GeneticVariabilityand Association among yield and yield related traits ofSesame(*Sesamumindicum*L.) genotype

ABSTRACT

A field experiment was carried out with 42 genotypes of sesame (*Sesamum indicum* L.) at the Niger Research Station, Navsari Agricultural University, Vanarasi, Ta. Vansda. The study was performed to evaluate the genetic variability, characters association, path analysis and genetic diversity based on yield and yield related traits.The highest genotypic coefficient of variation was observed for seed yield per plant followedby capsules per cluster and harvest index. High estimates of heritability coupled with highgenetic advance expressed as percentage of mean were observed for the traits *viz.*, capsulewidth, capsules per cluster, leaf area, harvest index and seed yield per plant indicating thatthese characters are under the control of additive gene effect. The seed yield per plant wasfoundtobesignificantandpositivelycorrelated withdaystomaturity, capsulelength,capsulewidth, capsules per cluster, 1000 seed weight and harvest index at genotypic and phenotypiclevels. The maximum direct effects as well as appreciable indirect influences were exerted byharvestindex,capsulewidth,capsulelengthand1000seedweight.D^2analysisindicatedwidergeneticdiversityamongtheforty-twogenotypeswhichweregroupedintenclustersindicatingthere is no formed relationship between geographical diversity and genetic diversity. ClusterIIIandXshowedthemaximuminterclusterdistanceof16.51.Hence,thegenotypesbelonging to the X, IX and VIII cluster could be used in hybridization program for obtaining a widespectrum of variability among the segregants. Among different eleven traits studied, leaf areafollowedbycapsulespercluster,harvestindex,capsulewidth,seedyieldperplantandcapsulelength contributed maximum towards the total genetic divergence. Results of mean clusteranalysisshowedthatclusterXrecordedhighestclustermeanforfourimportantyieldattributingcharactersandclusterIXfortwoimportantcharacters.Genotypesfromtheseclustermayproduceprogenieswith highgeneticvariation.

Keyword- Genetic variability, Heritability, Genetic advance, Path analysis, Cluster, Genetic divergence, D 2 technique, *Sesamumindicum*L.

Introduction

Sesame(*Sesamumindicum*L.)isoneofthemost important ancient cultivated oilseedscropgrowninAsiaandAfrica.ItbelongstoPedaliaceaefamilyhavingchromosomenumber (2n=26) and is an annual and oilseed crop. Sesame oil is characterized forits stability and quality hence it is regardedas“QueenoftheOilseed”.Thecropishighly tolerant to drought, grows well inmost of the well-drained soils and variousagroclimaticregions,andiswelladaptedtodifferentrotations.Sesameisself-pollinated crop with the cross pollination 4to5%andcrosspollinationmay occurthrough insect activity and environmentalcondition.Duetothestabilityofitshealthyoil, easiness of extraction and resistance todrought, sesame was popular in the ancientworld, Sesame is considered as a nutritiousoilseed crop being rich source of protein(18–25%),carbohydrate(13.5%),mineralsandpolyunsaturatedfattyacid(Bedigian,1986).Variationisaprerequisiteto start a breeding programme in any crop.Geneticvariabilityisnecessaryforcontinuedgeneticimprovementofcropspecies. Biometrical technique to evaluatethegeneticvariabilityandextentofheritability of economic character serve asusefultoolinevaluatingthesegregatingpopulation. Variation and selection are twobasicessentialityofgeneticimprovementinany crop. Yield is the resultant product ofvarious morphological,physiological andbiologicalcomponentswhichisdeterminedbygrowthanddevelopmentprocesses(Quarrie,2006) and more particularly byyieldrelatedtraitswhicharegreatlyinfluencedbybothgeneticandenvironmental factors (Wattoo, 2009). Ifinformationongeneticvariabilityisavailable then the selection based on yieldcomponenttraitsisadvantageous.Phenotypicandgenotypiccorrelationcoefficient and yield components and theircontributioninpathanalysisprovideinformation on their relative importance indeterminingtheyield(DeweyandLu,1959).

Genetic diversity is a fundamentalelementinplantbreedingwhichprovidetheinformationaboutgeneticrelatednessamong elite breeding material (Mukhtar *etal.*,2002).Geneticdiversityamonglandraceswillhelpintheselectionandbreedingofhighyielding, goodqualitycultivarsthatwillincreaseproduction(Mumtaz*etal.*,2010).Butlimitedstudyongenetic diversity has been done in sesame.Some genetic parameters like phenotypiccoefficientofvariation(PCV)andgenotypic coefficient of variation (GCV),heritabilityandgeneticgainhelptoevaluate genetic diversity of experimentalmaterials. Assessment of genetic diversityusingagro-morphologicalandmolecularmarkers is one of the effective methods fordiversity analysesinsesamethatcanbeused in future breeding program and alsosignificanttoimprovesesamevarieties.Diversityanalysisbasedonlyonmorphologicalcharactersarepronetoenvironmental bias due to biotic influencesandalsocomplexgeneticstructureofdifferentmorphologicaltraits(Pandey*etal.*,2015).

MaterialsandMethods

The experiment was conducted toevaluateforty-twogenotypesunderirrigatedcondition, in Randomized BlockDesign with three replications at ResearchFarm of Niger Research Station, NavsariAgriculturalUniversity,Vanarasi,Ta.Vansda, Dist. Navsari, Gujarat. The seedswere sown at 60 cm between rows and 15cm between plants in the row. Total area ofexperimentalunitwas24.5m^2.Thegenotypes were randomly assigned to theplots in every replication. The experimentwas laid out with one row of 2.10 m lengthof each genotype surrounded by one guardrows to avoid damage and border effects.All recommended practices were followedand timely plant protection measures weretakentimelytoavoiddamagethroughinsect-pests and diseases. Thedatawere recorded on five randomly selectedplantsfromeachgenotypeondifferent characters *viz.* days to 50% flowering, daystomaturity,plantheight(cm),capsulelength (cm),capsule width (cm), capsulespercluster,leafarea(cm^2),1000seedweight (g), oil content (%), harvest index(%)andseedyieldperplant(g).Thephenotypicandgenotypiccoefficientofvariabilitywascomputedasper BurtonandDe vane (1953). Heritability (h^2) in broadsense and genetic advance percent of meanwascalculatedforeachcharacteraccordingtothemethodsuggestedbyJohnson(1955)**.**Correlationcoefficientsforyieldandyieldcomponentswereevaluatedusing the formula suggested by PanseandSukhatme(1987).

ResultsandDiscussion

The experimental result showed that a wide range of variation by virtueof exhibiting highly significant genotypicdifferencesfornineoutofeleventraitsstudied *viz.*, days to 50% flowering, plantheight,capsulelength,capsulewidth,capsules per cluster, leaf area, 1000 seedweight, harvest index and seed yield perplantwhileremainingtwotraitsi.e.daystomaturityandoil contentshowedsignificantdifference(Table-1).Thissuggeststhatthe presence of substantial variation in the inherent genetic potential of the genotypes studied depicting the, possibility of selecting high yielding sesame genotypes.Similarresultsinrelatedtosesameformostofthecharacterswerealsoreportedby Valarmathi(2004), Raghuwanshi(2005), SarwarandHaq(2006),Gawali(2007),Parameshwarappa(2009) for days to 50%flowering,plantheight,capsulelength,1000 seed weight and seed yield per plant;Sumathiandmuralidharan(2010),Gidey*etal*.(2012),Bharathi*etal*.(2014),AbateandMekbib(2015a) andIqbal*etal*.(2016).

The estimates of GCVandPCVindicatedthatthevalues of PCV were higher than GCV formost of the traits due partly to interaction of thegenotypes with the environment or otherenvironmentalfactorsinfluencingtheexpressionofthesecharacters (Table 2).Thehighestvalue of GCV and PCV was observed forsome of the traits like capsulespercluster,harvestindexandseedyield per plant. High magnitude of GCVindicatedthepresenceofwidevariationforthe characters under study to allow furtherimprovement by selection of theindividualtrait.HighestimatesofGCVinsesamehave been also reported for seed yield perplant by Valarmathi (2004), Mandal *et al*.(2010),Gayathri(2011) and Gidey(2013).

Highestimatesofheritabilitycoupledwithhighgeneticadvanceexpressed as percentage of mean (Table2)were observed for the traits *viz.*, capsulewidth,capsulespercluster,leafarea,harvestindexandseedyieldperplantindicating that these characters are underthecontrolofadditivegeneeffect.Therefore,furtherimprovementinthesetraits using pure line selection wouldbeworthwhile.SimilarresultreportedbyReddy*etal.*(2001),Krishnaiah*etal.*(2002);forharvestindexbyMohanty(2020a).

Thecorrelationcoefficientsbetween seed yield per plant and yield componentcharactersandamongthemselveswereestimatedatgenotypicandphenotypiclevelsand arepresentedinTable-3 as Genotypic (r_g) and phenotypic (r_p)correlations coefficientaredescribedunder this table.Ingeneral,thevaluesofgenotypiccorrelationscoefficient werehigherthantheircorrespondingphenotypiccorrelations coefficient.This indicated that there was highdegreeofassociationbetweentwovariablesatgenotypiclevel,itsphenotypicexpression was deflated by the influence ofenvironment.Inthepresentstudy,seedyieldperplantwasfoundtobehighlysignificantly and positively correlated withcapsule length, capsule width, 1000 seedweight and harvest index at genotypic andphenotypiclevels. Positive and significant correlation between traits can be the result of strong coupling linkage between genes or the characters may be the result of pleiotropic genes that control these characters in the same direction (Kearsey and Pooni, 1996).

Table1:Analysisof variancefordifferentcharactersin sesame

Source ofVariation	d.f.	MSS					
		DFF	DM	PH	CL	CW	CC
Replications	2	3.431	12.077	33.599	0.002	0.012	0.023
Genotypes	41	13.295**	37.643*	140.027**	0.159**	0.106**	4.778**
Error	82	4.347	23.315	49.248	0.036	0.009	0.249

SourceofVariation	d.f.	MSS				
		LA	SW	OC	HI	SYP
Replications	2	3.970	0.016	0.320	0.502	0.909
Genotypes	41	102.905**	0.227**	9.218*	82.141**	6.154**
Error	82	5.289	0.043	5.457	4.957	0.429

*, ** Significant at 0.05 and 0.01 probability level respectively,

DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsule per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

Table 2: Range, mean, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and geneticadvanceas percent of mean fordifferentcharactersofsesame

Sr. No	Traits	Mean	GCV(%)	PCV(%)	h^2(%)	GA	GAM
1	DFF	39.45	4.38	6.86	40.69	2.27	5.75
2	DM	94.58	2.31	5.60	17.00	1.86	1.96
3	PH	104.47	5.27	8.54	38.06	6.99	6.69
4	CL	3.00	6.76	9.23	53.69	0.31	10.20
5	CW	1.10	16.26	18.42	77.95	0.33	29.57
6	CC	5.03	24.42	26.36	85.82	2.34	46.61
7	LA	45.21	12.62	13.60	86.02	10.90	24.11
8	SW	3.21	7.72	10.07	58.80	0.39	12.20
9	OC	39.88	2.81	6.50	18.69	1.00	2.50
10	HI	21.90	23.17	25.30	83.85	9.57	43.70
11	SYP	5.07	27.24	30.14	81.65	2.57	50.70

DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsule per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

Table3:Genotypic(r_g) andPhenotypic(r_p) correlationcoefficientsforyieldandyieldattributingtraitsinsesamegenotypes

Characters		DFF	DM	PH	CL	CW	CC	LA	SW	OC	HI	SYP
DFF	**rg**	**1.000**										
	rp	**1.000**										
DM	**rg**	0.416**	**1.000**									
	rp	0.130^{NS}	**1.000**									
PH	**rg**	-0.446**	-0.017^{NS}	**1.000**								
	rp	-0.166^{NS}	-0.075^{NS}	**1.000**								
CL	**rg**	-0.259**	0.025^{NS}	0.043^{NS}	**1.000**							
	rp	-0.175^{NS}	-0.025^{NS}	0.161^{NS}	**1.000**							
CW	**rg**	-0.206*	-0.045^{NS}	0.119^{NS}	1.079**	**1.000**						
	rp	-0.113^{NS}	-0.011^{NS}	-0.014^{NS}	0.689**	**1.000**						
CC	**rg**	0.122^{NS}	-0.030^{NS}	-0.232**	0.099^{NS}	0.242**	**1.000**					
	rp	0.132^{NS}	-0.014^{NS}	-0.149^{NS}	0.039^{NS}	0.205*	**1.000**					
LA	**rg**	0.012^{NS}	0.298**	0.244**	0.127^{NS}	0.047^{NS}	-0.264**	**1.000**				
	rp	-0.021^{NS}	0.095^{NS}	0.070^{NS}	0.036^{NS}	0.050^{NS}	-0.201*	**1.000**				
SW	**rg**	-0.272**	-0.406**	0.066^{NS}	0.862**	0.825**	0.260**	-0.069^{NS}	**1.000**			
	rp	-0.131^{NS}	-0.133^{NS}	0.042^{NS}	0.535**	0.575**	0.159^{NS}	-0.079^{NS}	**1.000**			
OC	**rg**	0.475**	-0.398**	-0.119^{NS}	-1.144**	-1.146**	-0.528**	0.074^{NS}	-0.984**	**1.000**		
	rp	0.059^{NS}	-0.098^{NS}	-0.040^{NS}	-0.407**	-0.454**	-0.205*	0.082^{NS}	-0.405**	**1.000**		
HI	**rg**	-0.427**	0.186*	0.215*	0.273**	0.293**	0.134^{NS}	-0.009^{NS}	0.320**	-0.747**	**1.000**	
	rp	-0.246**	0.033^{NS}	0.125^{NS}	0.206*	0.248**	0.096^{NS}	-0.023^{NS}	0.202*	-0.321**	**1.000**	
SYP	**rg**	-0.148^{NS}	0.235**	0.135^{NS}	0.848**	0.807**	0.243**	-0.083^{NS}	0.719**	-1.182**	0.592**	**1.000**
	rp	-0.083^{NS}	0.197*	0.069^{NS}	0.557**	0.619**	0.197*	-0.070^{NS}	0.515**	-0.525**	0.472**	**1.000**

*, ** Significant at 0.05 and 0.01 probability level respectively, DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsule per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

Table4:Genotypicpathcoefficientshowingdirectandindirecteffectsforyieldandyieldattributingtraitsin sesame genotype

Characters	DF	DM	PH	CL	CW	CC	LA	SW	OC	HI	SYP (r)
DF	**0.0592**	0.1798	-0.0401	-0.0045	-0.0358	-0.0080	-0.0026	-0.1566	-0.0529	-0.0861	-0.1476
DM	0.0246	**0.4324**	-0.0015	0.0004	-0.0078	0.0020	-0.0635	-0.2335	0.0443	0.0374	0.2348
PH	-0.0264	-0.0074	**0.0900**	0.0007	0.0207	0.0152	-0.0520	0.0377	0.0132	0.0434	0.1351
CL	-0.0153	0.0109	0.0038	**0.0173**	0.1874	-0.0065	-0.0271	0.4954	0.1272	0.0552	0.8483
CW	-0.0122	-0.0193	0.0107	0.0187	**0.1737**	-0.0159	-0.0101	0.4744	0.1275	0.0591	0.8066
CC	0.0073	-0.0130	-0.0208	0.0017	0.0420	**-0.0656**	0.0563	0.1494	0.0587	0.0270	0.2430
LA	0.0007	0.1289	0.0220	0.0022	0.0082	0.0174	**-0.2129**	-0.0394	-0.0082	-0.0018	-0.0829
SW	-0.0161	-0.1757	0.0059	0.0149	0.1434	-0.0171	0.0146	**0.5747**	0.1095	0.0646	0.7187
OC	0.0282	-0.1722	-0.0107	-0.0198	-0.1991	0.0346	-0.0157	-0.5653	**-0.1113**	-0.1507	-1.1820
HI	-0.0253	0.0802	0.0194	0.0047	0.0509	-0.0088	0.0019	0.1840	0.0831	**0.2017**	0.5918

Residualeffect= SQRT(1-1.0432), Numbersinboldindicatedirecteffects

DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsule per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

Table5:InterandintraclusterD^{2}valuesfordifferentclusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**6.19**									
II	9.11	**6.63**								
III	8.72	9.65	**5.46**							
IV	7.62	12.12	11.42	**0.00**						
V	7.44	10.39	11.02	4.35	**0.00**					
VI	8.14	13.49	11.85	4.55	5.68	**0.00**				
VII	7.95	10.90	12.44	4.79	5.02	6.61	**0.00**			
VIII	8.70	11.47	14.41	9.05	8.48	9.47	7.41	**0.00**		
IX	9.53	10.72	14.12	11.69	10.63	11.39	8.39	5.91	**0.00**	
X	11.15	13.44	16.51	8.41	7.95	9.99	7.27	9.17	12.04	**0.00**

Numbersinbold indicate intracluster D^2 values

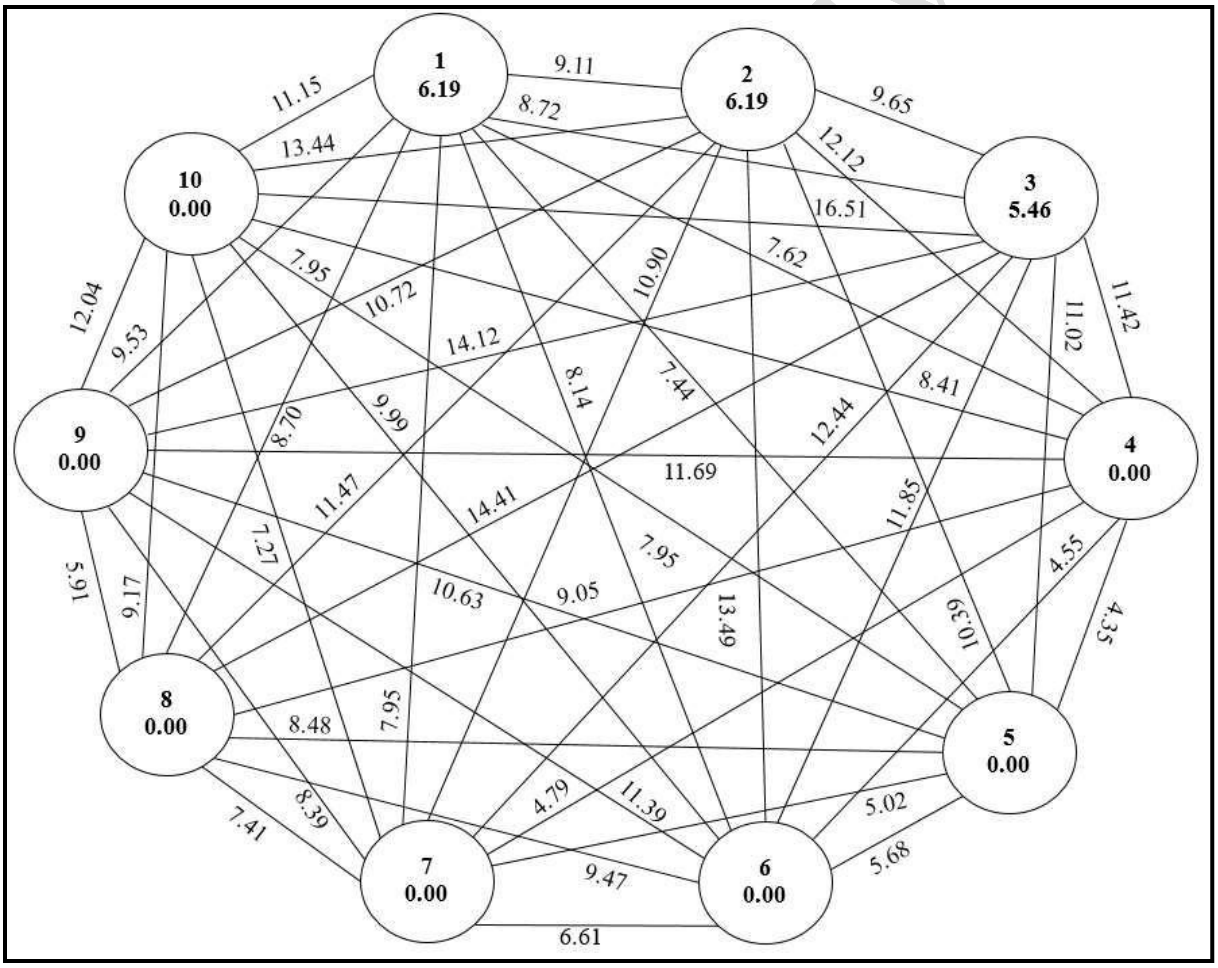

Figure 1. Cluster diagram indicating inter and intra cluster distance

Table6:Cluster means foryieldandyieldcontributingtraitsofsesamegenotypes

Cluster	DFF	DM	PH	CL	CW	CC	LA	SW	OC	HI	SYP
I	38.66	94.23	103.58	2.97	1.11	5.11	42.95	3.21	39.62	23.88	5.23
II	40.28	94.44	106.39	2.98	1.06	3.96	52.73	3.12	40.86	18.39	4.19
III	40.37	94.73	100.72	2.76	0.87	5.09	40.48	2.90	42.23	14.77	3.11
IV	39.33	91.33	98.20	3.30	1.33	6.33	39.97	3.73	36.93	20.47	7.23
V	43.00	94.17	111.70	3.17	1.27	6.13	43.87	3.37	38.77	18.53	7.73
VI	41.83	98.33	108.90	3.17	1.30	7.27	36.57	3.27	36.13	24.50	7.03
VII	39.67	91.50	101.77	3.33	1.33	7.00	49.13	3.70	38.30	22.73	6.67
VIII	38.33	101.50	106.13	3.23	1.17	4.73	48.00	3.53	38.10	33.53	8.00
IX	40.50	97.17	109.13	2.97	1.07	6.07	55.17	3.23	38.43	34.57	5.57
X	38.00	96.00	115.53	3.80	1.80	5.33	47.27	3.80	37.27	24.40	7.67
Over all mean	40.00	95.34	106.21	3.17	1.23	5.70	45.61	3.39	38.66	23.58	6.24

Table7:Percentagecontributionofeachcharacterstowardsdivergence

Sr.No.	Source	TimesRanked1st	Contribution%
1	DFF	5	0.58 %
2	DM	1	0.12 %
3	PH	8	0.93 %
4	CL	9	1.05 %
5	CW	62	7.20 %
6	CC	183	21.25 %
7	LF	270	31.36 %
8	SW	8	0.93%
9	OC	2	0.23 %
10	HI	165	19.16 %
11	SYP	148	7.19 %

DFF=Days to 50% flowering, DM=Days to maturity, PH=Plant height, CL=Capsule length, CW=Capsule width, CC=Capsule per cluster, LA=Leaf area, SW=1000 seed weight, OC=Oil content, HI=Harvest index, SYP=Seed yield per plant,

The positive genotypic associationhas been reported between seed yield perplantandcapsulelengthbyParmeswarappa*etal*.(2009),Rao*etal*.(2013),Abhijatha*etal*. (2017), Patil and Lokesha (2018); forseed yield per plant and 1000 seed weightby Bhuvan and Sharma (2004), Yol*etal*.(2010), Fazal*etal*. (2015), Imran and dash(2018); for seed yield per plant and harvestindex by Gidey*etal*. (2013), Bamrotiya*etal*. (2016a) and Patil and Lokesha (2018),respectively.Thepresentresultsoncorrelation coefficients revealed that, daysto maturity, capsule length, capsule width,capsules per cluster, 1000 seed weight andharvestindexwerethemostimportantattributes and may contribute considerablytowards higher seed yield per plant. Theinterrelationship among yield componentswould help in increasing the yield levelsandtherefore,moreemphasisshouldbegiven to these components while selectingbettertypesinsesameimprovementprogrames.

Pathcoefficientanalysiswascarriedoutwiththeobjectiveofpartitioningthegenotypiccorrelationofyield component with seed yield into directandindirecteffectsforelevenvariables.The seed yield was regarded as resultantvariablewhiletheothertraitsascausalvariable.Theestimatesofdirectandindirect effects of various traits along withtheir genotypic correlations with yield arepresentedinTable-4.Pathcoefficientanalysisrevealedthatdaysto50%flowering,daystomaturity,capsulelength,capsulewidth,1000seedweightandharvestindexexertedpositivedirecteffectsonseedyieldperplant.Inthe presentstudy,the residual effect at genotypic level was0.2732indicating, that all of the traits included in the study explained moderate percentage of variation in seed yield per plant (72.68%), while other factors not included in the study would explain 27.32%.Thesecharactersalsoexhibitedhighly significant and positive associationswith seed yield per plant and hence, theymay be considered as the most importantyieldcontributingcharactersandddueemphasisshouldbeplacedonthesecomponentswhile selectingforhighyieldingtypes in sesame.

TheMahalanobis'sD^{2}statisticswascomputedforallpossiblepairofpopulations under investigation. Forty-twogenotypes of sesame were grouped into tenclusters on the basis of relative magnitudeof D^{2}values following Tocher'smethod(Rao,1952).ClusterIwasthelargestcluster having twenty one genotypes. The secondlargest cluster II had nine while cluster IIIhad five genotypes, respectively whereascluster IV, V, VI, VII, VIII, IX and X weremono genotypic. Thus, the present resultsindicatedthatgeographicaldistributionandgenetic divergence did not follow the samepattern. Therefore, it can be concluded thatselectionofparentsforhybridizationshouldnotbebasedongeographicaldiversity only, but it should have a base ofboth geographical origin as well as geneticdivergence.SimilarfindingshavebeenreportedbyJadhavandMohrir(2013),Gogoi*etal.*(2018),Mohan(2014b),Ramprasad*etal.* (2019b), Soudharya*etal.*(2018b),Swathy*etal.*(2018)andMohanty*etal.* (2020b).

Intraandinterclusterdistance(Table5withfigure 1.) between all possible pairs of tenclusters were computed with the help ofmethodgivenbySinghandChaudhary(1977). The intra cluster distance rangedfrom 6.63 to 5.46. The cluster II exhibitedmaximumsintraclusterdistance(6.63)followed by the cluster I (6.19) and clusterIII (5.46). The intra cluster distance waszeroforclusterIV,V,VI,VII,VIII,IXandXindicatingthatgenotypeswithinthisclusterweresimilar.Theinterclusterdistance ranged from 16.51 to 4.35. TheinterclusterdistancebetweenclusterIIIand X (16.51) was maximum followed byclusterIIIandVIII(14.41),IIIandIX(14.12) and II and VI(13.49). The minimuminterclusterdistancewasobserved between cluster IV and V (4.35)followedbythatofclustersIVandVI(4.55),IVandVII(4.79),VandVII(5.02)andV and VI(5.68).

Ingeneral,intra-clusterdistancevalueswerelowerthantheinterclusterdistanceswhichindicatedsubstantialdiversitypresentamongthegenotypesstudied.Thus,thegenotypesincludedwithin a cluster tended to diverse less fromeachother.

Clustermeanfortheelevencharacters are presented in Table 6. Cluster I had a mean values greater than over all mean for Oil content and harvest index, but for the rest of traits it had mean values lower than the overall mean. Cluster II had a mean values greater than the overall mean for days to 50% flowering and oil content. Cluster III exhibited the lowest mean value for most of the traits viz., capsule length, capsule width, 1000 seed weightand harvest index. Cluster IV depicted mean value for second highest mean value for capsule width and 1000 seed weight. The lowest mean value for days to maturity, plant height and oil content was noticed in cluster IV.Cluster V depicted highest mean value for days to 50% flowering whereas second highest mean value for plant height and seed yield per plant. Cluster VI showed highest mean value for capsules per cluster. Besides this, it had lowest mean value for leaf area.Cluster VII exhibited second highest mean values for capsule length, capsule widthand capsules per cluste. Cluster VIII depicted highest mean value for days to maturity and seed yield per plant. Cluster IX depicted highest mean value for leaf area and harvest index. Cluster X showed highest mean value for most of traits *viz.* plant height, capsule length, capsule width and 1000 seed weight whereas lowest mean value for days to 50% flowering.

Itcouldbeconcludedthathighyielding genotypes coupled with desirabletraitslikeplantheight,capsulelength,capsule width, capsules per cluster, 1000seed weight, harvest index and seed yieldper plants could be selected as parents forhybridization programme from cluster X,IX, VI and VIII. Intercrossing genotypesfromthese clustersmightresultinwidearray of variability for exercising effectiveselection.

The component of D^2 due to eachcharactervariablewasrankedindescendingorderofmagnitude,rank-Ibeingassignedtothehighestvalue.Thepercent contribution of different characters todiversityispresentedinTable-7.Thepresentstudyrevealedthatleafarea(31.36%), capsulespercluster (21.25%),harvestindex(19.16%),capsulewidth(7.20%), seed yield per plant (7.19%) andcapsulelength(1.05%)werethemaincontributors to the total divergence. Thesesixcharactersaccountedfor87.21%oftotaldivergence. The contribution of remainingfivecharacterswas negligibletosmall.

Conclusion

The analysis of variance revealed the presence of sufficient variability among the genotypes for different characters.Maximum range of variation was observed for plant height followed by leaf area and days to maturity indicating the presence of wide variation for the characters.The values of phenotypic coefficient of variation were higher than genotypic coefficient of variation indicating the less influence of environmental factors in most of the characters. The highest genotypic coefficient of variation was observed for seed yield per plant followed by capsules per cluster and harvest index which indicated the presence of wide genetic variation for these characters.High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for the traits viz., capsule width, capsules per cluster, leaf area, harvest index and seed yield per plant indicating that these characters are under the control of additive gene effect. Therefore, further improvement in these traits using pure line selection would be worthwhile.The seed yield per plant was found to be significant and positively correlated with days to maturity, capsule length, capsule width, capsules per cluster, 1000 seed weight and harvest index at genotypic and phenotypic levels. The oil content had highly significant and negative association with seed yield per plantPath coefficient analysis showed days to 50% flowering, days to maturity, plant height, capsule length, capsule width, 1000 seed weight and harvest index positive direct effects on seed yield per plant. Hence, these traits were considered as the most important yield contributors and due emphasis should be given while attempting seed yield improvement in sesame.The genetic diversity analysis revealed the formation of ten clusters suggested the presence of wide genetic diversity among the forty-two genotypes studied.The geographic diversity was not associated with genetic diversity. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that leaf area followed by capsules per cluster, harvest index, capsule width, seed yield per plant and capsule length were the main contributors to the total divergence. These six characters accounted for more than 87.21% of total divergence in the material studied. Based on the maximum genetic distance, it is advisable to attempt intercrossing of the genotypes from cluster X, IX and VIII, which may lead to broad spectrum of favorable genetic variability for yield improvement in sesame.Thepresentstudysuggestedthatdays to maturity, capsule length, capsulewidth,capsulespercluster,1000seedweightandharvestindexshouldbeconsideredasselectioncriteriaf oryieldimprovementin sesame.

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