

**Genetic Characterization and nutritional analysis of Eastern and South African  
*Cleome gynandra* (spider plant) accessions**

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Science Degree in Plant Breeding and Biotechnology**


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## DECLARATION

This thesis is my original work and it has not been presented for a degree in any other university.

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Signed..........

Date.....25/7/2017.....

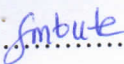
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## ABSTRACT

Sub-Saharan Africa is faced with a rapidly growing population, malnutrition, human diseases, increased food prices, political instability and high inflation. This calls for a multifaceted approach in bringing about food and nutritional security. African indigenous vegetables play a highly significant role in food security by providing valuable sources of energy and micronutrients to the underprivileged, in both urban and rural settings. Spider plant (*Cleome gynandra*), commonly known as African Spider Flower or Spider wisp, is an important leafy vegetable in most parts of Africa. It is highly nutritive and contains health promoting bioactive compounds important in combating malnutrition and reducing human degenerative diseases. Despite continued increase in production and consumption, there has been limited efforts towards its improvement. The aim of this study was: a) To determine the extent of phenotypic variation among selected Kenyan and South African spider plant accessions. b) To establish their nutrition composition for future improvement. c) To identify microsatellites or Simple Sequence Repeat (SSR) markers from a close relative of *C. gynandra* for which whole genome sequence is available, (*Tarenaya hassleriana*) that can be subsequently used for marker-assisted selection in *C. gynandra*. A total of 49 spider plant accessions were planted in the field at the University of Nairobi Field Station in a randomized complete block design with three replications for two seasons. Characterization of the spider plant accessions for various qualitative traits was done based on the list of modified Food and Agriculture Organization (FAO) spider plant descriptors. Days to 50% flowering, chlorophyll content, plant height, leaf length, leaf width, single leaf area, and number of leaves per plant were evaluated as quantitative traits while stem and flower colour, petiole and leaf colour, stem and petiole hairiness were evaluated as qualitative traits. Nutrition components vitamin C, beta carotene and total phenolics were determined at the

nutrition laboratories at the Department of Food Science and Technology, Jomo Kenyatta University of Agriculture and Technology. Broad sense heritability was estimated for the nutrition and yield related components. For bioinformatics analysis, the whole genome sequence of the close relative, *T. hassleriana* was searched for Simple Sequence Repeats (SSRs) using the Genome wide Microsatellite Analyzing Tool (GMATo) software with the objective of subsequently transferring these markers into *C. gynandra* for marker-assisted breeding. The parameters used for GMATo search were di-, tri-, tetra-, penta-, and hexa-nucleotide motifs. Estimates of Shannon-Weaver diversity index ( $H'$ ) for the qualitative characters were generally high ( $H' > 0.500$ ) indicating a greater inter-country than intra-country diversity. Unweighted Pair Group Method with Arithmetic mean (UPGMA) clustering method using stem and flower colour traits clustered the accessions into 2 major groups, each group consisting of Kenyan and South African accessions. Analysis of variance (ANOVA) showed significant difference for all the quantitative traits at  $P < 0.05$ . Positive correlation was observed between leaf yield and chlorophyll content ( $r=0.45$ ), plant height ( $r=0.69$ ) and number of primary branches ( $r=0.63$ ). There was a wide variation in vitamin C (63-281 mg/100g) content followed by beta-carotene (0.6-7.2 mg/100g) and total phenols (3.1-10.6 mg/100g). High heritability in broad sense heritability was estimated ranging between 78% and 99% among the quantitative traits with number of leaves per plant and plant height highest at 99% while leaf width exhibited the lowest percentage at 78%. Nutrition components namely; -Vitamin C, beta carotene and phenols expressed a high heritability  $>80\%$ . Bioinformatics analysis revealed a total of 76280 SSR motifs in the *T. hassleriana* genome. Dinucleotides were the most common SSRs at 88.1% (67192/76280) with AT being the most abundant motif at 39.9% (26862/67192). Statistical analysis in this study revealed a great variability among evaluated traits implying diversity

among the accessions. The presence of a considerable degree of compositional variability of the nutraceuticals among tested accessions suggests that spider plant can be a valuable source of genes for improvement of spider plant for vitamin and phenolic content. Considering all genetic parameters, selection based on vitamin C, phenols, beta carotene, plant height, number of leaves per plant and single leaf area would be effective for the improvement of nutrition quality and yield in vegetable spider plant. With the absence of *C. gynandra* whole genome sequence, cross-species transfer of molecular markers from a close relative such as *T. hassleriana* is the first step towards the development of molecular markers in *Cleome* for more efficient crop improvement.