➔DOI : 10.15740/HAS/AJBS/12.2/194-201
e ISSN-0976-8343 | ■ Visit us : *www.researchjournal.co.in*
ASIAN JOURNAL OF BIO SCIENCE
Volume **12** | Issue 2 | Oct., 2017 | 194-201

RESEARCH **P**APER

Genetic analysis of *Sesamum indicum* L. germplasm using RAPD markers

K. HANUMANTHA RAO[1], RAMESH CHOUDHARY[1] **AND** BHANWAR LAL JAT[2]

[1]Department of Agriculture, Bhagwant University, AJMER (RAJASTHAN) INDIA
[2]Department of Agricultural Biotechnology, Bhagwant University, AJMER (RAJASTHAN) INDIA
Email : hanumantharao.agri@gmail.com

Article Info : Received : 25.05.2017; Revised : 17.08.2017; Accepted : 15.09.2017

Genetic diversity among 14 sesame (*Sesamum indicum* L.) accessions was examined at DNA level by means of random amplified polymorphic DNA (RAPD) analysis. Twenty primers used to produce a total of 201 RAPD fragments, of which 120 (59.70%) were polymorphic. Each primer generated 4 to 15 amplified fragments with an average of 10.05 bands per primer. Based on pair-wise comparisons of RAPD amplification products, simple match similarity co-efficients were computed to assess the associations among the accessions. Pair-wise similarity indices varied from 0.63 to 0.91. A UPGMA cluster analysis based on these genetic similarities located most of the accessions far apart from one another, showing a high level of polymorphism. Genetically, all the genotypes were classified into four major clusters. A single accession (Kayamkulam) was relatively distinct from rest of the accessions and created independent cluster. In conclusion, even with the use of a limited set of primers, RAPD technique revealed a high level of genetic variation among sesame accessions collected from diverse ecologies of India. This high level of genetic diversity among the genotypes suggested that RAPD technique is valuable for sesame systematic and can be helpful for the upholding of germplasm banks and the competent choice of parents in breeding programmes.

Key words : RAPD, DNA, Genetic analysis, Germplasm, Sesame

How to cite this paper : Rao, K. Hanumantha, Choudhary, Ramesh and Jat, Bhanwar Lal (2017). Genetic analysis of *Sesamum indicum* L. germplasm using RAPD markers. *Asian J. Bio. Sci.*, **12** (2) : 194-201.**DOI : 10.15740/HAS/AJBS/12.2/194-201.**

INTRODUCTION

Sesame (*Sesamum indicum* L.) of the family Pedaliaceae, is one of the oldest oil crops being cultivated in Asia for more than 5000 years. The genus *Sesamum* contains more than 30 species of which *S. indicum* is the commonly cultivated (Nayar and Mehra, 1970 and Kobayashi *et al*., 1990). The exact natural origin of the sesame is mysterious. India and Africa are the two expected places of its origin. Ashri (1995) felt that settling the dispute on the origin of sesame will involve more detailed cytogenetic and fitting DNA comparisons. Sesame seeds are in high demand because of its significance in the confectionary industry universally. Sesame contains about 50–60 per cent odorless and colorless oil (Uzun *et al.,* 2003), which is of superior class with antioxidants, almost matching olive oil. Sesame oil is used as a cooking medium mainly in the Indian subcontinent and African countries. Small uses of sesame oil consist of pharmaceutical and skin care products and are synergic for insecticides (Hatam and Abbasi, 1994). Sesame oil also contains a high level of polyunsaturated fatty acids (Wood, 1999). It has a reducing consequence on plasma cholesterol and it also lowers the blood pressure (Sankar *et al.,* 2005). Potential reimbursement of sesame on human health has freshly rehabilitated the attention in this ancient crop (Laurentin and Karlovsky, 2006). Sesame is grown over 50 countries in the world.

According to FAO (Anonymous, 2003), over 7 million of hectares were harvested worldwide in 2005, producing almost three millions tons. India, Sudan, Myanmar, Uganda and China are the supreme sesame producers, covering 75 per cent of world production. Sesame has many returns as it needs a little water as compared to other crops such as cotton (half of sesame crop), etc. Its yield (413.6 kg/ha) is near to the ground as compared to other chief sesame producing countries of the world such as China and Egypt which are generating 897.7 and 1200 kg seed yield per hectare, respectively (Anonymous, 2011). In spite of being the first oilseed crop known to man, its extended history and importance sesame is a naturally neglected crop. Sesame has been mentioned as an 'orphan crop' because it is not commanded to any of the CGIAR institutes which could also be one of the reasons for lack of research works (Ashri, 1995). As a natural result of this condition, the use of molecular techniques for the enhancement of sesame is very restricted. Only a few reports are accessible on the use of molecular markers such as isozyme (Isshiki and Umezaki, 1997); RAPD (Bhat *et al.,* 1999); ISSR (Kim *et al.,* 2002); AFLP (Uzun *et al.,* 2003) and SSR (Dixit *et al.,* 2005). In India as well as in other countries, the average seed yield of sesame is quite low owing to lack of enhanced cultivars, making the plants vulnerability to diseases, pest and environmental stresses. Furthermore, properties such as undefined growth habit and asynchronous capsule ripening highlight seed shattering and there is a lack of inputs in the cultivation of sesame (Ashri, 1998). Lower productivity of the sesame has also been attributed to some extent to the use of conventional varieties (Hamid *et al.,* 2003). Comparatively, low seed yield is one of the most important reasons that sesame wants breeding to provide more yields (Furat and Uzun, 2010). Selection for good yield types should be very functional and donate to breeding programmes in our country. Hence, the first and prime need is the detection or cataloguing of sesame genotypes along with the assessment of genetic diversity widespread Indian sesame germplasm. Although genetic variation subsists for agronomically important characters, but the inadequate genetic information regarding Indian sesame populations is warning the access to helpful traits present among adapted landraces of sesame all over the country. This deficient genetic information about the sesame populations is the key factor for limited cultivation of modern varieties and small yield (Baydar *etal*., 1997) because efficient utilization of any sesame germplasm in a breeding programme need information on genetic variability, heritability and correlation among diverse characters in the germplasm. Among a large group of molecular markers, random amplified polymorphic DNA (RAPD) is suitable for the estimation of genetic diversity (Williams *et al.,* 1990) due to its simplicity, speed and relatively low cost. Being a quick and sensitive method, RAPD can be quickly and effectively applied to distinguish useful polymorphisms (Ko *et al.,* 1998). The resolving influence of this tool is numerous folds superior than morphological or biochemical markers and is much simpler and technically less demanding than RFLP and other new generation markers. RAPD markers have proved their significance for assortment analysis in a number of field crops such as rice (Rabbani *et al.,* 2008 and Pervaiz *et al.,* 2010) and horticultural plants like strawberry, common bean, *Neem*, turmeric (Jan *et al.,* 2011) and particularly in sesame (Ercan *et al.,* 2004). Since molecular based characterization of genotypes is independent of G x E interaction it may be a successful and competent tool to understand and validate the genotype variability between and within geographical regions and ultimately in conceding protection and crop development programme. In the present study, we report on the genetic diversity and genetic associations within the sesame accessions collected from different geographical areas of India through RAPD technique.

RESEARCH METHODOLOGY

Plant material:

Plant material for the study consisted of 14 sesame genotypes, collected from diverse ecologies of India (Table A). These accessions were selected on the basis of their agronomic presentation in field conditions. Around 15~25 seeds of each sesame accession were grown in the greenhouse. After 20 days of seed sowing, fresh leaflets were collected from 10 plants of each accession, bulked together and stored at -80°C till the leaves were subjected for the extraction of total genomic DNA.

DNA extraction and PCR analysis :

Total genomic DNA was extracted from the leaflet tissues of each sesame genotype using micro-prep DNA extraction protocol reported by Futon *et al.* (1995) with few alterations. Concentration of DNA was checked by visual evaluation of band intensity in contrast with lambda

Table A : List of sesame germplasm from India used for RAPD analysis

Sr. No.	Locality
ES-274	Madhya Pradesh
BHACHAU-7	Gujarat
RSS-106	Rajasthan
SSM	Rajasthan
Surya	Kerala
Kayamkulam	Kerala
Tilak	Tamil Nadu
GP286	Tamil Nadu
VRI(SV)1	Tamil Nadu
Tilarani	Tamil Nadu
Guj.Til-1	Gujarat
Guj.Til-2	Gujarat
Guj.Til-3	Gujarat
Guj.Til-4	Gujarat

DNA molecular standards of recognized concentrations with 0.8 per cent agarose gel. For PCR analysis all the extracted DNA samples were diluted to a running concentration of 20ng/µl with TE buffer. Altogether, 40 decamer oligonucleotides from Operon Technologies Inc. (Alameda, California, USA) were experienced for identifying polymorphisms. After a preliminary screen, 10 primers which proved obvious and reliable banding patterns and amplification were eventually selected to amplify the DNA of each sesame accession. Amplification reactions were carried out in a volume of 20µl. The reaction mixture contained 1x PCR buffer [10mM Tris-HCl (pH 8.3), 50mM KCl], 2mM $MgCl_2$, 0.25mM dNTP and 0.4mM of 10-mer primer (Operan Technologies Inc., Alameda, CA), 1 unit Taq DNA polymerase and approximately 20ng of genomic DNA. For the prevention of reaction mixtures evaporation a one drop of mineral oil was added. DNA thermocycler - 480 (Perkins Elmer Cetus, Norwalk, USA) was used for the DNA amplification. The thermal cycler was planned to 1 cycle of 5 min at 94°C for first strand separation, pursued by 45 cycles of 1 min at 94°C for denaturation, 1 min at 36°C for annealing the DNA double strand and 2 min at 72°C for primer extension. At last, 1 cycle of 7 min at 72°C was employed for concluding extension, followed by drenched at 4°C. The reproducibility of the amplification products was confirmed twice for each RAPD primer. After amplification, 10µl of amplification products plus loading dye were loaded in 1.3 per cent agarose gels for electrophoresis in 1xTBE (10mM Tris-Borate, 1mM EDTA) buffer to analyze the PCR products. A 1kb DNA ladder was used as a molecular size marker. After the complete run of electrophoresis, gels were carefully stained with ethidium bromide for 40 minutes and photographed under UV light by means of black and white film # 667 (Polaroid, Cambridge, Mass., USA).

Data analysis:

All RAPD product amplified by given primers were measured as a single locus and data were scored as the absence (0) or presence (1) of a DNA band for each of the primer-accession combination. The intensity of the DNA fragments was not taken into consideration and the bands with the same mobility were considered to be the same bands. Only main DNA fragments constantly amplified were scored and weak bands were not measured for analysis. The molecular size of the DNA fragments was deliberated from a standard curve based on known size of DNA fragments of a 1kb marker. Pair-wise comparisons of all the sesame accessions based on absence or presence of unique and shared DNA bands were utilized to make similarity co-efficients. The resulting similarity co-efficients were employed to assess the relationship among sesame genotypes with a cluster analysis by means of unweighted pair-group method with arithmetic averages (UPGMA) and then designed in the form of dendrogram. We selected this way of calculation over other general similarity indices because of the enlarged weighting of band matches versus that of non-matches. All calculations were carried out using NTSYS-pc, Version 2.1 package (Rohlf, 2000).

RESEARCH FINDINGS AND ANALYSIS

The genetic diversity and the relationships among 14 sesame genotypes were evaluated by RAPD markers using 20 primers. Fig. 1 shows the pattern of amplified products across sesame accessions generated with the primers OPK-07, OPK-08 and OPK-13, respectively. In most of the cases, sesame germplasm collections exhibited different banding patterns. Some of the accessions shared relatively lower number of bands with other germplasm accessions, showing their distant relationship to them. The accession 'Kayamkulam' demonstrated unique bands in contrast with all other sesame accessions. Interestingly, many primers showed

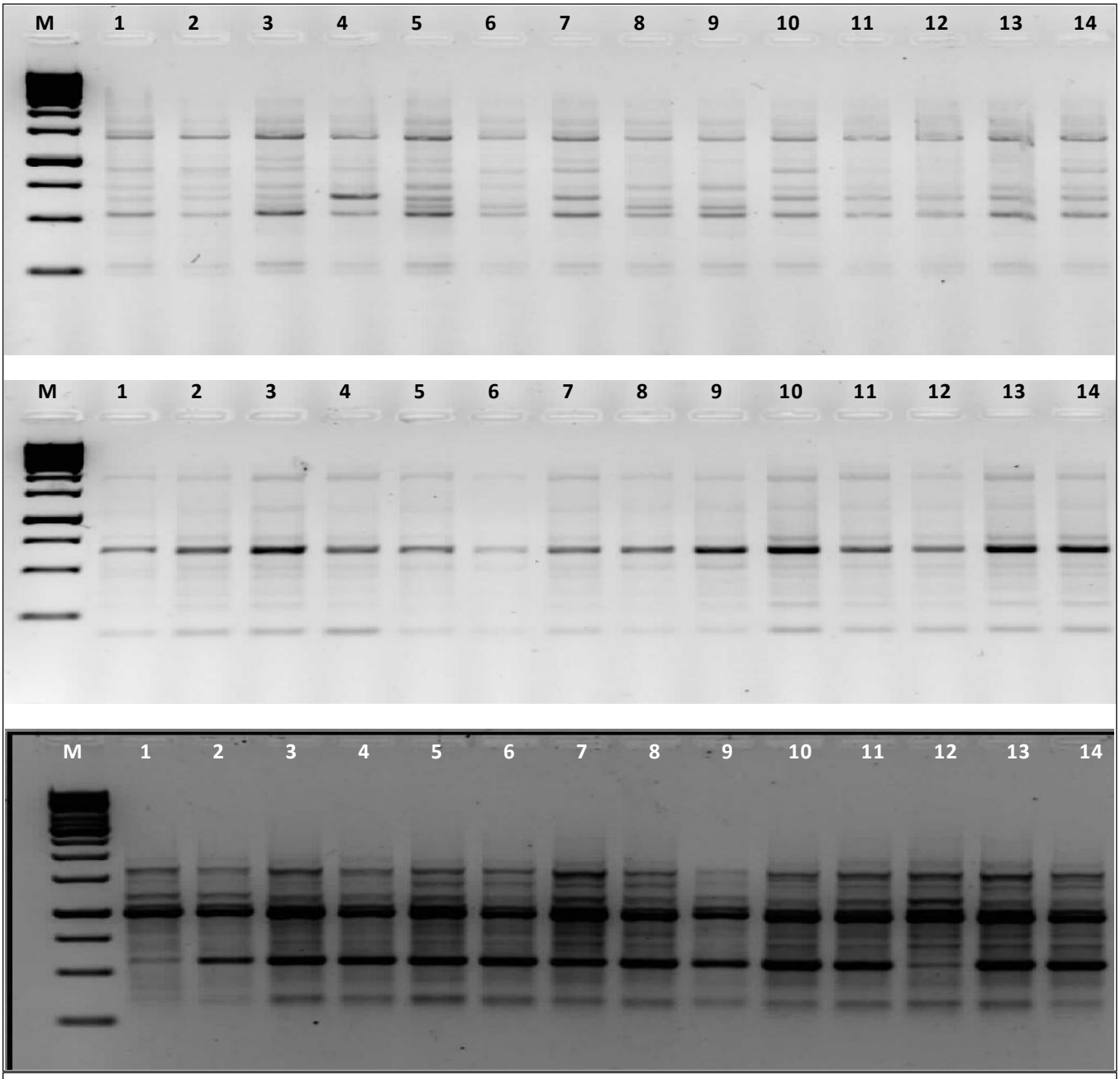

Fig. 1: Amplification of sesame accessions by RAPD markers OPK-07, OPK-08 and OPK-13. M = 1kb DNA ladder, 1 = ES-274, 2= BHACHAU-7, 3 = RSS-106, 4 = SSM, 5 = SURYA, 6 = KAYAMKULAM, 7 = TILAK, 8 = GP-286, 9 = VRI(SV)-1, 10 = TILARANI,11 = Guj.Til-1, 12 = Guj.Til-2, 13 = Guj.Til-3, 14 = Guj.Til-4.

characteristic bands in this accession which were not produced in any of the other collections. A total of 80 decamer primers were primarily screened for their potential to generate polymorphic patterns by means of four sesame accessions. Twenty primers that exhibited reliable and consistent banding patterns were chosen for the evaluation of variability across all the accessions. Remaining primers performed poorly and produced weak bands or did not amplify the DNA in some of the accessions utilized, were removed from the analysis. Each of the chosen 20 primers varied greatly in their ability to determine variability among the accessions. A total of

Table 1 : Primers used for generating RAPDs in Indian sesame genotypes

Sr. No.	Primer names	Sequence (5' - 3')	Amplified fragments (a)	Polymorphic fragments (b)	Percentage polymorphism (bx100/a)	Fragment size range (bp)
1.	OPA 10	GTGATCGCAG	15	11	73.33	330 - 6370
2.	OPA 11	CAATCGCCGT	4	1	25.00	577 - 2063
3.	OPA 13	CAGCACCCAC	8	5	62.50	370 - 2057
4.	OPC 11	AAAGCTGCGG	11	6	54.55	290 - 5760
5.	OPC 12	TGTCATCCCC	9	5	55.56	750 - 4450
6.	OPK 7	AGCGAGCAAG	11	4	36.36	780 - 5600
7.	OPK 8	GAACACTGGG	11	5	45.45	330 - 5110
8.	OPK 9	CCCTACCGAC	10	4	40.00	300 - 5830
9.	OPK 10	GTGCAACGTG	6	3	50.00	390 - 4650
10.	OPK 13	GGTTGTACCC	13	7	53.85	330 - 3150
11.	OPK 14	CCCGCTACAC	10	8	80.00	700 - 5670
12.	OPK 17	CCCAGCTGTG	7	5	71.43	390 - 2800
13.	OPK 18	CCTAGTCGAG	15	12	80.00	270 - 2690
14.	OPK 20	CACAGGCGGA	9	5	55.56	530 - 5110
15.	OPN 7	CAGCCCAGAG	11	7	63.64	460 - 3630
16.	OPO 20	ACACACGCTG	11	9	81.82	260 - 4800
17.	12 ES	GTAGGCGTCG	11	9	81.82	340 - 4210
18.	17 ES	GCCTCCTACC	10	5	50.00	670 - 4730
19.	22 ES	AGGCCCGATG	9	7	77.78	230 - 2550
20.	5 ES	GCATCACAGCCTGTTATTGCCTC	10	2	20.00	250 - 2660

201 amplification products were produced by 20 primers across 14 accessions, out of which 120 (59.70%) fragments were polymorphic (Table 1). The number of amplification products generated by each primer ranged from 4 (OPA- 11) to 15 (OPA-10) with an average of 10.05 fragments per primer. The size of the amplified fragments ranged from 800 (OPA-04) to 5000bp (OPD-08). A similarity matrix based on the proportion of shared RAPD fragments was utilized to set up the level of relatedness between the diverse sesame germplasm accessions. Pair-wise estimates of similarity for 14 accessions ranged from 0.63 to 0.91. Two pairs of accessions, 'RSS-106' and 'Guj.Til-1', and 'Guj.Til-1' and 'Guj.Til-2' were the closest genotypes with the highest similarity index, while 'Tilak' and 'Kayamkulam' were the least similar accessions. No accession was exactly similar to any other accession. Based on analysis carried out on Simple match similarity matrix via UPGMA, 14 accessions were grouped together into four clusters (Fig. 2). First cluster (A) consisted of two genotypes, second cluster (B) comprised of seven accessions, third cluster (C) was of four genotypes and fourth cluster (D) consisted of single genotype. As expected from the similarity estimates, cluster analysis positioned most of the sesame accessions far apart from each other showing a high level of genetic diversity. However, some of the accessions of the same locality were grouped together in the same cluster revealed a nearer genetic relationship (e.g. cluster B). One accession 'Kayamkulam' did not fall into any of groups and formed a separate cluster which was distant from all the other sesame accessions evaluated. RAPD markers have been used in this study to assess the genetic diversity among the Indian sesame genotypes. The selection of the RAPD technique was inspired by the fact that no DNA sequence knowledge is known about sesame crop and RAPD technique does not need any prior information of DNA sequencing. In addition it is simple to use for the evaluation of genetic diversity in sesame (Bhat *et al.*, 1999; Ercan *et al.*, 2004 and Salazar *et al.*, 2006). A high level of genetic variation was observed among the 14 Indian sesame genotypes. Though sesame is generally a self-pollinated crop but cross-pollination from 5 to 60 per cent has been reported in it (Yermamos, 1980). About 10 to 20 per cent of the genetic

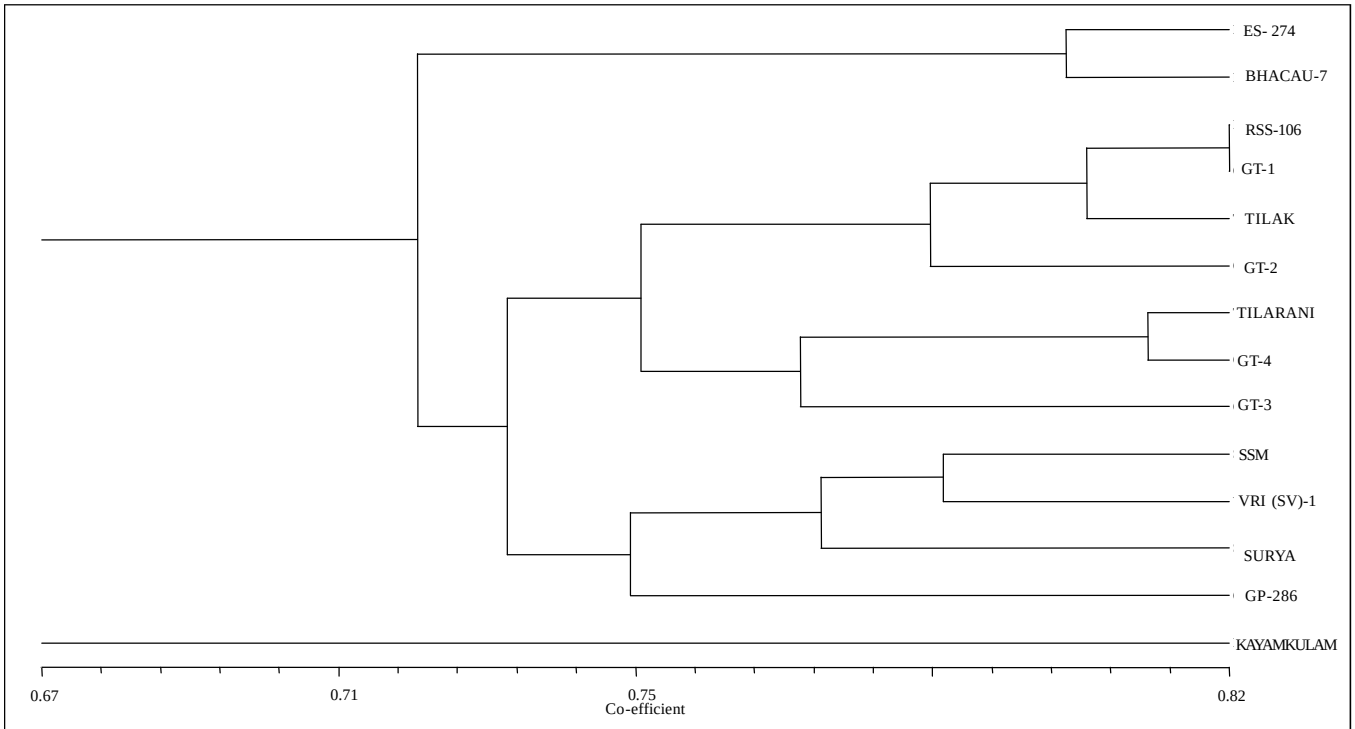

Fig. 2 : UPGMA cluster analysis (Dendrogram) of genetic relationship among 14 genotypes based on RAPD analysis

diversity among populations is due to cross-pollinations (Hamrick and Godt, 1989). Hence, some cross-pollination could clarify the high level of genetic diversity examined in the same sesame accessions. Our results are in agreement to other studies based on RAPD markers which have reported high level of genetic variations in sesame genotypes (Ashri, 1998; Bhat *et al.*, 1999; Ercan *et al.*, 2004 and Salazar *et al.*, 2006). The 10 RAPD primers noticed sufficient genetic diversity among the 14 sesame genotypes to allow for full separation. A number of other investigations have reported on the use of the same number of RAPD primers for evaluating genetic variation. Li and Midmore (1999) detected a high level of genetic diversity among germplasm of Chinese water chestnut with 14 RAPD primers. Similarly, Millan *et al.* (1996) reported a high level of genetic variation in rose germplasm using merely 10 RAPD primers. Schontz and Rether (1999) identified 37 lines of foxtail millet (*Setaria italica* L.) using just four RAPD primers, whereas genetic diversity of rice landraces and cultivars from Pakistan has successfully been assessed by RAPD markers (Rabbani *et al.*, 2008 and Pervaiz *et al.*, 2010).

Conclusion :

It should be noted that RAPD molecular markers could give high level of genetic diversity as compared to other molecular markers for example Isshiki and Umezaki (1997) identified a low level of genetic diversity in sixty eight sesame germplasms applying isozymes. Similarly Laurentin and Karlovsky (2006) noticed a very low genetic variation in thirty two sesame genotypes using AFLP molecular markers. Even Kim *et al.* (2002) reported a low level of genetic diversity in sesame germplasm collected from Korea and some other countries using microsatellite ISSR molecular markers. While Bhat *et al.* (1999) and Ercan *et al.* (2004) identified a very high level of genetic diversity among sesame accessions by means of RAPD molecular markers. In our study a high level of polymorphism was detected among sesame genotypes from diverse geographical regions of India. This was also supported by earlier RAPD marker results from other sesame investigations by applying the OPM-06 primer (100% polymorphism). In our study a high level of polymorphism (59.70%) observed is analogous to the 78 per cent polymorphism noticed in the evaluation of genetic diversity in Turkish sesame (Ercan *et al.*, 2004). Bhat *et al*. (1999) also observed 86.75 per cent polymorphism in a study of genetic diversity in Indian and exotic sesame germplasm. Although a considerable level of genetic diversity was present among diverse

sesame genotypes collected from various geographical regions of India, it was found that some accessions present geographically far apart clustered together in the identical group such as accession 'ES-273' (from Rajasthan) and 'BHACHAU-7' (from Gujarat) grouped together incluster A (Fig. 2). This could be a result of large movement of Indian farmers to various regions moving sesame seeds for farming into their new geographical locations. According to Stankiewicz *et al*., (2001) the human factor has earlier been revealed to be accountable for the lack of association between genetic and geographical detachment in some cases. The accession 'Kayamkulam' from Kerala region was found to be an extremely distinct genotype as it did not group with any other sesame accession. It seemed to be dissimilar species as it displayed a low level of similarity with all the other germplasm collections. This accession revealed certain unique bands which were not produced in any of the sesame collections evaluated. This result was further supported by its characteristic pattern of total seed proteins (data not shown) and important phenotypic features from the other genotypes. Some of the accessions evaluated appeared to be linked with their geographical sites and these genotypes from the similar geographical location were found to have a near genetic association. In conclusion, RAPD analysis showed a considerable level of genetic diversity among sesame accessions collected from different areas of India, even using as few as 20 RAPD primers. This high level of genetic variability among the sesame accessions proposed that the RAPD technique can be fruitful for the sesame systematics and selection of parents for breeding programmes.

LITERATURE CITED

Ali, M.A., Niaz, S., Abbas, A., Sabir, W. and Jabran, K. (2009). Genetic diversity and assessment of drought tolerant sorghum landraces based on morph-physiological traits at different growth stages. *POJ*, **2**: 214-227.

Anonymous (2000). *FAO production year book*. Food and Agriculture Organization of the United Nations, Rome Italy, **54** : 123.

Anonymous (2003). *FAO production yearbook, 2002*. Food and Agriculture Organization of the United Nations, Rome Italy, 271p.

Ashri, A. (1995). *Sesame research overview: current status, perspectives and priorities*. In: Bennet, M.R. and Wood, I.M.(Eds.), Proc. 1st Australian Sesame Workshop. Darwin and Katherine, Northern Territory.

Ashri, A. (1998). Sesame breeding. *Plant Breed. Rev.,* **16**: 179-228.

Baydar, H., Turgut, I. and Turgut, K. (1997). Variation of certain characters and line selection for yield, oil, oleic and linoleic acids in the Turkish sesame (*Sesamum indicum* L.) populations. *Turk. J. Agric. For.,***23**: 431-441.

Bhat, K.V., Babrekar, P.P. and Lakhanpaul,S. (1999). Study of genetic diversity in Indian and exotic sesame (*Sesamum indicum* L.) germplasm using random amplified polymorphic DNA (RAPD) markers. *Euphytica*,**110** : 21- 33.

Dixit, A., Jin, M.H. and Chung, J.W. (2005). Development of polymorphic micro satellite markers in sesame (*Sesamum indicum* L.). *Mol. Ecol. Notes,***5** : 736-738.

Ercan, A.G., Taskin, M. and Turgut, K. (2004). Analysis of genetic diversity in Turkish sesame (*Sesamum indicum* L.) populations using RAPD markers. *Genet. Resourc. Crop Evol.,***51**: 599-607.

Furat, S. and Uzun, B. (2010). The use of agro-morphological characters for the assessment of genetic diversity in sesame (*Sesamum indicum* L.). *POJ*, **3** : 85-91.

Futon, T.M., Chunwongse, J. and Tanksley, S.D. (1995). Microprep protocol for extraction of DNA from tomato and other herbaceous plants. *Plant Mol. Biol. Rep.*, **13**: 207-209.

Hamid, K.A., Ibrahim, A.S., Taha, M.B. and Ahmed, M.E. (2003). Performance, interrelationship and path analysis of some yield component in sesame. *U.J. Agric. Sci.,***11**: 305 - 320.

Hamrick, J.L. and Godt, M.J.W. (1989). Allozyme diversity in plant species. In: Brown, A.H.D., Clegg, M.T., Kahler, A.L. and Weir, B.S., Ed. *Plant population genetics, breeding and genetic resourses.* Sunderland, MA: Sinauer Associates, 43–63pp.

Hatam, M. and Abbasi, G.Q. (1994). Oilseed crops. In: *Crop production.* National Book Foundation, Islamabad. (Ed.). Nazir, S., Basher, E. and Bantel, R. pp. 319-389.

Isshiki, S. and Umezaki, T. (1997). Genetic variations of isozymes in cultivated sesame (*Sesamum indicum* L.). *Euphytica*, **93** : 375-377.

Jan, H.U., Rabbani, M.A. and Shinwari, Z.K. (2011). Assessment of genetic diversity of indigenous turmeric (*Curcuma longa* L.) germplasm from Pakistan

using RAPD markers. *J. Med. Plants Res.*,**5**: 823-830.

Kim, D., Zur, G., Danin-Poleg, Y. , Lee, S., Shim, K., Kang, C. and Kashi, Y. (2002). Genetic relationships of sesame germplasm collection as revealed by inter-simple sequence repeats. *Plant Breed.*,**121**: 259-262.

Kobayashi, T., Kinoshita, M., Hattori, S., Ogawa, T., Tsuboi, Y., Ishida, M., Ogawa, S. and Saito, H. (1990). Development of the sesame metallic fuel performance code. *Nucl. Technol.,* **89**: 183-193.

Ko, M.K., Yang, J., Jin, Y.H., Lee, C.H. and Oh, B.J. (1998). Genetic relationships of Viola species evaluated by random amplified polymorphic DNA analysis. *J. Hort. Sci. Biotech.*,**74**: 601-605.

Laurentin, H.E. and Karlovsky, P. (2006). Genetic relationship and diversity in sesame (*Sesamum indicum* L.) germplasm collection using amplified fragment length polymorphism (AFLP). *BMC Genet.*,**7**: 10.

Li, M. and Midmore, D.J. (1999). Estimating the genetic relationships of Chinese water chestnut [*Eleocharisdulcis* (Burm. f.) Hensch.] cultivated in Australia, using random amplified polymorphic DNAs (RAPDs). *J. Hort. Sci. Biotech.*,**74**: 224-231.

Masood, S., Ghafoor, A. and Javaid, A. (2003). *Characterization and evaluation of plant genetic resources*. Plant Genetic Resources Institute, NARC, Islamabad.

Millan, T., Osuna, F., Cobos, S., Torres, A.M. and Cubero, J.I. (1996). Using RAPDs to study phylogenetic relationships in Rosa. *Theor. Appl. Genet.*,**92**: 273-277.

Nayar, N.M. and Mehra, K.L. (1970). Sesame - its uses, botany, cytogenetics, and origin. *Econ. Bot.*,**24**: 20-31.

Nei, M. and Li, W.H. (1979). Mathematical models for studying genetic variation in terms of restriction endonucleases. *Proc. Natl. Acad. Sci. USA*,**76**: 5269-5273.

Pervaiz, Z.H., Rabbani, M.A., Shinwari, Z.K., Masood, M.S. and Malik, S.A. (2010). Assessment of genetic variability in rice (*Oryza sativa* L.) germplasm from Pakistan using RAPD markers. *Pak. J. Bot.*,**42**: 3369-3376.

Rabbani, M.A., Pervaiz, Z.H. and Masood, M.S. (2008). Genetic diversity analysis of traditional and improved cultivars of Pakistani rice (*Oryza sativa* L.) using RAPD markers. *Elect. J. Biotech.*,**11**: 1-10.

Rabbani, M.A., Masood, M.S., Shinwari, Z.K. and Shinozaki, K.Y. (2010). Genetic analysis of basmati and non-basmati Pakistani rice (*Oryza sativa* L.) cultivars using microsatellite markers. *Pak. J. Bot.*,**42**: 2551- 2564.

Rohlf, F.J. (2000). *NTSYSpc – numerical taxonomy and multivariate analysis system*. Version 2.01. Applied Biostatistics Inc., Exeter Software, NY, USA.

Salazar, B., Laurentin, H., Davila, M. and Castillo, M.A. (2006). Reliability of the RAPD technique for germplasm analysis of sesame (*Sesamum indicum* L.) from Venezuela. *Interciencia,* **31**: 456-460.

Sankar, D., Sambandam, G., Ramakrishna, R.M. and Pugalendi, K.V. (2005). Modulation of blood pressure, lipid profiles and redox status in hypertensive patients taking different edible oils. *ClinicalChem. Acta,* **355**: 97-104.

Schontz, D. and Rether, B. (1999). Genetic variability in foxtail millet, *Setaria italica* (L.) Beauv: identification and classification of lines with RAPD markers. *Plant Breed.,* **118**: 190-192.

Stankiewicz, M., Gadamski, G. and Gawronski, S.W. (2001). Genetic variation and phylogenetic relationships of triazine resistant and triazine susceptible biotypes of *Solanum nigrum* analysis using RAPD markers. *Weed Res.*,**41**: 287- 300.

Uzun, B., Lee, D. and Donini, P. (2003). Identification of a molecular marker linked to the closed capsule mutant trait in sesame using AFLP. *Plant Breed.*,**122**: 95-97.

Williams, J.G.K., Kubelik, A.R., Livak, J., Rafalski, J.A. and Tingey, S.V. (1990). DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acid Res.*,**18**: 6531-6535.

Wood, R. (1999). *The new whole foods encyclopedia: A comprehensive resource for healthy eating*. Penguin Putnam Inc., NEW YORK, U.S.A.

Yermamos, D.M. (1980). Sesame. In: *Hybridization of crop plants.* (Eds.): W.R. Fehr, H.H. Hadley. American Soc. Agron., CSSA, Madison.