



Research Article

IDENTIFYING PROMISING GENOTYPES FOR GENETIC DIVERGENCE AND PATH ANALYSIS IN SOYBEAN

[*Glycine max* (L.) Merr.]

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Abstract: Forty elite genotypes collected from different sources were evaluated for path analysis and genetic divergence studies. Forty genotypes were grouped into twelve groups with differing levels of divergence based on D_2 analysis. These genotypes were quite different, according to D_2 analysis, with D_2 values ranging from 6.94 to 26.25. The largest inter-cluster distance (28.25) was found between clusters IV and XII. The two clusters with the shortest inter-cluster distances, IV and V, were 6.94. Cluster VI (12.88) has the largest intra-cluster distance. In contrast, clusters III, IV, V, VII, VIII, IX, X, and XII only had one genotype. From the path analysis studies, we can conclude that the quantity of seeds produced per plant had positive direct effect with the traits like days to maturity, number of pods per plant, number of seeds per pod, number of branches per plant, weight of 100 seeds, and protein content. The genotypes KDS-344, DS-228, JS-335, JS-9305, HIMSO-1691, NRC-128, MACS-1701, MAUS-768, MacS-450, MACS-NRC-1647, may be useful for upcoming crop improvement programmes based on the examined divergence classes during this research project.

Keywords: Soybean, Genetic divergence, Path analysis, Significance

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Introduction

Soybean is an annual plant with a short, upright, semi-spreading to spreading growth habit and a broad range of heights, belonging to the family fabaceae (Leguminosae), sub family Fabioideae and genus Glycine. It is a diploid crop with basic chromosome number of $2n = 40$ that self-pollinates naturally. It is an important and extensively used oil seed crop that is farmed all over the world.

Because of its many industrial, nutritional, and agricultural applications, it is also known as the "miracle bean" or the "golden bean." Soybeans are rich in nutrients. It has around 38–42% high-quality protein and 18–20% oil that has been enhanced with essential fatty acids. Moreover, it contains 5% minerals and 35% carbs. The term "poor man's meat" refers to soybeans because of their high protein content and nutritional worth. It also contains isoflavones, which are good for human health and help prevent a number of illnesses like diabetes, cancer, osteoporosis, and coronary heart disease [1].

Nine oil crops—mustard, soybean, groundnut, sesamum, sunflower, linseed, safflower, niger, and rapeseed—are the primary source of vegetable oils in the nation. These seeds are typically grown over an area of around 26 million hectares under rain-fed conditions. Whereby more than 88% of the overall oil seed output is accounted for by soybean (34%), groundnut (29%) and mustard (27%).

Meanwhile, more than 80% of vegetable oil comes from mustard (35%), soybean (23%) and groundnut (25%). India is the world's largest importer of vegetable oils (15%), behind China and the US, and is heavily dependent on imports to satisfy its demand for edible oils. About 60% of imported edible oils are made up of palm oil, with soybean and sunflower oils coming in second and third, respectively. During the past few decades, there has been a significant increase in imports of edible oils [2]. Soybean is a highly self-pollinated crop and have minimum natural variation which result in limited chances for selection. The study of genetic variability offers selection of suitable parents for the combination of proper traits or allele in crop improvement programme. Genetic diversity is the study of diversity within a species. If there is more diversity, then the chances of selection of desirable genotypes for hybridization will be more.

This research will assist soybean farmers in lowering production losses and allowing crop harvesting to be postponed for two to three weeks in the case of a labour problem. Study of existing variability among the genotypes would provide wider base for selection [3-10].

Material and Method

The current research was carried out in the *Kharif* season of 2021 at the Post Graduate Research Farm, Botany Section, College of Agriculture, Dhule, Maharashtra. The following provides a description of the specific materials utilised, techniques employed, and statistical analysis performed throughout the inquiry. The experimental material used for the study consisted of 40 genotypes of soybean were obtained from Agricultural Research Station (ARS), Kasbe Digraj, Sangali. The list of genotypes used in the experiment is given in [Table-1].

The Post Graduate Research Farm is located in Northern Maharashtra's Scarcity Zone, or Agroclimatic Zone 6. It is located between latitudes 20.4°N and longitudes 74°E . At College of Agriculture, Dhule, the monsoon usually begins around the third week of June, with an average of 607 mm of rainfall every year. During the study period, the maximum temperature varied between 35.2 and 30.0°C , while the lowest temperature varied between 12.0 and 21.5°C . In the morning and evening, the relative humidity varied from 75 to 92 and 27 to 71 percent, respectively [11-24].

Path analysis was measured using traditional method. Wright (1921) proposed path analysis, which was further developed by Dewey and Lu (1959). Using path coefficient analysis, the genotypic correlation coefficient is separated into direct and indirect effects. It examines the direct and indirect effects of independent variables on the dependent variable.

If 'Y' is the effect and X_1 is the cause, the path coefficient for the path from cause X_1 to the effect Y is $\sigma X_1 / \sigma Y$.

Direct and indirect effects were worked out by using genotypic correlations as below:

Direct effect of X_1 on $y = PX_1Y$

Where,

PX_1 = Path coefficient of X_1 on Y .

Similarly, direct effects of other attributes on yield were worked out.

Indirect effect of X_1 viz. X_2 or $Y = PX_2Y \times r_{X_1X_2}$

Where,

PX_2Y = Path coefficient of the component character X_2 on Y .

$r_{X_1X_2}$ = Genotypic correlation between X_1 and X_2 .

Similarly, indirect effects in all possible combinations were calculated for all component characters. The residual effect (R) was calculated as below;

$$R = [1 - (PX_1 \cdot r_{X_1Y}) - (PX_2 \cdot r_{X_2Y}) - \dots (PX_n \cdot r_{X_nY})]^{1/2}$$

Where,

PX_1, PX_2, \dots, PX_n = Direct effects of respective characters on yield.

$r_{X_1}, r_{X_2}, \dots, r_{X_n}$ = Correlation coefficient between respective characters and yield.

Average intra cluster D2 is calculated by:

$$D2 = \sum D2_i / n$$

Where, D_i is the sum of distance between all possible combinations (n) of the population included in a cluster.

Average inter cluster D2 is calculated by:

$$D2 = \sum \text{distance between the population of cluster } i \text{ and } j / n_i \cdot n_j$$

Where,

n_i = number of populations in the cluster i .

n_j = number of populations in the cluster j .

Average intra and inter-cluster distance is calculated by:

$$D = \sqrt{D2}$$

Table-1 List of forty genotypes of soybean used for the present study

SN	Genotypes	Pedigree	Collected from
1	KDS- 753	JS 9305 x EC 241780	ARS, Digraj
2	KDS-344	JS 335 x EC241780	ARS, Digraj
3	KDS-992	JS 9305 x EC241780	ARS, Digraj
4	KDS-726	JS 9305 x EC241780	ARS, Digraj
5	KS-103	JS 335 x EC241780	ARS, Digraj
6	NRCSL-1	JS 335 x SL 525	ARS, Digraj
7	NRC-142	JS 9752 x PI 596540 x PI 542044	ARS, Digraj
8	AMS-100-39	Mutant JS 9305	ARS, Digraj
9	DS-228	JS 335 x Ankur	ARS, Digraj
10	DSB-33	DSB 21 x JS 9560	ARS, Digraj
11	JS-335	JS78-77 x JS 71-05	ARS, Digraj
12	JS-9305	Secondary selection from PS73-22	ARS, Digraj
13	MACS-NRC-1667	PI 542044	ARS, Digraj
14	MACS-450	Bragg x PS416	ARS, Digraj
15	DSB-38	DSB18 x EC 241780	ARS, Digraj
16	DS-3105	Pusa 9712 x JS 335	ARS, Digraj
17	DLSB-2	DSb 21 x SL958	ARS, Digraj
18	RVSM-2012-11	JS 2029 x PS 1475	ARS, Digraj
19	DSB-21	JS335 x EC 241778	ARS, Digraj
20	AS-15	(BR13 x GJS3)F2-2013-5-1-3-2	ARS, Digraj
21	HIMSO-1691	--	ARS, Digraj
22	JS-22-14	JS 20-53 x JS 20-34	ARS, Digraj
23	DLSB-1	SL 979 x DSB 21	ARS, Digraj
24	NRC-128	--	ARS, Digraj
25	VLS-101	VLS 75 x VLS 69	ARS, Digraj
26	PS1661	JS 97-52 x JS 335	ARS, Digraj
27	DSB-23	DSB 21 x JS 9560	ARS, Digraj
28	RVS-2012-20	--	ARS, Digraj
29	PS-1670	PS 1584 x JS 20-69	ARS, Digraj
30	MAUS-806	--	ARS, Digraj
31	RVS-2011-10	JS 335 x PS 1042	ARS, Digraj
32	MAUS-768	--	ARS, Digraj
33	ASB-9	LSB3 x NRC51	ARS, Digraj
34	MACS-1460	--	ARS, Digraj
35	MACS-1701	RKS 24 x MACS 450	ARS, Digraj
36	KDS-1096	KDS 378 x DSB 21	ARS, Digraj
37	KDS-1144	DS 228 x TYPE 49	ARS, Digraj
38	TS 20-5	--	ARS, Digraj
39	KSL-441	--	Krishidhan seeds
40	SUPERSTAR-211	--	Oswal seeds

Clustermeans

On the basis of the mean performance of the genotypes included in the cluster, cluster means for different characters were determined.

For genetic divergence studies, cluster combinations were divided into four divergent groups using the approach suggested by Arunachalam and Bandopadhyaya (1984). The mean (M) and standard deviation (S) of the intra and inter-cluster divergence (D) were computed in order to determine the level of parental divergence. The four divergent classes (DC), DC1, DC2, DC3, and DC4, are used to classify parental divergence.

Result and Discussion:

Path coefficient analysis is a standardized partial regression coefficient which divide the correlation coefficient into the measures of direct and indirect effects. In another term, it measures the direct and indirect influence of various independent traits on a dependent trait. The path analysis reveals whether the association of these characters with yield is due to their direct effect on yield or is a result of their indirect effects via component characters. In the current study procedure given by Dewey and Lu (1959) is used to estimate direct and indirect effect of various characters.

Path coefficients offer more reliable and consistent data that may be used in plant breeding initiatives. Direct selection for this character will be fruitful for yield enhancement if the relationship between yield and a character is the result of that character's direct influence. On the other hand, indirect selection through such a characteristic might be helpful in yield improvement if the connection is mostly the result of the character's indirect influence via another component trait. A further possibility is that a feature with a favourable direct influence on yield might, through another component trait, have a negative indirect effect. Direct selection for such a trait should be carried out to lessen the adverse indirect effect if the direct effect is large and positive but the correlation is negative.

When twelve characters were analysed using seed yield as the dependent variable, the number of pods per plant (0.8099), 100 seed weight (0.5176), days to maturity (0.1647), number of primary branches per plant (0.0867), number of seeds per pod (0.0630), and protein content (0.0587) were found to have the highest direct positive effects on seed yield. Conversely, the following characteristics had a negative direct impact on the amount of seeds produced per plant: days to 50% blooming (-0.1575), plant height (-0.0563), pod breaking percentage (-0.0344), days to 50% germination (-0.0281), and oil content (-0.0031). In addition to demonstrating a significant positive direct influence on seed output, the characteristics number of pods per plant and 100 seed weight also shown a high positive association with seed yield per plant.

It suggests that finding high yielding genotypes might be aided by direct selection based on this feature. Days to maturity and the number of main branches per plant were shown to have a modest positive direct influence on seed output per plant, but they did have a positive and significant correlation with it. Although it had a little positive direct impact on seed output per plant, the character number of seeds per pod exhibited a negative and substantial correlation with seed yield per plant. Conversely, plant height had a little negative direct impact on the total number of seeds produced per plant, but it was favourably and strongly linked with seed production.

Genetic diversity refer to variation within a species due to genetic factors. It is a potent source for heritable crop improvement. Genetic diversity may develop as a result of geographical separation, spontaneous mutation or hurdles in crossability. In plant breeding genetic diversity play a key role as hybrid between diverse line usually display higher heterosis than that of closely related parents. Therefore, the precise knowledge of genetic diversity is vital for efficient plant breeding program.

The D2 analysis of 40 soybean genotype was done as per Mahalanobis (1936). The calculated D2 values ranged in between 6.94 to 26.25. The maximum inter-cluster distance was observed between cluster IV and cluster XII (28.25). The lowest inter cluster distance was observed between cluster IV and V (6.94). The intra-cluster distance ranged between 0.00 to 12.88. Cluster VI (12.88) had the highest value of intra-cluster distance. However, cluster III, IV, V, VII, VIII, IX, X, XI and XII were mono genotypic. The wide range of D2 values shows a substantial level of genetic diversity among the genotypes.

Table-2 Genotypic path coefficient (Direct and Indirect effects) for twelve characters in forty genotype of soybean

Path analysis	Days to 50 per cent germination	Days to 50 per cent flowering	Days to maturity	Plant height(cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	100 seed weight(g)	Protein content(%)	Oil content(%)	Pod shattering(%)	Seed yield per plant(g)
Days to 50 per cent germination	-0.0281	0.018	-0.0318	0.0054	-0.0046	-0.0793	0.0121	-0.0026	-0.0144	-0.0004	-0.0032	-0.129
Days to 50 per cent flowering	0.0032	-0.1575	0.1286	-0.0056	0.0152	0.1535	-0.0028	-0.0926	-0.0014	0.0005	-0.0054	0.0358
Days to maturity	0.0054	-0.123	0.1647	-0.0166	0.0265	0.3117	0.007	-0.0935	-0.0055	0.0001	-0.0059	0.2711*
Plant height(cm)	0.0027	-0.0156	0.0486	-0.0563	0.0305	0.2727	-0.0124	-0.0163	-0.0127	0.0001	-0.0051	0.2362*
Number of primary branches per plant	0.0015	-0.0276	0.0504	-0.0198	0.0867	0.435	-0.0126	-0.0579	-0.0093	-0.0002	-0.0018	0.4442**
Number of pods per plant	0.0028	-0.0299	0.0634	-0.019	0.0466	0.8099	-0.0227	0.0337	-0.0128	-0.0006	-0.0052	0.8661**
Number of seeds per pod	-0.0054	0.0071	0.0184	0.0111	-0.0173	-0.2921	0.063	-0.0677	-0.0046	-0.0005	0.0036	-0.2843*
100 seed weight(g)	0.0001	0.0282	-0.0298	0.0018	-0.0097	0.0527	-0.0082	0.5176	-0.0034	-0.0002	0.0004	0.5495**
Protein content(%)	0.0069	0.0038	-0.0155	0.0121	-0.0137	-0.1769	-0.0049	-0.0298	0.0587	0.0017	0.0003	-0.1572
Oil content(%)	-0.0033	0.0275	-0.0074	0.0012	0.0069	0.1528	0.0091	0.0265	-0.0317	-0.0031	0.0042	0.182
Pod shattering (%)	-0.0026	-0.0246	0.0282	-0.0083	0.0047	0.1218	-0.0066	-0.0054	-0.0005	0.0004	-0.0344	0.0725

Table-3 Grouping of forty soybean genotype into different cluster

Clusters	No. of genotypes	Genotypes
I	21	KDS- 753, KDS-992, KDS-726, KS-103, NRCSL-1, NRC-142, AMS-100-39, DS-228, JS-335, DS-3105, RVSM-2012-11, HIMSO-1691, JS-22-14, NRC-128, VLS-101, PS1661, DSB-23, MAUS-768, MACS-1460, KDS-1096, KDS-1144
II	6	DSB-33, DSB-38, DLSB-1, PS-1670 RVS-2011-10, ASB-9
III	1	MACS-1701
IV	1	MAUS-806
V	1	KSL-441
VI	4	JS-9305, MACS-450, RVS-2012-20, SUPERSTAR-211
VII	1	KDS-344
VIII	1	AS-15
IX	1	MACS-NRC-1647
X	1	DLSB-2
XI	1	DSB-21
XII	1	TS20-5

Table-4 Average inter and intra-cluster distance (D2 values) in soybean

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	10.33	14.11	12.37	12.33	12.89	14.01	12.71	12.46	14.75	14.99	19.33	20.76
II		10.24	16.72	19.54	20.2	17.57	20.69	16.96	18.23	20.37	22.92	13.29
III			0	10.78	10.61	11.38	14.18	19.66	15.99	19.96	26.24	23.29
IV				0	6.94	12.27	12.78	16.15	15.98	17.6	22.54	28.25
V					0	12.14	11.7	17.08	17.81	17.1	21.81	26.87
VI						12.88	17.01	18.98	16.08	21.6	25.11	24.15
VII							0	14.04	13.43	10.58	17.06	27.01
VIII								0	17.8	11.89	13.28	22.78
IX									0	17.67	21.05	25.75
X										0	11.33	25.07
XI											0	26.55
XII												0

Table-5 Cluster mean for twelve character in forty soybean genotypes

Cluster	Days to 50 per cent germination	Days to 50 per cent flowering	Days to maturity	Plant height(cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Protein content(%)	Oil content(%)	Pod shattering(%)	Seed yield per plant(g)
I	4.07	43.31	100.38	57.27	4.43	63.11	2.58	12.19	38.99	17.77	38.76	15.36
II	4.08	43.5	99.42	54.25	4.18	56.43	2.53	11.64	41.09	16.89	32	13.16
III	3	42.5	99	48.3	4.1	51.6	2.64	13.02	38.1	17.34	2	13.44
IV	4	43	94	48.9	4.3	63.25	2.26	12.59	38.35	18.95	30	15.91
V	4.5	44	101.5	46.7	4.4	63.1	2.65	11.75	37.48	19.5	20	14.82
VI	4.25	37.75	93	49.96	3.55	42.63	2.8	11.78	38.49	18.27	21.5	10.37
VII	4	44	106.5	71.6	5	80.3	2.68	12.54	37.03	18.25	14	20.15
VIII	4	41	100	60.5	4.5	56.45	2.48	11.27	38.43	17.35	94	12.73
IX	4	35	97.5	83.9	3.8	53.95	2.39	12.19	38.77	17.7	4	14.17
X	4	48	104.5	73.4	5.9	51.55	2.28	10.85	37.16	17.2	30	11.29
XI	4	46.5	102	72	4.4	76.5	2.3	9.16	37.29	17.37	48	10.51
XII	3.5	46	106	52.3	4.1	36.2	3.05	10.1	41.63	16.29	26	8.31

Table-6 Character improvement on the basis of source cluster

SN	Characters	Source Cluster
1	Days to 50 per cent germination (earliness)	III
2	Days to 50 per cent flowering (earliness)	IX, VI
3	Days to maturity (earliness)	VI, IV, IX
4	Plant height(cm) (Tall)	IX, X, XI
5	Number of primary branches per plant (Highest)	X, VII
6	Number of pods per plant (Highest)	VII, XI, I, IV
7	Number of seeds per pod (Highest)	XII, VI, VII, V
8	100 seed weight(g) (Highest)	III, IV, VII
9	Protein content (%) (Highest)	XII, II
10	Oil content (%) (Highest)	V, IV, VI
11	Pod shattering (%) (lowest)	III, IX
12	seed yield per plant (Highest)	VII, I, IV

Conclusion

Five randomly chosen plants were observed for twelve features, including days to 50 per cent germination, days to 50 per cent flowering, days to maturity, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield per plant, protein content, oil content and pod shattering percentage. The forty genotypes showed quite significant differences among them. Based on average performance, it was

determined that the genotypes viz., NRC-128, KDS-344, KDS-726, DS-228, JS-335, JS-9305, MACS-1701, MACS-NRC-1647 and AMS-100-39 were better.

The characters number of pods per plant and 100 seed weight showed strong positive correlation with seed yield per plant and has also showed strong positive direct effect on seed yield. It indicate that direct selection based on this trait would help in identifying high yielding genotypes. The broad range of D2 values reflects a significant level of genetic diversity among the genotypes. In comparison to closely related parents, hybrids of diverse lines generally show higher heterosis thus crossing of clusters having higher inter cluster distances may produced a superior F1 progeny, which will consist of desirable agronomical and morphological characters. e.g., cluster II and cluster VII (20.69), cluster I and IX (14.75). On the basis of the analysed divergence classes, the genotypes KDS-344, DS-228, JS-335, JS-9305, HIMSO-1691, NRC-128, MACS-1701, MAUS-768, MACS-450, MACS-NRC-1647, etc., may prove valuable for future crop improvement programmes.

Application of research: Study of identification promising genotypes for genetic divergence and path analysis in soybean

Research Category: Genetic Divergence and Path analysis

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Study area / Sample Collection: Maharashtra and Madhya Pradesh

Cultivar / Variety / Breed name: Soybean [*Glycine max* (L.) Merr.]

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References

- [1] Khadar V. (2019) *Acta Scientific Nutritional Health*, 3(3), 44-498.
- [2] National Mission on Oilseeds and Oil palm (NMOOP) (2018) Available from, www.nfsm.gov.in/StatusPaper/NMOOP2018.pdf, 1-72.
- [3] Abady S.F., Merkeb and Dilnesaw Z. (2013) *J. Environ. Sci. Water Res.*, 2(8), 270-276.
- [4] The Soybean Processors Association of India (2021) Available from, www.sopa.org/statistics/worldsoybean-production.
- [5] Arunachalam V. and Bandopadhyay A. (1984) *Indian J. Genet.*, 44(3), 548-554.
- [6] Badkul A., Shrivastava A.N., Bisen R. and Mishra S. (2014) *Soybean Res.*, 2, 44-50.
- [7] Bairwa A., Shukla P.S., Singh K. and Dhaka N. (2020) *Int. J. Curr. Microbiol. App. Sci.*, 9(03), 978-985.
- [8] Balla M.Y. and Ibrahim S.E. (2017) *Open Access J.*, 2471-6774.
- [9] Banaszkievicz T. (2011) *Nutritional Value of Soybean Meal, Soybean and Nutrition*, Edited by Hany El-Shemy, IntechOpen, 1.
- [10] Baraskar V. V., Vachhani J.H., Kachhadia V.H., Patel M.B. and Barad H.R. (2015) *Electron. J. Plant Breed.*, 6(2), 570-573.
- [11] Carter T.Jr., Hymowitz T., Nelson R. (2004) *Springer*, 47-59.
- [12] Da Silva A.F., Dos Santos Silva F.C., Bezerra A.R.G., Sediama T., Rosa D.P. and Barros J.P.A. (2022) *Functional plant Breed. J.*, 4(2).
- [13] Hang Vu T.T., Cham Le T.T., Vu D.H., Nguyen T.T. and Ngoc T. (2019) *Asian J. Crop Sci.*, 11, 32-39.
- [14] Joshi D., Pushpendra, Singh K. and Adhikari S. (2018) *Int. J. Curr. Microbiol. App. Sci.*, 7(1), 700-709.
- [15] Kachhadia V.H., Baraskar V.V., Vachhani M.B., Patel M.B. and Barad H.R. (2014) *Electronic J. Plant Breed.*, 5(3), 563-566.
- [16] Kim M.Y., Van K., Kang Y.J., Kim K.H., Lee S.H. (2012) *Breed. Sci.*, 61, 445-452.
- [17] Kumar A., Pandey A., Aochen C. and Pattanayak A. (2014) *Proc. Natl. Acad. Sci., India, Sect. B Biol. Sci.*, 85(2), 397-405.
- [18] Mishra A.K. (2019) *Soybean Res.*, 17(1&2), 30-39.
- [19] Nagarajan D., Kalaimagal T. and Murugan E. (2015) *Int. J. Farm Sci.*, 5(3), 28-34.
- [20] Nag S.K. and Sarawgi A.K. (2021) *J. Pharm. Innov.*, 10(6), 475-478.
- [21] Nag S.K., Sarawgi A.K., Mehta N., Verulkar S.B. and Saxena R.R. (2017) *Bull. Env. Pharmacol. Life Sci.*, 6(4), 45-50.
- [22] Shadakshari T. V., Kalaimagal T., Senthil N., Boranayaka M.B., Kambegowda R. and Rajesha G. (2012) *Asian J. Bio. Sci.*, 6(1), 7-11.
- [23] Tyagi S. D. and Sethi J. (2011) *Res. J. Agric. Sci.*, 2(2), 288-290.
- [24] Verma S. (2019) *MSc Thesis, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, India*, 1-82.