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GENETIC VARIABILITY, EVALUATION AND CHARACTERIZATION OF SUNFLOWER (*HELIANTHUS ANNUUS* L.) GERMPLASM

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Keywords: Characterization, Evaluation, Genetic variability, Sunflower

Abstract

Fifty accessions of sunflower germplasm were characterized and evaluated for seed yield and its components traits to study the variability present among different germplasm lines. Significant amount of genetic variability was observed for all the characters under study. Seed yield and hull content were identified for highest genotypic (27.08 and 20.14%, respectively) and phenotypic coefficients of variation (27.89 and 20.64%, respectively) and also for high heritability (97.46 and 97.28%, respectively) coupled with high genetic advance (52.19 and 40.49%, respectively) over mean followed by duration of reproductive phase, oil content, 100-seed weight and plant height. Qualitative traits also showed wide variation among the accessions. Majority of the accessions were early in flowering, medium in maturity and medium in head diameter. Among all the accessions, ten lines were observed with short height and ten lines showed high oil content (> 40%). Maximum genetic distance was observed between the accessions EC-601800 and EC-512687 and utilization of these accessions has been advocated in breeding programme. The results of the present study can be useful for the formation of data base and reference lines, genotype identification and will also be helpful in amplification of future sunflower improvement programme.

Introduction

Sunflower (*Helianthus annuus* L.) is an important oilseed crop, which belongs to the genus '*Helianthus*' of the family Asteraceae. It is widely adopted and accepted for its high quality and nutritional edible oil. Due to its high economic importance, the developments of effective hybrids are required with superior yield and quality traits. Presence/existence of ample amount of genetic variability is prerequisite before embarking any breeding programme. Information of variability and heritability is useful to formulate selection criteria for improvement of seed yield and its component traits. Heritability estimates along with genetic advance is a more reliable measure in predicting the expected performance/progress to be achieved during selection. Hence, variability present in a gene pool of a crop species is important to plant breeder for breeding programme. The coefficients of variation expressed at phenotypic and genotypic levels are used to compare the variability among different characters for identifying the character association and selection of the superior genotype. A wide range of variation has been reported for seed yield and seed number (Velkov 1980) and other important yield attributing components (Virupakshappa and Sindagi 1988) in sunflower. The heritability estimates aid in determining the relative amount of heritable portion in variation and thus help plant breeder in selecting the elite lines from a diverse population. However, the heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. Classification of germplasm based on agronomic characters plays an important role in plant breeding to select valuable genetic resources to be utilized later in different breeding programmes. Further, characterization could be utilized for varietal identification in seed production programmes, maintaining the genetic purity of a genotype, and also DUS testing becomes easy in a well characterized genotype. Germplasm

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of a specific crop collected from the diverse sources offers greater genetic diversity and may further useful to widen the genetic base of crop species. Hence, the present study was conducted to evaluate the extent of genetic variability, heritability and genetic advance over mean for seed yield and its components traits in sunflower. Moreover, the present material was also characterized based on quantitative (8) and qualitative (26) traits by giving scores in accordance with the standard DUS guideline on sunflower.

Materials and Methods

The present study was conducted in the research farm of the Oilseeds Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, Haryana, India. Monthly average temperature (maximum and minimum) and rainfall during the research period are presented in Fig. 1.

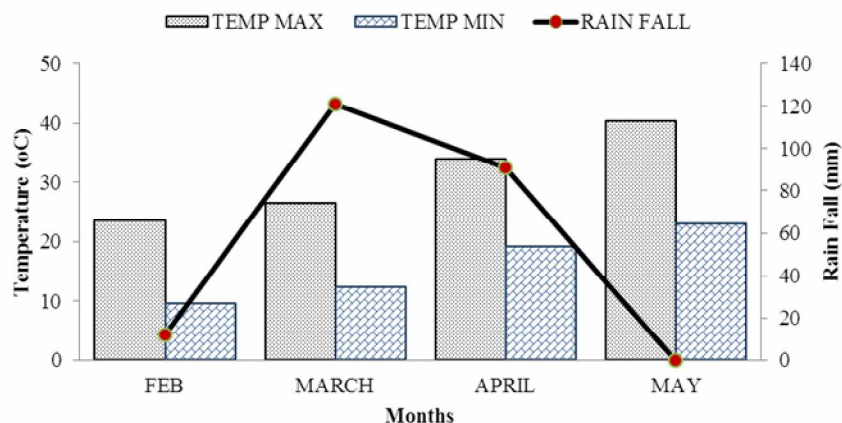


Fig.1. Monthly, average temperature (°C) and rainfall (mm) during crop season 2015.

The present study comprised 50 germplasm of sunflower lines, maintained by the Oilseeds Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar.

The experiment was laid out in a randomized complete block design (RCBD) with three replications, in spring season, 2015 having double row plot of 3.5 m length of each accession per replication maintaining row to row and plant to plant distance of 60 and 30 cm, respectively. Standard agronomic practices were performed uniformly for all the experimental units.

At maturity five plants from each accession were selected randomly for recording of data on yield and its related characters *viz.* days to 50% flowering, duration of reproductive phase (days), days to maturity, plant height (cm), stem girth (cm), head diameter (cm), seed yield (g), 100-seed weight (g), seed volume weight (g/100 ml), hull content (%) and oil content (%). The accessions were characterized on the basis of recommended qualitative characters as per DUS guidelines (Dhillon *et al.* 2010).

The genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were computed according to the methods suggested by Burton and Devane (1953), heritability (h^2) by Hanson *et al.* (1956) and expected genetic advance over mean (GAM) as suggested by Johnson *et al.* (1955). Dendrogram was prepared to form different clusters of accessions and to estimate genetic similarities among these by using the software XLSTAT.

Results and Discussion

The analysis of variance revealed highly significant differences for all characters (Table 1). Mean, range, genotypic and phenotypic coefficients of variation, heritability and genetic advance in *per cent* of mean for the respective characters were estimated (Table 2). The range of variation was maximum for plant height (102.00 – 169.07 cm) followed by seed yield (13.83 - 50.93 g) and hull content (31.13 - 65.70%), while it was lowest in the case of 100-seed weight (3.46 - 6.47 g) and stems girth (5.67 - 8.73 cm). The values of PCV were marginally higher than GCV. This indicates that the large amount of variation was contributed by genetic component and least by environment. Duration of reproductive phase and stem girth was most affected by environment as compared with the other characters. Very high values of PCV and GCV were obtained for seed yield (27.08 and 27.89%), hull content (20.14 and 20.64%), duration of reproductive phase (17.95 and 19.55%) and oil content (15.16% and 15.28%), which indicates significant role of these characters in the improvement of breeding programmes. These results are similar with those of Virupakshappa and Sindagi (1988), Gangappa (1991), Suma and Virupakshappa (1994), Patil *et al.* (1996), Reddy and Reddy (2006), Kalukhe *et al.* (2010). Moderate levels of PCV and GCV were obtained for the 100-seed weight, plant height, head diameter, seed volume weight and stem girth in the decreasing order of magnitude. These results are in agreement with the results obtained by Patil *et al.* (1996). However, low values were obtained for days to maturity (3.70 and 3.83%) (Satisha 1995). Seed yield per plant was identified for having high heritability (97.46%) while lowest for stem girth (57.50%).

Table 1. Analysis of variance for seed yield and yield component in sunflower.

Source of variation	Mean sum of square			CV (%)
	Replication	Genotype	Error	
	df	2	49	
Seed yield per plant (g)	15.802	284.142**	16.100	11.495
Days to 50% flowering (days)	4.740	46.324**	16.951	6.573
Duration of reproductive phase (days)	4.037	16.529**	3.250	11.734
Days to maturity (days)	3.927	46.357**	17.403	4.513
Plant height (cm)	13.716	1003.689**	15.507	3.080
Stem girth (cm)	2.116	1.271**	0.251	6.758
Head diameter (cm)	0.787	4.344**	1.091	8.332
100-seed weight (g)	0.062	1.852**	0.196	8.983
Seed volume weight (g/100 ml)	2.796	27.326**	2.228	4.178
Hull content (%)	17.387	311.118**	14.827	7.804
Oil content (%)	1.194	86.412**	1.331	3.284

Estimates of high heritability obtained by these characters were governed by additive gene effects (Panse 1957) and these characters are amendable for improvement by selection, particularly through mass selection (Krishnawat and Sharma 1988, Ashok *et al.* 2000). The high heritability magnitude indicates the reliability, which represent the high chance of the genotype to be recognized by its phenotypic expression. This result is in accordance with the previous results (Mogali 1993, Satisha 1995, Manjula 1997). Moderate heritability of oil content was reported by Fick 1974, Gangappa 1991, Makane *et al.* 2011).

The genetic advance in per cent of mean varied from 7.37 to 54.19 for days to maturity and seed yield per plant, respectively. High heritability values coupled with high genetic advance in per cent of mean was recorded for seed yield per plant, hull content and duration of reproductive phase. This indicates generous scope for improving these characters through simple selection. Similar results were also reported by Srivastava and Mishra (1976) and Singh *et al.* (1977). High heritability coupled with moderate genetic advance was observed for plant height, 100-seed weight and head diameter. Similar results were reported earlier by Manjula (1997) and Lakshmanaiah (1980). High heritability along with low genetic advance was noticed for the days to maturity, stem girth and days to 50% flowering and these results were in conformity with those of Kshirsagar *et al.* (1995) and Satisha (1995).

Table 2. Range, mean, coefficients of variation, heritability and genetic advance for 11 quantitative traits in sunflower.

Characters	Mean \pm SE	Range		Coefficient of variation		Heritability (b.s.)	Genetic advance	GAM
		Min.	Max.	Genotypic	Phenotypic			
SY	34.90 \pm 2.32	13.83	50.93	27.08	27.89	97.46	18.91	54.19
DF	62.64 \pm 2.38	56.33	71.33	6.20	6.27	93.06	7.90	12.61
RP	15.36 \pm 1.04	10.97	19.67	17.95	19.55	90.34	5.44	33.95
DM	92.43 \pm 2.41	86.33	101.00	3.70	3.83	82.63	6.46	7.37
PH	127.85 \pm 2.27	102.00	169.07	14.20	14.31	95.50	37.10	29.02
SG	7.42 \pm 0.29	5.67	8.73	7.86	8.78	57.50	1.08	14.50
HD	12.54 \pm 0.60	9.83	15.07	11.26	11.73	79.73	2.80	22.27
SW	4.93 \pm 0.26	3.46	6.47	15.06	15.93	73.76	1.45	29.33
SVW	35.73 \pm 0.86	30.52	45.52	8.10	8.45	78.97	5.71	15.98
HC	49.34 \pm 2.22	31.13	65.70	20.14	20.64	97.28	19.98	40.49
OC	35.13 \pm 0.67	27.35	45.81	15.16	15.28	95.52	10.89	30.99

GAM= Genetic advance as % of mean, SY = Seed yield per plant (g), DF = Days to 50% flowering (days), RP = Duration of reproductive phase (days), DM = Days to maturity (days), PH = Plant height (cm), SG = Stem girth (cm), HD = Head diameter (cm), SW = 100-seed weight (g), SVW = Seed volume weight (g/100 ml), HC = Hull content (%) and OC = Oil content (%).

Classification and characterization of all 50 sunflower accessions into different categories of quantitative traits was done (Table 3). The accession MR-6 showed the highest stem girth (8.7 cm) and seed volume weight (45.5g) and EC-512687 exhibited late maturity (97 days); highest plant height (169 cm). Encheva *et al.* (2008) and Onemli and Gucer (2010) reported significant differences in plant height, head diameter, and period of flowering of sunflower wild genotypes. The accessions RHA-265, HRHA-271-P3, RHA-297-P2, IB-43, ACC-350-2, MSF-1-7, AH-14, IHT-201, IHT-298, NDR-2 and GPB-07 showed early flowering (< 60 days) but considering maturity ACC-350-2 (86 days) was the earliest; but accessions EC-601746, EC-512687 and EC-601800 (71 days) were late in flowering but EC-512687, EC-152681 and EC-601746 (\geq 100 days) took highest number of days to mature which exhibited direct relation between earliness or lateness in flowering and maturity. Considering plant height EC-512687 was the tallest (169 cm) and MSF-2-16 (102 cm) was dwarf. Head diameter was largest in EC-152673 (15.1 cm); EC-152686 and EC-152687 (14.7 cm) but smallest in ACC-350-2 (9.8 cm). Considering oil per cent, the genotype MSF-1-4 (45.8%) produced the highest mean along with duration of reproductive

period (21) and EC-152686 (27.3%) produced the lowest mean oil content. Considering 100-seed weight, the genotype RHA-265 P₃ had the highest mean of 6.5 g and revealed to be a promising accession for confectionary purpose. Accessions which have high seed weight and oil content are categorized as potential accessions because seed weight is one of important considerable yield components (Dehkhoda *et al.* 2013, Rafiei *et al.* 2013, Ion *et al.* 2015). The lowest hull content (31%) was recorded from MR-6 and highest in HB-15 (65%). Maximum seed yield per plant was observed in accession EC-601755 (50.9g) followed by 1-OH-07-41 and GPB-6, which can be used for breeding for high yielding lines.

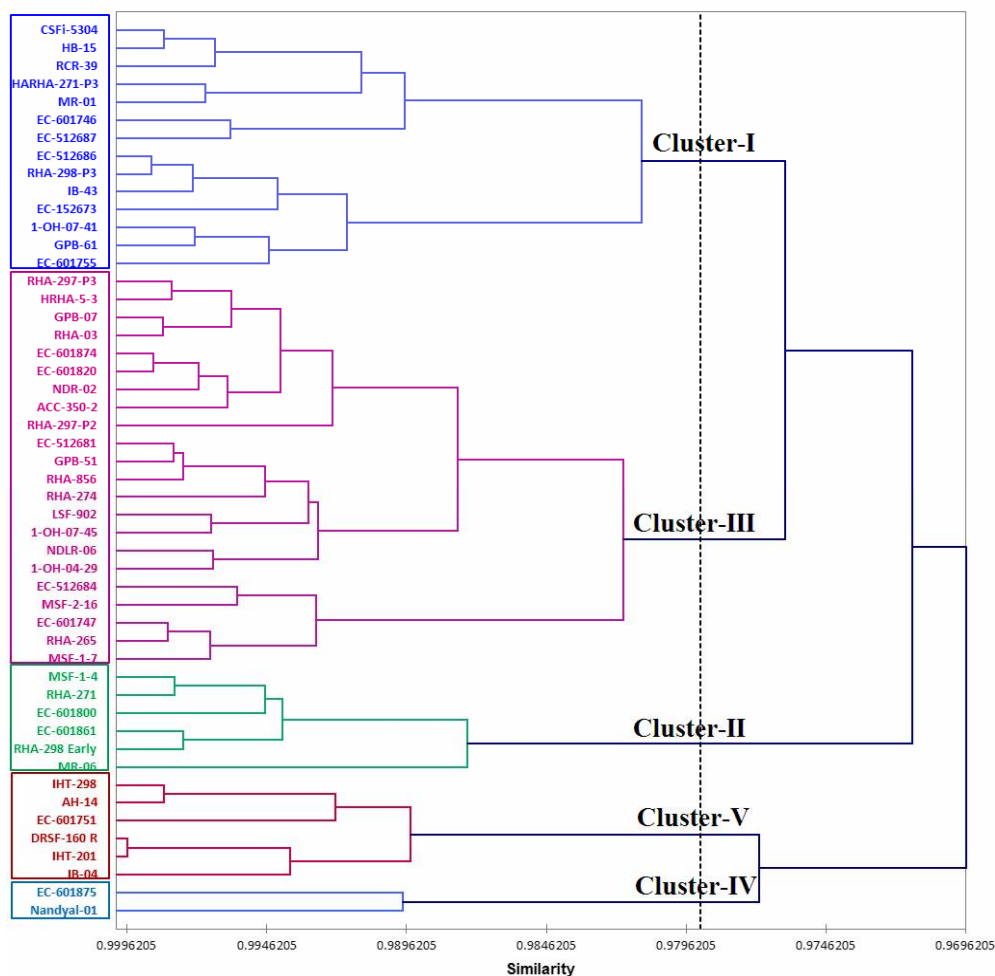


Fig. 2. Dendrogram showing the genetic distances amongst different sunflower accessions.

Qualitative traits such as leaf blistering, leaf colour, leaf serration, stem pigmentation and ray floret: shape, colour etc. were examined after 60 days after sowing. Classification and characterization of all the sunflower accessions on the basis of qualitative traits are presented in Table 4, which indicate wide variation for all the qualitative characters (except pollen colour) which is in conformity with the results reported by Makane *et al.* (2011). Tan and Tan (2011) also reported that the morphological variation on the characters was high. Out of 50 accessions, most

of accessions were absent for hypocotyl anthocyanine pigmentation, medium leaf size, cordate leaf shape, green leaf colour, medium leaf bristles, acute angle, erect leaf orientation of blade, elongate and yellow ray floret, convex head shape and black base colour of seed coat with grey strip. Sixty per cent of accessions were medium and 38% were coarse for leaf serration. This character could be used to distinguish extreme genotypes (Diederichsen 2010). About 50% and 99% accessions were absent on leaf petiole and bract anthocyanine pigmentation, respectively.

Table 3. Grouping of germplasm on the basis of quantitative characters.

Sl. No.	Characteristics	Expression	No. of accessions	Percentage
1	Days to 50% flowering (days)	Early (>60)	11	22
		Medium (60-75)	39	78
		Late (>75)	0	0
2	Plant height (cm)	Very short (<80)	0	0
		Short (80-110)	10	20
		Medium (111-140)	23	46
		Tall (141-170)	14	28
		Very tall (>170)	3	6
3	Head diameter (cm)	Small (<15)	35	70
		Medium (15-20)	15	30
		Large (>20)	0	0
4	Ray floret (number)	Few (<30)	1	2
		Medium (30-40)	27	54
		Many (>40)	22	44
5	100 seed weight	Low (<4)	12	24
		Medium (4-6)	32	64
		High (>6)	6	12
6	Seed length (cm)	Short (<1)	28	56
		Medium (1-1.5)	22	44
		High (>1.5)	0	0
7	Hull content (%)	Low (<25)	0	0
		Medium (25-30)	0	0
		High (>30)	50	100
8	Oil content (%)	Low (<35)	23	46
		Medium (35-40)	19	38
		High (40-43)	2	4
		Very high (>43)	6	12

Table 4. Grouping of germplasm on the basis of qualitative characters.

Sl. No.	Characteristics	Expression	No. of accessions	Percentage
1	Anthocyanin pigmentation	Absent	41	82
		Medium	6	12
		Strong	3	6
2	Leaf size (cm)	Small (<15)	5	10
		Medium (15-25)	37	74
		Large (>25)	8	16
3	Leaf shape	Lanceolate	0	0
		Triangular	5	10
		Cordate	42	84
		Rounded	3	6
4	Leaf colour	Light Green	9	18
		Green	33	66
		Dark Green	8	16
5	Leaf blistering	Absent	3	6
		Medium	31	62
		Strong	16	32
6	Leaf serration	Fine	1	2
		Medium	30	60
		Coarse	19	38
7	Leaf angle of lateral veins	Acute (<90°)	43	86
		Obtuse (>90°)	7	14
8	Leaf orientation of blade	Erect	31	62
		Drooping	19	38
9	Leaf petiole anthocyanin pigmentation	Absent	25	50
		Present	25	50
10	Stem pigmentation	Absent	49	98
		Present	1	2
11	Ray floret: Shape	Elongated	42	84
		Ovate	8	16
		Rounded	0	0
12	Ray floret: Colour	Light yellow	8	16
		Yellow	34	68
		Orange	6	12
		Purple	2	4
13	Disk floret: Colour	Yellow	13	26
		Orange	17	34
		Purple	20	40
14	Disk floret: Anthocyanin pig. of stigma	Absent	19	38
		Medium	19	38
		Strong	12	24

(Contd.)

Sl. No.	Characteristics	Expression	No. of accessions	Percentage
15	Disk floret: Pollen colour	White	0	0
		Yellow	50	100
16	Bract: Shape	Elongated	26	52
		Rounded	24	48
17	Bract: Anth. pign.	Absent	49	98
		Present	1	2
18	Plant: Natural position of closest lateral head to central head	Above	5	29.41
		Below	12	70.59
19	Head: Attitude	Inclined	9	18
		Vertical	21	42
		Half turned down	15	30
		Turned down	5	10
20	Head: Shape of grain side	Concave	3	6
		Flat	11	22
		Convex	29	58
		Irregular	7	14
21	Plant: Branching	Absent	33	66
		Present	17	34
22	Plant: Type of branching	Basal	0	0
		Overall	7	14
		Apical	10	20
23	Seed : Shape	Elongated	9	18
		Ovoid elongated	22	22
		Ovoid wide	19	38
24	Seed coat: Base colour	White	0	0
		Grey	2	4
		Brown	11	22
		Black	37	74
25	Seed coat: Stripe	Absent	30	60
		Present	20	40
26	Seed coat: Colour of stripe	White	1	5
		Grey	17	85
		Brown	2	10
		Black	0	0

Cluster analysis indicates the extent of genetic diversity in the material that could be used as parental lines in future breeding programmes (Sultana and Ghafoor 2008). The association among different accessions is presented in the form of dendrogram (Fig. 2) prepared using agglomerative hierarchical clustering methods (XLSTAT). Based on quantitative traits, all sunflower accessions by cluster analysis were divided into 5 groups. From the Fig. 2, most of the accessions were included in cluster III and I (22 and 14 accessions) followed by cluster II, cluster V (6 accessions) and cluster IV contains only two accessions. The accessions, which are lying nearer to each other in the dendrogram are more similar to one another than those lying away from each other. The

present dendrogram shows the relatively high magnitude of resemblance among the sunflower accessions in different clusters. Interestingly, the accession CSFI-5304 showed the extreme place from Nandyal-01 meaning thereby that they had maximum genetic distance between them. Likewise the positional distances between all the accessions on X-axis represent the genetic distances between these accessions and use of the accessions with maximum genetic distance is promoted in crossing programmes to develop sunflower hybrids with desirable combination of traits in them.

Table 5. Promising accessions of sunflower for different characters.

Characters	Accessions
Days to 50% flowering (<60 days)	RHA-265, MSF-1-7, HRHA-271-P ₃ , RHA-297-P ₂ , ACC-350-2, IHT-201, GPB-07, IB-43, MSF-2-16, DRSF-160 R, MSF-1-4, AH-14, IHT-298 and 1-OH-07-45.
Days to maturity (<90 days)	ACC-350-2, RHA-271, RHA-265, MSF-1-7, HRHA-271-P ₃ , IB-4, EC-601875, MR-1, MSF-2-16, CSFI-5304, MSF-1-4, DRSF-160 R, GPB-61 and EC-601751.
Head diameter (>15 cm)	RHA-297-P ₂ , RHA-298-P ₃ , MSF-1-7, IHT-201, 1-OH-07-41, 1-OH-07-45, CSFI-5304, LSF-902, NDLR-06, EC-152673, EC-512684, EC-512686, EC-601751, EC-601755 and EC-601874.
Plant height (<110 cm)	RHA-265, RHA-297-P ₂ , Nandyal-1, IB-4, ACC-350-2, MSF-2-16, MSF-1-7, IHT-298, AH-14 and EC-601875.
100-seed weight (>6 g)	RHA-297-P ₂ , RHA-298-P ₃ , AH-14, GPB-51, 1-OH-04-29 and NDLR-06.
Oil per cent (>40 %)	MSF-1-4, MR-6, EC-601800, EC-512681, RHA-271, 1-OH-07-41, EC-152673, EC-152687, MSF-2-16 and EC-512684.

The selection based on seed yield, plant height, duration of reproductive phase, hull content and oil yield would be more productive. As the selection is valuable for those characters having high heritability with high genetic advance, the lower variability coefficients for days to maturity indicated that there was less genetic variation for this trait in the material evaluated. No accession was found to be promising for all the quantitative characters. However, some accessions could be identified as promising for different traits (Table 5). Thus, a gene pool can be generated by constituting the germplasm lines of interest or by creating a broad based cross. Such material could be useful as a base population to develop promising populations and lines.

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(Manuscript received on 23 May, 2018; revised on 18 October, 2018)