*Original Research Article*

# GeneticVariability,PathanalysisanddivergencestudiedinSesame(*Sesamumindicum*L.)

## ABSTRACT

The study was conducted during *rabi*, 2020 at the at Niger Research Station, NavsariAgricultural University, Vanarasi, Ta. Vansda to assess the information on genetic variability,characterassociationandpathanalysisamong42genotypesofsesame(*Sesamumindicum*L.).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$^2$analysisindicatedwidergeneticdiversityamongtheforty-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, *Sesamumindicum*L.

## Introduction

Sesame(*Sesamumindicum*L.)isoneofthemost important ancient cultivated oilseedscropgrowninAsiaandAfrica.ItbelongstoPedaliaceaefamilyhavingchromosomenumber as (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. The Observationwere 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)**.**Correlationcoefficientsforyieldandyieldcomponentswereevaluatedutilizing the formula suggested by PanseandSukhatme(1987).

## ResultsandDiscussion

The present experimental materialshowed 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).Thissuggeststhatthereisamplescopetoidentifyhighyieldingtraitspossessinggenotypes.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),Gideyetal.(2012),Bharathietal.(2014),AbateandMekbib(2015a) andIqbal etal.(2016).

The estimates of genotypic (GCV)andphenotypic(PCV)coefficientsofvariability(Table-2)indicatedthatthevalues of PCV were higher than GCV forall the traits due partly to interaction of thegenotypes with the environment or otherenvironmentalfactorsinfluencingtheexpressionofthesecharacters.Thehighestvalue of GCV and PCV was observed forcapsulespercluster,harvestindexandseedyield per plant. High magnitude of GCVindicatedthepresenceofwidevariationforthe characters under study to allow furtherimprovement by selection of the individualtrait.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 (Table-2)were observed for the traits *viz.*, capsulewidth,capsulespercluster,leafarea,harvestindexandseedyieldperplantindicating that these characters are underthecontrolofadditivegeneeffect.Therefore,furtherimprovementinthesetraits using pure line selection would beworthwhile.SimilarresultreportedbyReddyetal.(2001),Krishnaiahetal.(2002);forharvestindexbyMohanty(2020a).

Thecorrelationcoefficientsbetween seed yield per plant and its elevencomponentcharactersandamongthemselveswereestimatedatgenotypicandphenotypiclevelsandarepresentedinTable-3 Genotypic ($r_g$) and phenotypic ($r_p$)correlationsaredescribedasunder.Ingeneral,thevaluesofgenotypiccorrelationswerehigherthantheircorrespondingphenotypiccorrelations.This indicated that though 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.Suchpositiveinterrelationshipbetweenseedyieldperplantandtheseattributeshasalsobeenreportedin sesamebyseveralresearchers.

**Table1:Analysisof variancefordifferentcharactersin sesame**

| Source ofVariation | d.f. | MSS | | | | | |
|---|---|---|---|---|---|---|---|
| | | Days to50%flowering | Days tomaturity | Plantheight(cm) | Capsule length(cm) | Capsule width(cm) | Capsules percluster |
| **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 |

| Sourceof Variation | d.f. | MSS | | | | |
|---|---|---|---|---|---|---|
| | | Leafarea(cm$^2$) | 1000seedweight(g) | Oilcontent(%) | Harvestindex (%) | Seed yield perplant(g) |
| **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 |

*and** indicatessignificanceat5% and1%levelsof probability,respectively

**Table 2: Range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and geneticadvanceas percent of mean fordifferent charactersofsesame**

| **Sr. No.** | **Characters** | **Range** | **Mean** | **Coefficient ofvariance** | | **Heritability $h^2$(%)** | **GeneticAdvance (GA)** | **GeneticAdvance as percent Mean(GAM)** |
|---|---|---|---|---|---|---|---|---|
| | | | | **GCV** | **PCV** | | | |
| **1** | Daysto50% flowering | 35.33 -43.33 | 39.45 | 4.38 | 6.86 | 40.69 | 2.27 | 5.75 |
| **2** | Daysto maturity | 85.67 – 101.50 | 94.58 | 2.31 | 5.60 | 17.00 | 1.86 | 1.96 |
| **3** | Plantheight(cm) | 88.40 – 116.90 | 104.47 | 5.27 | 8.54 | 38.06 | 6.99 | 6.69 |
| **4** | Capsulelength (cm) | 2.57 – 3.80 | 3.00 | 6.76 | 9.23 | 53.69 | 0.31 | 10.20 |
| **5** | Capsulewidth (cm) | 0.77 – 1.80 | 1.10 | 16.26 | 18.42 | 77.95 | 0.33 | 29.57 |
| **6** | Capsulesper cluster | 2.27 – 7.27 | 5.03 | 24.42 | 26.36 | 85.82 | 2.34 | 46.61 |
| **7** | Leaf area($cm^2$) | 36.30 – 56.43 | 45.21 | 12.62 | 13.60 | 86.02 | 10.90 | 24.11 |
| **8** | 1000seedweight (g) | 2.70 – 3.80 | 3.21 | 7.72 | 10.07 | 58.80 | 0.39 | 12.20 |
| **9** | Oilcontent(%) | 36.13 – 44.07 | 39.88 | 2.81 | 6.50 | 18.69 | 1.00 | 2.50 |
| **10** | Harvestindex (%) | 11.17 – 34.57 | 21.90 | 23.17 | 25.30 | 83.85 | 9.57 | 43.70 |
| **11** | Seed yieldper plant(g) | 2.03 – 8.00 | 5.07 | 27.24 | 30.14 | 81.65 | 2.57 | 50.70 |

**Table3:Genotypic($r_g$) andPhenotypic($r_p$) correlationcoefficientsforyieldandyieldattributingtraitsinsesamegenotypes**

| Characters | | DFF | DM | PH | CL | CW | CC | LA | SW | OC | HI | SYP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DFF** | $r_g$ | **1.000** | | | | | | | | | | |
| | $r_p$ | **1.000** | | | | | | | | | | |
| **DM** | $r_g$ | 0.416$^{**}$ | **1.000** | | | | | | | | | |
| | $r_p$ | 0.130$^{NS}$ | **1.000** | | | | | | | | | |
| **PH** | $r_g$ | -0.446$^{**}$ | -0.017$^{NS}$ | **1.000** | | | | | | | | |
| | $r_p$ | -0.166$^{NS}$ | -0.075$^{NS}$ | **1.000** | | | | | | | | |
| **CL** | $r_g$ | -0.259$^{**}$ | 0.025$^{NS}$ | 0.043$^{NS}$ | **1.000** | | | | | | | |
| | $r_p$ | -0.175$^{NS}$ | -0.025$^{NS}$ | 0.161$^{NS}$ | **1.000** | | | | | | | |
| **CW** | $r_g$ | -0.206$^{*}$ | -0.045$^{NS}$ | 0.119$^{NS}$ | 1.079$^{**}$ | **1.000** | | | | | | |
| | $r_p$ | -0.113$^{NS}$ | -0.011$^{NS}$ | -0.014$^{NS}$ | 0.689$^{**}$ | **1.000** | | | | | | |
| **CC** | $r_g$ | 0.122$^{NS}$ | -0.030$^{NS}$ | -0.232$^{**}$ | 0.099$^{NS}$ | 0.242$^{**}$ | **1.000** | | | | | |
| | $r_p$ | 0.132$^{NS}$ | -0.014$^{NS}$ | -0.149$^{NS}$ | 0.039$^{NS}$ | 0.205$^{*}$ | **1.000** | | | | | |
| **LA** | $r_g$ | 0.012$^{NS}$ | 0.298$^{**}$ | 0.244$^{**}$ | 0.127$^{NS}$ | 0.047$^{NS}$ | -0.264$^{**}$ | **1.000** | | | | |
| | $r_p$ | -0.021$^{NS}$ | 0.095$^{NS}$ | 0.070$^{NS}$ | 0.036$^{NS}$ | 0.050$^{NS}$ | -0.201$^{*}$ | **1.000** | | | | |
| **SW** | $r_g$ | -0.272$^{**}$ | -0.406$^{**}$ | 0.066$^{NS}$ | 0.862$^{**}$ | 0.825$^{**}$ | 0.260$^{**}$ | -0.069$^{NS}$ | **1.000** | | | |
| | $r_p$ | -0.131$^{NS}$ | -0.133$^{NS}$ | 0.042$^{NS}$ | 0.535$^{**}$ | 0.575$^{**}$ | 0.159$^{NS}$ | -0.079$^{NS}$ | **1.000** | | | |
| **OC** | $r_g$ | 0.475$^{**}$ | -0.398$^{**}$ | -0.119$^{NS}$ | -1.144$^{**}$ | -1.146$^{**}$ | -0.528$^{**}$ | 0.074$^{NS}$ | -0.984$^{**}$ | **1.000** | | |
| | $r_p$ | 0.059$^{NS}$ | -0.098$^{NS}$ | -0.040$^{NS}$ | -0.407$^{**}$ | -0.454$^{**}$ | -0.205$^{*}$ | 0.082$^{NS}$ | -0.405$^{**}$ | **1.000** | | |
| **HI** | $r_g$ | -0.427$^{**}$ | 0.186$^{*}$ | 0.215$^{*}$ | 0.273$^{**}$ | 0.293$^{**}$ | 0.134$^{NS}$ | -0.009$^{NS}$ | 0.320$^{**}$ | -0.747$^{**}$ | **1.000** | |
| | $r_p$ | -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** | $r_g$ | -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** |
| | $r_p$ | -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** |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **DFF** | = | Daysto 50%flowering | **DM** | =Daysto maturity | **PH** | =Plantheight(cm) | **CL** | =Capsulelength(cm) |
| **CW** | = | Capsulewidth(cm) | **CC** | =Capsulespercluster | **LA** | =Leaf area($cm^2$) | **SW** | =1000 seedweight(g) |
| **OC** | = | Oilcontent(%) | **HI** | =Harvestindex(%) | **SYP** | =Seed yieldperplant(g) | | |

**Table4:Genotypicpathcoefficientshowingdirectandindirecteffects foryieldandyield attributingtraitsin 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), Numbersinbold indicatedirecteffects

**DFF** = Daysto 50%flowering
**CW** = Capsulewidth(cm)
**OC** = Oilcontent(%)
**DM** =Daysto maturity
**CC** =Capsulespercluster
**HI** =Harvestindex(%)
**PH** =Plantheight(cm)
**LA** =Leaf area(cm$^2$)
**SYP** =Seed yieldperplant(g)
**CL** =Capsulelength(cm)
**SW** =1000 seedweight(g)

**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

**Fig1.Clusterdiagramindicatingintra andinter-clusterdistance**

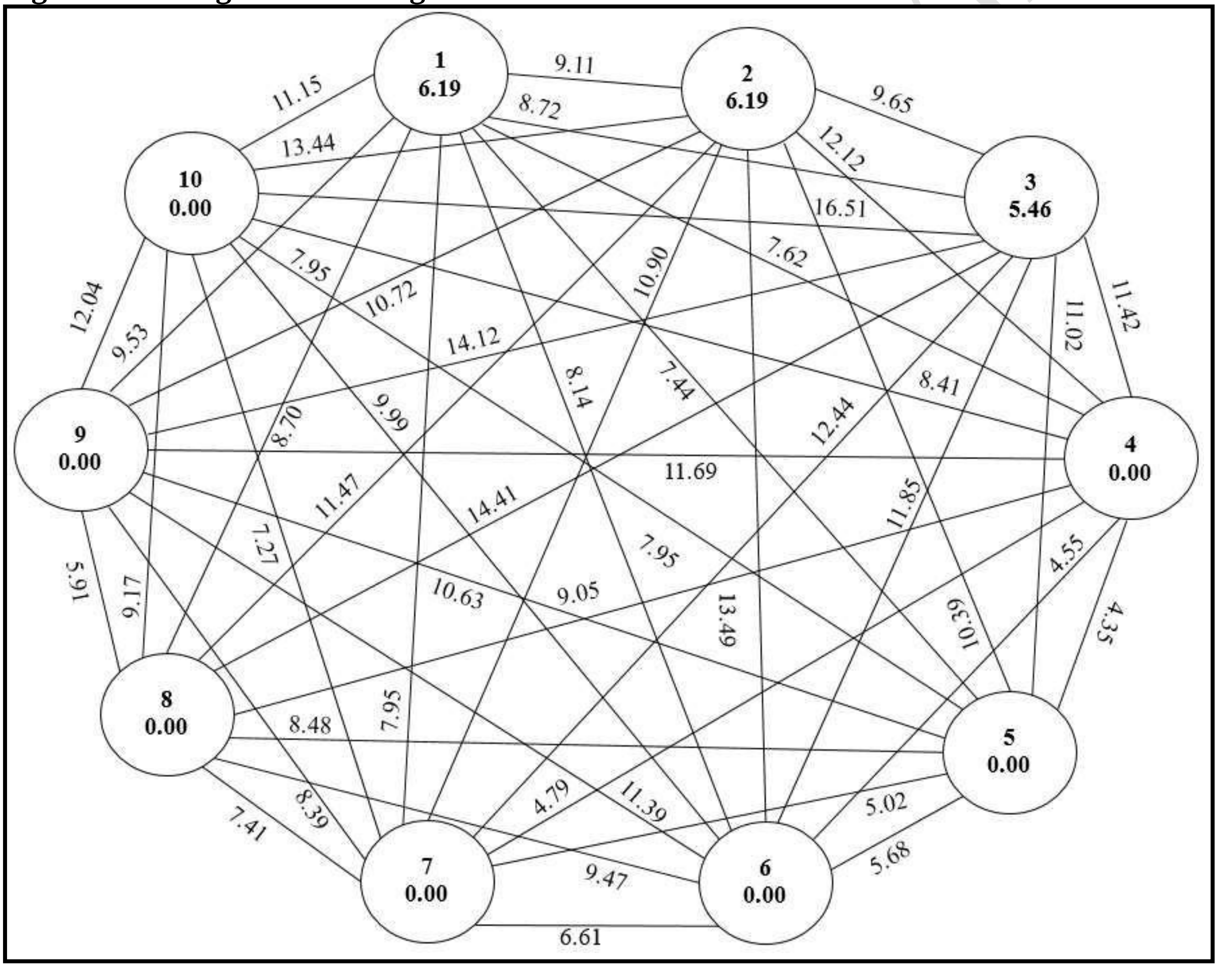

**Table6:Cluster means foryieldandyieldcontributingtraitsofsesamegenotypes**

| 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 |

**Table7:Percentagecontributionofeachcharacters towardsdivergence**

| Sr.No. | Source | TimesRanked1st | Contribution% |
|---|---|---|---|
| 1 | Daysto50 %flowering | 5 | 0.58 % |
| 2 | Daysto maturity | 1 | 0.12 % |
| 3 | Plantheight(cm) | 8 | 0.93 % |
| 4 | Capsulelength(cm) | 9 | 1.05 % |
| 5 | Capsulewidth (cm) | 62 | 7.20 % |
| 6 | Capsulespercluster | 183 | 21.25 % |
| 7 | Leaf area(cm$^2$) | 270 | 31.36 % |
| 8 | 1000seedweight(g) | 8 | 0.93% |
| 9 | Oilcontent(%) | 2 | 0.23 % |
| 10 | Harvestindex(%) | 165 | 19.16 % |
| 11 | Seedyieldperplant(g) | 148 | 7.19 % |

The positive genotypic associationhas been reported between seed yield perplantandcapsulelengthbyParmeswarappaetal.(2009),Raoetal.(2013),Abhijathaetal. (2017), Patil and Lokesha (2018); forseed yield per plant and 1000 seed weightby Bhuvan and Sharma (2004), Yol et al.(2010), Fazal et al. (2015), Imran and dash(2018); for seed yield per plant and harvestindex by Gidey et al. (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 selectingbettertypesinsesameimprovementprogrammes.

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 was0.2732whichsuggestedthattheremightbefew more component traits responsible toinfluencetheseedyieldperplantthanthosestudied.Thesecharactersalsoexhibitedhighly significant and positive associationswith seed yield per plant and hence, theymay be considered as the most importantyieldcontributingcharactersanddueemphasisshouldbeplacedonthesecomponentswhile 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's method(Rao,1952).ClusterIwasthelargesthaving 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 *et al.* (2019b), Soudharya*et al.*(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-clusterdistancevalueswerelowerthantheinter-clusterdistanceswhichindicatedsubstantialdiversitypresentamongthegenotypesstudied.Thus,the genotypesincludedwithin a cluster tended to diverse less fromeachother.

Clustermeanfortheelevencharacters are presented in Table 6. ClusterI exhibited third highest mean value for oilcontent(39.62%).Thesecondhighestmeanvalueforleafarea(52.73cm$^2$)andoilcontent(40.86%) whereaslowestmeanvalueofcapsulespercluster(3.96)andseedyield per plant (4.19 g) was recorded incluster II. Cluster III exhibited the lowestmeanvalueformostofthetraitsviz.,capsulelength(2.76cm),capsulewidth(0.87 cm), 1000 seed weight (2.90 g) andharvestindex(14.77%).ClusterIVdepictedmeanvalueforsecondhighestmeanvalueforcapsule width(1.33cm)and1000seedweight(3.73g).Thelowestmeanvaluefordaystomaturity (91.33days),plantheight(98.20cm)andoilcontent(36.93%)wasnoticedinclusterIV.ClusterV depicted highest mean value for days to50%flowering(43.00days)whereassecond highest mean value for plant height(111.70 cm) and seed yield per plant (7.73g). Cluster VI showed highest mean valueforcapsulespercluster(7.27).Besidesthis,ithadlowestmeanvalueforleafarea(36.57 cm2). Cluster VII exhibited secondhighestmeanvaluesforcapsulelength(3.33cm),capsulewidth(1.33cm)andcapsulespercluster(7.00).ClusterVIIIdepictedhighestmeanvalue for daystomaturity (101.50 days) and seed yield perplant (8.00 g). Cluster IX depicted highestmean value for leaf area (55.17 cm2) andharvest index (34.57%). Cluster X showedhighest mean value for most of traits *viz.*plant height (115.53 cm), capsule length(3.80cm),capsulewidth(1.80cm)and1000seedweight(3.80g)whereaslowestmeanvaluefor daysto50%flowering(38.00days).

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 todiversityispresentedinTable7.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

Thepresentstudysuggestedthatdays to maturity, capsule length, capsulewidth,capsulespercluster,1000seedweightandharvestindexshouldbeconsideredasselectioncriteriaforyieldimprovementin sesame.

### Reference

Abate,M.andMekbib,F.(2015a).AssessmentofgeneticvariabilityandcharacterassociationinEthiopianlow-altitude sesame (*Sesamum indicum* L.)genotypes.*J.Adv.Stud.Agric.Biol.Environ.Sci*., **2** (3): 55-66.

Abhijatha, A.; Arya, K.; Madhukar, K. andGogineni, S. (2017). Evaluation of

sesame(*Sesamumindicum*L.)genotypestothe

shaded uplands of southern region. *Int. J.Curr.Microbiol.Appl.Sci.*,**6**(7):332-339.

Bamrotiya, M. M.; Patel, J. B.; Malav, A.;Chetariya, C. P.; Ahir, D. and Kadiyara, J.(2016a).Geneticvariability,characterassociationandpathanalysisinsesame(*Sesamum Indicum* L.). *Int. J. Agric. CropSci.*,**8**(54): 2912-2916.

Bharathi, D.; Rao V. T.; Mohan, Y. C.;Bhadru,D.andVenkanna,V.(2014).Geneticvariabilitystudiesinsesame(*Sesamumindicum*L.).*Intern.J.Appl.Biol.Pharmac. Technol*, **5**:31-33.

Bhuvan,J.andSharma,M.K.(2004).Characterassociationstudiesinsesame(*Sesamumindicum*L.)underrainfedcondition.*Adv.PlantSci.*,**17**(1):313-316.

Bedigian,D.;Smyth,C.A.andHarlan,J. R.(1986).Patternsofmorphologicalvariation in *Sesamum indicum* (L.). *Econ.Bot.*,**40**: 353-365.

Dewey,D.R.andLuK.H.(1959).Correlation and path coefficient analysis ofcomponentsofcrestedwheatgrassseedproduction.*J. Agron.*, **51**: 515-518.

Fazal, A.; Mustafa, H. S. B.; Hasan, E. U.;Anwar,M.;Tahir,M.H.N.andSadaqat,H. A.(2015).Interrelationshipandpathcoefficient analysis among yield and yieldrelated traits in sesame (*Sesamum indicum*L.).*Nat. sci.*, **13** (5): 27-32.

Gawali, C. W.; Bhoite, K. D.; Pardeshi, S.R.;Mhaske,B.M.andWagh,M.P.(2007).Study of genetic variability and correlationstudies in sesame (*Sesamum indicum* L.).*Agril.Sci. Digest*, **27**: 282-284.

Gayathri, G. (2011). Heterosis breeding insesame (*Sesamum indicum* L.). Ph.D. (Ag)thesis,KeralaAgriculturalUniversity,Thrissur,p. 180.

Gidey,Y.T.;Kebede,S.A.andGashawbeza, G. T. (2012). Assessment ofgeneticvariability,geneticadvance,correlationandpathanalysisformorphological traits in sesame genotypes.*Intern.J. PlantBreed. Genet*, **7**:2-14

Gidey,Y.T.;Kebede,S.A.andGashawbeza, G. T. (2013). Assessment ofgeneticvariability,geneticadvance,correlationandpathanalysisformorphological traits in sesame genotypes.*Int.J. PlantBreed. Genet.*,**7** (1): 21-34.

Gogoi,L.R.;Singh,S.K.andSarma,R.N.(2018). Assessment of genetic diversity inindigenous sesame genotypes. *Int. J. Curr.Microbiol.Appl. Sci*.,**7** (6): 1509-1520.

Iqbal,A.;Akhtar,R.;Begum,T.andDasgupta, T. (2016). Genetic estimates anddiversitystudyinsesame(*Sesamumindicum* L.). *IOSR J. Agric. Veter. Sci.*, **9**:1-5.

Jadhav, R. S. and Mohrir, M. N. (2013).Geneticdivergenceanalysisinsesame(*Sesamum indicum* L.). *Electron. J. PlantBreed.*,**4** (1): 1090-1092.

Krishnaiah,G.;Reddy,K.R.andSekar,M. R.(2002).Variabilitystudiesinsesame. *CropRes.*, **24**(3): 501-504.

Mandal, R. K.; Suman, S. J.; Ojha, R. K.and Ram, S. (2010). Genetic variability inthegermplasmofsesame(*Sesamumindicum*L.).*Environ.Ecol.*,**28**(4):2556-2561.

Mohan,Y.C.(2014b).Variabilityandgeneticdivergenceinsesame(*Sesamumindicum*L.). *Int.J.Appl.Biol.Pharma.Tech.*,**5** (3): 222-225.

Mohanty,T.A.;Singh,U.K.;Singh,S.K.;Kushwaha,N.andSingh,D.(2020a).Studyofgeneticvariability,heritabilityandgeneticadvanceinsesame(*Sesamumindicum*L.)genotypes. *Int.J.Curr.Microbiol.App. Sci*, **9** (02): 347-356.

Mohanty,T.A.;Singh,U.K.;Singh,S.K.;Singh,D.andKushwaha,N.(2020b).Assessment of genetic diversity in sesame(*Sesamumindicum*L.)basedonagro-morphologicaltraits. *Curr.J.Appl.Sci.Technol.*,**39** (25): 101-107.

Mukhtar, M. S.; Rahman, M. and Zafar, Y.(2002).Assessmentofgeneticdiversityamongwheat(*Triticumaestivum*L.)

cultivars from a range of localities acrossPakistanusingrandomamplifiedpolymorphicDNAanalysis.*Euphytica*,**128**:417-425.

Mumtaz,S.A.;Naveed,M.andShinwari, Z.K.(2010).Assessmentofgeneticdiversityandgerminationpatterninselected cotton genotypes of Pakistan. *Pak.J.Bot*.,**42** (6): 3949-3956.

Pandey,S.K.;Das,A.;Rai,P.andDasgupta,T.(2015).Morphologicalandgeneticdiversityassessmentofsesame(*Sesamum indicum* L.) accessions differinginorigin.*Physiol.Mol.Biol.Plants*,**21**(4):519-529.

Patil,M.K.andLokesha,R.(2018).Estimationofgeneticvariability,heritability,geneticadvance,correlationsandpathanalysisinadvancedmutantbreedinglinesofsesame(*Sesamumindicum* L.). *J. Pharmacogn. Nat. Prod.*, **4**:151.

Quarrie,S.;Peki,Q.S.;Radosevi,R.;Rancic,D.andKaminska,A.(2006).DissectingawheatQTLforyieldpresentina range of environments: From the QTL tocandidategenes.*J. Exp. Bot.*,**57**:2627-2635.

Raghuwanshi,S.S.;Kachadia,V.H.;Vachhani,J.H.;Jivani,L. L.;Malav,A.K.and Bhati S. S. (2015). Selection indices ingroundnut(*Arachishypogaea*L.).*Electron.J.PlantBreed.*,**7**(1):140-144.

Ramprasad,E.;Jatothu,S.S.J.L.;Yamini, K.N.andDangi,K.S.(2019b).Analysisofgeneticdiversityinsesame(*Sesamumindicum* L.) advanced breeding lines andvarietiescollectedfrommajorbreedingcentersinIndia. *Electron.J.PlantBreed.*,**10** (3): 1269-1274.

Rao,V.T.;Bharathi,D.;Mohan,C.;Venkanna,V.andBhadru,D.(2013).Genetic variability and association analysisinsesame(*Sesamumindicum*L.). *CropRes.*,**46**: 122-125.

Rao,C.R.(1952).AdvancedStatisticalMethodsinBiometricalResearch,JohnWileyandSons,New York, 357-369.

Reddy,P.A.V.;Sekar,M.R.;Ranganatha,
A. R. G. and Dhanraj, A. (2001). Geneticvariability andheritability for seedyieldand its components in sesame (*Sesamumindicum*L.).*J.OilseedsR.*,**18**(2):173-175.Sarwar,G.andHaq,M.A.(2006).Evaluationforgeneticparametersanddisease resistance in sesame. *J. Agric. Res.*,**3**:44-46.

Singh, B. S. and Choudhary, R. K. (1977).Biometricalmethodsinquantitativegenetic analysis. Kalyani Publishers, NewDelhi,pp. 20-35.

Soundharya,B.;Hemalatha,V.;Shobha,R.andEdukondalu,B.(2017b).Geneticdivergencestudiesinsesame(*Sesamumindicum*L.)genotypes. *Int.J.Curr.Microbiol.Appl. Sci*,**6** (9): 2615-2619.

Sumathi, P. and Muralidharan, V. (2010).Analysis of genetic variability, associationand path analysis in the hybrids of sesame(*Sesamum indicum*L). *Trop. Agric. Res.Ext.*,**13** (3): 63-67.

Swathy,V.;Premnath,A.;Viswanathan,P.L.;Raveendran,M.andManonmani,S.(2018).Determinationofgeneticdivergencebasedonmorphologicaltraitsinsesame (*Sesamum indicum* L.). *ElectronicJ.Plant Breed.*, **9** (2): 747-752.
Valarmathi,G.;Kumar,M.andSaravana,
N.A.(2004).Geneticvariabilityandcorrelation studies for seed related traits insesame(*Sesamumindicum*L.).*SesameandSafflowerNewsletter*, p.19.

Wattoo,F.M.;Saleem,M.;Ahsan,M.;Sajjad,M.andAli,W.(2009).Geneticanalysisforyieldpotentialandqualitytraitsin maize (*Zea mays* L.). *Am.-Eurasian J.Sustain.Agric.*, **6** (6): 721-732.

Yol,E.;Karaman,E.;Furat,S.andUzun,
B. (2010). Assessment of selection criteriain sesame by using correlation coefficients,pathandfactoranalyses.*AustralianJ.CropSci.*,**4** (8): 598-602.