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Genetic variability studies for yield attributes and foliar disease resistance in groundnut (*Arachis hypogaea* L.)

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ABSTRACT

In the present investigation, estimates of genetic variability, heritability and genetic advance were assessed for nine different characters in the F_3 population derived from four groundnut crosses *viz.,* CO 7 × GPBD 4, TMV 2 × GPBD 4, TMV Gn 13 × GPBD 4 and VRI 2 × GPBD 4. Considering the mean performance, the cross derivative CO 7 × GPBD 4 registered superiority for the characters *viz.,* number of pods per plant, pod yield per plant (g), kernel yield per plant (g) and late leaf spot resistance. Apart from these characters, the cross VRI 2 × GPBD 4 and TMV 2 × GPBD 4 also showed superior mean performance for 100-pod weight (g) and rust score, respectively. High percentage of PCV, GCV, heritability coupled with high GAM values were recorded by number of pods per plant, 100-kernel weight (g), shelling (%), pod yield per plant (g), kernel yield per plant (g), late leaf spot score and rust score in various F_3 cross derivatives. Selection would be effective for these traits in respective crosses to obtain promising progenies. Regarding the population distribution, negative skewness was observed in the cross CO 7 × GPBD 4 for 100-pod weight (g), 100-kernel weight (g), shelling (%) and sound mature kernel (%). Similarly, platykurtosis was observed for late leaf spot and rust disease scores in VRI 2 × GPBD 4. Directional selection will effectively improve the mean performance of these traits.

Keywords: Genetic variability, Groundnut, Kernel yield, Late leaf spot, Pod yield, Rust

Groundnut (*Arachis hypogaea* L.) is an important crop both in subsistence and commercial agriculture in arid and semi-arid regions of the World. It is one of the most nourishing foods available in the World, grown as cash crop for oilseed, food and animal feed. The groundnut is particularly valued for its protein contents, which is of high biological value (Mondal and Badigannavar, 2016). The two major foliar diseases namely late leaf spot (*Phaeoisariopsis personata* Berk. and Curt.) and rust (*Puccinia arachidis* Speg.) affects the productivity of groundnut. These two diseases often occur together and causes up to 50-70% of yield losses in the crop (Subrahmanyam *et al.,* 1984). Development of cultivars resistant/tolerant to these diseases could be effective in decreasing the production costs, improving production quality and reducing the detrimental effects of chemicals on our ecosystem (Sreenivasulu *et al.,* 2015). The yield is a complex character, which is highly influenced by environmental variations. Information on nature and magnitude of variability present in the population due to genetic and non-genetic cause is an important pre-requisite for a systemic breeding programme (Prabhu *et al.,* 2015a). Genetic variability is essential for initiating an effective and successful breeding programme and it became imperative to study the level of genetic variability available in the existing genotype. The study of genetic advance with heritability estimates further clarify the nature of character which can be improved through selection (Savaliya *et al.,* 2009). Therefore, the present investigation was undertaken to study variability, heritability and genetic advance in four segregating F_3 populations of groundnut. The objectives of the present study are to evaluate groundnut cross derivatives for yield, yield attributes and foliar diseases, and to assess genetic parameters among them.

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MATERIALS AND METHODS

The present scientific investigation was carried out at Oilseeds Farm, Department of Oilseeds, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore during *kharif* 2014. Four crosses *viz*., CO 7 × GPBD 4, TMV 2 × GPBD 4, TMV Gn 13 × GPBD 4 and VRI 2 × GPBD 4 were made to develop foliar disease resistant groundnut lines with acceptable pod and kernel yield using five groundnut genotypes. Among the five, four genotypes *viz.,* CO 7, TMV 2, TMV Gn 13 and VRI 2 were susceptible, while GPBD 4 was resistant to foliar fungal diseases. Selection was done in F_2 generation for pod yield, kernel yield and foliar disease resistance. All the parents and F_3 progenies were evaluated in non-replicated trial. Recommended cultural practices were followed throughout the crop growing period. The spacing adopted was 30 × 10 cm. Observations were recorded and analysed in terms of mean and variability parameters on nine characters *viz.,* number of pods per plant, 100-pod weight (g), 100-kernel weight (g), shelling (%), sound mature kernel (%), pod yield

per plant (g), kernel yield per plant (g), late leaf spot (LLS) and rust disease scores. Nine point disease scale suggested by Subrahmanyam *et al.* (1995) was used to screen the lines for sources of resistance to late leaf spot and rust diseases. Standard statistical procedures were adopted for calculating the mean and various genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) in broad sense and genetic advance as per cent of mean (GAM). The range of coefficient of variation (CV) was categorized as per Sivasubramanian and Madhavamenon (1973): below 10% - low coefficient of variation; 10-20% - medium coefficient of variation; above 20% - high coefficient of variation. As suggested by Robinson *et al.* (1949), the heritability range was classified as: less than 30% - low heritability; 30-60% - moderate heritability; more than 60% - high heritability. Similarly, the range of genetic advance as per cent of mean (GAM) was grouped as: less than 10% - low GAM; 10-20% - medium GAM; more than 20% - high GAM (Johnson *et al*., 1955).

RESULTS AND DISCUSSION

Mean and genetic variability is the basic requirement for crop improvement as this provides wider scope for selection. Mean serves as a basis for eliminating undesirable crosses. Information on extent of genetic variability and role of important yield determining traits are paramount importance for their skillful engineering of new ideotype. The presence of variability in crop is important for genetic studies and consequently used for improvement and selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in material and the extent to which it is heritable. The results on the mean performance and various genetic parameters for nine yield and yield attributes of four segregating populations *viz*., CO 7 × GPBD 4, TMV 2 × GPBD 4, TMV Gn 13 × GPBD 4 and VRI 2 × GPBD 4 are presented hereunder.

Mean performance

Mean performance of parents: In a breeding programme, mean performance is the foremost important criteria to select an individual. Among the parents, CO 7 and TMV 2 recorded superiority for number of pods per plant while, the parent VRI 2 possessed higher mean value for 100-pod weight (g), 100-kernel weight (g), sound mature kernel (%), pod yield per plant (g) and kernel yield per plant (g). GPBD 4 exhibited superior mean performance for shelling (%) and late leaf spot score. Thus, VRI 2 was considered as desirable parent for yield improvement and GPBD 4 for late leaf spot resistance in groundnut (Table 1).

Mean performance of crosses: Among the crosses, CO 7 × GPBD 4 recorded superior mean performance for number of pods per plant, pod yield per plant (g), kernel yield per plant (g) and late leaf spot resistance. The cross VRI 2 × GPBD 4 exhibited higher mean value for 100-pod weight (g) whereas, the cross TMV 2 × GPBD 4 for rust resistance alone. Hence, considering the mean performance, the cross CO 7 × GPBD 4 is considered superior for yield improvement and late leaf spot resistance. No significance was observed for remaining traits in all the crosses.

Variability parameters

In the present study, the phenotypic and genotypic coefficient of variation exhibited wide range for all characters. All the four F_3 populations exhibited higher PCV values than the GCV values suggesting the influence of environmental factors for all the characters studied. Less difference observed between PCV and GCV in certain cases indicated greater role of genetic components and less influence by environment. Similar results were obtained by Ladole *et al.* (2009) and Shinde *et al.* (2010).The genetic parameters studied for various characters in F_3 generation (Table 2) are narrated below.

Table 1 Mean performance of parents for various traits in F_3 generation of groundnut

Parent / Trait	Number of pods per plant	100-pod weight (g)	100 kernel weight (g)	Shelling (%)	Sound mature kernel (%)	Pod yield per plant (g)	Kernel yield per plant (g)	LLS score	Rust score
CO 7	23.38*	89.23	29.47	58.56	90.02	16.30	9.90	3.93	2.25
TMV 2	24.80*	81.93	28.58	60.13	90.78	17.91	10.68	5.02	2.50
TMVGn 13	18.50	71.24	24.87	50.75	88.15	13.33	7.99	5.10	4.50
VRI 2	20.70	115.22*	38.10*	62.75	96.82*	20.71*	13.12*	5.80	3.20
GPBD 4	16.40	55.20	23.21	95.90*	90.39	8.64	8.29	2.80*	2.60
Grand mean	20.76	82.56	28.85	65.62	91.23	15.38	10.00	4.53	3.01
SE	1.96	9.15	2.25	6.90	2.41	2.27	1.29	0.53	0.37

*Significant @ 5% level of probability

Table 2 Estimates of genetic variability parameters in F_3 populations of groundnut

Character	Cross	Mean	PCV (%)	GCV (%)	h^2 (BS) (%)	GAM (%)	Skewness	Kurtosis
Number of pods per plant	C1	27.50*	55.34	48.05	86.83	48.45	0.49	0.65
	C2	11.70	57.68	19.10	33.11	44.45	1.00**	1.36**
	C3	15.30	50.20	34.40	68.53	65.58	0.14	-1.53
	C4	16.20	50.39	15.75	31.25	28.14	0.61**	0.60
100-pod weight (g)	C1	77.00	22.78	18.46	81.04	10.35	-0.81**	0.53
	C2	61.80	41.23	24.85	60.27	12.90	1.59**	4.87**
	C3	59.90	22.07	10.72	48.57	7.85	0.22	-0.18
	C4	88.20*	26.03	19.45	74.71	8.91	0.17	0.29
100-kernel weight (g)	C1	27.50	20.66	13.06	63.22	21.52	-0.62*	0.26
	C2	23.30	33.81	21.37	63.20	33.20	0.26	2.25**
	C3	20.20	23.08	16.92	73.28	35.90	-0.01	-0.73
	C4	29.90	24.61	15.67	63.67	21.73	0.44*	0.47
Shelling (%)	C1	55.50	27.87	22.92	82.24	16.11	-1.83**	3.70**
	C2	47.10	36.38	36.09	99.18	26.14	-1.01**	-0.07
	C3	53.50	26.75	9.01	33.68	6.71	0.94	-0.11
	C4	55.10	26.82	25.21	94.00	18.19	-1.62**	2.04**
Sound mature kernel (%)	C1	84.70	15.95	10.21	64.05	6.22	-0.71**	-0.13
	C2	83.20	24.59	22.57	91.81	11.27	-2.13**	5.41**
	C3	88.40	15.95	3.83	23.99	2.23	-0.83	-0.47
	C4	91.20	14.19	12.58	88.66	7.55	-2.52**	8.73**
Pod yield per plant (g)	C1	18.60*	56.88	48.33	84.97	70.83	0.25	-0.43
	C2	7.00	73.56	41.61	56.56	141.96	1.76**	5.08**
	C3	8.40	53.05	41.35	77.95	139.37	0.37	-0.81
	C4	13.70	82.81	64.84	78.29	107.35	5.96**	55.21**
Kernel yield per plant (g)	C1	11.20*	61.74	46.02	74.55	107.29	0.44	0.18
	C2	3.90	87.79	40.30	45.90	227.97	1.75**	4.85**
	C3	5.00	65.63	42.57	64.87	218.33	0.36	-0.46
	C4	8.20	89.77	65.41	72.87	173.07	5.51**	49.30**
LLS score	C1	2.40*	28.9	25.8	79.3	47.3	0.71**	-0.70
	C2	4.00	35.5	19.5	30.1	22.0	0.09	-0.74
	C3	5.70	26.7	-	-	-	-0.35	-0.47
	C4	6.40	33.3	28.2	71.8	49.3	-0.10	-0.90*
Rust score	C1	2.70	32.8	15.3	21.8	32.8	-0.32	-0.76
	C2	2.20*	45.5	42.5	87.4	81.9	0.59*	1.18*
	C3	5.30	35.8	33.3	86.5	63.7	1.10	0.67
	C4	5.10	35.1	28.9	67.5	48.9	-0.07	-1.08**

C1 - CO 7 × GPBD 4; C2 - TMV 2 × GPBD 4; C3 - TMV Gn 13 × GPBD 4; C4 - VRI 2 × GPBD 4
*,**Significant @ 5% and 1% level of probability, respectively.

Number of pods per plant: Two of the four crosses *viz.,* CO 7 × GPBD 4 and TMV Gn 13 × GPBD 4 exhibited high PCV, GCV, heritability coupled with high GAM for the trait number of pods per plant. Similar results have been reported by Savaliya *et al.* (2009), Shinde *et al.* (2010), Priyadharsini (2012), Anitha (2013), John *et al.* (2013) and Prabhu *et al.* (2015a). The crosses, TMV 2 × GPBD 4 and VRI 2 × GPBD 4 recorded high PCV and medium GCV for this trait, as reported by Anitha (2013). Similarly, moderate heritability and high GAM was possessed by the cross TMV 2 × GPBD 4 and VRI 2 × GPBD 4. This is similar to the findings of Shoba *et al.* (2009).

100-pod weight (g): High PCV and GCV values for 100-pod weight (g) was recorded by the cross TMV 2 × GPBD 4. Ali *et al.* (2000), Ladole *et al.* (2009) and Prabhu *et al.* (2015a)

also reported high PCV and GCV values for the trait 100-pod weight (g) in groundnut. High PCV and medium GCV were exhibited by three crosses, CO 7 × GPBD 4, TMV Gn 13 × GPBD 4 and VRI 2 × GPBD 4. Similar results were reported by Anitha (2013) and John *et al.* (2013). High heritability and medium GAM were recorded by the crosses, CO 7 × GPBD 4 and TMV 2 × GPBD 4 for 100-pod weight (g). The cross VRI 2 × GPBD 4 possessed high heritability and low GAM values whereas, the cross TMV Gn 13 × GPBD 4 recorded moderate heritability and low GAM values.

100-kernel weight (g): PCV, GCV, heritability and GAM values were higher for 100-kernel weight (g) in cross TMV 2 × GPBD 4 alone, among the four crosses under study. Such higher estimates of PCV, GCV, heritability and genetic advance have already been indicated by Savaliya *et al.* (2009), Shoba *et al.* (2009), Shinde *et al.* (2010), Hiremath *et al.* (2011), Padmaja *et al.* (2013a), Padmaja *et al.* (2013b), Thirumala *et al.* (2014) and Prabhu *et al.* (2015a). The crosses *viz.,* CO 7 × GPBD 4, TMV Gn 13 × GPBD 4 and VRI 2 × GPBD 4 exhibited high PCV, medium GCV, high heritability and high GAM values. Shoba *et al.* (2009) also reported the same for 100-kernel weight (g) in groundnut.

Shelling (%): High PCV, GCV, heritability and GAM values were recorded by the cross TMV 2 × GPBD 4 for the trait shelling (%). Similar results were given by Ali *et al.* (2000). The crosses, CO 7 × GPBD 4 and VRI 2 × GPBD 4 exhibited high PCV, GCV, heritability and medium GAM values. This is in accordance with Hiremath *et al.* (2011), John *et al.* (2013) and Thirumala *et al.* (2014). Similarly, the cross TMV Gn 13 × GPBD 4 possessed high PCV, low GCV, moderate heritability and low GAM. These observations are in agreement with the findings of Vishnuvardhan *et al.* (2012) and Padmaja *et al.* (2015).

Sound mature kernel (%): For sound mature kernel per cent, high PCV and GCV values were recorded in the cross TMV 2 × GPBD 4. Similar findings were reported by Hiremath *et al.* (2011) and Prabhu *et al.* (2015a) for sound mature kernel (%). Medium PCV and GCV were observed in the cross CO 7 × GPBD 4 and VRI 2 × GPBD 4 while, medium PCV and low GCV were recorded by TMV Gn 13 × GPBD 4. Sound mature kernel (%) in TMV Gn 13 × GPBD 4 exhibited medium PCV and low magnitudes of GCV, heritability and GAM values indicating the limited scope of selection for this trait. Similar reports were given by John *et al.* (2013). The cross TMV 2 × GPBD 4 possesses higher heritability and medium GAM for sound mature kernel (%). These results are in accordance with John *et al.* (2013). Remaining crosses *viz.,* CO 7 × GPBD 4 and VRI 2 × GPBD 4 showed high heritability coupled with low GAM values for this trait. Concomitant results were obtained by Hiremath *et al.* (2011) and Maurya *et al.* (2014).

Pod yield per plant (g): All the four crosses recorded high PCV, GCV, heritability coupled with GAM for pod yield per plant (g) except the cross TMV 2 × GPBD 4. Higher values for pod yield per plant (g) were earlier reported by Shinde *et al.* (2010), Narasimhulu *et al.* (2012), Priyadharsini (2012), Anitha (2013), John *et al.* (2013), Narasimhulu *et al.* (2013), Thirumala *et al.* (2014) and Prabhu *et al.* (2015a). The cross TMV 2 × GPBD 4 exhibited higher values for PCV, GCV and GAM while, moderate value for heritability. These findings were similar to the findings of Shoba *et al.* (2009).

Kernel yield per plant (g): High PCV and GCV values coupled with high heritability and GAM were exhibited by the entire cross derivatives for kernel yield per plant (g), except for the cross TMV 2 × GPBD 4. Concomitant results have been reported by Savaliya *et al.* (2009), Dolma *et al.* (2010), Shinde *et al.* (2010), Narasimhulu *et al.* (2012), Priyadharsini (2012), Anitha (2013), John *et al.* (2013), Narasimhulu *et al.* (2013), Thirumala *et al.* (2014) and Prabhu *et al.* (2015a) for the trait kernel yield per plant (g) in groundnut. Similarly, moderate heritability coupled with high GAM values were recorded by the cross TMV 2 × GPBD 4.Shoba *et al.* (2009) also reported similar kind of results.

Late leaf spot score: All the cross derivatives showed higher PCV and GCV values except TMV 2 × GPBD 4 and TMV Gn 13 × GPBD 4 which showed medium and low GCV respectively for late leaf spot. High PCV and GCV values were noticed earlier by Dolma *et al.* (2010), Narasimhulu *et al.* (2013), Padmaja *et al.* (2013a), Ashish *et al.* (2014) and medium/low GCV values by Vishnuvardhan *et al.* (2012) and Padmaja *et al.* (2013 b). High heritability coupled with high GAM for the trait late leaf spot were recorded in two of the cross combinations *viz.,* CO 7 × GPBD 4 and VRI 2 × GPBD 4. Dolma *et al.* (2010), Vishnuvardhan *et al.* (2012), Narasimhulu *et al.* (2013), Padmaja *et al.* (2013a), Padmaja *et al.* (2013b) and Ashish *et al.* (2014) reported the same for late leaf spot score. The remaining crosses, TMV 2 × GPBD 4 and TMV Gn 13 × GPBD 4 possessed high PCV, low to medium GCV, heritability and GAM values. This results are in accordance with Prabhu *et al.* (2015 a).

Rust score: Rust score exhibited high PCV, GCV, heritability coupled with high GAM for all the four crosses in F_3 generation except CO 7 × GPBD 4. Similar results were reported by Narasimhulu *et al.* (2013), Ashish *et al.* (2014), Shridevi *et al.* (2014) and Prabhu *et al.* (2015 a). In CO 7 × GPBD 4, the trait rust score registered high PCV and high GAM values while, the GCV and heritability recorded medium and low values, respectively. Medium/low value

results are in accordance with John *et al.* (2008) and Vishnuvardhan *et al.* (2012).

Population distribution

Skewness and kurtosis reflects the nature of variability existing in a genetic population under study. The frequency distribution was studied for the quantitative traits under third and fourth order statistics *viz.,* skewness and kurtosis.

Skewness: Skewness characterizes the degree of asymmetry in the population. A positively skewed distribution indicates that the individuals of the population bunched up towards the lower mean values whereas, negatively skewed distribution exhibits that the individuals are clustered towards higher mean values. In the present investigation, significant and positive skewness was observed in the cross CO 7 × GPBD 4 (late leaf spot), TMV 2 × GPBD 4 [number of pods per plant, 100-pod weight (g), pod yield per plant (g), kernel yield per plant (g) and rust score] and VRI 2 × GPBD 4 [number of pods/plant, 100-kernel weight (g), pod yield per plant (g) and kernel yield per plant (g)]. Similarly, significant and negative skewness were exhibited for 100-pod weight (g), 100-kernel weight (g), shelling (%) and sound mature kernel (%) in the cross CO 7 × GPBD 4 whereas, the cross TMV 2 × GPBD 4 and VRI 2 × GPBD 4 possessed for shelling (%) and sound mature kernel (%). No significant skewness was noticed for remaining traits in all the four crosses. The results are in accordance with Prabhu *et al.* (2015 b).

Kurtosis: Similarly, kurtosis characterizes the relative peak size and flatness of a population distribution compared to normal distribution (Balanda and MacGillivray, 1988). Positive kurtosis indicates leptokurtic distribution, negative kurtosis indicates platykurtic distribution and zero value indicates normal or mesokurtic distribution (Pearson, 1929).Leptokurtosis were registered in the cross CO 7 × GPBD 4 for the trait shelling (%) whereas, the cross CO 7 × COG 0437 exhibited the same for number of pods/plant, 100-pod weight (g), 100-kernel weight (g), sound mature kernel (%), pod yield per plant (g), kernel yield per plant (g) and rust disease score indicating the presence of narrow variability for the particular trait. Hence selection cannot be made for these traits Anitha (2013). Similarly, the cross VRI 2 × GPBD 4, recorded leptokurtic nature for the traits *viz.,* shelling (%), sound mature kernel (%), pod yield per plant (g) and kernel yield per plant (g). Platykurtosis was possessed by the traits late leaf spot score and rust score in the cross VRI 2 × GPBD 4 while, mesokurtic nature of distribution was observed for the remaining traits in all the four crosses. Hence, directional selection will effectively improve the meanperformance of these traits.

In any breeding programme, mean performance is one of the basic selection criteria for categorizing of superior performing progenies and eliminating undesirable genotypes/crosses. High GCV values indicate the greater extent of variability present in the character and can be improved through selection. Heritability and genetic advance are useful tools for breeders in determining the direction and magnitude of selection. A relative comparison of heritability estimates and expected GAM will give an idea about the nature of gene action governing a particular trait. High value of heritability together with high genetic advance for any character indicates additive gene action and selection will be rewarding for improvement of such traits whereas, high heritability associated with low genetic advance might attribute to the presence of non-additive gene action which indicates dominance/epistasis and their response to selection would be poor. An insight into the nature and degree of distribution present in population is of utmost importance as it forms the basis for selection in any crop improvement programme (Table 3).

Table 3 Selection indices for yield and yield attributes in F3 populations of groundnut

Characters	Superior mean	Gene effects	Skewness	Kurtosis	Selection
Number of pods per plant	CO 7 × GPBD 4	Additive	Symmetric	Mesokurtosis	✓
100-pod weight (g)	VRI 2 × GPBD 4	Non additive	Symmetric	Mesokurtosis	X
Pod yield per plant (g)	CO 7 × GPBD 4	Additive	Symmetric	Mesokurtosis	✓
Kernel yield per plant (g)	CO 7 × GPBD 4	Additive	Symmetric	Mesokurtosis	✓
Late leaf spot score	CO 7 × GPBD 4	Additive	Positive	Mesokurtosis	✓
Rust score	TMV 2 × GPBD 4	Additive	Positive	Leptokurtosis	✓

Considering the mean performance, the cross derivative CO 7 × GPBD 4 registered superiority for the characters *viz.,* number of pods/plant, pod yield per plant (g), kernel yield per plant (g) and late leaf spot resistance. Apart from these characters, the cross VRI 2 × GPBD 4 [100-pod weight (g)] and TMV 2 × GPBD 4 (rust score) also showed higher mean performance. High percentage of PCV, GCV, heritability coupled with high GAM values were recorded by number of pods per plant (CO 7 × GPBD 4 and TMV Gn 13 × GPBD 4), 100-kernel weight (g) and shelling (%) (TMV 2 × GPBD

4), pod yield per plant (g) and kernel yield per plant (g) (CO 7 × GPBD 4, TMV Gn 13 × GPBD 4 and VRI 2 × GPBD 4), late leaf spot score (CO 7 × GPBD 4 and VRI 2 × GPBD 4) and rust score (TMV 2 × GPBD 4, TMV Gn 13 × GPBD 4 and VRI 2 × GPBD 4). Hence, selection would be effective for these traits in respective crosses to obtain promising progenies.

Regarding the population distribution, negative skewness was observed in the cross CO 7 × GPBD 4 for 100-pod weight (g), 100-kernel weight (g), shelling (%) and sound mature kernel (%). The trait shelling (%) and sound mature kernel (%) also recorded negative skewness for the cross TMV 2 × GPBD 4 and VRI 2 × GPBD 4. Similarly, platykurtosis was observed forlate leaf spot and rust disease scoresin VRI 2 × GPBD 4. Symmetric distribution / mesokurtic nature was noticed in most of the traits understudy. Thereby, directional selection will effectively improve the mean performance of these traits. Hence, based on mean performance and various genetic parameters, the cross CO 7 × GPBD 4 is considered as superior for number of per plant, pod yield per plant (g), kernel yield per plant (g) and late leaf spot resistance in groundnut.

REFERENCES

Ali N, Malik S N, Bashir K and Mirza M Y 2000. Genetic variability, heritability and correlation studies in groundnut. *Sarhad Journal of Agriculture,* **16**: 533-536.

Anitha B K 2013. Identification of quantitative trait loci for oil yield and marker assisted backcross for high oleic acid in groundnut (*Arachis hypogaea* L.). Ph.D. (Ag.) Thesis, Tamil Nadu Agricultural University, Coimbatore.

Ashish J, Nadaf H L and Gangadhara K 2014. Genetic analysis of rust and late leaf spot in advanced generation recombinant inbred lines of groundnut (*Arachis hypogaea* L.). *International Journal of Genetic Engineering and Biotechnology*, **5**(2): 109-114.

Balanda K P and MacGillivray H L 1988. "Kurtosis: A Critical Review". *The American Statistician*, **42**(2): 111-119.

Dolma T, Sekhar M R and Reddy K R 2010. Genetic variability, correlation and path analysis for yield and its components and LLS resistance in groundnut (*Arachis hypogaea* L.). *Journal of Oilseeds Research*, **27**(2): 154-157.

Hiremath C P, Nadaf H L and Keerthi C M 2011. Induced genetic variability and correlation studies for yield and its component traits in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, **2**(1): 135-142.

John K, Vasanthi R P and Venkateswarlu O 2008. Estimates of genetic parameters and character association in F_2 segregating populations of Spanish × Virginia crosses of groundnut (*Arachis hypogaea* L.). *Legume Research*, **31**(4): 235-242.

John K, Vasanthi R P, Sireesha K and Giridharakrishna T 2013. Genetic variability studies in different advanced breeding genotypes of Spanish bunch groundnut (*Arachis hypogaea* L.). *International Journal of Applied Biology and Pharmaceutical Technology*, **4**(2): 185-187.

Johnson H W, Robinson H F and Comstock R E 1955.Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**: 314-318.

Ladole M Y, Wakode M M and Deshmuk S N 2009. Genetic variability and character association studies for yield and yield contributing traits in groundnut, *Arachis hypogaea* (L.). *Journal of Oilseeds Research*, **26**: 123-125.

Maurya M K, Rai P K, Kumar A, Singh B A and Chaurasia A K 2014. Study on genetic variability and seed quality of groundnut (*Arachis hypogaea* L.) genotypes. *International Journal of Emerging Technology and Advanced Engineering,* **4**(6): 818-823.

Mondal S and Badigannavar A M 2016. Development of high protein groundnut (*Arachis hypogaea* L.) mutant through induced mutagenesis. *Journal of Oilseeds Research*, **33**(2): 98-101.

Narasimhulu R, Kenchanagoudar P V and Gowda M V C 2012. Study of genetic variability and correlations in selected groundnut genotypes. *International Journal of Applied Biology and Pharmaceutical Technology*, **3**(1): 355-358.

Narasimhulu R, Kenchanagoudar P V, Gowda M V C and Sekhar L 2013. Genetic variability and correlation studies for selection of multiple disease resistance lines in two crosses of peanut. *Bioinfolet*, **10**: 183-186.

Padmaja D, Eswari K B, Brahmeswararao M V and Madhusudhan Reddy S 2013a. Genetic variability parameters for yield components and late leaf spot tolerance in BC_1F_2 population of groundnut (*Arachis hypogaea* L.). *International Journal of Innovative Research and Development*, **2**(8): 348-354.

Padmaja D, Brahmeswararao M V, Eswari K B and Madhusudhan Reddy S 2013 b. Genetic variability, heritability for late leaf spot tolerance and productivity traits in a recombinant inbred line population of groundnut (*Arachis hypogaea* L.). *Journal of Agriculture and Veterinary Sciences*, **5**(1): 36-41.

Padmaja D, Eswari K B, Brahmeswararao M V and Prasad G S 2015. Genetic variability studies in F_2 population of groundnut (*Arachis hypogaea* L.). *Helix*, **2**: 668-672.

Pearson K 1929. Inequalities for moments of frequency functions and for various statistical constants. *Biometrika*, **21**(1-4): 361-375.

Prabhu R, Manivannan N, Mothilal A, Ibrahim S M 2015a. Estimates of genetic variability parameters for yield and yield attributes in groundnut (*Arachis hypogaea* L.). *International Journal of Agriculture, Environment and Biotechnology*, **8**(3): 729-737.

Prabhu R, Manivannan N, Mothilal A, Ibrahim S M 2015b. Nature and degree of distribution for yield and yield attributes in six backcross populations of groundnut (*Arachis hypogaea* L.). *Plant Archives*, **15**(2): 997-1001.

Priyadharshini M 2012. Molecular marker analysis for yield and yield component traits under non stress and drought stress conditions in groundnut (*Arachis hypogaea* L.).Ph.D. (Ag.) Thesis, Tamil Nadu Agricultural University, Coimbatore.

Robinson H F, Comstock R E and Harvey P H 1949. Estimates of heritability and the degree of dominance in corn. *Agronomy Journal*, **41**: 353-359.

Savaliya J J, Pansuriya A G, Sodavadiya P R and Leva R L 2009. Evaluation of inter and intraspecific hybrid derivatives of groundnut (*Arachis hypogaea* L.) for yield and its components. *Legume Research*, **32**(2): 129-132.

Shinde P P, Khanpara M D, Vachhani J H, Jivani L L and Kachhadia V H 2010. Genetic variability in Virginia bunch groundnut. *Plant Archives*, **10**(2): 703-706.

Shoba D, Manivannan N and Vindhiyavarman P 2009. Studies on variability, heritability and genetic advance in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, **1**: 74-77.

Shridevi A J, Nadaf H L, Gowda M V C, Bhat R S, Patil R K, Motagi B, Kenchanagowda P, Mukri G, Archana B, Ganagshetty P, Gangadhar K and Jaggal L 2014. Marker detection and genetic analysis for rust resistance of recombinant and backcross inbred lines in groundnut (*Arachis hypogaea* L.). *Indian Journal of Genetics*, **74**(2): 213-221.

Sivasubramanian S and Madhavamenon P 1973. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*, **60**: 1093-1096.

Sreenivasulu S, Jain P K and Sastry T P 2015. Impact of farmer field school on extent of adoption of improved practices by groundnut farmers. *Journal of Oilseeds Research,* **32**(1): 106-109.

Subrahmanyam P, McDonald D, Waliyar F, Reddy L J, Nigam S N, Gibbons R W, Rao V R, Singh A K, Pande S, Reddy P M and SubbaRao P V 1995. Screening methods and sources of resistance to rust and late leaf spot of groundnut. *Information Bulletin No. 47,* ICRISAT, Patancheru, India, pp. 24.

Subrahmanyam P, Williams J H, McDonald D and Gibbons R W 1984. The influence of foliar diseases and their control by selective fungicides on a range of groundnut (*Arachis hypogaea* L.) genotypes. *Annals of Applied Biology*, **104**: 467-476.

Thirumala R V, Venkanna V, Bhadru D and Bharathi D 2014. Studies on variability, character association and path analysis on groundnut (*Arachis hypogaea* L.). *International Journal of Pure and Applied Bioscience*, **2**(2): 194-197.

Vishnuvardhan K, Vasanthi R P, Reddy K H P and Reddy B V B 2012. Genetic variability studies for yield attributes and resistance to foliar diseases in groundnut (*Arachis hypogaea* L.). *International Journal of Applied Biology and Pharmaceutical Technology*, **3**(1): 390-394.

Influence of phosphorus application on seed yield, quality and phosphorus uptake pattern of Indian mustard (*Brassica juncea*) cultivars

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ABSTRACT

A field experiment was conducted during *rabi* 2012-13 at the Punjab Agricultural University, Ludhiana on low P soil to study the response of Indian mustard [*Brassica juncea* (L.) Czern and Coss] cultivars to applied phosphorus. Application of phosphorus up to 15 kg/ha of P_2O_5 significantly increased the concentration and uptake of P in plants at all the growth stages, in seed and stover at harvest, and seed yield, oil content, oil yield and protein yield whereas similar increase with application of 30 over 15 kg/ha of P_2O_5 was significant for P concentration in seed and stover, P uptake at 90 and 120 DAS, stover and total P uptake (seed+ stover) and oil content. Seed yield (1766 kg/ha), oil yield (625 kg/ha) and protein yield (291 kg/ha) produced with application of 30 kg/ha of P_2O_5 was 9.9, 11.2 and 8.9 per cent, respectively more than that produced without application of phosphorus. Among cultivars, NRCHB 601 has significantly out performed all other cultivars for P concentration and uptake, seed-, oil- and protein-yield. Total P uptake at maturity by NRCHB 601 (21.52 kg/ha) was significantly more (18.8-54.8%) than rest of the cultivars. Cultivar NRCDR 2 contained significantly higher oil content (40.2%) than rest of the test cultivars, but, its oil yield was significantly lower than that of NRCHB 601.

Keywords: *Brassica juncea,* Cultivars, Oil, Phosphorus, Protein, Uptake, Yield

Phosphorus (P) is involved in carbohydrate metabolism, glycolysis, energy transfer, photosynthesis, respiration, redox reactions, protein activation, carbon allocation, division and enlargement of meristematic cells in plants (Marschner, 1995; Brady and Weil, 2002). Its low mobility and fixation in soils make it one of the least available mineral nutrients required by plants resulting in its deficiency in crop fields all over the world (Vance *et al.,* 2003; Lynch, 2007). In India, about 50% soils are low and 40% medium in available P (Muralidharudu *et al.,* 2011). In Indian Punjab, about 68% soils have been reported low to medium in available phosphorus (Benbi *et al.,* 2011).

Phosphorus availability to winter crops is limited due to low temperature and lack of adequate moisture for P uptake and solubilisation of fixed forms of P in the semi-arid region of the country. Bolland and Gilkes (1998) reported that only 10-20 per cent of the applied phosphorus was directly used by the crop and even lower amount was availed by the succeeding crops in rotation. Application of P is expensive because almost entire amount of phosphatic fertilizers used in India is imported. Genetic improvement of P nutrition traits in crops is considered to be more economical and sustainable than application of P fertilizers alone (Vance *et al.,* 2003; Yan, 2005). High P fixation and low P uptake rate make it imperative to exploit P efficient cultivars to reduce fertilizer requirements and sustain productivity on low P soils (Fageria *et al.,* 2008). Rapeseed-mustard group of crops are next to soybean in terms of area and production and rank first in terms of vegetable oil supply in India. Indian mustard [*Brassica juncea* (L.) Czern & Coss] with a share of about 80 per cent in area and production is the most important among different rapeseed-mustard crops in the country (Bannor and Mathur, 2015; Singh *et al.,* 2016). Rapeseed-mustard group of crops have relatively high P requirement. Keeping in view the important role of Indian mustard in vegetable oil economy and high cost and poor efficiency of applied P, the present study was carried out to find out the P efficient cultivars.

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MATERIALS AND METHODS

The field experiment was conducted during *rabi* 2012-13 at research farm of Oilseeds Section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana (30° 56' N latitude, 75° 48' E longitude, 247 metre above the mean sea level). The soil of experimental field was loamy sand in texture, free from salts (EC 0.10, 0.08 dS/m), slightly alkaline in reaction (pH 7.8, 8.2) with low organic carbon content (0.37%, 0.17%), low in available nitrogen (245, 140 kg/ha), low in Olsen's available phosphorus (11.7, 11.7 kg/ha) and rich in $NaHCO_3$ extractable potassium (165, 215 kg/ha) at 0-15 and 15-30 cm soil depth, respectively.

Treatments comprising three doses of phosphorus (0, 15 and 30 kg P_2O_5/ha) in the main plots and 14 genotypes of Indian mustard (RLC 1, PBR 210, PBR 91, RLM 619, RL 1359, PBR 357, ELM 123, NRCDR 2, NRCHB 601, Pusa Bold, Varuna, MLM 19, NPJ 79 and PLM 2) in the sub plots

were replicated thrice. The test genotypes were sown on 5th November, 2012 in a plot each measuring 18.0 m^2 (3.0 m x 6.0 m) and were harvested on 8th April, 2013. All other recommended agronomic practices were followed. The net plot size was 9.0 m^2 (1.8 m x 5.0 m).

Phosphorus as per treatments was applied through single super phosphate (16% P_2O_5) at the time of sowing. Nitrogen @ 50 kg/ha in the form of urea (46% N) and potassium @ 15 kg/ha through muriate of potash (60% K_2O) were applied at time of field preparation for sowing. Another dose of urea to supply 50 kg/ha of N was top dressed after first irrigation.

The plants were cut at periodic intervals from base in the 0.5 metre row length from second outer most row in each plot, dried first under shade and later in oven at 65±2 °C till constant weight and computed as dry matter accumulation (DMA) in kg/ha. These dried samples were finally ground to pass through one mm seive. For seed and stover yield, six inner rows were separately harvested, dried and weighed for biomass yield before threshing for seed yield.

Phosphorus content in plant at different growth stages, seed and stover was determined by Vanado-molybdo-phosphoric yellow colour method (Jackson, 1967). The oil content as well as protein content in the seed were determined directly with NIRS (Near Infrared Reflectance Spectroscopy) Model FOSS 6500 by using non-destructive method of oil estimation using equation developed for mustard samples (Alexander *et al.,* 1967). The uptake of phosphorus at different growth stages, by seed and stover at harvest, protein yield and oil yield were worked out by multiplying per cent content with respective yields.

RESULTS AND DISCUSSION

Doses of phosphorus

Content/concentration: Phosphorus (P) concentration in plants decreased consistently with advancement of age of the crop up to 120 DAS (Table 1). But, it increased with the application of P up to 30 kg/ha of P_2O_5 irrespective of crop growth stages. Though such an increase was significant up to 15 kg/ha of P_2O_5 from 30 DAS to 120 DAS, whereas at maturity, significant increase in seed as well as stover P concentration was discerned up to 30 kg/ha of P_2O_5. Kumar and Yadav (2007) and Deo and Khandelwal (2009) reported significant increase in P concentration in plant with increase in its dose.

The oil content increased consistently and significantly with each increasing dose of P up to 30 kg/ha of P_2O_5 (Table 1). Tyagi and Rana (1992) and Lickfett *et al.* (1999) also reported similar positive effect of P application on oil content. Phosphorus in a constituent of phospholipids, therefore its increasing application increases oil (fat) content. Since phosphorus was applied through single super phosphate which also contains sulphur which is involved in oil synthesis, higher dose of phosphorus indirectly increased availability of sulphur for oil synthesis. However, there was no marked influence of P application on seed protein content. This might be due to use of P mainly to meet the requirements of plant biomass build up and seed formation as the DMA and seed yield increased with P application, thus leaving relatively lesser amount for protein synthesis. Patel and Shelke (1998) and Hocking *et al.* (2003) observed that higher levels of phosphorus application did not affect seed protein content.

Uptake and yields: There was consistent increase in P uptake with advancing age of the crop up to maturity (Table 2). It increased from 0.19 kg/ha of P_2O_5 at 30 DAS to 1.56 kg/ha at 60 DAS to 6.84 kg at 90 DAS to 7.53 kg/ha at 120 DAS. Application of 30 kg/ha of P_2O_5 resulted in higher P uptake compared to lower levels at all growth stages (Table 2). Application of 15 kg/ha of P_2O_5 resulted in significantly higher P uptake than control at all growth stage up to maturity, whereas application of 30 kg/ha of P_2O_5 resulted in significantly higher P uptake than 15 kg/ha of P_2O_5 at 90 and 120 DAS, in stover as well as total P uptake (seed + stover) at maturity. Thus application of 30 kg/ha of P_2O_5 resulted in 14.2 per cent more total phosphorus uptake (seed + stover) than that obtained with 15 kg/ha of P_2O_5 which in turn removed 28.9 per cent more phosphorus over control (13.18 kg/ha). Reddy and Sinha (1988) obtained significant increase in phosphorus uptake in Indian mustard with P application up to 30 kg/ha of P_2O_5.

Application of P increased the seed, oil and protein yields up to 30 kg/ha of P_2O_5 and such an increase with 15 kg/ha of P_2O_5 over control was significant (Table 2). Seed yield produced with application of 30 kg/ha of P_2O_5 (1766 kg/ha) was 9.9 and 2.5 per cent more than that obtained with control and 15 kg/ha of P_2O_5, respectively whereas application of 15 kg/ha of P_2O_5 increased the seed yield (1723 kg/ha) over control by 7.2 per cent. Application of 30 and 15 kg/ha of P_2O_5 increased oil yield over control (625 kg/ha) by 11.2 and 7.8 per cent, respectively and protein yield over control (291 kg/ha) by 8.9 and 7.5 per cent, respectively. Higher yield with successive phosphorus doses may be ascribed to higher DMA, more number of siliquae per plant, seeds per siliqua and 1000-seed weight (Chouksey *et al.,* 2016). Similar positive and significant relationship between seed yield and components of yield such as number of siliquae per plant, number of seeds per siliqua, 1000-seed weight, DMA have also been reported by Mir *et al.* (2010). The increase in oil yield accrued from increase in seed yield and oil content with increasing dose of phosphorus whereas, the protein yield increased mainly due to significant improvement in seed yield with phosphorus application.

Cultivars

Content/concentration: Significant differences were recorded among cultivars for P concentration at all the

growth stages including seed and stover at maturity (Table 1). Cultivars NRCHB 601 contained highest P concentration at all growth stages. Phosphorus concentration in NRCHB 601 at 30 DAS (0.34%) was significantly higher than rest of cultivars whereas at all other growth stages including seed and stover at maturity, it was on par with RLC 1. Cultivar NRCHB 601 also recorded statistically similar P concentration with that of Pusa Bold at 60, 90 and 120 DAS and stover at maturity, and with RL 1359 at 90 and 120 DAS. Cultivar NPJ 79 registered the lowest P concentration at 30, 60 and 90 DAS and in seed at maturity, whereas PLM 2 at 120 DAS and MLM 19 in stover at maturity registered the lowest P concentration. Aziz *et al.* (2006), Kumar and Yadav (2007), Siddiqui *et al.* (2008) and Duan *et al.* (2009) also reported differences in shoot phosphorus concentration among *Brassica* cultivars. Such differential in *Brassica* cultivars may be ascribed to their genetic variation for phosphorus acquisition.

Cultivar NRCDR 2 registered significantly higher oil content (40.2%) than rest of the test cultivars (Table 1). Cultivar NRCDR 2 also registered the highest seed protein content (18.9%) and was at par with Varuna, PBR 210, NRCHB 601, RLM 619, Pusa Bold and RL 1359. Whereas low erucic acid containing cultivars, ELM 123 (37.5%, 16.4%) and RLC 1 (37.7%, 16.9%) registered significantly lower seed oil and seed protein content than all other cultivars. Earlier Rana and Pachauri (2001) and Kumar and Yadav (2007) reported significant variation in oil content while Kundu and Dhaka (1996) documented significant differences in seed protein content among Indian mustard cultivars.

Uptake and yields: Differences in P uptake among cultivars were significant at all crop growth stages (Table 2). Cultivar NRCHB 601 registered significantly higher uptake of P at all growth stages than rest of cultivars whereas, NPJ 79, MLM 19 and ELM 123 registered lower P uptake than all other cultivars at different growth stages, seed and stover at maturity. The highest total (seed + straw) P uptake (21.52) registered by NRCHB 601 was significantly higher than rest of the cultivars with increase ranging from 3.4 kg/ha (18.8%) over RLC 1 to 7.62 kg/ha (54.8%) over MLM 19. Lowest total phosphorus uptake was recorded by MLM 19 (13.9 kg/ha) which was at par with NPJ 79 (14.73 kg/ha) and significantly lower than all other cultivars. Observed differences in P uptake were mainly due to similar differences in DMA at different growth stages, seed and stover yields at maturity in different cultivars. Genotypes NRCHB 601 also attained highest P content in seed and stover than rest of the genotypes (Table 1). Genetic variations for phosphorus acquisition, uptake and utilization have been reported in oilseed Brassica by Akhtar *et al.* (2006) and Aziz *et al.* (2011).

Table 1 Effect of phosphorus application and cultivars of Indian mustard on phosphorus content at different growth stages, seed oil content and seed protein content

Treatment	Phosphorus content (%)						Oil content (%)	Seed protein content (%)
	Days after sowing				Maturity			
	30	60	90	120	Seed	Stover		
Doses of phosphorus (kg P_2O_5/ha)								
0	0.23	0.16	0.10	0.08	0.57	0.07	38.9	18.1
15	0.29	0.19	0.12	0.11	0.62	0.10	39.1	18.1
30	0.30	0.20	0.13	0.12	0.65	0.12	39.3	17.9
SEm±	0.011	0.004	0.004	0.004	0.007	0.003	0.003	-
LSD (p=0.05)	0.03	0.01	0.01	0.01	0.02	0.01	0.1	NS
Cultivars								
RLC 1	0.30	0.20	0.13	0.11	0.66	0.11	37.7	16.9
PBR 210	0.26	0.18	0.11	0.10	0.61	0.08	39.1	18.6
PBR 91	0.27	0.18	0.12	0.10	0.62	0.09	39.7	18.3
RLM 619	0.28	0.18	0.12	0.10	0.59	0.12	39.6	18.6
RL 1359	0.29	0.19	0.13	0.11	0.60	0.09	39.6	18.5
PBR 357	0.27	0.18	0.12	0.10	0.59	0.09	39.1	18.2
ELM 123	0.26	0.17	0.11	0.09	0.63	0.09	37.5	16.4
NRCDR 2	0.25	0.17	0.11	0.10	0.60	0.11	40.2	18.9
NRCHB 601	0.34	0.22	0.15	0.12	0.67	0.12	39.6	18.6
Pusa Bold	0.30	0.20	0.13	0.11	0.64	0.10	39.5	18.5
Varuna	0.27	0.18	0.12	0.10	0.59	0.10	39.2	18.7
MLM 19	0.23	0.16	0.10	0.10	0.59	0.08	38.5	17.4
NPJ 79	0.22	0.16	0.10	0.10	0.57	0.10	39.6	17.7
PLM 2	0.26	0.17	0.11	0.09	0.61	0.10	39.0	17.4
SEm±	0.015	0.010	0.010	0.005	0.005	0.015	0.20	0.25
LSD (P=0.05)	0.03	0.02	0.02	0.01	0.01	0.03	0.40	0.5

Cultivar NRCHB 601 produced the highest seed yield (1907 kg/ha) which was significantly higher (6.3-30.4%) than all other test genotypes (Table 2). Similarly NRCHB also 601 produced significantly higher oil yield (755 kg/ha) and protein yield (354 kg/ha) than all other cultivars except Pusa Bold (709 kg/ha, 332 kg/ha, respectively) with increases ranging from 6.5 to 30.4 per cent in case of oil yield and 6.6 to 36.7 per cent in case of protein yield than rest of the cultivars. The seed-, oil- and protein-yield produced by NPJ 79 (1462, 579 and 259 kg/ha, respectively) were at par with MLM 19 (1534, 590, 266 kg/ha, respectively) and with ELM 123 (278 kg/ha) only for protein yield and significantly lower than rest of the cultivars for seed-, oil- and protein- yield. The highest seed yield produced by NRCHB 601 may be mainly due to more number of siliquae per plant and number of seeds per siliqua than other cultivars (Chouksey *et al.,* 2016). Similarly lower yields by MLM 19 and NPJ 79 were due to their significantly lesser number of branches per plant, lower number of seeds per siliqua and 1000-seed weight than rest of the cultivars. Yadav and Yadav (2005) and Rana and Pachauri (2001) reported similar differences among Indian mustard cultivars for seed yield. Differences in phosphorus uptake at different growth stages, in seed and stover, and oil yield and protein yield among cultivars were mainly due to similar differences in DMA at different growth stages and seed yield with NRCHB 601 showing distinct superiority over other cultivars for these traits.

Thus, P concentration and P uptake in plants at different growth stages, seed yield, oil content and oil yield and protein yield increased with application of phosphorus up to the highest test dose of 30 kg/ha of P_2O_5. Among cultivars, NRCHB 601 out performed all other cultivars for P concentration and uptake, seed-, oil- and protein-yield. Cultivar NRCDR 2 registered significantly higher oil content (40.2%) than rest of the test cultivars.

Table 2 Effect of phosphorus application and cultivars of Indian mustard on phosphorus uptake at different growth stages, seed yield, oil yield and protein yield

Treatment	Phosphorus uptake (kg/ha)							Seed yield (kg/ha)	Oil yield (kg/ha)	Seed protein yield (kg/ha)
	Days after sowing				Maturity					
	30	60	90	120	Seed	Stover	Seed + Stover			
Doses of phosphorus (kg $_P2_O5$/ha)										
0	0.14	1.12	5.29	5.35	9.18	4.00	13.18	1607	625	291
15	0.20	1.65	7.11	8.03	10.72	6.27	16.99	1723	674	313
30	0.23	1.89	8.12	9.23	11.52	7.89	19.41	1766	695	317
SEm±	0.01	0.12	0.29	0.34	0.35	0.21	0.52	27.0	10.1	6.12
LSD (p=0.05)	0.03	0.32	0.80	0.96	0.98	0.59	1.45	75	28	17
Cultivars										
RLC 1	0.20	1.66	7.30	7.55	11.43	6.69	18.12	1728	652	291
PBR 210	0.18	1.63	6.57	7.40	10.78	5.17	15.95	1767	690	328
PBR 91	0.19	1.47	7.01	6.98	10.31	5.01	15.32	1663	660	304
RLM 619	0.21	1.52	7.19	7.24	10.27	7.48	17.75	1741	690	324
RL 1359	0.20	1.55	7.31	7.94	10.46	5.52	15.98	1743	691	323
PBR 357	0.19	1.56	7.12	7.12	10.18	5.75	15.93	1724	674	315
ELM 123	0.17	1.31	6.23	6.28	10.67	5.03	15.70	1694	635	278
NRCDR 2	0.18	1.33	6.34	7.07	9.90	6.64	16.54	1650	664	311
NRCHB 601	0.25	2.04	9.09	9.63	12.78	8.74	21.52	1907	755	354
Pusa Bold	0.20	1.61	7.49	8.05	11.48	5.99	17.47	1793	709	332
Varuna	0.19	1.51	6.93	6.74	9.81	5.68	15.49	1663	653	310
MLM 19	0.15	1.24	5.50	7.10	9.05	4.85	13.90	1534	590	266
NPJ 79	0.14	1.33	5.96	7.36	8.33	6.40	14.73	1462	579	259
PLM 2	0.20	1.58	6.59	6.92	10.44	6.69	17.13	1711	668	298
SEm±	0.015	0.13	0.47	0.60	0.54	0.69	0.78	55.6	23.0	11.0
LSD (P=0.05)	0.03	0.26	0.95	1.20	1.08	1.38	1.55	111	46	22

REFERENCES

Akhtar M S, Oki Y, Adachi T, Murata Y and Khan M H R 2006. Phosphorus starvation induced root mediated pH changes in solubilisation and acquisition of sparingly soluble P sources and organic acids exudation by *Brassica* cultivars. *Soil Science and Plant Nutrition*, **52**: 623-633.

Alexander D E, Silvelas L, Collinis F I and Rodgers R C 1967. Analysis of oil content of maize by wide line NMR. *Journal of American Oil Chemists Society*, **44**: 555-558.

Aziz T, Ahmed I, Farooq M, Maqsood M A and Sabir M 2011. Variation in phosphorus efficiency among *Brassica* cultivars. Internal utilization and phosphorus remobilization. *Journal of Plant Nutrition*, **34**: 2006-2017.

Aziz T, Rahmatullah, Maqsood M A, Tahir M A, Ahmad I and Cheema M A 2006. Phosphorus utilization by six *Brassica* cultivars (*Brassica juncea* L.) from tri-calcium phosphate, a relative insoluble compound. *Pakistan Journal of Botany*, **38**: 1529-1538.

Bannor R K and Mathur S 2015. Integration of mustard markets in Rajasthan State of India. *Journal of Oilseeds Research*, **32**(2): 158-166.

Benbi D K, Manchanda J S, Gosal S K, Walia S S, Toor A S and Minhas P S 2011. Soil health issues for sustaining agriculture in Punjab. *Research Bulletin 4/2011,* Directorate of Research, Punjab Agricultural University, Ludhiana, India, pp. 42.

Bolland M A and Gilkes R J 1998. The chemistry and agronomic effectiveness of phosphorus fertilizers. In: *Nutrient Use in Crop Production*, Rengel Z (ed), The Howorth Press, New York. pp. 139-163.

Brady N C and Weil R R 2002. Soil phosphorus and potassium. In: *The Nature and Properties of Soils* (13th ed). NJ: Prentice-Hall, Inc.

Chouksey H 2013. Variability in Indian mustard (*Brassica juncea* L.) cultivars for response to phosphorus. M.Sc. thesis, Punjab Agricultural University, Ludhiana. pp.73.

Deo C and and Khandelwal R K 2009. Effect of zinc and phosphorus on yield, nutrient uptake and oil content of mustard grown on the gypsum treated sodic soil. *Journal of the Indian Society of Soil Science*, **57**: 66-70.

Duan H Y, Shi L, Ye X S, Wang Y H and Xu F S 2009. Identification of phosphorus efficient germplasm in oilseed rape. *Journal of Plant Nutrition*, **32**: 1148-1163.

Fageria N K, Baligar V C and Li Y C 2008. The role of nutrient efficient plants in improving crop yields in the twenty-first century. *Journal of Plant Nutrition,* **31**: 1121-1157.

Hocking P J, Mead J A, Good A J and Diffey S M 2003. The response of canola (*Brassica napus* L.) to tillage and fertilizer placement in contrasting environments in southern NSW. *Australian Journal of Experimental Agriculture,* **43** : 1323-1335.

Jackson M L 1967. *Soil Chemical Analysis.* Prentice-Hall of India Private Limited, New Delhi.

Kumar H and Yadav D S 2007. Effect of phosphorus and sulphur levels on growth, yield and quality of Indian mustard (*Brassica juncea*) cultivars. *Indian Journal of Agronomy*, **52**: 154-157.

Kundu S and Dhaka R P S 1996. Protein, oil and glucosinolate contents in some elite genotypes of Indian mustard (*Brassica juncea* L. Czern & Coss). *Journal of Oilseeds Research*, **13**: 149-150.

Lickfett T, Matthaus B, Velasco L, and Mollers C 1999. Seed yield, oil and phytate concentration in the seeds of oilseed rape cultivars as affected by different phosphorus supply. *European Journal of Agronomy*, **11**: 293-299.

Lynch J P 2007 Roots of the second green revolution. *Australian Jurnal of Botany*, **55**: 493-512.

Marschner H 1995. *Mineral Nutrition of Higher Plants.* 2nd edition, Academic Press, London. 889 pp.

Mir M R, Mobin M, Khan N A, Bhat N A, Lone NA, Bhat K A, Razvi S M, Wani S A, Wani N, Akhter S, Rashid S, Masood, NH and Payne W A 2010. Effect of fertilizers on yield characteristics of mustard (*Brassica juncea* L. Czern & Coss). *Journal of Physiology*, **2**: 20-24.

Muralidharudu Y, Sammi Reddy K, Mandal B N, Subba Rao A, Singh K N and Sonekar S 2011. *GIS Based Soil Fertility Maps of Different States of India,* AICRP-STCR, IISS, Bhopal, pp. 224.

Rana D S and Pachauri D K. 2001. Sensitivity of zero erucic acid genotypes of Oleiferous Brassica to plant population and planting geometry. *Indian Journal of Agronomy,* **46**: 736-740.

Reddy B N and Sinha M N 1988. Yield and phosphorus utilization of mustard as influenced by phosphorus at various levels of N and moisture regimes. *Fertiliser News,* **33**: 31-37.

Siddiqui M H, Mohammad F, Khan M N and Khan M M A 2008. Cumulative effect of soil and foliar application of nitrogen, phosphorus, and sulphur on growth, physico-biochemical parameters, yield attributes, and fatty acid composition in oil of erucic acid-free rapeseed-mustard genotypes. *Journal of Plant Nutrition*, **31**: 1284-1298.

Singh B, Malik V, Amarjeet, Abha T, Yadav P K and Singh J 2016. Response of Indian mustard (*Brassica juncea* L.) hybrids to different spacings on aridisols. *Journal of Oilseeds Research*, **33**(2) : 108-113.

Tyagi M K and Rana N S 1992. Response of mustard (*Brassica juncea*) cultivars to phosphorus. *Indian Journal of Agronomy*, **37**: 841-842.

Vance C P, Uhde-Stone C and Allan D L 2003. Phosphorus acquisition and use: Critical adaptations by plants for screening a non-renewable resources. *New Phytologist*, **157**: 423-447.

Yadav S S and Yadav R D 2005. Response of mustard (*Brassica juncea* L. Czern & Coss) varieties to different sowing times under semi-arid conditions of Rajasthan. *Journal of Oilseeds Research*, **22**: 261-262.

Yan X 2005. The roots of phosphorus efficient soybean: theories and practices. In: *Plant Nutrition for Food Security, Human Health and Environmental Production*, Li C J, Zhang F S, Dobermann A, Hinsinger P, Lambers H, Li X L, Marschner P, Maene L, McGrath S, Oenema O, Zhu Y G (eds), Tsinghua University Press, Beijing, pp. 36-37.

Determination of fatty acid profile of branded and unbranded processed foods commonly available in the Indian market with special reference to trans fatty acids

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ABSTRACT

Adverse health effects from the consumption of trans fatty acids (TFA) have led to efforts to decrease the consumption of foods containing these lipids. There is a need for up to date information on TFA levels in foods to support decision-making by regulators on labelling and health claims. In this context, the present study provides detailed information about the fatty acid profile with special reference to TFA of selected branded and unbranded Indian processed foods. Products were analysed for fatty acid composition by using GC. Results showed that the amount of TFA, SFA, MUFA and PUFA varied considerably among the analyzed samples. Among the products analyzed, vanaspati showed highest fat content, chocos showed highest SFA content (82%), boondi showed highest UFA content (74%) and cake showed highest TFA. The major trans forms in all samples were elaidic acid and linolelaidic acid (C18:2, trans-6). Vaccenic acid was detected only in health drinks (0.33%). Six out of 15 product labels were misrepresenting the TFA content. Stringent regulations are required for reducing TFA content of commonly consumed foods in India.

Keywords: Branded and unbranded processed foods, Fatty acid composition, Trans fatty acids

Trans fatty acids (TFA) by definition are geometric isomers of monounsaturated and polyunsaturated fatty acids having at least one carbon-carbon double bond with hydrogen on opposite sides of the double bond (trans configuration). There are two major sources of TFAs, those that occur naturally at low levels in ruminant fats and those that are formed during the production of partially hydrogenated vegetable oils at high levels (Phillips *et al.,* 2010). In addition to industrial hydrogenation, TFA can also be produced by heating oils above 180°C (Wolff, 1994) and frying of oils at high temperatures.

The major TFA formed by partial hydrogenation of vegetable oils, derived from oleic acid is elaidic acid, whereas the main TFA resulting from rumen bio-hydrogenation is vaccenic acid (Tardy *et al.,* 2011) and also palmitelaidic acid (C16:1 $\triangle$9t or 16:1 trans-9) from other ruminant fats (Mozaffarian and Cao, 2010). TFA isomers differ between the industrial TFA (I-TFA) and ruminant TFA (R-TFA) with elaidic acid (t9-C18:1) predominant in I-TFA and vaccenic acid (t11-C18:1) predominant in R-TFA (Scientific Advisory Committee on Nutrition, 2007).

The World Health Organization (WHO) predicted that coronary heart disease (CHD) will remain as the third killer of the world in the coming decades (Mackay and Mensah, 2004). Consumption of TFA predicts higher risk of coronary heart disease and possibly diabetes mellitus (Mozaffarian *et al.,* 2006). Major dietary sources of TFA include bakery products, fast foods, meat, deep fried and frozen foods, packaged snacks, margarines and partially hydrogenated fats directly used for cooking and also ruminant derived foods (dairy products and meat) (Micha and Mozaffarian, 2008). TFA can be formed during heating of unsaturated fatty acids. Thus, frying foods in vegetable oils can lead to the formation of TFA even if no such fatty acids are introduced into the oil prior to cooking. Typically 0.2-1% of total fat may be converted to TFA when vegetable oils are used for deep frying over long periods (Health Canada, 2006). TFA have been taken up by the commercial food industry as an ingredient that can reduce costs, enhance attractiveness, texture to baked goods, shelf-life and reduce refrigeration requirements. WHO recommended a TFA intake of less than 2.2 g/day (1% of overall energy intake) in 2003 (WHO, 2003). Food regulation worldwide has been amended with respect to nutrition labelling and health claims on TFA. As a result, mandatory nutrition labelling of TFA came into effect in many countries such as Korea, United States, Canada and Denmark. Prevention of Food Adulteration Act of India, 1955 require that the foods in which hydrogenated vegetable fats or bakery shortening is used shall declare on the label that "Hydrogenated vegetable fats or bakery shortening used contains trans fats" and a health claim of 'trans fat free' may be made where the TFA is less than 0.2 g per serving of food. According to latest recommendations, TFA in oil should not exceed 2%. However, the laboratory tests conducted by a Delhi based Centre for science and environment (CSE) found TFA levels to be as high as 23% in some vanaspati brands liberally consumed in India (Dhaka

et al., 2011). The present study was designed to determine the fatty acid profile of processed foods (labelled as well as un-labelled products) that are commonly available in Indian market with special reference to TFA and to check whether the claims made on labels of processed foods are genuine. This study also provides valuable information which can be utilized for laying down regulations and also highlights the necessity of bringing regulation on un-labelled products.

MATERIALS AND METHODS

Samples for study: A total of 30 food items were selected, and among these, 15 were branded which include cooking butter, vanaspathi (hydrogenated fat), fat spread, brown bread (brand 4), brown bread (brand 5), crispy snack, cake, potato chips, chocos, health drink, noodles, soup mix, Alu bhujia, biscuits and choco cream biscuits. Fifteen unbranded samples included samosa, jalebi (traditional Indian deep fried sweet made of refined wheat flour), bun (local), namak para (traditional crispy deep fried snack made of refined wheat flour, semolina, ghee), biscuits, boondi (water droplet sized deep fried crispy Indian snack prepared from gram flour), chegodi (rice flour rings - a traditional south Indian savoury snack), potato chips, muruku (crunchy deep fried Indian savoury snack), gulab jamun, pizza bread, vegetable curry puff, ragi biscuit, trans-esterified fat and cake which were commonly consumed by people, that might contain a high TFA content. Processed food samples were procured from the super markets, local bakeries and other retail agents in Hyderabad, India, which were selected through market survey.

Total fat and fatty acid analysis: The moisture content of samples was analysed by following standard procedure of IS 1155:1968, reaffirmed, (2010) using hot air oven. Total fat was analysed by Gerhardt soxtherm fat analyser by the method described by AOAC (2003.06, 19th Edition). Fatty acids were analysed by AOAC (2001. 996.06). The isolated fat was trans-esterified using 0.5 M methonolic KOH to form fatty acid methyl esters (FAME). Fatty acids were estimated by GC, 7890B of Agilent Technologies with 7693 Auto sampler, equipped with flame ionization detector and split injector. Injector temperature was at 260°C and samples were injected (1 µl) with split ratio of 10:1 by the auto sampler. Carrier gas (Nitrogen) flow rate was 30 ml/min. Column used was Agilent-DB-FFAP, a nitroterephthalic-acid-modified polyethylene glycol (PEG) of high polarity for the analysis of volatile fatty acids, with the length 30m x 250 µm, diameter 0.25mm, film thickness of 0.25µm. The temperature program was at set with the initial temperature of 100°C, hold time, 5 min, rising at an increasing rate to 240°C at the rate of 4°C /min and held for 5 min. Total run time was 45 min. Nitrogen was used as carrier gas at a column flow rate of 1.0 ml/min. Detector temperature was at 280°C. EZ Total Chrome software was used for running the GC and calculation of fatty acid composition. FID Hydrogen gas flow rate was 30 ml/min. Zero air flow was 300 ml/min and make up flow was 25 ml/min. The fatty acid content was measured based on area normalization.

Standards used were 47885-U Supelco® 37 Component FAME Mix, 10 mg/mL in methylene chloride. For individual trans-fatty acids standards, Supelco trans-9-Eliadic methyl ester, 10 mg/ml in heptane, trans-9, 12-Octadecadienoic (linoleliadic) methyl ester and trans-11-Vaccenic methyl ester, were used. After injecting the 37-FAME standard, individual trans-fatty acid methyl ester standards were also injected and the retention times were compared under standard conditions described above to ascertain that the individual standard peaks were coinciding exactly with the peaks in the combined standard. Samples were processed and injected as standards. Sample fatty acid composition was compared with standard fatty acid composition and percentages calculated by normalization of peak areas.

RESULTS AND DISCUSSION

Branded and unbranded products including biscuits, bread, bun, puffs, samosa, health drink, soup mix, noodles, and some traditional foods were analyzed for total fat, trans fat and complete fatty acid composition. Among the total food products 15 were branded and 15 were unbranded samples.

Total fat content of branded and unbranded food products: The total fat (g/100 g food) contents of 15 branded and 15 unbranded samples are given in the Table 3 and 4, respectively. Total fat content in the branded samples analyzed was in the order: Vanaspathi > cooking butter > fat spread > crispy snack > potato chips > cake > Alu bhujia > choco cream biscuit > biscuit > soup mix > chocos > brown bread (brand 4) > brown bread (brand 5) > health drink > noodles. The total fat content in the unbranded samples was in the order: trans-esterified fat > boondi > biscuits > namak para > potato chips > muruku > chegodi > samosa > cake > vegetable curry puff > ragi Biscuit > jalebi > gulab jamun > pizza bread > bun (local). The type of fatty acids present in any food product will attain significance with respect to health implications, only if the total fat content is higher. The higher the fat content, intakes will be more, and simultaneously, the presence of unhealthy fatty acids like SFA and TFA will attain significance with respect to pre-disposing to heart diseases. Foods that are high in trans or saturated fatty acids are associated with an increased risk of cardiovascular disease and diabetes (Mozaffarian *et al*., 2006).

Saturated fatty acid content of branded and unbranded food products: Tables 1 and 3 shows saturated fatty acid content of branded food items. The SFA content of the 15

food products in the branded category ranged from 37.6% to 82.07%. The highest amount of saturated fat (82.07%) in branded samples was found in chocos while it was lowest (37.62%) in soup mix. The predominant fatty acids present in these items which had high fat content as well as high SFA was palmitic acid, which ranged from 37.2 to 55.3%. Stearic acid (C18:0) was the second dominant saturated fatty acid present in all food samples. The highest amount of stearic acid was found in cooking butter (17.9%) while it was lowest in soup mix (1.18%). Other SFA like butyric acid (C4:0), caprylic acid (C6:0), capric acid (C10:0), lauric acid (C12:0), myristic acid (C14:0), arachidic acid (C20:0) and behenic acid (C22:0) were also determined in lower concentrations in other foods.

Tables 2 and 4 shows saturated fatty acid content of unbranded food items. The dominant fatty acid among the saturated group was palmitic acid (C16:0), which ranged from 17.8% in boondi to 40.0% in trans-esterified fat. In unbranded food items also, palmitic acid was the predominant fatty acid. This indicates that a greater amount of fats rich in palmitic acid is used in food preparation or due to repeated reuse of oil for frying. Reheating of oils increases SFA and may be the reason for higher SFA in food samples in the present study. Palmitic (16:0) acid content increased with prolonged frying where as linoleic acid (18:2) and linolenic acid (18:3) fatty acid content was decreased (Alireza *et al.,* 2010). Lower fatty acids of shorter chain length were detected in almost trace amounts in these food products, while stearic acid (18:0) was the second highest fatty acid present in unbranded food items.

Table 1 Fatty acid composition of branded food items

Brand No.	Sample Name	Fatty acid composition (%)																	
		Total fat (%)	Butyric acid (C4:0)	Caproic acid (C6: O)	Caprylic acid (C8: 0)	Capric acid (C10: 0)	Lauric acid (C12:0)	Myristic acid (C14:0)	Myristoleic acid (C14:1)	Palmitic acid (C16:0)	Stearic acid (C18:0)	Oleic acid (C18: 1n9cis)	Elaidic acid (C18: 1,n9 trans)	Linoleic acid (C18: 2n6cis)	Linolelidic acid (18:2,n6 Trans)	α-Linolenic acid (18:3)	Arachidic acid (C20:0)	Behenic acid (C22:0)	Vaccenic acid (C18:1, n11T)
Brand 1	Cooking butter	72		0.52	0.7	1.93	2.62	11.9	-	37.2	17.9	21.6	2.5	0.66	2.50	-	-	-	-
Brand 2	Vanaspathi								-										
Brand 3	Fat spread	57		-	0.22	0.42	5.63	2.56	-	39.72	4.51	37.6	-	9.36	-	-	-	-	-
Brand 4	Brown bread	1.0	-	-	-	-	-	-	-	62.8	8.32	19.3	-	9.57	-	-	-	-	-
Brand 5	Brown bread	0.7	-	-	-	-	-	1.53	-	60.2	10.6	22.6	0.46	4.60	-	-	-	-	-
Brand 6	Crispy snack	29	-	-	-	-	0.25	1.12	-	44.0	-	36.62	9.54	-	8.46	-	-	-	-
Brand 7	Cake	14	-	-	-	-	1.1	1.25	-	40.7	1.32	35.4	11.8	-	8.47	-	-	-	-
Brand 8	Potato chips	28	-	-	0.17	0.05	0.18	0.93	-	37.08	1.37	38.45	7.80	12.22	-	-	0.60	-	-
Brand 9	Chocos	1.5	-	-	1.38	-	1.16	2.17	1.64	67.21	10.15	16.29	-	-	-	-	-	-	-
Brand 10	Health drink	0.24	-	-	-	-	0.65	1.13	-	40.83	1.26	40.0	7.4	-	-	-	-	-	0.33
Brand 11	Noodles	0.2	-	-	-	-	-	-	-	45.0	-	17.0	-	38.4	-	-	-	-	-
Brand 12	Soup mix	2.2	-	-	-	-	3.01	1.83	-	31.6	1.18	37.0	2.92	21.4	0.17	0.92	-	-	-
Brand 13	Alu Bhujia	14	-	-	-	-	0.2	1.06	-	42.45	5.58	40.66	-	9.47	0.14	-	0.43	-	-
Brand 14	Biscuits	8	-	-	-	-	0.12	0.93	-	42.54	5.25	39.1	-	12.1	-	-	-	-	-
Brand 15	Choco cream biscuits	14	-	-	-	-	0.25	1.14	-	46.1	4.6	36.7	-	7.3	-	-	-	-	-

Table 2 Fatty acid composition of unbranded food items

Sample Name	Total Fat (%)	Fatty acid composition (%)																
		Butyric acid (C4:0)	Caproic acid (C6: O)	Caprylic acid (C8: 0)	Capric acid (C10: 0)	Lauric acid (C12:0)	Myristic acid (C14:0)	Myristoleic acid (C14:1)	Palmitic acid (C16:0)	Stearic acid (C18:0)	Oleic acid (C18:1 n9cis)	Elaidic acid (C18:1,n9 trans)	Linoleic acid (C18: 2n6cis)	Linolelidic acid (18:2,n6 Trans)	α-Linolenic acid (18:3)	Arachidic acid (C20:0)	Behenic acid (C22:0)	Vaccenic acid (C18:1,n11T)
Samosa	21	-	-	0.26	0.17	0.64	1.8	-	32.9	1.98	20.4	6.18	33.82	0.33	-	0.39	-	-
Jalebi	6.0	-	-	0.26	-	0.34	1.38	-	50.0	1.72	34.5	7.84	-	3.93	-		-	-
Bun (local)	1.2	-	-	-	-	-	0.44	1.81	23.3	9.75	39.44	1.01	23.84	-	-		-	-
Namak para	22	-	-	-	-	0.59	1.23	-	44.3	1.55	37.2	7.03	-	8.10	-		-	-
Biscuits	27	-	-	-	-	0.97	1.46	-	50.1	1.04	33.6	6.7	-	6.17	-		-	-
Boondi	36	-	-	0.3	-	-	-	-	17.8	1.70	31.6	4.42	42.8	0.41	-		0.70	-
Chegodi	23	-	-	-	-	-	1.12	-	46.8	0.57	40.0	4.54	5.56	0.10	-		-	-
Potato chips	24	-	-	-	-	-	1.21	-	47.2	0.88	34.79	10.2	-	5.70	-	-	-	-
Muruku	24	-	-	-	-	-	-	-	19.4	5.9	31.7	0.95	42.1	-	-	-	-	-
Gulab Jamun	4.4	0.37	1.04	0.86	1.67	4.56	9.13	0.65	37.88	11.1	25.5	-	2.84	-	-	-	-	1.69
Pizza bread		-	-	-	-	1.03	1.15	-	37.6	1.34	36.8	-	16.1	-	0.42	-	-	0.35
Vegetable curry puff	20	-	-	-	0.27	4.12	2.39	-	46.4	1.5	32.7	8.0	-	4.11	-	-	-	0.53
Ragi Biscuit	14	-	-	-	-	0.27	1.25	-	49.24	4.69	36.11	-	8.44	-	-	-	-	-
Trans-esterified fat	92					0.73	1.37	-	49.01	4.96	34.79	-	7.80	-	-	0.38	-	-
Cake	18	-	-	-	-	0.71	1.19	-	41.64	1.01	39.99	6.64	0.34	8.48	-	-	-	0.34

Table 3 Total fatty acid composition of branded samples

Brand No.	Sample name	Total fat content (%)	Total SFA (%)	Total UFA (%)	TFA content given on label (%)	TFA found after analysis (%)
Brand 1	Cooking butter	72	72.77	22.26	3	5
Brand 2	Vanaspathi	100	61.67	28.48	10	9.86
Brand 3	Fat spread	57	53.06	46.96	Not detectable	0
Brand 4	Brown bread	1.0	71.12	28.87	Traces	0
Brand 5	Brown bread	0.7	72.33	27.2	0	0.46
Brand 6	Crispy snack	29	45.37	36.62	0	18
Brand 7	Cake	14	44.37	35.4	0	20.27
Brand 8	Potato chips	28	40.38	50.67	Not > 0.1	7.8
Brand 9	Chocos	1.5	82.07	17.93	0	0
Brand 10	Health drink	0.24	43.87	40	0	7.4
Brand 11	Noodles	0.2	45	55.4	0.1	0
Brand 12	Soup mix	2.2	37.62	59.32	Traces	3.09
Brand 13	Alu Bhujia	14	49.72	50.13	0	0.14
Brand 14	Biscuits	8	48.84	51.2	0	0
Brand 15	Choco cream biscuits	14	52.09	44	Not > 0.1%	0

Table 4 Total fatty acid composition of unbranded samples

Sample Name	Total fat content (%)	Total SFA (%)	Total UFA (%)	Total TFA (%)
Samosa	21	38.14	53.82	6.51
Jalebi	6.0	53.7	34.5	11.77
Bun (Local)	1.2	33.49	63.28	1.01
Namak para	22	47.67	37.2	15.13
Biscuits	27	53.57	33.6	12.87
Boondi	36	20.5	74.4	4.83
Chegodi	23	48.49	45.56	4.64
Potato chips	24	49.29	34.79	15.90
Muruku	24	25.3	73.8	0.95
Gulab Jamun	4.4	66.61	28.34	-
Pizza bread	2.7	41.12	53.32	-
Vegetable curry puff	20	54.68	32.7	12.11
Ragi Biscuit	14	55.45	44.55	-
Trans-esterified fat	92	56.45	42.59	-
Cake	18	44.55	39.99	15.12

Unsaturated fatty acid content of branded and unbranded food products: Tables 3 and 4 shows unsaturated fatty acid content of branded and unbranded food items. The total amount of unsaturated fat in branded samples ranged from 17% in chocos to 59% in soup mix in branded food samples. The types of fatty acids present in food items attains significance only if the total fat content in the foods is present in higher amounts like in cooking butter, vanaspathi, fat spread, crispy snack, potato chips, choco cream biscuits and cake. In these food items, the total unsaturated fatty acid content ranged from 22.3 to 50.7%. Among all these 15 food items, the predominant unsaturated fatty acid was oleic acid which ranged from 16.3% in chocos to 40.7% in Alu bhujia. Linoleic acid, which is an n-3 PUFA, was the other fatty acid present in amounts ranging from 0.66 in cooking butter to 38.4% in noodles. In food products with fat content higher than 14%, around 10% of linoleic acid was present. Among the unbranded food items, total UFA ranged from 32.7% in vegetable curry puffs to 74.4% in boondi. Among these products, those with fat content more than 14% and UFA content more than 40% could be of significance in terms of their beneficial effects on health. Among the MUFA, oleic acid (C18:1 cis-9) was the major fatty acid present. The amount of oleic acid ranged from 20.4% in samosa to 40% in chegodi. Linoleic acid content was also significantly high ranging from 33.8 to 42.8% in fried items like samosa, muruku and boondi among unbranded samples.

Trans fatty acid content of branded and unbranded food products: Tables 3 and 4 show trans fatty acid content of branded and unbranded food items. In branded samples the amount of total TFA ranged from 0.14 in Alu bhujia to

20.3% in cake. Total TFA was higher in cake (20.3%), crispy snack (18%), potato chips (7.8%), vanaspathi (9.86%), cooking butter (5%), among the food products having higher fat content. The TFA content assumes significance in terms of their ill effects on the health of consumers, only if fat content is also high. Hence, consumption of the above listed products might prove to be harmful if consumed in large amounts and at higher frequencies. The major TFA observed in all samples was elaidic acid (C18:1 trans-9) and linolelaidic acid (C18:2, trans-6) in the range of 0.46-11.8%. Out of 15 branded samples, four samples contained elaidic acid (C18:1 trans-9) at more than 7% (7.4, 7.8, 9.5, 11.8%), four samples had less than 3% and six samples did not contain any TFA. Linolelaidic acid (C18:2, trans-6) was present in two samples (chat masti crispy snack and cake) at 8.5% and two samples has less than 2%, while cooking butter and vanaspathi had 2.5% and 4.6%, respectively. Six samples did not contain any TFA and vaccenic acid was detected only in health drink (0.33%). Presence of vaccenic acid in health drink could be due to presence of ingredients such as dried skimmed milk, dried whey and milk proteins (as presented on label) which are of animal origin. Vaccenic acid is a TFA which is known to be produced in the rumen of epigastric animals naturally during the partial biohydrogenation of linoleic acid (Adlof *et al.,* 2000; Lock *et al.,* 2004) and it acts as a precursor for the endogenous synthesis of cis9, trans11-conjugated linoleic acid (CLA) via the action of the Δ^9 desaturase enzyme in both humans and animals (Adlof *et al.,* 2000; Turpeinen *et al.,* 2002).

TFA was present in almost all unbranded foods except 4 out of 15 and its content ranged from 0.6% to 15% of total fatty acids. TFA content was higher (> 2%) in potato chips (15.9%), namak para (15%), biscuits (12%), vegetable curry puff (12%), jalebi (11%), samosa (6%), boondi (4.8%) and chegodi (4.64%). Since these food items also contain higher fat content, excess consumption might prove harmful to health. Out of 15 unbranded samples, the major TFA observed in all samples was elaidic acid (C18:1 trans-9) and linoleliadic acid (C18:2, trans-6) in the range of 1-10% and 0.1-8.4%, respectively. Among the 15 food items, eliadic acid was not detected in four samples and linoleliadic acid was not detected in six samples. In terms of classifying them in order of harmfulness with respect to higher fat as well as higher TFA content, namak para is more harmful followed by biscuits followed by potato chips, vegetable curry puffs, cake and jalebi.

An adult with a daily energy intake of 2000 k cal is recommended to limit TFA intake to less than 2.2g/d and SFA intake to less than 22.2 g/d. For a sedentary worker the permitted RDA from SFA is 10% i.e. 180 k.cal and from TFA is 1% i.e. 18 k.cal. If the person consumes a high fat diet, resultant energy may exceed the permitted level exposing the individual to many health issues. Majority of bakery food items were having TFA, whose values had almost crossed the limit recommended by WHO. Serving size is an important factor which contributes to total fat and TFA intake. For example one piece of puff weighing 100g contributes a TFA content of 12%. The resultant energy from TFA alone will be 216 kcal. It is more than the limit specified by WHO i.e. <1% of the total energy should come from TFA. If the same person consumes some similar food products on a daily basis, TFA intake will increase further. On studying the quality of fat in all these products, it was observed that higher TFA is present in many of the products. These results show that the amount of TFA, SFA, MUFA and PUFA varied considerably among the analyzed samples because of the differences in hydrogenation process conditions such as temperature, pressure, type and amount of catalyst and agitation rate that affect the resulting TFA content of the starting oil. There is a need of strong food regulations in all countries to bring levels of TFA in the processed foods to negligible levels.

Table 3 shows the presence or absence of TFA on the nutrition label of the 15 branded processed food items analyzed in the present study. A comparison was made between the information provided on the label with respect to TFA content and the actual TFA content analyzed in the present study. It was observed that the TFA content was more than what was mentioned on the labels of some of the food products. Among those whose label was misrepresenting the TFA content are cooking butter, which had 5% TFA as opposed to 3% provided on the label, crispy snack, which contained 18% TFA, respectively as opposed to 0% indicated on the label, cake which had 20.27% TFA as opposed to 0% on the label, potato chips had 7.8% TFA as opposed to 0% claimed on the label and health drink and soup mix had 7.4 and 3.1% TFA as opposed to claims of 0% on the label. Six food items had 0% as claimed on the label while 2 items had trace amounts when the label indicated 0%. Only vanaspathi had 9.86% TFA and the label indicated 10% TFA. Hence, it can be observed that in 6 out of 15 items, the 0% TFA claims on labels were false. These results show that the amount of TFA, SFA, MUFA and PUFA varied considerably among the analyzed samples. A high percentage of TFA was found in most of the samples. Stringent regulations are required for reducing TFA content of commonly consumed foods in India.

REFERENCES

Adlof R O, Duval S and Emken E A 2000. Biosynthesis of conjugated linoleic acid in humans. *Lipids*, **35**: 131-135.

Alireza S, Tan C P, Hamed and Che M Y B 2010. Effect of frying process on fatty acid composition and iodine value of selected vegetable oils and their blends. *International Food Research Journal*, **17**(2): 295-302.

AOAC 2003.06. *Official Methods of Analysis,* Association of Official Analytical Chemists.

AOAC 2001.996.06. *Official Methods of Analysis,* Association of Official Analytical Chemists.

Bendsen N T, Christensen R, Bartels E M and Astrup A 2011. Consumption of industrial and ruminant trans fatty acids and risk of coronary heart disease: a systematic review and meta-analysis of cohort studies. *European Journal of Clinical Nutrition*, **65**: 773-783.

Dhaka V, Gulia N, Ahlawat K and Khatkar B 2011. Trans fats - sources, health risks and alternative approach - A review. *Journal of Food Science and Technology*, **48**: 534-541.

Lock A L and Bauman D E 2004. Modifying milk fat composition of dairy cows to enhance fatty acids beneficial to human health. *Lipids*, **39**: 1197-1206.

Mackay J and Mensah G 2004. The atlas of heart disease and stroke. Geneva: WHO. Available at URL: www.who.int/cardiovascular_diseases/en/cvd_atlas_25_future.pdf

Micha R and Mozaffarian D 2008. Trans fatty acids: effects on cardio metabolic health and implications for policy. *Prostaglandins, Leukotrienes and Essential Fatty Acids*, **79**: 147-152.

Mozaffarian D, Cao H, King I B, Lemaitre R N, Song X, Siscovick D S and Hotamisligil G S 2010. Trans-palmitoleic acid, metabolic risk factors and new-onset diabetes in U.S. adults. *Annals of Internal Medicine*, **153**: 790-799.

Mozaffarian D, Katan M B, Ascherio A, Stampfer M J and Willett W C 2006. Trans fatty acids and cardiovascular disease. *New England Journal of Medicine*, **354**: 1601-1613.

Phillips K, Ruggio D and Amanna K 2010. Optimization of standard gas chromatographic methodology for the determination of trans fat in unlabeled bakery products. *Food Analytical Methods*, **3**: 277-294.

Scientific Advisory Committee on Nutrition 2007. Update on trans fatty acids and health. Position statement, London: TSO. http://www.sacn.gov.uk/pdfs/ sacn_trans_fatty_acids_report.pdf [Accessed 4.01.12].

Tardy A L, Morio B, Chardigny J M and Malpuech B C 2011. Ruminant and industrial sources of trans-fat and cardiovascular and diabetic diseases. *Nutrition Research Reviews*, **24**: 111-117.

Turpeinen A M, Mutanen M, Aro A, Salminen I, Basu S, Palmquist D L and Griinari J M 2002. Bio-conversion of vaccenic acid to conjugated linoleic acid in humans. *American Journal of Clinical Nutrition*, **76**: 504-510.

U.S. Food and Drug Administration 2003. Food labelling: trans fatty acids in nutrition labeling, nutrient content claims, and health claims. 68. Federal Register 41433-41506.

Watkins C 2004. Trans Symposium a rousing success. *Inform*, **15**: 229-231.

Wolff R L 1994. Cis-trans isomerization of octadecatrienoic acids during heating. Study of pinolenic (cis-5, cis-9, cis-12 18:3) acid geometrical isomers in heated pine seed oil. *Journal of the American Oil Chemists Society*, **71**: 1129-1134.

WHO 2003. Diet, nutrition and the prevention of chronic diseases. Report of a Joint WHO/FAO Expert Consultation. World Health Organization Technical Report Series 916.

Integrated disease management of phyllody of sesame (*Sesamum indicum* L.)

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ABSTRACT

Sesame phyllody is an important disease caused by a pleomorphic phytoplasma which is transmitted by a leafhopper, *Orosius albinctus.* The affected plants become stunted and floral parts are modified in to leafy structures bearing no fruits and seeds causing yield loss up to 59.6 per cent. In this view, a field experiment was conducted at Agriculture Research Sub-Station, Hanumangarh, Rajasthan for the effective management of sesame phyllody through the application of antibiotics, botanicals and insecticides. The experiment was carried out to study the efficacy of seed treatment with imidacloprid and foliar spray of insecticides + combination of streptocycline + copper oxychloride. The treatment comprising seed treatment with imidacloprid 70WS @ 5g/kg seed followed by two sprays of thiomethoxam 25WG @ 0.25 g/l at 40 and 50 DAS and one spray of streptocycline 150 ppm+ copper oxychloride 50WP @ 2g/l at 60 DAS gave minimum disease incidence of 2.5%, highest seed yield of 918 kg/ha as well as maximum cost benefit ratio of 1: 3.32 followed by seed treatment with imidacloprid 70WS @ 5g/kg seed + two sprays of thiacloprid 21.7SC @1ml/l + one spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2g/l which was significantly superior over standard check with a per cent disease incidence of 11.7% and seed yield of 547 kg/ha.

Keywords: Antibiotics, Botanicals, Insecticides, Phyllody, Phytoplasma asteris, Sesame

Sesame (*Sesamum indicum* L.), domesticated over 3000 years ago, is an important and ancient oil-yielding crop. Among the other oilseed field crops, sesame is one of the most important crops in the world for edible oil production, and it is produced mainly in India, Myanmar, China, Sudan, Ethiopia, Uganda, Nigeria, Paraguay, Niger, Tanzania, Thailand, Pakistan and Turkey (Anonymous, 2010). Sesame is one of the important crops for Turkey, because Turkey is secondary centre of diversity for this crop. Having great amount of diversity, the genetic resources of sesame used as source of breeding (Tan, 2010). In India, it is grown in 1.9 m. ha, ranked first in area (46.5%) and second in seed production after China (DES, 2013). Sesame seed is a rich source of protein (20%), edible oil (50%), oleic acid (47%) and linolenic acid (39%) (Uzun *et al.,* 2008; Kumaraswamy *et al.,* 2015). It is also a rich source of natural antioxidants viz., sesamoline, sesamin and sesamol (Shyu and Hwang, 2002). Although sesame is widely used for different purposes, it has low productivity due to non-availability of high-yielding varieties, resistant variety to biotic and abiotic stresses, low harvest index, seed shattering, and indeterminate growth habit (Ashri, 1998; Chauhan *et al.,* 2016).

Many diseases attack sesame, but only a few of them such as Fusarium wilt, charcoal rot, stem and root rot, bacterial blight, bacterial leaf spot, Cercospora leaf spot, Alternaria leaf spot, Powdery mildew, leaf curl and phyllody are considered to be important diseases of sesame in the world and it occurs wherever sesame is cultivated (Beech, 1981; Sataur, 1981; Serry and Sataur, 1981; Tan, 2010; Sujatha *et al.,* 2015). Among major biotic constraints, phyllody characterized by floral virescence and proliferation is major limiting factor affecting sesame crop (Tan, 2010). About one per cent increase in disease intensity reduces its yield by 8.36 kg/ha (Maiti *et al.,* 1988). Association of phytoplasma has been confirmed with phyllody disease in India on the basis of symptoms, electron microscopy and molecular approaches but only up to group level (Vasudeva and Sahambi, 1955; Abraham *et al.,* 1977; Manjunatha *et al.,* 2012). Phyllody or "Green Flowers" is one of the most important and destructive diseases of sesame in Turkey. The incidence of this disease increased day by day in sesame growing areas. The incidence of this disease was reported as high as 100% in India and 90% in Burma (Beech, 1981).Turkmenoglu and Ari (1959) observed phyllody symptoms on native sesame varieties in Aegean Region of Turkey and they have never seen an economical damage of this disease on native sesame varieties. However, the foreign sesame varieties showed as high as 50% symptoms and damage, whereas native varieties which were growing near the foreign varieties did not show so much symptoms as the others. They indicated that the native varieties were almost resistant against this disease. Phyllody is associated with a mycoplasma-like organism (MLO) in the phloem of affected plants (Vasudeva and Sahambi, 1955; Klein 1977; Beech, 1981). It is transmitted by leafhopper (Vasudeva and Sahambi, 1955). Pal and Pushkarnath (1935) reported that the systemic nature of the disease was caused by a virüs. However, it was showed that

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disease to be transmitted by two species of Cicadellid leafhoppers, *Orosius albicinctus* and *O. argentatus* (Vasudeva and Sahambi, 1955, Gowanlock *et al.,* 1976). Beech (1981), reported that phyllody in sesame is transmitted in India and Australia by Cicadellid leafhoppers in the genus *Orosius.* In common with most other MLO, the sesame MLO can be transmitted to a range of other crops. Hence, looking to the seriousness of the disease, present investigation was undertaken by using seed treatment of insecticides and foliar application of insecticides with combination of antibiotics, botanicals and fungicides for effective management of sesame phyllody.

MATERIALS AND METHODS

A field trial was laid out during *kharif* 2013-2015 to evaluate efficacy of insecticide as seed treatment as well as foliar application of different insecticides, botanicals and combination of antibiotic + fungicidal sprays for the control of vector (*Orosius albicinctus*) of phyllody on sesame. The trial was laid out in the field of SKRAU, Bikaner, ARSS, Hanumangarh farm in randomized block design with three replications using variety RT-346 in 3 x 2.7 m plot size with row to row spacing at 30 cm and plant to plant spacing of 10 cm. The spray of insecticides, antibiotics+ fungicide and botanicals were applied at 40, 50 and 60 days after sowing, respectively as per treatment. The field was ploughed well and fertilizers were applied as per recommendation. Weeding was done regularly and two irrigations were applied. The trial consisting of following eight treatments *viz.,* T1- Seed treatment with imidacloprid 70WS @ 5g/kg seed, T2 - T1+ two spray of imidacloprid 17.8 SL @ 0.25 ml/l at 40 and 50 DAS + one spray of streptocycline 150 ppm + copper oxychloride 50WP@ 2gm/l at 60 DAS, T3- T1 + two sprays of acetamiprid 20SP @ 0.3g/l + one spray of streptocycline 150 ppm+ copper oxychloride 50WP @2g/l, T4- T1+ two sprays of thiacloprid @ 1ml/l + one spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2 g/l, T5 - T1 + two sprays of thiomethoxam @ 0.25 g/l + one spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2 g/l, T6 - T1 + two sprays of lambda cyhalothrin 5EC @ 1ml/l + one spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2g/l, T7 - T1 + two sprays of azadirachtin @ 0.03 ml/l + one spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2g/l and T8 - Control. The observations on disease incidence were recorded at weekly intervals up to the maturity of crop.Observations on per cent disease incidence of phyllody were recorded on plot basis up to maturity of crop. Per cent disease incidence was calculated by using the following formula:

$$\text{Per cent disease incidence} = \frac{\text{No. of plants infected}}{\text{Total no.of plants observed}} \times 100$$

The yield obtained from each plot was recorded after threshing. Data were analyzed using arc sin transformation using single factor analysis of variance (ANOVA). Cost benefit ratio was also calculated.

RESULTS AND DISCUSSION

The results revealed that all the tested treatments are significantly superior in reducing the phyllody disease and increasing grain yield of sesame as compared to control during *kharif* 2013 to 2015 (Table 1). Pooled data of three years indicated that among all the treatments, treatment comprising of seed treatment with imidacloprid @ 5g/kg seed + two sprays of thiamethoxam at 40 and 50 DAS + one spray of streptocycline + copper oxychloride at 60 days after sowing gave significantly less disease incidence of 2.5% and highest grain yield of 918 kg/ha followed by treatment module comprising of seed treatment with imidacloprid @ 5g/kg seed + two sprays of thiacloprid at 40 and 50 DAS + one spray of streptocycline + copper oxychloride at 60 days after sowing (3.6% phyllody and 848 kg/ha yield) as compared to control where maximum incidence 11.71% of phyllody and minimum grain yield of 547 kg/ha was recorded (Table 1). It is clear from the data that only seed treatment with imidacloprid @ 5g/kg seed was less effective in disease management, as leafhopper vector attack the crop at later stage and that time the efficacy of treated insecticide was very negligible and vector may successfully transmit the disease. Eventhough the phyllody disease was recorded in different treatments but the incidence was very low in treatment. The influence of treatments on seed yield revealed that it was significantly higher with the application of seed treatment alone as well as combination of seed treatment with insecticides and spray of insecticides, botanicals in combination with antibiotic and fungicide (6.62 to 9.18 q/ha) compared to control (5.47 q/ha) (Table 1). The result presented in Table 1 reveals a positive return and highest cost benefit ratio (1:3.32) in the module comprising of seed treatment with imidacloprid + two sprays of thiacloprid at 40 and 50 DAS followed by single spray of streptocycline + copper oxychloride at 60 days after sowing. These results are in agreement with Jyothirmai et al. (2002) who reported that application of imidacloprid 70WS seed treatment at 5g/kg seed + imidacloprid 0.01% foliar spray drastically reduced leafhoppers population and increased the pod yield of groundnut. Pathak *et al.* (2013) reports that to manage phyllody disease by check the vector population through systemic insecticide is only way to control this disease. Venkanna *et al.* (2010) reported that foliar application of imidacloprid @ 26.7g a.i./ha at 25 and 40 days after sowing was found to be significantly effective in reducing leafhoppers on groundnut and also superior among various neonicotinoid group og insecticides *viz.,* acetamiprid and thiamethoxam. Dey *et al.* (2005) reported that imidacloprid

70WS @ 5-10g/kg seed and imidacloprid 20SL @ 100-125 ml/ha were found highly effective and significantly superior to Carbosulfan 25DS @ 50 g/kg in controlling the leafhopper (*Amrasca biguttulabiguttula*) in okra. This study represents the integrated disease management combinations were best for the management of vector population at prophylactic as well as foliar sprays. Though, the disease is transmitted by the leafhopper, so that to manage the disease, leafhopper must be checked.

In our present study, leaf hopper was controlled by the foliar application of different insecticides and finally a common spray of combination of antibiotic and fungicide was applied for creating resistance in plant against phyllody disease. Hence, it can be concluded from the results of present investigation that module comprising seed treatment with imidacloprid 70WS @ 5g/kg seed + two sprays of thiamethoxam 25WG @ 0.25 ml/l at 40 and 50 DAS + one spray of streptocycline 150 ppm+ copper oxychloride 50WP @ 2 g/l at 60 days after sowing followed by seed treatment with imidacloprid 70WS @ 5g/kg seed + two sprays of thiacloprid @ 1ml/l at 40 and 50 DAS + one spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2g/l at 60 days after sowing was most effective as well as economically beneficial treatments to manage the phyllody of sesame.

Table 1 Integrated disease management of sesame phyllody (*kharif,* 2013-2015)

T. No.	Treatments	*Kharif* 2013		*Kharif* 2014		*Kharif* 2015		Mean		CBR
		Phyllody (%)	Yield (kg/ha)	Phyllody (%)	Yield (kg/ha)	Phyllody (%)	Yield (kg/ha)	Phyllody (%)	Yield (kg/ha)	
T1	Seed treatment with imidacloprid 70WS @5g/kg seed	10.69 (18.30)	786	10.4 (18.68)	648	9.0 (17.35)	416	10.03 (18.11)	662	2.64
T2	T1 + Two sprays of imidacloprid 17.8SL @ 0.25 ml/l + One spray of streptocycline 150 ppm + copper oxychloride50WP @ 2gm/l	6.80 (14.90)	902	7.5 (15.83)	763	7.33 (15.68)	463	7.2 (15.47)	709	2.69
T3	T1+ Two sprays of acetamiprid 20SP @ 0.3g/l + One spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2g/l	8.66 (17.07)	856	8.0 (16.3)	717	6.33 (14.53)	486	7.66 (15.96)	686	2.59
T4	T1+ Two sprays of thiacloprid @ 1ml/l + one spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2gm/l	2.84 (10.76)	1064	3.8 (11.13)	902	4.16 (11.63)	579	3.6 (11.17)	848	3.07
T5	T1 + Two sprays of thiamethoxam 20WG @ 0.25 g/l + One spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2 g/l	2.54 (9.17)	1087	2.9 (8.62)	995	2.16 (8.27)	671	2.53 (8.68)	918	3.32
T6	T1 + Two sprays of lambda cyhalothrin 5EC @ 1ml/l + One spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2 g/l	3.38 (10.87)	1041	4.9 (12.80)	856	4.83 (12.52)	555	4.37 (12.06)	817	3.10
T7	T1 + Two sprays of azadirachtin @ 0.03 ml/l + One spray of streptocycline 150 ppm + copper oxychloride 50WP @ 2gm/l	6.98 (15.28)	925	7.86 (16.24)	786	8.2 (16.56)	440	7.68 (16.00)	717	2.74
T8	Control	11.65 (19.04)	740	13.33 (22.39)	532	10.16 (18.47)	370	11.71 (19.96)	547	2.18
	Mean	14.38	925.8	15.25	775.4	14.37	497.6	14.67	732	
	CV (%)	13.53	13.8	15.6	16.9	14.34	18.36	6.78	5.00	
	CD (P=0.05)	2.41	158.4	2.95	162.5	2.55	113.3	1.23	45.41	

*Figures in parentheses are arc sine transformed values

REFERENCES

Abraham E V, Natarajan K and Murugaesan M 1977. Damage by pests and phyllody to *Sesamum indicum* in relation to time sowing. *Madras Agriculture Journal*, **64**: 298-301.

Anonymous 2010. Sesame production data. http://faostat.fao.org.

Ashri A 1998. Sesame breeding. *Plant Breeding Review*, **16**: 179-228.

Beech D F 1981. Phyllody - its impact on yield and possible control measures. In: *Sesame: Status and Improvement,* Ashri A and Poetiary P (Eds.) FAO Plant Production and Protection Paper No. 29, Rome, Italy, pp. 73-80.

Chauhan S, Rao V P, Reddy A P K, Jayasree G and Reddy S N 2016. Response of sesame (*Sesamum indicum* L.) to irrigation scheduling based on climatological approach and N fertigation levels. *Journal of Oilseeds Research*, **33**(1): 38-44.

DES 2013. Agricultural Statistics Database, Directorate of Economics and Statistics, Department of Agriculture and Cooperation Government of India, http:// www.dacnet.nic.in and FAO. Agricultural data. Organization of the United Nations, Rome, Italy. http://faostat.fao.org.

Dey P K, Jana S K, Chakraborty G and Somchoudhury A K 2005. Evaluation of imidacloprid (70WS-20SL) against sucking pest complex of okra, *Abelmoschus esculentus. Journal of Entomological Research*, **29**(3): 215-218.

Gowanlock D, Greber R, Behncken G M and Finlay J 1976. Electro-microscopy of mycoplasma-like bodies in several Queensland crop species. Second National Plant Pathology Conference, Brisbane, Australia.

Jyothirmai T, Murali K T, Ramaiah M, Padmavathamma K and Ramakrishna Rao A 2002. Efficacy of different insecticides against jassids on groundnut. *Journal of Entomological Research*, **26**(4): 291-295.

Klein M 1977. Sesame phyllody in Israel. *Journal of Phytopathology*, **88**(2): 165-171.

Kumaraswamy H H, Jawaharlal J, Ranganatha A R G and Chander Rao S 2015. Safe sesame (*Sesamum indicum* L.) production: Perspectives, practices and challenges. *Journal of Oilseeds Research*, **32**(1): 1-24.

Maiti S, Hegde M R and Chattopadhyay S B 1988. *Handbook of Oilseed Crops,* 317 pp. Oxford and IBH Publishing Co. (Pvt.). Ltd, New Delhi.

Manjunatha N, Prameela H A, Rangaswamy K T and Palanna K B 2012. Phyllody phytoplasma infecting sesame in South India. *Phytopathogenic Mollicutes*, **2**: 29-32.

Pal B P and Pushkarnath 1935. Phyllody: A possible virus disease of sesamum. *Indian Journal of Agricultural Sciences*, **5**: 517-522.

Pathak D M, Patel D R and Patel R R 2013.Control of sesame phyllody caused by PLO's. *International Journal of Forestry and Crop Improvement*, **4**(1): 47-48.

Sataur M 1981. Fungi, bacteria, viruses, mycoplasma, nematodes and insectsattacking sesame. In: *Sesame: Status and Improvement*, Ashri A and Poetiary P (Eds.), FAO Plant Production and Protection Paper No. 29, Rome, Italy, pp. 81-84.

Serry M and Sataur M 1981. Major diseases of sesame and sources of resistance in Egypt. In: *Sesame: Status and Improvement,* Ashri A and Poetiary P (Eds.), FAO Plant Production and Protection Paper No. 29, Rome, Italy, pp. 71-72.

Shyu Y S S and Hwang L S 2002. Antioxidant activity of white and black sesame seeds and their hull fractions. *Food Research International*, **35**: 357-365.

Sujatha M, Prashant K S and Jawaharlal J 2015. Identification of *Podosphaera xanthii* causing powdery mildew on sesame (*Sesamum indicum* L.). *Journal of Oilseeds Research*, **32**(2): 183-185.

Tan A S 2010. Screening phyllody infected sesame varieties and seed transmission of phyllody under natural conditions in Turkey. *Journal of Ayub Agricultural Research Institute*, **20**: 26-33.

Turkmenoglu Z and Ari O 1959. A virus disease-phyllody virus-noted on sesame in the Aegean Region. *BitkiKoruma Bülteni*, **1**(2): 12-17.

Uzun B, Arslan C and Furat S 2008. Variation in fatty acid compositions, oil content and oil yield in a germplasm collection of sesame (*Sesamum indicum* L.). *Journal of American Oil Chemists Society*, **85**: 1135-1142.

Vasudeva R S and Sahambi H S 1955. Phyllody in sesamum (*Sesamum orientale* L.). *Indian Phytopathology*, **8**: 124-129.

Venkanna Y, Ranga Rao G V and Dharma Reddy K 2010. Bioefficacy of neonicotinoid insecticides against thrips, *Scirtothrips dorsalis* and leafhoppers, *Empoasca kerri* in groundnut. *Indian Journal of Plant Protection*, **38**(2): 134-138.

Changes in edible oil preference and present-day consumption status of households : A case of Tamil Nadu state, India

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ABSTRACT

Traditionally, in India, a variety of edible oils are used for consumption. The type of edible oil being consumed varied across regions. While one region prefers rapeseed-mustard oil, the other region enjoys peanut, sesame and coconut oils. On the whole, rapeseed and mustard oil and peanut oil are the most popularly consumed edible oils in the country. In the study state, Tamil Nadu, the foremost edible oil consumed is peanut oil besides other oils. The technological, economic and policy changes after liberalization induced drastic changes in consumer's preference for food including edible oils. The Markov Chain Analysis for rural and urban Tamil Nadu revealed that there is a perceptible shift in edible oil consumption from traditional peanut oil to Other Edible Oils (OEO's). The possible reason for these shifts are increased urbanization and changing lifestyles, increased awareness, availability of oils in loose pack form in varied quantities available even in remote areas, change in relative prices of oils, and increased income levels of rural and urban households. The secondary data published by National Sample Survey Organisation for Tamil Nadu state did not clearly disintegrate the OEO's, primary survey was employed for this study. The results based on 1000 households revealed that the dominant edible oil consumed was non-traditional sunflower oil in both rural and urban regions. The per capita consumption of edible oils was also higher in recent years indicating higher consumption demand. The results from this study affirm that peanut oil, which was traditionally consumed by households as first preference, has been replaced by non-traditional oils like sunflower oil owing to various macroeconomic factors like price, cost of cultivation and imports. The change call for more concerted efforts to supply these non-traditional oils in the future as the demand were expected to be high. Further, it also implies need for increasing the capacities of edible oil industries as the overall consumption of edible oil is increasing over years. This study highlights the need for suitable policy options for edible oil processing and marketing specifically for sunflower oil besides traditional oils and trade on edible oils.

Keywords: Consumption dynamics, Edible oil, Markov chain, Tamil Nadu state

In the agricultural economy of India, oilseeds are important next only to food grains in terms of area, production and value. India accounts for about 13% of world oilseeds area, 8% of world oilseeds output, and 6% of world vegetable oil production (Hegde, 2003). The Indian edible oil market is the fourth-largest in the world after USA, China and Brazil. The diverse agro-ecological conditions in the country are favourable for growing several annual edible oilseed crops, *viz.,* peanut, rapeseed-mustard, soybean, sunflower, sesame, safflower and niger. Among these, peanut, rapeseed-mustard and soybean, account for nearly 77% of oilseeds area and 86% of oilseeds production (Damodaram and Hegde, 2007; Richard and Mathur, 2015). Despite favourable climatic conditions and highest area under oilseeds (26 m ha), India is the second largest consumer after China, meeting more than half of its requirements of edible oil through imports.

In India, the demand for oilseeds and vegetable oil is increasing due to high population growth, increasing *per capita* income and urbanisation (Sudhakarababu and Hegde, 2011). The process of rapid urbanization and global integration bring about new dietary needs and general lifestyles changes (Popkin, 1999; Regmi and Dyck, 2001). Economic growth is the driving force for the significant change in consumer demand for food including the edible oils (Govindaraj, 2010; Govindaraj and Suryaprakash, 2013; Govindaraj *et al.,* 2015). Many Asian countries including India which are in economic and demographic transition has already exhibited dramatic changes in food consumption patterns (Shetty, 2002; Pingali and Khwaja, 2004). The per capita consumption of edible oil in India was around 11.2 kg/ capita/year, which is less than the world average of 17.8 kg/per capita/year (Ramesh and Murughan, 2008).

On production font, Tamil Nadu is one of the most important oilseeds cultivating state in India with 0.448 million ha producing 1.113 million tonnes of oilseeds (Singh, 2014). The major edible oilseed crops grown in this state are peanut, sesame and sunflower. Traditionally, peanut oil is the major edible oil consumed in this state, however due to rapid economic and income growth [it is one of the fastest growing state with average Gross Domestic Product (GDP) growth of

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more than 5% in the last decade], urbanization (it is the most urbanised state as according to 2001 census, 44% percentage of population, i.e., 27.2 million live in urban areas and in terms of degree of urbanisation and town density) and increased literacy levels [literacy level in this state was 80% as against national level 74% (GOI, 2011)], the consumption pattern of edible is changing in the recent years. Besides these factors, the population of Tamil Nadu state is also expected to reach 70.6 million by 2020 from the 2010 population level of 67.0 million (Census of India, 2001).

There are several studies that highlighted the changes in consumption pattern in India like i) reduced per capita consumption of rice and increased consumption of wheat and wheat based products, ii) rise in high protein and energy dense diets (animal based products) and increase in consumption of fruits and vegetables (Kumar, 1998; Radhakrishan and Venkatareddy, 2002; Pingali, 2006; Mittal, 2006). Nevertheless, none of these studies focussed on the changes in edible oil consumption at the national or state (disaggregated) level, though, it is imperative for planning demand-driven oilseed production and for formulating appropriate trade policy. Further, the national household surveys do not account for the major edible oils being consumed presently like sunflower, rice bran, soybean oils, etc. In this background, the present study was designed to assess the temporal shift in consumption of major edible oils and to ascertain the present-day edible oil consumption pattern in Tamil Nadu state, India.

MATERIALS AND METHODS

Data and sampling: Both secondary and primary data were used in the present study. The secondary data from five quinquennial and National Sample Survey Organisation (NSSO) rounds i.e. 43rd (July 1987 - June 1988), 50th (July 1993 - June 1994), 55th round (July 1999-June 2000), 61st (July 2004 - June 2005) and 66th (July 2009 - June 2010) on consumption pattern of households were used for analysing the temporal shift in consumption of major edible oil groups. The primary data collected through household survey during 2010 was used to ascertain the present-day pattern of edible oil consumption by households (since the secondary data published by NSSO comprise only five oils [Vanaspati/margarine, mustard oil, peanut oil, coconut oil and Other Edible Oils (OEO's) and no details are available on the consumption of other oils by households like sunflower oil, sesame oil, palm oil etc]. For the study on present consumption pattern of edible oils in Tamil Nadu, a multistage random sampling technique was followed to select the sampling households. In the first stage, five zones (north, south, west, central and east) were identified and one district was randomly selected to represent each zone. In the second stage, one taluk in each of the selected districts and one block in the selected taluk were identified randomly. In the third stage, three village clusters were selected in each of the identified blocks. The household samples surveyed in the identified districts were considered as urban samples. In the fourth stage, the households were randomly selected in both rural and urban areas. The household edible oil consumption data was collected using primary survey with the help of pre-tested questionnaires developed for the purpose. Five hundred households each were selected in rural and urban areas and interviewed to know the present-day pattern of edible oil consumption.

Model specification: The temporal shift in consumption of edible oils were analysed by employing a first order finite Markov Chain Model which captured the net effect of changes in the consumption of edible oil over a period of time. Markov Chain Analysis (MCA) was employed to ascertain the shift in consumption of edible oils from 43rd round (1987-88) to 66th round (2009-10).The estimation of the transitional probability matrix (P) was central to this analysis. The element P_{ij} of the transitional probability matrix indicated the probability that share would switch from commodity 'i' to commodity 'j' over time. The diagonal elements P_{ij} where i=j indicated the probability that the commodity retaining its value share. In the context of the current application, the change in edible oil consumption was treated as a random process. The average share of the selected edible oil (commodity) from among the edible oils (commodity group) in any period (round) depends only on the share of the previous period and which was algebraically denoted below:

$$E_{jt} = \sum_{i=1}^{n} [Ei_{t-1}]P_{ij} + e_{it} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots(1)$$

where,

E_{jt} = shift in per capita share of j^{th} commodity (edible oil) during the round t

E_{it}-1 = per capita share of ithcommodity (edible oil) during the round t-1

P_{ij} =probability that share will shift from the i^{th} commodity (edible oil) to j^{th} commodity (edible oil)

e_{it} = error-term which is statistically independent of e_{it}-1, and

n = number of commodities (edible oils)

The transitional probabilities P_{ij}, which can be arranged in a(c×r) matrix, had the following properties:

$$\sum_{i=1}^{n} P_{Ij} = 1 \quad \text{and} \quad 0 \leq P_{ij} \leq 1$$

The probability matrix was estimated using 43rd round to 66th round of data. The transition probability matrix was estimated in Linear Programming (LP) frame work by a method referred to as minimization of Mean Absolute Deviation (MAD); the LP formulation is as per expression below:

$$\text{Min, } OP^* + I_e \qquad \ldots\ldots\ldots\ldots\ldots\ldots (2)$$

Subject to

$$X P^* + V = Y$$

$$GP^* = 1$$

$$P^* \geq 0$$

where, P*is a vector of the probabilities P_{ij}, O is a null vector; I is an appropriately dimensional vector of edible oil; e is the vector of absolute errors (| U |); Y is the vector of proportion of *per capita* shares of other edible oils; X is a block diagonal matrix of lagged values of Y; V is the vector of errors; and G is a grouping matrix to add the row elements of P arranged in P* to unity. P* vectors were arranged to obtain the transitional probability matrix which indicated the overall structure of the transitions that had taken place in the system. Essentially, the transitional probability matrix captures the dynamics of the changes in *per capita* consumption of edible oils in Tamil Nadu in value terms. The individual probabilities P_{ij} indicate the probability of the shift from the commodity 'i' to commodity 'j'.

RESULTS AND DISCUSSION

Consumption pattern of edible oil in rural Tamil Nadu: The comparison of monthly *per capita* consumption of edible oils across income classes in rural Tamil Nadu across five NSSO rounds (43rd, 50th, 55th, 61st and 66th) revealed that during 43rd round (1987-88), the major oils consumed by the rural households were peanut oil and Other Edible Oils (OEO's). The quantity of peanut oil consumed was 0.17 kg *per capita* per month followed by OEO's (0.04 kg *per capita*/month) (Table 1). Over the periods, the *per capita* consumption of peanut oil increased and reached a peak of 0.27 kg *per capita*/month during the 55th round (1999-2000), and thereafter it declined to 0.18 kg *per capita*/month during 66th round (2009-10). This decline in peanut oil consumption in recent years in rural Tamil Nadu was compensated by higher consumption of OEO's. The *per capita* peanut oil consumption increased by only 6% since the base period consumption (1987-88), whereas, a leapfrog jump of 975% in OEO's consumption was observed during 66th round (2009-10). Thus, it could be concluded that there is perceptible temporal shift in consumption of edible oil from traditional peanut oil to other oils in rural Tamil Nadu. Besides shift in edible oil consumption, the *per capita* oil consumption per month also tripled from 0.22 kg during 43rd round (1987-88) to 0.61 kg during the recent 66th round (2009-10) in rural Tamil Nadu.

Consumption pattern of edible oil in urban Tamil Nadu: Similar to rural households, the major oils consumed among urban households was peanut oil and OEO's. The peanut oil consumption was 0.20 kg *per capita*/month during 43rd round (1987-88) and increased to 0.27 kg during the 50th round (1993-94) and started declining thereafter and stood at 0.121 kg *per capita*/month during 66th round (2009-10). This indicated that, the consumption of peanut oil has declined in urban Tamil Nadu also in recent years. It also revealed that the decline in peanut oil consumption started after 50th round (1993-94) in urban areas, whereas, in rural areas the decline was observed after the 55th round (1999-2000) affirming lag in consumption shift from traditional (peanut) to newer oils between the urban and rural areas. The OEO's consumption in urban Tamil Nadu had increased from 0.14 kg *per capita*/ month during 43rd round to 0.57 kg during 66th round. Hence, it could be concluded that, the peanut oil consumption was declining, whereas, the OEO's consumption showed increasing trend in urban Tamil Nadu (Table 2). The results also revealed that in urban Tamil Nadu the *per capita* consumption of peanut oil and coconut oil declined by 29% and 70%, respectively, whereas the OEO's consumption increased by 190% from the base year consumption (1987-88). The decline in *per capita* consumption of peanut oil and coconut oil was overcompensated by higher level of consumption of OEO's. The consumption increase in OEO's might be due to increased awareness about the health benefits of these oils. Moreover, some of the OEO's like sunflower, rice bran oil, palm oil, etc., were priced lower than the peanut and coconut oil inducing shift in consumption. Besides shift (from traditional to newer oils) in consumption in urban areas, the total edible oil consumption *per capita*/month also increased from 0.37 kg during 43rd (1987-88) to 0.70 kg during 66th round (2009-10). The total edible oil consumption *per capita* per month has increased in both rural and urban regions, but consumption was higher in urban areas *vis-à-vis* rural areas (Table 2).

Expenditure pattern and compositional changes in edible oil consumption in rural Tamil Nadu: The shift in edible oil consumption or which oil has given way to which oil in Tamil Nadu state was studied by Markov Chain Analysis. The edible oil commodity-wise monthly *per capita* expenditure for all the income classes from round 43rd (1987-1988) to round 66th (2009-10) was used to analyse the shift or compositional changes in edible oil consumption for rural Tamil Nadu. Before analysing the shift in *per capita* expenditure, the *per capita* per month expenditure share across rounds was compared (Table 3).

It was observed that consumption expenditure share of edible oils like vanspathi/margarine, mustard oil and peanut oil decreased over years (Table 3). The peanut oil share decreased substantially from 84% in 43rd round (1987-88) to 33% during 66th round (2009-10) in value terms. The coconut oil share showed some fluctuations but during the last round its share was only 1.85%. However, during the same period, substantial increase in consumption expenditure share of Other Edible Oils (OEO's) was observed from a meagre 12% during 43rd round (1987-88) to 65% during 66th

round (2009-10) and it affirms shift in expenditure pattern among the edible oils.

The transitional probability matrix presented in Table 4 provides a broad indication of changes/shift in edible oil consumption pattern in rural Tamil Nadu from 43rd to 66th round. The row elements in a transitional probability matrix provide the information on the extent of shift in consumption expenditure across different edible oils with the passage of time. The column elements indicate the probability of gain in consumption expenditure share by particular edible oil from other edible oils (the losing item). The diagonal elements indicate the probability of retention of consumption expenditure by that particular edible oil. The results for rural Tamil Nadu indicated that, the highest retention probability of 1.00 expenditure share was for OEO's followed by probability of 0.84 for peanut oil. Vanaspati/Margarine was expected to gain less in consumption expenditure from mustard oil (0.02 probability) and peanut oil (0.002 probability). Mustard oil does not gain from any of the edible oils, whereas, peanut oil was expected to gain in consumption expenditure from Vanaspati/margarine by 0.52 probability and mustard oil by 0.65 probability, implying that a portion of Vanaspati/margarine or mustard oil were being replaced by peanut oil. The OEO's gain in consumption expenditure from mustard oil (0.13 probability) and coconut oil (1.00 probability) implied that there was shift in per capita consumer expenditure towards OEO's from mustard and coconut oils. The probability of vanaspati losing its share to other oils was 0.52 and 0.48 for peanut oil and coconut oil, respectively. It can be concluded from the above results that people are switching from traditional oils to OEO's in rural areas. The traditional peanut oil given way to OEO's by 0.13 probability, implying that peanut consumers are slowly shifting to OEO's in rural areas.

Table 1 Monthly *per capita* consumption of edible oils in rural Tamil Nadu - 43rd to 66th rounds of NSSO Survey

Edible oil type	Quantity (kg)				
	43rd round (1987-88)	50th round (1993-94)	55th round (1999-00)	61st round (2004-05)	66th round (2009-10)
Vanaspati/Margarine	0.00	0.00	0.00	0.00	0.00
Mustard oil	0.00	0.00	0.00	0.00	0.00
Peanut oil	0.17	0.24	0.27	0.23	0.18 (5.9)
Coconut oil	0.00	0.01	0.01	0.00	0.01
Other Edible Oils (OEO's)	0.04	0.11	0.14	0.21	0.43 (975.0)
Total	0.22	0.38	0.43	0.44	0.61 (177.3)

Source: compiled from different surveys publication of NSSO; Note: Figures in parentheses indicate per cent change over 43rd round

Table 2 Monthly *per capita* consumption of edible oils in urban Tamil Nadu - 43rd to 66th rounds of NSSO Survey

Edible oil type	Quantity (kg)				
	43rd round (1987-88)	50th round (1993-94)	55th round (1999-00)	61st round (2004-05)	66th round (2009-10)
Vanaspati/Margarine	0.01	0.00	0.00	0.002	0.003
Mustard oil	0.00	0.00	0.00	0.000	0.000
Peanut oil	0.20	0.27	0.22	0.143 (-28.5)	0.121 (-39.5)
Coconut oil	0.01	0.01	0.01	0.003 (-70.0)	0.014 (-40.0)
Other Edible Oils (OEO's)	0.14	0.20	0.31	0.405 (190.0)	0.561 (300.7)
Total	0.37	0.48	0.54	0.553 (49.5)	0.699 (88.9)

Source: compiled from different surveys publication of NSSO; Note: Figures in parentheses indicate per cent change over 43rd round

Table 3 Monthly *per capita* consumption expenditure on edible oils in rural Tamil Nadu (₹/month)

Round (Year)	Vanaspati/Margarine	Mustard oil	Peanut oil	Coconut oil	Other edible oils	Total oil
43rd (1987-88)	0.03 (0.59)	0.06 (1.17)	4.27 (83.72)	0.15 (2.94)	0.59 (11.56)	5.1 (100)
50th (1993-94)	0.02 (0.17)	0.05 (0.44)	8.32 (73.96)	0.31 (2.76)	2.55 (22.67)	11.25 (100)
55th (1999-00)	0.00 (0.00)	0.02 (0.12)	10.35 (62.05)	0.51 (3.06)	5.8 (34.77)	16.68 (100)
61st (2004-05)	0.03 (0.12)	0.01 (0.04)	12.64 (52.33)	0.19 (0.79)	11.28 (46.71)	24.15 (100)
66th (2009-10)	0.04 (0.12)	0.00 (0.00)	11.48 (33.19)	0.64 (1.85)	22.43 (64.86)	34.58 (100)

Source: compiled from different surveys publication of NSSO; Note: Figures in parentheses indicate percentage to total expenditure on edible oils

Table 4 Shift in the pattern of edible oil consumption in rural Tamil Nadu - Probability transition matrix for 43rd to 66th rounds of NSSO survey

Edible oil type	Vanaspati/Margarine	Mustard oil	Peanut oil	Coconut oil	Other edible oils
Vanaspati/Margarine	0	0	0.517	0.483	0
Mustard oil	0.018	0.333	0.649	0	0
Groundnut oil	0.002	0	0.843	0.030	0.1263
Coconut oil	0	0	0	0	1.0000
Other Edible Oils (OEO's)	0	0	0	0	1.0000

Expenditure pattern and compositional changes in edible oil consumption in urban Tamil Nadu: The monthly *per capita* consumption expenditure for different edible oils across all classes for urban Tamil Nadu revealed that, the expenditure share of edible oils like Vanaspati/margarine, mustard oil, peanut oil and coconut oil decreased substantially over the rounds (Table 5). The peanut oil share decreased substantially from 68% in the 43rd round to 19% during 66th round whereas, vanspathi/margarine share decreased from 3.6% to 0.7% during the same period. However, the expenditure on OEO's increased substantially from 26% to 78% during 43rd to 66th round implying more consumption of OEO's in the recent years compared to traditional oils.

The results of transitional probability estimated for urban Tamil Nadu indicated that the highest retention probability (0.91) was for OEO's followed by peanut oil (0.45 probability) (Table 6). Vanaspati/margarine was expected to gain in consumption expenditure from peanut oil and OEO's was less likely. Mustard oil does not gain significantly from any of the oils, whereas, peanut oil was expected to gain in from coconut oils by probability of one, Vanaspati/margarine by 0.77 and OEO's by 0.09 probability. The OEO's gain in consumption expenditure from peanut oil (0.52 probability) indicating preference of OEO's in place of traditional peanut oil. The probability of vanaspati losing its share was 0.77 and 0.16 for peanut oil and coconut oil, respectively. Mustard oil loses its expenditure share completely to OEO's. In case of urban Tamil Nadu, the above empirical results imply that there is shift in consumption from peanut oil (traditional oil) to OEO's in urban areas.

Present-day pattern of edible oil consumption: Due to limitation in the NSSO data published in India in which only five oils were considered *viz.,* Vanaspati/margarine, mustard oil, peanut oil, coconut oil and Other Edible Oils (OEO's) and details about other oils like sunflower oil, sesame oil, soybean oil, palm oil, etc., is lacking, primary data was collected to assess the present-day pattern (type and quantity) of edible oil consumption in rural and urban Tamil Nadu. The results revealed that, in the present primary survey, about 0.660 kg of edible oil *per capita*/month was consumed by the sample rural households (Table 7). The major oil consumed in rural areas was sunflower (0.203 kg) followed by peanut oil (0.139 kg), palm oil (0.153 kg), sesame (0.102 kg), and coconut oil (0.54 kg). The consumption of sunflower oil was more than the traditional peanut oil. Among the total oil expenditure, 30% was spent by households on sunflower oil, followed by 25% on sesame oil, 23% on peanut oil, 12% on palm oil, 9% on coconut oil and 1% on other oils that includes rice-bran oil, soybean oil and corn oil (Table 7). Hence, it could be concluded that, at present, the highest per capita consumption and expenditure in rural Tamil Nadu was sunflower oil followed by peanut oil.

Among the urban households, the major oil consumed, at present, was sunflower (0.372 kg *per capita*/month) followed by peanut oil (0.142 kg), palm oil (0.128 kg), sesame oil (0.101 kg), coconut oil (0.027 kg) and 0.011 kg of other oils (rice-bran oil, soybean and corn oil). It could be inferred that, similar to rural areas, the *per capita* consumption of sunflower oil was higher than peanut oil in urban areas. Among the total oil expenditure, 43% was spent by households on sunflower oil followed by 22% on sesame oil, 20% on peanut oil, 9% on palm oil, 4% on coconut oil and 1% on other oils.

Table 5 Monthly *per capita* consumption expenditure on edible oils in urban Tamil Nadu (₹/month)

Round (Year)	Vanaspati/ Margarine	Mustard oil	Peanut oil	Coconut oil	Other Edible Oils (OEO's)	Total oil
43rd (1987-88)	0.27 (3.61)	0.00 (0.00)	5.08 (68.01)	0.2 (2.68)	1.92 (25.70)	7.47 (100)
50th (1993-94)	0.15 (1.21)	0.04 (0.32)	9.5 (76.49)	0.31 (2.50)	2.42 (19.48)	12.42 (100)
55th (1999-00)	0.12 (0.55)	0.02 (0.09)	8.63 (39.35)	0.52 (2.37)	12.64 (57.64)	21.93 (100)
61st (2004-05)	0.10 (0.32)	0.01 (0.03)	8.03 (25.32)	0.20 (0.63)	23.38 (73.71)	31.72 (100)
66th (2009-10)	0.30 (0.68)	0.02 (0.05)	8.22 (18.75)	1.03 (2.35)	34.26 (78.17)	43.83 (100)

Source: compiled from different survey publications of NSSO; Note: Figures in parentheses indicate percentage to total expenditure on edible oils

Table 6 Shift in the pattern of edible oil consumption in urban Tamil Nadu - Probability transition matrix for 43rd to 66th rounds of NSSO survey

Oil type	Vanaspati/ Margarine	Mustard oil	Peanut oil	Coconut oil	Other Edible Oils (OEO's)
Vanaspati/Margarine	0	0.074	0.771	0.155	0
Mustard oil	0	0	0	0	1
Groundnut oil	0.007	0	0.448	0.029	0.517
Coconut oil	0	0	1	0	0
Other Edible Oils (OEO's)	0.001	0	0.085	0	0.914

Table 7 Monthly *per capita* consumption of edible oils by sample households in Tamil Nadu during 2010

Areas/Oil type	Rural		Urban	
	Quantity (kg)	Value (₹)	Quantity (kg)	Value (₹)
Peanut oil	0.139	11.55 (23.17)	0.142	11.80 (20.23)
Sunflower oil	0.203	14.81 (29.71)	0.372	25.23 (43.26)
Sesame oil	0.102	12.38 (24.83)	0.101	13.07 (22.41)
Coconut oil	0.054	4.41 (8.84)	0.027	2.33 (3.99)
Palm oil	0.153	5.97 (11.97)	0.128	5.21 (8.93)
Other oils*	0.010	0.72 (1.44)	0.011	0.68 (1.16)
Total oils	0.660	49.84 (100)	0.780	58.32 (100)
Sample size (n)	500		500	

Note: Figures in parentheses indicate percentage to total expenditure on edible oils;* indicate rice bran oil, soybean oil and corn oil.

There is heterogeneity in the consumption of edible oils in underdeveloped countries between the rural and urban areas (Oshima, 1962). Hence, the long term changes and present-day consumption pattern of edible oils was studied independently for rural and urban regions of Tamil Nadu. In rural areas, the consumption of traditional oils like peanut oil had declined drastically over the period, whereas, the consumption of OEO's had increased. Similar trend was observed in urban regions with differences in period of shift in consumption of edible oils. The Markov chain analysis also affirms shift in consumption pattern of edibles in the study region. The decline in peanut oil consumption started after 50th round (1993-94) in urban areas, whereas, in rural areas, the decline was observed after the 55th round (1999-2000) indicating lag in consumption shift from traditional (peanut) to newer oils between the urban and rural areas. The lag in shift might be due to differences in income levels, education levels, awareness and perception about different oils, and penetration and acceptance levels of households in the rural and urban areas.

Besides shift in edible oil consumption, the *per capita* oil consumption per month from 1987-88 to 2009-10 also tripled and doubled in rural and urban regions, respectively, implying rapid increase in consumption of edible oils in rural than urban areas. However, the *per capita* consumption was higher in urban areas *vis-à-vis* rural areas and it might due to difference in income and number and type of food commodities in the consumption basket of urban and rural households. Over a period, the expenditure on traditional peanut oil decreased substantially, whereas, significant increase in expenditure on Other Edible Oils (OEO's) in both rural and urban regions. The present-day consumption pattern study to identify the dominant oil preferred in recent years revealed sunflower oil as the most preferred and consumed by households followed by peanut oil in both urban and rural areas. The preference for newer oils available in the market like rice-bran oil, soybean and corn oil is least.

Literature had shown that there has been shift in consumption of food commodities in India, from coarse to fine cereals, from low to high value commodities like fruits, vegetables, milk and milk products, meat, fish, egg, etc. (Kumar, 1998; Hanumantha Rao, 2000; Mittal, 2006; Sivaramane *et al*., 2009). The present study has brought out very clearly the shift in edible oil consumption and also identified the important oils consumed by the households in rural and urban regions in recent years. The possible reason for these shifts are increased urbanization (changing lifestyles), increased awareness about health benefits of different oils, changes in processing and acceptance of these oils by households (solvent extraction oils over the traditional oil separated through expellers), distribution (availability of oils in packet form in different quantities even in remote rural areas), and marketing of edible oils (excessive advertisements for edible oils promotion, change

in relative prices of edible oils and change in income levels in both rural and urban regions recent years.

In majority of the developed countries olive oil is consumed whereas in developing countries in South Asia, especially India, the traditional oil consumption is changing. In the studied state (Tamil Nadu) the traditional edible oil consumption pattern (peanut oil) is no longer static and households exhibit strong preference for non-traditional oils. The consumption of traditional edible oil like peanut had declined whereas, Other Edible Oils (OEO's) consumption has increased in rural as well as urban areas. It might be due higher education levels in both rural and urban areas thereby increased awareness about the health benefits of OEO's besides the product related development in OEO's like improved processing methods, efficient packaging, distribution and marketing of edible oils and complex interaction between social, economic and product related factors. Besides shift in oil preference, the per capita edible oil consumption had also increased in both rural and urban areas. The preference for newer oils and overall increase in *per capita* consumption of edible oils will likely to continue in the coming years in a faster pace in consonance with demographic, economic and social factor changes in Tamil Nadu. It implies, three important aspects firstly, on production front household preferred edible oils (demand-driven) like sunflower, sesame etc., should be augmented in mission mode to meet the edible oil demand domestically. Secondly, the industries involved in edible oil processing and marketing need to concentrate on the household preferred oils rather than traditional oils only to make a dent in the emerging edible oil market or to retain their market share. Thirdly, the preference of edible oils by households gives an indication to the importers or the exporters which oil one should concentrate.

REFERENCES

Damodaram T and Hegde D M 2007. *Oilseeds Situation in India: A Statistical Compendium.* Directorate of Oilseeds Research, Hyderabad, India.

Census of India 2001. Population projections for India and states 2001-2006. In: *Report of the Technical Group on Population Projections contributed by the National Commission on Population,* Office of the Registrar General and Census Commission, New Delhi. http://www.educationforallinindia.com/Population_Projection_Report_2006.pdf. Accessed on 10 July 2012.

Census of India 2011. State of Literacy. http://censusindia.gov.in/2011-prov-results/data_files/india/Final_PPT_2011_chapter6.pdf. Accessed on 28 August 2014.

Govindaraj G 2010. Dynamics of edible oils in Tamil Nadu: An econometric analysis. Ph.D. Thesis, University of Agricultural Sciences, Bangalore, India.

Govindaraj G and Suryaprakash S 2013. Determinants of edible oil choice by households in Tamil Nadu India. *Ecology of Food and Nutrition*, **52**: 497-514.

Govindaraj G, Suryaprakash S and Sivaramane N 2015. Household demand and supply projections of major edible oils in Tamil Nadu State, India. *Journal of Oilseeds Research*, **32**(1): 80-86.

Hanumantharao C H 2000. Declining demand for food grains in rural India: causes and implications. *Economic and Political Weekly*, January 22: 201-206.

Hegde D M 2003. Vegetable oils scenario in India: past, present and future. *Renewable Energy Science Series*, 12: 1-17.

Kumar P 1998. Food demand and supply projections for India. *Agricultural Economics Policy Paper 98-01*, Indian Agricultural Research institute, New Delhi.

Mittal S 2006. Structural shift in demand for food: projections for 2020. *Working Paper 184,* Indian Council for Research on International Economic Relations (ICRIER), New Delhi. http://www.icrier.org/pdf/WP_184.pdf. Accessed on 21 January 2014.

Pingali P 2006. Westernization of Asian diets and the transformation of food systems: Implications for research and policy. Food Policy, **32**: 281-298.

Pingali P and Khwaja Y 2004. Globalisation of Indian diets and the transformation of food supply systems. Paper presented at the Inaugural Keynote address to the 17th Annual conference of the Indian Society of Agricultural Marketing, Hyderabad, 5-7 February 2004. http://www.eldis.org/vfile/upload/1/document/0708/DOC15357.pdf. Accessed on 25 August 2015.

Popkin B 1999. Urbanization, lifestyle changes and the nutrition transition. *World Development,* **27**(11): 1905-1916.

Radhakrishan R and Venkata Reddy K 2002. Food Security and Nutrition: Vision 2020. http://planningcommission.nic.in/reports/genrep/bkpap2020/16_bg2020.pdf. Accessed on November 2014.

Ramesh P and Murugan M 2008. *Edible oil consumption in India.* www.ameft.com/picture/upload /file/08.pdf. Accessed on 25 July 2013.

Regmi A and Dyck J 2001. Effects of urbanization on global food demand. In: Regmi A (Ed.) *Changing Structures of Global Food Consumption and Trade*. ERS WRS 01-1. Economic Research Service, United States Department of Agriculture, Washington DC. http://www.ers.usda.gov/media/293645/wrs011_1_.pdf. Accessed on 2 January 2015.

Richard B K and Mathur S 2015. Integration of mustard markets in Rajasthan State of India. *Journal of Oilseeds Research*, **32**(2): 158-166.

Shetty P S 2002. Nutrition transition in India. Public Health and Nutrition, Feb 5(1A): 175-182. http://www.ncbi.nlm.nih.gov/pubmed/12027282. Accessed on 2 Febuary 2014.

Singh R P 2014. Status paper on oilseeds crops. Directorate on Oilseeds Development, Ministry of Agriculture, Government of India, Hyderabad. http://nmoop.gov.in/Publication/Status_Paper.pdf. Accessed on 10 January 2014.

Sivaramane N, Singh D R and Arya P 2009. An econometric analysis of household demand for major vegetables in India. *Indian Journal of Agricultural Marketing*, **23**(1): 66-76.

Sudhakarbabu S N and Hegde D M 2011. Best management practices for increasing productivity and resource use efficiency in oilseeds. *Journal of Oilseeds Research*, **28**(1): 1-23.

Classification of soybean pest data using decision tree algorithm

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ABSTRACT

Classification of large volume of data especially in agriculture is a challenging task. Decision tree method is generally used for the classification, because it is the simple hierarchical structure for the user understanding and decision making. In the present study, the various classification techniques have been applied with *Spodoptera* spp. solitary larvae data set of soybean, for classifying into four classes based on Economic Threshold Level (ETL), using R statistical language. Out of six classification methods tested, it was found that C4.5 (decision tree) was effective with accuracy of 78 per cent followed by Naïve Bayes and kNN algorithms both with 72 per cent accuracy.

Keywords: C4.5 classification, Data mining, Decision tree classification, Soybean pest data

Data Mining is the process of discovering the interesting patterns or information from the data in large databases. The data sources can include databases, data warehouses, the web, other information repositories, or data that are streamed into the system dynamically. Han and Kamber (2005) had defined the data mining as knowledge discovery in databases, knowledge extraction, pattern analysis, data archeology and business intelligence. Alagukumar and Lawrance (2015a and b), stated that data mining techniques have become a popular tool for analyzing large amount of data. Srinivasan and Aggarwal (2003) had discussed that data mining techniques have become a popular research tool for agriculture data to identify and exploit patterns and relationships among large number of variables and to predict the outcome of a pest using the historical datasets.

Priyam *et al.* (2013) applied ID3, C4.5, and CART algorithms on the educational data for predicting the student's performance in examination. The algorithms are applied on student's internal assessment data to predict their performance in the final exam. They mentioned that C4.5 is the best algorithm for small datasets because it provides better accuracy and efficiency than other algorithms. Hssina *et al.* (2014) have focused on the key elements of their construction from a set of data and then they presented the algorithm ID3 and C4.5 that respond to classification. Finally they compared ID3 and C4.5, which confirmed that the most powerful and preferred method in machine learning is certainly C4.5.

One of the major challenges in agriculture data analysis is the prediction prognosis especially in pest data to determine the control measures. In the current study the pest data of *Spodoptera* spp. solitary larvae in soybean crop collected throughout Maharashtra state under Crop Pest Surveillance and Advisory Project (CROPSAP) during 2009-2013 was used and various classifying techniques/ algorithms were tested to find out the suitable and effective technique for classifying the pest data based on Economic Threshold Level (ETL) in to four categories.

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MATERIALS AND METHODS

Classification technique plays a vital role in agricultural data experiments, for purposes of classifying pest samples and prediction using agricultural pest data.

Data formats

In the present study the Spodoptera spp. pest data from soybean crop recorded at farmers' fields from various villages of Maharashtra under CROPSAP has been used. The dataset can be in the form of a M x N matrix D, where the row X={ x1,x2,x3… xm} represents the fields / villages and column P={p1,p2,p3…, pn} represents pests as shown in Table 1. Category column represents the actual class of the pest sample based on Economic Threshold Level (ETL). For the current study *Spodoptera* spp. solitary larvae data of soybean crop is used, where they are classified based on ETL of 4 larvae per metre row length as white (no pest is observed), green (≤1.99), yellow (2.00 to 3.99) and red (≥4.00).

a) Classification techniques: Han and Kamber (2005) discussed that classification is a data mining technique which assigns an object to one of several predefined categories based on the attributes of the object. The input dataset termed as the training data set (*Spodoptera* spp. solitary larvae / metre row length in soybean), which contains the number of predefined labels each having a number of attributes. The attributes are either continuous or categorical.

The main aim is to use the training data set to build a model, which can be used to classify unknown label data set.

b) Decision tree: Han and Kamber (2005) have also stated that Decision Tree is a supervised classification, which predicts both the classifier and regression models. Classification trees are mainly used to classify an object to a predetermined class based on the attributes. Safavian and Landgrebe (1991), surveyed classification techniques and explained the classification trees. A Tree is a set of nodes, a node with no incoming edge and zero or more outgoing edge is called as Root, a node with exactly one incoming edge and one or more outgoing edge is called as Internal node and all other nodes are known as Leaf node which has exactly one incoming edge and no outgoing edge. Using the Training set the classifier model has been developed; testing set was applied on the classification model to predict the previously unknown class.

C4.5 is one of the Decision tree Classification Algorithms developed by Quinlan (1996 and 2014). It uses Gain ratio as a Splitting Criteria by calculating entropy and splitting information of an attribute. It can handle numeric attributes and missing values. The C4.5 decision tree classification is faster than ID3 algorithm and also ID3 cannot deal with missing values. Decision tree is constructed by examining a set of training samples whose class labels are known. These features of known samples are applied in order to determine the properties of unknown samples. The C4.5 Classification Algorithm provides accurate result, takes less memory space for large data set, less time to build a model and short searching time.

c) Algorithm : Decision tree classification: Let the class label be represented as {C1, C2,….,Ck}. There are number of possibilities for the content of the set of training samples T in the given node of decision tree. If S is any set of samples, let f(Ci,S) stand for the number of samples in S that belong to class Ci (out of k possible classes), and |S| denotes the number of samples in the set S. Then the entropy of the set S:

$$Info(s) = -\sum_{i=1}^{k}\left(\left(\frac{f(C_i,S)}{|S|}\right) * \log_2\left(\frac{f(C_i,S)}{|S|}\right)\right)$$

After set T has been partitioned in accordance with n outcomes of one attribute test X:

$$Info_x(T) = \sum_{i=1}^{n}\left(\left(\frac{|T_i|}{|T|}\right) * info(T_i)\right)$$

Criterion: then select an attribute with the highest gain value Gain(X)=Info(T)-info_x (T)

Input:
D, Training dataset with class labels

Output:
Generates Decision tree Classification model for predicting results.

Classification Model Construction Procedure:

Begin
Step1. Read the training dataset from agricultural pest data
Step2. Compute entropy value for all attributes
Step3. Select best attribute having highest gain ratio according to the entropy value
Step4. Create a decision node based on the best attribute in step 3
Step5. Split the dataset based on newly created decision node in step 4
Step6. For all sub-dataset in step 5, call the algorithm recursively to get a sub-tree
Step7. Attach the tree obtained in step 6 to the decision node in step 4
Step8. Return tree
Step9. Decision tree Classification model for predicting result is the output
End

RESULTS AND DISCUSSION

In this study the above discussed method has been implemented with the soybean *Spodoptera* spp. pest data set collected from CROPSAP Project of Maharashtra. The experimental research was implemented using R statistical language. The R software can be downloaded from the link https://cran.r-project.org/. The experimental dataset has huge volume of data regarding the pests and other relevant information. The research implements the decision tree classifications and other traditional classification algorithms for the soybean pest dataset. Confusion matrix is a visualization tool which is commonly used to present the accuracy of the prediction. The confusion matrix is represented in table 2.

The confusion matrix is used to show the relationship between outcomes and predicted classes. The effective classification model is calculated with number of correct and incorrect classifications for each possible value of the variable being classified in the confusion matrix. The accuracy of a classifier for a given test set is the percentage of test set tuples that are correctly classified by the classifier.

$$Accuracy = \frac{Number\ of\ correct\ predictions}{Total\ number\ of\ predictions} = \frac{TP + TN}{TP + TN + FP + FN}$$

$$ErrorRate = \frac{Number\ of\ wrong\ predictions}{Total\ number\ of\ predictions} = \frac{FP + FN}{TP + TN + FP + FN}$$

In this study the various classification techniques have been applied and experimented with the *Spodoptera* spp. solitary larvae data set of soybean. The Classification System of decision tree (C4.5) on agriculture data is shown in Figure 1. Normally the classification techniques are divided into two parts such as training phase and test phase. This represents the classification and prediction step of the present system. Initially the agriculture pest data has been passed as training data set. The best attributes has been selected using entropy value and selected attributes have been used to generate the tree and form the classification model. Finally the test data

have been passed into the classification model and predict the pest level from the agriculture soybean data set. The Figure 2 represents the visualization of the classification based on ETL. Here the *Spodoptera* spp. solitary larvae data is classified, such as green, white and yellow based on the ETL values as explained in the previous section.

Table 1 Agriculture pest data format

Samples	Attributes				Category by ETL value for respective pest
	Pest1	Pest2	…	Pestn	
x1	p(1,1)	p(1,2)	…	p(1,n)	White
x2	p(2,1)	p(2,2)	…	p(2,n)	Green
x3	p(3,1)	p(3,2)	…	p(3,n)	Yellow
…	…	…	…	…	Red
…	…	…	…	…	Green
xm	p(m,1)	p(m,2)	…	p(m,n)	Yellow

Table 2 Confusion matrix

Actual Class	Predicted Class	
	TP	FN
	FP	TN

The accuracy of the different classifiers on the soybean pest dataset is presented in Table 3, indicated that C4.5 (decision tree) classification method is highly effective with 78 per cent accuracy. This was followed by Naïve Bayes and kNN algorithms each with 72 per cent accuracy. Ripper and oblique (decision trees) and LDA algorithm had 60, 50 and 46 per cent accuracy respectively. The Figure 3 represents the comparative analysis of the decision tree classification performance with traditional classification algorithm. The various classification algorithms are tested with Iris Flower bench mark dataset and tested how it was performing with Decision tree classification algorithms. Finally, the classification algorithms are tested with soybean pest dataset and calculated classification performance using accuracy measures. Thus from the accuracy measures for the classification algorithms for the Iris Flower dataset and soybean pest dataset, it can be observed that C4.5, Naïve Bayes and kNN classifiers are more accurate than the other classifiers. Priyam *et al.* (2013) and Hssina *et al.* (2014) also confirmed the same. Also, the oblique decision tree classifier and LDA classifier is the least accurate for both the datasets. C4.5 is used in classification problems and it is the most used algorithm for building Decision tree. It is suitable for real world problems as it deals with numeric attributes and missing values. The algorithm can be used for building smaller or larger, more accurate decision trees and the algorithm is quite time efficient. Compared to ID3, C4.5 performs by default a tree pruning process, which leads to smaller trees, more simple rules and more intuitive interpretations. For the classification of agricultural pest data in to different classes C4.5 can be used, which gives more accurate classification system, thus enabling us to quickly classify the large volume of data into different classes assisting in quick pest management decision making.

Table 3 Accuracy of different methods on agriculture data

Method	Accuracy on Agriculture data
C4.5 (Decision Tree)	78 %
RIPPER (Decision Tree)	60 %
Oblique (Decision Tree)	50 %
Naïve Bayes	72 %
kNN	72 %
LDA	46 %

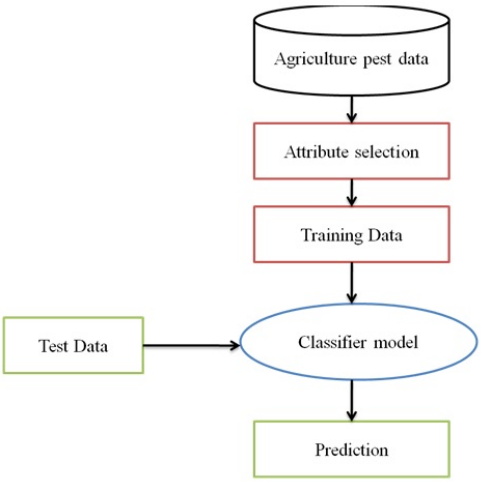

Fig. 1. The classification approach on agriculture data

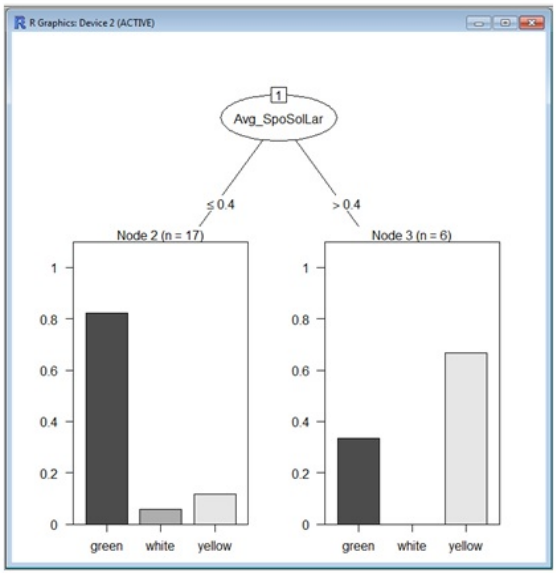

Fig. 2. Decision tree for pest data

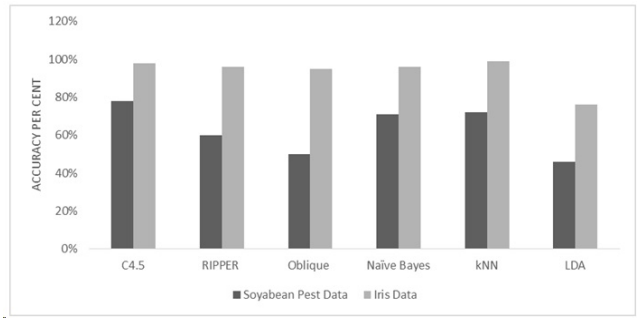

Fig. 3. Comparative analysis of different methods on soybean pest data and Iris flower data set

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REFERENCES

Alagukumar S and Lawrance R 2015. A selective analysis of microarray data using association rule mining. *Procedia Computer Science*, **47**: 3-12.

Alagukumar S and Lawrance R 2015 Algorithm for microarray cancer data analysis using frequent pattern mining and gene intervals. *International Journal of Computer Applications*, **1** : 9-14.

Han J and Kamber M 2005. *Data Mining: Concepts and Techniques.* Elsevier Publications, pp. 744.

Hssina B, Merbouha A, Ezzikouri H and Erritali M 2014. A comparative study of decision tree ID3 and C4. 5. *International Journal of Advanced Computer Science and Applications*, **4**(2): 13-19.

Srinivasan P and Aggarwal C C 2003. On the use of conceptual reconstruction for mining massively incomplete data sets. *IEEE Transactions on Knowledge and Data Engineering*, **15**: 1512-1521.

Priyam A, Abhijeeta R G, Ratheeb A and Srivastava B S 2013. Comparative analysis of decision tree classification algorithms. *International Journal of Current Engineering and Technology*, **3**: 334-337.

Quinlan J R 1996. Improved use of continuous attributes in C4.5. *Journal of Artificial Intelligence Research*, **4**: 77-90.

Quinlan J R 2014. *C4.5: Programs for Machine Learning.* Elsevier Publications, pp. 302.

Safavian S R and Landgrebe D 1991. A survey of decision tree classifier methodology. IEEE Transactions on Systems. *Man and Cybernetics*, **21**: 660-674.

Genetic diversity in castor (*Ricinus communis* L.) pistillate lines using EST-SSR markers

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ABSTRACT

Genetic diversity is essential for crop genetic improvement. Genetic diversity among breeding lines helps breeders in selecting parents for hybrid production with maximum heterosis and combining useful genes in a genetic background. However, heterosis levels in castor hybrids are not up to the desired extent due to narrow range of diversity between male and female lines and development of parents from few common sources. The objective of the study was to assess the diversity and genetic relationship of castor pistillate lines using EST-SSR markers. Sixty percent of the SSR used were polymorphic and 59 alleles were observed with an average of 2.4 alleles per locus. Dice similarity coefficient of UPGMA cluster analysis was used to construct dendrogram and observed five clusters. The Dice coefficient ranged from 0.48 to 0.84. Low level of genetic variation was observed in castor at DNA level with SSR markers.

Keywords: Castor, EST-SSRs, Genotypes, Pistillate lines

Castor (*Ricinus communis* L.) is one of the ancient oilseed crops of the world. It is a Euphorbiaceous plant belonging the monospecific genus *Ricinus.* Castor is considered to be native of tropical Africa, but is cultivated in many tropical and subtropical regions of the world (Goverts *et al.,* 2000). It is one of the most important non-edible oilseed crop and is mainly grown for castor oil and cake which are primarily used in industries. Genetic diversity is essential for crop genetic improvement and thus the most important consideration in any plant breeding programme. Genetic diversity among breeding lines helps breeders in selecting parents for hybrid production with maximum heterosis and combining useful genes in a genetic background (Kavani *et al.,* 2016). However, heterosis levels in castor hybrids are not up to the desired extent due to narrow range of diversity between male and female lines and development of parents from few common sources. As there is no source for CMS system in castor, the success of castor hybrids relied on the development of VP-1 from TSP-10 R, an exotic source pistillate line from USA. Limited studies on pistillate mechanism indicated the role of recessive genes in N type, dominant and epistatic effects in S type and a combination of N and S type in NES type. Diversification of pistillate source was necessitated due to genetic homogeneity caused by VP-1 and its derivatives in majority of the pistillate lines developed in India (Lavanya, 2002). Diversified sources like DPC11, DPC17 and DPC19 were developed either from germplasm accessions or hybridization between diverse sources (Lavanya, 2009). Studies on genetic diversity of the different sources of pistillate and male lines (breeding lines) are essential to diversify the base of parental material to avoid the genetic vulnerability to major diseases like *Fusarium* wilt and *Botryotinia* grey mold and ultimately help in increasing the heterosis and productivity of the crop to the desired extent.

The genetic diversity of castor genotypes have been characterized based on morphological traits, agronomic characters, biotic and (or) abiotic stress and (or) biochemical characteristics (Anjani *et al.,* 1999; Rao *et al.,* 2003; Sunil *et al.,* 2005; Lavanya and Gopinath, 2008; Rajiv Kumar *et al.,* 2015) and also DNA markers (Wang *et al.,* 2007; Allan *et al.,* 2008; Bajay *et al.,* 2009; Foster *et al.,* 2010; Qiu *et al.,* 2010; Vividik *et al.,* 2014; Kanti *et al.,* 2015). In the present study, we examined the genetic diversity of castor genotypes using EST-SSR markers with an aim to assess genetic diversity among pistillate lines which are more prominently used in the crossing programme and to select diverse lines for use in hybrid development.

Twenty genotypes were selected to evaluate genetic diversity using EST-SSR markers and provide information for the castor breeding programmes (Table 1). The seed samples were obtained from ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad. Genomic DNA was extracted from bulk sampling of a minimum of ten individual plants for all genotypes, following the procedure described by Doyle and Doyle (1987). Forty SSRs (Pranani *et al.,* 2011) were used for screening the genotypes. DNA amplification was performed in the Master cycler Gradient Eppendorf version 2.1 (Eppendorf, USA) programmed according to Williams *et al.* (1990) with minor modifications. DNA was pre-denatured at 94°C for 5 min followed by 35 cycles of denaturation at 92°C for 30 sec, primer annealing at 56°C for 30 sec and primer extension at 72°C for 30 sec. The last cycle was followed by final

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extension at 72°C for 7 min. The amplified products were electrophoresed in 6% polyacrylamide sequencing gels. Data was scored for different alleles and analysesd using NTSYS (Rohlf, 1992). The similarity matrices were constructed for each marker type. The corresponding dendrograms were constructed by applying unweighted pair group method with arithmetic mean (UPGMA) clustering algorithm. The number of polymorphic bands/alleles (n) and polymorphic information (PIC) were calculated as described by Tessier *et al.* (1999).

Table 1 List of castor genotypes used for genetic diversity studies

Genotype	Sex expression	Morphological characters
DPC-9	Pistillate	Green, spiny, zero bloom, normal plant type
DPC-19	Pistillate	Green, spiny, double bloom, normal plant type
DPC-21	Pistillate	Green, spiny, double bloom, normal plant type
VP-1	Pistillate	Green, spiny, triple bloom, dwarf plant type
M-568	Pistillate	Green, spiny, triple bloom, dwarf plant type
M-574	Pistillate	Green, spiny, triple bloom, dwarf plant type
DPC-16	Pistillate	Red, spiny, zero bloom, normal plant type
DPC-17	Pistillate	Red, spiny, zero bloom, normal plant type
DPC-15	Pistillate	Red, non-spiny, double bloom, dwarf, papaya leaf type
NES-6	Pistillate	Red, non-spiny, double bloom, normal plant type
NES-22	Pistillate	Red, non-spiny, double bloom, dwarf plant type
Geetha	Pistillate	Red, non-spiny, double bloom, normal plant type
DPC-18	Pistillate	Red, non-spiny, double bloom, normal plant type
DPC-20	Pistillate	Red, non-spiny, double bloom, normal plant type
DCS-107	Male	Green, spiny, double bloom, normal plant type
DCS-94	Male	Green, spiny, triple bloom, normal plant type
DCS-106	Male	Green, non-spiny, double bloom, normal plant type
DCS-89	Male	Red, non-spiny, double bloom, normal plant type
DCS-105	Male	Red, spiny, triple bloom, normal plant type
DCS-78	Male	Green, spiny, double bloom, normal plant type

Out of 40 EST-SSR markers screened 24 (60%) were polymorphic, whereas 16 loci were monomorphic. A total of 59 polymorphic alleles were detected, and the number of alleles detected on a single locus ranged from 1 to 3, with an average of 2.4 alleles per locus. The molecular size of the alleles ranged from 154 to 298 bp. The highest number of alleles (3) was observed with nine primers (CES06, CES09, CES10, CES28, CES49, CES61, CES65, CES123, and CES143). The observed allelic frequencies ranged from 0.1 to 0.9, with an average of 0.45.

Genomic DNA markers have been extensively used genetic diversity studies in castor. These included gSSRs (Bajay *et al.,* 2009), gSSRs and AFLP (Allan *et al.,,* 2008), RAPD, ISSRs (Bhavesh *et al.,* 2010) and SNP (Foster *et al.,* 2010) markers. Nine SSR loci showed higher than average number of alleles 2.4 per locus, respectively. The genetic distance and allelic diversity is low among the castor genotypes studied. Allan *et al.* (2008) also found low allelic diversity; the nine SSR loci yielded 28 alleles total with an average of 3.1 alleles per locus and found limited genetic diversity and structure for populations in genome wide diversity studies in castor. Nybom (2004) also reported low genetic diversity in castor. The number of polymorphic bands/alleles and polymorhic information (PIC) was presented in Table 2. The PIC values ranged from 0.19 to 0.70 with a mean of 0.44 for SSRs.

Dice similarity coefficient of UPGMA cluster analysis was used to construct a dendrogram which illustrated the overall genetic relationship among the 20 castor genotypes. The dice coefficient ranged from 0.48 to 0.84.The dendrogram resulting from the NTSYS-pc version 2.02 was depicted in Fig. 1. The analysis classified the set of parental lines into five major clusters (I, II, III IV and V). The first cluster included 5 genotypes while the second and third clusters consisted of 7 and 5 genotypes, respectively. The fourth cluster was sub classified into two clusters IVA and IVB with two genotypes each. The fifth cluster is monotypic with single genotypes (DCS 78). There are two major sources of pistillate expression *viz.,* S and NES type based on their genetic basis and mechanism of pistillate expression (Ankineedu and Rao, 1973; Lavanya and Solanki, 2010). The first cluster consists of the non-revertant pistillate line DPC-9 with distinct characters was used in the development and release of two hybrids like DCH-177 and YRCH-1 and DPC 19, DPC 21, DPC-20 and Geetha which has 48-1 background. The second cluster consists of 6 pistillate lines and one male line (DCS-106). It includes NES6, NES22 and DPC-15 and DPC-16, which were developed using NES source of pistillate line (Lavanya and Solanki, 2010). DPC-17 is a new pistillate line, cross derivative of M-619 x JI-225 is a revertant type of pistillate line. It also consists of one male line DCS-106 derived from a multiple cross involving four F1s and six different parents. The third cluster included first pistillate line of S type VP-1 and two mutant lines M568 and M574 developed form VP-1 through radiations. Interestingly, the fourth cluster consists of all male lines *viz*., DCS 107, DCS 74, DCS 89 and DCS 105.

In conclusion, low level of allelic diversity was observed in castor lines studied even through morphologically they are diverse. The finding of low genetic variation in castor at DNA level reveal the use of alternative methods like mutations, interspecific and intergeneric crosses to enhance the genetic base of castor to enhance seed yield and oil production and productivity.

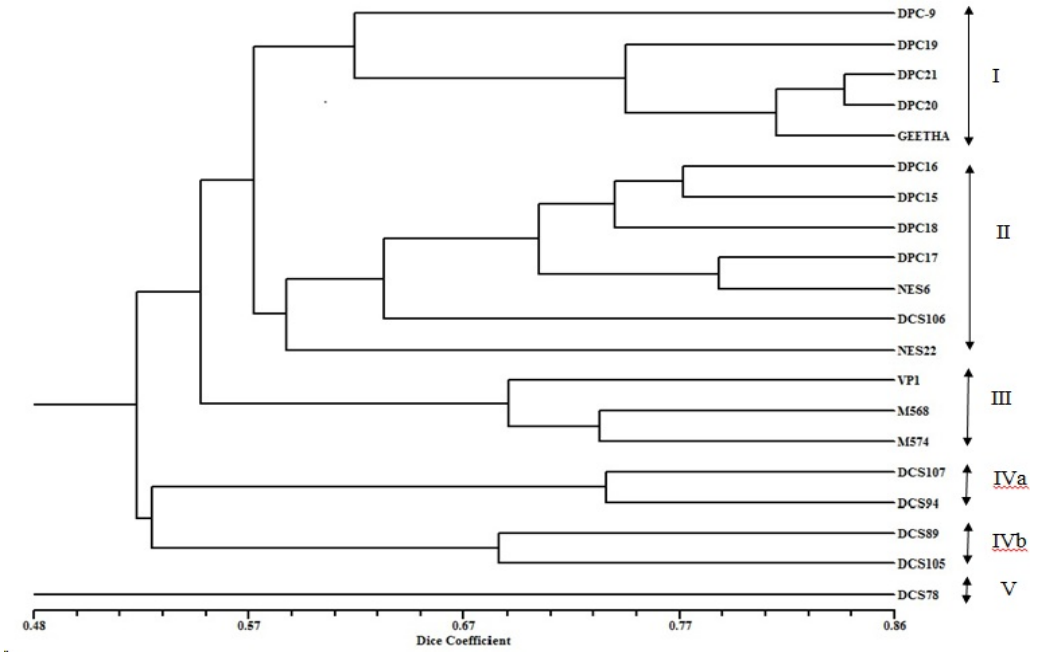

Fig.1. Dendrogram resulting from an UPGMA cluster analysis of 20 castor genotypes based on Dice coefficient

Table 2 Number of polymorphic bands (n) and PIC values of EST-SSR primers

Primer	n	PIC
CES-06	3	0.70
CES-09	3	0.70
CES-10	3	0.76
CES-15	2	0.50
CES-25	2	0.39
CES-28	3	0.61
CES-39	2	0.27
CES-48	2	0.19
CES-49	3	0.35
CES-56	2	0.44
CES-61	3	0.54
CES-65	3	0.43
CES-73	2	0.27
CES-80	2	0.48
CES-123	3	0.43
CES-125	2	0.27
CES-126	2	0.34
CES-128	2	0.39
CES-137	2	0.53
CES-140	2	0.27
CES-143	3	0.48
CES-157	2	0.52
CES-168	2	0.42
CES-170	2	0.51
Average	2.4	0.44

REFERENCES

Allan G, Williams A, Rabinowicz P D, Chan A P, Ravel J and Keim P 2008. Worldwide genotyping of castor bean germplasm (*Ricinus communis* L.) using AFLP and SSRs. *Genetic Resources and Crop Evolution*, **55**: 365-378.

Anjani K, Yadav W S and Duhoon S S 1999. Collecting castor (*Ricinus communis* L.) germplasm in north western India. *Plant Genetic Resources Newsletter*, **120**: 48-51.

Ankineedu G and Ganga Prasada Rao N 1973. Development of pistillate castor. *Indian Journal of Genetics and Plant Breeding*, **33**: 416-422.

Bajay M M, Pinheiro J D, Batista C E A, Nobrega M B M and Zucchi M I 2009. Development and characterization of microsatellite markers for castor (*Ricinus communis* L.), an important oleaginous species for biodiesel production. *Conservation of Genetic Resources*, **1**(1): 237-239.

Bhaavesh B G, Nitish Kumar, Amritpal S S, Bhupendra S P, Ravikiran R, Subhash N and Jadeja G C 2010. Assessment of genetic diversity in castor (*Ricinus communis* L.) using RAPD and ISSR markers. *Industrial Crops and Products*, **32**: 491-498.

Doyle J J and Doyle J L 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin*, **19**: 11-15.

Foster J F, Allan G J, Chan A P, Pablo D, Rabinowicz, Jacques Rave, Paul J Jackson and Paul Keim 2010. Single nucleotide polymorphisms for assessing genetic diversity in castor bean (*Ricinus communis*). *BMC Plant Biology*, **10**: 13.

Govaerts R, Frodin D G and Radcliffe-Smith A 2000. World checklist and bibliography of *Euphorbiaceae* (with Pandaceae). Redwood Books Limited, Trowbridge, Wiltshire.

Kanti M, Ramya K T, Anjani K and Usha kiran B 2015. Agro-morphological and molecular diversity in castor (*Ricinus communis* L) germplasm collection from Andaman and Nicobar islands, India. *Czech Journal of Genetics and Breeding*, **12**: 4-10.

Kavani R H, Vachhani J H, Madariya R B, Jadeja S R and Dobariya K L 2016. Combining ability for seed yield and its components in castor (*Ricinus communis* L.). *Journal of Oilseeds Research*, **33**(1): 22-25.

Lavanya C 2002. Sensitivity and variations of sex expression in response to environmental changes in castor. *Indian Journal of Genetics and Plant Breeding*, **62**: 232-237.

Lavanya C and Gopinath V 2008. Study on inheritance of morphological characters and sex expression in pistillate lines of castor. *Indian Journal of Genetics and Plant Breeding*, **68**: 275-282.

Lavanya C and Solanki S S 2010. Crop improvement of castor: the challenges ahead. In: *Research and Development in Castor: Present Status and Future Strategies*, Hegde (Ed.), Indian Society of Oilseeds Research, Hyderabad, pp. 36-55.

Lavanya C 2009. Diversification of the pistillate base using geographically diverse castor germplasm. Proceedings of National Symposium on "Recent Global Developments in the Management of Plant Generic Resources", 17-18th December 2009, NBPGR, New Delhi.

Nybom H 2004. Comparison of different nuclear DNA markers for estimating intraspecific genetic diversity in plants. *Molecular Ecology*, **13**: 1143-1155.

Pranavi B, Sitaram G, Yamini K N and Dinesh kumar V 2011. Development of EST-SSR markers in castor bean (*Ricinus communis* L.) and their utilization for genetic purity testing of hybrids. *Genome*, **54** (8): 685-691.

Qiu L, Yang C, Tian B, Yang J B and Liu A 2009. Exploiting EST database for the development and characterization of EST-SSR markers in castor bean (*Ricinus communis* L). *BMC Plant Biology*, **10**: 278-287.

Rajiv Kumar, Patel J A, Patidar D, Patel N, Patel S, Sapre S and Ravi Shah 2015. Effect of ethrel spray on ISF induction in pistillate line of castor SKP-84. *Journal of Oilseeds Research*, **32**(1): 100-101.

Rao C H, Lavanya C, Anjani K, Sujatha M, Lakshmamma P and Mukta N 2003. Crop improvement in castor. In: *Castor in India*, Hegde, D.M., Sujatha, M., Singh, N.B. (Eds.). Directorate of Oilseeds Research, Hyderabad, pp. 14-35.

Rohlf F J 1992. NTSYS-PC: *Numerical Taxonomy and Multivariate Analysis System Version 2.02k*. State University of New York, Stony Brook, New York.

Sunil N, Ashok Kumar A, Ashokvardhan Reddy P and Varaprasad K S 2005. Collection of diversity in castor (*Ricinus communis* L.) germplasm from parts of Andhra Pradesh. *Indian Journal of Plant Genetic Resources*, **18**: 187-190.

Tessier C, David J, This P, Boursiquot J M and Charrier A 1999. Optimization of the choice of molecular markers for varietal identification in *Vitis vinifera* L. *Theoretical and Applied Genetics*, **98**: 171-177.

Vivodik M, Balazova Z and Galova Z 2014. RAPD analysis of genetic diversity of castor bean. *International Journal of Biological, Veterinary, Agricultural and Food Engineering*, **98**: 171-177.

Wang H Y, Wei Y M, Yan Y H and Zheng Y L 2007. EST-SSR DNA polymorphism in durum wheat (*Triticum durum* L.) collections. *Genetics*, **48**: 35-42.

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

Hybrid purity assessment of safflower (*Carthamus tinctorius* L.) F_1s using inter-simple sequence repeats (ISSRs)

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ABSTRACT

Twelve hybrids were developed using four lines and three testers parents of safflower. Genetic purity of these twelve safflower hybrids was tested using 7 ISSR primers which showed polymorphism between parents. ISSR primers UBC 807, UBC 812, UBC 815, UBC 834, UBC 840, UBC 841 and UBC 842 could differentiate parents and identify true hybrids in 2,4,1,1,1,2, and 2 crosses, respectively. Hybrid seed production in safflower is a challenge due to easy selfing of female parents and thus degrades the quality of seed lot. These ISSR primers can be used to test the hybrid purity in hybrid seed production.

Keywords: Hybrid genetic purity, ISSR, Safflower

Safflower (*Carthamus tinctorius* L.) is an oilseed crop that belongs to the family Asteraceae. The genus *Carthamus* has 25 species, of which *C. tinctorius* is the only cultivated one, and has 2n = 24 chromosomes. It is dicotyledonous, herbaceous, and annual plant. It has adapted to grow in hot, dry climates and well-drained soil. Safflower is mainly cultivated for its seed, which is used primarily for edible oil. In the past, the crop is grown for its flowers used for coloring and flavoring foods, making dyes and medicine (Suneel Kumar *et al.,* 2016). In recent years, development of high yielding cultivars has been a major objective of safflower breeding in order to overcome the constraints during safflower cultivation. There exists abundant variability among the safflower germplasm collections for various traits which need to be harnessed for breeding high yielding varieties. However, the proper and precise utilization of these lines in breeding programmes depends on their characterization for qualitative and quantitative traits. Information on nature and degree of genetic divergence would help the plant breeders in choosing the right type of parents for purposeful hybridization. The importance of selection of parents on the basis of genetic distance to get heterotic effect in F_1 generation and higher frequency of better segregants in subsequent generations has been reported by earlier researchers in oilseed crop like linseed. Mahalanobis D^2 statistics (1936) as described by Rao, (1952) has been successfully used by plant breeders in different crops for isolating genetically diverse genotypes. In the present study an attempt has been made to utilize this useful technique for selection of parents for hybridization in safflower breeding programme.

Inter-simple sequence repeats (ISSR) PCR using primers based on dinucleotide, tetranucleotide or pentanucleotide repeats has now become in fashion among the researchers (Zietkiwicz *et al.,* 1994). For its advantages of simple procedure, low cost, good stability, high reproducibility, ISSR marker has been successfully used in genetic mapping (Tanyolac, 2003), germplasm identification (Potter *et al.,* 2002) and genetic diversity analysis (Wu *et al.,* 2005). Until now, few studies have been carried on the genetic variations of *C. tinctorius* using RAPD markers (Guo *et al.,* 2003; Amiri *et al.,* 2001) and isozymes (Zhang, 2000). The objective of the presented study is to assess the genetic diversity of 13 parents through ISSR marker and assess the hybrid purity of F_1's of these parents.

Table 1 Enlist of parents and crosses in L x T design

Lines
- GMU 224
- MMS-white (GMS line)
- MSV-10-5-1 (GMS line)
- TMS-3-6-7-9 (TGMS line)

Testers
- GMU 1303
- GMU 1769
- RVS-2012-13

Crosses
- GMU 224 x GMU 1303
- GMU 224 x GMU 1769
- GMU 224 x RVS-2012-13
- MMS-white x GMU 1303
- MMS-white x GMU 1769
- MMS-white x RVS-2012-13
- MSV-10-5-1 x GMU 1303
- MSV-10-5-1 x GMU 1769
- MSV-10-5-1 x RVS-2012-13
- TMS-3-6-7-9 x GMU 1303
- TMS-3-6-7-9 x GMU1769
- TMS-3-6-7-9 x RVS-2012-13

The experimental material for the present study comprised 7 parents and 12 F_1s were planted in 2013-14 at the Research cum Instructional Farm of Indira Gandhi Krishi Vishwavidyalay, Raipur. Experiment was laid out in a randomized complete block design. The names of the 7 parents and 12 F_1s are given in Table 1. Genomic DNA was extracted from young leaves following the cetyl tri methyl ammonium (CTAB) procedure described by Saghai-Maroof *et al.* (1984). Extracted DNA concentration was quantified by using the NanoDrop spectrophotometer and qualified using PAGE. Eleven ISSR primers were used for the PCR (Table 2).

Table 2 List of ISSR primers used for detecting polymorphism

ISSR PRIMERS	PRIMER SEQUENCES
UBC 807	AGA GAG AGA GAG AGA GT
UBC 809	AGA GAG AGA GAG AGA GG
UBC 835	AGA GAG AGA GAG AGA GYC
UBC 824	TCT CTC TCT CTC TCT CG
UBC 840	GAG AGA GAG AGA GAG AYT
UBC 842	GAG AGA GAG AGA GAG AYG
UBC 834	AGA GAG AGA GAG AGA GYT
UBC 811	GAG AGA GAG AGA GAG AC
UBC 815	CTC TCT CTC TCT CTC TG
UBC 812	GAG AGA GAG AGA GAG AA
UBC 841	GAG AGA GAG AGA GAG AYC

The amplified products were separated on 5% polyacrylamide gel and stained with ethidium bromide. Images were photographed and captured by Gel Doc 2000TM (Bio-Rad, USA). Amplified products were scored by the presence or absence of male parent bands for the ISSR markers.

Eleven ISSR primers were also used to test the hybridity of F_1's. The seven primers which gave polymorphic results with parents used to test the hybridity of F_1's. ISSR primer UBC 807, UBC 812, UBC 815, UBC 834, UBC 840, UBC 841 and UBC 842 were screened on all the hybrids. Result of banding pattern for UBC 807 in cross between P_3 and P_2 (MMS-white X RVS-2012-13) had the fragment size of 500 bp and the band was present in F_1 hybrid and male parent i.e., RVS-2012-13 (P_2) which ultimately shows that F_1 hybrid is a true hybrid P_3 X P_2 (MMS-white X RVS-2012-13) (Fig. 1). In another cross between P_7 and P_4 (TMS-3-6-7-9 X GMU 1303) produced a band size of 550 bp which was also present in F_1 hybrid and male parent i.e., GMU 1303 (P_4). This proves the F_1 is a true hybrid between the parent P_7 (TMS-3-6-7-9) and parent P_4 (GMU 1303). All other parents and hybrids showed monomorphic pattern with primer UBC 807. In case of primer UBC 812, a cross between P_6 and P_2 (MSV-10-5-1 X RVS-2012-13) produced a fragment of 700 bp size which was present in F_1 hybrid and male parent i.e., RVS-2012-13 (P_2) shows that the F_1 is a true hybrid between the female parent P_6 (MSV-10-5-1) and male parent P_2 (RVS-2012-13).

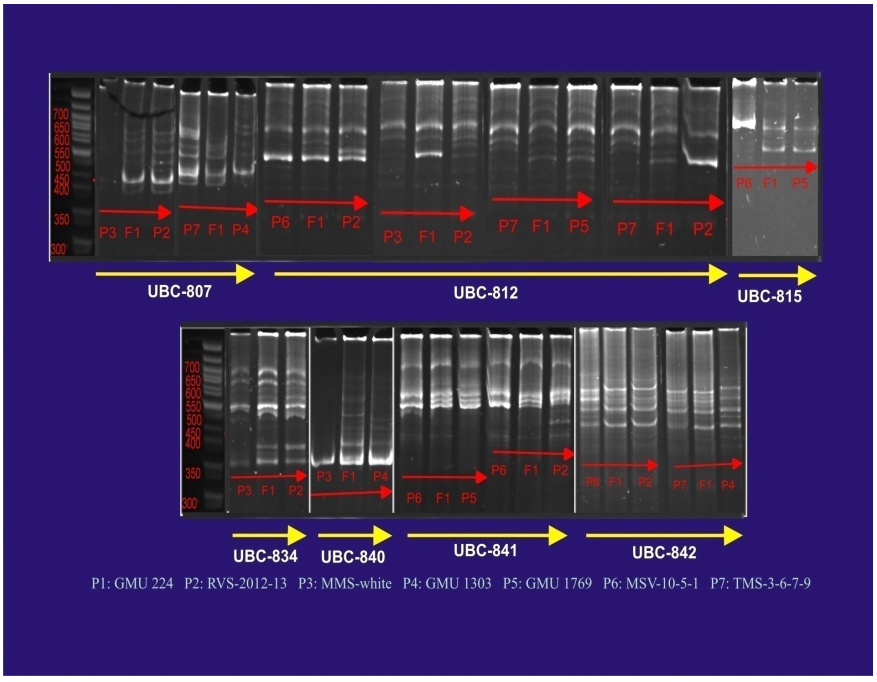

Fig. 1. Result of hybridity test through ISSR markers

In another cross between P_3 and P_2 (MMS-white X RVS-2012-13) produced a band size of 700 bp which was also present in F_1 hybrid and male parent i.e., RVS-2012-13 (P_2). This shows that the F_1 is a true cross hybrid between the female parent P_3 (MMS-white) and male parent P_2 (RVS-2012-13). In another cross between P_7 and P_5 (TMS-3-6-7-9 X GMU 1769) produced a band size of 500 bp which was also present in F_1 hybrid and male parent i.e., GMU 1769 (P_5). This indicated that the F_1 was a true hybrid between the female parent P_7 (TMS-3-6-7-9) and male parent P_5 (GMU 1769). In another cross between P_7 and P_2 (TMS-3-6-7-9 X RVS-2012-13) produced a band size of 700 bp which was also present in F_1 hybrid and male parent i.e., RVS-2012-13 (P_2). This showed that the F_1 is a true hybrid between the female parent P_7 (TMS-3-6-7-9) and male parent P_2 (RVS-2012-13). All other parents and hybrids showed monomorphic pattern for primer UBC 812.

In case of ISSR primer UBC 815, a cross between P_6 and P_5 (MSV-10-5-1 X GMU 1769) produced a fragment of 650 bp size which was present in F_1 hybrid and male parent i.e., GMU 1769 (P_5) shows that the F_1 is a true cross hybrid between the female parent P_6 (MSV-10-5-1) and male parent P_5 (GMU 1769)). All other parents and hybrids showed monomorphic pattern for primer UBC 815. In case of UBC 834, a cross between P_3 and P_2 (MMS-white X RVS-2012-13) produced a fragment of 400 bp size which was present in F_1 hybrid and male parent i.e., RVS-2012-13 (P_2) shows that the F_1 is a true hybrid between the parent P_3 (MMS-white) and parent P_2 (RVS-2012-13). All other parents and hybrids showed monomorphic pattern for primer UBC 834.

In case of UBC 840, a cross between P_3 and P_4 (MMS-white X GMU 1303) produced a fragment of 450 bp size which was present in F_1 hybrid and male parent i.e., GMU 1303 (P_4) shows that the F_1 is a true hybrid between the parent P_3 (MMS-white) and parent P_4 (GMU 1303). All other parents and hybrids showed monomorphic pattern for primer UBC 840. In case of ISSR primer UBC 841, a cross between P_6 and P_5 (MSV-10-5-1 X GMU 1769) produced a fragment of 700 bp size which was present in F_1 hybrid and male parent i.e., GMU 1769 (P_5) shows that the F_1 is a true hybrid between the parent P_6 (MSV-10-5-1) and parent P_5 (GMU 1769). In another cross between P_6 and P_2 (MSV-10-5-1 X RVS-2012-13) produced a band size of 766 bp which was also present in F_1 hybrid and male parent i.e., RVS-2012-13 (P_2). This indicated that the F_1 is a true hybrid between the parent P_6 (MSV-10-5-1) and parent P_2 (RVS-2012-13). All other parents and hybrids showed monomorphic pattern for primer UBC 841.

The ISSR primer UBC 842, when tested with hybrid between P_6 and P_2 (MSV-10-5-1 X RVS-2012-13) produced a fragment of 500 bp size which was present in F_1 hybrid and male parent i.e., RVS-2012-13 (P_2) showed that the F_1 is a true hybrid between the parent P_6 (MSV-10-5-1) and parent P_2 (RSV-2012-13). All other parents and hybrids showed monomorphic pattern for primer UBC 841. In another cross between P_7 and P_4 (TMS-3-6-7-9 X GMU 1303) produced a band size of 550 bp which was also present in F_1 hybrid and male parent i.e., GMU 1303 (P_4). This shows that the F_1 is a true hybrid between the parent P_7 (TMS-3-6-7-9) and parent P_4 (GMU 1303). All other parents and hybrids showed monomorphic pattern for primer UBC 842.

The result of experiment indicated that ISSR marker can be used for identification of trueness of hybrids. This study revealed the existence of sufficient variability among the genotypes and improvement program either through selection or through hybridization program has good scope.

REFERENCES

Amiri R M, Azdi S B, Ghanadha M R and Abd M C 2001. Detection of DNA polymorphism in landrace populations of safflower in Iran using RAPD-PCR technique. *Iranian Journal of Agricultural Sciences*, 32(4): 737-745.

Guo M L, Jiang W, Zhang Z Z, Zhang G, Mao J F, Yin M and Su Z W 2003. Randomly amplified polymorphic DNA technique in molecular identification of germplasms of *Carthamus tinctorius* L. *Academic journal of Second Military Medical University*, 24(10): 1116-1119.

Mahalanobis P C 1936. On the generalized distance in statistics. *Proceedings of National Academy of Science*, 12: 49-55.

Potter D, Gao F Y, Aliello G, Leslie C and Granahan G 2002. Inter-simple sequence repeat markers for fingerprinting and determining genetic relationships of walnut (*Juglans regia*) cultivars. *Journal of the American Society for Horticultural Science*, 127: 75-81.

Rao C R 1952. *Advanced Statistical Methods in Biometrical Research,* John Wiley and Sons, Inc., New York, pp. 390.

Saghai-Maroof M A, Biyashev R M, Yang G P, Zhang Q and Allard R W 1984. Extraordarily polymorphic microsatellite DNA in barly: species diversity, chromosomal locations, and population dynamics. *Proceedings of the National Academy of Sciences, USA*. 91: 5466-5470.

Suneel Kumar E, Aparna Kuna, Padmavathi P, Durga Rani Ch V, Supta Sarkar and Sowmya M 2016. Changes in antioxidant content in selected cultivars of safflower (*Carthamus tinctorius* L.) leaves during different stages of maturity. *Journal of Oilseeds Research*, 33(1): 51-55.

Tanyolac B 2003. Inter-simple sequence repeat (ISSR) and RAPD variation among wild barely (*Hordeum vulgare* subsp. *spontaneum*) populations from west Turkey. *Genetic Resources and Crop Evolution*, 50(6): 611-614.

Wu W, Zheng Y L, Chen L, Wei Y M, Yang R W and Yan Z H 2005. Evaluation of genetic relationships in the genus *Houttuynia* Thunb. in China based on RAPD and ISSR markers. *Biochemical Systematics and Ecology*, 33: 1141-1157.

Zhang Z W 2000. Studies on genetic diversity and classification of safflower (*Carthamus tinctorius* L.) germplasm by isozyme techniques. *Journal of Plant Research*, 1(4): 6-13.

Zietkiwicz E, Rafaliski A and Labuda D 1994. Genome fingerprinting by simple sequence repeat (SSR)-anchored polymerase chain reaction amplication. *Genomics*, 20(2): 176-183.

Assessment of variability for yield, component traits and reaction to foliar fungal diseases in back cross population of groundnut (*Arachis hypogaea* L.)

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ABSTRACT

Three BC_1F_1 populations *viz.,* TMV (Gn) 13 × GPBD 4, CO 7 × GPBD 4 and TMV 2 × GPBD 4 along with their parental lines of groundnut were evaluated for variability, heritability and genetic advance. High magnitude of PCV and GCV coupled with broad sense heritability and genetic advance as per cent of mean for these characters studied such as number of pods per plant, shell weight per plant, rust disease score, late leaf spot (LLS) disease score, pod yield per plant and kernel yield per plant in all the populations. So, it could be concluded that these characters were under the control of additive type of gene action and hence selection may be effective for these traits in these populations.

Keywords: Back cross, Genetic variability, Groundnut, Heritability, Late leaf spot, Rust

Groundnut (*Arachis hypogaea* L.) is one of the most important oilseed crops of India. Even though India ranks first in area, its production and productivity was low due to several biotic and abiotic factors (Basha *et al.*, 2016; Mondal and Badigannavar, 2016). Among the biotic stresses, the two fungal diseases *viz*., late leaf spot (LLS) caused by *Cercosporidium personata* [(Berk. and Curt.) Deighton] and rust caused by *Puccinia arachidis* Speg. are widespread and economically more important. These diseases often occur together and cause yield loss up to 50-70% in the crop (Subrahmanyam *et al.*, 1985). Therefore, the use of groundnut varieties resistant to late leaf spot and rust are considered important and an effective way to manage these diseases. Development of cultivars resistant/tolerant to rust and late leaf spot could be effective in decreasing the production costs, improving production quality and reducing the detrimental effects of chemicals on our ecosystem. Genetic variability is the basic requirement for crop improvement as it provides wider scope for selection (Bhargavi *et al.*, 2016; Sreenivasulu *et al.,* 2015). Knowledge of association among quantitative characters and foliar diseases score will enable the breeders to create new variations by effecting crosses between carefully chosen parents and to suggest about the direction and intensity of selection for the matter. In such cases, creation of new variability through hybridization followed by selection is the best option for the improvement of crop plants. With this framework, hybridization were attempted to develop three rust and LLS disease resistance introgressed BC_1F_1 population to study the extent of variability, heritability and amount of genetic gain expected to occur during the selection for yield parameters and foliar disease resistance. Heritability is the portion of phenotypic variation which is transmitted from parent to progeny. Higher the heritable variation, greater will be the possibility of fixing the characters by selection. Hence, heritability studies are of foremost importance to judge whether the observed variation for a particular character is due to genotype or due to environment. Heritability estimates may not provide clear predictability of the breeding value. For predicting the effect of selection, heritability estimates along with genetic advance are more useful than the heritability estimates alone (Burton, 1952; Johnson *et al.,* 1955). With this background, the present study was planned to assess the selection potential for kernel yield and component characters with foliar fungal disease resistance in the back cross derived progenies.

The experimental material for the present study comprised of 155 plants [44 from TMV (Gn) 13 × GPBD 4, 87 from CO 7 × GPBD 4 and TMV 2 × GPBD 4] of three BC_1F_1back across populations by crossing recurrent parents *viz.,* TMV (Gn) 13, CO 7 and TMV 2 with a resistant donor GPBD 4 [derived from the cross KRG 1 × CS 16 (Gowda *et al*., 2002)]. Recurrent parents were susceptible to rust and late leaf spot diseases but having highest pod yield and oil content. The donor parent is resistance to rust and LLS diseases. Observations were recorded on each individual plant. Parameters considered in the present study were number of pods per plant, hundred-pod weight (g), hundred-kernel weight (g), shelling weight (g), shelling per cent, sound mature kernel, rust and LLS disease score, pod yield per plant (g) and kernel yield per plant (g).

Disease scoring for rust and LLS was carried out at Department of Oilseeds, TNAU, Coimbatore, India during *rabi*/summer 2016. Both recurrent and donor parental genotypes were also sown as control. The genotypes were subjected to field screening for rust and LLS reaction using infector row technique (Subrahmanyam *et al.,* 1995) in which

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Co Gn 4 and TMV 2 were planted at regular interval of 10 rows and on border rows around the field to maintain effective inoculum load. Disease scoring for rust and LLS was done at 90 days after sowing by using a modified 9-point scale (Subrahmanyam *et al.,* 1995). Statistical methods suggested by Burton (1952) for variability, Lush (1940) for heritability, Johnson *et al.* (1955) for genetic advance as per cent of mean were adopted to find out the respective estimates. Further categorization of estimates was made based on the suggestions of Sivasubramanian and Madhavamenon (1973) for variability (< 10% - Low; 10-20% - Medium; > 20% - High), .Johnson *et al.* (1955) for heritability (< 30% - Low; 30-60% - Moderate; > 60 - High) and genetic advance as percent of mean (< 10% - Low; 10-20% - Medium; > 20% - High).

A survey of genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability estimates, genetic advance are absolutely necessary to start an efficient breeding program (Atta *et al.,* 2008). The genetic variability studies in back cross derived progenies of three crosses indicated high mean and wider range for all the traits under evaluation. This suggested the existence of sufficient genetic variability in these populations. Narrower difference between the values of GCV and PCV indicated that the environmental effect was small for the expression of these characters and these traits are governed by additive gene action (Abinasa *et al.,* 2011; Vijayakumar *et al.,* 2013).

The general mean value for each trait, range among the progenies and estimates of genetic parameters like phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean for different characters of three back cross populations are presented in Tables 1 and 2. All the three back cross derived progenies recorded the high estimates of PCV and GCV for all the traits except *viz*., hundred-pod weight, shelling per cent and sound mature kernel suggested that there is a high phenotypic and genotypic variation for all the traits except these three traits. This indicates that there is an ample scope for selection of promising plants from the present population for yield and its components. Shoba *et al.* (2009), Sawargaonkar *et al.* (2010), Anitha (2013), Thirumala *et al.* (2014) and Prabhu *et al.* (2015) also reported high genetic variability for yield and its component characters in segregating generations of groundnut.

The high estimates of PCV and moderate/high GCV were observed for hundred pod weight in all the three back cross derived populations. This result was accordance with findings of Ali *et al.* (2000) and Ladole *et al.* (2009). Moderate/low estimates of PCV and low/moderate of estimates GCV were recorded for shelling per cent and sound mature kernel in the progenies of all the three back cross populations. This suggested the reduced level of variability for these traits and difficulty of manipulating these traits through plant breeding. Therefore, selection would be ineffective. These results are in accordance with the findings of Khedikar *et al.* (2008), Hiremath *et al.* (2011) and Prabhu *et al.* (2015).

High PCV and GCV were recorded for rust and LLS incidence, indicating that there is high variability and ample scope for selecting rust and LLS resistant segregants from these populations. The results are similar with the findings of Yadawat *et al.* (2015) in rust score in F_2 population of wheat, Prabhu *et al.* (2015) for rust and LLS score and Khedikar (2008) for LLS score in RIL population of groundnut.

Heritability is a significant parameter for the selection of an efficient population improvement method. Single plant selection in the earlier generations may be much effective for a character if the trait that is highly heritable. The high estimates of heritability were observed in the present study for yield and yield related traits like number of pods per plant, shell weight per plant, shelling per cent, pod yield per plant and kernel yield per plant in all the three back cross populations. This suggested that heritability is due to the additive genetic effects and selection could be effective for these traits and the possibility of improving kernel yield through direct selection for kernel yield related traits. Anitha *et al.* (2013) and Prabu *et al.* (2015), also reported high heritability estimates for number of pods per plant, shell weight per plant, shelling per cent pod and kernel yield per plant, which support the present findings. Hence selection for these traits is suggested to improve the yield.

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al.,* 1955). High heritability accompanied with high genetic advance as per cent of mean was recorded for number of pods per plant, shell weight per plant, pod yield per plant and kernel yield per plant in all the crosses. This indicates the lesser influence of environment on expression of these traits and prevalence of additive gene action in their inheritance; hence selection of these traits in breeding program would facilitate the improvement of kernel yield. The present findings are in agreement with the findings of Sawargaonkar *et al.* (2010), Anitha (2013), Thirumala *et al.* (2014) and Prabhu *et al.* (2015).

Moderate/ high heritability coupled with moderate/ high genetic advance as per cent of mean was recorded for sound mature kernel, shelling per cent, hundred-pod weight and hundred-kernel weight, which implies the existence of additive gene effect in all the three backcross derivatives. These results are in accordance with the findings of Ali *et al.* (2000), Khedikar *et al.* (2008), Shoba *et al.* (2009), Ladole *et al.* (2009), Hiremath *et al.* (2011) and Prabhu *et al.* (2015).

Table 1 Mean, range, phenotypic and genotypic coefficients of variation, heritability (B.S.), genetic advance expressed as per cent of mean for different characters of three back cross populations

Crosses	Mean	Range	SE	PCV	GCV	h^2 (bs)	GAM
			Number of pods per plant				
C1	24.22	5.00 - 33.00	1.10	30.53	25.70	70.90	46.97
C2	16.37	5.00 - 32.00	0.67	38.20	29.42	59.30	49.16
C3	15.29	4.00 - 32.00	1.32	42.36	33.37	62.08	57.06
			100-Pod weight (g)				
C1	67.38	34.50 - 97.60	2.19	21.76	14.46	44.16	20.85
C2	86.60	39.90 - 104.80	1.89	20.40	16.00	61.51	27.23
C3	56.97	24.70 - 104.90	3.65	31.39	24.80	62.43	42.52
			100-Kernel weight (g)				
C1	24.31	9.52 - 37.40	1.24	34.12	21.86	41.06	30.40
C2	41.64	13.20 - 54.00	1.23	27.62	23.00	69.35	41.56
C3	22.56	6.21 - 45.60	2.11	45.83	36.11	62.08	61.74
			Shell weight per plant (g)				
C1	6.51	2.23 - 9.91	0.31	31.86	26.35	68.39	47.29
C2	4.67	2.89 - 8.00	0.20	39.54	30.64	60.05	51.53
C3	3.84	2.99 - 8.14	0.38	48.10	37.32	60.19	62.83
			Shelling (%)				
C1	57.42	35.36 - 66.57	0.88	10.26	8.00	60.87	13.55
C2	64.73	49.08 - 90.67	0.73	10.45	8.76	70.33	15.95
C3	61.99	43.53 - 75.66	1.48	11.66	10.03	74.02	18.73
			Sound mature kernel (%)				
C1	90.82	60.00 - 100.00	1.41	10.39	8.31	63.88	14.41
C2	92.85	60.00 - 100.00	0.88	8.84	6.39	52.24	10.02
C3	90.16	75.00 - 100.00	1.87	10.15	7.96	61.56	13.56
			Rust score				
C1	1.66	1.00 - 3.00	0.10	33.24	25.94	60.89	43.92
C2	1.50	1.00 - 3.00	0.07	38.89	30.29	60.66	51.19
C3	1.79	1.00 - 2.50	0.14	34.53	26.90	60.74	45.51
			LLS Score				
C1	2.27	1.00 - 3.00	0.10	27.26	21.74	63.62	37.64
C2	2.64	1.00 - 4.00	0.08	27.80	23.96	74.29	44.82
C3	2.65	1.50 - 3.50	0.14	26.47	21.95	68.80	39.52
			Pod yield per plant (g)				
C1	18.25	6.53 - 27.60	0.82	30.18	23.58	61.07	39.99
C2	13.88	3.99 - 28.30	0.59	39.38	30.63	60.49	51.69
C3	12.25	2.06 - 18.62	1.11	44.39	34.41	60.06	57.86
			Kernel yield per plant (g)				
C1	9.35	1.22 - 16.58	0.53	38.31	29.72	60.18	50.02
C2	8.90	2.34 - 19.24	0.38	40.33	31.33	60.33	52.80
C3	9.44	1.05 - 15.20	0.74	56.61	44.41	61.56	75.62

Table 2 Estimates of variability parameters for yield and foliar diseases in three BC_1F_1 generation of groundnut

Crosses	Mean	Range	SE	PCV	GCV	h2 (bs)	GAM
			Pod yield per plant (g)				
C1	18.25	6.53 - 27.60	0.82	30.18	23.58	61.07	39.99
C2	13.88	3.99 - 28.30	0.59	39.38	30.63	60.49	51.69
C3	12.25	2.06 - 18.62	1.11	44.39	34.41	60.06	57.86
TMV (Gn) 13	17.80						
CO 7	12.40						
TMV 2	11.20						
GPBD 4	14.65						
			Kernal yield per plant (g)				
C1	9.35	1.22 - 16.58	0.53	38.31	29.72	60.18	50.02
C2	8.90	2.34 - 19.24	0.38	40.33	31.33	60.33	52.80
C3	9.44	1.05 - 15.20	0.74	56.61	44.41	61.56	75.62
TMV (Gn) 13	9.30						
CO 7	8.55						
TMV 2	8.21						
GPBD 4	10.85						
			Rust score				
C1	1.66	1.00 - 3.00	0.10	33.24	25.94	60.89	43.92
C2	1.50	1.00 - 3.00	0.07	38.89	30.29	60.66	51.19
C3	1.79	1.00 - 2.50	0.14	34.53	26.90	60.74	45.51
TMV (Gn) 13	3.82						
CO 7	3.60						
TMV 2	4.00						
GPBD 4	2.00						
			LLS Score				
C1	2.27	1.00 - 3.00	0.10	27.26	21.74	63.62	37.64
C2	2.64	1.00 - 4.00	0.08	27.80	23.96	74.29	44.82
C3	2.65	1.50 - 3.50	0.14	26.47	21.95	68.80	39.52
TMV (Gn) 13	3.70						
CO 7	4.00						
TMV 2	3.60						
GPBD 4	2.50						

C1: TMV (Gn) 13 × (TMV (Gn) 13 × GPBD 4); C2: CO 7 × (CO 7 × GPBD 4); C3: TMV 2 × (TMV 2 × GPBD 4);
PCV: Phenotypic coefficient of variation (%); GCV: Genotypic coefficient of variation (%); h^2: Heritability;
GAM: Genetic advance expressed as per cent of mean; SE: Standard Error

For rust and LLS incidence, high heritability coupled with high genetic advance as per cent of mean was recorded. This suggested the effectiveness of selection for rust and LLS resistance plants from these back crosses derived populations. High GAM results are in accordance with Shridevi *et al.* (2014) for rust score, Yadawat *et al.* (2015) for rust score in F_2 population of wheat, Prabhu *et al.* (2015) for rust and LLs score and Khedikar (2008) for LLS score in RIL population of groundnut.

On the basis of above findings, it is evident from the present finding that substantial genetic variability was envisaged for yield and its component traits in all the three BC_1F_1 population of crosses *viz.,* TMV (Gn) 13 × GPBD 4, CO 7 × GPBD 4 and TMV 2 × GPBD. It also exhibited high

heritability coupled with high genetic advance as per cent of mean for number of pods per plant, 100-pod weight, shell weight per plant, pod yield per plant, kernel yield per plant and rust and LLS resistance. Therefore, these traits should be taken into account while selecting superior and desirable plants for further evolving high yielding and rust and LLS resistant genotype in groundnut.

REFERENCES

Abinasa M, Ayana A and Bultosa G 2011. Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. var. durum) genotypes. *African Journal of Agricultural Research*, **6**: 3972-3979.

Ali N Malik, Bashir S N and Mirza M Y 2000. Genetic variability, heritability and correlation studies in groundnut. *Sarhad Journal of Agriculture*, **16**: 533-536.

Anitha B K 2013. Identification of quantitative trait loci for oil yield and marker assisted backcross for high oleic acid in groundnut (*Arachis hypogaea* L.). Ph.D. (Ag.) Thesis, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu.

Ashish J, Nadaf H L and Gangadhara K 2014. Genetic analysis of rust and late leaf spot in advanced generation recombinant inbred lines of groundnut (*Arachis hypogaea* L.). *International Journal of Genetic Engineering and Biotechnology*, **5**(2): 109-114.

Atta B M, Haq M A and Shah T M 2008. Variation and inter relationships of quantitative traits in chickpea (*Cicer arietinum* L.). *Pakistan Journal of Botany*, **40**(2): 637- 647.

Basha S A, Raghavendra G, Ramanjaneyulu A V and Srinivas A 2016. Influence of biocontrol agents and fungicides on vegetative parameters of groundnut (*Arachis hypogaea* L.) under greenhouse conditions. *Journal of Oilseeds Research*, **33**(1): 91-94.

Bhargavi H, Srinivasa Reddy M, Tirumala Reddy S, Kavitha P, Reddy U V B and Ramesh Babu P V 2016. Productivity of groundnut (*Arachis hypogaea* L.) as influenced by varieties and plant densities. *Journal of Oilseeds Research*, **33**(1): 83-86.

Burton G W 1952. Quantitative inheritance in grasses. *Proceedings 6th International Grassland Congress*, **1**: 24-84.

Gowda M V C, Motagi B N, Naidu G K, Diddimani S B and Sheshagiri R 2002. GPBD 4: a Spanish bunch groundnut genotype resistant to rust and late leaf spot. *International Arachis Newsletter*, **22**: 29-32.

Hiremath C P, Nadaf H L and Keerthi C M 2011. Induced genetic variability and correlation studies for yield and its component traits in groundnut (*Arachis hypogaea* L.). *Electronic Journal of Plant Breeding*, **2**(1): 135-142.

Johnson H W, Robinson H F and Comstock R E 1955. Estimation of genetic variability and environmental variability in soybean. *Agronomy Journal*, **47**: 314-318.

Khedikar Y P 2008. Molecular tagging and Mapping of resistance to late leaf spot and rust in groundnut (*Arachis hypogaea* L.). Ph.D. Thesis, University of Agricultural Science, Dharwad, Karnataka.

Ladole M Y, Wakode M M and Deshmuk S N 2009. Genetic variability and character association studies for yield and yield contributing traits in groundnut (*Arachis hypogaea* L.). *Journal of Oilseeds Research*, **26**: 123-125.

Lush J L 1940. Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proceedings American Society of Animal Production*, **33**: 293-301.

Mondal S and Badigannavar A M 2016. Development of high protein groundnut (*Arachis hypogaea* L.) mutant through induced mutagenesis. *Journal of Oilseeds Research*, **33**(2): 98-101.

Prabhu R, Manivannan N, Mothilal A and Ibrahim SM 2015. Estimates of genetic variability parameters for yield and yield attributes in groundnut (*Arachis hypogaea* L.). *International Journal of Agriculture, Environment and Biotechnology*, **8**(3): 551-559.

Sawargaonkar S L, Giri R R and Hudge B V 2010. Character association and path analysis of yield component traits and late leaf spot disease traits in groundnut (*Arachis hypogaea* L.). *Agricultural Science Digest*, **30**(2): 115-119.

Shoba D, Manivannan N and Vindhiyavarman P 2009. Studies on variability, heritability and genetic advance in groundnut (*Arachis hypogaeae* L.). *Electronic Journal of Plant Breeding,* **1**: 74-77.

Shridevi A J, Nadaf H L, Gowda M V C, Bhat R S, Patil R K, Motagi B, Kenchanagowda P, Mukri G, Archana B, Ganagshe Y P, Gangadhar K and Jaggal L 2014. Marker detection and genetic analysis for rust resistance of recombinant and backcross inbred lines in groundnut (*Arachis hypogaea* L.). *Indian Journal of Genetics and Plant Breeding*, **74**(2): 213-221.

Sivasubramanian S and Madhava Menon P 1973. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*, **60**: 1093-1096.

Sreenivasulu S, Jain P K and Sastry T P 2015. Impact of farmer field school on extent of adoption of improved practices by groundnut farmers. *Journal of Oilseeds Research*, **32**(1): 106-109.

Subrahmanyam P D, McDonald F, Waliyar L J, Reddy S N, Nigam R W, Gibbons V R, Rao P, Singh A K, Pande S, Reddy P M and Subba Rao P V 1995. Screening methods and sources of resistance to rust and late leaf spot of groundnut. *Information Bulletin No. 47.* ICRISAT, Patancheru, India, pp. 24.

Subrahmanyam P, Moss J P, McDonald D, Rao P, V S Rao and Gibbons V R 1985. Resistance to leaf spot caused by *Cercosporidium personatum* in wild Arachis species. *Plant Disease*, **69**: 951-954.

Thirumala R V, Venkanna V, Bhadru D and Bharathi D 2014. Studies on variability, character association and path analysis on groundnut (*Arachis hypogaea* L.). *International Journal of Pure and Applied Bioscience*, **2**(2): 194-197.

Vijaykumar Hokrani H, Rudra Naik, Nadaf H L, Desai S A, Deshpande S K, Kalappanavar I K and Patil B N 2013. Genetic studies in free threshable advanced segregating population of tetraploid wheat (*Triticum dicoccum*). *Karnataka Journal of Agricultural Sciences*, **26**(1): 10-13.

Association analysis for yield and component traits in sunflower (*Helianthus annuus* L.)

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ABSTRACT

Ninety genotypes of sunflower were evaluated for the estimation of correlation and path analysis. Data were recorded for yield and its component traits *viz*., days to 50% flowering, days to maturity, duration of reproductive phase, plant height, stem girth, head diameter, 100-seed weight, seed filling percentage, hull content (%), protein content (%), oil content (%) and seed yield per plant (g). The seed yield per plant showed positive and significant correlation with seed filling percentage, head diameter, oil content and 100-seed weight showed negative correlation with days to 50% flowering, days to maturity and hull content. This shows that head diameter, 100-seed weight, seed filling percentage and oil content are the major yield contributing traits to be given more selection pressure for improving yield. The path coefficient analysis showed that 100-seed weight had the highest direct and positive effect on seed yield per plant followed by head diameter, plant height and oil content had positive direct effects on seed yield. So, direct selection of genotypes for seed yield through these traits may be effective.

Keywords: Correlation and path analysis, Genotypes, Sunflower

Sunflower (*Helianthus annuus* L.), belonging to the family 'Asteraceae' is an important oilseed crop and is the preferred source of oil for domestic consumption and cooking worldwide (Hu *et al.,* 2010). Sunflower has a great potential in bridging the gap between the demand and supply of edible oil in future as this oil is considered as good from health point of view due to presence of polyunsaturated fatty acids. In sunflower, seed yield and oil content are complex traits which are affected by different factors which may act individually or collectively. The knowledge of association of several characters with yield and among themselves will be, therefore, very essential for planning a successful breeding programme (Chandirakala *et al.,* 2015). The efficiency of selection mainly depends on the direction and magnitude of association between yield and its components. Correlation describes the mutual relationship between the variables and helps to improve different characters simultaneously. If correlation between dependent and independent variable is due to the direct effects of the character, it reflects a true relationship between them and selection can be practiced for such a character in order to improve the dependent variable. But the actual contribution of each character can be provided by partitioning of correlation coefficient into its direct and indirect effects. Path coefficient analysis is a reliable statistical technique which provides means not only to quantify the inter relationships of different yield components but also indicate whether the influence is directly reflected in the yield or takes some other pathway for ultimate effects. To better understand the cause and effect relationship between different pairs of characters, the study of correlation in conjunction with path analysis is essential (Vairam and Gnanamalar, 2016). Therefore, the path coefficient analysis was also undertaken to understand the direct and indirect effects of various traits on seed yield.

Ninety sunflower genotypes selected from sunflower germplasm maintained at the Oilseeds Section, Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar were used for the experiment (Table 1). The experiment was conducted at the Research Farm of CCS Haryana Agricultural University, Hisar during spring, 2013. All 90 genotypes were grown in a randomized block design with three replications in single row plots of 3 m length, keeping row to row distance of 45 cm and plant to plant distance of 30 cm for each genotype. All the recommended package of practices were followed to raise the crop. Observations were recorded on the characteristics like days to 50% flowering, days to maturity, duration of reproductive phase, plant height at harvest (cm), stem girth (cm), head diameter (cm), 100-seed weight (g), seed filling percentage, hull content (%), protein content, oil content (%) and seed yield per plant (g). Protein content of each genotype was estimated using micro- Kjeldal method, whereas oil content of seeds was determined by the method of AOAC (1995).

Seed yield is a quantitative character which is governed by several contributing traits. Hence, it is important to understand the association of different characters with seed yield for enhancing the usefulness of selection criterion to be followed while developing varieties. Estimates of genetic association along with phenotypic correlation show the inherent association as well as indicate the level of phenotypically expressed correlation influenced by the environment. Correlation between different characters could

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arise due to linkage or pleiotropy. Correlation due to linkage can be manipulated or changed through recombination but it could be impossible to overcome the correlation due to pleiotropy. High magnitude of genotypic correlation coefficient to that of phenotypic correlation coefficient shows a good amount of strong inherent association between different attributes (Safavi *et al.,* 2011).

Days to 50% flowering exhibited positive correlation with days to maturity, plant height, seed filling percentage and protein content and negative correlation with duration of reproductive phase, head diameter, oil content and seed yield per plant (Table 2). Binodh *et al.* (2008) have reported the similar results for seed yield. Head diameter had positive correlation with 100-seed weight, oil content and seed yield which confirmed the findings of Rao (2013) and Sujatha and Nadaf (2013). Positive correlations of 100-seed weight were observed with seed filling percentage and seed yield, whereas negative correlation was observed with hull content. Machikowa and Saetang (2008) also observed similar results for seed yield. Oil content was found to be positively correlated with seed yield. Similar findings were reported by Chander and Sheoran (2014).

Seed yield exhibited positive correlation with head diameter, 100-seed weight, seed filling percentage and oil content and negative correlation with days to 50% flowering, days to maturity and hull content. Similar results for one or more characters were reported by Kumari and Sheoran (2012) and Prabhakaran *et al.* (2013). These studies show that head diameter, 100-seed weight, seed filling percentage and oil content are the major yield contributing traits to be given more selection pressure for improving yield.

The correlation coefficient indicates only linear relationship existing between pair of characters. The path analysis helps to resolve the correlations further and provides a clear picture in which component traits contribute towards dependent variable. The path coefficient analysis takes into account the cause and effect relationship between the variables which is unique in partitioning the associations into direct and indirect effects through other dependent variables. The critical evaluation of path coefficient table in which diagonal values are direct effects and off-diagonal values are indirect effects revealed that all the direct effects were less than one which indicates that influences due to multicolinearity were minimal (Gravois and Helms, 1992). Partitioning of genotypic correlation between seed yield per plant and its component characters revealed that the direct effects were, in general, of higher magnitude than that of their indirect effects for all the characters (Table 3).

Table 1 List of 90 genotypes selected for the study

1	ACGIP-1436	31	EC-601801	61	GPB-07
2	AKSFI-33	32	EC-601806	62	GPB-18
3	AKSFI-52-4	33	EC-601820	63	GPB-50
4	AKSFI-54-3	34	EC-601871	64	GPB-61
5	AKSFI-58-3	35	EC-601875	65	GPB-67
6	AKSFI-71	36	EC-601885	66	GPB-07-1
7	AKSFI-78	37	EC-601889	67	GPN-145
8	AKSFI-186	38	EC-601896	68	GPN-215
9	AKSFI-190	39	EC-601906	69	LSF-902
10	AKSFI-197	40	EC-601926	70	MR-6
11	CGP-17	41	EC-601935	71	NDR-2
12	CGP-39-1	42	EC-601953	72	P35R-PAU
13	CGP-112	43	EC-601957	73	RCR-22-2
14	CSF1-5311	44	EC-601963	74	RCR-24-11
15	CSF1-5313	45	EC-601971	75	RCR-39
16	CSF1-5317	46	EC-601974	76	RCR-72
17	DRSF-106	47	EC-623009	77	RHA-271
18	DRSF-120	48	EC-623013	78	RHA-859
19	EC-512673	49	EC-623015	79	RHA-298
20	EC-512674	50	EC-623016	80	RHA-2
21	EC-512676	51	EC-623017	81	RHA-3
22	EC-512684	52	EC-623019	82	R-101
23	EC-512687	53	EC-623020	83	R-102
24	EC-601746	54	EC-623024	84	R-103
25	EC-601747	55	EC-623025	85	R-105
26	EC-601748	56	EC-623026	86	R-107
27	EC-601755	57	EC-623028	87	1-OH-07-8
28	EC-601758	58	EC-623031	88	1-OH-07-62
29	EC-601767	59	EC-623032	89	1-OH-07-65
30	EC-601769	60	GPB-02	90	1-OH-07-108

Table 2 Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among twelve characters in sunflower

Character	Days to 50% flowering	Days to maturity	Duration of reproductive phase	Plant height (cm)	Stem girth (cm)	Head diameter (cm)	100-seed wt. (g)	Seed filling per cent	Hull content (%)	Protein content (%)	Oil content (%)	Seed yield/ plant (g)
Days to 50% flowering		0.790**	-0.155*	0.168**	0.110	-0.136*	0.024	0.308**	0.056	0.208**	-0.136*	-0.170**
Days to maturity	0.853		0.062	0.261**	0.128*	-0.147*	-0.219**	0.166**	0.132*	0.070	-0.090	-0.348**
Duration of reproductive phase	-0.13	0.075		0.094	-0.006	0.112	-0.004	-0.081	0.139*	-0.233**	0.134*	-0.045
Plant height (cm)	0.188	0.276	0.111		0.144*	0.014	-0.038	0.012	0.053	-0.167**	-0.025	-0.021
Stem girth (cm)	0.192	0.173	-0.063	0.16		0.234**	0.099	-0.097	-0.047	0.164**	-0.193**	-0.029
Head diameter (cm)	-0.146	-0.223	0.184	-0.126	0.373		0.377**	0.016	-0.082	0.064	0.140*	0.468**
100-seed wt. (g)	0	-0.245	-0.013	-0.042	0.126	0.523		0.156*	-0.195**	0.061	0.087	0.655**
Seed filling per cent	0.345	0.174	-0.094	0.014	-0.127	0.024	0.163		-0.089	0.046	0.121*	0.128*
Hull content (%)	0.061	0.135	0.150	0.051	-0.077	-0.143	-0.219	-0.092		-0.319**	-0.049	-0.215**
Protein content (%)	0.221	0.077	-0.254	-0.179	0.215	0.113	0.068	0.044	-0.337		-0.047	0.043
Oil content (%)	-0.171	-0.099	0.159	-0.039	-0.29	0.152	0.095	0.132	-0.062	-0.060		0.251**
Seed yield per plant (g)	-0.190	-0.37	-0.05	-0.03	-0.026	0.600	0.711	0.119	-0.235	0.038	0.273	

*, ** = Significant at 5% and 1% level of probability, respectively

Table 3 Path coefficient analysis of seed yield per plant with its component characters in sunflower

Character	Days to 50% flowering	Days to maturity	Duration of reproductive phase (days)	Plant height (cm)	Stem girth (cm)	Head diameter (cm)	100-seed wt (g)	Seed filling per cent	Hull content (%)	Protein content (%)	Oil content (%)	Genotypic correlation with seed yield/plant
Days to 50% flowering	**0.036**	0.031	-0.005	0.007	0.007	-0.005	0.000	0.013	0.002	0.008	-0.006	-0.190
Days to maturity	-0.133	**-0.156**	-0.012	-0.043	-0.027	0.035	0.038	-0.027	-0.021	-0.012	0.016	-0.37
Duration of reproductive phase (days)	0.020	-0.012	**-0.154**	-0.017	0.010	-0.028	0.002	0.015	-0.023	0.039	-0.025	-0.05
Plant height (cm)	0.026	0.039	0.016	**0.141**	0.022	-0.018	-0.006	0.002	0.007	-0.025	-0.006	-0.03
Stem girth (cm)	-0.044	-0.040	0.015	-0.037	**-0.231**	-0.086	-0.029	0.029	0.018	-0.050	0.067	-0.026
Head diameter (cm)	-0.064	-0.098	0.081	-0.056	0.165	**0.441**	0.231	0.011	-0.063	0.050	0.067	0.600
100-seed wt. (g)	0.000	-0.112	-0.006	-0.019	0.058	0.238	**0.456**	0.074	-0.100	0.031	0.043	0.711
Seed filling (%)	-0.006	-0.003	0.002	0.000	0.002	0.000	-0.003	**-0.017**	0.002	-0.001	-0.002	0.119
Hull content (%)	-0.003	-0.007	-0.008	-0.003	0.004	0.008	0.012	0.005	**-0.055**	0.019	0.003	-0.235
Protein content (%)	-0.003	-0.001	0.004	0.003	-0.003	-0.002	-0.001	-0.001	0.005	**-0.014**	0.001	0.038
Oil content (%)	-0.020	-0.011	0.018	-0.005	-0.033	0.017	0.011	0.015	-0.007	-0.007	**0.114**	0.273

R square = 0.6902; Residual effect = 0.5566

100-seed weight had the highest direct and positive effect on seed yield per plant, followed by head diameter, plant height, oil content and days to 50% flowering thereby, suggesting the usefulness of all these mentioned characters for component selection method to improve seed yield per plant in sunflower. Similar findings for one or more characters were reported by Iqbal *et al.* (2013) and Zia *et al.* (2013). The direct negative effects were observed for days to maturity, duration of reproductive phase, stem girth, seed filling percentage, hull content and protein content. 100-seed weight, which showed highest direct effect, was also contributing to yield indirectly through head diameter, seed

filling percentage, stem girth, oil content (%) and protein content (%). Head diameter also contributed to yield indirectly through 100-seed weight, stem girth, oil content (%) and duration of reproductive phase. The residual effect (0.556) indicates that the component characters under study were responsible for about 45% of variability in seed yield per plant. So, from the combined results of correlation coefficient and path analysis, it may be concluded that head diameter, 100-seed weight, seed filling percentage and oil content are the major yield contributing traits to be given selection pressure for improving yield. Similar results were reported by Deengra *et al.* (2010).

Positive and significant correlations of seed yield were recorded with 100-seed weight, seed filling percentage, oil content and head diameter which revealed that the selection based on these traits would ultimately improve seed yield. It is also suggested that hybridization of genotypes possessing combination of above characters is most useful for obtaining desirable high yielding segregation. Path coefficient analysis revealed that the traits, 100-seed weight, head diameter, plant height, oil content and days to 50% flowering had positive and direct effects on seed yield per plant, while the characters, days to maturity, duration of reproductive phase, stem girth, seed filling percentage, hull content and protein content showed direct negative effects. Hence, it would be rewarding to lay stress on these yield contributing characters for the improvement of yield. The results of correlation and path coefficient analysis indicated that the traits, 100-seed weight, head diameter, plant height and oil content should be given due consideration while performing selection for seed yield in segregating generations of sunflower.

REFERENCES

AOAC 1995. *Official Methods of Analysis. Association of Official Agricultural Chemists*, 11th Edition. Washington D.C. pp. 16.

Binodh A K, Manivannan N and Vindhyavarman P 2008. Character association and path analysis in sunflower. *Madras Agricultural Journal*, **95**: 425-428.

Chander S and Sheoran R K 2014. Studies on correlation and path coefficient analysis for seed yield in sunflower hybrids (*Helianthus annuus* L.). *Proceedings of National Seminar on Reorientation of Agricultural Research to ensure National Food Security*, Jan 6-7, 2014, Directorate of Research, CCS HAU, Hisar, pp. 63.

Chandirakala R, Ameena P and Manivannan N 2015. Metroglyph analysis on genetic diversity in germplasm accessions of sunflower (*Helianthus annuus* L.). *Journal of Oilseeds Research,* **32**(2): 170-173.

Deengra S K, Kumar N, Kumar V and Dhaka R P S 2010. Correlation and path coefficient analysis in sunflower (*Helianthus annuus* L.). *Progressive Agriculture,* **10**(2): 318-322.

Dewey D R and Lu K H 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal,* **51**: 515-518.

Gravois K A and Helms R S 1992. Path analysis of rice yield and yield components as effected by seeding rate. *Agronomy Journal*, **84**: 1-4.

Hu J, Seiler G and Kole C 2010. *Genetics, Genomics and Breeding of Sunflower.* Routledge, USA, pp. 342.

Iqbal M, Ijaz U, Smiullah, Iqbal M, Mahmood K., Najeebullah M, Abdullah, Niaz S and Sadaqat H A 2013. Genetic divergence and path coefficient analysis for yield related attributes in sunflower (*Helianthus annuus* L.) under less water conditions at productive phase. *Plant Knowledge Journal*, **2**(1): 20-23.

Kumari S and Sheoran R K 2012. Genetic variability, heritability and character association in sunflower. *Research on Crops,* **13**(2): 566-572.

Machikowa T and Saetang C 2008. Correlation and path coefficient analysis on seed yield in sunflower. *Suranaree Journal of Science and Technology*, **15**(3): 243-248.

Prabhakaran V, Reddy S M, Reddy T D and Ranganatha A R G 2013. Character association and path analysis in sunflower (*Helianthus annuus* L.). *Journal of Oilseeds Research*, **30**(1): 65-67.

Rao V T 2013. Association analysis in sunflower (*Helianthus annuus* L.). *International Journal of Applied Biology and Pharmaceutical Technology*, **4**(1): 1-4.

Safavi A S, Safavi S M and Safavi S A 2011. Genetic variability of some morphological traits in sunflower (*Helianthus annuus* L.). *American Journal of Crop Research*, **17**: 19-24.

Sujatha K and Nadaf H L 2013. Correlation for yield and yield related trait in mutant and segregating genotypes in sunflower (*Helianthus annuus.* L). *Molecular Plant Breeding*, **4**: 265-266.

Vairam N and Gnanamalar R P 2016. Combining ability studies in sunflower (*Helianthus annuus* L.). *Journal of Oilseeds Research*, **33**(1): 72-74.

Wright S 1921. Correlation and causation. *Journal of Agricultural Research*, **20**: 557-585.

Zia U Z, Sadaqat H A, Tahir M H N and Sadia B 2013. Correlation and path coefficient analysis of various traits in sunflower (*Helianthus annuus* L.). *Journal of Global Innovation in Agricultural and Social Sciences*, **1**(1): 5-8.

Performance of safflower and linseed intercropping system with different row proportions under rainfed conditions

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ABSTRACT

Field experiment was conducted at Main Agricultural Research Station, Raichur, Karnataka during *rabi* season of 2015-16 to study the yield performance and economics of safflower and linseed intercropping system with different row proportions. The results revealed that, among various intercropping systems safflower + linseed in 1:2 row proportion recorded significantly higher safflower equivalent yield of 1686 kg/ha followed by safflower + linseed in 1:1 row proportion 1450 kg/ha. The land equivalent ratio was significantly highest in safflower + linseed in 1:2 row proportion (1.20) followed by safflower + linseed in 2:1 row proportion (1.03). Higher net return was recorded in safflower + linseed in 1:2 row proportion (₹ 23,212/ha) followed by sole linseed (₹ 19,376/ha) and sole safflower (₹ 18,979/ha). However, higher B: C was recorded in safflower + linseed (1:2) row proportion (2.22).

Keywords: Intercropping system, LER, Linseed, Safflower

The productivity of dryland crops is very low because of low and erratic rainfall, variation in soil fertility and improper management of resources by the farmers. To bridge this gap, crop diversification is required for increasing the productivity and profitability per unit area per unit time (Shubha *et al.,* 2015). In Northern Karnataka linseed is cultivating under rainfed area during *rabi* season as a sole crop or mixed cropping with safflower and safflower without proper row proportion but this proportion has no substantial gain in productivity of linseed and difficulties in cultural practices during crop growth. To increase the productivity of cropping system under rainfed condition, investigation was carried out to find out the remunerative intercropping system to be productive and economically viable with suitable row proportions.

Field experiment was conducted during *rabi* season of 2015-16 at Main Agricultural Research Station, University of Agricultural Science, Raichur, Karnataka on medium black soil under rainfed agro eco-system. The soil was medium in organic carbon (5.3 g/kg), low in available nitrogen (115.28 kg/ha), high phosphorous (59.21 kg P_2O_5/ha) and high potassium (473.55 kg K_2O /ha) with pH (7.78). Safflower (cv. S-144) and linseed (cv. NL-115) were intercropped in 1:1, 1:2, 2:1 and 2:2 row proportions and both crops were grown as sole crop at their recommended row spacing (60 cm for safflower and 30 cm for linseed) along with mixed cropping of safflower and linseed totaling seven treatments. The experiment was laid out in a randomized complete block design with four replications. Both the crops were sown simultaneously and recommended dose of fertilizers were applied to sole crops and in intercropping system. The components crops received fertilizer at the time of sowing in proportion to their plant density in the form of urea, DAP and MOP. The crops were sown as per the row proportions during second fortnight of October. The rainfall received during 2015-16 was 677.5 mm, while during cropping period, it was 95.5 mm. The growth and yield observations were recorded from net plots and seed yield of various crops were converted on hectare basis in kilograms. The economics of each system was computed with prevailing prices of each commodity during the year. The yield was further computed in terms of safflower equivalent yield, land equivalent ratio, gross returns as well as B:C ratio to assess the system productivity and viability.

Seed yield of safflower was influenced significantly due to intercropping systems with different row proportions and plant population. Sole safflower recorded significantly higher seed yield (1398 kg/ha) and it was on par with mixed cropping of safflower and linseed (1298 kg/ha) and safflower + linseed (1:2) row proportion (1289 kg/ha). Reduction in yield of safflower due to various intercropping combinations were in the order of safflower + linseed (1:2), safflower + linseed (1:1), safflower + linseed (2:2) and safflower + linseed (2:1) (Table 1). Seed yield of safflower under intercropping system was reduced to an extent of 85 per cent in 2:1, 64.10 per cent in 1:2, 24.37 per cent in 1:1, 8.45 per cent in 1:2 and 7.7 per cent in mixed cropping of safflower and linseed as compared to sole safflower. Variation in the safflower yield might be due to several causes *viz.,* variation in population levels, planting geometry, crop combinations, inter and intra species competition for light, moisture, nutrients, space, etc. Further, inter and intra species competition for available resources owing to higher population levels per unit area under intercropping systems is another reason. Similarly, Manjithkumar *et al.* (2009) also obtained lower yield of safflower under intercropping systems. The lower seed yield of safflower was produced

when it was intercropped with linseed in 2:2 row ratios as compared to the rest of the treatment combinations. Comparable seed yield of safflower could be attributed to comparable performance of yield and growth component of safflower. Superior values of yield in solitary stand of safflower might be attributed to competition free environment and optimum population level compared to intercropping treatments. The results are in conformity with the findings of Manjithkumar *et al.* (2009) and Gobade et al. (2015), where they reported that yield of safflower and other *rabi* crops were always highest in sole cropping system as compared to other different intercropping system.

Safflower when grown with linseed in mixed cropping system attributed to higher values of yield components *viz.,* number of seed per capitulum, seed weight per plant and test weight. The other factor which indirectly influenced the seed yield are growth attribute *viz.,* number of leaves per plant, leaf area, number of primary and secondary branches per plant, dry matter accumulation and its distribution in various plant parts. Thus, an attempt was made to identify and analyse the growth components which have led to the difference in the seed yield of safflower in light of observation made on yield components, dry matter distribution and growth attributes.

The seed yield of linseed showed significant variations due to intercropping system. Linseed performed better under pure stand compared to intercropping with varying row proportions. Among intercropping system, linseed was superior under safflower + linseed with different row proportion and inferior under mixed cropping with safflower. The variations in linseed yield could be attributed to variation in the yield attributes and population levels. The higher seed yield of linseed might be contributed by higher number of capsules per plant, capsule weight (g), seeds per capsule and test weight (g). The higher yield of linseed under safflower + linseed (1:2) may be attributed to least competition offered by safflower. These results are in conformity with the findings of Sarkar *et al.* (2003). They reported that, higher seed yield of linseed when intercropped with lentil. Intercropping of lentil + linseed in 5:1 row ratio resulted bonus yield of linseed.

Crop equivalent yield is an important index for assessing the performance of different crops under a given circumstance. Based on the price structure, economic yield of component crops is converted into base crop yield i.e., safflower equivalent yield (SEY). Safflower equivalent yield showed marked differences due to intercropping system at varying row proportion. The SEY was significantly higher in safflower + linseed in 1:2 (1686 kg/ha) as compared to sole crop of safflower followed by the safflower + linseed (1:1) (1450 kg/ha) (Table 1). The higher SEY in safflower + linseed (1:2) was due to higher yield obtained by both safflower and linseed and higher market price of linseed. These results are in conformity with the finding of Aladkatti *et al.* (2011) and Prasad *et al.* (1993). Gobade *et al.* (2015) reported higher safflower equivalent yield (SEY) in sorghum + safflower (2:1) (2322 kg/ha) intercropping system compare to other row proportion. Lower SEY was recorded in safflower + linseed (2:1) (1031 kg/ha), safflower + linseed (2:2) (1144 kg/ha) and sole safflower (1398 kg/ha). This might be due to less plant survival and absence of linseed in case of sole safflower. The productivity of a cropping system is mainly determined by the efficiency of the component crops in utilization of resources. The overall productivity of the intercropping of linseed with safflower relies on the main crop as well as compatibility with other crops.

Significantly higher LER was recorded when safflower intercropped with linseed in 1:2 row proportion (1.20) when compared to sole linseed (1.0) and sole safflower (1.0) (Table 1). Result shows that the highest LER value was achieved in safflower density of 8 plants/row and linseed densities of 16 plants/rows (LER=1.10) which is equal to 10 per cent increase in agricultural profitability compared to monocultures of two crops. The lower LER as 0.81 was obtained in six safflower and 16 linseed plants. Reduction of LER in higher densities can be due to inter-competition between linseed and safflower, which was confirmed by Hemayati *et al.* (2002). Similarly, Sarkar *et al.* (2003) also reported higher LER under intercropping systems. Tanwar *et al.* (2011) reported that intercropping systems of linseed with chickpea were found more LER and advantageous than sole cropping.

Significantly higher gross returns was recorded in safflower + linseed in 1:2 (₹ 42,158/ha) and was followed by safflower + linseed (₹ 36,242/ha) (Table 1). These results confirmed by Deshpande and Sawant (1997), they reported that gross returns was highest under toria + safflower (₹ 18,291/ha) and mustard + safflower (₹ 20,149/ha) intercropping system of 6:2 row ratio followed by toria + safflower (₹ 11,151/ ha) and mustard + safflower (₹ 17,210/ha) intercropping system of 4:2 row ratio. Significantly lowest gross returns was noticed in safflower + linseed (2:1) (₹ 25770/ha) these results were also confirmed by Deshpande and Sawant (1997) reported that 6:2 row ratio gave highest gross returns when it intercropped with linseed, lentil and amaranthus.

Significant difference observed with respect to net returns among the various treatments comprising of row proportion. Significantly higher net returns was recorded in safflower + linseed in 1:2 (₹ 23,213/ha). The higher net returns from these treatments was mainly because of higher yield level of both the crops and higher market price of component crop as compared to other treatment combinations. These results confirmed by Deshpande and Sawant (1997), they reported that net returns was highest under toria + safflower (₹ 14,037/ha) and mustard + safflower (₹ 14,937/ha) intercropping system of 6:2 row ratio followed by toria + safflower (₹ 11,551/ha) and mustard + safflower (₹

12,366/ha) intercropping system of 4:2 row ratio. Significantly lower net return was noticed in safflower + linseed (2:2) (₹ 8,123/ha) (Table 1). Similarly, this result also conformity to result of Yaragattikar and Itnal (2002), where safflower + ber gave higher net returns (₹ 16,485/ha) as compared to sole safflower (₹ 5,485/ha).

Benefit Cost ratio was varied among the treatments, where higher B: C was recorded in safflower + linseed (2:1) this could be attributed to lower cost of cultivation (Table 1). The higher economical advantage of these intercropping systems was due to higher seed yield from intercrops besides higher market price. Similar results were reported by Korwar *et al.* (1998), Deshpande and Sawant (1997) and Yaragattikar and Itnal (2002).

Table 1 Seed yield of safflower, seed yield of linseed, safflower equivalent yield, LER and economics of the systems as influenced by different row proportion and spacing

Treatment	Safflower seed yield (kg/ha)	Linseed seed yield (kg/ha)	SEY	LER	Gross returns (Rs./ha)	Net returns (Rs./ha)	B:C ratio
T1 – Safflower + linseed (1:1) 30 cm rows	1124	163	1450	1.03	36242	17638	1.94
T2 – Safflower + linseed (1:2) 30 cm rows	1289	199	1686	1.20	42158	23212	2.22
T3 – Safflower + linseed (2:1) 30 cm rows	755	138	1031	0.73	25770	8123	1.46
T4 – Safflower + linseed (2:2) 30 cm rows	852	146	1144	0.81	28596	11343	1.65
T5– Mixed cropping of safflower and linseed (100:20)	1298	61	1419	1.01	35483	18239	2.05
T6 – Sole safflower (60 cm x 30 cm)	1398	-	1398	1.00	34949	18979	2.18
T7 – Sole linseed (30 cm x 5 cm)	-	716	1433	1.00	35817	19376	2.17
S.Em.±	73	13.96	78	0.02	-	1093	0.11
CD (P=0.05)	224	43.01	240	0.06	-	3368	0.35

SEY - Safflower equivalent yield; LER - Land equivalent ratio

REFERENCES

Aladakatti Y R, Hallikeri S S, Nandagavi R A, Hugar A Y and Navee N E 2011. Effect of intercropping of oilseed crops on growth, yield and economics of cotton (*Gossypium hirsutum*) under rainfed conditions. *Karnataka Journal of Agricultural Sciences,* **24**(3): 280-282.

Deshpande S L and Sawant A R 1997. Safflower intercropping in lentil and amaranthus. *Proceedings of 4th International Safflower Conference,* 2-7th June 1997, Bari, Italy, pp. 62-64.

Gobade S M, Patil C B and Gokhale D N 2015. To quantify production potential of non-spiny safflower to other *rabi* crop and intercropping system. *National Academy of Agricultural Sciences*, **22**(5): 1087-1089.

Hemayati S, Siadat A and Sadeghzade F 2002. Evaluation of intercropping of two corn hybrids in different densities. *Iranian Journal of Agricultural Sciences*, **25**: 73-87.

Korwar G R, Osman M, Tomar D S and Singh R P 1998. *Dryland Horticulture Extension Bulletin,* Central Research Institute for Dryland Agriculture, Hyderabad, pp. 9-12.

Manjithkumar B R, Chidenand M, Mansur P M and Salimath S C 2009. Influence of different row proportions on yield components and yield of *rabi* crops under different intercropping systems. *Karnataka Journal of Agricultural Sciences*, **22**(5): 1087-1089.

Prasad M, Meena B L and Prasad R 1993. Effect of intercropping in upland cotton on growth and yield of component crops. *Indian Journal of Agronomy*, **38**(2): 342-344.

Sarkar R K, Malik G C and Pal P K 2003. Effect of intercropping lentil (*Lens culinaris*) and linseed (*Linum usitatissimum* L.) under varying plant density and row arrangement on productivity and advantages in system under rainfed condition. *Indian Journal of Agronomy*, **49**(4): 241-243.

Shubha G V, Biradar S A, Satyanaraynrao, Koppalkar B G, Govindappa M R, Ajithkumar K and Rajanna 2015. Performance of sorghum and linseed intercropping system with different row proportion and planting geometry under rainfed condition. *Journal of Oilseeds Research*, **32**(1): 97-99.

Tanwar S P S, Rokadia P and Singh A K 2011. Effect of row ratio and fertility levels on chickpea (*Cicer arietinum*) and linseed (*Linum usitatissimum*) intercropping system. *Indian Journal of Agronomy*, **56**(3): 217-222.

Yaragattikar A T and Itnal C J 2002. Studies on ber based intercropping systems in the Northern Dry Zone of Karnataka. *Karnataka Journal of Agricultural Sciences*, **16**(1): 22-25.