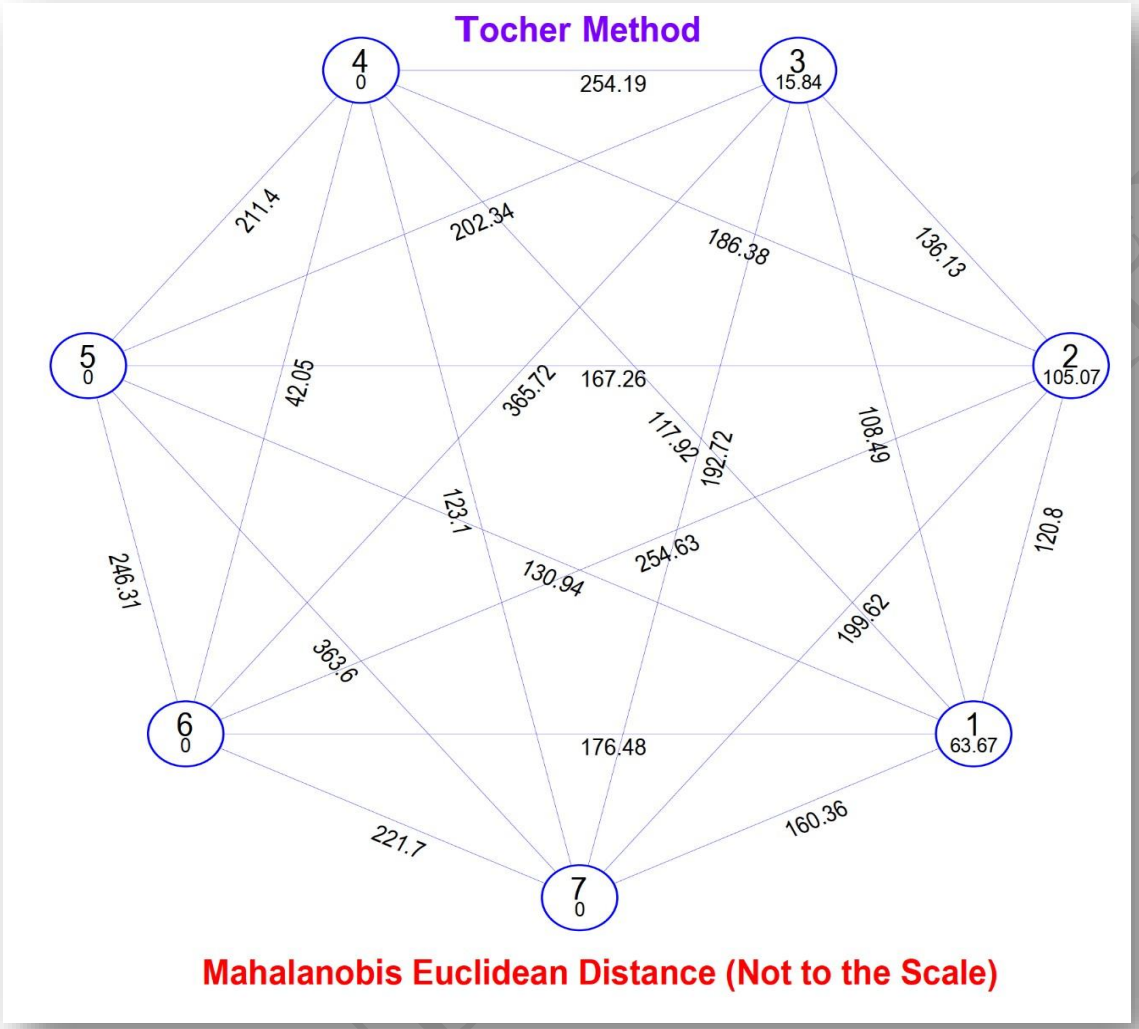


Fig.3:Interand intraclusterdistance of40genotypesofrice

Table6:ClusterMeanof13biometricaltraitsof40ricegenotypes

	Cluster -I	Cluster -II	Cluster -III	Cluster -IV	Cluster -V	Cluster -VI	Cluster -VII
DF50	108.9	98.54	82.83	115.33	107.33	118.67	105.00
DM	138.55	125.92	117.00	142.33	141.63	145.33	131.00
PH	151.94	134.91	113.84	163.28	177.68	159.59	125.00
PL	25.50	27.89	39.03	24.30	29.80	24.43	27.97
FLL	40.59	41.69	24.24	55.25	45.13	78.59	35.81
FLW	1.17	1.34	1.17	0.88	1.00	0.97	1.83
NTH	7.89	10.96	8.40	9.33	7.94	9.80	15.60
NPH	7.64	10.50	8.40	7.73	7.40	9.00	14.00
NSPP	196.59	234.94	228.90	191.73	204.93	167.80	210.60
BYH	50.49	78.85	35.43	60.53	114.00	68.80	51.50
TW	19.67	23.40	26.00	13.73	15.34	17.36	23.10
HI	36.93	52.40	52.85	33.42	32.57	25.75	44.00
GYH	17.96	40.68	18.67	20.13	37.14	17.80	22.66

DF50: Days to 50% flowering, **DM:** Days to maturity, **FLL:** Flag leaf length (cm), **FLW:** Flag leaf width (cm)**,PH:** Plant height (cm)**, NTH:** Number of tillers per Hill, **NPH**: Number of Panicles per Hill, **PL:** Panicle length(cm),**NSPP**:NumberofSpikeletsperPanicle,**BY:**BiologicalYield(g),**HI:**Harvestindex(%),**TW:**Testweight(g),**GYPP:**GrainYieldperPlant(g)

Interandintraclusterdistance

Interandintraclusterdistancesarefurnishedin Table5.Theintraclustervaluesrangedfrom0to105.07. The maximum intra cluster distance was observed in cluster II (105.07). The minimumintra cluster distance for cluster IV, V, VI and VII exhibited zero. The inter cluster distance differedfrom 42.05 (between IV and VI) to 365.72 (between III and VI). Other inter cluster distance werebetweenthesevalues.Thehighestinterclusterdistanceobservedbetweenclusters VI andclusterIII(365.72) followed by cluster VII and cluster V (363.6), cluster VI and cluster II (254.63), cluster IVand cluster III (254.19) and cluster VI and cluster V (246.31). The minimum inter-cluster distanceobserved between cluster VI and IV (42.05), cluster III andcluster I (108.49), and cluster IV andclusterI(117.92).

~~**Interandintraclusterdistance**~~

~~Inthepresentstudy,thehighestinterclusterdistanceobservedbetweenclusterVIandclusterIII(365.72)followedbyclusterVIIandclusterV(363.6),clusterVIandclusterII(254.63),cluster IV and cluster III (254.19) and cluster VI and cluster V (246.31). Therefore, thegenotypes belonging to the clusters VI and III followed by cluster VII and V may be usedasparentstoproducetransgressivesegregants.~~

Clustermeans

Theresultsofclustermeanwere furnishedinTable6. **No results and Discussion**

Contributiontowardsdivergence

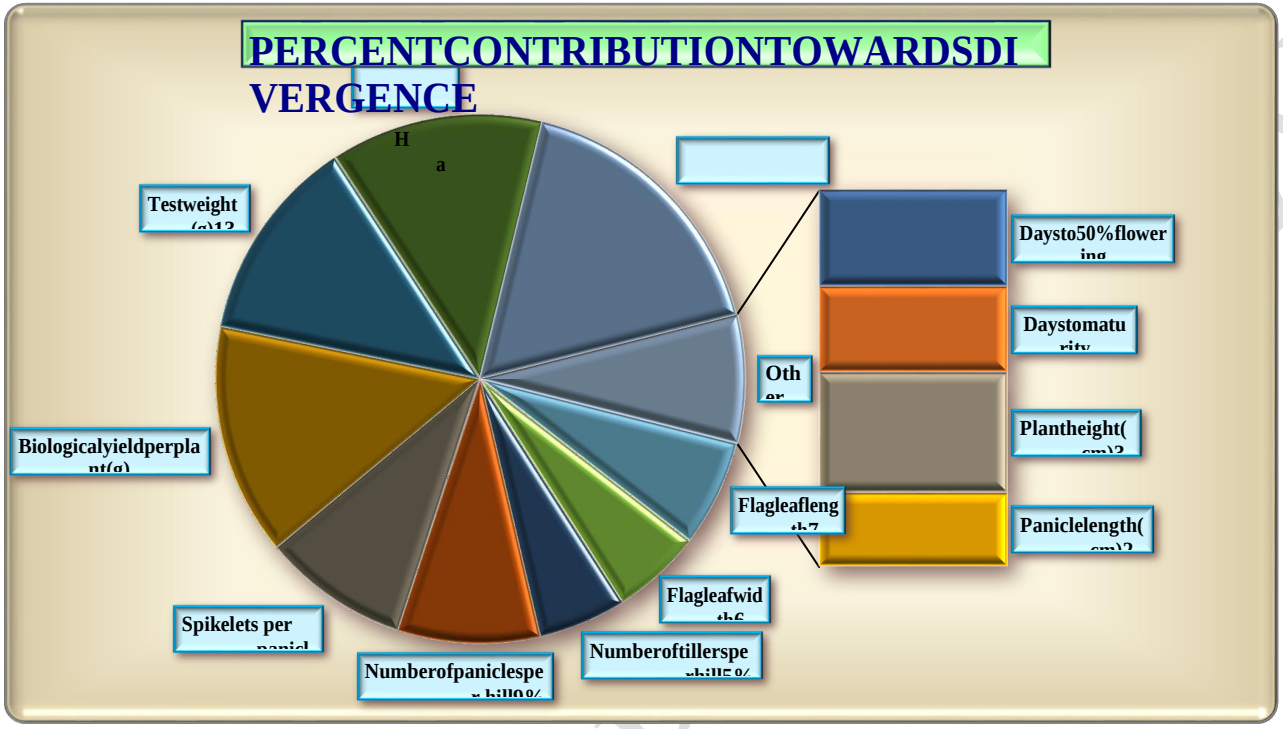
Thepercentcontributionof13biometricaltraitsof40ricegenotypestowardsgeneticdivergence wasestimatedandgiveninTable7~~andFigure4.~~Thetraitgrainyieldperhill(17.3%)had maximum contribution towards to genetic divergence followed by biological yield (14.2%),harvest index (13.0 %), test weight (12.6%), number of spikelets per panicle (8.96%), number ofpaniclesperhill (8.67%),flagleaflength(6.54%),flagleafwidth(5.54%),numberoftillersperhill(5.36%),plantheight(2.5%),daysto50%flowering(2.0 %),daystomaturity(1.79 %),paniclelength(1.54%).

Table7:

Percentcontributionof13biometricaltraitsof40ricegenotypestowardsgeneticdivergence

SL.NO.	Source	Contribution%	Timesranked1st
1	**Daysto50%flowering**	2.00	16.00
2	**Daystomaturity**	1.79	14.00
3	**Plantheight(cm)**	2.50	19.00
4	**Paniclelength(cm)**	1.54	12.00
5	**Flagleaflength(cm)**	6.54	51.00
6	**Flagleafwidth(cm)**	5.54	43.00
7	**Numberoftillersperhill**	5.36	42.00
8	**Numberofpaniclesperhill**	8.67	68.00
9	**NumberofSpikeletsperpanicle**	8.96	70.00
10	**Biologicalyieldperplant(g)**	14.20	111.00
11	**Testweight(g)**	12.60	98.00
12	**HarvestIndex(%)**	13.00	101.00
13	**Grainyieldperplant(g)**	17.30	135.00

~~Fig:4PiechatPercentcontributionof13biometricaltraits of40ricegenotypestowardsgeneticdivergence~~



CONCLUSION

Considerable variability existed in the genotypes for all the characters studied. These werethe genotypes with high mean values in desirable direction i.e., From the present investigation it isconcluded that among 40 genotypes of rice, Nellore Dhanyarasi showed early flowering (77 days),IR-64 had characters like early maturity (108 days), high grain yield per plant is seen in ShuatsDhan-6 (62.1 g), JHARA SEL showed high plant height (185 cm) and high biomass is seen inShuats Dhan-6 (123.6 g), Swathi showed high panicle length (43.7 cm). Highest GCV and PCVwere depicted for grain yield per plant, biological yield, harvest index and number of spikeletsper panicle. The highest heritability was observed for grain yield per plant followed by harvestindex, flag leaf length, biological yield and number of spikelets per panicle. The GeneticAdvance(GA) as in percent of mean is high for grain yield per plant, biological yield, harvest index andnumberofspikeletsperpanicle.BasedonD^{2}values40genotypesgroupedinto7clusters.Among7clusters,clusterIhadagreaternumberofgenotypes(26)followedbyclusterII(8),III(2),IV,V,VIandVII(1)genotypeeach.ClusterVIandclusterIII(365.72)followedbyclusterVIIandclusterV (363.6), were most diverse from each other and the genotypes present in these clusters provide abroad spectrum of variability in segregation and may be used as parents in the future hybridizationprogrammetodevelopdesirablegenotypesforgrainyieldimprovementinricegenotypes.Thetraitgrainyieldperhillhadmaximumcontributiontowardstogeneticdivergencefollowedbybiological yield,harvestindex, and testweight.Therefore,allthesecharactersshouldbegivendueconsiderationduringselectionforcropimprovement.

References

AbigailSeneega,T.V.,Gnanamala,R.P.,Parameswari,C.,Vellaikumar.S.andPriyanka,A.R.(2019) Geneticvariability and association studies in F2 generation of rice (*Oryza sativa* L.). *Electronic Journal ofPlantBreeding*,**10**(2):512-517.

Al - Jibouri, H. A., Miller, P.A. and Robinson, H.F. (1958). Genotypic and environmental variancesinuplandcottoncrossofinterspecific origin.*AgronomyJournal*,50:633-637.

Allam, C.R., Jaiswal, H.K., Qamar, A., Venkateshwarlu, C. and Reddy, Y.S. (2015). Variability,heritability and genetic advance studies in some indigenous genotypes of basmati rice(*Oryzasativa* L.).*Electronic JournalofPlantBreeding*,**6**(2):506-511

Arivoli,V.,Saravanan,KandPrakash,M.(2007).AStudyonD^{2}AnalysisinRice. *InternationalJournalofPlantSciences*,**4**(1):157-160.

Awasthi,L.P.,Misra,C.H.andPandey,V.K.(2005). GeneticDivergenceinIndianAromaticRice. *Crop Research*,**30**(2):199-201.

Akinwale,M.G.,Gregorio,G.,Nwilene,F.,Ogunbayo,S.AandOdiyi,A.C.(2011). Heritabilityandcorrelationcoefficientanalysisforyieldanditscomponentsinrice(*OryzasativaL.*).*AfricanJournalofPlantScience*,**5**(3): 207-212.

Banumathy,S.,Manimaran,R.,Sheeba,A.,Manivannan,N.,Ramya,B.,Kumar,D.andRamasubramanian, G.V. (2010). Genetic Diversity Analysis of Rice Germplasm Lines forYieldAttributing Traits. *ElectronicJournalofPlantBreeding*,**1**(4):500-504.

Basavaraja,T.,Asifi,M.,Mallikarjuni,S.K.andGangaprasad,S.(2013). Variability,heritabilityandgeneticadvanceforyieldandyieldattributingcharactersindifferentlocalrice(*OryzasativaL.*).cultivars. *AsianJournalofBioscience*,**8**:60-62.

Beevi, H.A. and Venkatesan, M. (2015). Genetic Divergence Studies in Rice (*Oryza sativa* L.)Genotypes Under Natural Saline Condition. *Journal of the Andaman Science Association*,**20**(1):35-38.

Chauhan, J.S. and Singh, K.H. (2003). Genetic Divergence Analysis Using Quality Traits in UplandRice(*OryzasativaL.*).*AnnalsofAgriculturalResearch*,**24**(3):673-675.

Das, P., Kundu, Avijit, Mandal, N. and Indrani, D. (2004). Genetic Divergence in LandRaceCollectionsofRice(*Oryza sativaL.*).*JournalofInteracademicial*,**8**(4):488-494.

Deepak, Naik, Rao, A., Sarawgi, A. K and Singh, P. (2006). Genetic Divergence Studies inScentedRice. *JournalofPlantSciences*,**5**(2): 197-200.

Devi, K.R., Parimala, K. and Cheralu, C. (2016). Assessment of Genetic Parameters in ExoticGermplasmofRice(*Oryza sativaL.*).*BIOINFOLET*,**13**(1B):190-196.

Fisher, R.A., Yates, F. (1967). Statistical tables for biological, Agricultural and Medical Research,CongressGroupLimited,London.

Harsh, Shekhawat, V.S., Singh R.P. and Yashpal. (2015). Studies on Genetic Variabilty, HeritabiltyandGeneticAdvanceinRice(*OryzasativaL.*)GermplasmLines.*AnnalsofAgri-BioResearch*,**20**(1):22-25.

Islam, M.J., Raffi. S.A., Hossain, M.A. and Hasan, A.K. (2015). Analysis of genetic variability,heritability and genetic advance for yield and yield associated traits in some promisingadvancedlinesofrice(*OryzaSativa* L.).*ProgressiveAgriculture*,**26**(1):26-31.

Veni,M. andNadarajan,N.(2006). Correlationandpathanalysisininter sub-specificricegenotypes. *CropRes.*,**6**(2):286-289.

Vijaya,I.andShailaja,H.(2016). Assessmentofgeneticparametersforyieldanditsrelatedtraitsin F2 population of KRH-4 hybrid rice (*Oryza sativa* L). *International Journal of AgriculturalScienceand Research*,**6**(3):87-96.

Vinoth, R., Shivramakrishnan, R., Sivaji, M., Tamilkumar, P., Kumar, B and Marker, S.(2016). Geneticanalysisandcorrelationstudiesforgrainyieldinrice(*Oryzasativa*L.)undertheAllahabadagroclimaticregion,*InternationalJournalofForestryandCropImprovement*,**7**(1):93-100.

Vivek,S.,Surendra,S.,Singh,S.K.,Singh,H.,Shukla,VandSingh,S.(2004). Analysisofvariabilityand heritability in new plant type tropical Japonica rice (*Oryza sativa* L.). *Environment andEcology*,**22**(1): 43-45.