



Research Article

EVALUATION OF BAEL (*AEGLE MARMELLOS* CORREA.) GENE POOL OF KYMORE PLATEAU AND SATPURA HILL REGION

PARIHAR N. AND PANDEY C.S.*

Department of Horticulture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, 482004, India

*Corresponding Author: Email - shekharptc@gmail.com

Received: March 15, 2019; Revised: March 24, 2019; Accepted: March 25, 2019; Published: March 30, 2019

Abstract: The twenty genotypes (JAM-1 to 20) of the bael selected from different locations of Kymore plateau and Satpura hill region of MP from the existing plant population was evaluated for fruit characteristics of plants to find out superior genotypes. The present investigation reveals that many genotypes are valuable for one or other traits but considering the most important traits like higher pulp percentage, and less number of seeds and fruit weight, the genotypes JAM-8 is most superior with pulp% (73.18), less number of seed (53.16), TSS-38.70 oBrix followed by JAM-1, JAM-2, JAM3, JAM-10, JAM-12 and JAM-17 which may be include for further utilization and multiplication of quality planting material.

Keywords: Bael (*Aegle marmelos*), Genotypes, Pulp, Fruit size, Skull thickness, Seed

Citation: Parihar N. and Pandey C.S. (2019) Evaluation of Bael (*Aegle marmelos* Correa.) Gene Pool of Kymore Plateau and Satpura Hill Region. International Journal of Genetics, ISSN: 0975-2862 & E-ISSN: 0975-9158, Volume 11, Issue 3, pp.- 571-574.

Copyright: Copyright©2019 Parihar N. and Pandey C.S. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

Introduction

Bael (*Aegle marmelos* Correa.) also known as Shriphal, Baelpatra, Bengal quince belongs to the family Rutaceae. In India, it is distributed throughout the country but concentrated area under bael is in eastern parts of the Gangetic plains and nearby areas particularly in Uttar Pradesh, Bihar, West Bengal and Orissa. It is also available in wild form in sub-Himalayan tract from Rajasthan to West Bengal, Central and Southern India. Bael is a nutritious and medicinal fruit, which is most suitable for water scarce areas of the country. The fruit is rich in vitamins and minerals. The percentage content of some of the minerals, viz. phosphorus, potassium, calcium, magnesium and iron is 0.137, 0.746, 0.188, 0.127 and 0.007%, respectively. It is also rich in riboflavin, vitamin A, carbohydrates etc [1,2]. Various chemical constituents viz, alkaloids, coumarins and steroids have been isolated and identified from different parts of the bael tree. Marmelocin is probably the therapeutically active factor of bael fruit and is known as the panaceae of the stomach ailments. The aroma component of bael fruits was studied by Totikoma *et al.* [24]. The kymore plateau and satpura hills region of Madhya Pradesh have wide distribution of bael genotypes particularly in dry, undulating, forest and tribal areas which provides a tremendous scope and potential for cultivation of this fruit tree. This has created the necessity to breed new high yielding varieties. To improve the quality of variety in all aspects, presence of genetic variability in a population is pre requisite for planning any successful and effective crop improvement programme. Greater variability in crop plants provides an opportunity for selecting desirable types which may fulfil the needs of the growers. In view of the above facts, the present studies in bael entitled "Evaluation of Bael (*Aegle marmelos* Correa.) Gene pool of Kymore plateau and Satpura hill region" has been carried out with the objective to assess the variability in different physical traits of fruits as well as to mark the "Elite types" for further utilization and multiplication.

Materials and Methods

On the basis of information available from the local markets, villagers, farmers, state department of Horticulture and Farm Forestry, the potential locations of Madhya Pradesh especially Kymore plateau and Satpura hill region were selected

for survey. On the basis of visual appearance, liking and experience of villagers, the 20 genotypes were selected from different locations from the existing plant population and plant was tagged to study their morphological characteristics of plants and traits of their fruits. 3 randomly selected fruits were taken/treatment for analysis. The experiment was laid out in Completely Randomized Design (CRD) with three repetitions [16]. The observations were recorded and analyzed using standard procedure. The length of the fruits was measured from stem end to calyx end in centimetre with the help of Vernier callipers. The width (Transverse diameter) of the fruits was measured from the cut pieces in centre of fruits with the help of Vernier callipers. The volume of fruit was recorded by water displacement method with the help of measuring cylinder and was expressed in millilitres. The weight of fruit was taken with the help of electronic weighing machine and average weight of fruit was calculated. The taste of the fruit was observed as sweet, medium sweet and less sweet. The thickness of skull was measured with the help of Vernier callipers in mm. The skull weight of fruit was taken with the help of electronic weighing machine and average weight of skull was calculated. The pulp weight of fruit was recorded after the pulp extraction and average pulp weight was calculated in gram.

Result and discussion

Distinguishing features of genotypes on the basis of physical characters are as follows.

Fruit length (Polar diameter cm)

Fruit length was significantly affected by the different genotypes of bael. It varied from 7.25 cm to 13.19 cm. The maximum fruit length was recorded in the genotype JAM-2 followed by JAM-1, JAM-12, JAM-17 and JAM-3as compared to other genotypes. While, lowest fruit length was noted in genotype JAM-16. Variation in polar diameter of fruit was due to inherent genetic makeup of genotype, which may influence this morphological expression through the activity of endogenous growth regulators. The findings are also in agreement with the findings of Ghosh and Gayen [1]; Jaiswal *et al.* [3]; Kaushik, *et al.* [5]; Mishra *et al.* [9]; Prasad and Singh [17]; Lal [8]; Rai *et al.* [19]; Kaushik *et al.* [4]; Nath *et al.* [12]; Shrivastava and Singh [23]., Rai and Mishra [18]., Pandey *et al.* [15];

SN	Accession number	Details of location
1	JAM-1	G-59 Krishi Nagar, Adhartal, Jabalpur
2	JAM-2	F-51 Krishi Nagar, Adhartal, Jabalpur
3	JAM-3	G-16 Krishi Nagar, Adhartal, Jabalpur
4	JAM-4	G-3 Krishi Nagar, Adhartal, Jabalpur
5	JAM-5	Near Krishak Bhavan, Guest House No.2, JNKVV Jabalpur
6	JAM-6	Imaliya farm, Block Panagar, Jabalpur (IM-1)
7	JAM-7	Imaliya farm, Block Panagar, Jabalpur (IM-2)
8	JAM-8	Behind ICAR building JNKVV Jabalpur (ICAR-1)
9	JAM-9	Behind ICAR building JNKVV Jabalpur (ICAR-2)
10	JAM-10	Forestry Research farm Imaliya, Jabalpur (FR-1)
11	JAM-11	Forestry Research farm Imaliya, Jabalpur(FR-2)
12	JAM-12	Campus, Jabalpur (TFRI)
13	JAM-13	Forestry Research farm Imaliya, Jabalpur (FR-3)
14	JAM-14	Village Iswarpur, Ghansore, Dist. Seoni (IB-1)
15	JAM-15	Village Iswarpur, Ghansore, Dist. Seoni (IB-2)
16	JAM-16	Village Nidhani, Ghansore, Dist. Seoni
17	JAM-17	Near Railway crossing Bargi, Jabalpur
18	JAM-18	Sikara, Ghansore, Dist. Seoni
19	JAM-19	Shiv Mandir Bargi Nagar, Jabalpur (SM-1)
20	JAM-20	Shiv Mandir Bargi Nagar, Jabalpur (SM-2)

(JAM- Jawahar *Aegle marmelos*)

Pandey *et al.* [14]; Singh and Mishra [22]; and Pandey *et al.* [13].

Fruit width (Transverse diameter cm)

Fruit width varied from 8.40 cm to 11.47 cm. Significantly maximum fruit width was recorded in the genotypes JAM-2 and JAM-17, and which were at par with each other. However, the minimum fruit width was observed in JAM-4. Variation in transverse diameter of fruit was due to inherent genetic makeup of genotype, which may influenced this morphological expression through the activity of endogenous growth regulators. The findings are also in agreement with the findings of Ghosh and Gayen [1], Jaiswal *et al.* [3]; Kaushik *et al.* [5]; Mishra *et al.* [9]; Prasad and Singh [17]; Lal [8]; Rai *et al.* [19]; Kaushik *et al.* [4]; Shrivastava and Singh [23]; Pandey *et al.* [15]; Pandey *et al.* [14]; Singh and Mishra [21]; and Pandey *et al.* [13].

Table-1 Fruit length (Polar diameter cm), fruit width (Transverse diameter cm), fruit volume (ml) and fruit weight (g) as influenced by different genotypes of bael

Genotypes	Fruit length (Polar diameter cm)	Fruit width (Transverse diameter cm)	Fruit volume (ml)	Fruit weight (g)
JAM-1	12.30	9.95	432.03	557.00
JAM-2	13.19	11.47	851.17	1001.60
JAM-3	10.18	8.51	380.67	406.67
JAM-4	8.57	8.40	323.83	344.03
JAM-5	7.57	9.33	289.10	370.77
JAM-6	8.90	10.35	494.53	600.00
JAM-7	8.10	9.13	362.33	385.00
JAM-8	8.67	8.97	357.37	376.63
JAM-9	9.17	9.00	350.50	406.33
JAM-10	9.17	8.90	428.53	458.93
JAM-11	9.20	9.50	378.37	412.33
JAM-12	11.02	9.90	838.93	916.40
JAM-13	8.20	10.03	450.00	535.53
JAM-14	9.30	10.11	473.10	523.33
JAM-15	9.79	8.97	363.33	374.43
JAM-16	7.25	9.02	321.10	336.77
JAM-17	10.95	10.68	632.77	681.10
JAM-18	8.89	8.63	317.20	331.10
JAM-19	9.27	9.80	449.87	508.87
JAM-20	9.63	9.60	459.77	518.33
S.Em±	0.22	0.33	24.61	17.981
C.D.5% level	0.63	0.94	70.60	51.584

Fruit volume (ml)

Fruit volume range from 289.10 ml to 851.17 ml and significantly highest 851.17 ml and 838.93 ml fruits volume were recorded in the genotypes JAM-2 and JAM-12, respectively and which were at par with each other. However, the minimum fruits volume was observed in JAM-5. The findings are also in agreement with the findings of Ghosh and Gayen [1]; Lal [8]; Rai *et al.* [19]; Singh and Mishra [22].

Table-2 Skull thickness (mm), skull weight (g), pulp weight (g) and number of locules per fruit as influenced by different genotypes of bael

Genotypes	Skull thickness (mm)	Skull weight (g)	Pulp weight (g)	No. of locules /fruit
JAM-1	2.69	117.43	414.20	13.40
JAM-2	2.53	184.30	778.67	15.57
JAM-3	3.13	74.40	309.80	15.33
JAM-4	3.20	107.40	201.77	13.83
JAM-5	2.83	128.37	220.83	14.00
JAM-6	2.73	182.97	383.63	15.60
JAM-7	2.58	112.23	251.77	16.67
JAM-8	2.67	105.13	275.60	13.63
JAM-9	2.47	128.03	260.40	11.43
JAM-10	2.61	103.43	334.80	13.73
JAM-11	2.97	128.50	265.83	12.67
JAM-12	3.10	244.80	635.47	14.33
JAM-13	2.54	183.33	307.40	15.00
JAM-14	1.95	141.20	372.67	13.53
JAM-15	2.74	149.77	213.43	12.43
JAM-16	2.91	118.33	198.47	12.87
JAM-17	3.11	159.87	486.05	13.53
JAM-18	2.06	117.33	177.10	13.43
JAM-19	2.53	113.87	359.97	16.10
JAM-20	3.07	160.53	339.87	14.44
S.Em±	0.11	6.97	16.10	0.41
C.D.5% level	0.32	19.99	46.20	1.16

Fruit weight (g)

Fruit weight varied from 331.10 g to 1001.60 g. The maximum fruit weight 1001.60 g was recorded in the genotype JAM-2 followed by JAM-12, JAM-17 and JAM-6 as compared to other genotypes. While, lowest fruit weight was noted in genotype JAM-18. The findings are also in agreement with the findings of Ghosh and Gayen [1]; Kumar *et al.* [7]; Kaushik, *et al.* [5]; Prasad and Singh [17]; Lal [8]; Rai *et al.* [19]; Kaushik *et al.* [4]; Ram and Singh [20]; Nath *et al.* [12]; Shrivastava and Singh [23]; Rai and Mishra [18]; Nidhi and Gehlot [12]; Pandey *et al.* [15]; Pandey *et al.* [14]; Kenghe and Potdar [6]; Mitra *et al.* [11]; Singh and Mishra [22]; and Pandey *et al.* [13].

Skull thickness (mm)

Skull thickness varied from 1.95 mm to 3.20 mm. significantly lowest skull thickness (1.95 mm) was observed in JAM-14 followed by JAM-8 (2.06mm) and which were at par with each other. However, the maximum 3.20mm skull thickness was recorded in the genotypes JAM-4. The findings are also in agreement with the findings of Mishra *et al.* [9]; Lal [8]; Nath *et al.* [12]; Shrivastava and Singh [23]; Pandey *et al.* [15]; Pandey *et al.* [14]; Mitra *et al.* (2010) [11]; and Pandey *et al.* [13].

Skull weight (g)

Skull weight varied from 74.40 g to 244.80 g. The minimum skull weight 74.40 g skull weights were noted in genotype JAM-3 followed by JAM-10 (103.43 g), JAM-8 (105.13 g) and JAM-4 (107.40 g) as compared to other genotypes. While the maximum 244.80 g was recorded in the genotype JAM -12. The findings are in agreement with findings of Pandey *et al.* [15]; Pandey *et al.* [14]; And Pandey *et al.* [13].

Pulp weight (g)

The maximum pulp weight was recorded in the genotype JAM -2 followed by JAM-12 and JAM-17 as compared to other genotypes. While, lowest pulp weights was noted in genotype JAM-18. The findings are in agreement with findings of Ghosh and Gayen [1]; Nidhi and Gehlot [12]; Pandey *et al.* [15]; and Pandey *et al.* [14].

Table-3 Response of different genotypes of bael on number of seeds per locules, number of seeds per fruit and seed weight per fruit (g)

Genotypes	No. of seeds /locules	No. of seeds /fruit	Seed weight /fruit (g)
JAM-1	8.33	111.67	20.20
JAM-2	9.77	147.83	26.63
JAM-3	7.23	109.00	22.60
JAM-4	8.97	123.17	35.33
JAM-5	10.51	148.13	21.55
JAM-6	8.74	132.83	23.36
JAM-7	7.00	116.00	21.00
JAM-8	3.90	49.73	9.23
JAM-9	6.00	67.83	17.87
JAM-10	8.63	129.03	20.67
JAM-11	8.87	116.00	17.96
JAM-12	9.30	128.27	36.11
JAM-13	10.20	148.67	20.80
JAM-14	10.20	138.43	16.11
JAM-15	7.67	97.33	11.20
JAM-16	6.67	86.00	19.87
JAM-17	8.33	114.43	35.17
JAM-18	5.67	73.33	10.10
JAM-19	9.33	153.20	35.01
JAM-20	8.87	127.87	17.91
S.Em±	0.44	3.60	0.93
C.D.5% level	1.26	10.32	2.68

Table-4 Ratio of fruit weight: seed weight, fruit weight: pulp weight, fruit weight: fruit volume and pulp weight: seed weight of different genotypes of bael

Genotypes	Fruit weight: seed weight	Fruit weight: pulp weight	Fruit weight: fruit volume	Pulp weight: seed weight
JAM-1	27.58	1.34	1.29	20.52
JAM-2	37.70	1.29	1.18	29.29
JAM-3	18.03	1.31	1.07	13.74
JAM-4	9.74	1.71	1.06	5.71
JAM-5	17.32	1.68	1.29	10.30
JAM-6	25.81	1.56	1.22	16.52
JAM-7	18.47	1.53	1.07	12.08
JAM-8	40.79	1.37	1.05	29.85
JAM-9	22.75	1.56	1.17	14.58
JAM-10	22.26	1.37	1.07	16.25
JAM-11	22.96	1.57	1.09	14.77
JAM-12	25.38	1.44	1.09	17.61
JAM-13	25.70	1.78	1.23	14.70
JAM-14	32.62	1.41	1.11	23.25
JAM-15	33.44	1.75	1.03	19.06
JAM-16	17.03	1.70	1.05	10.04
JAM-17	19.40	1.40	1.08	13.85
JAM-18	32.89	1.91	1.05	17.45
JAM-19	14.58	1.41	1.15	10.32
JAM-20	28.91	1.53	1.13	18.96
S.Em±	0.98	0.06	0.04	0.82
C.D.5% level	2.82	0.17	0.13	2.35

Number of locules per fruit

Number of locules per fruit was significantly affected by the different genotypes of bael. The maximum number of locules per fruit was recorded in the genotype

JAM-7 followed by JAM-19, JAM-6 and JAM-2. While, lowest number of locules per fruit was noted in genotype JAM-9. Our findings are also in conformity with findings of Mishra *et al.* [9]; Pandey *et al.* [14]; Singh and Mishra [22].

Number of seeds per locules

Number of seeds per locules was significantly affected by the different genotypes of bael and ranged between 3.90-10.51. The minimum 3.90 number of seeds per locules was noted in genotype JAM-8 followed by JAM-18, JAM-9, JAM-16 and JAM-7. However, maximum number of seed 10.51 per locules was recorded in the genotype JAM-5. Similar results have been reported by Singh and Mishra [22]; and Pandey *et al.* [13].

Number of seeds per fruit

Number of seeds per fruit of bael varied from 49.73 to 153.20. The significantly minimum 49.73 number of seeds per fruit was noted in genotype JAM-8 followed by JAM-9, JAM-18, JAM-16 and JAM-15 as compared to other genotypes. While, maximum number of seed 153.20 per fruit was recorded in the genotype JAM-19. The findings are in agreement with findings of Mishra *et al.* [9]; Rai *et al.* [19]; Ram and Singh [20]; Shrivastava and Singh [23]; Rai and Mishra [18]; Pandey *et al.* [15]; Pandey *et al.* [14]; Mitra *et al.* [11]; Singh and Mishra [22]; and Pandey *et al.* [13].

Seed weight per fruit (g)

Seed weight per fruit range from 9.23 g to 36.11 g. The significantly minimum 9.23 g/fruit seed weight was noted in genotype JAM-8 followed by JAM-18 and JAM-15 and which were at par with each other. Whereas, the maximum seed weight 36.11 g per fruit was recorded in the genotype JAM-12. The findings are in agreement with findings of Rai *et al.* [19]; Rai and Mishra [18]; Pandey *et al.* [15]; Pandey *et al.* [14]; Singh and Mishra [22]; and Pandey *et al.* [13].

Fruit weight: seed weight

The significantly maximum ratio (40.79) of fruit weight and seed weight was recorded in the genotype JAM-8 followed by JAM-2, JAM-15, JAM-18 and JAM-14. Whereas, the lowest 9.74 ratio of fruit weight and seed weight was noted in genotype JAM-4.

Fruit weight: pulp weight

Genotype JAM -18 was recorded the significantly maximum 1.91 ratios of fruit weight and pulp weight followed by JAM-13, JAM-15, JAM-4 and JAM-16 as compared to other genotypes. While, lowest 1.29 ratios of fruit weight and pulp weight was noted in genotype JAM-2. The findings are in agreement with findings of Pandey *et al.* [15].

Fruit weight: fruit volume

Ratio of fruit weight and fruit volume was significantly affected by the different genotypes of bael. The maximum 1.29 ratio of fruit weight and fruit volume was recorded in the genotype JAM-1 and JAM-5 followed by JAM-13, JAM-6, JAM-2 and JAM-9. While, lowest 1.03 ratio of fruit weight and fruit volume was noted in genotype JAM-15.

Pulp weight: seed weight

Significantly highest 29.85 and 29.29 ratio of pulp weight and seed weight were recorded in the genotype JAM-8 and JAM-2, respectively and which were at par with each other. Whereas, the lowest ratio of pulp weight and seed weight (5.71) was noted in genotype JAM-4. Similar results have been reported by Nidhi and Gehlot [12].

Conclusion

On the basis of present investigation, it is found that many genotypes are valuable for one or other traits but considering the most important traits like higher pulp percentage, and less number of seeds and fruit weight, the genotypes JAM-8 is most superior with pulp% (73.18), No of seed (53.16), TSS-38.70 oBrix followed by JAM-1, JAM-2, JAM3, JAM-10, JAM-12 and JAM-17 which may be include for further utilization and multiplication of quality planting material.

Application of Research: Study showed many genotypes are valuable for one or other traits but considering the most important traits like higher pulp percentage, and a smaller number of seeds and fruit weight.

Research Category: Horticulture-Crop Improvement

Abbreviation: JAM: Jawahar *Aegle marmelos*

Acknowledgement / Funding: Authors are thankful to Jawaharlal Nehru Krishi Vishwa Vidyalyaya, Jabalpur, 482004, India

***Research Guide or Chairperson of research: Dr C.S. Pandey**

University: Jawaharlal Nehru Krishi Vishwa Vidyalyaya, Jabalpur, 482004, India

Research project name or number: M.Sc. (Ag) Horticulture thesis

Author Contributions: All authors equally contributed

Author statement: All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

Study area / Sample Collection: Kymore plateau and Satpura hill region, Madhya Pradesh

Cultivar / Variety name: *Aegle marmelos* Correa

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

References

- [1] Ghosh D. Kand Gayen P. (1993) *Progressive Horticulture*, 22 (1-4), 6-11.
- [2] Gopalan C.B.M., Ramashastry B.V. and Balasubramaniam S.C. (1985) *Nutritive value of Indian foods*, ICMR, Hyderabad pp 47.
- [3] Jaiswal H. R., Misra K.K., and Vijai Singh (1999) *Scientific Horticulture*, 6, 25-30.
- [4] Kaushik R. A., Yamdagni R. and Dhawan S. S. (2002) *Haryana Journal of Horticultural Sciences*, 31 (1/2), 32-34.
- [5] Kaushik R. A., Yamdagni R. and Dhawan S.S. (2000) *Haryana Journal of Horticultural Sciences*, 29 (1/2), 44-45.
- [6] Kenghe R.N. and Potdar S.N. (2009) *Journal of Maharashtra Agricultural Universities*, 34 (2), 205-207.
- [7] Kumar Dinesh, Rajput C.B.S. and Singh S.P. (1996) *Recent Horticulture*, 3 (1), 49-51.
- [8] Lal G. (2002) *Current Agriculture*, 26 (1/2), 127-129.
- [9] Mishra K.K., Rajesh Singh, Jaiswal H.R. (2000) *Indian Journal of Agricultural Sciences*, 70 (10), 682-683.
- [10] Mitra S.K., Maity C.S., Mani D. and Ghosh B. (2010) *Acta Horticulture*, 864, 49- 51.
- [11] Nath Vishal, Pandey Devendra and Das Bikash (2003) *Indian Journal of Plant Genetic Resources*, 16 (3), 222 - 225.
- [12] Nidhi and Gehlot, Rakesh (2007) *Research on Crops*, 8 (1), 189-190
- [13] Pandey D., Tandon D.K., Umesh Hudedamani and Tripathi M. (2013) *Indian Journal of Horticulture*, 70 (2), 170-178.
- [14] Pandey D., Shukla S.K., and Akhilesh Kumar (2008a) *Journal of Tropical Forestry*, 24 (1/2), 31-36.
- [15] Pandey D., Shukla S.K. and Kumar A. (2008) *Indian Journal of Horticulture*, 65 (2), 226-229.
- [16] Panse V.C. and Sukhatme P.V. (1985) *Statistical methods for agricultural workers*. ICAR Publications, New Delhi. pp 155.
- [17] Prasad Yogesh and Singh R.P., (2001) *Haryana Journal of Horticultural Sciences*, 30 (1/2), 70-71.
- [18] Rai Deepti and Misra K.K. (2005) *Indian Journal of Horticulture*, 62 (2), 152-154.
- [19] Rai Deepti, Mishra K.K. and Singh V.P. (2002) *Progressive Agriculture*, 34 (1), 35-38.
- [20] Ram D. and Singh I.S. (2003) *Progressive Horticulture*, 35 (2), 199-201.
- [21] Singh V.P. and Mishra K.K. (2008) *Environment and Ecology*, 26 (3), 1208-1210.
- [22] Singh V.P. and Mishra K.K. (2010a) *Progressive Agriculture*, 10 (1), 132-134.
- [23] Srivastava K.K. and Singh H.K. (2004) *Agric. Sci. Digest*, 24 (1), 65-66.
- [24] Totikoma Y. Shimono Y., Kobayashi A. and Yamanishi T. (1982) *Agril. Biological Chemistry*, 46(7), 1873-1877.