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Research Article

Genetic Variation of New Purple-Fleshed Sweet Potato (*Ipomoea batatas* L.) Genotypes in Indonesia by Multivariate Analysis

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Purple-fleshed sweet potato (PFSP) is a major staple food and feed material in tropical countries. The pandemic of COVID-19 that encouraged healthy lifestyles worldwide further increases the importance of PFSP. Despite its importance, the investment in research to improve PFSP in Indonesia was left behind. The objective of the research was to estimate the genetic variation and genetic distance of new PFSP genotypes prior to variety release. The research trials were arranged in a randomized block design, with nine new PFSP genotypes from polycrosses breeding as treatments and three check varieties in four growing environments in West Java, i.e., Cilembu, Jatinangor, Maja, and Karangpawitan during one season. Agronomic traits data were analyzed by the multivariate analysis. The principal component analysis (PCA) showed high genetic variation of PFSP in four environments. The eigenvalue ranges from 1.92 to 5.29 in Cilembu which contributed to 80.958% variability, 0.543–6.177 which contributed variability to 92.135% in Jatinangor, 0.824–5.695 in Karangpawitan which contributed to 92.117%, and 0.822–4.797 in Maja which contributed to 86.133%. Storage root length, storage root diameter, number of roots per plant, total root weight per plant, number of marketable/commercial roots, marketable/commercial root weight, number of roots per plot, and total storage root weight have a discriminant value of more than 0.7 in PC 1. Agglomerative hierarchical clustering (AHC) showed a wide distribution obtaining two clusters in Cilembu with euclidean distance 1.92–5.29, Jatinangor 1.72–6.09, Karangpawitan 1.28–6.38, and Maja 2.05–5.09. High genetic variation in the four environments greatly supports to the development of PFSP new varieties.

1. Introduction

Purple-fleshed sweet potato (PFSP) has been developed in various countries along with the growing market demand for healthy food. The pandemic due to COVID-19 has increased public awareness to start a healthy lifestyle [1]. One of the efforts in a healthy lifestyle is to increase the immune system or body resistance. The immune system can be improved by consuming nutritious, diverse, balanced, and safe foods. PFSP is used in various commercial products as well as a natural food colorant [2–5]. PFSP has a deep purple color in the root and skin. The purple coloration comes from natural pigments, namely, anthocyanins [6–9]. The high anthocyanin content makes purple sweet potato a functional food that is very beneficial for health.

The assembly of superior varieties of PFSP through a plant breeding program is an effort to increase the production and productivity of PFSP. Genetic variation of PFSP provides an opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer preferred traits and breeder preferred traits [10, 11]. The process of plant breeding activity to produce superior sweet potato genotypes starts from recombinations through handcrosses/controlled crosses or uncontrolled crosses/polycrosses, followed seedling nurseries and field trials where morphological characterization and yield evaluation are carried out [12].

Multivariate analysis is the most popular approach to estimate genetic variation among germ plasm collections. This method may have three main purposes, i.e., summarizing information, eliminating "noise" from the data sets, and revealing the structure of the data sets [13, 14], and furthermore, it can also be used for determining grain yield stability and identifying genotypic groups possessing desirable traits [15]. Genetic variation in sweet potato can be estimated using an analysis of plant morphological and agronomic traits such as yield [16]. The information obtained through this analysis can be used as a reference in determining genetic relationships and potential genetic variations that can be produced [17, 18], thus facilitating the selection of PFSP genotypes with the desired advantages. The principal component analysis (PCA) and agglomerative hierarchical clustering (AHC) analysis are the preferred tools for agronomic characterization of sweet potato genotypes and their grouping on a similarity basis.

Multivariate analysis has been widely used to analyze genetic variation in sweetpotato. Afuape et al. [19] reported the genetic variation of sweet potato based on nine agronomic and eight morphological traits. Characterization and evaluation of South African sweet potato genotypes were also performed by Laurie and Booyse [20]. The objective of this study was to estimate the genetic variation and genetic distance of PFSP genotypes for the development of new superior sweet potato varieties in Indonesia.

2. Materials and Methods

2.1. Genetic Materials. Genetic material evaluated in the research included nine genotypes of PFSP developed by Laboratory of Plant Breeding, Faculty of Agriculture, Universitas Padjadjaran, Indonesia, and three commercial varieties (Table 1).

2.2. Field Experimental Details. The 9 new PFSP genotypes were evaluated in experimental trials at four environments in West Java, Indonesia, including Cilembu, Sumedang, Jatinangor, Sumedang, Karangpawitan Garut, and Maja Majalengka. The agroclimate of the locations is presented in Table 2.

The experiment was laid in a randomized block design (RBD) which consisted of three replications at each environment. The experimental plot consisted of 3 m × 5 m, and 75 plants were planted in each plot. During the crop cultivation, standard crop management practices were applied, and the plots were manually harvested. The traits including storage root length, storage root diameter, number of roots per plant, total root weight per plant, number of marketable/commercial roots, marketable/commercial root weight, number of roots per plot, total storage root weight, specific gravity, and level of sweetness were measured in raw storage roots used digital refractometer [22]. Traits measured following sweet potato descriptor [22].

2.3. Data Analysis. The data were subjected to analysis of variance using PBStat.com (Central Library Agricultural University, Bogor, Indonesia). PCA was used to classify PFSP genotypes and see how high contribution to the traits of PFSP genotype appearance. Genetic variation and genetic relationship distance based on similarity between objects under study were analyzed using AHC based on the "*t*" Euclidean coefficient. The NTSyspc version 2.11xAnalysed computer software was used for PCA and AHC.

3. Results and Discussion

3.1. Analysis of Variance. The analysis of variance indicated that among PFSP genotypes, there was a significant difference on ten traits based on Table 3. Number of marketable/commercial roots, marketable/commercial root weight, number of roots per plot, total storage root weight, and level of sweetness indicated significant variation at the $p \leq 0.01$ and $p \leq 0.05$. Variations on these five traits were important to identify because yield and other yield-contributing traits as highly necessary for PFSP improvement criteria.

The variation in the significant F values of the ten traits indicated that PFSP genotypes used at each location had a different response. Topography and weather conditions were different at each location. Sweet potato yield is largely influenced by genotype or clone (G), environment (E), and genotype by environment interaction (GEI) [23]. GEI leads to differential response of genotypes across growing environments and may limit selection response [24, 25]. According to Ngailo et al. [26] and Karuniawan et al. [27] difference in potency and quality of sweet potato storage root yield is caused by variations in the environment. Understanding the differential response of crop genotypes to changes in environmental conditions is an important key in plant breeding [28]. This makes GEI crucial for PFSP selection and variety release.

In this study, nine genotypes of PFSP were used. These genotypes have the potential to be developed and released as superior varieties. Genetic variation is the basic capital to obtain superior genotypes in plant breeding and to study the relationship between phenotypic and genotypic traits [29]. Therefore, it is necessary to test in several agroecosystems to determine the genetic variation of the 9 new superior PFSP genotypes.

3.2. Principal Component Analysis. Multivariate analysis can identify differences between traits through principal component analysis (PCA). This method is used to determine the traits that have an influence on genetic variation. PCA allows researchers to obtain representative important information and determine the relationship between variables in a data set [30, 31]. PCA is also used to estimate the most influential traits or variables in the variation of a population [30]. In this study, the principle component (PC) analysis partitioned the total variance into four PCs contributing maximum to the total diversity among the genotypes due to the study of various traits.

Main component analysis is a technique used to determine the contribution of one trait to variability to easily

Table 1: Pedigree of 12 PFSP genotypes evaluated in the study.

No.	Genotype	Pedigree	Status
1	G1	Local variety (rancing)	Check
2	G2	Kyushu no. 109 (♀) × Satsumahikari (♂) (check)	Check
3	G3	MSU 03028 (♀) (check)	Check
4	G4	L RCK (♀) × polycross	New clone
5	G5	IND11 (♀) × polycross	New clone
6	G6	F2 (♀) × polycross	New clone
7	G7	M2 (♀) × polycross	New clone
8	G8	57 (97) (♀) × polycross	New clone
9	G9	L CLMB (♀) × polycross	New clone
10	G10	199035.5 (♀) × polycross	New clone
11	G11	Malang 9 (♀) × polycross	New clone
12	G12	T1 (♀) × polycross	New clone

Table 2: Agroclimatology of the location in West Java, Indonesia.

No.	Location	Type of agroclimatology
1	Cilembu, Sumedang	AII2. Climate type of wet; yearly rain of >2500 mm; number of continuous dry months per year, 3–7; number of continuous wet months, 5–9; potential of crop index, 2
2	Jatinangor, Sumedang	AII2. Climate type of wet; yearly rain of >2500 mm; number of continuous dry months per year, 3–7; number of continuous wet months, 5–9; potential of crop index, 2
3	Maja, Majalengka	AII2. Climate type of wet; yearly rain of >2500 mm; number of continuous dry months per year, 3–7; number of continuous wet months, 5–9; potential of crop index, 2
4	Karangpawitan, Garut	BI3. Climate type of dry: yearly rain of 1500–2500 mm; number of continuous dry months per year, >7; number of continuous wet months, 3-4; potential of crop index, 1

(Ministry of Agriculture of Republic of Indonesia [21]).

Table 3: Analysis of variance of ten agronomic traits observed.

Traits	Sumedang (Cilembu)	Sumedang (Jatinangor)	Majalengka	Garut	G	GxE	CV
SRL	1.5271	2.246	0.824	1.834	4.141**	0.699	20.097
SRD	1.2164	5.202**	5.630*	5.344**	3.484**	1.328	19.125
NRP	0.888	1.357	1.732	3.562**	2.087	1.335	31.101
TRWP	3.273**	4.338**	2.040	7.316**	3.225**	1.649*	59.595
NRM	6.958**	5.214**	2.345*	4.931**	2.440*	3.614**	56.529
MRW	3.277**	7.818**	2.932*	4.614**	2.346*	3.479**	61.630
NRPL	15.382**	7.190**	4.702**	6.383**	2.795*	4.788**	31.575
TSRW	6.459**	7.523**	2.839*	21.911**	3.140**	8.765**	25.578
BRIX	7.793**	22.343**	9.464**	12.097**	2.408*	7.656**	7.1017
SG	0.214*	1.540	29.962**	3.208**	2.517*	1.651*	2.273

SRL: storage root length, SRD: storage root diameter, NRP: number of roots per plant, TRWP: total root weight per plant, NRM: number of marketable/commercial roots, MRW: marketable/commercial root weight, NRPL: number of roots per plot, TSRW: total storage root weight, BRIX: level of sweetness, SG: specific gravity; **, *: significant at the 0.01 and 0.05 probability levels, respectively.

determine the trait that can represent a genotype [32]. The results of the PCA analysis showed three main axial components that have eigenvalues more than 0.7 (Table 4). The eigenvalue is a description of the level of effectiveness of a factor in extracting the maximum variance of each analyzed variable [33]. Tables 4 and 5 show the principal component (PC) that forms variability from the 10 traits observed. The determination of the PC is based on an eigenvalue more than 0.70 PC [34] and a cumulative percentage more than 80% [33]. PC divides the total variance into several factors.

The eigenvalue ranged from 0.822 to 3.360 which contributed to 80.958% cumulative in Cilembu Sumedang. Primary component 1 (PC 1) covers 32.605% of the variability with a variation of 12 genotypes given the biometric traits, namely, total root weight per plant, marketable/commercial root weight, and total storage root weight. PC 2 covers 21.466% variability from variations in 12 genotypes given the trait storage root diameter. PC 3 covers 17.622% variability given the trait specific gravity. For PC 4, it covers 8.223% and no contributing traits in PC 4. PC values more than 0.70 [34].

Table 4: Factor loadings, of agronomic trait markers, contributed to variability in PFSP at Cilembu Sumedang.

Parameters	PC 1	PC 2	PC 3	PC 4
SRL	0.5098	0.1455	0.2438	0.5365
SRD	0.5399	0.7039	0.2702	−0.3078
NRP	0.3639	0.2804	−0.5865	0.5181
TRWP	0.9215	−0.0346	0.0217	0.0635
NRM	0.1334	−0.7565	−0.5580	0.0198
MRW	0.7334	−0.3696	−0.2251	−0.3128
NRPL	0.4081	0.3945	−0.5682	−0.1312
TSRW	0.8596	0.1934	0.2044	−0.0913
BRIX	0.5769	−0.7115	0.1456	−0.0562
SG	0.1836	−0.3772	0.7359	0.2008
Eigenvalue	3.360	2.146	1.766	0.822
Variability (%)	33.605	21.466	17.662	8.223
Cumulative (%)	33.605	55.072	72.735	80.958

SRL: storage root length, SRD: storage root diameter, NRP: number of roots per plant, TRWP: total root weight per plant, NRM: number of marketable/commercial roots, MRW: marketable/commercial root weight, NRPL: number of roots per plot, TSRW: total storage root weight, BRIX: level of sweetness, and SG: specific Gravity.

Table 5: Factor loadings, agronomic trait markers, contributed to variability in PFSP at Jatinangor Sumedang.

Parameters	PC 1	PC 2	PC 3	PC 4
SRL	0.930	0.243	0.104	0.133
SRD	0.708	0.387	−0.411	0.311
NRP	0.716	−0.393	0.047	0.406
TRWP	0.862	−0.325	0.006	−0.194
NRM	0.966	−0.050	0.141	−0.135
MRW	0.951	0.062	0.157	−0.190
NRPL	0.867	−0.070	0.007	−0.295
TSRW	0.913	0.209	0.068	−0.199
BRIX	0.081	0.892	−0.336	−0.035
SG	0.242	−0.618	−0.709	−0.206
Eigenvalue	6.117	1.703	0.848	0.543
Variability (%)	61.177	17.038	8.482	5.436
Cumulative (%)	61.177	78.216	86.698	92.135

SRL: storage root length, SRD: storage root diameter, NRP: number of roots per plant, TRWP: total root weight per plant, NRM: number of marketable/commercial roots, MRW: marketable/commercial root weight, NRPL: number of roots per plot, TSRW: total storage root weight, BRIX: level of sweetness, and SG: specific gravity.

Eigenvalue was between 0.543 and 6.177 which gives variability of as high as 92.135% in Jatinangor Sumedang (Table 5). PC 1 covered 61.177% of variability with a variation of nine genotypes and three commercial varieties as checks given the traits storage root length, storage root diameter, number of roots per plant, total root weight per plant, number of marketable/commercial roots, marketable/commercial root weight, number of roots per plot, and total storage root weight. The PC 2 showed 17.038% variability Brix. PC 3 variability was at 8.482%, and PC 4 variability was at 5.436%.

There are no contributing traits for PC 3 and PC 4. The research on multivariate analysis of sweet potato has also been reported by Lestari [35], based on that study PCA identified the number of roots per plot and total storage root weight as well as stand count at harvest as important traits

Table 6: Factor loadings, agronomic trait markers, contributed to variability in PFSP in Garut.

Parameters	PC 1	PC 2	PC 3	PC 4
SRL	0.473	0.436	0.352	0.557
SRD	0.620	−0.078	0.701	−0.109
NRP	0.643	−0.597	0.378	0.238
TRWP	0.938	0.114	−0.111	0.043
NRM	0.879	0.399	−0.140	−0.144
MRW	0.844	0.435	−0.198	−0.158
NRPL	0.950	−0.171	−0.012	−0.006
TSRW	0.930	0.055	−0.272	0.050
BRIX	−0.421	0.586	0.566	−0.346
SG	−0.599	0.403	−0.089	0.524
Eigenvalue	5.695	1.456	1.234	0.824
Variability (%)	56.955	14.563	12.349	8.249
Cumulative (%)	56.955	71.518	83.868	92.117

SRL: storage root length, SRD: storage root diameter, NRP: number of roots per plant, TRWP: total root weight per plant, NRM: number of marketable/commercial roots, MRW: marketable/commercial root weight, NRPL: number of roots per plot, TSRW: total storage root weight, BRIX: level of sweetness, and SG: specific gravity.

that could be used to differentiate the sweet potato genetic materials from landraces.

The diversity in agronomic traits consists of four axes with a cumulative value of 92.117% and the eigenvalue ranged from 0.824 to 5.695 in Garut (Table 6). Contributing variation showed from the discriminant values in Table 5. The variation on the first axis (PC 1) is 56.955%, which is contributed by the traits of total root weight per plant, number of marketable/commercial roots, marketable/commercial root weight, number of roots per plot, and total storage root weight which have a discriminant value of more than 0.7. The variability of PC 2 is 14.563%. PC 3 is 12.349% contributed by root diameter. PC 4 is 8.249%. There are no traits that contribute significantly to the variation in PC 2 and PC 4.

The eigenvalue of Majalengka ranged from 0.822 to 4.797 which contributed to 86.133% (Table 7). PC 1 covers 47.975% of variability with a variation of 12 genotypes given the biometric traits, namely, number of marketable/commercial roots, marketable/commercial root weight, number of roots per plot, and total storage root weight. PC 2 covers 16.782% variability from variations in 12 genotypes given the trait root diameter. PC 3 covers 13.151%, and PC 4 covers 8.224%, with no contributing traits in PC 3 and PC 4.

The scatter plots are shown in a graphic biplot as determined by the PC values that give the highest contribution to variability. PC 1 and PC 2 are the component values that give the highest contribution towards the variability of a trait. In Cilembu Sumedang, the PC 1 and PC 2 values are 33.605% and 21.466%.

The variability values of the two components for each PFSP genotype are scattered within the biplot forming 4 quadrants (Figure 1). The figures show that the different morphological traits and PFSP genotypes are found in four different quadrants. This shows that there are traits in the PC that have relatively high variability and are important in separating genotypes. Location Cilembu Sumedang (Figure 1), quadrant I has a positive value showing the biometric

Table 7: Factor loadings, agronomic trait markers, contributed to variability in PFSP at Majalengka.

Parameters	PC 1	PC 2	PC 3	PC 4
SRL	0.589	0.614	0.001	0.301
SRD	0.294	0.730	0.165	−0.491
NRP	0.485	−0.447	0.509	0.403
TRWP	0.242	−0.372	0.671	−0.410
NRM	0.941	−0.023	−0.281	0.030
MRW	0.929	−0.121	−0.221	−0.046
NRPL	0.947	0.031	−0.047	0.171
TSRW	0.930	0.128	0.033	−0.127
BRIX	0.440	−0.627	−0.518	−0.330
SG	−0.602	0.011	−0.420	0.022
Eigenvalue	4.797	1.678	1.315	0.822
Variability (%)	47.975	16.782	13.151	8.224
Cumulative (%)	47.975	64.758	77.909	86.133

SRL: storage root length, SRD: storage root diameter, NRP: number of roots per plant, TRWP: total root weight per plant, NRM: number of marketable/commercial roots, MRW: marketable/commercial root weight, NRPL: number of roots per plot, TSRW: total storage Root weight, BRIX: level of sweetness, and SG: specific gravity.

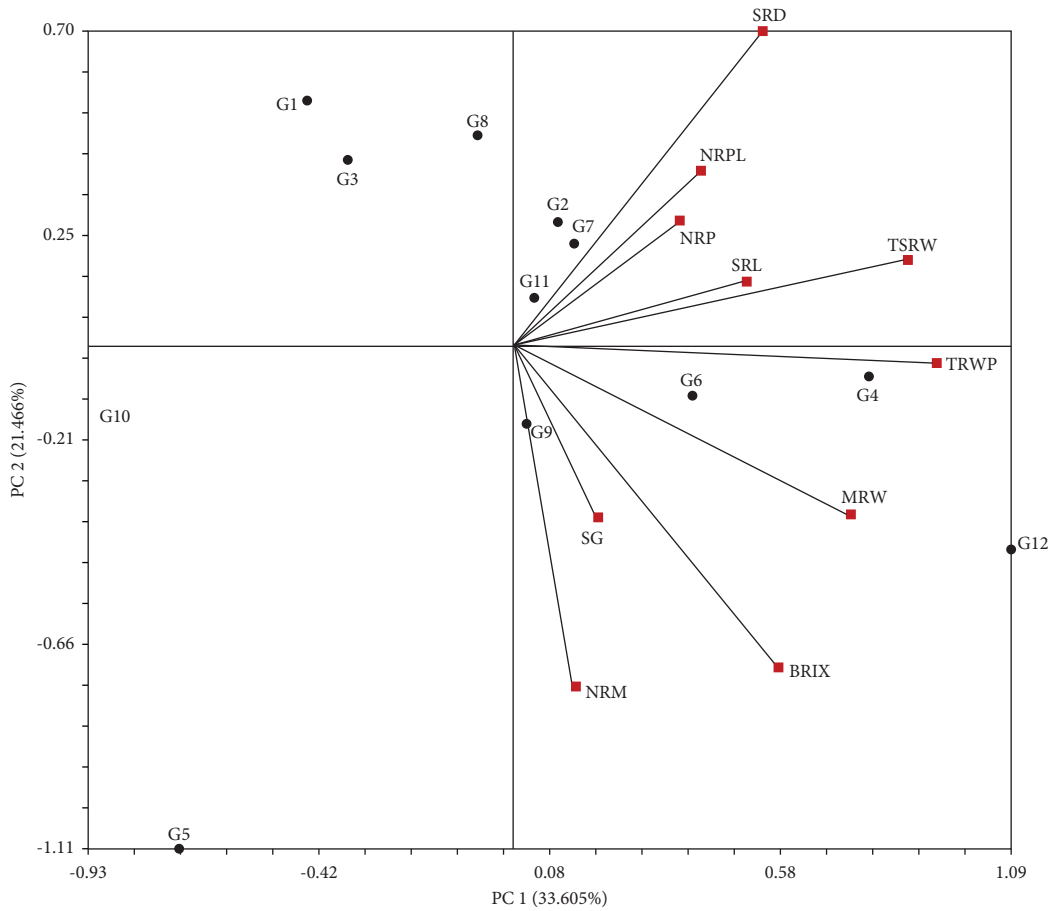

Figure 1: Distribution pattern of nine genotypes PFSP and three commercial varieties as checks based on ten agronomic traits in Cilembu Sumedang.

traits storage root diameter, number of roots per plot, number of roots per plant, storage root length, and total storage root weight are tightly related or linked. Genotypes in quadrant 1 (G2, G7, and G11) are closely related, and they have a high levels of similarity. For Jatinangor Sumedang (Figure 2), traits with positive values are brix, storage root diameter, storage root length, total root weight, and marketable/commercial root weight.

Genotypes that have high similarities in Jatinangor Sumedang are G4, G9, and G12. Different traits in the same quadrant mean that they are closely and positively related. The opposite is true if they are in different quadrants. In

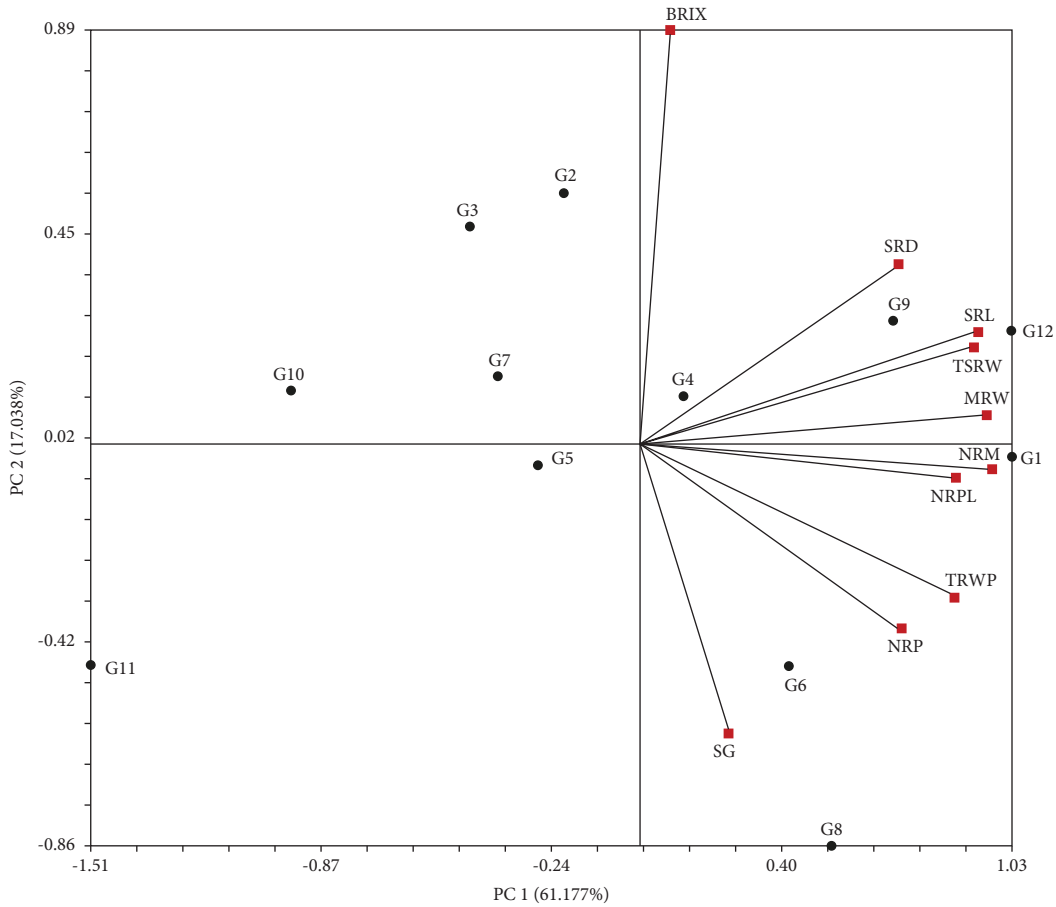

Figure 2: Distribution pattern of nine genotypes PFSP and three commercial varieties as checks based on ten agronomic traits in Jatinangor Sumedang.

Jatinangor Sumedang, the PC 1 and PC 2 values are 61.177% and 17.038% traits that are located separately have traits that are different and can be used as a marker of morphological traits. Position closeness between two objects can be interpreted as the similarity of the object's properties.

The figures show that the different morphological traits and PFSP genotypes are found in four different quadrants in Garut with the PC 1 and PC 2 values are 56.955% and 14.563% (Figure 3). Quadrant I has a positive value showing that the traits are storage root length, marketable/commercial root weight, number of marketable/commercial roots, total root weight per plant, and total storage root weight are closely and positively related. Genotypes that have high similarities in Jatinangor Sumedang are G12, G2, and G4. The closer the two objects are the trait indicated by the values of the variables is more similar.

For Majalengka (Figure 4), the traits with positive values are storage root diameter, storage root length, total storage root weight, and number of roots per plant. Jain and Patel [36] show that traits with positive values have a significant contribution to diversity. Genotypes that have high similarity are G1, G6, and G2. The opposite is true if they are in different quadrants. Depiction of a biplot can provide information regarding the correlation between the traits observed by genotypes in the form of groupings.

3.3. Agglomerative Hierarchical Clustering (AHC) Analysis. Cluster analysis is a method used in grouping a set of traits into clusters. In the AHC analysis, the closeness of the relationship is measured by the value of the Euclidean distance. Euclidean is basically a value that shows the distance between two points or data in different dimensions [37]. The results of the cluster analysis presented in the form of a dendrogram showed that there were differences in the level of similarity of each sweet potato genotypes based on agronomic traits in four locations. Euclidean distance value in the range of 0-1 indicates a small dissimilarity, whereas its value more than 1 indicates a large dissimilarity coefficient [38].

Clustering resulted in two main clusters with Euclidean values on the dendrogram of agronomic traits ranging from 1.92 to 5.29 in Cilembu Sumedang (Figure 5). Euclidean distance of more than one indicates that the sweet potato genotypes are broad [39]. The dendrogram shows that the distribution of the 12 PFSP genotypes is wide. The dendrogram of agronomic traits showed that PFSP genotypes were divided into two main clusters, namely, the main cluster I with 10 genotypes and the main cluster II with 2 genotypes. Each main cluster is divided into two different subclusters at a Euclidean distance of 4.45.

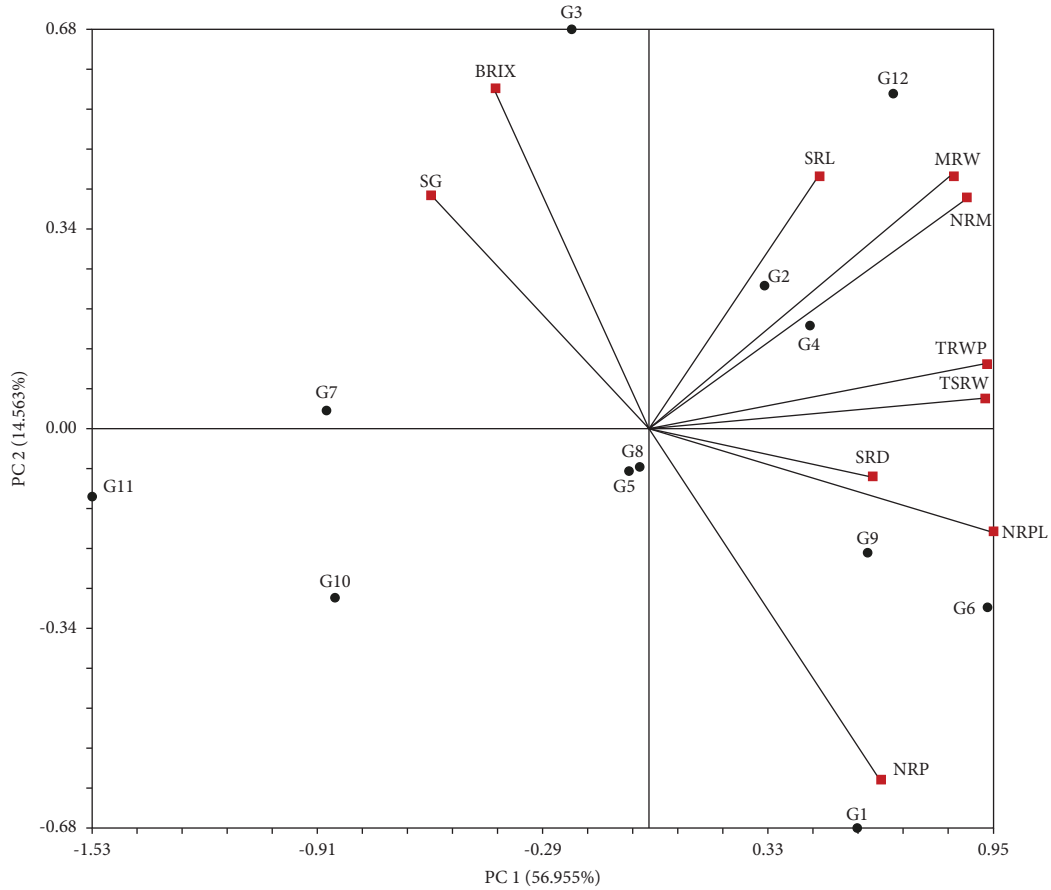

Figure 3: Distribution pattern of nine genotypes PFSP and three commercial varieties as checks based on ten agronomic traits in Garut.

Subcluster I.1 consisted of nine genotypes, namely, G1, G3, G2, G7, G9, G11, G6, and G8, while subcluster I.2 consisted of two genotypes, namely, G4 and G12. There were two genotypes, namely, G5 and G10 in cluster II. The highest similarity values were found in G2 and G7. Genotypes in the same cluster tend to have similarities in agronomic traits. Genetic distance has an important role in plant breeding in addition to genetic variation. Genetic distance studies, especially based on agronomic traits, can help plant breeders in determining parents with different characteristics for plant breeding activities [40]. Genetic distance shows the relationship between two different individuals based on the traits they have, where the farther the relationship between two accessions in a population, the higher the genetic variation.

The existence of PFSP genotypes found in the same subcluster was caused by the similarity of agronomic traits. The accuracy of this cluster analysis is determined by the number of traits observed. The level of dissimilarity among genotypes in the dendrogram has a Euclidean distance of 1.72–6.09 (Figure 6). The level of dissimilarity between genotypes is high in the dendogram with two main clusters. The dendrogram shows that the distribution of the 12 genotypes in Jatinangor Sumedang is wide.

Each main cluster is divided into two different subcluster at a Euclidean distance of 5.00. Subcluster I.1 consists of five genotypes, namely, G1, G12, G9, G6, and G8, while subcluster I.2 consists of six genotypes, namely G2, G3, G4, G5, G7, and G10. There was one genotype in cluster II, namely, G11 subcluster produce different level of genetic distance with PFSP genotypes. Clusters can group heterogeneous data into more homogeneous classes based on dissimilarity between data [38]. The highest similarity values were found in genotypes G1 and G12.

The level of dissimilarity among genotypes in the dendrogram has a Euclidean distance of 1.28–6.38 (Figure 7). The level of dissimilarity between genotypes is high in the dendrogram with two main clusters. The dendrogram shows that the distribution of the 12 genotypes in Garut is wide. The level of dissimilarity among genotypes in the dendogram has a Euclidean distance of 1.28–6.38.

Subcluster I.1 consisted of eight genotypes, namely, G1, G9, G2, G4, G8, G5, G12, and G6, while subcluster I.2 consisted of three genotypes, namely, G3, G7, and G10. There was one genotype in cluster II, namely, G11. The highest similarity values were found in genotypes G2 and G7. Based on agronomic traits, the genetic distances in 12 PFSP genotypes in Garut were widely. Estimating the relationship between genetic variation and relationships among germplasm accessions facilitates the selection of parents with different genetic background necessary for the breeding program [28, 41–43]. The greater the genetic distance, the opportunity to obtain the desired trait with a high heritability value is getting bigger.

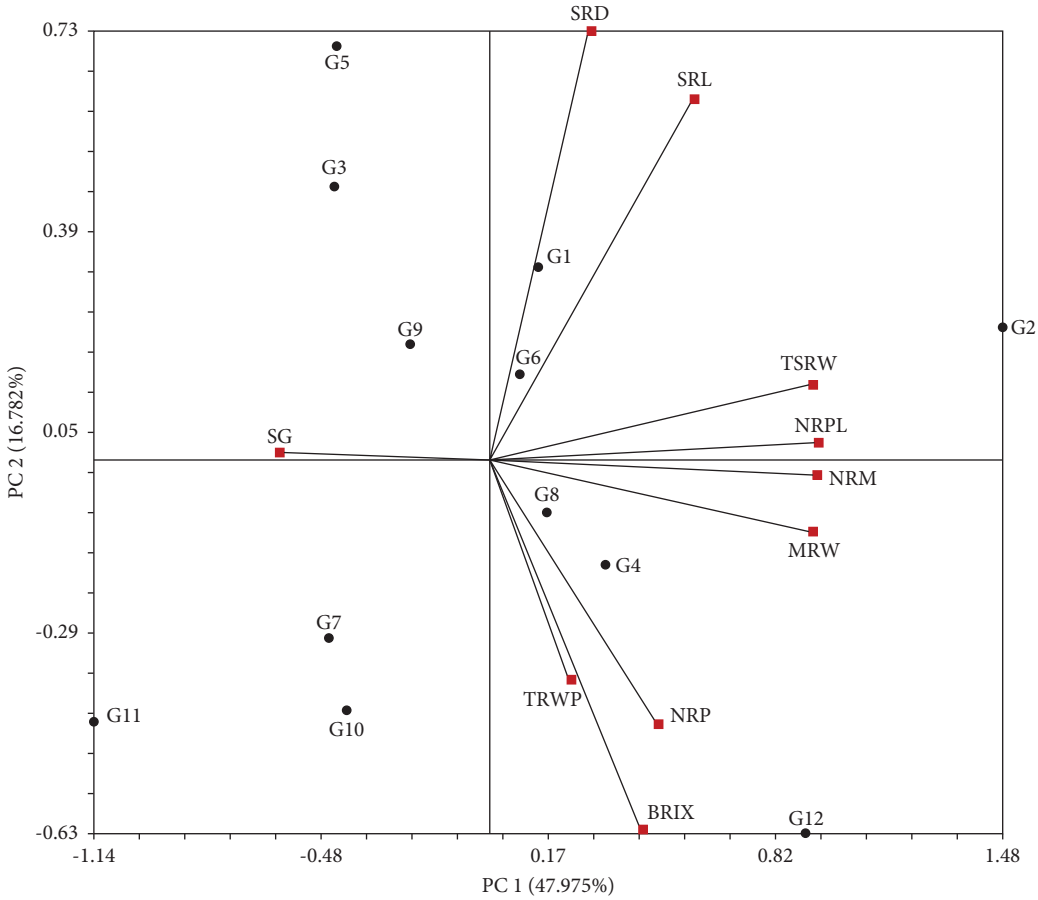

Figure 4: Distribution pattern of nine genotypes PFSP and three commercial varieties as checks based on ten agronomic traits in Majalengka.

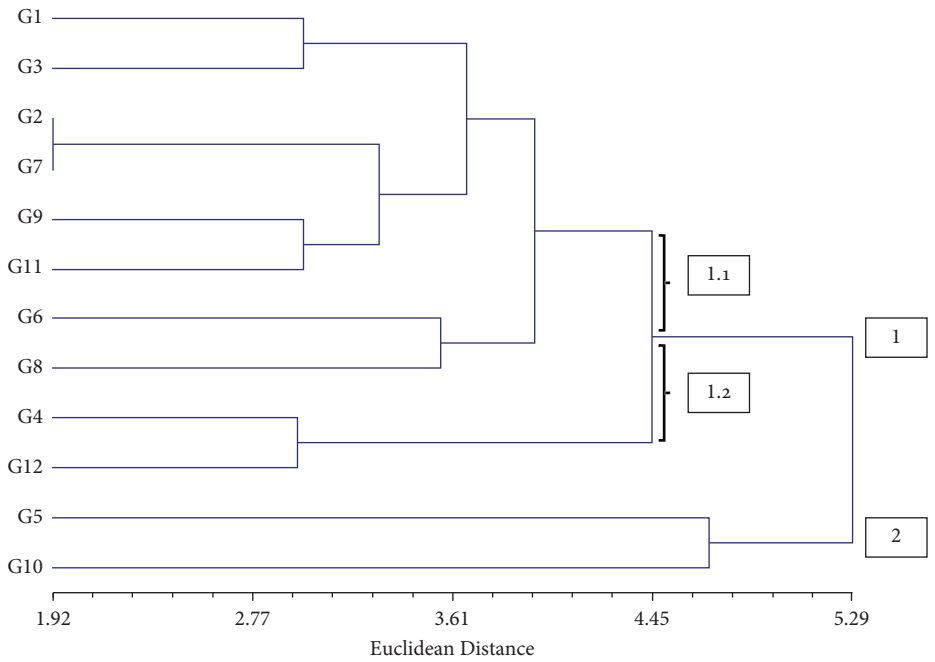

Figure 5: Dendrogram for nine genotypes of PFSP and three commercial varieties as checks based on agronomic traits in Cilembu Sumedang.

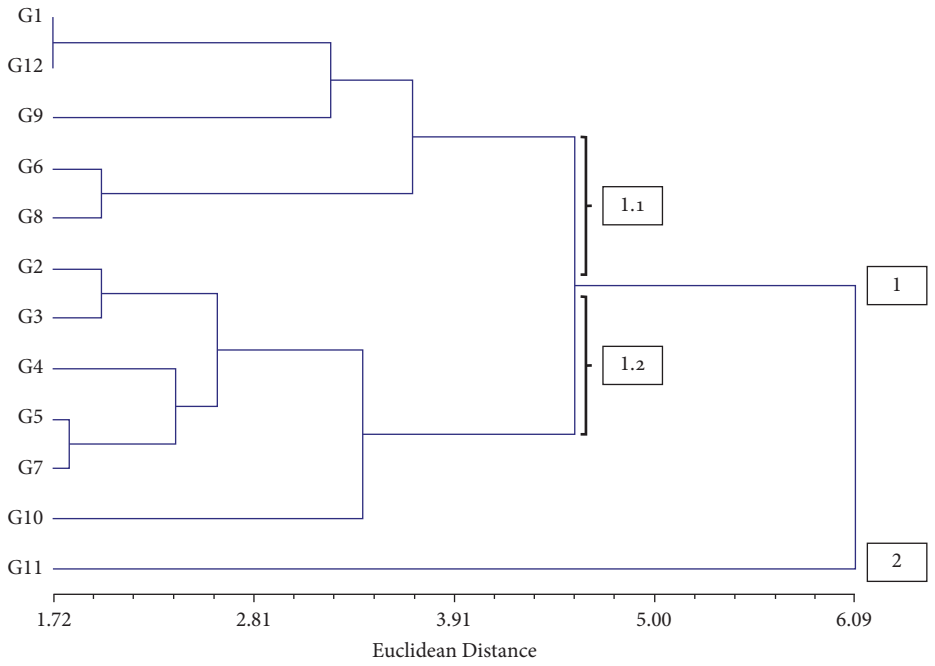

Figure 6: Dendrogram for nine genotypes of PFSP and three commercial varieties as checks based on agronomic traits in Jatinangor Sumedang.

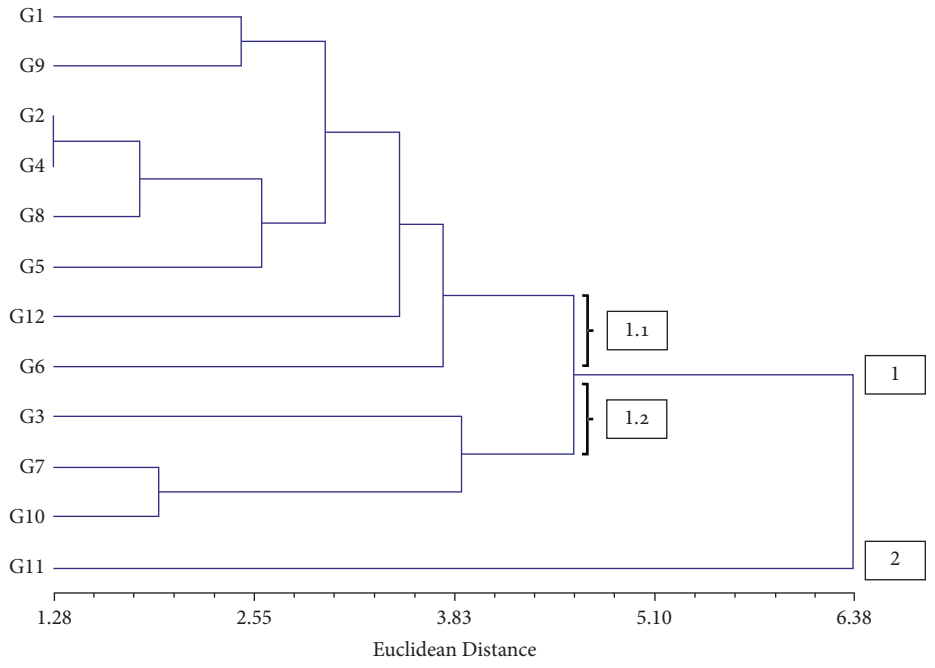

Figure 7: Dendrogram for nine genotypes of PFSP and three commercial varieties as checks based on agronomic traits in Garut.

Agronomic traits in the dendrogram showed that PFSP genotypes were divided into two main clusters in Majelengka, namely, the main cluster I with ten genotypes and the main cluster II with one genotype (Figure 8). Each main cluster is divided into two different subclusters at a Euclidean distance of 4.94. Subcluster I.1 consisted of nine genotypes, namely, G1, G9, G3, G5, G9, G7, G6, G4, G12, and G8, while subcluster I.2 consisted of two genotypes, namely, G10 and G11. There was one genotype, namely, G2 in cluster II. The highest similarity values were found in genotypes G2 and G7.

The dendrogram shows that the distribution of 12 PFSP genotypes in Majalengka with Euclidean distance 2.05–5.09. The dendrogram shows that the distribution of the 12 PFSP genotypes in Majalengka is wide. Differences in genetic variation can occur based on agronomic traits. Genetic

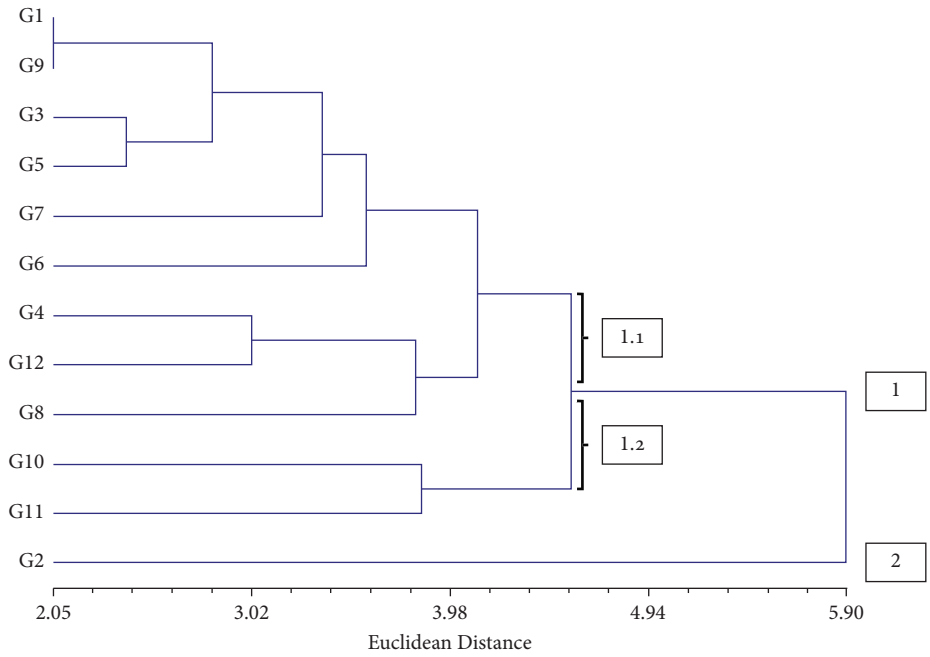

Figure 8: Dendrogram for nine genotypes of PFSP and three commercial varieties as checks based on agronomic traits in Majalengka.

variation information is essential as a reference in determining the genetic material to be developed, with data related to plant genetic variation, and the opportunity to produce superior sweet potato varieties with wide genetic variation will be even greater.

4. Conclusions

Multivariate analysis showed the high genetic variations in nine PFSP genotypes and three commercial varieties as checks were assessed in four environments. Eigenvalue range from 1.92 to 5.29 in Cilembu Sumedang which contributed to eigenvalue ranged from 0.822 to 3.360 which contributed to 80.958% variability, eigenvalue range of 0.543–6.177 which contributed variability to 92.135% in Jatinangor Sumedang, eigenvalue range from 0.824 to 5.695 in Karangpawitan Garut which contributes to 92.117%, and eigenvalue range from 0.822–4.797 which contributed to 86.133% in Maja Majalengka. The cluster analysis of PFSP genotypes showed a wide distribution obtaining two clusters in Cilembu Sumedang with euclidean distance 1.92–5.29, Jatinangor Sumedang range of 1.72–6.09, Karangpawitan Garut range of 1.28–6.38, and Maja Majalengka range of 2.05–5.09. High genetic variation in agronomic traits of PFSP genotypes in four environments was found in almost all traits observed in. In general, information from PFSP high genetic variation can be used to determine contributing traits and as a basis for selection for variety releases. PFSP genotypes are recommended for further stability test in many environments and seasons.

Data Availability

All data generated or analyzed to support the findings of this study are included in this published article.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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