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Genetic diversity studies in exotic germplasm lines for yield related traits in soybean (*Glycine max* (L.) Merrill)

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Abstract
Knowledge of the naturally occurring diversity helps to identify diverse groups of soybean genotypes that can be useful for the breeding program. Therefore, this study aims to identify traits that influence the soybean genotypes in cluster formation using k-*means* cluster analysis. 144 exotic germplasm lines including checks *viz*., DSb 21, JS 335, EC 241780 and EC 241778 were evaluated in augmented block design and grouped into eight clusters. Maximum number of genotypes were grouped in the cluster V (39 genotypes) followed by cluster I (35 genotypes), cluster VII and cluster VIII (20 genotypes each). The formation of distinct solitary clusters may be due to the fact that exotic germplasm lines belong to different regions which may be responsible for this type of genetic diversity. It could be seen that clusters vary much with respect to mean expression of various characters which resulted in distinct clusters. There were significant differences between the mean of clusters for all the traits. The inter-cluster distance was maximum between clusters II and VI (D=55.64) followed by clusters VII and VIII (D=53.07). The minimum inter-cluster distance was observed between clusters I and III (D=7.07). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. The traits *viz*., number of pods per plant (41.82), seed yield per plant (18.24), number of branches per plant (17.47) and days to 50 % flowering (13.42) exhibited major contribution towards the diversity while, days to maturity (9.05) contributed the least towards total genetic diversity. The genotypes *viz*., DSb 21 of cluster VI, EC 242104 of cluster I, EC 241780 and EC 241778 of cluster IV and JS 335 of cluster V were identified as genetically diverse parents, which can be utilized for future crop improvement programme.

Keywords: k cluster analysis, genetic diversity, exotic germplasm and soybean

Introduction
Soybean (*Glycine max* (L.) Merrill) owes worldwide reputation by virtue of its high quality protein and low cholesterol edible oil. It has an average protein content of 40 per cent and is protein rich source than any of the common vegetable or animal food sources. Soybean seeds also contain about 20% oil on a dry matter basis of which 85 per cent is unsaturated and cholesterol free. In view of potentiality and wide range of agricultural, industrial and medicinal values, soybean is rightly described as "nature's unique gift" to mankind, otherwise also known as a 'miracle crop'. The area under soybean cultivation expanded significantly as a result of its nutritive, economic importance and diverse domestic usage. It is also a prime source of vegetable oil in the international market.

Currently, soybean ranks first as on oilseed crop both in area and production in India. Over a decade, area under soybean increasing consistently besides its spread to new areas all over India from 3000 ha in 1969 to 10.80 million ha during 2018-19. Soybean production increased from 2.49 million tonnes in 1991-92 to 12.10 million tonnes during 2018-19. This corresponds to a growth rate of 15-20 per cent per annum which obviously one of the highest for any crop in recent past and resulted in radical improvement of rural economy.

At present, soybean occupies an area of 127.19 million hectare producing 364.33 million tonnes with the productivity of 2864 kg per hectare in the world (Anon., 2018-19). In India it occupies an area of 10.80 million hectare with the production of 12.10 million tonnes and productivity of 1120 kg hectare (Anon., 2018). In India, major soybean producing states are Madhya Pradesh, Maharashtra, Rajasthan, Karnataka and Telangana.

Although the cultivation of soybean is very wide in world the productivity is high as compared to India. Therefore, improving productivity of soybean is the major concern of the breeders.

Hence, an assessment of genetic diversity is a pre-requisite to improve crop yield. For any crop improvement programme, analysis of genetic diversity is the first and foremost step. Information on genetic diversity among genotypes has several important applications for crop improvement. This information can be useful to classify germplasm for identification of cultivars, assist in selection of parents for hybridization and reduce number of genotypes needed to ensure sampling of a broad range of genetic variability. Genetically diverse parents is a pre-requisite to improve the chances of selecting better segregants for various characters. When such parents are utilized in hybridization programme, they are likely to produce high heterotic effect and wide spectrum of variability (Barh *et al*., 2014) [3]. The challenge is to select which genotype to be used in breeding programme from available germplasm, those carrying favorable rare alleles absent in elite germplasm.

The choice of parents is of paramount importance in any breeding programme. It is rather a difficult task for a plant breeder. Selection of parents on the basis of *per se* performance is good but there is a possibility of related lines being chosen resulting in limited or no advances under selection and, therefore, there is a need for emphasis on a wide genetic base by the utilization of world collection on genetic criterion. Selection of parents on the basis of geographical diversity is another way of choosing parents and this has led to success in some cases but this need to be supplemented with genetic diversity (Brown, 1978, Frankel and Souel, 1981, Frankel *et al.*, 1995) [7]. The measures based on genetic criteria qualifying diversity have become important in classifying material for the use by the breeders. Therefore, further study is needed to know genetic variation within available gene pool through divergence study and to make strategies for incorporating useful diversity or to facilitate the introgression of genes of interest into commercial varieties.

The present study was envisaged to measure the genetic diversity among the germplasm lines of soybean and to identify divergent parents for future hybridization programmes for yield improvement.

Material and methods

The experimental material comprised of 144 exotic germplasm lines including checks *viz*., DSb 21, JS 335, EC 241780 and EC 241778 (Table 1). These exotic germplasm lines were from different geographical regions (Table 2) which were collected from international institute AVRDC, Taiwan and national institutes *viz*., IISR, Indore, ARI, Pune, NBPGR, New Delhi and JNKV, Jabalpur. These lines were evaluated at Main Agricultural Research Station, University of Agricultural Sciences, Dharwad in augmented block design during *Kharif* 2015. Each line was raised in one row of 5 m length with a spacing of 45 x 10 cm. The observations were recorded for yield and yield components *viz.*, days to 50% flowering, number of branches per plant, days to maturity, number of pods per plant and seed yield per plant. In all the entries, five random plants were tagged in each line for recording the observations. Days to 50 % flowering (DFF) was recorded as number of days taken from the date of sowing to the day on which 50 per cent of plants flowered on each individual line; number of branches per plant (NB) was recorded by counting the total number of branches present on main stem of each plant at the time of harvest; days to maturity (DM) was documented as number of days taken from date of sowing to physiological maturity of the plant was recorded as days to maturity; number of pods per plant (NPP) was recorded by counting total number of pods produced in each plant in five randomly tagged plants and seed yield per plant (SYP) was documented as seeds obtained from each individual plant in five randomly tagged plants were weighed in grams.

Mean of five plant observations was used for the statistical analysis. The non-hierarchical Euclidean cluster analysis based on k-*means* method was used for assessing the genetic divergence for yield related traits in exotic germplasm lines. The statistical analysis was performed employing SPSS software. k-*means* was used for describing an algorithm that assigned each item to the cluster having nearest means (Queen, 1967) [15].

Table 1: Exotic germplasm lines and checks used for genetic diversity studies during *kharif* 2015

Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes
1	EC 1028	42	EC 250578	83	EC 333920	124	EC 457419
2	EC 10027	43	EC 250588	84	EC 333934	125	EC 49393
3	EC 100031	44	EC 250607	85	EC 338597	126	EC 65772
4	EC 100772	45	EC 250608	86	EC 34057	127	EC 685246
5	EC 104817	46	EC 250619	87	EC 34078	128	EC 685250
6	EC 107416	47	EC 251329	88	EC 34079	129	EC 685251
7	EC 114520	48	EC 251334	89	EC 34092	130	EC 685252
8	EC 114573	49	EC 251341	90	EC 34500	131	EC 685255
9	EC 116343	50	EC 251358	91	EC 340924	132	EC 685256
10	EC 118420	51	EC 251401	92	EC 36816	133	EC 685258
11	EC 118443	52	EC 251409	93	EC 37937	134	EC 7048
12	EC 12570	53	EC 251411	94	EC 376065	135	EC 85705
13	EC 14426	54	EC 251 456	95	EC 377552	136	EC 9172587
14	EC 242091	55	EC 251501	96	EC 380322	137	EC 93413
15	EC 14476	56	EC 251516	97	EC 383165	138	EC 94625
16	EC 14573	57	EC 251762	98	EC 385243	139	EC 95291
17	EC 149988	58	EC 274755	99	EC 389148	140	EC 95815
18	EC 15966	59	EC 287754	100	EC 389151	141	EC 241778 (C)
19	EC 16119	60	EC 30832	101	EC 389178	142	EC 241780 (C)
20	EC 16738	61	EC 308334	102	EC 389400	143	DSb 21 (C)
21	EC 172607	62	EC 309512	103	EC 39219	144	JS 335 (C)
22	EC 175529	63	EC 309538	104	EC 39362		
23	EC 177744	64	EC 309545	105	EC 39491		
24	EC 187456	65	EC 315213	106	EC 39516		

25	EC 184337	66	EC 3251	107	EC 39536		
26	EC 19923	67	EC 325092	108	EC 390981		
27	EC 225114	68	EC 325099	109	EC 391158		
28	EC 221329	69	EC 325101	110	EC 391336		
29	EC 2388	70	EC 325102	111	EC 391346		
30	EC 232019	71	EC 329158	112	EC 392532		
31	EC 241309	72	EC 33875	113	EC 392580		
32	EC 241761	73	EC 33917	114	EC 394839		
33	EC 241766	74	EC 33922	115	EC 396052		
34	EC 242018	75	EC 33940	116	EC 396053		
35	EC 242038	76	EC 333868	117	EC 397158		
36	EC 242104	77	EC 333875	118	EC 4435		
37	EC 242105	78	EC 333881	119	EC 42081		
38	EC 245984	79	EC 333886	120	EC 457161		
39	EC 245989	80	EC 333891	121	EC 457175		
40	EC 2581	81	EC 333904	122	EC 457286		
41	EC 25269	82	EC 333909	123	EC 457406		

Table 2: Source / origin of exotic germplasm lines utilized in genetic diversity studies

Source/Origin	Name of the Germplasm
USA	EC 10031, EC 100772, EC 107416, EC 114520, EC 114573, EC 242091, EC 24139, EC 241761, EC 241766, EC 242038, EC 242104, EC 242105, EC 251501, EC 308334, EC 329158, EC 333868, EC 333875, EC 333881, EC 333886, EC 333891, EC 333904, EC 333909, EC 333920, EC 333934, EC 39491, EC 65772, EC 241780, EC 241778
China	EC 16119, EC 281762
Australia	EC 14426
Brazil	EC 399512, EC 309538, EC 309545
Argentina	EC 251329, EC 251334, EC 251341, EC 251358, EC 251401, EC 251401, EC 251409, EC 251411, EC 251456, EC 251516, EC 377552
Philippines	EC 274755, EC 287754
Hungary	EC 325092, EC 325099, EC 325101, EC 325102, EC 34057, EC 34078, EC 34079, EC 34092
Russia	EC 95815
Taiwan	EC 245984, EC 245989, EC 250588, EC 250607, EC 250608, EC 250619
Indonesia	EC 4435
Canada	EC 36816

Reaction for rust resistance

The severity of rust was scored between 65-90 days after sowing based on percent leaf area infected by using 0-9 scale given by Mayee and Datar (1986).

0: Immune (<1%)
1: Highly resistant (1-10%)
3: Moderately resistant (11-25%)
5: Moderately susceptible (26-50%)
7: Susceptible (50-75%)
9: Highly susceptible (>75%)

Results and discussion

The precise information about the degree of relationship between different genotypes is very much essential for an effective breeding programme. Genetic diversity between lines indicates the difference in gene frequencies. The multivariate analysis has been demonstrated to classify biological populations and to identify factors influencing their genetic divergence (Rao, 1960) [17]. The varieties involving the parents with more diversity among them are expected to exhibit higher amount of heterotic expression and also broad spectrum of variability in segregating generations (Naik *et al*., 2006) [11].

The k-*means* cluster analysis provides a measure of magnitude of divergence between the groups under comparison. It considers the means of the characters under study, and their consequence (Queen, 1967) [15]. The technique has been applied in several crops to select genotypes for further breeding programmes (Shabbir *et al.* 2016) [16].

In the present investigation the algorithm k-*means* cluster analysis was employed to group 144 genotypes into eight clusters, based on the mean values of yield related traits (Table 3). Maximum number of genotypes were grouped in the cluster V (39 genotypes) followed by cluster I (35 genotypes), cluster VII and cluster VIII (20 genotypes each). The formation of distinct solitary clusters may be due to the fact that exotic germplasm lines belong to different regions which may be responsible for this type of genetic diversity. It could be seen that clusters vary much with respect to mean expression of various characters which resulted in distinct clusters. There were significant differences between the mean of clusters for all the traits. The genotypes from cluster II are highly divergent from the genotypes of clusters VI and of medium divergence from the genotypes of cluster VII and cluster VIII. The results of cluster mean analysis clearly indicated that the cluster VI exhibited maximum cluster mean values for the traits *viz*., seed yield per plant, number of pods per plant, number of branches per plant and cluster II exhibited minimum cluster mean values for the traits *viz*., days to 50 % flowering, number of branches per plant, days to maturity and number of pods per plant. Therefore, it can be concluded that the genotypes of the cluster VI exhibited maximum potentiality for yield related traits while, the genotypes from the cluster II had low potentiality for yield related traits. These findings are similar to the reports of Maharaddi (1996) [10], Ramgiry *et al.* (1999) [16], Ganesh Moorthy and Sheshadri (2002) [8], Aravind (2006) [2] and Parameshwar (2006) [12-13].

Table 3: Clustering of 140 exotic germplasm lines and four checks in eight clusters in soybean

Cluster	Number of germplasm lines	Name of the Exotic germplasm
I	35	EC 100031, EC 118420, EC 149988, EC 187456, EC 242038, EC 242104, EC 245984, EC 25269, EC 250607, EC 251341, EC 251358, EC 251411, EC 251501, EC 251516, EC 274755, EC 30832, EC 309512, EC 315213, EC 33922, EC 33940, EC 333868, EC 333875, EC 333920, EC 333934, EC 34092, EC 389178, EC 39219, EC 39516, EC 390981, EC 394839, EC 42081, EC 457161, EC 457286, EC 457419, EC 65772.
II	16	EC 10027, EC 14573, EC 250588, EC 251401, EC 325099, EC 325101, EC 325102, EC 329158, EC 33917, EC 333886, EC 333909, EC 34079, EC 392532, EC 392580, EC 685250, EC 685258.
III	10	EC 1028, EC 116343, EC 250619, EC 251334, EC 251762, EC 34057, EC 377552, EC 39536, EC 685252, EC 95291.
IV	2	EC 241780 (C), EC 241778 (C).
V	39	EC 100772, EC 104817, EC 107416, EC 114573, EC 12570, EC 15966, EC 16119, EC 177744, EC 184337, EC 225114, EC 221329, EC 2388, EC 232019, EC 241309, EC 242018, EC 242105, EC 245989, EC 250578, EC 250608, EC 251329, EC 251 456, EC 287754, EC 308334, EC 309538, EC 333891, EC 338597, EC 340924, EC 36816, EC 389151, EC 39491, EC 391336, EC 396052, EC 457175, EC 457406, EC 49393, EC 685246, EC 685255, EC 685256, JS 335(C).
VI	2	EC 385243, DSb 21 (C).
VII	20	EC 114520, EC 118443, EC 14426, EC 242091, EC 14476, EC 16738, EC 19923, EC 2581, EC 33875, EC 380322, EC 383165, EC 389400, EC 396053, EC 4435, EC 7048, EC 85705, EC 9172587, EC 93413, EC 94625, EC 95815.
VIII	20	EC 172607, EC 175529, EC 241761, EC 241766, EC 251409, EC 309545, EC 3251, EC 325092, EC 333881, EC 333904, EC 34078, EC 34500, EC 37937, EC 376065, EC 389148, EC 39362, EC 391158, EC 391346, EC 397158, EC 685251.

Inter-cluster distances

The maximum inter-cluster distance observed was 55.64 between cluster II and VI followed by 53.07 between cluster VI and VIII (Table 4). The lowest inter-cluster distance was observed between cluster I and III (7.07) followed by cluster II and VIII (9.41). Cluster I was farthest to cluster VI (33.69) and nearest to cluster III (7.07). similarly, cluster II was nearest to cluster VIII (9.41) and farthest to cluster VI (55.64), cluster III was nearest to cluster VII (12.08) and farthest to cluster VI (32.56), cluster IV was nearest to cluster VI (20.07) and farthest to cluster VIII (42.29), cluster V was nearest to cluster VIII (9.71) and farthest to cluster VI (44.26), while cluster VI was nearest to cluster VII (20.82) and farthest to cluster VIII (53.07). With respect to cluster VII, the cluster VIII was farthest (32.90) and cluster VIII nearest to the cluster II (9.41).

The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. It is true that larger the divergence between genotypes, higher would be the heterosis when hybrid programme is planned to develop yield superior varieties (Bekele *et al*., 2012). In this context, genotypes from cluster I (EC 242104) cluster V (JS 335), cluster VI (DSb 21) and cluster IV (EC 241780 and EC 241778) can be used as parents in hybridization programme.

Table 4: Estimates of average inter-cluster distances for yield related traits in soybean

Cluster	I	II	III	IV	V	VI	VII	VIII
I		22.60	7.07	26.23	10.68	33.6	13.40	19.63
II			23.59	47.80	12.42	55.64	34.90	9.41
III				29.36	13.86	32.56	12.08	23.37
IV					35.76	20.07	20.14	42.29
V						44.26	23.70	9.71
VI							20.8	53.07
VII								32.90
VIII								

Cluster mean analysis and per cent contribution of traits towards the divergence

Significant cluster means were observed for all the traits studied (Table 5). The cluster VI recorded maximum cluster mean value of 91.5 for days to maturity, 89.9 for number of pods per plant, 37.5 for days to 50 % flowering, 13.49 for seed yield per plant and 6.2 for number of branches per plant. Whereas, cluster II exhibited minimum cluster mean value of 82.75 for days to maturity, 35.26 for number of pods per plant, 33.75 for days to 50 % flowering and 4.28 for number of branches per plant. The maximum cluster means for seed yield per plant was registered by cluster IV (13.49) followed by cluster III (13.27) while, minimum was observed in cluster VIII (9.29). Cluster II showed minimum cluster mean values of 33.75 and 82.75 for the days to 50 % flowering and days to maturity respectively. The maximum cluster mean observed for days to 50 % flowering (37.5) and days to maturity (91.5) was in cluster VI.

The traits *viz*., number of pods per plant (41.82), seed yield per plant (18.24), number of branches per plant (17.47) and days to 50 % flowering (13.42) exhibited major contribution

towards the diversity while, days to maturity (9.05) contributed the least towards total genetic diversity.

The characters contributing maximum to the divergence should be given greater emphasis in deciding the clusters for the purpose of further selection and choice of parents for hybridization. Contribution of each character towards genetic divergence was estimated based on number of times it appeared in the first rank. The results depicted that the most important traits which contributed maximum to total genetic divergence are; number of pod per plant, seed yield per plant, number of branches per plant and days to 50 % flowering. They accounted for about 90% of total genetic divergence in the material. Looking to these results number of pods per plant should be considered as an important trait when selecting parents for hybridization programme.

Based on the cluster means, cluster VI for seed yield per plant, number of pods per plant, number of branches per plant, days to 50 % flowering and cluster II for early maturity are considered to be superior. Thus, crosses among the genotype(s) of these clusters would exhibit high heterosis and is also likely to produce new recombinants with desired traits in soybean.

The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used either for direct adoption or for hybridization followed by selection. In the present study, seed yield per plant, an important contributing trait to genetic diversity, was larger in the genotype DSb 21 of cluster VI. This genotype was also high in number of pods per plant. The genotype in the cluster I (EC 242104) differed from other clusters in respect of rust resistance. Also the genotypes grouped in the cluster IV (EC 241780 and EC 241778) were found to be rust resistant. These lines can be used in hybridization programme for rust resistance. The genotype of cluster V (JS 335) was early maturing and this genotype can be utilized in development of early maturing varieties. Therefore, genotypes of these clusters may be utilized in future breeding programme for creating wide spectrum of variability for different yield contributing characters. This will facilitate to isolate superior genotypes with higher seed yield.

Table 5: Cluster mean values and percent contribution for yield related traits in soybean

Characters	Cluster								F	Percent contribution
	I	II	III	IV	V	VI	VII	VIII		
Days 50 % flowering	36.54	33.75	34.7	46	34.9	37.5	34.9	37.15	7.56**	13.42
Number of branches per plant	4.72	4.28	5.06	5.8	4.63	6.2	5.39	4.35	8.38**	17.47
Days to maturity	89.83	82.75	83.4	103.5	88.79	91.5	88.35	91.35	24.06**	9.05
Number of pods per plant	56.31	35.26	58.5	76.5	45.87	89.9	69.51	37.03	243.19**	41.82
Seed yield per plant (g)	12.62	9.45	13.27	10.86	11.39	13.49	12.87	9.29	51.57**	18.24

Reaction of exotic germplasm lines for rust resistance

Among 144 exotic germplasm lines including resistant and susceptible checks screened under field condition, four lines recorded highly resistant reaction (DSb 21, EC 241780, EC 241778 and EC 242104), 9 lines recorded moderately resistant reaction, 5 lines registered moderately susceptible reaction, 46 lines were found to be susceptible and 80 lines exhibited highly susceptible reaction (Table 6). In the present study EC 242104 which exhibited highly resistant reaction, can be utilized in future breeding programmes for development of resistant genotypes. These results are in conformity with the earlier reports of Patil *et al*., (2004), Hartman *et al*., (2005), Parameshwar (2006) [12-13], Twizeyimana *et al*., (2007) [20] and Shivakumar *et al.* (2011) [19]. The new source of resistance can be used in combination with already identified resistance genes.

Table 6: Reaction of exotic germplasm lines for rust resistance during *kharif* 2015 at Dharwad

Sl. No.	Germplasm lines	Grade (0-9 Scale)	Reaction	Sl. No.	Germplasm lines	Grade (0-9 Scale)	Reaction	Sl. No.	Germplasm lines	Grade (0-9 Scale)	Reaction
1	EC 1028	7	S	51	EC 251401	7	S	101	EC 389178	7	S
2	EC 10027	7	S	52	EC 251409	9	HS	102	EC 389400	9	HS
3	EC 100031	3	MR	53	EC 251411	9	HS	103	EC 39219	9	HS
4	EC 100772	7	S	54	EC 251 456	7	S	104	EC 39362	9	HS
5	EC 104817	9	HS	55	EC 251501	9	HS	105	EC 39491	9	HS
6	EC 107416	9	HS	56	EC 251516	9	HS	106	EC 39516	9	HS
7	EC 114520	9	HS	57	EC 251762	7	S	107	EC 39536	9	HS
8	EC 114573	9	HS	58	EC 274755	9	HS	108	EC 390981	9	HS
9	EC 116343	9	HS	59	EC 287754	3	MR	109	EC 391158	7	S
10	EC 118420	5	MS	60	EC 30832	9	HS	110	EC 391336	3	MR
11	EC 118443	9	HS	61	EC 308334	3	MR	111	EC 391346	7	S
12	EC 12570	9	HS	62	EC 309512	9	HS	112	EC 392532	9	HS
13	EC 14426	5	MS	63	EC 309538	9	HS	113	EC 392580	7	S
14	EC 242091	7	S	64	EC 309545	9	HS	114	EC 394839	9	HS
15	EC 14476	3	MR	65	EC 315213	9	HS	115	EC 396052	7	S
16	EC 14573	9	HS	66	EC 3251	5	MS	116	EC 396053	7	S
17	EC 149988	7	S	67	EC 325092	9	HS	117	EC 397158	9	HS
18	EC 15966	3	MR	68	EC 325099	9	HS	118	EC 4435	9	HS
19	EC 16119	7	S	69	EC 325101	7	S	119	EC 42081	7	S
20	EC 16738	7	S	70	EC 325102	7	S	120	EC 457161	9	HS
21	EC 172607	7	S	71	EC 329158	9	HS	121	EC 457175	7	S
22	EC 175529	7	S	72	EC 33875	9	HS	122	EC 457286	7	S

23	EC 177744	7	S	73	EC 33917	9	HS	123	EC 457406	9	HS
24	EC 187456	7	S	74	EC 33922	5	MS	124	EC 457419	9	HS
25	EC 184337	7	S	75	EC 33940	9	HS	125	EC 49393	9	HS
26	EC 19923	7	S	76	EC 333868	7	S	126	EC 65772	9	HS
27	EC 225114	7	S	77	EC 333875	9	HS	127	EC 685246	9	HS
28	EC 221329	5	MS	78	EC 333881	9	HS	128	EC 685250	9	HS
29	EC 2388	7	S	79	EC 333886	9	HS	129	EC 685251	9	HS
30	EC 232019	7	S	80	EC 333891	9	HS	130	EC 685252	9	HS
31	EC 241309	7	S	81	EC 333904	7	S	131	EC 685255	9	HS
32	EC 241761	7	S	82	EC 333909	7	S	132	EC 685256	9	HS
33	EC 241766	7	S	83	EC 333920	9	HS	133	EC 685258	9	HS
34	EC 242018	9	HS	84	EC 333934	3	MR	134	EC 7048	9	HS
35	EC 242038	7	S	85	EC 338597	9	HS	135	EC 85705	9	HS
36	EC 242104	1	HR	86	EC 34057	9	HS	136	EC 917258	9	HS
37	EC 242105	9	HS	87	EC 34078	9	HS	137	EC 93413	9	HS
38	EC 245984	7	S	88	EC 34079	9	HS	138	EC 94625	9	HS
39	EC 245989	9	HS	89	EC 34092	9	HS	139	EC 95291	9	HS
40	EC 2581	9	HS	90	EC 34500	9	HS	140	EC 95815	9	HS
41	EC 25269	7	S	91	EC 340924	9	HS	141	EC 241778 (RC)	1	HR
42	EC 250578	3	MR	92	EC 36816	9	HS	142	EC 241780 (RC)	1	HR
43	EC 250588	9	HS	93	EC 37937	9	HS	143	DSb 21 (RC)	1	HR
44	EC 250607	7	S	94	EC 376065	9	HS	144	JS 335 (SC)	9	HS
45	EC 250608	7	S	95	EC 377552	9	HS				
46	EC 250619	7	S	96	EC 380322	9	HS				
47	EC 251329	7	S	97	EC 383165	9	HS				
48	EC 251334	7	S	98	EC 385243	3	MR				
49	EC 251341	7	S	99	EC 389148	9	HS				
50	EC 251358	7	S	100	EC 389151	9	HS				

RC-Resistant check, SC- Susceptible check

HR-Highly resistant, R-Resistant; MR-Moderately resistant; MS-Moderately susceptible; S-Susceptible; HS-Highly susceptible

References

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