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The genetic diversity of leaf vegetable jute mallow (*Corchorus spp.*): A review

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ABSTRACT

Corchorus spp. is among traditional vegetable which is very nutritious and has been in use in many households in Africa. It contains high level of carotenoids (150µg/100g), vitamin C, Iron (190µg/g), 1.3% Calcium and 25.0% protein. The leaves are used in treatment of diseases and have wide antibacterial properties. It is semidomesticated and sometimes grows as a volunteer crop. Its status in some parts of Tanzania as a wild plant renders it unappealing for consideration in crop development programs. There is limited scientific information on its diversity for use as a vegetable in crop improvement and is a potential area for research. Variations exist among different accessions based on leaf shapes and color. Diversity studies by using molecular markers, proteins and isozymes are reported by several authors. There is low variation within species and high among species. Most of released varieties have a narrow genetic base. Conservation of this species in Africa is scarcely reported.

Key words: *Corchorus spp.*, Genetic diversity, Jute mallow, Leaf yield, Morphological characterization.

INTRODUCTION

In tropical Africa, there are various types of vegetable species (Grubben and Denton 2004). African traditional vegetables have significant roles in our diet, food availability, food diversity, economic growth and sustainability. They are a source of income as they can be marketed or traded locally, regionally and exported (Weinberger and Msuya 2004). Several traditional vegetables are not used as food only but are also consumed for their protective and healing properties as well (Keding *et al.* 2007).

Variation in morphological and physiological characters among *Corchorus* species has been documented by several researchers (Schippers 2000; Kar *et al.* 2009; Benor *et al.* 2012; Mandal *et al.* 2013; Soliman *et al.* 2014). Molecular markers techniques have also been used to detect variation in *Corchorus* species in which both within and among genotype variation has been observed (Basu *et al.* 2004; Benor *et al.* 2011; Banerjee *et al.* 2012; Ghosh *et al.* 2014). Other markers that have been used to study genetic diversity of Jute mallow include proteins and isozymes. Collection and conservation of germplasm accessions in different national and international gene banks is also reported by several authors.

This review paper aims at exploring the current state of jute mallow research as a leaf vegetable consumed in many rural areas in East Africa. In light of this review work, a

platform for identification of promising accessions for yield, quality and desirable horticultural traits for use in breeding programs and improvement of jute mallow can be established.

Origin and geographical distribution: The origin of *Corchorus spp.* has been investigated by several authors, white jute is said to be originated from Indo-Burma while the dark jute is said to be originated from Africa due to variation in morphological traits (Xiong 2008). Now it is well established that the two cultivated species (*C. olitorius* and *C. capsularis*) in Asia originated from Africa through the study conducted by using nuclear and chloroplast simple sequence repeats (SSRs) (Kundu *et al.* 2013). This is also supported by a wide spread plant types present in the continent and occurrence of several related species (Kundu 1951; Benor *et al.* 2012). On the other hand, secondary centers of origin are considered to be Bangladesh, North India and Myanmar (Basu *et al.* 2004; Grubben and Denton 2004).

The species are known to occur in diverse ecological habitats and are widely distributed across Africa, from North to the South and from West to East (Mir *et al.* 2008). The plant is found in open acacia bushland, grassland, cultivated lands and near pans and dams in several countries such as Kenya, Tanzania, Botswana, Zambia and Zimbabwe (Nguni and Mwila 2007). Eight species of *Corchorus* and

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the two cultivated species occur in India in diverse ecological conditions and habitats (Mir *et al.* 2008). *Corchorus* is also cultivated in Caribbean, Brazil, Cyprus, Greece, Crete, Bangladesh, China, Japan and in the middle East (Grubben and Denton 2004; Thompson *et al.* 2010). The variation in *Corchorus spp.* is said to be due to adaptation to various climates and habitats or occurrence over large geographical areas resulting in spatially isolated populations (Knight *et al.* 2005; Benor *et al.* 2011). Zhang *et al.* (2015) noted that different centers of origin for the two cultivated species of jute mallow (*C. olitorius* and *C. capsularis*) caused their differences, i.e. strong sexual incompatibility barrier.

Taxonomy and botanical description: Jute mallow belongs to the family *Malvaceae*. At least 50-60 species are well known and 170 different names are used to describe them under the genus *Corchorus* in Index Kewensis (Edmonds 1990; Palve and Sinha 2005; Mir *et al.* 2008).

The cultivated species (*C. olitorius* and *C. capsularis*) are diploid ($2n=14$) and they undergo regular meiosis. As for the identified wild species, the chromosome numbers of around 21 species have been reported. Majority of these wild species are diploid though tetraploid species ($2n=28$) are also known (Edmonds 1990).

Most of the species are annual herbs reaching a height of up to 2.4 m. Jute mallow can be unbranched or with very few primary and secondary branches. It has alternate simple, lanceolate leaves. The leaves margins range from finely serrate to coarsely serrate or lobed margin. The plant has small yellow flowers with five petals which are hermaphrodite (Norman 1972). The stem is long, slender and color varies from full green to dark red in case of *C. capsularis* and green or colored light red or deep red in case of *C. olitorius*. It has a round pods for *C. capsularis* and elongated pods for *C. olitorius*. It has a well branched tap root system.

Use and nutritional importance: *C. olitorius* and *C. capsularis* are mainly cultivated in Asia and Latin America countries as a major source of natural fiber (Roy *et al.* 2006; Roy 2013). In Africa, *C. olitorius* is grown as vegetable crop (Krebs 2001; Grubben and Denton 2004; Kinabo *et al.* 2006; Dansi *et al.* 2008; Benor *et al.* 2012). Little is reported for these species as fiber crop in Africa (Benor *et al.* 2010). Nevertheless plants with short and branched stems with small leaves are used as leafy vegetable widely in Africa, Asia and Europe (Velempini *et al.* 2003).

Jute mallow like other traditional leafy vegetables represents a cheap but quality nutrition for large segments of the population in urban and rural areas (Freiberger *et al.* 1998; Kinabo *et al.* 2006; van Rensburg *et al.* 2007; Lewu and Mavengahama 2010; Anbukkarasi and Sadasakthi, 2016). Its leaves contain an average of 15% dry matter, 4.8 g protein, 259 mg calcium, 4.5 mg iron, 4.7 mg vitamin A,

92 µg folate, 1.5 mg nicotinamide and 105 mg ascorbic acid per 100 g leaves (Grubben and Denton 2004; Odhav *et al.* 2007; Dansi *et al.* 2008). The production of mucilage from the leaves is a property appreciated to make sources that can be used together with starchy foods. A relish and potherb can also be produced by boiling the leaves like spinach (Benor *et al.* 2010).

Apart from food value, *Corchorus* species are medicinal plants widely used for treatment of various diseases. The commonly used species include *C. olitorius*, *C. capsularis* and *C. aestuans*. These are used to treat general diseases and are also remedies for heart disease, enemas, parturition and febrifuges (Burkill 2004). Other diseases include chronic cystitis, gonorrhoea, dysuria, and toothache (Hillocks 1998). The seeds are used to treat fever and have wide antibacterial properties (Pal *et al.* 2006). *C. fascicularis* is used as soap and soap substitute. The mucilage from *C. olitorius* is also used as source of fatty acids, oils and waxes. *C. capsularis* is a source of glycosides, saponins and steroids (Benor *et al.* 2010).

Genetic Diversity of Jute mallow

Morphological diversity: Genetic variation within individual species (*C. olitorius* and *C. capsularis*) is limited due to self-pollination (Hossain *et al.* 2002). *Corchorus* species are thus characterized by a high level of inter-specific variability, but a low degree of intra-specific variability (Kar *et al.* 2009).

Studies on morphological characteristics of jute mallow have been reported by several researchers. Nath and Denton (1980) observed large morphological and physiological variation in leaves of *C. olitorius* grown by farmers in Nigeria. Variation in leaf shapes particularly was used to separate different local cultivars of *C. olitorius*. Considerable variation in other morphological traits was also observed by Akoroda (1985) in several local morphotypes.

Variation in number of vegetative characters among three Egyptian cultivars of *C. olitorius* was also reported by Soliman *et al.*, (2014). Denton and Nwangburuka (2012) conducted a study on six morphological characters (plant height at maturity, number of leaves per plant, fresh leaf weight, stem weight, total plant weight and harvest index). In their study, clustering scores among the principal component analyses suggested a strong relationship among individuals in the cluster.

In another study, forty from *C. incifolus* and another forty from *C. olitorius* were used by Ogunkanmi *et al.* (2010). In this study, they reported a continuous distribution of mean value for the parameters they measured except for number of leaves in *C. olitorius* which indicated superiority of a leafy vegetable over other genotypes (Ogunkanmi *et al.* 2010).

Begum and Kumar (2011) characterized 25 released varieties and seven common knowledge varieties of both

species using 17 morphological characters for Distinctiveness Uniformity and Stability testing. Out of 17 morphological traits, eight were monomorphic, seven dimorphic and two polymorphic in *C. capsularis*.

In another study Palve and Sinha (2005) used 6 accessions of *C. capsularis* and 7 accessions of *C. olerius* to study variation and interrelationships among fiber yield attributes. Highly significant differences were observed among accessions for plant height, number of days to first flowering and fiber strength. Benor *et al.* (2012) used 101 accessions of *C. olerius* species to study genetic diversity and relationships inferred from molecular and morphological data. It was found in their study that qualitative traits, those related to leaf morphology, branching habit and stipule color were the taxonomically very informative traits.

In efforts to widen a base for assessment of jute mallow traits, (Mandal *et al.* 2013) conducted a study on pollen grains. Pollen morphological parameters revealed differences between the two species and a correlation matrix revealed no significant relationship between them. These are associated with reproductive outcomes and heredity and they are important in detailing morphological variations which define taxonomic relationships among plant taxa at different levels.

Morphological assessment with respect to vegetative characters of *Corchorus spp.*: Crop improvement programmes on jute mallow for selection of varieties with finer and high quality fiber have received considerable attention over years in Asia and India. However, improvement programs on jute mallow as a vegetable has been very limited (Nyadanu *et al.* 2016).

Morphological studies on several accessions have been done in Nigeria to separate segregating populations into different leaf types (National Horticultural Research Institute, 1986).

A study to determine heritability, genetic advance and association of quantitative vegetative characters with leaf yield of *C. olerius* was conducted by Nwangburuka and Denton (2012) on 15 accessions, in which significant difference was found among the genotypes for all characters studied except in stem weight per plant, suggesting a prospect for meaningful selection for improvement of jute mallow.

In Benin, forty cultivars of *Corchorus spp.* were evaluated for their genetic diversity with reference to all phenotypic traits. Results led to grouping the target plant materials into six classes based on all quantitative traits under the study.

Choudhary *et al.* (2013) conducted a study on seventeen genotypes belonging to six Jute mallow species to assess leaf area and foliage yield and some nutritional parameters. They were able to link foliage yield and nutritional content in which leaf area and foliage yield were

found to have positive phenotypic correlation with potassium mineral content.

In this regard, only few studies on genetics of leaf yield traits have been conducted in Jute mallow and only few accessions have been used (Palit, *et al.* 1996; Denton and Nwangburuka 2012; Osawaru *et al.* 2012). These few common parents in breeding programs leads to narrow genetic base of existing varieties thus make them susceptible to crop biotic and abiotic stresses (Kamannavar *et al.* 2015). In order to improve leaf yield of Jute mallow, the knowledge required is not only of the diversity and genetic variability of the available germplasm but also of genetic architecture of leaf yield traits and its attributes. Descriptive data for each accession conserved by gene banks facilitate the efficient use of accessions in research and plant breeding for improvement of the respective crop (Kristkova *et al.* 2008).

In view of this, genetic evaluation of the current germplasm by focusing on leaf yield related traits is important in order to identify the lines which have high yield and well adapted to specific environment.

Genetic diversity based on Biochemical markers

Protein: When proteins are used as genetic markers and conducted according to proper laboratory procedures, their electrophoretic migration rates are generally highly heritable and ample polymorphism are available for many germplasm management purposes (Bretting and Widrechner 1995). The variation in banding pattern of different proteins are assumed to be equal to the variation in genes coding for these proteins (Osawaru *et al.* 2012). In a study conducted by using proteins to determine the relationship among three *Corchorus* species, traits such as growth habit and stem features appeared to be uniform. Determinate and medium branching habit and erect stems among the accessions studied as important traits for leaves production which are needed by farmers (Osawaru *et al.* 2012). Seed protein polymorphism derived from electrophoretic banding pattern using SDS-PAGE in two cultivated Jute species (*C. olerius* and *C. capsularis*) and seven wild species was conducted by Das and Maiti (1998). The results of this study indicated distinct polymorphism in electrophoretic banding pattern and led to detection of polypeptide bands ranging from medium (25.0kD to 49.9kD) to low (<25.0kD). Seven polypeptide bands ranging from 9.73 to 88.79kD were also recognized among 14 accessions of Jute mallow screened by Isuosuo and Akaneme (2015). These bands were moderately dissimilar showing moderate heterogeneity. Generally few studies have been conducted on Jute mallow by using protein as markers. However, this technique has been used effectively to study genetic diversity among and between genotypes in different plant species (Thanh and Hirata 2002; Chandra 2008; Meena and Shukla 2013). More reliable and useful information in detailing the

diversity among Jute mallow genotypes can be generated by using these markers.

Isozymes: Isozymes are defined as structurally different molecular forms of an enzyme with qualitatively the same catalytic function. They result from amino acid alterations which cause changes in net charge or the spatial structure (conformation) of the enzyme molecules and thus their electrophoretic mobility (Dziechciarkova *et al.* 2004). In jute mallow, Ali *et al.* (2012) used allozymes/isozymes banding pattern to measure the genetic diversity of six leaf mutants of tossa Jute. The result of cluster analysis from the constructed dendrograms showed only two groups of peroxidases and five groups of esterase. The two clusters of peroxidase revealed 20% similarity with Jaccards similarity coefficient of 0.1 among the researched genotypes in both clusters.

In another study (Khatun and Alam 2010) confirmed the species status of *C. trilocularis* and *C. pseudo-olitorius* by using isozyme assay. The activities of isozyme systems such as esterase, acid phosphatase and peroxidase used in their study and their banding pattern were different in the two species, indicating their usefulness in establishing the identity of the two species. For instance in acid phosphatase, *C. pseudo-olitorius* showed two bands which were dark and thick, while in *C. trilocularis* two light bands were observed. Similar work has been done in *C. aestuans*, a wild *Corchorus* species. In esterase system, five bands were observed while in peroxidase only one light band was observed. In acid phosphatase, two bands were observed, one thick and one light band. One band in both esterase and peroxidase system was common for all species of wild Jute, while the rest were specific for *C. aestuans* (Khatun *et al.* 2011). The specific bands can be used as markers for *C. aestuans*.

Isozyme assay of three species of *Corchorus* (*C. fascicularis*, *C. pseudo-capsularis* and *C. tridens*) was carried out by (Khatun *et al.* 2011). The banding properties in esterase and acid phosphatase were different in three species. In peroxidase *C. fascicularis* showed a dark and thick band while *C. pseudo-capsularis* had light thick band. The bands in peroxidase can be used as markers for these two species. Generally, the activities of different isozyme systems such as esterase, acid phosphatase and peroxidase have proved to be powerful tools in studying genetic diversity of different plant species. In jute mallow only few studies have been reported on the use of isozymes as markers. Many studies have been reported on the use of DNA markers (genomic DNA and chloroplast DNA), the approach that has been used to study the genetic diversity in other crop species.

Genetic diversity by using DNA markers: Genetic diversity studies by using molecular markers have been

reported by different authors. (Haque *et al.* 2007) conducted a study in which eighteen genotypes of two cultivated species (*C. olitorius* and *C. capsularis*) were evaluated by using RAPD markers. In this study, the genotypes representing the two species formed two major clusters. The use of Amplified Fragment Length Polymorphism (AFLP) in Jute mallow is reported by (Basu *et al.* 2004). In their study, 305 polymorphic bands were detected by AFLP markers by using 10 pairs of primers (EcoRI and MseI) from 49 genotypes of amplified template DNA of the two Jute mallow species. This marker revealed a high level of variation between *C. olitorius* and *C. capsularis* suggesting the distant relationship and different maternal origins. (Benor *et al.* 2012) employed AFLP in evaluation of genetic diversity of 101 *C. olitorius* accessions. Their analysis indicated low genetic diversity within the population as well as low Neis' gene diversity index which ranged from 0.0457 to 0.0955. Generally, there is low genetic diversity at species level.

Another study was conducted by (Ghosh *et al.* 2014) by using 63 genotypes of *C. olitorius* and *C. capsularis*. Both Simple Sequence Repeats (SSR) and AFLP markers were used in this study in which the combination of data from both primers divided the 63 genotypes into two different clusters. The similarity between the two species was low (0.003) indicating the divergence which exists in DNA sequences of these two species.

(Mir *et al.* 2008) used 81 genotypes of commercially cultivated jute (45 *C. olitorius* and 36 *C. capsularis*) to study fiber related traits. This study revealed a quantitative nature of fiber yield related traits with more likelihood of dominance component in genetic variance. It was further noted that a subset of 45 set of SSRs derived from *C. olitorius* were more transferable to *C. capsularis* when they were used to study DNA polymorphism in *C. capsularis*. Average number of alleles for individual SSRs and average polymorphic information content (PIC) was low in both species. Similar study was also conducted by (Huq *et al.* 2009) by using 16 genotypes of elite Jute varieties from the same two species by using SSR markers. In this study, twenty seven SSR primer pairs yielded a total of 171 different alleles, where the average alleles per locus were 6.33 ± 2.04 . They also attained high polymorphism (92.2%) despite the crop being self-pollinated and incompatible for inter-specific crosses. Clustering of their data by using UPGMA resulted into two groups belonging to both species. This pattern of clustering is similar to those obtained in other studies by using RAPD and AFLP markers.

In another study, 172 SSRs were used to assess genetic diversity and population structure in 292 genotypes of two cultivated Jute species including indigenous and exotic accessions. In their study, PIC values did not differ significantly in the two species and 596 alleles were detected. In both distance based analysis and structure based analysis,

the exotic and indigenous genotypes were in separate groups (Banerjee *et al.* 2012).

Inter simple sequence repeats (ISSR) markers are also reported by several authors in Jute mallow. (Qi *et al.* 2003) used 27 accessions of *Corchorus* consisting of two species *C. urticifolius* and *C. trilocularis* and unknown wild species to investigate their genetic diversity by using ISSR primers. In their study, 283 bands were amplified by 25 primers in which 92.85% of the amplified bands were polymorphic making an average of 10.48 bands per primer. After cluster analysis, the accessions were grouped into three clusters belonging to different species. In another study, (Roy *et al.* 2006) used ISSR and other markers to study genetic diversity of 20 exotic germplasm and 20 commercial varieties of cultivated jute from *C. capsularis* and *C. olitorius*. Again, the results showed 98.44% polymorphism across all the species and low level of polymorphism within the species.

Sequence Tagged Microsatellite Sites (STMS) was used by (Roy *et al.* 2006) to study genetic diversity in Jute mallow. These markers employ a pair of primers with sequences similar to the single copy of a sequence flanking microsatellite repeats, which upon amplification detects the variation which exist among individuals in terms of number of repeat motifs at a specific locus. In their study, all six STMS markers showed polymorphism among the four species of *Corchorus* under study and this polymorphism ranged from 50 to 100 with PIC ranging from 0.1 to 0.5.

Sequence related amplified polymorphism (SRAP) is reported by Soliman *et al.* (2014) in which three genotypes of leafy vegetable Jute mallow were evaluated for genetic diversity and phylogenetic relationships. The results from different primer combinations indicated highest percentage polymorphism (72.7%) using Me4-Em3 combination and the lowest polymorphism (14.3%) were recorded in Me4-Em4 combination.

In efforts to quantify genetic diversity and to characterize accessions in germplasm collections, microsatellite markers and other DNA markers are useful tools by considering their advantages over other markers. They are unlimited in number and are not affected by environmental factors, growth stage and agronomic practices (Mir *et al.* 2009). In many studies conducted, the diversity of the genotypes at species level is very low for many accessions of Jute mallow and hence it is important to focus on the variation that exists between different species and establish how this variation can be used to improve the crop.

Conservation: Jute mallow, like other traditional leaf vegetables has been neglected by researchers, policy makers and agriculturists thus reducing its biodiversity and loss of indigenous knowledge (Agong *et al.* 2013). There is therefore

a need of both in-situ and ex-situ conservation measures to ensure that the available genetic resources are not lost. In Africa, attempts to conserve the germplasm of *Corchorus* spp. in national and institutional gene banks had been done in Nigeria, Ethiopia, Kenya, Sudan and Zambia (Attere, 1997). In Nigeria, National Horticultural Research Institute (NIHORT) maintains a large germplasm collection of local landraces that have been characterized (Opabode and Adebooye 2005). Thirteen species of *Corchorus* are found in National Herbarium of Addis Ababa University in Ethiopia. Among these species, *C. urticifolius* is very rare, indicating high risk of genetic erosion in Ethiopia (Benor *et al.* 2011). In Tanzania, the National Plant Genetic Resources Center (NPGRC) contains only nine accessions of *Corchorus* of unknown species (National Report of PGR, FAO 2009), despite the high number of species reported to be found in the country by survey conducted by (Edmonds 1990) and (Benor *et al.* 2010). Two more accessions were collected in collaboration with other international centers and conserved at facilities of CGIAR and the world vegetable centre (AVRDC). In 2013, the World Vegetable Center (WorldVeg) in Tanzania had 2,659 vegetable accessions of 48 species (Agong *et al.* 2013). Among these accessions, 35 were accessions of jute mallow from one species. However, currently due to active collection of important indigenous vegetables, the germplasm collection of Jute mallow contains 104 accessions, from different countries in the world comprised of several species. WorldVeg gene bank in Africa is an important source of vegetable germplasm for breeding, research, and any other uses from public and private sectors.

CONCLUSION

In order to improve jute mallow as a leaf vegetable, the current germplasm should be exploited to come up with varieties with desirable horticultural traits. Based on the knowledge generated by studying the genetic diversity of present germplasm, it is also possible to lay down the strategies for its conservation. Several studies have been conducted by using molecular markers to study the genetic diversity of jute mallow. However, it is the enrichment and refinement of these markers as well as their validation that will contribute significantly to the genomic research and breeding of jute mallow.

The presence of a vast array of germplasm in Africa and East Asia should be considered as a potential source of breeding materials for breeders. It is well documented that the currently cultivated species of jute mallow have a very narrow genetic base. The option of reaching out the wild species with superior traits; such as drought tolerance, tolerance to low temperatures and resistance to diseases remains very important. Improved genotypes of jute mallow will broaden the nutritional base of leaf vegetables and increase its utilization.

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