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## Biochemical studies in bael (*Aegle marmelos* Correa.) gene pool of Kymore plateau and Satpura hill region

**Nilesh Parihar and CS Pandey**

### Abstract

The present investigation was carried out during 2011-2013 at Department of Horticulture, College of Agriculture, JNKVV, and Jabalpur (M.P.). The experimental material was comprised of twenty genotypes of the bael to assess the chemical characteristics of fruits for finding out superior genotypes in quality. Significantly highest 44.00 Brix total soluble solid were recorded in the genotype JAM-15, lowest 0.130% acidity was noted in genotype JAM-15. The maximum reducing sugar (7.77%) was recorded in the genotype JAM-9 and maximum non-reducing sugar (4.60%) and total sugar (11.97%) was recorded in the genotype JAM-7.

**Keywords:** Bael (*Aegle marmelos*) genotypes, total soluble Solids and acidity

### 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 (Gopalan *et al.*, 1985)<sup>[1]</sup>. Various chemical constituents viz, alkaloids, coumarin 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 panacea of the stomach ailments. The aroma component of bael fruits was studied by Totikoma *et al.* (1982)<sup>[21]</sup>.

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 fulfill the needs of the growers. In view of the above facts, the present studies in bael entitled "Variability studies in 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 chemical traits of fruits and 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 chemical characteristics of their fruits. 3 randomly selected fruits were taken/treatment for chemical analysis in Completely Randomized Design (CRD) with three repetition. The fruits were chemically analyzed using standard procedure.

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**Table 1:** Treatment details

S. No.	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*)

## Result and Discussion

Bael genotypes were evaluated based on quality characters of fruit. Distinguishing features of genotypes on the basis of quality traits are as follows.

### Total Soluble Solid (<sup>o</sup> Brix)

Significantly highest 44.00, 43.43, 42.30 and 41.97<sup>o</sup> Brix total soluble solid were recorded in the genotype JAM-15, JAM-20, JAM-12 and JAM-7, respectively. However, the lowest 32.0<sup>o</sup> Brix T.S.S. was noted in genotype JAM-2. Total soluble solids were higher at the ripe stage. Similar results have been reported by Kumar *et al.* (1996) [4], Kaushik, *et al.* (2000) [3], Prasad and Singh (2001) [14], Rai *et al.* (2002) [15], Kaushik *et al.* (2002) [2], Ram and Singh (2003) [16], Shrivastava and Singh (2004), Sheoran *et al.* (2007) [18], Nidhi and Gehlot (2007) [8], Saroj *et al.* (2008) [17], Pandey *et al.* (2008) [11], Pandey *et al.* (2008a) [10], Parihar *et al.* (2009) [13], Mitra *et al.* (2010) [7], Singh and Mishra (2010a) [19] and Pandey *et al.* (2013) [9].

### Acidity (%)

Significantly lowest 0.130% acidity was noted in genotype JAM-15 followed by JAM –9 (0.133%), JAM –20 (0.133%), JAM –6 (0.140%), JAM –12 (0.140%), JAM –1 (0.150%), JAM –7 (0.150%), JAM –18 (0.150%) and JAM –4 (0.157%) and which were at par with each other. However, the highest 0.233% acidity were recorded in the genotype JAM-19. Acidity was higher at green stage. Similar results have been reported by Kaushik, *et al.* (2000) [3], Kaushik *et al.* (2002) [2], Ram and Singh (2003) [16], Sheoran *et al.* (2007) [18], Nidhi and Gehlot (2007) [8], Verma and Gehlot (2007) [22], Saroj *et al.* (2008) [17], Pandey *et al.* (2008) [11], Pandey *et al.* (2008a) [10], Parihar *et al.* (2009) [13], Singh and Mishra (2010a) [19], Mitra *et al.* (2010) [7] and Pandey *et al.* (2013) [9].

### Reducing sugar (%)

The significantly maximum reducing sugar (7.77%) was recorded in the genotype JAM-9 followed by JAM-6, JAM-12, JAM-1 and JAM-7 and which were at par with each other. Therefore, the lowest 4.93% reducing sugar was noted in genotype JAM-19. Similar results have been reported by Mishra *et al.* (2000) [6], Prasad and Singh (2001) [14], Ram and Singh (2003) [16], Sheoran *et al.* (2007) [18], Nidhi and Gehlot (2007) [8], Verma and Gehlot (2007) [22], Pandey *et al.* (2008) [11], Pandey *et al.* (2008a) [10] and Pandey *et al.* (2013) [9].

### Non- reducing sugar (%)

The significantly maximum (4.60%) non-reducing sugar was recorded in the genotype JAM-7 followed by JAM-6, JAM-12, JAM-18, JAM-11, JAM-14 and JAM-8 and which were at par with each other. While, the lowest 2.10% non-reducing sugar was noted in genotype JAM-2. The findings are in agreement with findings of Prasad and Singh (2001) [14], Ram and Singh (2003) [16] and Pandey *et al.* (2013) [9].

### Total sugar (%)

The significantly maximum (11.97%) total sugar was recorded in the genotype JAM-7 followed by JAM-6, JAM-12, JAM-9, JAM-18, JAM-20, JAM-1 and JAM-8 and which were at par with each other. While, the lowest 7.53% total sugar was noted in genotype JAM-2. The findings are in agreement with findings of Mishra *et al.* (2000) [6], Ram and Singh (2003) [16], Shrivastava and Singh (2004), Sheoran *et al.* (2007) [18], Nidhi and Gehlot (2007) [8], Verma and Gehlot (2007) [22], Pandey *et al.* (2008) [11], Pandey *et al.* (2008a) [10] and Pandey *et al.* (2013) [9].

**Table 2:** Total Soluble Solid (<sup>0</sup> Brix), acidity (%), reducing sugar (%), non- reducing sugar (%) and total sugar (%) as influenced by different genotypes of bael.

Genotypes	Total Soluble Solid ( <sup>0</sup> Brix)	Acidity (%)	Reducing sugar (%)	Non- reducing sugar (%)	Total sugar (%)
JAM-1	40.77	0.150	7.48	3.49	10.97
JAM-2	32.00	0.203	5.43	2.10	7.53
JAM-3	41.20	0.163	7.13	2.30	9.43
JAM-4	40.00	0.157	6.81	2.93	9.73
JAM-5	37.70	0.163	7.20	2.23	9.43
JAM-6	38.83	0.140	7.76	4.12	11.88
JAM-7	41.97	0.150	7.37	4.60	11.97
JAM-8	38.70	0.170	6.87	3.87	10.70
JAM-9	39.53	0.133	7.77	3.60	11.40
JAM-10	39.53	0.167	5.83	3.17	9.00
JAM-11	39.67	0.167	6.40	4.00	10.40
JAM-12	42.30	0.140	7.67	4.13	11.80
JAM-13	37.43	0.177	5.80	2.80	8.70
JAM-14	36.00	0.187	6.47	3.93	10.11
JAM-15	44.00	0.130	7.27	2.93	10.20
JAM-16	36.20	0.187	6.40	2.73	9.17
JAM-17	35.43	0.207	5.57	3.80	9.37
JAM-18	39.43	0.150	7.33	4.13	11.37
JAM-19	29.77	0.223	4.93	2.90	7.83
JAM-20	43.43	0.133	7.30	3.70	11.00
S.Em±	0.92	0.011	0.38	0.27	0.54
C.D.5% level	2.64	0.030	1.09	0.78	1.54

### Summary & Conclusion

On the basis of present investigation it is concluded that many genotypes are valuable in one or other trait i.e.-

1. The genotype JAM-15, JAM-20, JAM-12 and JAM-7 recorded significantly highest 44.00, 43.43, 42.30 and 41.97<sup>0</sup> Brix total soluble solid respectively.
2. The genotype JAM-15 recorded lowest 0.130% acidity followed by JAM –9, JAM –20, JAM –6, JAM –12, JAM –1, JAM –7, JAM –18 and JAM –4 which were at par with each other.
3. The genotype JAM-9 recorded maximum reducing sugar (7.77%) followed by JAM-6, JAM-12, JAM-1 and JAM-7.
4. The genotype JAM-7 recorded maximum non-reducing sugar (4.60%) followed by JAM-6, JAM-12, JAM-18, JAM-11, JAM-14 and JAM-8.
5. The genotype JAM-7 recorded maximum total sugar (11.97%) followed by JAM-6, JAM-12, JAM-9, JAM-18, JAM-20, JAM-1 and JAM-8.

### Application of Research

Based on research findings, the different superior genotypes may be utilized for further utilization in crop improvement and multiplication programme.

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