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Genetic Diversity Analysis of Fodder Oats (*Avena sativa* L.) Germplasm by Microsatellite Markers

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ABSTRACT

The present study was undertaken to assess the genetic diversity in the ninety six oat (*Avena sativa* L.) elite cultivars representing the collection from various eco-geographical regions of India. The molecular diversity analysis using 40 SSR markers clustered all the 96 cultivar into ten clusters and significant level of distinction (dissimilarity coefficient ranged from 0.12 to 0.96) was depicted among the lines indicating a high degree of divergence among these lines. Genotypic pairs having utmost genetic dissimilarity (0.96) were OL1634 and OL1688, OL1702 and OL1688, OL1705 and OL1634, UPO03-3 and OL 1688, and UPO03-3 and OL1705 that can be used as parents in purposeful hybridization programs. Polymorphic Information Content (PIC) values ranged from as low as 0.06 to as high as 0.75 (AM 7). Owing to their highest *PIC* values, primer pairs AM7 (0.75), AM2 (0.69) and AM10 (0.69) can be further used in association mapping studies in oat. The Un-weighted Pair Group Method with Arithmetic Mean (UPGMA) based dendrogram revealed the cluster V (19 genotypes) as the largest and cluster X (3 genotypes) as the smallest one. Thus, genotypes within clusters can be predicted as similarity pool in further oat improvement programs. The selected panel of SSR markers performed well in detection of genetic diversity patterns and can be recommended for future germplasm characterization studies in oats.

Keywords: Dissimilarity coefficient, Molecular diversity analysis, Polymorphic information Content, SSRs.

INTRODUCTION

The genus *Avena* belongs to the grass family Poaceae. Oat (*A. sativa* L.) is an economically important crop and ranks sixth in world cereal production after wheat, rice, maize barley and sorghum (FAO, 2012). It is an important winter forage crop in many parts of the world and is also grown as multipurpose crop for grain, pasture, and forage. Differing from other cereal grains such as wheat and barley, it is rich in the antioxidants α-tocotrienol, α-tocopherol, and avenanthramides, as well as total dietary fibre including the soluble fibre β-glucan (Oliver *et al*., 2010). In recent years, with the advent of exaggerated dairy industry in our country, oat has fascinated the attention of breeders for its improvement due to its nutritious quality fodder for livestock and its grains as animal feed with high net energy gains (Ruwali *et al*., 2013). Hence, the first and foremost need is the identification or cataloguing of oats genotypes along with the

assessment of genetic diversity prevalent in different geographical regions in the world. Moreover, there are different genetic approaches for assessment of genetic diversity in

germplasm accessions, breeding lines, and segregating populations based on morpho-agronomic traits and DNA markers. Among them, the use of DNA marker technology in varietal improvement has progressed rapidly during the last decade. The discovery and use

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of molecular markers based on DNA differentiation offers great opportunity to understand and identify the diverse genetic material in crop species. Molecular markers are indispensable tools for characterizing genetic resources by detecting variation of the DNA sequences among cultivars and, therefore, directly bypass the problems related to environmental effects and thus have many applications of value to crop improvement. In oats, extensive studies have been done for genetic diversity analysis using molecular markers such as Random Amplified Polymorphic DNA (RAPD) (Loskutov, 2007; Loskutov and Perchuk, 2000; Hanif et al., 2008; Abbas et al., 2008; Boczkowska et al., 2014), restriction fragment length polymorphism (RFLP) (Pal, 2002), Sequence-Characterized Amplified Region (SCAR) and Cleaved Amplified Polymorphic Sequence (CAPS) (Orr and Stephen, 2008). But, at certain point, these studies were to be less edifying due to highly monomorphic nature as well as in bi-parental mapping population. Therefore, SSRs are the logical choice to characterize genetic variability for understanding phylogenetic and evolutionary patterns owing to their high reliability, effectiveness in assessment of crop germplasm at genetic level (O'Neill et al., 2003) and being used extensively in studies of variability and genotype characterization. These markers are PCR based (Weber and May, 1989), co-dominant (Litt and Luty, 1989) and consist of short tandem repeats of between 1 and 6 base pairs (Queller et al., 1993). As compared to RFLP and AFLP analysis, assays involving SSRs are rapid, cost effective (Jannink and Gardner, 2005), work well with minute or even degraded samples of DNA, and display consistency in scoring of alleles with clear comparisons across various gels (Queller et al., 1993). These characteristics, along with an evenly dispersed genomic distribution, are properties which make SSRs ideal genetic markers (Morgante and Olivieri, 1993; Powell et al., 1996). To date, 174 oat genomic microsatellites have been identified from SSR-enriched libraries, related species, and by mining sequence databases (Li et al., 2000, Holland et al., 2001, Pal et al., 2002, Jannink and Gardner, 2005, Oliver et al., 2010, Wight et al., 2010). In addition, 216 microsatellites with good PIC (0.42) have been mined from available Expressed Sequence Tag (EST) databases in oat (Becher, 2007); however, the availability of this EST-based resource is restricted. Montilla- Bason et al., (2013) utilized 31 of these existing SSR markers having very high PIC values (mean 0.80) and successfully identified four clusters among 177 oat accessions consisting of cultivars, two groups of four white oat landraces, and red oat accessions. More recently, Boczkowska et al. (2014) employed eight ISSR primers, with mean PIC value of 0.24, as part of a larger study to measure genetic variation in pre-1939 Polish oat varieties. Thus, the purpose of this study was to assess the genetic diversity among oat germplasms based on microsatellite markers (SSRs).

MATERIALS AND MTHODS

The experimental material comprised of 96 elite cultivars from diverse eco-geographic regions of the country (Figure 1) maintained at the experimental area of Forage Research Farm, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana. The names and origin of the plant material used in the present investigation is given in Table 1. Dendrogram was constructed using symmetric matrix of euclidean distance coefficients based on UPGMA using DARwin 5.0 (Perrier *et al.*, 2006)

Isolation of Genomic DNA

Total genomic DNA of 96 *Avena sativa* accessions was isolated from young leaves from four-week old plants following the procedure of Poulsen *et al.* (1993). DNA samples were evaluated

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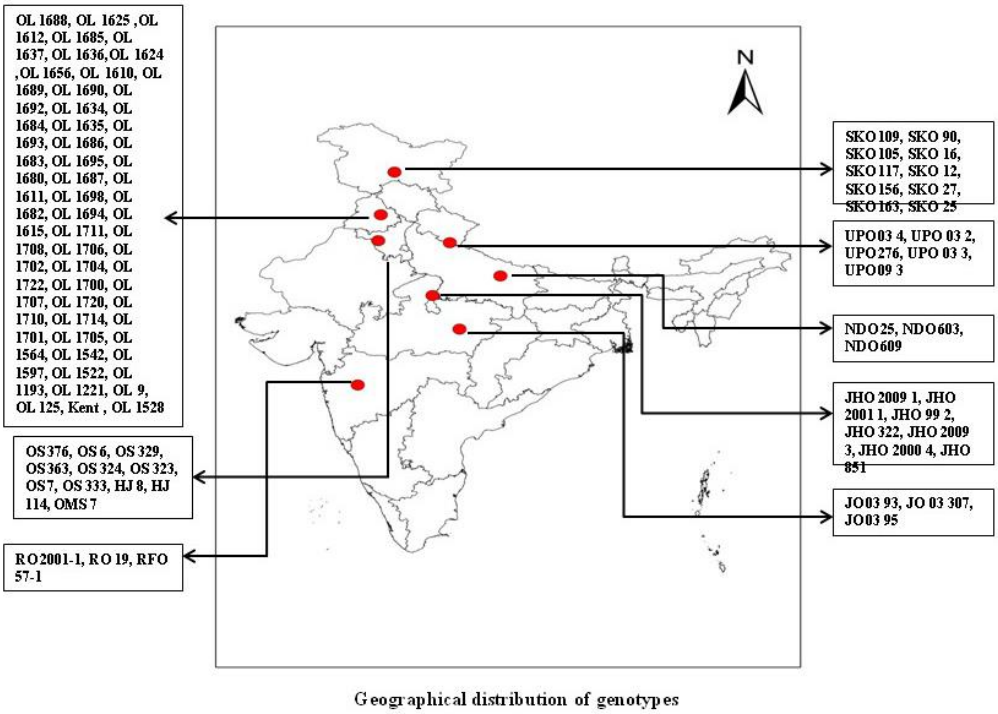

Figure 1. Geographic distribution of 96 germplasm accessions on Indian map.

both quantitatively and qualitatively using spectrophotometer and λ (lambda) DNA (concentration marker), respectively.

Selection of Primers

For the present study, 40 SSR primer pairs (Table 2) belonging to AM, CWM, WISC series were selected from the published source. AM series were provided by Li *et al*. (2000), the WISC primers were developed by Zhu and Kaeppler (2003), and CWM series was provided by Gao *et al.* (2003).

SSR Analysis

PCR amplification of SSR markers was carried out using reaction mixture containing 50 ng of template DNA, 1X PCR buffer, 1.5 mM MgCl2, 200µM of dNTPs, 0.4 µM each of forward and reverse primers and 1 unit of Taq DNA polymerase. Amplification was performed using the following conditions: denaturation at 94 ºC for 4 minutes; 40 cycles of 1 minute denaturation at 94 ºC, 1 minute annealing at temperatures adjusted depending upon the SSR primer sequence, 1 min extension at 72ºC and a final extension at 72ºC for 10 minutes. The SSR amplification products were separated in a vertical denaturing 6% polyacrylamide. DNA fragments were revealed using the ethidium bromide staining procedure. The gels were stained for 30-35 minutes and visualized under UV light and photographed using photo gel documentation system (Alphaimager HP, Alpha Innotech).

RESULTS AND DISCUSSION

Summarized data for number of alleles detected per primer pair and the Polymorphic Information Content (PIC) values for each of the 40 SSR primers are presented in Table 3. PCR amplification results by one primer are presented in Figure 2. A total of 129 alleles were detected by 40

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Table 1. The list of all the germplasm accessions evaluated for diversity analysis.

S No	Genotype	Origin	S No	Genotype	Origin	S No	Genotype	Origin	S No	Genotype	Origin
1	OL 1688	Ludhiana	25	OL 1694	Ludhiana	49	UPO 03 2	Pantnagar	73	SKO 90	J & K
2	OL 1625	Ludhiana	26	OL 1615	Ludhiana	50	UPO 276	Pantnagar	74	SKO 105	J & K
3	OL 1612	Ludhiana	27	OL 1711	Ludhiana	51	UPO 03 3	Pantnagar	75	SKO 16	J & K
4	OL 1685	Ludhiana	28	OL 1708	Ludhiana	52	UPO 09 3	Pantnagar	76	SKO 117	J & K
5	OL 1637	Ludhiana	29	OL 1706	Ludhiana	53	HJ 8	Hisar	77	SKO 12	J & K
6	OL 1636	Ludhiana	30	OL 1702	Ludhiana	54	HJ 114	Hisar	78	SKO 156	J & K
7	OL 1624	Ludhiana	31	OL 1704	Ludhiana	55	NDO 25	Faizabad	79	SKO 27	J & K
8	OL 1656	Ludhiana	32	OL 1722	Ludhiana	56	NDO 603	Faizabad	80	SKO 163	J & K
9	OL 1610	Ludhiana	33	OL 1700	Ludhiana	57	NDO 609	Faizabad	81	SKO 25	J & K
10	OL 1689	Ludhiana	34	OL 1707	Ludhiana	58	JHO 2009 1	Jhansi	82	OL 1564	Ludhiana
11	OL 1690	Ludhiana	35	OL 1720	Ludhiana	59	JHO 2001 1	Jhansi	83	OL 1542	Ludhiana
12	OL 1692	Ludhiana	36	OL 1710	Ludhiana	60	JHO 99 2	Jhansi	84	OL 1597	Ludhiana
13	OL 1634	Ludhiana	37	OL 1714	Ludhiana	61	JHO 322	Jhansi	85	OL 1522	Ludhiana
14	OL 1684	Ludhiana	38	OL 1701	Ludhiana	62	JHO 2009 3	Jhansi	86	OL 1193	Ludhiana
15	OL 1635	Ludhiana	39	OL 1705	Ludhiana	63	JHO 2000 4	Jhansi	87	OL 1221	Ludhiana
16	OL 1693	Ludhiana	40	OS 376	Hisar	64	JHO 851	Jhansi	88	OL 9	Ludhiana
17	OL 1686	Ludhiana	41	OS 6	Hisar	65	RO 2001 1	Rahori	89	OL 125	Ludhiana
18	OL 1683	Ludhiana	42	OS 329	Hisar	66	RO 19	Rahori	90	Kent	Ludhiana
19	OL 1695	Ludhiana	43	OS 363	Hisar	67	RFO 57 1	Rahori	91	EC 605830	Exotic collection
20	OL 1680	Ludhiana	44	OS 324	Hisar	68	JO 03 93	Jabalpur	92	EC 605839	Exotic collection
21	OL 1687	Ludhiana	45	OS 323	Hisar	69	JO 03 307	Jabalpur	93	EC 605833	Exotic collection
22	OL 1611	Ludhiana	46	OS 7	Hisar	70	JO 03 95	Jabalpur	94	EC 605829	Exotic collection
23	OL 1698	Ludhiana	47	OS 333	Hisar	71	OMS 7	Hisar	95	EC 605832	Exotic collection
24	OL 1682	Ludhiana	48	UPO 03 4	Pantnagar	72	SKO 109	J&K	96	OL 1528	Ludhiana

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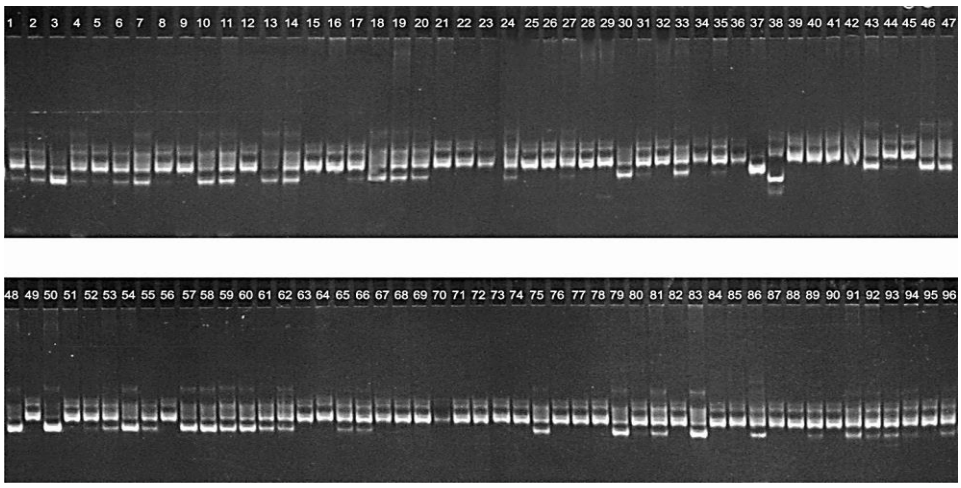
Table 2. The list of SSR primers and their sequence information used in present study.

S No	Primer	Repeat motif	Left primer 5' to 3'	Right primer 5' to 3'	Tm (°C)
1	AM1	(AG)(CAGAG)	*GGATCCTCCACGCTGTTGA*	*CTCATCCGTATGGGCTTTA*	46
2	AM2	AG	*TGAATTCGTGGCATAGTCACAAGA*	*AAGGAGGGCATAGGGAGGTATTT*	49
3	AM3	AG	*CTGGTCATCCTCGCCGTTCA*	*CATTTAGCCAGGTTGCCAGGTC*	51
4	AM4	AG	*GGTAAGGTTTCGAAGAGCAAAG*	*GGGCTATATCCATCCCTCAC*	48
5	AM5	AG	*TTGTCAGCGAAATAAGCAGAGA*	*GAATTCGTGACCAGCAACAG*	46
6	AM6	AG	*AATGAAGAAACGGGTGAGGAAGTG*	*CCAGCCCAGTAGTTAGCCCATCT*	52
7	AM7	AG	*GTGAGCGCCGAATACATA*	*TTGGCTAGCTGCTTGAAACT*	48
8	AM8	AG	*CAAGGCATGGAAAGAAGTAAGAT*	*TCGAAGCAACAAATGGTCACAC*	47
9	AM9	AG	*CAAAGCATTGGGCCCTTGT*	*GGCTTTGGGACCTCCTTTCC*	48
10	AM10	AG	*AAAATCGGGGAAGGAAACC*	*GAAGGCAAAATACATGGAGTCAC*	46
11	AM11	(AG)(AAAG)	*TCGTGGCAGAGAATCAAAGACAC*	*TGGGTGGAGGCAAAAACAAAAC*	49
12	AM12	AG	*TGCTGAAGTGAACAATCGC*	*CCTTCTCCAACAACTCTAC*	44
13	AM13	AG	*CGGCGTGATTTGGGGAAGAAG*	*CTAGTAACGGCCGCCAGTGTGCTG*	54
14	wisc48	AG	*CAATGGGCATTGAGAGATTAAG*	*TATGGCTGGTGGAGTTGTTTTG*	52
15	CWM26	A	*GGCAGCAGCAAAAGCAGGTC*	*ACTCACAATAGGGCGAAATG*	55
16	CWM27	A	*AGCATCCTCGCATTTCTTGTA*	*GCAGCCGCTTTTGATTCTA*	55
17	CWM28	A	*CGCATGGAAGCTCACAAGTTT*	*TTGCTGAGATGGCTGGAAGGAG*	55
18	CWM29	AAC	*CGCATGCAAGCTCACAAGT*	*GCTGAGGCTGCTGGTAGGAGAC*	55
19	CWM30	AAC	*GCGGTGCCAAGCCATCC*	*ACATTGCAGGTAGCGTCTCT*	55
20	CWM31	AAC	*ATGCAGGGATGTTGTATTG*	*CTGTGGGTTTTGCTGAGAT*	55
21	CWM32	AAC	*GCGGTGCCAAGCCATCCA*	*CACATTGCAGGTAGCGTCTCT*	55
22	CWM33	AAC	*CAGCGCATGGAAGATCACAA*	*GTT GGAGCCCTGGCCTAATGGA*	55
23	CWM34	AAC	*GCAGCCATCCATAGCGTCG*	*TG AAATGGTGCCCTGATGATGGAG*	55
24	CWM35	AAC	*ATGCAGGGATGTTGTATTG*	*GAGGCTGTTGGAAGGAGAC*	55
25	CWM36	AAC	*CATGCAGGGATGTTGTCTTG*	*ATATTGCTGCTGAGGCTGTTGG*	55
26	CWM37	A	*AGCATCCTCGCATTTCTTGTA*	*GCAGCCGCTTTTGATTCTA*	55
27	CWM38	A	*TTGGTCGTTGTAGCGGTGAAA*	*AATTGTAAAACGACGGCCAGTAAT*	55
28	CWM39	A	*TCCTGCGCCCCTGATGTAAT*	*TAATAAATGCGCCCCTCCCAGAAG*	50
29	CWM40	A	*TCGCTCCCTACGCCGCAGAAT*	*A TGTAAAAGGCCCGCCAGTGAGC*	55
30	CWM41	A	*TTCACCGGTGCCGATTTACAG*	*AGGGATGGCGCCGGGATGGTGAGGAG*	50
31	CWM42	A	*TGTCCCGTTGCCAGTTTTGTT*	*TAG ATTACCGCGGGCCAGTGAGC*	50
32	CWM43	A	*AGCGTGGAGGAAGTGGAG GG*	*GGGTGGGTGGGGTAG 55*	55
33	CWM44	A	*AATGGAAGGTGGGGGTTTGA*	*GGGGCGCCGGTGTTTTT 5*	55
34	CWM45	AAC	*GCGCATGGAAGCTCACAAG*	*TTTTGAAGAAGCCCTGGCCTGATGGATA*	55
35	CWM46	ATG	*GGTTGCCCTGGTGATGAAG*	*ATAAACAAGGATGCCGTGGAG*	55
36	CWM47	ATCCCT	*ATCGCCGCCTCCAGCA*	*ACCAGACGACGCCGACGAGGACGAG*	55
37	CWM48	ATG	*GATCGGCGACTTCCTCCCT*	*ACCCCGCTCTTTCCCCAATAAT*	55
38	CWM49	A	*TCGCTCCCTACGCCGCAGAAT*	*TGTAAAAGGCCCGCCAGTGAGC*	55
39	CWM50	AAC	*AGCGCATGGAAGATCACAA*	*GGAGCCCTGGCCTAATGGA*	55
40	CWM51	A	*GCGTATGCGTGCCAAAAA CG*	*ATAATCAAAAAGCGGTCACTAC*	55



Genotypes are marked by order (1-96) as per sequence given in table 1

Figure 2. PAGE Plate: Polymorphism pattern from amplification of genomic DNA of 96 test genotypes with SSR primer CWM 51.

Table 3. Alleles amplified and *PIC* values of primers.

S No	Primer	Number of alleles amplified	*PIC* value	S No	Primer	Number of alleles amplified	*PIC* value
1	AM1	2	0.33	21	CWM33	2	0.34
2	AM2	4	0.69	22	CWM34	3	0.55
3	AM3	2	0.37	23	CWM35	4	0.57
4	AM4	2	0.36	24	CWM36	4	0.58
5	AM5	3	0.56	25	CWM37	2	0.16
6	AM6	3	0.57	26	CWM38	2	0.37
7	AM7	5	0.75	27	CWM39	3	0.49
8	AM8	4	0.48	28	CWM40	4	0.23
9	AM9	6	0.63	29	CWM41	4	0.37
10	AM10	5	0.69	30	CWM42	4	0.40
11	AM11	4	0.54	31	CWM43	3	0.41
12	AM12	4	0.53	32	CWM44	3	0.30
13	AM13	3	0.43	33	CWM45	3	0.59
14	CWM26	3	0.31	34	CWM46	2	0.53
15	CWM27	4	0.60	35	CWM47	2	0.37
16	CWM28	2	0.28	36	CWM48	3	0.50
17	CWM29	4	0.48	37	CWM49	2	0.38
18	CWM30	3	0.40	38	CWM50	2	0.06
19	CWM31	3	0.45	39	CWM51	3	0.48
20	CWM32	2	0.36	40	WISC 48	4	0.63

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primers in the 96 genotypes with an average of 3.22 alleles per primer. To mention but a few, the main causes of this divergence may be the deletions, insertions, and chromosomal inversion at the DNA level which generate polymorphism or allelic diversity. However, Fu *et al.* (2007) found higher level of diversity by observing the number of alleles per primer pair ranged from 1 (CWM204) to 24 (AM3) and averaged 4.8 alleles. These differences in our study pertaining to the number of alleles detected are primarily due to the use of high resolution 6% polyacrylamide gel, lines from different geographic regions and SSR markers used. Total number of allele amplified for each primer ranged from 2 to 6. The maximum number of alleles (6) was amplified by AM9. The lower average number of alleles amplified per SSR marker and that by the individual marker in the present study is due to the use of local *Avena sativa* accessions, which had no ploidy changes and had not been used by any of the studies enlisted above. So, these genotype specific alleles couldn't add on to the alleles amplified per primer and the average alleles per primer.

Polymorphic Information Content (PIC) Values

PIC values ranged from 0.06 to 0.75 with an average of 0.45. The highest *PIC* value was recorded by AM7 (0.75), followed by AM2 (0.69), AM10 (0.69), WISC 48 (0.63) and AM9 (0.63). *PIC* values of each primer pair ranged from 0.02 to 0.95 with an average of 0.35 reported by Fu *et al.* (2007) in *Avena sterilis*. These polymorphic primers can be used in further molecular studies like association mapping, tagging of gene of interest, and the so called approach Marker Assisted Selection (MAS).

Cluster Analysis in Germplasm Collection Based on SSR Data

Ten clusters were obtained upon clustering the 96 genotypes under study (Figure 3) with the symmetric matrix of DICE coefficients based on UPGMA using DARwin 5.0 (Perrier *et al.*, 2006). The perusal of the clustering analysis revealed that the individuals within any one cluster were more closely related than the individuals in different clusters (Table 4). The cluster I consisting of 19 genotypes was the largest amongst all and was closely followed by cluster V having 14 genotypes. Among all, cluster X was the smallest one consisting of three genotypes. The check cultivars OL 9 and KENT used in the present study fell in clusters II and IX, respectively. The clustering pattern thus obtained in the study confirmed the discriminating power and reliability of the SSR markers for genetic diversity studies.

The dissimilarity coefficients ranged from 0.12 to 0.96 signifying a high degree of dissimilarity among the *A. sativa* accessions evaluated in the present investigation. Genotypic pairs having utmost genetic dissimilarity of 96% were OL1634 and OL1688, OL1702 and OL1688, OL1705 and OL1634, UPO03-3 and OL1688, UPO03-3 and OL1705. These results showed that genotypes OL1634, OL1688, OL1705, OL1702 and UPO03-3 were implicated to get high dissimilarity, consequently, they can be used to facilitate as mapping population in various mapping studies as well as establishing the utility of microsatellite markers in identifying diverse pairs. In contrast, the minimum genetic dissimilarity of about 12% was observed between the lines SKO12 and OMS7, SKO12 and SKO16, SKO12 and HJ114, SKO16 and OL1695 .This marked a possibility that the SSR markers used in the study may be linked to the genomic region in these genotypes. OL1684 was grouped into the separate cluster from OL1615, so, they being diverse as reported by the SSR study could be used to develop mapping populations for number of tillers/plant, green fodder yield, and dry fodder yield because they have extreme value for these traits and also are present

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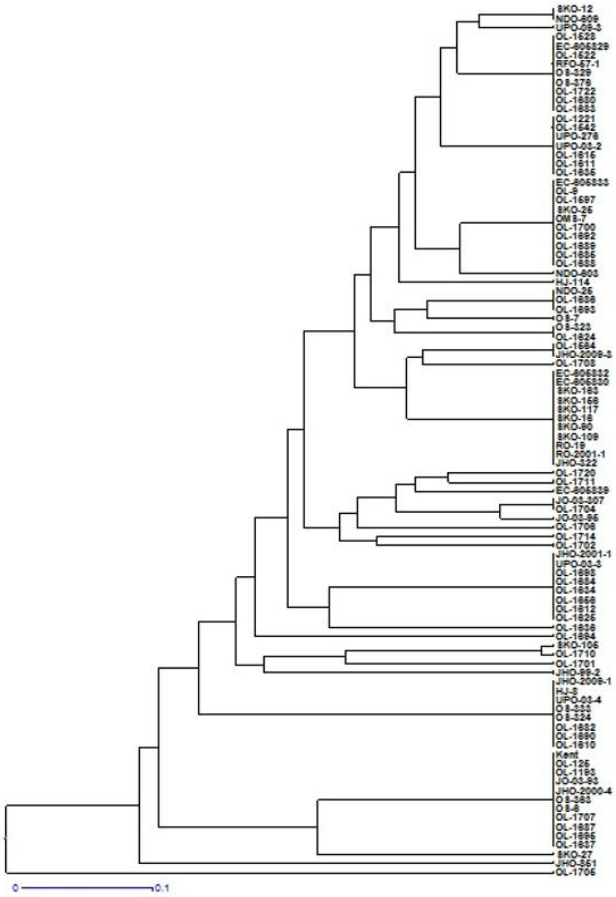

Figure 3. Dendrogram obtained by SSR marker analysis using UPGMA method.

Table 4. Clustering pattern obtained by SSR analysis.

Cluster	Number of genotypes	Genotypes
I	19	SKO12, NDO609,UPO00-3, OL1528, EC605829, OL1622, RFO57-1, OS329, OS376, OL1722, OL1680, OL1683, OL1221, OL1542, UPO276, UPO03-2, OL1615, OL1611, OL1635
II	11	EC 165833,OL9, OL1597, SKO25, OMS7, OL1700, OL1692, OL1689, OL1688, NDO603
III	7	HJ114, NDO25, OL1693, OS7, OS323, OL1624,OL1625
IV	14	OL1684, JHO2009-3, OL1708, EC605832, EC605830, SKO163, SKO109, SKO117, SKO18, SKO90, SKO169, RO19, RO2001-1, JHO322
V	9	OL1720, OL1711, EC605839, JO03-307, OL1704, JO 03-95, OL1708, OL1714, OL1702
VI	9	JHO2001-1, UPO03-3, OL1693, OL1684, OL1634, OL1658, OL1612, OL1625, OL1638
VII	5	OL1694, SKO105, OL1710, OL1701, JHO99-2
VIII	8	JHO 2009-1, HJ 8, UPO 03-4, OS 333, OS 324, OL 1682, OL 1690, OL 1710
IX	11	KENT, OL125, OL1193, JO03-93, JHO2000-4, OS 363, OS8, OL1707, OL1687, OL1696, OL1637
X	3	SKO27, JHO851, OL1705

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in separate clusters. While excellent mapping population for number of leaves/plant could be developed between UPO03-4 and UPO276, as they have extreme values for the target character, as well as they are placed in the extreme groups by the SSR dendrogram. Similarly, genes for plant height could be mapped from a mapping population using any genotypes among OL1625, OL1686, UPO03-4, JHO99-2 and JO03-93 because all have extreme trait values, as well as are grouped in distinct groups by microsatellite analysis. Greater number of genotypes in a single cluster manifests that these genotypes were more closely related and had less genetic variation among them. It further implies that hybridization program employing these genotypes inhabiting a common cluster will be of little use in oat improvement program. In studies of SSR diversity in accessions of *Triticum aestivum* L., Huang *et al*. (2002) observed that not all accessions originating from a geographic region clustered in the same group. The authors concluded that either similar genetic variation occurred independently among accessions in the different geographical regions or that the artificial transfer of accessions between regions resulted in the incorrect/false determination of geographical origin. SSRs with similar attributes could be exploited for genome/ species differentiation, because repetitive sequences associated with SSRs are relatively stable and genome-specific (Li *et al*., 2000). Additionally, these results probably linked with the morphological attributes of the same cultivars and need to be validated through precise investigation for association either through bulk segregation analysis or near isogenic lines (Tanhuanpaa *et al*., 2007).

CONCLUSIONS

Conclusively, induction of diverse oat genotypes followed by their utilization in the well defined scientific oat hybridization program could be a useful tool to cater the overall fodder oats cultivar development program. Further, among marker discriminating indices, *PIC* (Polymorphic Information Contents) are believed to be more reliable indices for selecting a marker or combination of markers for characterization of germplasm. Also, between marker systems, microsatellites (SSRs) could be suitable for studying genetic diversity among oats genotypes because of their ability to produce more number of bands per reaction, while their co-dominant nature with high value of expected heterozygosity will make them more suitable for genome mapping.

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تحلیل تنوع ژنتیکی ژرم پلاسم های جو دو سر (*Avena sativa* L.) با نشانگر های ریزماهواره ای

ر. کاپور ، و خ. چاودهاری

چکیده

هدف از این پژوهش ارزیابی تنوع ژنتیکی در ۹۶ کولتیوار الیت جودوسر (*Avena sativa* L.) بود که نمونه های جمع آوری شده از مناطق مختلف بوم-جغرافیایی هندوستان بودند. با تجزیه و تحلیل تنوع ملکولی با استفاده از ۴۰ SSR، همه این ۹۶ کولتیوارها در ده خوشه متمایز در سطح معنا دار دسته بندی شد(ضریب عدم تشابه بین ۰/۱۲۰ تا ۰/۹۶) که نشاندهنده درجه واگرایی بالایی بین این رگه ها بود. جفت های ژنوتیپیک با بیشترین عدم تشابه (۰/۹۶) عبارت بودند از OL 1634 وOL1688، OL1702 و OL1688، OL 1705 وOL 1634، UPO 03-3 وUPO 03-3، UPO 03-3 وOL1705 که می توان آنها را به عنوان والد ها در برنامه های دورگ گیری هدفمند به کار گرفت. مقدار محتوای اطلاعاتی چند شکلی (PIC) از مقدار کم ۰/۰۶ تا مقدار زیاد ۰/۷۵ (AM7) تغییر میکرد. به علت داشتن بالاترین مقدار PIC، جفت های آغاز گر AM 7 (۰/۷۵) و AM2 (۰/۶۹) و AM10 (۰/۶۹) را میتوان در مطالعات association mappingدر جو دو سر استفاده کرد. روش Un-weighted Pair Groupبا دندروگرام مبتنی برمیانگین حسابی آشکار ساخت که خوشه V(شامل ۱۹ ژنوتیپ) بزرگترین خوشه و خوشه X (شامل ۳ ژنوتیپ) کوچکترین خوشه بود. به این قرار، در برنامه های بهبود و اصلاح ژنتیکی جو دو سر می توان ژنوتیپ های درون خوشه ها را به عنوان مجموعه ای مشابه قلمداد کرد. در این پژوهش، مجموعه انتخاب شده SSRها در شناسایی الگوهای تنوع ژنتیکی به خوبی عمل کرد و می توان آن ها را در مطالعات بیشتر برای تشخیص ژرم پلاسم ها در جو دو سر توصیه کرد.

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