



DIVERSITY STUDIES ON MORPHOLOGICAL ATTRIBUTES OF SEGREGATING SWEETPOTATO [*Ipomoea batatas* (L.) Lam] GENOTYPES

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ABSTRACT

Sweetpotato (*Ipomoea batatas* (L.) Lam) is one of the most important root crops in the world, particularly in sub-Saharan Africa. Collecting and characterizing plant materials have been the basis for crop improvement. Diversity studies have long been seen as vital for rational management and use of crop germplasm. Thirty-two newly developed clones (progenies) and their parents (TIS 8164 (M1), Centennial (F2), UMUSPO/3 (Mother Delight) F1, UMUSPO/2 (M3) and Tio Joe (F5)). The data generated were analyzed for morphological diversity using principal component analysis (PCA), which was used in identifying the few characters that significantly influenced the observed variation among the progenies. In summary, this study revealed that ground cover, vine internode length, predominant skin colour, secondary skin colour, flower colour, flower habit, mature leaf, leaf lobe type and leaf lobe number were important descriptor traits that characterize the observed variations in segregating sweetpotato. It also helped to identify progenies and parents that were less susceptible to the sweetpotato virus disease for breeding purposes, and to farmers for a good yield.

Keywords: Sweetpotato, morphological characterization, diversity, and segregating population

Introduction

Sweetpotato (*Ipomoea batatas* (L.) Lam) is a dicotyledonous plant which belongs to the family *Convolvulaceae* (Degross, 2000). It is believed to have originated in Central America, though other centres of origin have been proposed (Austin, 2000). It is a widely grown and important staple food in many parts of the tropics and sub-tropics, especially in the developing countries of the world (Edmond, 1971). Globally, it is the seventh most important food crop in the world (FAO, 2012). The crop is grown for multipurpose uses. Roots and vines are used both for human food and for animal feed. The demand for new varieties with high productivity for both roots and forage has increased, especially for farmers operating in mixed crop-livestock systems (Lukuyu and Agili, 2013). One of the main characteristics of sweetpotato is its high phenotype and genotype variability (Veasey *et al.*, 2007) that confers adaptability to different edaphic climatic conditions. In the process of developing new varieties of species, new clones are developed through hybridization of selected parents. As the variability contained in the genome of a species find expressions as visible characteristics that form the phenotype (Hidalgo, 2003), segregating population such as those developed through bi-

parental crosses provides a rich platform to study variation. Studying the structure of variation within such highly segregating progenies will generate valuable information that can refine morphological characterization of sweetpotato genotypes as well as understand the traits that define the extent of the observed diversity. Through characterization, diversity that exists in a germplasm population can be estimated and effectively studied (Sinha *et al.*, 2013). This is because descriptors correspond to characteristics or attributes whose expressions are easily detected by the naked eye, be recorded, have high heritability, high taxonomic and agronomic value, easy to measure or evaluate (Hidalgo, 2003). Morphological characterization in sweetpotato is done by assessing variations in the vine, leaf, flower and storage root characteristics (Huaman, 1991). This method has been used for identifying sweetpotato cultivars, detecting unique character traits and correlation with characteristics of agronomic importance (Karuri *et al.*, 2010). Standard descriptor lists often used for sweetpotato characterization provide an international format and universally understood language for plant genetic resource data (Huaman, 1991). The International Plant Genetic Resources Institute (IPGRI) Descriptor for

Sweetpotato is the standard descriptor used for sweetpotato characterization (IBPGR, 1997). This study aims at evaluating the extent of morphological diversity within a segregating sweetpotato population, and the determination of the important traits that influence the observed variation among a segregating population.

Materials and Methods

The planting materials consisting of four node vine cuttings of 32 sweetpotato progenies and six parents were obtained from the Sweetpotato Breeding Program of the National Root Crops Research Institute, Umudike. Each progeny was from a family of male and female parents. The experiment was laid out in a randomized complete block design (RCBD) with three replicates. The plot size was 6.0 m² (2.0 m by 3.0 m) containing 20 plants per plot with inter-plot spacing of 0.5 m between plots. Plant spacing of 1.0 m by 0.3 m was used. The sweetpotato vines were planted on the crest of the ridge, slanting at an angle of 45°. Planting was done in June, 2017 after the soil was sufficiently moistened. First weeding was done manually at four weeks after planting before fertilizer application at the rate of 400 kg per hectare of NPK (15:15:15) was carried out. Subsequent weeds found were rogued.

Data collection: Morphological data were collected three months after planting. Measurements were done on three plants chosen randomly from the middle portion of the main stem per plot and averaged for the variable in each of the clones and parents as recommended by Huaman (1991). Qualitative characters were scored using a scale of 0 to 9. The following variables were scored: Plant growth characteristics: plant type (habit) (PT), ground cover (GC); mature vine characteristics: vine internode length (VIL), predominant vine colour (PVC), secondary vine colour (SVC), vine tip pubescence (VTP); mature leaf characteristics: general outline of leaf (GOL), leaf lobes number (LLN), leaf lobed type (LLT), mature leaf size (MLS), shape of central leaf lobe (SCLL), mature leaf colour (MLC), immature leaf colour (ILC); flowering habit (FH).

Data analysis: The data collected were analyzed for morphological diversity using principal component analysis based on correlation matrix to identify the few characters that significantly influenced the observed variation among the segregating progenies and their parents for both above and below ground attributes; and to also determine the progeny clusters with parent-like traits according to Afuape et al. (2019).

Results and Discussion

Vine Characters

Principal component analysis (PCA) for the six morphological descriptor traits for vine characters

among the 32 progenies and their parents is presented in Table 2. Only three principal components had eigen values above 1.0. Principal component 1 was responsible for 29.8% of the observed total variation, while PC 2 and PC 3 were responsible for 21.7% and 17.2 of the total variation, respectively. Ground cover (0.596), vine internode length (0.525) were the traits with the highest influence on the 29.8% contributed by PC 1. Secondary vine colour (-0.408) and plant type (0.337% also showed moderate influence on PC 1. While the 21.7% variation contributed by PC 2 was largely influence by predominant vine colour (0.655), vine tip pubescence (-0.583) and plant type (0.440), the 17.2 % variation of PC 3 was mainly as a result of the influence of secondary vine length (0.686).

The PCA biplot analysis for vine characters revealed the relationships between the 32 progenies, their six parents and the vine descriptors. Genotypes that are very close to a particular trait expresses high values for that trait, and those found between two traits possess moderate for each of the traits. Genotypes around traits that are directly opposite have low expression for the opposite traits. Parent genotype Tio Joe and CL1/F₂M₁/4 were distinct for good ground cover and long vine length. Genotypes with pronounced vine tip pubescence included UMUSPO/2, (parent), UMUSPO/3 (parent), CL1/F₅M₁/14, CL1/F₂M₁/26, CL1/F₂M₁/49, while TIS 87/0087 had moderate values for ground cover and vine tip pubescence. For predominant vine colour, CL2/F₂M₁/51 had unique expression of the trait, while CL2/F₂M₁/06, CL2/F₁M₁/02 and CL1/F₅M₁/15 had same colour but fairly distinct from that of CL2/F₂M₁/51. For secondary vine colour, the genotypes around the trait shared some semblance of secondary colours on the vines, but there were still enough differences to distinguish one from the other. All the genotypes around the origin of all the traits have moderate expressions for all the vine descriptor traits.

Flower Characters

Three descriptor traits were used to characterize the flowers of the segregating genotypes and their parents (Table 3). Out of the three principal components, only PC1 with eigen value above 1.0 and variance contribution of 44.4% was relevant. PC2 contributed 32.8% to the total variation though. All the three descriptors had large influence on the observed 44.4% variation contributed by PC1 with flower colour (0.669) being the most discriminant among them, followed by flowering habit (0.550). Using all the three descriptors Using the three descriptors will be the best idea for use in characterizing plant part with very few descriptors such as sweetpotato flower. From the PCA biplot analysis for flower characters (Figure 2), most of the genotypes clustered around flower colour and flowering habit, depicting they could also be used to characterize a progeny

population. Parent genotype UMUSPO/2 has a distinct immature leaf colour from the other parents, with only very few progenies sharing this trait with it. All the genotypes that clustered away from the three descriptor traits either had moderate and distinguishable expression of the three traits or were totally distinct from the progenies expressing the traits. Such totally distinct traits could have arisen from the preponderance of mutation which has been noted in sweetpotato (Takagi, 1993).

Leaf characters

The results of the PCA performed on six morphological leaf traits of the total genotypes are presented in Table 4. Out of the six PCs, only two had >1.0 eigen value with cumulative variance of 69.4%. Principal component 1 (PC 1) contributed 51.5% while PC 2 contributed 17.9% to the total observed variance. Four of the descriptor traits (leaf lobe type, mature leaf shape, leaf lobe number and shape of central leaf lobe) were the important descriptors that accounted for the 51.5% variance contributed by PC 1. For PC 2, only leaf size (0.758) and mature leaf colour (-0.623) were important in PC 2. For the characterization of moderate number of genotypes, the six leaf descriptor traits can be used. However, for a large number of genotypes, leaf lobe type, mature leaf shape, leaf lobe number and shape of central leaf lobe will be adequate.

The biplot analysis for the leaf descriptor traits of the characterized genotypes showed that four of the six traits were closely related as the more acute the angle between any two traits, the stronger the correlation between them. In this regard, there is a strong correlation among leaf lobe type, mature leaf shape, shape of central leaf lobe and leaf lobe number. Progenies CL1/F1M5/1, CL1/F5M1/13, CL1/M5M1/1, CL1/F2M1/8 had elevated values for the four traits, while CL2/F2M1/06, CL1/F2M1/22 and CL2/F2M1/15 had average performance for leaf lobe number and leaf size. Progeny CL1/F5M1/15 had a distinct mature leaf colour, Progenies CL2/F2M1/57 and UMUSPO/2 that were located at the intersection of the two zero origins were average for all the traits. All the genotypes opposite leaf lobe type, mature leaf shape, shape of central leaf lobe and leaf lobe number and below the horizontal zero line were common for the traits, and were UMUSPO/3, TIS 8164, TIS 87/0087 and Centennial (parents) type. Progeny CL1/M1F2/4 had unique features that were different from every other genotype.

There is high variability among sweetpotato genotypes which Maguia *et al.*, (2013) had reported were largely caused by natural mutations and environmental influence on such traits as root flesh and skin colour, as well as leaf and vine characteristics. Diversity studies have been done on the crop using morphological descriptors in various

parts of the world to highlight the structure and extent of the variations. The extent and distribution of the variation in sweetpotato is essential for sound conservation strategies whereby conservation and sustainable use of phenotypic resources are essential to meet the demand for future use (Karuri *et al.*, 2010). Morphological diversity and relationship among sweetpotato varieties are very important, not only for germplasm conservation, but also for breeding purposes especially during the selection of varieties having superior qualities (Laurie *et al.*, 2004). This study showed that there is high level of phenotypic diversity exhibited among the segregating progenies using morphological characters. Among the progenies studied and their parents, most of the morphological characters were highly variable.

The sweetpotato descriptor manual has over 40 descriptor traits for morphological characterization. It will be near impossible to use the whole traits to characterize a large sweetpotato germplasm. Principal components analysis is a procedure for identifying a smaller number of uncorrelated variables, called "principal components", from a large set of data (Jolliffe, 2002). The goal of principal components analysis is to explain the maximum amount of variance with the fewest number of principal components, which was used in identifying the few characters that significantly influenced the observed variation among the progenies and their parents for both above and below ground attributes (Abdi and Williams, 2010). However, this work has revealed fewer descriptor traits that can be effectively used to characterize a given sweetpotato germplasm including a segregating population. From this study, vine internode length, secondary vine colour, predominant vine colour, vine tip pubescence and ground cover (vine descriptor traits), flower colour and flower habit (flower descriptor traits), mature leaf shape, leaf lobe type, shape of central leaf lobe, leaf lobe number, immature leaf colour and leaf size (leaf descriptor traits), and predominant root skin colour and secondary skin colour (root descriptor traits) have been identified as trait descriptors that can sufficiently be used in studying sweetpotato germplasm for morphological variation. In their work, and as found by this study, Afuape and Nwachukwu (2005) also identified flowering habit, leaf lobe type, shape of central leaf lobe, leaf lobe number, predominant root skin colour and immature leaf colour as descriptors capable of discriminating among genotypes. Ochieng (2019) equally identified vine internode length and leaf size as descriptors with high discriminating power. However, Afuape and Nwachukwu's (2005) work further showed that secondary root skin colour may not be much of importance when characterizing locally assembled landraces which could share many traits.

Conclusion

Findings show that the 32 progenies and 6 parents of sweet potatoes used for this study have high morphological diversity in both the above (vine, leaf, flower) and below (root) attributes in the population. While the whole descriptor traits in the IPBGR Sweetpotato Descriptor Manual should be used for small germplasm collection, fewer traits that can still be used to adequately discriminate among the large collections include: vine internode length, ground cover, flower colour, flower habit, mature leaf shape, leaf lobe type, shape of central leaf lobe, leaf lobe number, Predominant skin colour and secondary skin colour. This study hereby recommends that these identified descriptor traits are good for vine internode length, ground cover, flower habit, flower colour, mature leaf shape, leaf lobe number and predominant skin colour are good discriminant descriptor traits for segregating sweetpotato genotype and the progenies that cluster together in the PCA biplot analysis for each descriptor trait can be used in core collection of sweetpotato.

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Table 1a: List of 32 progenies of sweetpotato used in the study

Progenies	Pedigree	
	Female parent	Male parent
CL1/F2M1/22	Centennial	TIS 8164
CL1/F5M1/2	Tio Joe	TIS 8164
CL1/F5M1/15	Tio Joe	TIS 8164
CL1/F5M1/14	Tio Joe	TIS 8164
CL2/F1M1/02	UMUSPO/3	TIS 8164
CL2/F2M1/55	Centennial	TIS 8164
CL2/F2M1/22	Centennial	TIS 8164
CL2/F2M1/15	Centennial	TIS 8164
CL2/F2M1/06	Centennial	TIS 8164
CL2/F2M1/51	Centennial	TIS 8164
CL1/F5M1/3	Tio Joe	TIS 8164
CL1/F2M1/30	Centennial	TIS 8164
CL1/F5M1/13	Tio Joe	TIS 8164
CL1/M1F5/1	Tio Joe	TIS 8164
CL2/F2M1/57	Centennial	TIS 8164
CL1/F2M1/7	Centennial	TIS 8164
CL2/F2M1/03	Centennial	TIS 8164
CL1/F2M1/49	Centennial	TIS 8164
CL1/M1F2/4	Centennial	TIS 8164
CL1/F2M1/26	Centennial	TIS 8164
CL1/F5M1/6	Tio Joe	TIS 8164
CL2/F2M1/36	Centennial	TIS 8164
CL1/F5M6/1	Tio Joe	Ex-Igbariam
CL1/M5M1/1	Solo-Abuja	TIS 8164
	Centennial	TIS 8164
CL2/F2M1/57	Centennial	TIS 8164
CL1/F2M1/8	Centennial	TIS 8164
CL1/F5M2/1	Tio Joe	TIS 87/0087
CL2/F2M1/50	Centennial	TIS 8164
CL1/F2M1/33	Centennial	TIS 8164
CL1/F2M14	Centennial	TIS 8164
CL2/F2M1/46	Centennial	TIS 8164

Table 1b: Lists of parents used in the study

1	TIS 8164 (M1)
2	TIS 87/0087 (M2)
3	UMUSPO 2 (M3)
4	UMUSPO/3 (MOTHER'S DELIGHT) F1
5	Centennial (F2)
6	Tio Joe (F5)

Table 2: Identification of important sweetpotato vine descriptor traits using principal component analysis

Characters (traits)	PC 1	PC 2	PC 3
Plant type	0.337	0.440	-0.150
Vine internode length (cm)	0.525	0.172	0.241
Predominant vine colour	-0.191	0.655	0.378
Secondary vine colour	-0.408	0.052	0.686
Vine tip pubescence	0.230	-0.583	0.477
Ground cover	0.596	0.070	0.280
Eigen value	1.790	1.303	1.032
% variance contribution	29.8	21.7	17.2
% Cumulative variance contribution	29.8	51.8	69.0

Table 3: Identification of important sweetpotato flower descriptor traits using principal component analysis

Character (traits)	PCA 1	PCA 2	PCA 3
Flower colour	0.699	0.010	0.7 15
Immature flower colour	-0.457	0.775	0.436
Flower habit	0.550	0.631	-0.546
Eigen value	1.333	0.984	0.683
% variance contribution	44.4	32.8	22.8
% cumulative variance contribution	44.2	77.2	100

Table 4: Identification of important sweetpotato leaf descriptor traits using principal component analysis

Character (Traits)	PC 1	PC 2
Leaf size	0.025	0.758
Mature leaf shape	0.504	-0.023
Leaf lobe type	0.525	0.017
Shape of central leaf lobe	0.474	0.167
Mature leaf colour	-0.026	-0.623
Leaf lobe number	0.494	0.095
Eigen value	3.088	1.075
% variance contribution	51.5	17.9
% cumulative variance contribution	51.5	69.4

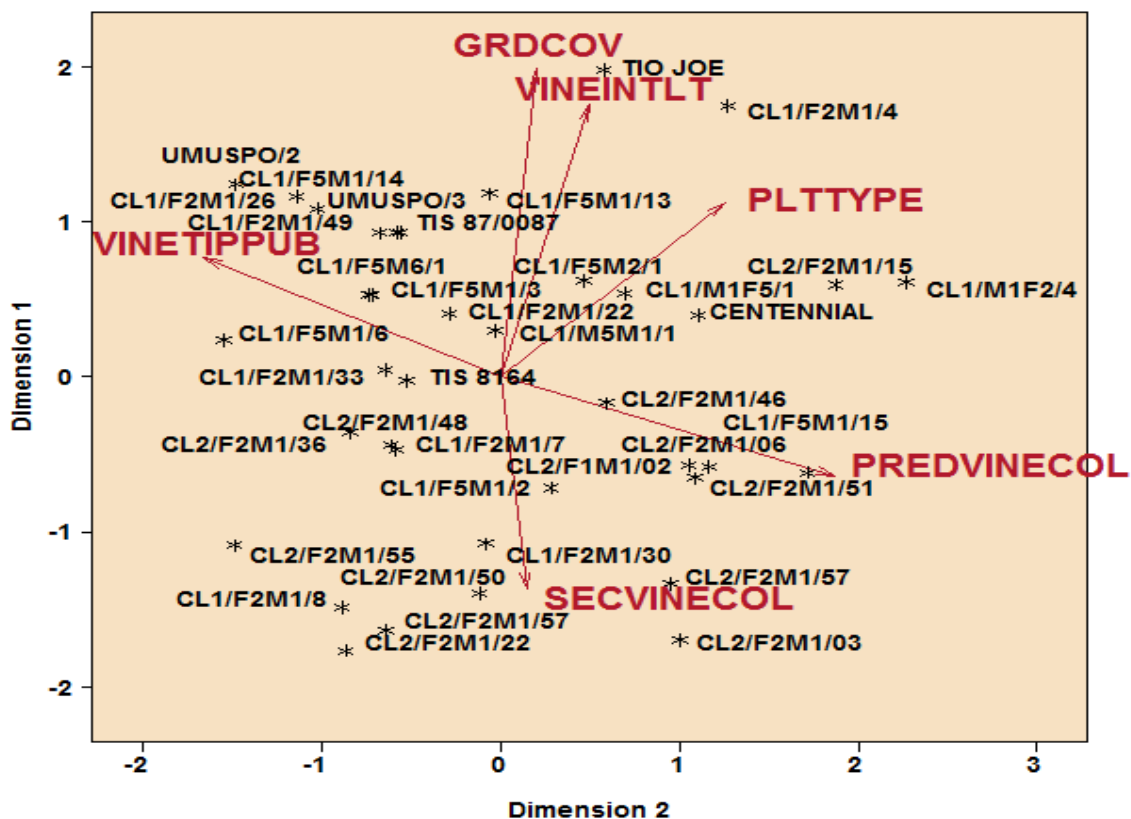


Figure 1: PCA biplot analysis of relationship between segregating progeny population and the parents for six vine descriptor traits. Keys: GRDCOV=Ground Cover; VINE INTLT=Vine internode length; PLTTYPE=Plant type; PREDVINECOL = Predominant vine colour; SECVINECOL= Secondary vine colour; F₅ = Tio Joe; F₁= UMUSPO/3; M₁ = TIS 8164; M₂ = TIS 87/0087; M₃ = UMUSPO/2; F₂ –Centennial

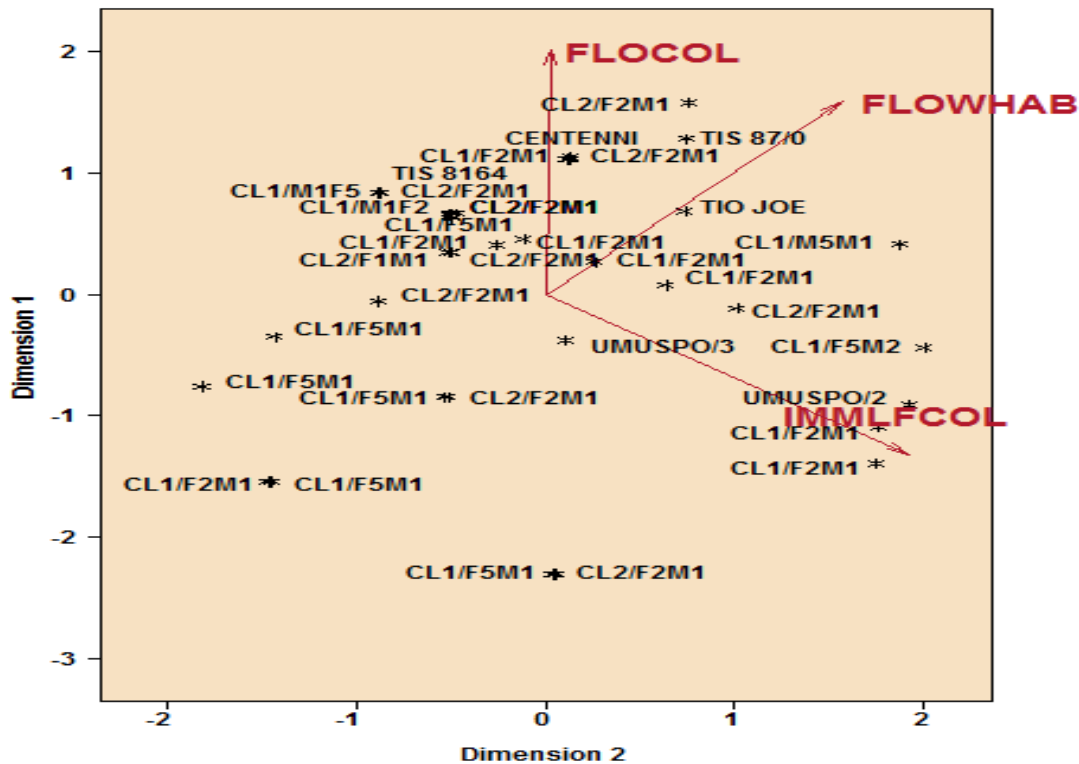


Figure 2: PCA biplot analysis of relationship between segregating progeny population and the parents for three flower descriptor traits. Keys: F₅ = Tio Joe; F₁ = UMUSPO/3; M₁ = TIS 8164; M₂ = TIS 87/0087; M₃ = UMUSPO/2; F₂ –Centennial. FLOCOL - Flower Colour, FLOWHAB – Flower habit, IMMLFCOL – Immature flower colour

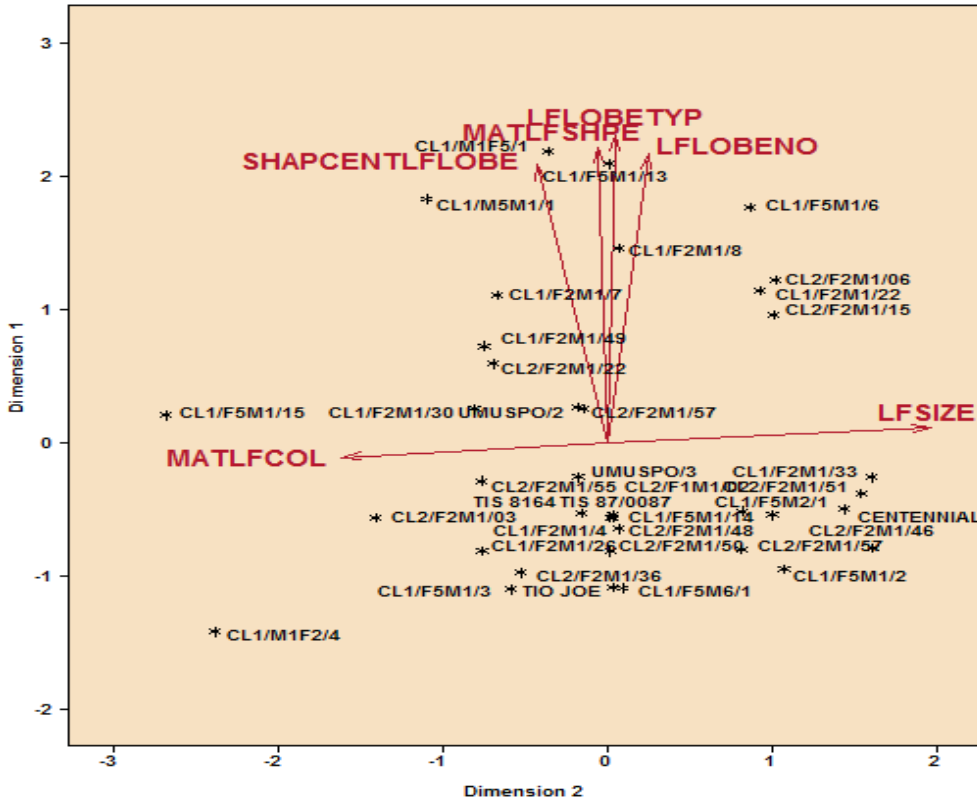


Figure 3: PCA biplot analysis of relationship between segregating progeny population and their parent for 6 leaf descriptor traits. LFLOBETYP – leaf lobe type, MATLFSHAPE, Mature leaf shape, SHAPCENTLOBE – shape of central leaf lobe, LFLOBENO-leaf lobe number, LFSIZE – leaf size, MATLFCOL – mature leaf colour. F₅ – Tio Joe, F₁ – UMUSPO/3, M₁ – TIS 8164, M₂ – TIS 87/0087, M₃ – UMUSPO/2, F₂ –Centennial.