Research Application Summary

Importance of cowpea production, breeding and production constrains under dry areas in Africa

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Abstract

Cowpea [*Vigna unguiculata* (L.) Walp.] is an important grain legume which is widely grown in sub-Saharan Africa (SSA) for food and feed. Its grain is composed of high levels of protein, energy and micro- and macro-nutrients. Young and succulent leaves of cowpea are consumed as cooked vegetables in some parts of SSA. In SSA, including Namibia, cowpea productivity is considerably low due to a wide array of abiotic and biotics stresses and socio-economic constrains. Therefore, breeding improved varieties incorporating farmers-preferred traits remains an overriding consideration to boost the productivity of cowpea in the region. This review summarizes challenges and constraints to cowpea production, breeding methods and progress, genetic variation and analysis of cowpea. Furthermore, information on participatory varietal selection (PVS) is presented to highlight farmers' desire and preference in the selection of cowpea varieties for large-scale production and ultimate adoption. The literature presented herein may serve as baseline information for cowpea breeders, agronomists or producers in Namibia or similar agro-ecologies in SSA.

Keywords: Breeding, genetic variation, cowpea, mutation breeding, Namibia, participatory variety selection

Résumé

Le niébé [*Vigna unguiculata* (L.) Walp] est une légumineuse à grains importante qui est largement cultivée en Afrique Subsaharienne (ASS) pour l'alimentation humaine et animale. Son grain est composé de niveaux élevés de protéines, d'énergie et de micro et macro-nutriments. Les jeunes feuilles succulentes du niébé sont consommées comme légumes cuits dans certaines parties de l'ASS. En Afrique subsaharienne, notamment en Namibie, la productivité du niébé est considérablement faible en raison d'un large éventail de stress abiotiques et biotiques et de contraintes socio-économiques. Par conséquent, la sélection de variétés améliorées incorporant des caractères préférés des agriculteurs

demeure une considération primordiale pour augmenter la productivité du niébé dans la région. Cette revue résume les défis et les contraintes de la production du niébé, les méthodes de sélection et le progrès, la variation génétique et l'analyse du niébé. En outre, des informations sur la sélection variétale participative (PVS) sont présentées pour souligner le désir et la préférence des agriculteurs dans la sélection des variétés de niébé pour une production à grande échelle et une adoption finale. La littérature ici-présentée pourrait servir d'informations de base pour les sélecteurs du niébé, les agronomes ou les producteurs en Namibie ou des agro-écologies similaires en Afrique subsaharienne.

Mots clés: sélection, variation génétique, niébé, sélection par mutation, Namibie, sélection participative de variétés

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.; 2n =2x = 22) is an important legume crop widely grown under low input production systems and in arid and semi-arid agro-ecologies of the world. Cowpea grain is composed of high proportion of protein (17 to 25 %) which is rich in two essential amino acids, lysine and tryptophan (Ibro *et al.*, 2014). Cowpea is also known as southern pea, black eye pea, crowder pea, lubia, niebe, coupe or frijole. Reports (Padulosi and Ng, 1997; Agbogidi, 2010) indicate that cowpea belongs to the family Fabaceae and sub-family Faboideae. It is predominantly a self-fertilizing crop. China, Turkey, India, Brazil and USA are the leading producers of cowpea in the world (Pasquet, 2000; Ba *et al.*, 2004). West Africa is the major cowpea producing region in Sub-Saharan Africa (SSA), where Nigeria and Niger stand first and second respectively covering 80% of the total regional production during the past 14 years (Aboki and Yuguda, 2013).

Cowpea is one of the most preferred crops and a valuable component in the farming systems of the majority of resource poor rural households in SSA for its various attributes (Gnanamurthy *et al.*, 2012; Molosiwa *et al.*, 2016). The crop has the ability to grow under harsh environmental conditions where other major crops fail to grow. Its foliage is regarded as an important source of high-quality livestock feed. Cowpea has the ability to restore soil fertility through nitrogen fixation useful in crop rotation with the major cereal crops (Dugje *et al.*, 2009; Gnanamurthy *et al.*, 2012). In Namibia, cowpea is the third most important staple crop after pearl millet and sorghum. In the country cowpea is prepared in various food forms such as boiled grains, or peeled grains pounded into a mash or soup (Fleissner and Bagnall-Oakeley, 2001).

There was no systematic cowpea research and development program over the past years in Namibia. Therefore, in the country cowpea yields have been low varying from 100-599 kg ha^{-1} (Horn *et al.*, 2015) compared to potential yields of 1500 to 3000 kg ha^{-1} reported elsewhere (Gbaye and Holloway, 2011). Using a participatory rural appraisal (PRA) study conducted across four cowpea growing regions, it was found that 70.2% farmers in the northern Namibia still grew local unimproved cowpea varieties, while only 29.8% used improved varieties either singly or in combination (Horn *et al.*, 2015). In the country only the following three improved varieties: Nakare [IT81D-985], Shindimba [IT89KD-245-1] and Bira [IT87D-453-2] are commercially available. During the same study farmers

reported poor yields of the local varieties due to their susceptibility to drought and heat stresses. In the study areas, farmers indicated other constrains affecting cowpea production such as field and storage pests (aphids, leaf beetles, pod borers and bruchids) and low soil fertility. Furthermore, 79.5% of the farmers indicated that parasitic weeds such as *Striga gesnerioides* (Willd.) Vatke and *Alectra vogelii* (Benth.) affected cowpea production in Namibia (Horn *et al*., 2015). Various national research programs and the International Institute of Tropical Agriculture (IITA) are actively involved in developing improved cowpea varieties globally. Consequently, nematode resistant (e.g. varieties CE-31, Frade Preto, CE-28, CE-01, CE-315and CE-237) (Oliveira *et al*., 2012) or Striga and Alectra tolerant varieties were developed and released through conventional breeding techniques (Timko *et al*., 2007; Kabambe *et al*., 2013). Furthermore, early maturing, high yielding and pest resistant cultivars have been developed by the IITA and the Agricultural Research Institute of Senegal (ISRA) (Dugje *et al*., 2009) which are widely grown in Nigeria, Niger and Senegal. In Namibia a well-established cowpea improvement program is required to develop farmers-preferred and locally adapted varieties for sustainable production and productivity.

Production constraints to cowpea: Biotic constraints
Fungal diseases. The most destructive fungal disease of cowpea includes leaf smut (false smut or black spot), caused by *Protomycopsis phaseoli* (Bailey *et al*., 1990; Singh, 2005). Fungal diseases cause leaf smut, stem rot as well as root rot (Bailey *et al*., 1990). Yield losses varying from 20 to 100% have been reported due to fungal diseases (Mbeyagala *et al*., 2014). Sources of resistance to fungal pathogens have been identified, and screening techniques are well developed (Adejumo *et al*., 2001; Gbaguidi *et al*., 2013; Pujari *et al*., 2015). Yield losses due to fungal diseases have been reported in several African countries. However, serious epidemics were reported in Nigeria, the Sudan savanna and Sahel (Adejumo *et al*., 2001; Singh, 2005). So far there is no study that reported fungal diseases of cowpea in Namibia.

Viral diseases. Thottappilly and Rossel (1992) and Adejumo *et al*. (2001) reported eight virus strains affecting cowpea production and productivity in Africa. Cowpea viruses are transmitted by aphids, beetles and other parasitic pests that live and feed on the crop. The common cowpea viruses include yellow mosaic comovirus, mottle virus, and southern bean mosaic sobemovirus, which are beetle-transmitted. Aphid-borne viruses of cowpea include mosaic potyvirus and cucumber mosaic cucumovirus. Some cowpea viruses are transmitted by whitefly such as cowpea golden mosaic virus and cowpea mild mottle carlavirus. The red mosaic virus has negative effect on rhizobium bacterial growth and development that led to a reduction of 20 to 45% root nodulation (Taiwo *et al*., 2014). Mbeyagala *et al*. (2014) suggested that introducing new cowpea genotypes into a new growing environment may bring viral epidemics. A number of landrace cowpea varieties such as WC32, WC18, NE43, NE15, and WC35B were reported to be resistant to virus strains (Taiwo *et al*., 2014). It is not known whether viral diseases are causing economic yield losses of cowpea production in Namibia. In the country no study has been conducted on parasitic plants or pathogens limiting cowpea production.

Bacterial diseases. The common and serious bacterial diseases of cowpea reported in the literature are bacterial blight caused by *Xanthomonas campestris* pv. vignicola and bacterial pustule caused by *Xanthomonas campestris* pv. vignaeuguiculatae (Viswanatha *et al*., 2011). The two pathogens were reported to cause yield reductions reaching up to 71% in pod, 68% in seed and 53% in fodder

in susceptible varieties in India (Viswanatha *et al.*, 2011). The bacteria cause yellowing of the leaves progressively showing irregular to round spots during moderate infection. This will lead to senescence and dropping of leaves. Some bio-control agents have been reported being effective in controlling bacterial blight disease of cowpea (Reddy *et al.*, 2013). There is no information available on bacterial diseases of cowpea in Namibia.

Root knot nematodes. Root knot nematodes cause major loss in cowpea production hindering nutrient and water absorption from the soil (Haegeman *et al.*, 2012). Gheysen and Mitchum (2011) reported the negative effect of nematodes in cowpea growth and development including interfering and limiting auxin transport and plant cell differentiation pathways. The root knot nematode species, *Meloidogyne incognita* and *M. javanica*, are frequently prevalent in cowpea fields (Oliveira *et al.*, 2012). Some transgenic cowpea cultivars such as CE-31, Frade Preto, CE-28, CE-01, CE-315and CE-237 were reported to possess considerable resistance to nematodes (Oliveira *et al.*, 2012). Nematode infestation in cowpea production can also be prevented through cultural practices such as cleaning of field from infected crop residues after harvest and crop rotation practices (Gheysen and Mitchum, 2011).

Parasitic weeds. *Striga gesnerioides* (Willd.) Vatke and *Alectra vogelii* (Benth) are the two major parasitic weeds affecting cowpea production in SSA. The weeds grow and attach themselves on the root surfaces of the host where they absorb nutrients (Figure 1). Alectra causes serious yield losses in cowpea production in Namibia (Horn *et al.*, 2015). Various authors Noubissietchiagam *et al.* (2010) documented the negative effects of Striga on cowpea production. Seeds of the parasitic weed are able to remain dormant in the soil for over 20 years making it difficult to control using traditional methods (Kabame *et al.*, 2002; Kabambe *et al.*, 2013). One of the possible ways in controlling Striga and Alectra is by reducing its seed bank in the soil. This can be achieved by removing the parasitic weeds after germination and before flowering and seed set. Timko *et al.* (2007); Kabambe *et al.* (2013) reported some of the progress made in breeding cowpea for resistance to Striga and Alectra using conventional breeding methods.

Figure 1. Cowpea field infested by *Alectra vogelii* (Benth) (left) and an uprooted Alectra plant attached to cowpea roots as parasitic weed (right). Photos taken at Bagani Research Station in Namibia during cropping 2014/15 season.

Insect pests. Insect pests attack cowpea both in the field and in-stores. Several studies (Ngakou *et al*., 2008; Boukar and Fatokun, 2009; Dugje *et al*., 2009) reported the major field pests of cowpea including *Aphis craccivora* (Koch), bruchids (*Callosobruchus maculatus* (Fabricius)), beetles (*Ootheca mutabilis)*, maruca, leafhoppers and foliage beetles. The pests occur throughout the vegetative growing stages of the plant, feeding on the leaves and also act as virus vectors. In Namibia, farmers described the predominant field pests including aphids as causing yield losses of 77.8%, leaf beetles (53.2%) and pod borers (60%) and bruchids (100%) (Horn *et al*., 2015). In SSA bruchids are the leading pests of cowpea affecting stored grains (Figure 2). Bruchids damage cowpea grains which may lead to losses reaching up to 100% (Stejskal *et al*., 2006; Gbaguidi *et al*., 2013; Horn *et al.,* 2015). No effective commercial pesticides or resistance genes have been reported in controlling bruchids (Stejskal *et al*., 2006; Gbaye and Holloway, 2011).

Production constraints to cowpea: Abiotic constraints
Drought and heat stresses and poor soil fertility. Drought and heat stresses and poor soil fertility are the major abiotic factors affecting cowpea production and productivity. The negative effects of heat and drought stress in sub-Saharan Africa including Namibia have been reported since 1968. Abiotic stresses led to the loss of many landraces varieties of crops including pearl millet, sorghum and legumes (Hall, 2004). Cowpeas are sensitive to severe droughts especially during pod setting and grain filling stages (Hall, 2004). Heat stress above a threshold temperature of 16 C caused 4 to 14% loss in pod set and grain yield. Poor soil fertility is another major constraint limiting cowpea production. In Namibia, cowpea production is carried out in soils with poor fertility levels and most farmers do not apply fertilizers (Horn *et al*., 2015).

Socio-economic constraints in cowpea production. Sabo *et al*. (2014) and Horn *et al*. (2015) outlined a number of socio-economic constraints adversely affecting cowpea production in sub-Sahara Africa. These includes non-availability of market preferred varieties, low yield potential,

Figure 2. Cowpea seeds infested by bruchids (*Callosobruchus maculatus*) at Omahenene Research Station of Namibia during 2013/2014 season.

high cost of farmland preparation, lack of improved production and harvesting tools, high cost and absence of labour, high cost and adulteration of pesticides, poor harvest prices, and underdeveloped marketing channels.

Other major constrains to cowpea production in many SSA countries includes lack of defined value chain and poor development of cowpea as a commodity crop. There is no efficient transport systems and cowpea trading is not organized due to limited value addition and lack of cowpea enterprises (Fakayode *et al.*, 2014). In Nigeria and other west African countries farmers solely survive on cowpea farming which is the major economic mainstay and business (Aboki and Yuguda, 2013). In this region cowpea trade enables farmers to buy other cereal grains and farm inputs such as fertilizers (Fakayode *et al.*, 2014). In Namibia farmers earn cash incomes from sales of cowpea grains (Horn *et al.*, 2015) though the monetary values of cowpea products are low. The full economic potential of cowpea will only be realized if other value added products especially those targeted at the ever growing urban population, are introduced. Waddington *et al*. (2010) suggested that converting cowpea into baby food might bring about a rise in the price of the commodity which will also bring higher returns to the producer. Cowpea is an important weaning food in many communities in Africa and Asia. In SSA its demand is particularly high (Ibro *et al.*, 2014). Raising the average yield per hectare of the crop will therefore increase the annual global production and hence the revenue.

Various reports indicated that that the potential yields of cowpea can reach up to 3,000 kg ha^{-1} if most of the constraints are alleviated (Aboki and Yuguda, 2013). Therefore, targeted cowpea breeding is needed to improve production and productivity of the crops incorporating farmers' and consumers and preferences. Introduction of new value added cowpea products into the market would significantly raise revenues from cowpea production.

Genetic diversity in cowpea. Genetic diversity is fundamental in plant breeding programs. The genetic diversity of cowpea has declined due to various biotic and abiotic factors (Fang *et al.*, 2007). Farmers in Namibia reported loss of their local varieties overtime due to damage by insect pests both in the field and in storage and due to frequent droughts (Stejskal *et al.*, 2006; Horn *et al.*, 2015). Loss of genetic diversity may also arise due to artificial selection of better performing varieties, while discarding poor performing types from a narrow genetic base. Genetic variation may be restricted within specific breeding programs in the absence of a complementary pre-breeding programs (Gbaguidi *et al.*, 2013). Studies conducted using germplasms collections from the continents of north America, Asia and Africa revealed a narrow genetic base of cowpea (Fang *et al.*, 2007). The same study further indicated a strong genetic relatedness among germplasm collections of US and Asia with that of African cowpea collections. The authors indicated that most cowpea genotypes in the world are originated from Africa. Genetic variation arises at a slow pace under natural evaluation especially in cowpeas where the predominant mode of reproduction is through self-fertilisation. Gbaguidi *et al*. (2013), reported loss of genetic diversity of cowpea in Africa at a rate of 28 to 60% in some agro-ecologies.

A well-characterized germplasm is useful to incorporate economic traits through designed

crosses. Genetic diversity analysis can be carried out using DNA markers such as amplified fragment length polypomrshism (AFLP), simple sequence repeat (SSR), randomly amplified polymorphic DNA (RAPD) and single nucleotide polymorphism (SNPs). DNA based molecular markers are more reliable and robust methods for the characterization of genetic diversity. These genetic markers have been successfully applied in genetic diversity analysis of many crop plants including cowpea (Ogunkanmi *et al*., 2008; Tantasawat *et al*., 2010; Adetiloye *et al*., 2013).

Genetic diversity is routinely assessed using agro-morphological or phenotypic markers. In cowpea breeding both quantitative and qualitative phenotypic characters are extensively used in germplasm characterization, classification and selection. Quantitative traits include: number of branches per plant, days to 50% flowering, days to 50 maturity, number of pods per plant, pod length, pod width, seed weight, number of seeds per pod, seed yield (Molosiwa *et al*., 2016). Uses of phenotypic characteristics is a common approach because they form the most direct measure of the phenotype, readily available and relatively cheaper requiring simple equipment. However, phenotypic markers are subject to environmental influences in the field that may mask the concrete genetic variation among genotypes. The combined use of phenotypic and molecular markers may allow estimation of genetic diversity more reliably and efficiently. Effective field-based high-throughput phenotyping platforms (HTPPs) are recently advocated for which may improve the efficiency of selection in plant breeding programs (Araus and Cairns, 2014) .

Breeding cowpea. Various national and international research programs notably at IITA are actively developing improved cowpea cultivars with high yields, early maturity, and pest and disease resistance (Dugje *et al*., 2009). Most of these breeding programs use conventional and molecular breeding tools to harness cowpea genetic variation for breeding. Furthermore, the International Atomic Energy Agency (IAEA) has been supporting Member States in genetic improvement of various crops including cowpea through the use of artificial mutagenesis such as gamma rays, x-rays, and ethylmethanesulphonate (EMS) (Mba *et al*., 2010). This has led to development and release of improved cowpea cultivars in Africa, Asia, and Latin America (Viswanatha *et al*., 2011; Reddy *et al*., 2013). Further, most cowpea breeding initiatives aim at broadening the genetic bases of the crop to adapt to various cropping systems and agro-ecologies, and in the development of consumer-preferred varieties with enhanced nutritional quality (Singh *et al*., 2003; Lima *et al*., 2011). The following breeding methods have been widely used in cowpea improvement programs:

Pure-line selection. The concept of this selection method was proposed by the Danish botanist Johanssen in 1903 on the basis of his studies on Princess beans (*Phaseolus vulgaris*). This method is suitable for highly self-fertilizing crop species such as wheat, barley, sorghum, peas, cowpea etc. Pure-line selection involves selection of promising individuals from a large number of segregating populations after systematic crosses or induced mutagenesis. Selected individuals are harvested individually and continuously selfed and selected to develop and release pure-line cultivars.

Pedigree breeding. Unlike pure-line breeding, pedigree breeding maintains detailed record of the relationship between the selected plants and their progenies. In this method each progeny in every generation can be traced back to the F_2 plant from which it was selected from. It is commonly applied in selection of desirable plants from the segregating populations of self- pollinated crops. Pedigree method is useful especially when improving some specific traits lacking in an already established variety. It is widely used in the selection of new and superior recombinant individuals.

It is a useful procedure in transgressive breeding scheme to select individuals with unique attributes such as disease resistance, plant height or maturity.

Backcross breeding. Backcross breeding was proposed by Harian and Pope in 1922. It is used to transfer few genes into an established cultivar of self- or cross-fertilising crop. Backcrossing leads to increased homozygosity allowing selection of desirable genotype in homozygous and desirable genetic backgrounds.

Single seed descent selection method. This selection procedure was first suggested by Goulden in 1941 and subsequently modified by Brim 960. In this method, only a single seed collected from each of the F_2 plants is kept and bulked to grow the F_3 generation. This process continues up to the F_5 and F_6 generations, whereby a desired level of homozygosity is achieved. In the F_6, large number of single plants are selected and their progeny grown separately. In the F_7 and F_8, selection of best performing lines are selected for preliminary and national yield traits.

Bulk population breeding. Bulk population method is also known as mass selection or population breeding. It was first used by Nilsson Ehle in 1908. It refers to a population grown in bulk plot from F_1 to F_5 with or without selection. A portion of the bulk seed is used to grow the next generation and individual plant selection is often started in the F_6 or later generation. Bulk selection method is useful to increase the frequency of desirable types through positive mass selection. It is suitable for studies on the survival of genes and genotypes in populations and it offers greater chances of isolation of transgressive segregants than pedigree method.

Mutation breeding. Mutations are the ultimate source of genetic variation, a raw material for plant breeding programs (van Harten 1998). Induced mutation derived through the use of gamma rays, x-rays, or EMS is a powerful tool for crop genetic enhancement and breeding. Appropriate dose of radiation should be established on target genotypes before large scale mutagenesis is undertaken (Tshilenge-Lukanda et al., 2012). Optimizing the dose of radiation is the first step in induced mutation breeding. This is important because its predictable value guide the researcher in the choice of the ideal dose depending on the plant materials and desired outcome (Horn and Shimelis, 2013). Induced mutations provides considerable genetic variation within a reasonably short period of time when natural genetic variation of the crop is limiting for breeding. Mutagens bring about desirable changes including plant height, growth types, genetical, biochemical, physiological or morpho-genetical changes (Girija and Dhanavel, 2009).

Various improved cultivars of major crops such as wheat, rice, barley, cotton, peanuts, beans have been developed through induced mutation platforms of the Joint FAO/IAEA Division of the Nuclear Techniques in Agriculture in the 1950s (Ahloowalia and Maluszynski, 2001; Slabbert *et al.*, 2004). Maluszynski (2001) outlined some of the major success of induced mutation breeding and varieties released globally. The Netherlands, USA and Japan are classified as top countries in releasing cultivars derived through mutation breeding techniques. About 1142 mutant cultivars were released in Asia, the highest number in the

world, while only 48 mutant varieties were released in Africa (Maluszynski, 2001). The Mutant Varieties Database (MVD) of FAO (Food and Agriculture Organisation of the United Nations) and the International Atomic Energy Agency (IAEA) maintained a list of 2,252 crop cultivars developed through artificial mutations (Nielen, 2004). These cultivars were released across 59 countries worldwide, mainly in continental Asia (1 142 cultivars), Europe (847) and North America (160) (Maluszynski, 2001; Maluszynski *et al.,* 2009). Studies indicate that induced mutagenesis has successfully modified several plant traits such as plant height, maturity, seed shattering resistance, disease resistance, oil quality and quantity, malting quality, size and quality of starch granules of cowpea (Goyal and Khan, 2010; Singh *et al.,* 2013).

Genotype by environment interaction. Genotype by environment interaction (G E) is a differential response of genotypes when grown across environments (Yan and Hunt, 1998; Annicchiarico, 2002). Multi-environmental trials (METs) are required to quantify the magnitude of genotype $\times$ environment interaction and to recommend varieties with narrow or broader adaption (Ramburan *et al.,* 2012). G x E trials are valuable for cultivar recommendation or for the final stages of selection of elite breeding material (Annicchiarico, 2002). Data generated through G×E interaction studies may assist crop ecologists, agronomists and plant breeders to define ecological regions, mega-environments and ecotypes (Annicchiarico *et al.,* 2011). Two types of genotype environment interaction (GEI) are distinguishable: cross-over or qualitative and non-cross-over or quantitative (Annicchiarico and Iannucci, 2008). Cross-over or qualitative interaction is observed when there is change in ranking of cultivars when grown in different environments, while non-cross-over interaction is the interaction that is observed when genotypes show changes in magnitude of performance but the rank order of genotypes across environments remains unchanged (Jalata, 2011). For cultivar development, the cross-over type of interaction is more important than the non-cross-over type. This is because the cross-over interaction complicates the selection of high yielding genotypes due to inconsistent performance of test genotypes across locations (Annicchiarico *et al.,* 2010; Jalata, 2011).

Genotype environment interaction has an advantage to crop improvement that targets broad adaptation, but it can also represent opportunities for genetic improvement for specific sites (Annicchiarico *et al.,* 2010). However, G×E interactions may present a barrier to crop improvement because it can contribute to temporal and spatial instability of crop yields (Annicchiarico, 2002). The advantage of G×E interactions is that it can offer opportunities for selection and adoption of genotypes showing positive or negative interaction with the location and its environmental conditions allowing the exploitation of specific or broad adaptation and yield stability (Gurmu *et al.,* 2009; Mohammed *et al.,* 2016).

Several methods have been proposed to analyze and interpret the genotype environment interaction. These include: contrasts (Yan and Hunt, 1998), linear regression (Finlay and Wilkinson, 1963), additive main effect and multiplicative interaction (AMMI) (Fleischmann *et al.,* 2016) and multivariate analysis such as principal component analysis. Also, the genotype plus the genotype by environment interaction (GGE) biplot has been reported as a method of choice in analyzing G×E data (Aruna *et al.,* 2011; Adinurani *et al.,* 2015). The GGE biplot has been used in mega-environment analysis (Yan and Rajcan, 2002; Casanoves *et al.,* 2005), genotype and test environment evaluation (Yan and Rajcan, 2002; Blanche *et al.,* 2009), trait association (Yan and

Rajcan, 2002) and heterotic pattern analysis (Blanche *et al.*, 2007). The GGE biplot is constructed by plotting the two principal components (PC1 and PC2) derived from the singular value decomposition (SVD) of environmental centered data (GGE matrix) such that three component matrices are generated, i.e., the singular value matrix (array), the genotype eigenvector matrix, and the environment eigenvector matrix. The GGE biplot is more powerful than other tools and has the merit of showing graphically the which-won-where pattern of data compared to other methods of analyzing genotype by environment interaction and stability (Yan and Wu, 2008; Adinurani *et al.*, 2015). In this situation, both genotype and genotype environment interaction can be effectively exploited by selecting superior genotypes for each mega-environment (Yan and Rajcan, 2002). Two concepts of stability have been reported, the static or biological and the dynamic or agronomic stability (Kang, 1998). Under the static concept, a genotype is indicated to be stable when its performance does not change with change in environmental conditions while under the dynamic concept a genotype is considered to be stable when it yields well relative to the productive potential of test environments.

Participatory rural appraisal (PRA) and participatory variety selection (PVS). Participatory research techniques have been successfully used to identify farmers' perceived production constraints, preferred crop varieties and traits for deployment of production packages and suitable crop varieties (Alam and Ihsan, 2012). Depending on the breeding goal and the environment, farmers could contribute significantly at different stages of crop cultivar design, development, release and adoption (Nkongolo *et al.*, 2008). Participatory variety selection is an approach to provide choices of varieties to the farmers for increasing production in their diversity of socioeconomic and agro-ecological condition (Belay *et al.*, 2006). PVS is a more rapid and cost effective way of identifying farmer preferred cultivars if a suitable choice of cultivars exists. Various researchers including Hoffmann *et al.* (2007), vom Brocke *et al.* (2010) and Rusinamhodzi and Delve, (2011) have reported the importance of PVS. Understanding farmers' requirements and trait preferences, as well as their farming systems is essential for wide adoption of newly developed crop varieties and production technologies (vom Brocke *et al.*, 2010; Rusinamhodzi and Delve, 2011). The major objectives for PVS are to promote the adoption and dissemination of new varieties and site-specific resource conservation technologies; to obtain farmers' assessments of new improved lines/varieties and specific traits; to understand farmers' criteria in evaluating improved germplasm; to obtain feedback from farmers for breeding purposes; and finally to demonstrate the value of combining improved varieties with resource conservation techniques (Hoffmann *et al.*, 2007). In PVS, the participants are selected based on their indigenous knowledge and selection is done based on farmers' selection criteria such as diseases, pest and drought tolerance, yield, grain characteristics, etc. (vom Brocke *et al.*, 2010). According to Nkongolo *et al.* (2008) field extension workers and the village chiefs are more familiar with farmers in the study sites and are often helpful during PVS. It is therefore recommended for current and future breeding programme to be conducted towards meeting the specific farmers' needs and preferences. Moreover, breeding aiming at specific agricultural practices and production constraints for specific regions and developing cultivars with wide adaptation is encouraged.

Conclusions

Cowpea is the major food crop and a source of cheap protein for most of resource poor households in SSA including Namibia. This literature showed the gap in global research efforts directed at improving cowpea, one of the orphan crops globally. Concerted research and development efforts is required to develop improved cultivars of cowpea for sustainable and enhanced production. The need of multi-disciplinary collaborations between breeders, farmers, processors, consumers, traders and gene banks should not be overlooked in efforts to boost cowpea production and beneficiation along the value chains. In the past various international organizations such as the IAEA and IITA and national breeding programs contributed significantly in developing improved cowpea germplasm and generation of scientific knowledge. These programs developed and released useful cowpea varieties. Evaluation of developed genetic resources is essential under the target environments prior to recommendation for large scale production. In Namibia cowpea research and development is in its infancy. Only three improved cultivars are available and widely grown in the country over the years. The country requires a cowpea breeding program focusing on developing varieties with short maturity, drought, pest and disease tolerance. In the country farmers face yield losses due to parasitic weeds (Striga and Alectra) and insect pests. Farmers reported to have lost their cowpea germplasm overtime. This requires creation of genetic pool of the crop for cultivar development incorporating farmers-preferred traits. Mutation breeding is an important tool for genetic enhancement and breeding improved crop varieties for specific environments. Mutation breeding can be regarded as an efficient breeding tool and procedure for cowpea breeding which is the main focus of our current work.

Acknowledgements

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