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Evaluation of Thompson Seedless and its Clone Based on Fruit Characteristics under Indian Condition

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ABSTRACT

The present study was conducted during fruiting season during October, 2023 to April, 2024 at the experimental farm of ICAR-National Research Centre for Grapes, Pune, Maharashtra, India to evaluate clones for fruit morphology by multivariate analysis and estimate similarity distances among different clones. In this study, 13 clones belonging to Thompson Seedless (Tas-A-Ganesh, Manik Chaman, Sonaka, Maruti Seedless, Ambe Seedless, SSN, Sudhakar Seedless, Pusa Seedless, 2A clone and H-5-Clone) were characterized considering pomological diversity under Indian conditions. A total of 15 berry and bunch attributes were characterized in clones for the distinctness. A high variability (60.38%) was found in the evaluated grape cultivars, and significant differences were found between them in all fruit attributes. The morphological quantitative traits such as bunch weight, bunch length, berry weight, number of berries bunch^{-1}, berry diameter, berry length and TSS were in following range 62.13–224.67 g, 8.0–17.50 cm, 46.0–127.0 g, 60.0–154.0, 7.50–15.87 mm, 11.30–19.24 mm and 18.0–22.4 °Brix respectively which indicated a wide level of diversity in the clonal varieties. There were high positive correlations between bunch and berry traits particularly weight and length while negative correlation between total soluable solid (TSS) and titratable acidity (TA). Principal component analyses showed a considerable fruit diversity in the studied grape varieties. Clonal selection and conservation of the highly diverse autochthonous grapes are therefore recommended.

KEYWORDS: Grape, clonal selection, fruit trait, clonal diversity

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1. INTRODUCTION

The first individual clonal selection took place more than 100 years ago. The concept of clonal selection was utilized by Biolette for the first time in Muscat of Alexandria but the most useful result has been obtained in Chardonnay (Chadha and Shikhamany, 1999). Clonal selection has been increasingly used as a tool for grapevine improvement since the late 1950s. The first purpose of clonal selection was to create virus-free populations from healthy mother plants. In the second stage, viticultural criteria have been included in the clonal selection programmes (Atak et al., 2014). A clone refers to the vegetative propagation of a grapevine with a clearly defined identity, characterized by stable phenotypic traits and health attributes, which remain consistent unless a new mutation occurs (Aurand, 2017; van Leeuwen et al., 2019). Cultivars propagated vegetatively differ genetically from each other. Clonal selection is mainly based on the genetic variability, conditions available during its growth period and health of cultivars. Due to their polyclonal origin and the slow accumulation of genetic changes over time, cultivars exhibit genetic heterogeneity (Sefc et al., 2009). To choose healthy and high-quality clones, clonal selection studies have been conducted using a variety of grape cultivars and rootstocks. In viticulture, clonal selection is a fundamental step in developing grape varieties, playing a crucial role in productivity, quality, and sustainability across all wine-growing regions (Ruhl et al. 2003). As van Leeuwen et al. (2019) emphasize, clonal variation significantly impacts vine health and adaptability to environmental changes. To maintain flavor consistency and ensure uniformity, grapevine breeders prefer plant material that closely matches the original selected clone. Clonal selection involves both genetic and sanitary evaluations, balancing genetic diversity with varietal purity. This approach minimizes the risks of propagating vines affected by mutations or infected with viruses and related diseases. Genetic diversity within a variety often results from its polyclonal origins and the gradual accumulation of mutations over time (Vondras et al., 2019). The clonal selection process includes field evaluations, assessments of agronomic and oenological traits, health testing, and clone identification. Clones with superior health and desirable traits are preserved for long-term cultivation. Comparative trials under uniform conditions help determine a clone's grape production potential, leading to certification and distribution to growers (Loureiro et al., 2011).

Clonal selection yielded very good results in India. Among the wide range of grape varieties, Thompson Seedless is one of the most well-known cultivars worldwide. Due to its sweet, juicy berries and seedlessness nature, this cultivar has been propagated across diverse climatic regions, contributing significantly to the global grape industry. Currently in India, Thompson Seedless is the ruling grape variety occupying 78.96% of the area with its clones (Anonymous, 2024). Grapevines are clonally propagated to preserve the cultivar's genetic, enological, and agronomic traits. However, mutations result into greater diversity of clones or selections. Clones can exhibit differences in agronomic performance, including yield, berry weight, and the number of berries cluster^{-1} (Burin et al., 2011; Dimovska et al., 2012; Suklje et al., 2016; Urra et al., 2023). The assessment of grape diversity is a key element of germplasm characterization and conservation, which is necessary to maintain and improve crop production (Villano et al., 2023). Traditionally, morphological characterization was the only tool to distinguish grapevine clones (Douhovnikoff and Dodd, 2003).

Maharashtra is major grape growing state in the country with diversity in cultivation of Thompson Seedless and its clones. In different grape growing districts, growers have identified clones from Thompson Seedless at local level. The performance is also seen well in these areas. Considering this, study was conducted to evaluate these clones for fruit morphology by multivariate analysis to reveal grouping characteristics and estimate similarity distances among different clones to reveal the fruit diversity of clones growing in India.

2. MATERIALS AND METHODS

The present study was conducted during October, 2023 to April, 2024 at the experimental farm of ICAR-National Research Centre for Grapes, Pune, Maharashtra, India. Thirteen clones belonging to Thompson Seedless were evaluated with replicates of five vines for each clone (Table 1). Pune is located in Mid-West Maharashtra at an altitude of 559 m above sea level with a latitude of 18.32°N and longitude of 73.51°E. The region is characterized by a hot and dry climate with an average temperature of 25°C to 32°C and relative humidity of 45–55%. Annual precipitation varies between 600 and 900 mm. Due to tropical conditions of the region, single cropping and double pruning approach is being adopted. All the standard cultural recommended practices were followed during the period of study.

Fruit characterization of each clone was performed according to the descriptor list for Vitis Species (Anonymous, 2007). Fifteen fruit characters were used to assess the range of variation among the cultivars. Parameters related to the fruit were measured, calculated and visually estimated at harvest stage (full maturity). Quantitative traits were measured by laboratory equipment such as digital caliper, weighing balance, measuring scale. Bunch and berry parameters (length and width) were measured with measuring scale.

Table 1: Information about Thompson seedless and its clone

Variety	Developed by	Year
Thompson seedless	William Thompson, California	1875
Tas-e-Ganesh	Shri Vasant Rao Arve, Tasgaon, Sangli	1970
Sonaka	Nanasaheb Kale, Nanaj, Solapur	1977
Sonaka (Mutant)	Nanasaheb Kale, Nanaj, Solapur	1982
Manik Chaman	Shri T. R. Dabade	1982
Maruti Seedless	Mr. Maruti Mali, Mhaisal	1994
Ambe Seedless	Mr. Vital Mali, Bedag, Sangli	2007
Pusa Seedless	IARI, New Delhi	1970
Sudhakar Seedless	Mr. Sudhakar Kshirsagar, Nasik.	2015
SSN	Mr. Sarjerao Narute	2018
2A Clone	Introduced from USA	NA
H-5-Clone	Introduced from Australia	NA

Weight of bunch and berry was recorded by electronic balance. The fruit juice was used for analysis of total soluable solid (TSS), titratable acidity (TA), and pH (Table 2).

The differences between fruit character among the studied cultivars were detected using one way analysis of variance (ANOVA) by SAS software. Coefficient of variation (CV) were calculated as a variation index. The Pearson correlation coefficients were used to determine between the traits using SPSS software version 29. Principal component analysis (PCA) was applied to investigate the relationships among the clones using SPSS® software. In addition, bi-plot was generated using SPSS statistics software.

3. RESULTS AND DISCUSSION

3.1. Fruit traits

Significant differences were observed between fruit character in the studied clonal varieties of Thompson Seedless. Mean, standard deviation, minimum, maximum, and CV % values for fruit characteristics are presented in Table 3. Maximum bunch weight was recorded in Sudhakar Seedless (224.3 g) while the minimum in 2A Clone (62.13 g). Berry weight ranged from 46.0 g (H-5 Clone) to 127.0 g (SSN). Number of berries bunch^{-1} varied from 60 (SSN) to 154 (Pusa Seedless). Large variation was observed in bunch length and bunch width among the varieties, ranging from 8.0 cm (Vijay Chaman) to 17.5 cm (H-5 Clone) and 4.5 cm (Ambe Seedless) to 14.0 (Sudhakar Seedless). The result of the present study is in agreement with the results of Somkuwar et al. (2024) who reported a variation in bunch weight (78.5 g to 530 g) and berry weight (76.5 g to 225.6 g) in different grape varieties. Two different berry shapes (short elliptical and long elliptical) as well as three bunch shape (conical, cylindrical and winged cylindrical) were noted. The dominant berry color was yellowish green (Figure 1).

Table 2: Thompson seedless and its clone studied with their fruit characteristics

Varieties	Bunch weight (g)	50 berry weight (g)	No. of berries	Berry diameter (mm)	Berry length (mm)	Bunch length (cm)	Bunch width (cm)	Peduncle length (cm)
Thompson seedless	140.00	80.50	93.00	12.20	13.60	13.50	7.50	3.20
TAS A Ganesh	191.00	69.50	94.00	11.70	12.90	15.00	7.00	2.00
Sonaka	155.67	67.00	75.00	10.40	14.40	12.80	6.50	1.80
Sonaka Mutant	183.00	81.00	69.00	7.50	11.30	15.00	8.50	2.50
Manik Chaman	125.33	51.00	81.00	10.70	15.80	12.40	4.50	1.30
Maruti seedless	179.00	71.00	146.00	12.10	13.90	13.50	6.20	1.90
Ambe	79.83	56.00	84.00	8.80	15.90	8.60	4.50	1.30
Pusa seedless	209.50	83.00	154.00	13.30	14.30	12.00	10.00	2.50
Sudhakar seedless	224.67	52.50	65.00	15.87	16.80	17.00	14.00	2.30
S.S.N	196.50	127.00	60.00	12.56	19.24	14.50	9.50	3.50
Sultana seedless	107.83	70.50	86.00	14.85	15.63	15.50	9.50	1.90
2A-Clone	62.13	78.00	85.00	9.70	12.20	11.00	8.00	2.30
H-5 Clone	204.17	46.00	97.00	10.60	12.80	17.50	6.20	1.30
Vijay Chaman	75.50	74.00	78.95	13.05	14.86	8.00	5.70	1.20

Table 2: Continue...

Table 2: Thompson seedless and its clone studied with their fruit characteristics

Varieties	Pedicel length (cm)	Skin thickness (mm)	TSS (^{0}Brixs)	Acidity (%)	Juice pH	Berry shape	Bunch shape
Thompson seedless	0.50	0.22	20.30	0.68	3.47	Short elliptical	Winged cylindrical
TAS A Ganesh	0.50	0.20	22.30	0.71	3.41	Short elliptical	Conical
Sonaka	0.30	0.09	20.00	0.45	3.65	Long elliptical	Conical
Sonaka Mutant	0.50	0.21	22.40	0.56	3.54	Short elliptical	Conical
Manik Chaman	0.50	0.07	19.00	0.71	3.85	Short elliptical	Winged cylindrical
Maruti seedless	0.30	0.04	19.20	0.68	3.94	Round	Cylindrical
Ambe	0.50	0.06	21.80	0.86	3.65	Long elliptical	Winged cylindrical
Pusa seedless	0.60	0.21	22.00	1.09	3.45	Short elliptical	Conical
Sudhakar seedless	0.50	0.18	21.70	0.00	3.36	Short elliptical	Conical
S.S.N	0.60	0.12	20.80	0.00	3.67	Long elliptical	Winged cylindrical
Sultana seedless	0.40	0.22	19.80	0.00	3.78	Short elliptical	Conical
2A-Clone	0.60	0.20	20.60	0.94	4.06	Short elliptical	Conical
H-5 Clone	0.30	0.15	18.00	0.98	3.45	Short elliptical	Winged cylindrical
Vijay Chaman	0.34	0.23	20.80	0.94	3.28	Long elliptical	Winged cylindrical

3.2. Correlations among the traits

The data presented in Table 4 and Figure 2 showed the correlation between the fruit parameters. Bunch weight showed significant positive correlation with bunch length (r=0.74), bunch width (r=0.50), berry diameter (r=0.26) and number of berries bunch^{-1} (r=0.20), which is in accordance with the previous findings (Khadivi Khub et al., 2014; Vafaee et al., 2017; Migicovsky et al., 2017; Abiri et al., 2020). Significant positive correlation existed between berry diameter and berry length (r=0.51) and also between berry diameter and bunch width (r=0.61). Bunch length and bunch width (r=0.52) was positively correlated indicating that these parameters can be used to predict each other. This relation has also been reported by Khadivi Khub et al. (2014). Negative correlation (r=-0.04) was observed for total soluble solid (TSS) and titratable acidity (TA). Vafaee et al. (2017) also reported a negative correlation between TSS and TA. These parameters can be used to predict other ones, and could be considered of importance for the characterization of varieties.

Table 3: Descriptive statistics for measured fruit variables between the studied clonal cultivars

Sl. No.	Variable	Minimum	Maximum	Mean	SD	CV (%)
1.	Bunch weight (g)	62.13	224.67	152.44	54.39	35.67
2.	50 berry weight (g)	46.00	127.00	71.93	19.86	27.60
3.	No of berries bunch^{-1}	60.00	154.00	90.57	27.42	30.37
4.	Berry diameter (mm)	7.50	15.87	11.67	2.27	19.42
5.	Berry length (mm)	11.30	19.24	14.55	2.06	14.13
6.	Bunch length (cm)	8.00	17.50	13.31	2.80	21.01
7.	Bunch width (cm)	4.50	14.00	7.69	2.53	32.90
8.	Peduncle length	1.20	3.50	2.07	0.71	34.05
9.	Pedicel length	0.30	0.60	0.46	0.11	24.35
10.	Skin thickness (mm)	0.04	0.23	0.16	0.07	43.86
11.	TSS (°Brixs)	18.00	22.40	20.62	1.34	6.47
12.	Acidity (%)	0.00	1.09	0.61	0.37	60.88
13.	Juice pH (%)	3.28	4.06	3.61	0.23	6.38
14.	Bunch shape (code)	2.00	4.00	3.36	0.63	18.86
15.	Berry shape (code)	2.00	4.00	3.14	0.66	21.09

Figure 1: Fruit's pictures of studied grape varieties

Any future plant breeding programme might find this information to be very useful. Also, a close relationship trait could facilitate or hinder gene introgression, since strong selection for a desirable trait could favor the presence of another desirable traits from germplasm. To achieve maximum yield and superior quality fruit, for example, cross combination could be performed between varieties with very large berry size and high TSS.

3.3. Principal component analysis

PCA based on a correlation matrix was performed to estimate fruit differentiation between clonal selections from Thompson Seedless and to determine whether data reduction obtained through the new set of variables (PCs) revealed a pattern of variation consistent with grouping when the largest components of the overall variance were contributed by differences between groups. A PC loading of more than 0.59 was considered significant for each factor, showing six components and accounting for 86.85% of the total variance (Table 5). The first three PCs explained 60.65% of the variance (27.29, 19.25, and 14.11%, respectively), showing that these parameters have the highest variation between the varieties and had the greatest impact on the difference between them. The highest loading point on the PC1 corresponded to variables in bunch weight, bunch length and bunch width. The variables with the highest loading on the second PCA (PC2) axis were 50 berry weight and berry shape. The highest loadings on the third components (PC3) were acidity and TSS. Berry size can be inferred from the variables that indicated a strong connection with PC1. Furthermore, the data sets with several associated variables are effectively reorganized into smaller sets of components using this type of analysis. These results in some cases are in agreement with result reported in other grape studies (Guan et al., 2020, Abiri et al., 2020). Khadivi-Khub et al., (2014) studied sixteen fruit parameters in 23 grapes cultivars and explained 53.98% of the variance (19.23, 17.74, and 17.01%, respectively) in first three PCs, indicating that these attributes have the highest variation between the cultivars. Similarly Abiri et al., (2020) observed 77.37% of total variances were explained by the first 12 components. Vafaee et al. (2017) used PCA to study grape cultivars and observed that 85.84% of the total variation was explained by 12 PCs.

A PCA biplot (Figure 3) showed the relationship between the clonal varieties of Thompson Seedless and morphological variables. The results revealed that, 15 quantitative traits or variables (berry weight, berry length, bunch width, Skin thickness and peduncle length) had a strong correlation with varieties viz., Thompson Seedless, Sonaka Mutant and SSN and these variables had their positive contribution in these varieties which included them in a similar group. In the opposite direction, at the left lower quadrant there were only two morphological traits viz., juice pH and number of berries bunch^{-1} which were mostly similar in genotypes (Sonaka, Manik Chaman, Maruti Seedless and H-5 clone)

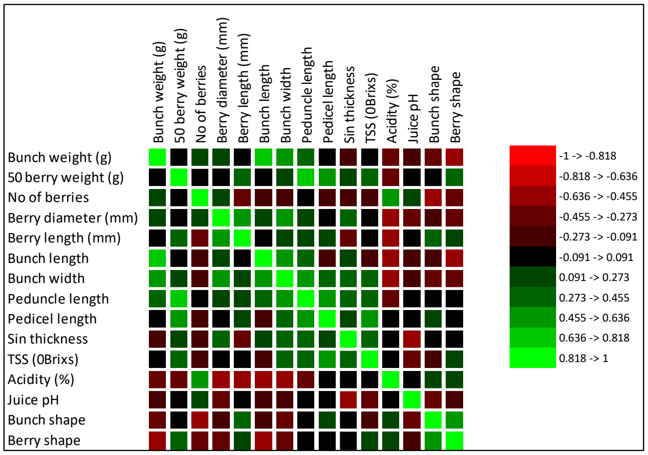

Figure 2: Correlation between different fruit character in studied clonal cultivars

Table 4: Pearson's correlation between different fruit character in studied clonal cultivars

Variables	Bunch weight	50 berry weight (g)	No of berries bunch^{-1}	Berry diameter (mm)	Berry length (mm)	Bunch length (cm)
Bunch weight	1.000					
50 berry weight (g)	0.102	1.000				
No of berries bunch^{-1}	0.204	-0.078	1.000			
Berry diameter (mm)	0.262	0.065	0.130	1.000		
Berry length (mm)	0.071	0.305	-0.294	0.51^{8*}	1.000	
Bunch length	0.741*	-0.067	-0.095	0.271	-0.040	1.000
Bunch width	0.509*	0.258	-0.110	0.611*	0.249	0.526*
Peduncle length	0.373	0.782*	-0.069	0.173	0.173	0.302
Pedicel length (mm)	0.020	0.463	-0.106	-0.031	0.186	-0.095
Skin thickness (mm)	-0.034	0.190	-0.116	0.283	-0.324	0.123
TSS (°Brixs)	0.101	0.297	-0.116	-0.045	-0.026	-0.197
Acidity (%)	-0.267	-0.290	0.519*	-0.473	-0.595	-0.515
Juice pH	-0.394	0.081	0.116	-0.284	-0.018	-0.128
Bunch shape	-0.268	0.024	-0.465	-0.135	0.329	-0.240
Berry shape	-0.429	0.331	-0.399	-0.332	0.260	-0.548

Table 4: Continue...

Variables	Bunch width (cm)	Peduncle length (cm)	Pedicel length (mm)	Sin thickness	TSS (°Brixs)	Acidity (%)	Juice pH	Bunch shape	Berry shape
Bunch weight									
50 berry weight (g)									
No of berries bunch^{-1}									
Berry diameter (mm)									
Berry length (mm)									
Bunch length									
Bunch width	1.000								
Peduncle length	0.575*	1.000							
Pedicel length (mm)	0.383	0.592*	1.000						
Skin thickness (mm)	0.450*	0.290	0.258	1.000					
TSS (°Brixs)	0.387	0.337	0.586*	0.378	1.000				
Acidity (%)	-0.587	-0.406	-0.044	0.012	-0.047	1.000			
Juice pH	-0.240	-0.006	0.088	-0.472	-0.379	-0.053	1.000		
Bunch shape	-0.323	-0.079	0.152	0.053	-0.146	0.137	-0.330	1.000	
Berry shape	-0.430	-0.089	0.021	-0.043	0.109	0.108	-0.137	0.602	1.000

in this quadrant. The morphological variables present in the upper left side quadrant had a strong correlation with genotypes present in this quadrant. Similarly, the variables present on the lower right side had a strong correlation with genotypes present in a similar quadrant. The results also showed that grapes variables present near to the center of the axis were closely related to each other and had less contribution in diversity. While variables away from the center of the axis showed a high level of variations in grapes genotypes.

In the present investigation, the largest variability was observed between fruit traits. Bunch weight is a very important characteristic because of its economic importance. Some varieties such as Sudhakar Seedless, Maruti seedless, Tas-E Ganesh shown large berry with high bunch weight. This could be explained by the fact that the berry size was

Table 5: Eigenvalues and proportion of total variability and eigenvectors of six principal components (PCs) for studied grape varieties

Variables	PC1	PC2	PC3	PC4	PC5	PC6
Bunch weight (g)	0.711^{**}	-0.259	-0.014	-0.017	0.324	0.591^{**}
50 berry weight (g)	0.228	0.525^{**}	0.083	-0.346	-0.031	0.179
No of berries bunch^{-1}	-0.06	-0.324	0.29	-0.18	-0.417	0.558^{**}
Berry diameter (mm)	0.288	-0.089	-0.206	0.228	-0.595^{**}	0.03
Berry length (mm)	0.162	0.242	-0.48	-0.078	-0.325	0.216
Bunch length (cm)	0.605^{**}	-0.302	-0.159	0.109	0.533^{**}	0.037
Bunch width (cm)	0.555^{**}	-0.043	0.038	0.091	-0.108	-0.17
Peduncle length (cm)	0.373	0.169	0.138	-0.271	0.134	0.141
Pedicel length (mm)	0.217	0.295	0.272	-0.238	0.009	0.014
Skin thickness (mm)	0.194	0.11	0.364	0.392	-0.07	-0.285
TSS (°Brixs)	0.19	0.243	0.595^{**}	0.06	-0.033	-0.095
Acidity (%)	-0.336	-0.05	0.515^{**}	0.058	-0.062	0.306
Juice pH (%)	-0.117	-0.096	-0.112	-0.634^{**}	-0.025	-0.361
Bunch shape (code)	-0.13	0.382	-0.186	0.276	0.167	0.29
Berry shape (code)	-0.187	0.567^{**}	-0.094	0.043	0.069	0.147
Eigenvalue	4.09	2.88	2.11	1.74	1.193	0.991
% of variance	27.29	19.25	14.11	11.62	7.95	6.60
Cumulative %	27.29	46.54	60.66	72.29	80.24	86.85

(**Eigenvalue significant ≥ 0.51)

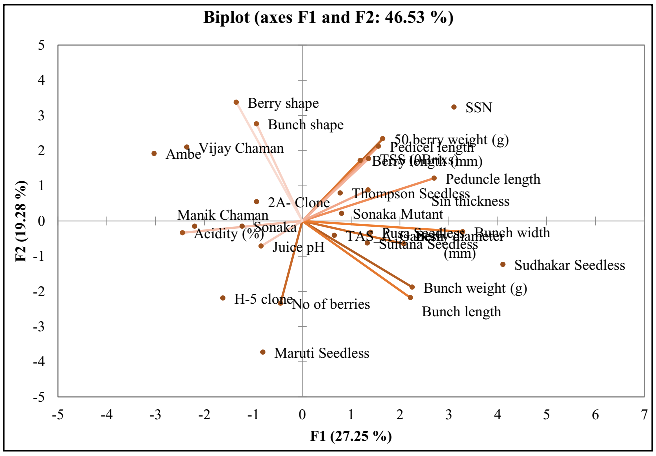

Figure 3: PCA biplot of 14 grape varieties for quantitative fruit traits

probably one of the first parameters to be considered in a traditional farmer's selection process. Although the most important variables in distinguishing grape genotypes have been berry size, certain dimensional traits of berry can also be important. Besides, the skin color of berry is a very important quality attribute, and also serves in estimating the stage of maturity of the berry. Berry skin color also has a significant impact on consumer perception of fruit quality, especially as regards the attractiveness of fruit (Ekhvaia and Akhalkatsi, 2010).

4. CONCLUSION

Most of the fruit characteristics differed significantly between the clonal varieties examined. It facilitated the selection and use of the most desirable characteristics of interest and highlights the possibility of further improving the quality of grapes. A significant positive correlation was observed between economic traits, such as bunch length, bunch width, berry length, and berry width, suggesting that selection for these characteristics would lead to crop improvement.

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