



Genetic variability of star gooseberry in north east India

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ABSTRACT

Assessment of genetic variability is the prerequisite for development of improved genotypes through planned breeding programme. Therefore, an investigation was carried out to identify superior genotypes of star gooseberry of Mizoram, India and to determine variability for physical and biochemical traits during 2017-2018. The matured fruits of 30 genotypes were analyzed for physico-chemical traits like fruit weight, fruit length, fruit diameter, fruit volume, specific gravity, pulp weight, pulp-seed ratio, pulp percentage, seed weight, moisture content, TSS, acidity, ascorbic acid, total sugars, reducing sugar, non-reducing sugar, sugar: acid ratio, TSS: acid ratio. The study reveals significant variation among the genotypes with respect to all these parameters. Out of all the genotypes, MZU-HAMP-SGS-3, MZU-HAMP-SGS-10 and MZU-HAMP-SGS-13, MZU-HAMP-SGS-19, MZU-HAMP-SGS-20, MZU-HAMP-SGS-21 showed the overall superiority in all the parameters. Therefore, from the present investigation, it can be concluded that MZU-HAMP-SGS-3, MZU-HAMP-SGS-10 and MZU-HAMP-SGS-13, MZU-HAMP-SGS-19, MZU-HAMP-SGS-20, MZU-HAMP-SGS-21 can be considered as elite star gooseberry genotypes for future improvement programme.

Keywords: *Phyllanthus acidus* Skeels, Genetic diversity, Mizoram

INTRODUCTION

Star gooseberry (*Phyllanthus acidus*) (L.) Skeels a close relative of aonla belongs to Euphorbiaceae family is one of the earliest known tribal fruit grown in abundance in India and other Asian countries. The fruits are rich in ascorbic acid, niacin, riboflavin, carotene, calcium, phosphorus, iron and other health promoting substances like flavonoids and phenolics (Mishra, 10). The antioxidants rich fruits have immense medicinal properties like purgative, hepatoprotective, anti-diabetics and anti-nociceptive.

The knowledge of the magnitude of genetic variation among fruit characters and their heritability is very much important for predicting genetic progress in breeding programme and developing efficient breeding strategies in a highly out crossing species (Rajan *et al.*, 12). Although, newly developed molecular markers are valuable in gene based diversity studies, but have the limitations of high cost. In contrast, morphological traits could feasibly be used for parental selection and germplasm classification in plant breeding programs.

In Mizoram, north-eastern India, star gooseberry trees are found growing wild in the natural forests or semi wild in marginal land or in home gardens without commercial cultivation. As majority of them are from seedling origin, hence a tremendous variations exist in their morphology and physico-chemical traits in the naturally scattered populations. Despite of its immense potential as medicinal plant, no

systematic efforts have so far been made to identify promising star gooseberry genotypes based on their Horticultural traits. So the present study was made to develop adequate phenotypic markers for the identification and management of star gooseberry genotypes for their further intended use.

MATERIALS AND METHODS

The surveying of star gooseberry genotypes and collection of fruits from six districts of Mizoram viz., Aizawl, Lunglei, Serchhip, Mamit, Champhai and Kolasib comprising of 30 different villages was conducted during the fruiting season of 2017-2018. The details of the genotypes and their sources are described in Table 1. The collected specimens were immediately brought to the departmental laboratory, Dept. of HAMP, Mizoram University for analysis of physico-chemical characters.

For measuring the physical parameters, 20 randomly selected fruits were taken from each of three replications during March-April. The data on fruit weight were recorded with the help of electronic balance, while fruit and seed size were measured with digital vernier caliper. The fruit volume was measured by water displacement method. The specific gravity was measured by dividing the fruit weight by the fruit volume. The standard method (AOAC, 1) was followed to determine the titratable acidity, reducing, non-reducing and total sugars of fruit. Visual titration method was followed for the estimation of ascorbic acid and the result was expressed in mg per 100 g

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Table 1. Genotypes and their sources

Sl. No.	Genotypes	Location	Latitude	Longitude	Elevation (m. a. m. s. l.)
1.	MZU-HAMP-SGS-1	Sairang	23°48'31"N	92°39'23"E	165
2.	MZU-HAMP-SGS-2	Seling	23°43'29"N	92°51'18"E	748
3.	MZU-HAMP-SGS-3	Reiek	23°40'39"N	92°36'20"E	1232
4.	MZU-HAMP-SGS-4	Aibawk	23°33'32"N	92°42'23"E	793
5.	MZU-HAMP-SGS-5	Darlawn	24°00'52"N	92°55'28"E	1088
6.	MZU-HAMP-SGS-6	Rawpui	23°08'45"N	92°53'55"E	756
7.	MZU-HAMP-SGS-7	Hnahthial	22°57'55"N	92°55'48"E	761
8.	MZU-HAMP-SGS-8	Tuipui D	22°54'18"N	92°55'50"E	257
9.	MZU-HAMP-SGS-9	Leite	22°54'06"N	92°54'40"E	713
10.	MZU-HAMP-SGS-10	Thiltlang	23°01'13"N	92°55'16"E	783
11.	MZU-HAMP-SGS-11	Chhiahtlang	23°22'39"N	92°50'43"E	897
12.	MZU-HAMP-SGS-12	Baktawng	23°32'10"N	92°50'45"E	1176
13.	MZU-HAMP-SGS-13	Tlungvel	23°36'16"N	92°51'14"E	1151
14.	MZU-HAMP-SGS-14	N. Vanlaiphai	23°07'48"N	93°03'42"E	1371
15.	MZU-HAMP-SGS-15	Keitum	23°13'55"N	92°54'40"E	703
16.	MZU-HAMP-SGS-16	Khamrang	23°56'02"N	92°39'14"E	200
17.	MZU-HAMP-SGS-17	Kawnpui	24°02'39"N	92°40'18"E	825
18.	MZU-HAMP-SGS-18	Bilkhawthlir	24°02'08"N	92°43'04"E	473
19.	MZU-HAMP-SGS-19	Thingdawl	23°37'59"N	92°43'18"E	871
20.	MZU-HAMP-SGS-20	Bualpui N	24°05'39"N	92°41'01"E	964
21.	MZU-HAMP-SGS-21	Lengte	23°46'19"N	92°36'00"E	483
22.	MZU-HAMP-SGS-22	Lengpui	23°49'53"N	92°37'46"E	407
23.	MZU-HAMP-SGS-23	Rawpuichhip	23°47'07"N	92°33'37"E	773
24.	MZU-HAMP-SGS-24	Dampui	23°48'55"N	92°29'35"E	988
25.	MZU-HAMP-SGS-25	Tuidam	23°55'39"N	92°22'06"E	700
26.	MZU-HAMP-SGS-26	Zohnuai	23°44'31"N	92°42'26"E	869
27.	MZU-HAMP-SGS-27	Zuangtui	23°45'40"N	92°44'42"E	998
28.	MZU-HAMP-SGS-28	Kawlkuh	23°36'51"N	92°05'00"E	1119
29.	MZU-HAMP-SGS-29	Khawzawl	23°31'52"N	93°11'02"E	1254
30.	MZU-HAMP-SGS-30	Durtlang	23°47'09"N	92°43'48"E	1077

(Freed, 3). The data were statistically analysed by using completely randomized Design (CRD) and the analysis of variance (ANOVA) for each parameter was performed using PROC GLM of statistical analysis system (SAS) software (version 9.3; SAS Inc, Cary, NC). Mean separation for different treatments and parameters was performed using least significant different (LSD) test ($P \leq 0.05$).

RESULTS AND DISCUSSION

The genotypes studied during the course of present study varied significantly with respect to physical characteristics of fruit (Table 2). Among all

the genotypes, the highest fruit weight was recorded in MZU-HAMP-SGS-21 (5.32g), followed by MZU-HAMP-SGS-19 (5.29 g), MZU-HAMP-SGS-13 (5.17 g), MZU-HAMP-SGS-10 (5.04 g), MZU-HAMP-SGS-20 (4.85 g), MZU-HAMP-SGS-3 (4.74 g), and MZU-HAMP-SGS-27 (4.54 g), while the lowest fruit weight was observed in MZU-HAMP-SGS-5 (2.57 g). The rich variation in fruit weight could be due to highly heterozygous and diverse genetic background of parents. Since, all the plants are of seed origin, there might be differences in the genetic make-up of the plants, which might have contributed the variations in fruit weight among the genotypes. Our study is in

Table 2. Fruit physical parameters among different genotypes.

Genotypes	Fruit weight (g)	Fruit length (mm)	Fruit diameter (mm)	Specific gravity (cc)	Pulp weight (g)	Pulp content (%)	Seed length (mm)	Seed diameter (mm)	Seed weight (g)
MZU-HAMP-SGS-1	4.01	15.79	21.79	0.96	3.81	95.01	6.33	7.80	0.20
MZU-HAMP-SGS-2	3.33	14.94	20.52	0.96	3.12	93.77	6.39	7.67	0.21
MZU-HAMP-SGS-3	4.74	16.18	23.22	0.98	4.60	96.98	5.49	6.86	0.14
MZU-HAMP-SGS-4	3.84	15.66	21.37	1.07	3.60	93.72	6.73	7.34	0.24
MZU-HAMP-SGS-5	2.57	13.64	18.29	0.79	2.40	93.43	6.05	6.28	0.17
MZU-HAMP-SGS-6	3.88	15.75	20.99	1.05	3.66	94.20	5.97	7.98	0.22
MZU-HAMP-SGS-7	3.80	15.21	21.35	1.05	3.57	94.02	5.93	8.30	0.23
MZU-HAMP-SGS-8	3.51	15.46	20.41	1.08	3.32	94.18	6.17	7.57	0.19
MZU-HAMP-SGS-9	3.54	15.63	20.35	1.33	3.36	94.73	6.10	7.82	0.19
MZU-HAMP-SGS-10	5.04	16.41	23.39	1.06	4.89	97.03	5.23	6.43	0.15
MZU-HAMP-SGS-11	4.30	15.96	22.62	0.99	4.13	95.99	6.02	8.37	0.17
MZU-HAMP-SGS-12	4.46	15.81	22.83	1.12	4.24	94.86	5.57	5.55	0.22
MZU-HAMP-SGS-13	5.17	15.77	24.39	1.18	5.01	96.84	5.38	6.62	0.16
MZU-HAMP-SGS-14	3.93	14.80	21.67	1.07	3.71	94.40	5.54	8.75	0.22
MZU-HAMP-SGS-15	3.66	14.71	21.24	0.91	3.52	96.19	4.97	7.58	0.14
MZU-HAMP-SGS-16	3.38	14.43	20.65	1.15	3.20	94.64	5.67	8.59	0.18
MZU-HAMP-SGS-17	3.94	14.88	21.98	1.20	3.76	95.18	5.17	8.96	0.19
MZU-HAMP-SGS-18	3.62	14.31	21.26	1.10	3.43	94.83	5.40	8.79	0.19
MZU-HAMP-SGS-19	5.29	16.23	23.69	1.05	5.13	96.89	5.14	7.10	0.16
MZU-HAMP-SGS-20	4.85	16.37	23.27	0.99	4.68	96.56	5.08	6.85	0.16
MZU-HAMP-SGS-21	5.32	16.21	23.14	0.98	5.16	96.92	5.07	6.44	0.16
MZU-HAMP-SGS-22	4.11	15.67	21.10	1.05	3.89	94.62	5.96	7.91	0.22
MZU-HAMP-SGS-23	3.88	15.38	21.24	1.01	3.67	94.66	5.63	7.10	0.21
MZU-HAMP-SGS-24	4.51	15.37	22.83	1.41	4.28	94.81	5.43	8.32	0.23
MZU-HAMP-SGS-25	3.77	14.93	20.82	1.14	3.52	93.45	5.97	8.24	0.25
MZU-HAMP-SGS-26	3.90	15.27	21.66	1.25	3.67	93.94	6.34	7.80	0.23
MZU-HAMP-SGS-27	4.54	15.77	21.37	1.12	4.32	95.24	5.35	8.13	0.22
MZU-HAMP-SGS-28	4.14	15.66	21.80	1.03	3.91	94.38	5.97	8.24	0.23
MZU-HAMP-SGS-29	4.19	15.89	21.38	1.11	3.99	95.23	5.37	7.99	0.20
MZU-HAMP-SGS-30	3.85	15.05	21.25	1.14	3.64	94.51	5.44	7.95	0.21
S.Em (±)	0.38	0.41	0.70	0.11	0.38	0.77	0.19	0.43	0.02
CD _{0.05}	0.79	0.86	1.47	0.22	0.80	1.61	0.40	0.90	0.04

close conformity with the findings of Sharma (13), Hazarika *et al.* (5), and Singh *et al.* (15) who also reported the similar variations in fruit weight of aonla.

The data presented in Table 2 revealed that the highest fruit length was recorded in MZU-HAMP-SGS-10 (16.41 mm), which was significantly higher than all other genotypes except MZU-HAMP-SGS-20 (16.37 mm), MZU-HAMP-SGS-19 (16.23 mm), MZU-HAMP-SGS-21 (16.21 mm), and MZU-HAMP-

SGS-3 (16.18 mm), with which it was found statistically *at par*. Similarly, MZU-HAMP-SGS-13 had the highest diameter (24.39 mm), and MZU-HAMP-SGS-9 exhibited the lowest diameter of fruits (20.35 mm). The variation in fruit length and diameter may be attributed to differences in genetic features of the individual genotypes and soil and climatic condition. More or less similar kinds of variability in fruit length were observed by Chandra *et al.* (2), Hazarika *et al.*

(5), Singh *et al.* (15) and Hazarika and Lalitluangkimi (4). Shukla *et al.* (14) reported variation in fruit diameter among different aonla genotypes.

The star gooseberry genotypes varied significantly with respect to fruit volume (Fig. 1). The highest fruit volume was recorded in MZU-HAMP-SGS-21 (5.43 cc) having similarity statistically with MZU-HAMP-SGS-19 (5.03 cc), while it was lowest in MZU-HAMP-SGS-9 (2.67 cc). Our results are in the line with the findings of Chandra *et al.* (2), Hazarika *et al.* (5), Singh *et al.* (15), Singh and Singh (17) and Hazarika and Lalitluangkimi (4), from North-east India who also reported variation in fruit volume among aonla genotypes. The variation in fruit volume among star gooseberry genotypes may be due to differences in their genetic make-up and prevailing agro-climatic conditions, i.e. nutrient, soil, light, water and altitude under which the plants are growing. Similarly, the maximum (1.33 g/cc) and minimum (0.79 g/cc) specific gravity of fruit were observed in MZU-HAMP-SGS-9 and MZU-HAMP-SGS-5 genotypes respectively (Table 2), as also reported by Hazarika *et al.* (5), Singh *et al.* (15) Singh and Singh (17), and Hazarika and Lalitluangkimi (4). The variation in specific gravity among different star gooseberry genotypes might be due to differences in fruit weight and volume which contributes towards the specific gravity of the fruits.

Among all the genotypes, the highest pulp content was recorded in MZU-HAMP-SGS-21 (5.16 g), followed by MZU-HAMP-SGS-19 (5.13 g), MZU-HAMP-SGS-13 (5.01 g), MZU-HAMP-SGS-10 (4.89 g), MZU-HAMP-SGS-20 (4.68 g), and MZU-HAMP-SGS-27 (4.32 g) without having significant difference, while the lowest pulp content was noticed in MZU-HAMP-SGS-5 (2.40 g). Among all the genotypes, MZU-HAMP-SGS-10 recorded the highest pulp percentage (97.03 %), whereas MZU-HAMP-SGS-5 yielded the fruits with lowest content of fruit pulp (93.43 %) (Table 2). Such variation in pulp characters may be attributed due to the

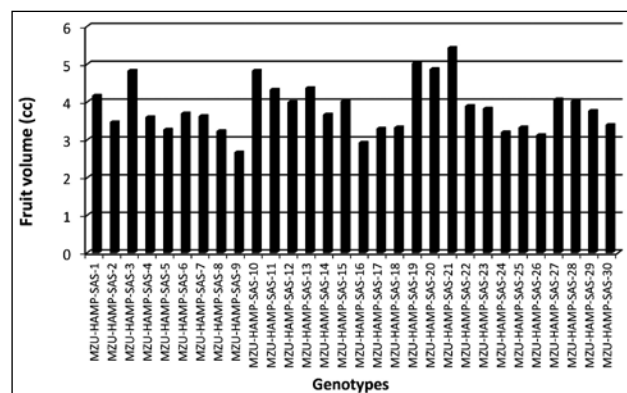


Fig. 1. Fruit volume among the different genotypes

difference in pulp length, pulp width and pod thickness. The similar findings in aonla have also been reported by various researchers (Sharma, 13 Hazarika and Lalitluangkimi, 4; Hazarika *et al.*, 5).

The various genotypes tested showed the significant variations respect to seed parameters of star gooseberry. Among all the genotypes, the longest seeds were observed in MZU-HAMP-SGS-4 (6.73 mm), while these were the shortest in HAMP-SGS-15 (4.97 mm). MZU-HAMP-SGS-17 was found to have the highest seed diameter (8.96 mm), while MZU-HAMP-SGS-12 proved worse (5.55 mm) in respect of this trait. Similarly, maximum seed weight was recorded in MZU-HAMP-SGS-25 (0.25 g), which was closely followed by MZU-HAMP-SGS-3, while MZU-HAMP-SGS-15 tended to produce the lightest seeds (0.14 g) of star gooseberry (Table 2). For an ideal variety, lower weight and small size of seed are the desirable characters. These observations revealed a positive correlation among pulp weight, seed weight and fruit weight. The genotypes produced higher fruit weight may be due to higher pulp weight and less seed weight. This clearly indicated that, during selection of any genotype based on fruit, the breeder should give emphasis on fruit pulp content rather than fruit weight alone. Our results is in the line with the findings of Chandra *et al.* (2) and Singh *et al.* (15) Singh and Singh (17) who reported variation in seed parameters among aonla genotypes.

It is evident from the data presented in Fig. 2 that among the different genotypes of star gooseberry, MZU-HAMP-SGS-3 (33.69) recorded the significantly highest pulp: seed ratio having similarity statistically with MZU-HAMP-SGS-10 (32.67), MZU-HAMP-SGS-21 (32.32), MZU-HAMP-SGS-19 (31.44) and MZU-HAMP-SGS-13 (30.82), however it was lowest in the fruits of MZU-HAMP-SGS-25 (14.41). The differences in pulp: seed ratio might be due to variations in pulp and seed weight among the individual genotypes.

The fruit quality traits in the studied populations of different star gooseberry fruits varied significantly are presented in Fig. 3 and Table 3. Comparison of data on moisture content revealed that the fruits of MZU-HAMP-SGS-20 exhibited the highest content of moisture (90.90 %), while the lowest was recorded in MZU-HAMP-SGS-28 (79.19%). The similar variations in the moisture content of aonla fruits have also been reported by Hazarika *et al.*, (5) and Hazarika and Lalitluangkimi (4). Similarly, the fruits of genotype MZU-HAMP-SGS-3 were found most juicy (47.13%) having similarity statistically with MZU-HAMP-SGS-10 (42.67%), MZU-HAMP-SGS-13 (42.15%), MZU-HAMP-SGS-20 (42.08%) and MZU-HAMP-SGS-19 (41.58 %), while the lowest juice content was recorded in HAMP-SGS-29 (23.08%). The rich variation in moisture and juice

could also be due to highly heterozygous and diverse genetic background of parents. The similar variation in the content of juice in aonla was also reported by Hazarika *et al.* (7,8).

The genotypes varied significantly with respect to TSS of the fruits (Table 3). The content of TSS was highest in MZU-HAMP-SGS-19 (8.50 °B) having similarity statistically with MZU-HAMP-SGS-3 (8.22 °B), MZU-HAMP-SGS-20 (8.17 °B), MZU-HAMP-SGS-21

(8.03 °B), and MZU-HAMP-SGS-13 (7.97 °B), while the lowest TSS was recorded in MZU-HAMP-SGS-2 (6.73 °B). The variation in TSS among the genotypes may be due to different genetical make-up of the individual genotypes and agro-climatic conditions. The fruits growing in arid region with limited availability of water tend to accumulate more, and thus had the higher TSS in fruits (Meghwal and Azam, 9), as also observed in the present study. The breeders during selection of

Table 3. Chemical characteristics of the fruits among different genotypes.

Genotypes	Juice (%)	TSS (°B)	Acidity (%)	Ascorbic Acid (mg/100 g)	Total Sugars (%)	Reducing sugars (%)	Non-reducing sugars (%)	Sugar: acid ratio	TSS : acid ratio
MZU-HAMP-SGS-1	28.29	7.83	2.18	41.75	3.27	1.95	1.25	1.50	3.59
MZU-HAMP-SGS-2	35.59	6.73	2.24	36.34	3.68	2.31	1.30	1.64	3.01
MZU-HAMP-SGS-3	47.13	8.22	2.14	45.37	4.82	3.28	1.46	2.25	3.84
MZU-HAMP-SGS-4	27.19	7.02	2.22	39.77	3.24	1.97	1.21	1.46	3.16
MZU-HAMP-SGS-5	35.76	7.63	2.66	40.27	3.29	2.09	1.14	1.23	2.87
MZU-HAMP-SGS-6	31.57	7.53	2.35	40.60	3.43	2.15	1.22	1.46	3.21
MZU-HAMP-SGS-7	35.04	7.73	2.73	33.77	3.48	1.94	1.46	1.27	2.83
MZU-HAMP-SGS-8	36.93	7.43	2.37	40.11	3.40	1.93	1.40	1.44	3.15
MZU-HAMP-SGS-9	36.22	7.67	2.37	41.78	3.51	2.14	1.30	1.48	3.24
MZU-HAMP-SGS-10	42.67	7.87	2.07	46.86	4.27	3.04	1.17	2.07	3.81
MZU-HAMP-SGS-11	24.58	8.07	2.42	41.38	2.86	1.52	1.28	1.18	3.34
MZU-HAMP-SGS-12	23.99	7.77	2.68	42.71	3.15	1.97	1.12	1.17	2.90
MZU-HAMP-SGS-13	42.15	7.97	2.16	46.41	4.55	3.14	1.34	2.10	3.68
MZU-HAMP-SGS-14	32.47	7.73	2.32	36.65	3.36	2.00	1.29	1.44	3.33
MZU-HAMP-SGS-15	35.89	7.67	2.37	39.71	3.12	1.68	1.37	1.32	3.24
MZU-HAMP-SGS-16	28.86	7.87	2.43	43.60	2.87	1.64	1.17	1.18	3.23
MZU-HAMP-SGS-17	26.36	7.27	2.25	38.70	3.28	1.95	1.26	1.45	3.23
MZU-HAMP-SGS-18	25.86	7.60	2.28	40.50	3.40	2.14	1.19	1.49	3.33
MZU-HAMP-SGS-19	41.58	8.50	2.20	46.31	4.56	3.22	1.28	2.09	3.88
MZU-HAMP-SGS-20	42.08	8.17	2.13	44.92	4.28	3.03	1.19	2.01	3.84
MZU-HAMP-SGS-21	39.07	8.03	2.17	43.86	4.74	3.21	1.46	2.19	3.71
MZU-HAMP-SGS-22	23.73	8.07	2.27	38.98	3.63	2.42	1.15	1.60	3.56
MZU-HAMP-SGS-23	27.18	7.30	2.53	38.18	3.78	2.21	1.49	1.49	2.89
MZU-HAMP-SGS-24	27.74	7.93	2.67	35.67	3.30	2.10	1.14	1.24	2.97
MZU-HAMP-SGS-25	28.71	7.17	2.33	42.71	3.63	2.33	1.24	1.56	3.07
MZU-HAMP-SGS-26	24.79	7.10	2.37	40.67	3.16	1.92	1.18	1.34	3.00
MZU-HAMP-SGS-27	28.96	7.03	2.50	43.41	3.39	2.09	1.24	1.36	2.82
MZU-HAMP-SGS-28	27.48	7.13	2.40	42.17	3.41	2.22	1.13	1.42	2.98
MZU-HAMP-SGS-29	23.08	7.87	2.23	36.11	3.43	2.05	1.31	1.53	3.53
MZU-HAMP-SGS-30	28.56	7.90	2.78	34.60	3.99	2.70	1.23	1.44	2.85
S.Em (±)	3.84	0.29	0.06	1.05	0.27	0.27	0.16	0.12	0.15
CD _(0.05)	8.02	0.60	0.13	2.08	0.55	0.57	0.34	0.25	0.31

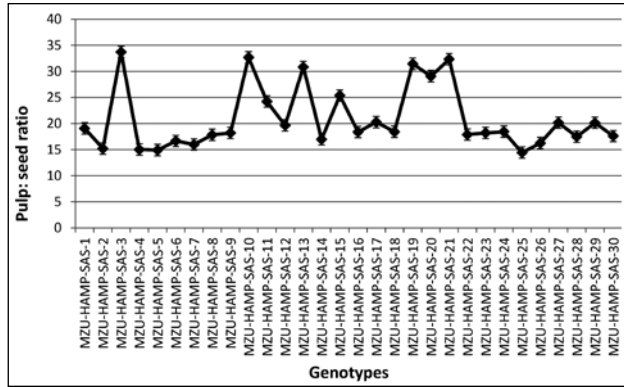


Fig. 2. Pulp: seed ratio among different genotypes

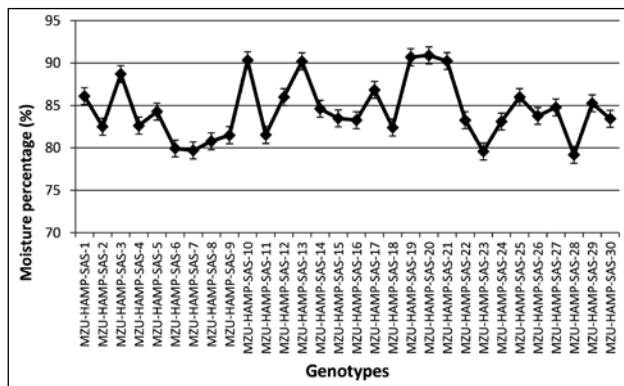


Fig. 3. Moisture percentage among different genotypes

superior genotypes should emphasize total soluble solids content of the fruit.

Titrateable acidity is directly related to the concentration of dominant organic acid, which is an important parameter in maintaining fruit quality. It is clear from the data (Table 3) that of the various genotypes, MZU-HAMP-SGS-30 tended to show the highest content of titrateable acids (2.78 %), while its lowest value was registered with MZU-HAMP-SGS-10 (2.07%) Variation among genotypes for acidity might be due to different genetic make-up of the plants (Prakash *et al.*, 10) which has also proved in our study. The variation in acidity among different germplasms has also reported by Shukla *et al.* (14) and Hazarika and Lalitluangkimi (4) in aonla.

Ascorbic acid contributes to the nutritional value of fruits juices, as it protects the body against accumulation or retention of the toxic mineral lead. It also acts as antioxidant as well as co-factor functions for enzyme metabolism inside the body. In the present investigation, the highest content of ascorbic acid was recorded in MZU-HAMP-SGS-13 (46.41 mg/100 g) which was statistically *at par* with MZU-HAMP-SGS-19 (46.31 mg/100g), MZU-HAMP-SGS-3 (45.37

mg/100 g) and MZU-HAMP-SGS-20 (44.12 mg/100 g) (Table 3). It is a fact that, if TSS increases, the ascorbic acid also increases because the precursor of ascorbic acid is glucose- 6-phosphate (Prakash *et al.*, 11), which was also confirmed from our study. The similar findings have also been reported by several researchers (Hazarika *et al.*6; Singh *et al.* 16; Hazarika and Lalitluangkimi, 4).

Of the various genotypes of star gooseberry, the highest content of total sugars was recorded in MZU-HAMP-SGS-3(4.82%), which did not differ significantly from MZU-HAMP-SGS-21(4.74%), MZU-HAMP-SGS-19 (4.56%), MZU-HAMP-SGS-13 (4.55%) and MZU-HAMP-SGS-10 (4.27%). Similarly, MZU-HAMP-SGS-3 and MZU-HAMP-SGS-11 showed the highest reducing (3.28 %) and non-reducing (1.49 %) sugars, respectively. The variation in sugar content among the genotypes may be due to differences in TSS, as sugar is the predominating component of TSS. Our study is in close conformity with the findings of Hazarika and Lalitluangkimi (4), Hazarika *et al.* (5), Sharma (13) and Singh *et al.* (15).

Sugar: acid and TSS: acid ratio are commonly used as measure of fruit maturity, and also considered an important factor in consumer acceptability of fruit. In the present investigation, significant variation was observed among the genotypes in sugar: acid and TSS: acid ratio (Table 3). Among all the genotypes, MZU-HAMP-SGS-3 and MZU-HAMP-SGS-19 exhibited the highest sugar: acid (2.25) and TSS: acid ratio (3.88). Our study is in close conformity with the findings of, Singh *et al.* (16), Singh and Singh (17) and Hazarika and Lalitluangkimi (4).

Identification and description of the genetic variability is preliminary requirements for exploitation of useful traits in plant breeding. Preference of consumers always depends on physical parameters of fruits like fruit weight, fruit diameter, pulp content and pulp: seed ratio of any fruit. In *Phyllanthus acidus* more fruit weight, bigger size, more pulp content and pulp: seed ratio, greater is the acceptability by the consumer. Among biochemical constituents of the fruits, consumers always prefer fruits with high juice, ascorbic acid, TSS, low acidity and high sugar: acid ratio. Similarly, for development of a new variety, breeders also choose germplasms with these desirable qualities. From the summary of the present investigation, it can be concluded that MZU-HAMP-SGS-3, MZU-HAMP-SGS-10 and MZU-HAMP-SGS-13, MZU-HAMP-SGS-19, MZU-HAMP-SGS-20, MZU-HAMP-SGS-21 can be considered as elite *Phyllanthus acidus* genotypes for use in various purposes. The result of the present work might help the breeders in selecting the most diverse genotypes with similar pomological fruit quality and

yield related traits to begin crossing and breeding programs. Detailed investigation with more number of genotypes from varied eco-geographical areas by using different statistical tools may help to identify and establish more superior varieties from this biodiversity hot-spots.

AUTHORS' CONTRIBUTION

Conceptualization (TKH); Designing of the experiments (TKH); Contribution of experimental materials (TKH, RN); Execution of field/lab experiments and data collection (RN); Analysis of data and interpretation (TKH); Preparation of the manuscript (TKH, RN).

DECLARATION

The authors declare that there is no conflict of interest

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