www.ThePharmaJournal.com

The Pharma Innovation

Bijjam Chandra Reddy
PG Students, Department of Genetics and Plant Breeding, Dr. PDKV university Akola, College of Agriculture Nagpur, Maharashtra, India

Beena M Nair
Linseed Breeder, AICRP on Linseed and Mustard, Dr. PDKV university Akola, College of Agriculture, Nagpur, Maharashtra, India

Shilpa Rananaware
Agriculture Assistant, AICRP on Linseed and Mustard, Dr. PDKV university Akola, College of Agriculture Nagpur, Maharashtra, India

Shailendra Sagar Prajapati
Ph.D., Scholar, Department of Plant Breeding & Genetics, Jawaharlal Nehru Krishi Vishwavidyalaya, Jabalpur, Madhya Pradesh, India

Mahesh Gujar
PG Students, Department of Genetics and Plant Breeding, Dr. PDKV university Akola, College of Agriculture Nagpur, Maharashtra, India

Arpita Mate
PG Students, Department of Genetics and Plant Breeding, Dr. PDKV university Akola, College of Agriculture Nagpur, Maharashtra, India

Jyoti Shinde
PG Students, Department of Genetics and Plant Breeding, Dr. PDKV university Akola, College of Agriculture Nagpur, Maharashtra, India

Corresponding Author:
Bijjam Chandra Reddy
PG Students, Department of Genetics and Plant Breeding, Dr. PDKV university Akola, College of Agriculture Nagpur, Maharashtra, India

Genetic diversity in exotic linseed germplasm for yield and yield contributing traits

Bijjam Chandra Reddy, Beena M Nair, Shilpa Rananaware, Shailendra Sagar Prajapati, Mahesh Gujar, Arpita Mate and Jyoti Shinde

Abstract
176 genotypes along with two check varieties (PKV NL 260, TL 99) were evaluated in augmented block design for eleven quantitative characters *viz.*, days to 50 % flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant^{-1}, number of capsule plant^{-1}, seed yield plant^{-1} (g), 1000 seed weight (g), % bud fly infestation, % alternaria blight infestation, powdery mildew (score), flower size (mm). At AICRP on Linseed and Mustard farm, College of Agriculture, Nagpur. Mahalanobis D² statistics were used for genetic diversity of eleven quantitative characters to identify potential parents for linseed programme aimed for yield improvement. The analysis of dispersion for eleven characters using Wilk's criterion, revealed highly significant difference between genotypes for all eleven characters. The 178 genotypes were grouped into thirteen clusters by Tocher's method. The maximum inter cluster distance was recorded between cluster XII and XIII (D²=40.20) and in between cluster VII and XII (D²=37.76) whereas minimum inter cluster distance was found in between cluster V and cluster VI (D²=7.39). The canonical analysis revealed that differentiation for eleven characters among 178 genotypes was completed in five phases indicated the importance of number of capsule plant^{-1}, days to 50% flowering, seed yield plant^{-1} for selecting parents. The canonical analysis and cluster means studied together revealed the importance of bud fly infestation%, number of capsule plant^{-1}, seed yield plant^{-1}, as an important contributing character towards the total divergence. The parents EC0041764, EC0041726, EC0001465, EC0001403, EC0541211, EC0541224, EC0041598, EC54225, EC41562, EC004140 can be used for further hybridization programme. These genotypes on hybridization with the existing check varieties may also be used for their improvement.

Keywords: Clusters, Genetic divergence, linseed, D² statistics

Introduction
Linseed is one of the most important oilseed crops for industrial as well as food, feed, and fiber purposes. Linseed oil has various industrial and medicinal uses (Chauhan *et al.,* 2009). Linseed has an increasing demand in agro based industries but still the average productivity is very low as compared to other countries, due to non adaption of applied production technologies. The study of genetic diversity plays significant role by providing basis in making selection of parents for hybridization programme in crop improvement programme. Mahalanobis D² Statistics is a powerful tool to measure the degree of divergence among group genotypes based on multiple characters and for selecting efficient parents for hybridization programme in out breeding and self-pollinated crops. (Rao, 1952 [11]; Murty and Arunachalam 1966) [14]. The studies on divergence of the germplasm are very useful for developing high yielding, disease, and insect-pest resistant cultivars. The selection of suitable divergent parents for hybridization is required because the cross involving diverse parents offer great possibility of obtaining desirable segregants in the segregating generations (Moll and Robinson, 1962) [9].

Materials and Methods
The present investigation involving 176 genotypes along with two checks (PKV NL 260, TL 99) of linseed were planted in Augmented Block Design during *Rabi* 2021-22. Each genotype was grown in single row having spacing of 30cm x 5 cm at experimental section AICRP on Linseed and Mustard farm, College of Agriculture Nagpur. Recommended agronomic practices were followed to raise the crop. Five competitive plants from each genotype were selected randomly to record observations on eleven traits *viz.*, days to 50 % flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant^{-1},

to record observations on eleven traits viz., days to 50 % flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant[-1], number of capsule plant[-1], seed yield plant[-1] (g), 1000 seed weight (g), % bud fly infestation, % alternaria blight infestation, powdery mildew (score), flower size (mm). The collected data were subjected to analysis of genetic divergence in 178 genotypes by using Mahalanobis D^2 statistics (1936), Wilk's criterion as described by Rao (1952) [11]. Inter and intra cluster distance were calculated by method suggested by Rao (1952) [11] selection of parents for hybridization from different clusters were done on the basis of mean statistical distance as suggested by Bhatt (1970).

Results and Discussion

The data on the mean squares due to the genotypes were highly significant for all eleven characters studied *i.e.* days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant[-1], number of capsule plant[-1], seed yield plant[-1] (g), 1000 seed weight (g), bud fly infestation (%), alternaria blight infestation (%), Powdery mildew infestation (%), flower: corolla size (mm) indicating the presence of considerable genetic variation among the genotypes for the characters studied. The wide variability for yield contributing characters in linseed were observed by the Dhirhi *et al.* (2016) [15] and Paul *et al.* (2017) [16].

Table 1: Analysis of dispersion

Source of variations	DF	Sum of squares	Mean squares
Varieties	177	1.4532E17	8.2103E14*
Error	353	1.1486E02	3.2540E-01
Total	530	1.4532E17	2.7419E14

* Significant at 5% level

Table 2: Contribution of different characters towards divergence

Sr. No.	Characters	Time ranked 1st	Percent Contribution
1	Plant height (cm)	448	2.84%
2	Number of capsules plant[-1]	3195	20.28%
3	Number of branches plant[-1]	1289	8.18%
4	Alternaria infestation %	3862	24.52%
5	Bud fly infestation%	235	1.49%
6	Powdery mildew infestation%	1261	8.00%
7	Days to maturity (days)	0	0.00%
8	1000 seed weight (g)	278	1.76%
9	Days to 50% flowering (days)	1575	10.00%
10	Seed yield plant[-1](g)	2739	17.39%
11	Flower: corolla size (cm)	871	5.53%
	Total	15753	
	Tochers cut-off value	271.75	

The analysis of dispersion for the test of significance of difference in the mean values based on the Wilk's criterion revealed highly significant difference among genotypes for eleven characters. Diversity analysis was also carried out in linseed by Pali and Mehta (2015) [17], Paul *et.al.* (2017) [18] also reported significant divergence among the genotypes for all the characters studied in linseed (Table 1).
Data revealed that the contribution of alternaria blight infestation % was maximum (24.52) % followed by number of capsule plant[-1] (20.28 %), seed yield plant[-1] (17.39 %), days to 50 % flowering (10.00 %), number of primary branches plant[-1] (8.18 %) powdery mildew infestation% (8.00%),

flower size (5.53 %), plant height (2.84 %), 1000 seed weight (g), (1.76 %), bud fly infestation % (1.49 %), days to maturity (0.0%).This indicates that characters like number of capsule plant[-1], seed yield plant[-1], days to 50%flowering were important traits contributing towards genetic divergence. (Table 2).
In the present investigation, 178 genotypes were grouped into thirteen clusters were done by Tocher's method. All the 178 genotypes were grouped into thirteen clusters on the basis of D² statistics. The cluster I was largest comprising of 130 genotypes, followed by cluster II comprising of 27 genotypes, cluster III comprising of 11 genotypes, cluster IV, cluster V, cluster VI, cluster VII, cluster VIII, cluster IX, cluster X, cluster XI, cluster XII, cluster XIII comprising single genotypes in each cluster. The checks PKV NL 260, TL 99 grouped into cluster I along with 128 genotypes. This indicates that there are many germplasms which were highly diverse from the check and hence offers good scope for improvement (Table 3).
The value of first five canonical vectors and canonical roots are presented in Table 4. The first five canonical roots accounted for 82.96 per cent of the observed variability in the material studied (λ1= 31.53%, λ2=18.65 %, λ3=14.31 %, λ4=11.39 %, λ5=7.08 %). The overall contributions of the five canonical roots to the total variability among 178 genotypes were 82.96 per cent suggesting the major portion of differentiation in first five phases. This indicates that differentiations for eleven characters among 178 genotypes were completed in five phases. Further coefficient in first five canonical vectors shows that out of eleven characters' number of capsules plant[-1], alternaria blight infestation %, seed yield plant[-1], days to 50 % flowering,1000 seed weight, powdery mildew infestation%, bud fly infestation%, number of branches plant[-1], plant height contributed in vector I accounting for 31.53 % of total variation. Characters number of capsules plant[-1], number of branches plant[-1], days to 50 % flowering, seed yield plant[-1], days to maturity, powdery mildew infestation% were important characters in vector II which accounted for 18.65 % of total variation. Flower size, seed yield plant[-1], days to maturity, 1000 seed weight, plant height were important characters in vector III which accounted for 14.31 % of total variation. The important characters in vector IV number of capsule plant[-1], alternaria blight infestation %, days to maturity are accounted for 11.39 % of total variation. The important characters in vector V are 1000 seed weight, days to 50 % flowering,1000 seed weight, number of capsules plant[-1], plant height, seed yield plant[-1] accounted for 7.08 % of total variation. This suggested that parent selected on the basis of number of capsule plant-1, days to 50 % flowering, alternaria blight infestation %, bud fly infestation% etc. may expected to be genetically diverse (Table 5).
The intra cluster distance range from 0.00 to 18.71. Cluster III possessed highest intra cluster distance (D²=18.71) followed by cluster II (D²=16.76). The maximum intra cluster value marked greatest divergence amid several genotypes within the cluster. Cluster I (D²=13.57) showed least intra cluster distance indicating minimum genetic diversity among the genotypes of that group. Therefore, the hybridization between the genotypes belonging to the clusters possessing low inter cluster distance were unlikely to achieve heterotic recombinants in segregating generations. So, it is suggested to attempt crosses between the genotypes belonging to clusters

separated by large inter-cluster distance. Ananda and Murty, (1968) [2] also proposed hybridization between lines belonging to clusters separated by large inter cluster distance in linseed. Present finding is in accordance with the findings of earlier linseed worker like Nizar and Mulani (2015) [1] and Kumar *et al.*, (2017) [19]. The average inter cluster distance was maximum between cluster XII and XIII (D²=40.20), followed by cluster VII and cluster XII (D²=37.76), cluster IV and cluster XIII (D²=37.40) and cluster VIII and cluster XIII (D²=35.91), cluster I and cluster XII (D²=33.36) and cluster V and cluster XII (D²=33.21) indicated wide in genetic diversity between these clusters. It is therefore, suggested that crosses should be pursued between the genotypes belongs to cluster XII and XIII, VII and cluster XII may produce desirable transgressive segregants. Meanwhile the inter cluster distance was found to be minimum between cluster V and cluster VI (D²=7.39) expressing less divergence between the genotypes of these cluster pairs or we could say they were genetically similar to each other (Table 6).

The variance for cluster means for all the characters indicated that the maximum variation was accounted for number of capsules plant⁻¹ (1702.43) followed by plant height (114.36), bud fly infestation % (88.72), days to 50 % flowering (32.12), powdery mildew infestation % (27.37), seed yield plant⁻¹ (19.70), number of branches plant⁻¹ (8.41), alternaria infestation% (8.24), flower size (5.72), days to maturity (0.94), 1000 seed weight (0.68). A wide variation has been confirmed from one cluster to another in respect of cluster mean from the above observation, which pointed out that genotypes having distinct mean performance for various characters were separated into different clusters. Similar findings were also observed by Fulkar *et al.*, (2007) [4] and Kanchan and Rao (2008) [5]. (Table 7). All possible cluster combinations beyond the mean statistical distance $\overline{D}$ = 10.56 have been arranged in descending order in Table 6. The maximum inter-cluster distance. ($\overline{D}$ =33.36) was observed between the cluster I and cluster XII. The genotype showing highest mean superiority for seed yield plant⁻¹, number of capsules plant⁻¹ are included in cluster XII is EC0041764. Check i.e., PKV NL 260 showing mean superiority in bud fly resistance included in cluster I. Other parents which showed bud fly resistance, number of capsules plant⁻¹, seed yield plant⁻¹ are EC0541224, EC0541218-A, EC0006160, EC0001388, EC41765, EC07188299, EC0541225, EC004181, EC0718828, included in clusters III x XII ($\overline{D}$ =29.51), EC041643 in cluster IX x XII ($\overline{D}$ = 27.31), EC0541218 in cluster IV x XII ($\overline{D}$ = 29.36), EC0041735 in cluster V x XII ($\overline{D}$ = 33.21) were significantly superior for seed yield plant⁻¹ with resistance in bud fly infestation over the other parents and were identified potential parents for further hybridization programme (Table 8). In conclusion, an appreciable extent of genetic divergence was observed among 178 genotypes of linseed. On the basis of the above analysis, it can be concluded that the selection of parental material for hybridization programme must be carried out from the farthermost clusters showing superior mean performance may help in obtaining transgressive segregants or heterotic cross, which may help in booming seed yield instead of those based on geographic diversity, which might not be a fruitful exercise for the finding of useful divergent parents.

Table 3: Grouping of genotypes into different clusters

Cluster	Number of genotypes	Name of the genotypes
I	130	EC41659, EC41741, EC98994, EC51904, EC0541202, EC99001, EC0041700, EC0399084, EC0041469, EC0541194, EC0110474, EC0541198, EC0022388, EC0001443, EC0001550-B, EC0001459, EC1628, EC0001437, EC0007005-B, EC0118743, EC1645, EC0041734, EC0001433, EC0041467, EC80490, EC0001476, EC0041720, EC0541195, EC1066, EC1386, EC1588, EC45890, EC0041687-A, EC41623, EC0041762, EC0541227, EC0520246, EC14539, EC0000526, EC0541205, EC0001457, EC1474, EC1424, EC0041672, EC541196, EC0115174, EC0399086, EC0041528, EC0001432, EC0520247, EC0041562, EC0718850, EC0541212, EC0009827, EC0041753, EC0041672-1, EC0041601-A, EC0541213, EC0541223, EC0541226, EC541194, EC0541226, EC0022872, EC0000541-A, EC0041621, EC0541215, EC41466, EC0541213, EC0541215, EC541196, EC0041650, EC0000522, EC0541210, EC0399082, EC0541220, EC041667, EC0041621-B, EC0041737, EC0041400, EC0000531-A, EC0001395, EC0041723, EC0001551, EC0041774-A, EC0041687, EC0041607-2, EC00414678-B, EC0041768, EC244634, EC0001475, EC0041478, EC0041647, EC0541219, EC054214, EC0455084, EC0718826, EC0718831, EC0001395-1, EC0041615, EC0041649, EC0041622, EC0541203, EC0115148, EC0541207, EC00411623, EC0041644, EC0041758, EC0110289, EC0158985, EC22648, EC0002711, EC0041535, EC0541204, EC0541216, EC0718824, EC0718834, EC718830, EC718835, EC0718842, EC0718843, EC0718847, EC0080490, EC0001396, EC0718851, EC0541213, EC0041646, EC000545, PKV-NL-260, TL 99.
II	27	EC0041619, EC0001451, EC22813, EC718846, EC0541217, EC0541201, EC718823, EC0041582, EC000564, EC0041598, EC0718845, EC0041579, EC0718825, EC0041726, EC0001465, EC0011748, EC0000538, EC0718852, EC0041755, EC0022813-B, EC0399085, EC0541211, EC0041601-A, EC0001403, EC004154-A, EC054119, EC001419.
III	11	EC0006160, EC0541218-A, EC0001388, EC0041765, EC07188229, EC0718827, EC0541224, EC541225, EC0041495-1, EC004181, EC0718828.
IV	1	EC0541218
V	1	EC0041735
VI	1	EC0041653
VII	1	EC541206
VIII	1	EC0012538
IX	1	EC041643
X	1	EC0000543
XI	1	EC0023208
XII	1	EC0041764
XIII	1	EC0718848

Table 4: Values of first five vectors

Sr. No.	Characters	Vector I	Vector II	Vector III	Vector IV	Vector V
1	Plant height	0.04334	0.00538	0.04725	0.05943	0.39798
2	Number of capsules plant[-1]	0.54752	0.42177	-0.00643	0.60411	0.10726
3	Number of branches plant[-1]	0.28401	0.21298	-0.34286	-0.14649	-0.48986
4	Alternaria infestation %	0.49345	-0.74698	-0.23600	0.14944	-0.15912
5	Bud fly infestation %	0.08043	-0.08855	-0.11063	-0.23048	0.11313
6	Powdery mildew infestation%	0.09262	0.30127	-0.20161	-0.32967	-0.36487
7	Days to maturity	-0.03188	0.22239	0.03688	0.03430	0.05820
8	1000 seed weight	0.00987	-0.22705	0.20514	-0.18502	0.09381
9	Days to 50% flowering	0.14634	0.10855	-0.49427	-0.43731	0.43473
10	Seed yield plant[-1]	0.57158	0.08239	0.60862	-0.44419	0.10213
11	Flower size	-0.09950	-0.02369	0.33679	-0.04435	-0.45529

Table 5: Five canonical roots and their contribution expressed as per cent of the total variation

Root	Eigen value	Contribution in per cent
$\lambda 1$	8333.82	31.53
$\lambda 2$	4930.19	18.65
$\lambda 3$	3780.96	14.31
$\lambda 4$	3010.00	11.39
$\lambda 5$	1871.35	7.08
Total	21926.32	82.96
Sum of all canonical roots		100
Residual		17.04

Table 6: Average intra and inter cluster distance D^2 values

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	13.57	20.24	20.26	18.46	20.97	20.78	16.58	16.86	22.90	18.48	17.68	33.36	27.48
II		16.76	21.30	23.24	19.06	18.88	21.91	22.32	19.16	19.18	20.90	24.44	27.12
III			18.71	22.66	24.51	25.22	22.25	26.96	22.15	21.12	22.99	29.51	25.98
IV				0.00	27.13	28.69	25.16	17.80	26.25	23.21	23.77	29.36	37.40
V					0.00	7.39	15.71	26.14	12.05	27.29	25.38	33.21	25.31
VI						0.00	14.56	24.34	14.38	25.37	23.69	32.94	26.71
VII							0.00	23.54	16.97	24.31	22.49	37.76	26.22
VIII								0.00	29.44	18.07	18.00	32.33	35.91
IX									0.00	26.81	28.50	29.72	27.31
X										0.00	11.07	27.69	28.00
XI											0.00	33.08	27.61
XII												0.00	40.20
XIII													0.00

$^-$D = 10.56, Bold figures are average intra cluster distance

Table 7: Cluster means for eleven characters

Cluster	Plant Height (cm)	No. of Capsules plant[-1]	No. of branches plant[-1]	Alternaria infestation %	Bud fly infestation %	Powdery mildew infestation %	Days to maturity	1000 seed weight (g)	Days to 50 % flowering	Seed yield plant[-1] (g)	Flower size (mm)
1	57.20	68.08	5.98	3.44	16.09	16.87	105.99	8.67	57.98	1.61	21.00
2	58.34	102.43	7.55	5.97	23.56	18.25	106.05	9.37	59.51	3.21	20.69
3	61.88	117.30	7.64	4.29	21.65	23.00	106.39	8.32	65.69	1.72	15.59
4	76.33	125.33	4.93	1.40	4.67	13.33	106.00	10.30	51.67	1.87	20.88
5	62.83	79.60	6.00	9.50	15.83	14.67	106.00	8.53	55.00	1.85	21.88
6	53.50	69.07	4.00	9.17	22.02	14.67	105.00	8.83	59.00	2.28	22.88
7	69.33	49.37	4.80	6.17	19.23	9.33	106.33	9.40	66.00	1.02	20.38
8	48.17	55.00	4.50	1.60	15.73	10.67	103.33	10.20	50.00	3.08	25.88
9	77.17	128.17	6.57	8.87	35.17	9.33	106.67	9.60	61.00	1.52	19.38
10	52.33	75.67	8.17	2.37	43.00	30.67	107.00	9.40	62.00	3.17	21.88
11	53.83	38.13	7.00	3.17	20.67	40.67	106.67	9.80	61.33	2.90	22.88
12	62.50	186.70	6.93	5.20	25.17	14.67	107.00	8.40	62.00	5.83	19.38
13	39.50	63.83	15.50	7.70	19.00	26.67	106.00	7.40	70.33	1.13	19.88
SD	10.69	41.26	2.9	2.87	9.42	5.23	0.97	0.82	5.67	4.44	2.4
VAR	114.36	1702.43	8.41	8.24	88.72	27.37	0.94	0.68	32.12	19.70	5.72

Table 8: Selection of genotypes based on inter cluster distances and cluster means

Clusters	Distance between clusters	Selection based on Seed yield plant⁻¹ and bud fly infestation%
I & XII	33.36	PKV NL 260 X EC0041764
V & XII	33.21	EC0041735 X EC0041764
III & XII	29.51	EC0006160XEC0041764, EC541218-AXEC0041764, EC0541224XEC0041764, EC0001388XEC0041764, EC41765XEC0041764, EC07188229XEC0041764, EC0718828XEC0041764, EC541225XEC0041764, EC004181X EC0041764
IV & XII	29.36	EC0541218XEC0041764
IX & XII	27.31	EC041643XEC0041764

References

1. Abdul NM, Mulani RM. Genetic diversity in indigenous and exotic linseed germplasm (Linum usitatissimum L.). Electronic Journal of Plant Breeding. 2015 Nov 11;6(3):848-854.
2. Ananda II and Murty BR. Genetic divergence and hybrid performance in linseed. Indian J. Genet. 1968;28:178-185.
3. Chauhan MP, Singh S, Singh AK. Post-harvest Uses of Linseed. Journal of Human Ecology. 2009 Dec 1;28(3):217-219.
4. Fulkar PL, Ghorpade PB, Maheswari JJ, Patil SR, Reddy MN, Pavithran C. Evaluation of linseed germplasm for genetic divergence and choice of parents. Journals of Soil and Crops. 2007;17(2):333-338.
5. Kumari K, Rao SS. Genetic divergence in linseed (Linum usitatissimum L.). Journal of Agricultural Sciences. 2008;42(1):15-19.
6. Khan MA, Mirza MY, Amjad M. Assessment of genetic diversity in germplasm of linseed (Linum usitatissimum L.). Pakistan J. Agric. Res. 2013 Sep 1;26(3):178-184.
7. Mahalanobis PC. A statistical study at Chinese head measurement. Asiatic Society. Bengal. 1928;25(3):301-77.
8. Mahto JL, Singh SN. Genetic divergence in linseed under rain fed conditions of Chotanagpur. J. Res. 1996;6(8):85-87.
9. Moll RH, Robinson RF. Heterosis and genetic diversity in variety crosses of maize. Crop Sci. 1962 May;2(3):197-209.
10. Nizar MA, Mulani RM. Genetic diversity in indigenous and exotic linseed germplasm (Linum usitatissimum L.). Electronic Journal of Plant Breeding. 2005 Nov 11;6(3):848-854.
11. Rao CR. Advanced statistical methods in biometrical research. 1st Edition. John Wiley and Som, New work; c1952. p. 390.
12. Savita SG. Diversity of linseed germplasm for yield and yield components. M. Sc. (Agriculture) in Genetics and Plant Breeding. Dissertation. Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad; c2006. p. 108.
13. Shafi N. Crop Production. National Book Foundation, Islamabad; c1994. p. 36.
14. Murty BR, Arunachalam V. The nature of divergence in relation to breeding systems in some crop plants. Indian Journal of Genetics and Plant Breeding. 1966;26:188-98.
15. Dhirhi R, Prasad K, Shukla AK, Sarkar S, Renganathan T, Pushpavanam S, Kaza M. Experimental study of rotating dry slag granulation unit: operating regimes, particle size analysis and scale up. Applied Thermal Engineering. 2016 Aug 25;107:898-906.
16. Dhirhi R, Prasad K, Shukla AK, Sarkar S, Renganathan T, Pushpavanam S, Kaza M. Experimental study of rotating dry slag granulation unit: operating regimes, particle size analysis and scale up. Applied Thermal Engineering. 2016 Aug 25;107:898-906.
17. Pali V, Mehta N, Verulkar SB, Xalxo MS, Saxena RR. Molecular diversity in flax (Linum usitatissimum L.) as revealed by DNA based markers. Int J Plant Res. 2015;28:157-65.
18. Paul J, Parthasarathy S, Gupta P. Exporting challenges of SMEs: A review and future research agenda. Journal of world business. 2017 Apr 1;52(3):327-42.
19. Kumar S, Soukup M, Elbaum R. Silicification in grasses: variation between different cell types. Frontiers in Plant Science. 2017 Mar 28;8:438.