



# Production constraints and breeding approaches for cowpea improvement for drought prone agro-ecologies in Sub-Saharan Africa

Lydia N. Horn<sup>a,b,\*</sup>, H. Shimelis<sup>b</sup>

<sup>a</sup> Zero Emissions Research Initiative, Multi-disciplinary Research Center, University of Namibia, Windhoek 12007, Namibia

<sup>b</sup> University of KwaZulu-Natal, African Centre for Crop Improvement, Private Bag X01, Scottsville 3209, Pietermaritzburg, South Africa

## ARTICLE INFO

### Article history:

Received 28 May 2019

Received in revised form 9 March 2020

Accepted 12 March 2020

Available online 24 March 2020

### Keywords:

Breeding

Genetic variation

Cowpea

Namibia

Participatory variety selection

## 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 contains high levels of protein, energy, micro- and macro-nutrients. In SSA cowpea productivity is considerably low due to a wide array of abiotic and biotic stresses, and socio-economic constraints. This review summarizes challenges and constraints to cowpea production, breeding methods and progress, genetic variation and analysis of cowpea. Therefore, this review could serve as baseline information for cowpea breeders, agronomists and producers in Namibia as well as for similar agro-ecologies in SSA.

© 2020 Published by Elsevier Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

## 1. Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.;  $2n = 2x = 22$ ) is an important legume crop which is widely grown under low input production systems and in arid and semi-arid agro-ecologies of the world. It is predominantly a self-fertilizing crop. Cowpea grain contains a high proportion of protein (19 to 35%) which is rich in two essential amino acids, lysine and tryptophan (Abadassi, 2015; Ibro et al., 2014). Cowpea is also known as southern pea, black eye pea, crowder pea, lubia, niebe, coupe or frijole. Cowpea belongs to the family Fabaceae and sub-family Faboideae (Agbogidi, 2010). Apart from Nigeria which produces the most quantity of cowpea grains annually at approximately 2.14 million metric tonnes, USA, Peru, Serbia, Sri Lanka, China were listed among the world-leading producers of cowpea during the past three years (FAOSTAT, 2017). About 6.5 million metric tons of cowpea is being produced annually on about 14.5 million hectares worldwide (Boukar et al., 2018). 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; ; Boukar et al., 2018).

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 (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. In addition, cowpea has the ability to restore soil fertility through nitrogen fixation, making it a good crop to use in crop rotation with major cereal crops (Daryanto et al., 2015). In Namibia, cowpea is ranked third important staple crop after pearl millet and sorghum and its richness in proteins contribute to satisfy the food needs of both kids and adults. It is prepared in different food forms such as boiled grains, peeled grains pounded into a mash and fresh green pods. Cowpea yields have been low varying from 100 to 599 kg.ha<sup>-1</sup> compared to potential yields of 1500 to 3000 kg.ha<sup>-1</sup> (Gbaye and Holloway, 2011). The low yield is often associated with the use of unimproved local varieties, poor soil fertility, drought and other biotic and abiotic stresses. In the country, only the following three varieties are available which were initially imported from the International Institute of Tropical Agriculture (IITA): Nakare [IT81D-985], Shindimba [IT89KD-245-1] and Bira [IT87D-453-2]. But the varieties are not commercially available and do not carry farmers-preferred quality traits. Therefore, 70.2% farmers in the northern Namibia were still found to grow local cowpea varieties, while only 29.8% used improved varieties either singly or in combination (Horn et al., 2015). Other cowpea production constraints are field and storage pests (aphids, leaf beetles, pod borers and bruchids) and low soil fertility. Parasitic weeds such as *Striga gesnerioides* (Willd.) Vatke and *Alectra vogelii* (Benth.) affect cowpea production (Horn et al., 2015). IITA has been involved in developing improved cowpea varieties globally. Consequently, nematode resistant (e.g. varieties CE-31, Frade Preto, CE-28, CE-01, CE-315 and CE-237)

\* Corresponding author.

E-mail address: [Lhorn@unam.na](mailto:Lhorn@unam.na) (L.N. Horn).

(Oliveira et al., 2012) or *Striga gesnerioides* and *Alectra vogelii* tolerant varieties were developed and released (Kabambe et al., 2013; Timko et al., 2007). Furthermore, early maturing, high yielding and pest resistant cultivars have been developed by the IITA and the Agricultural Research Institute of Senegal (ISRA) which are widely grown in Nigeria, Niger and Senegal. In Namibia, the Ministry of Agriculture Water and Forestry also released seven mutant cowpea varieties during 2017. Therefore, the objective of this review was to summarize challenges and constraints to cowpea production, breeding methods and progress of cowpea improvement in order to provide baseline information for cowpea breeders, agronomists and producers in Namibia and for similar agro-ecological niches in SSA.

## 2. Production constraints to cowpea

### 2.1. Biotic constraints

#### 2.1.1. Fungal diseases

More than 40 species of fungi have been reported to cause diseases in cowpea (Bailey et al., 1990). The most destructive fungal disease of cowpea includes leaf smut (false smut or black spot), caused by *Protomyces phaseoli* (Bailey et al., 1990). Fungal diseases cause leaf smut, stem rot, as well as root rot (Bailey et al., 1990). Yield losses due to serious epidemics were reported in Nigeria, the Sudan savanna and Sahel (Adejumo et al., 2001). The losses ranged from 20 to 100% (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).

#### 2.1.2. Viral diseases

More than 20 viruses are known for their negative effects on cowpea production worldwide. These viruses contribute to 90% yield losses or even total crop failure reported in some areas (Mbeyagala et al., 2014). It is not known whether viral diseases cause economic yield losses in cowpea production in Namibia. However, the aphid attack on cowpea results in 100% yield loss in some years (Horn et al., 2015). According to Mbeyagala et al. (2014), the common viral diseases in cowpea are cowpea aphid borne mosaic (CABMV), cucumber mosaic virus (CMV), cowpea mild mottle virus (CPMMV) and cowpea severe mosaic virus (CPSMV). These include yellow mosaic comovirus, mottle virus, and southern bean mosaic sobemovirus, which are beetle transmitted while some cowpea viruses such as cowpea golden mosaic virus and cowpea mild mottle carlavirus are transmitted by whiteflies. The red mosaic virus has a negative effect on rhizobium bacterial growth and development. This had led to 20 to 45% reduction in root nodulation (Taiwo et al., 2014). Viral epidemics could also be transferred from one location to another through the introduction of

newly infected cowpea genotypes into a viral free environment (Mbeyagala et al., 2014). The spread of these viruses could be controlled by growing resistant varieties. Several landraces of cowpea in Uganda, such as WC32, WC18, NE43, NE15, and WC35B were reported to have resistance to virus strains (Taiwo et al., 2014). The impact of the virus on the crop differs significantly in disease reaction among genotypes within and among agro-ecological zones (Mbeyagala et al., 2014).

#### 2.1.3. Bacterial diseases

Bacterial pathogens cause yield reductions reaching up to 71% in pod, 68% in seed and 53% in fodder in susceptible varieties (Viswanatha et al., 2011). The common and serious bacterial diseases of cowpea are bacterial blight caused by *Xanthomonas campestris* pv. *vignicola* and bacterial pustule caused by *Xanthomonas campestris* pv. *vignaeuigiculatae* (Viswanatha et al., 2011). Common symptoms are progressively yellowing of the leaves showing irregular to round spots during moderate infection. This leads to senescence and drooping of leaves. Some bio-control agents have been reported being effective in controlling bacterial blight disease of cowpea. However, the best recommended and economical method is the use of host plant resistance. For any successful crop improvement programme, identification and use of resistant sources against pests and diseases is essential. According to Viswanatha et al. (2011), resistant Lines are used as donor in development of cowpea varieties resistant to bacterial blight disease in breeding programme.

#### 2.1.4. Root-knot nematodes

Root-knot nematodes cause a major loss in cowpea production by hindering nutrient and water uptake (Haegeman et al., 2012). Gheysen and Mitchum (2011) reported some 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). Resistance to nematodes is found in some cowpea cultivars such as CE-31, Frade Preto, CE-28, CE-01, CE-315 and CE-237 (Oliveira et al., 2012). Nematode infestation can also be controlled through cultural practices such as cleaning of the field from infected crop residues after harvest and by crop rotation (Gheysen and Mitchum, 2011).

#### 2.1.5. 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 (Fig. 1). *Alectra vogelii* causes serious yield losses in cowpea in Namibia (Horn et al., 2015).



Fig. 1. Cowpea field infested by *Alectra vogelii* (A) and an uprooted *Alectra vogelii* plant attached to cowpea roots as a parasitic weed (B).



Noubissietchiagam et al. (2010) documented the negative effects of *S. gesnerioides* on cowpea production. Seeds of the parasitic weed are able to remain dormant in the soil for over 20 years, making it difficult to eradicate using traditional methods (Kabambe et al., 2013). One of the possible ways in controlling *S. gesnerioides* and *A. vogelii* is by reducing its seed bank in the soil (Kabambe et al., 2013) and through intensification of resistant genotypes (Christopher et al., 2018). This can be achieved by removing the parasitic weeds after germination and before flowering and seed set.

Kabambe et al. (2014) reported the progress made in identifying cowpea resistant to *Alectra vogelii*. Line IT99K-494-6 was identified for higher yield and resistance to *A. vogelii* (Kabambe et al., 2014). In addition, Line IT97K-499-35, developed at IITA carried resistant to most races of the parasitic weed *S. gesnerioides* (Huynh et al., 2016). Furthermore, cowpea genotypes Kir/Nya-005 and Mbe/Mach-022 were identified with complete resistant to *A. vogelii* (Karanja et al., 2013). Germplasm screening can be used to test resistance (levels of exudates produced) mechanisms of the crop against germination of the parasite (Christopher et al., 2018). Chemical substances called Alectrol or Strigolactone released by some cowpea genotypes are prerequisite to germination and have shown to support few or no *A. vogelii* germination (Christopher et al., 2018). Even with the discovery of resistant cultivars, adoption of suitable cultural practices is still required in controlling the parasitic weeds. Cultural control methods such as the use of trap and catch crops were found effective to control *A. vogelii* (Rugare et al., 2013). Trap crops are plants that are grown as host to stimulate germination of parasitic weeds; however, parasitic plants are immediately destroyed before flowering. Practice of crop rotation is also a recommended cultural method in controlling insect pests and parasitic weeds in cowpea fields (Kabambe et al., 2013).

### 2.1.6. Insect pests

Insect pests attack cowpea both in the field and in stores (Gbaguidi et al., 2013). Dugje et al. (2009) and Ngakou et al. (2008) reported *Aphis craccivora* (Koch), bruchids (*Callosobruchus maculatus* (Fabricius)), beetles (*Ootheca mutabilis*), maruca (*Maruca vitrata*), leafhoppers and foliage beetles as major field pests of cowpea. The pests occur throughout the vegetative growth stages of the plant, feeding on the leaves and also act as virus vectors. In Namibia, field pests including aphids cause yield losses of 77.8% followed by leaf beetles (53.2%), pod borers (60%) and bruchids (100%) (Horn et al., 2015). In SSA bruchids topped the list in destroying stored grains (Fig. 2). Cowpea grains damage by bruchids often results in 100%



**Fig. 2.** Cowpea seeds infested by bruchids (*Callosobruchus maculatus*) at Omahenene Research Station, Namibia during 2013/2014 season. Note: bruchids can cause 100% grain loss if not controlled.

**Table 1**

List of improved cowpea varieties released in Africa between 2008 and 2016. Source: Boukar et al. (2018).

Year of release	Country and variety released
2008	Nigeria: IT97K-499-35,
2009	Nigeria: IT89KD-288, IT89KD-391, Niger: IT97K-499-35, IT97K-499-38, IT98K-205-8
2010	Niger: IT99K-573-1-1, Mali: IT97K-499-35, IT93K-876-30:
2011	Nigeria: IT99K-573-1-1, IT99K-573-3-1, Mozambique: IT82E-16, IT00K-1263, IT97K-1069-6, Malawi: IT99K-494-6
2012	Tanzania: IT99K-7-21-2-2-1, IT99K-573-1-1
2013	Burkina Faso: IT99K-573-2-1, IT98K-205-8, Benin: IT95K-193-12
2015	Nigeria: IT07K-292-10, IT07K-318-33, Tanzania: IT00K-1263, IT99K-1122, Swaziland: IT05K-321-2, IT97K-390-2, IT82E-16, IT-82E-18, IT99K-494-4, Sierra Leon: IT99K-573-2-1, IT99K-573-1-1
2016	South Sudan: IT90K-277-2, IT07K-211-1-8, Ghana: IT99K-573-2-1, IT99K-573-1-1

grain losses if not controlled (Gbaguidi et al., 2013; Horn et al., 2015; Stejskal et al., 2006). Yet no effective commercial pesticide or resistance genes have been reported for controlling bruchids (Gbaye and Holloway, 2011; Stejskal et al., 2006). Studies on insect-pests in stored grains in Namibia found that there were some natural enemies in grain storage facilities. This suggested that natural enemies were potential for pest bio-control in the grain stores (Stejskal et al., 2006). Further research is needed to investigate on how the natural enemies could be effectively used to control insect-pests in storehouses.

### 2.1.7. Control measures for biotic constraints

For any successful crop improvement programme, identification and use of resistant sources against pests and diseases is essential. According to Viswanatha et al. (2011), breeders make use of resistant lines (V-16 showed highly resistant, APC-140, HC-03-02 moderately resistant, GC-4, P-695 moderately susceptible and highly susceptible reactions C-152) as a donor in development of cowpea varieties resistant to bacterial blight disease in their breeding programmes. Similarly, cowpea landrace varieties such as WC32, WC18, NE43, NE15, and WC35B were reported to be resistant to virus strains in Uganda (Taiwo et al., 2014). In Malawi Line IT99K-494-6 was released for high yield and resistance to the parasitic weed *A. vogelii* (Kabambe et al., 2014). The discovery of resistant lines encourages researchers and plant breeders to breed for more cowpea varieties with resistance and traits of interest (Abadassi, 2015). Past research effort by the IITA has contributed to the release of cowpea varieties (Table 1) for different purposes in Africa (Boukar et al., 2018).

## 2.2. Abiotic constraints

### 2.2.1. Drought and heat stresses and poor soil fertility

Drought and heat stresses, as well as poor soil fertility, are the major abiotic factors affecting cowpea production and productivity in SSA. Abiotic stresses cause a loss in many crops such as pearl millet, sorghum and legumes (Hall, 2004). Cowpea is favoured for its ability to withstand drought and grow in poor soils, although it can be sensitive to severe droughts, especially during pod setting and grain filling stages (Hall, 2004). Heat stress above a threshold temperature of 16 °C may cause 4 to 14% loss in pod set and grain yield depending on cultivars (Hall, 2004). Cowpea plants can produce more than 1000 kg.ha<sup>-1</sup>, but this figure can drastically reduce to approximately 360 kg.ha<sup>-1</sup> especially when drought stress occurs at flowering stage (Boukar et al., 2018). A low yield of 360 kg. ha<sup>-1</sup> is within the yield per hectare levels reported in many Sub-Saharan countries. Improved cowpea varieties with better

adaptation to drought condition and early maturity could be recommended to mitigate the effects of abiotic stresses. Daryanto et al. (2015) reported that drought led to severe yield reduction. This was confirmed in a study on monoculture legume yield responses to drought under field conditions between 1980 and 2014, whereby the amount of water reduction in the soil showed a positive correlation with yield reduction in cowpea (Agbicodo et al., 2009). Through molecular techniques, researcher identified RNA sequences for drought-sensitive and drought-tolerant effects with two cowpea genotypes (CB46, drought-sensitive, and IT93K503-1, drought-tolerant) (Barrera-Figueroa et al., 2011).

Unlike drought, soil fertility may be improved by adding organic matter such as manure or the use of chemical fertilizers following recommendations (Kimiti and Odee, 2010). The IAEA ([www.iaea.org/topics/improving-soil-fertility](http://www.iaea.org/topics/improving-soil-fertility)) defined soil fertility as an ability of soil to sustain plant growth and optimize crop yield. This can be enhanced through organic and inorganic fertilizers applied to the soil. Most farmers in SSA, including Namibia, believe that cowpea does not require fertilization, hence grown on poor soil compared to pearl millet and sorghum which are grown on manure applied side of the field (Horn et al., 2015). Despite their ability to fix atmospheric Nitrogen, soil amendments were found to be useful in enhancing cowpea rhizobia populations which varied from  $4.89 \times 10^2$  rhizobia.g<sup>-1</sup> soil to  $1.074 \times 10^3$  rhizobia.g<sup>-1</sup> soil in cowpea variety IT95K-52-34 (Kimiti and Odee, 2010). Due to poor soil fertility combined with other biotic and abiotic stresses, cowpea production has declined in Africa over the past year, compared to other producing countries in the world (FAOSTAT, 2017). In addition, a larger area of land in Africa has been dedicated to cowpea production but did not improve production because of low yield of 275 kg. ha<sup>-1</sup> in Africa, compared to 1790 kg. ha<sup>-1</sup> recorded in the developed world such as the USA (Boukar et al., 2018). This suggests that Africa needs to increase breeding efforts towards climate smart crops with resistance to abiotic and biotic stresses.

### 2.3. Socio-economic constraints

Some of the socio-economic constraints adversely affecting cowpea production in Sub-Sahara Africa were outlined by Horn et al. (2015) and Ibro et al. (2014). These include non-availability of market preferred varieties, low yield potential, high cost of farmland preparation, lack of improved production and harvesting tools, high cost and absence of labor, high cost and adulteration of pesticides, poor harvest prices, and underdeveloped marketing channels. Other major constraints reported in West African countries include lack of defined value chain and poor development of cowpea as a commodity crop. It is reported that farmers in Nigeria and other West African countries solely survive on cowpea farming which is the major economic mainstay and business (Aboki and Yuguda, 2013). In this region, cowpea trades enable farmers to buy other cereal grains and farm inputs such as fertilizers after selling their produce. Despite the effort made, lack of efficient transport, value addition and cowpea enterprises are still an obstacle to marketing (Fakayode et al., 2014).

On the other hand, farmers in Namibia earn little incomes from sales of cowpea grains (Horn et al., 2015) since the monetary values of raw cowpea products are low and production is also low. However, the full economic potential of cowpea could be realized if other value added products, especially those targeted at the ever-growing urban population, are introduced (Waddington et al., 2010). 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. Since cowpea is an important weaning food in many African and Asian communities, its demand could increase with value addition and product development (Ibro et al., 2014). It is also believed that product development and value addition would

increase demand for raw cowpea materials. This will require an increase in production, raising the average yield per hectare of the crop to increase the annual global production and hence the revenue. The world's highest production in cowpea was attained during 2012 and 2013 with 8,045,107 and 8,030,174 metric tons respectively, while in 2011 production dropped and only 44,742 metric tons was recorded (Fig. 3). Increased production could be achieved by provision of inputs such as improved varieties, technical assistance and fertilizers among others.

### 3. Analysis of genetic diversity

Crop genetic diversity is important as it offers an opportunity to plant breeders for developing new and improved cultivars with desirable characteristics which includes both farmers' and breeders' preferred traits (Govindaraj et al., 2015). It is reported that genetic diversity in cowpea has declined over the past years due to various biotic and abiotic factors (Fang et al., 2007). Some farmers reported loss of their local varieties overtime due to frequent droughts, damage by insect pests both in the field and in storage (Horn et al., 2015; Stejskal et al., 2006). Gbaguidi et al. (2013) reported loss of genetic diversity in African cowpea at an increasing rate of 28 to 60% in some agro-ecologies. It is postulated that artificial selection for better performing varieties could have accelerated the loss of genetic diversity because of negative selection against poor performing types from a narrow genetic base. In addition, genetic variation also is restricted within specific breeding programmes in the absence of complementary pre-breeding programmes (Gbaguidi et al., 2013). Studies on germplasms collected from North America, Asia and Africa revealed a narrow genetic base of cowpea (Fang et al., 2007). The same studies further have shown a strong genetic relatedness among germplasm collections of USA and Asia with that of African cowpea collections. Well-characterized germplasm is useful to incorporate economic traits through designed crosses. Genetic diversity is routinely assessed using agro-morphological or phenotypic markers (Govindaraj et al., 2015). In cowpea breeding, both quantitative and qualitative phenotypic characters are extensively used in germplasm characterization, classification and selection (Molosiwa et al., 2016). 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 and seed yield (Molosiwa et al., 2016). Use 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 real genetic variation among genotypes. However, molecular marker techniques are regarded as powerful in determining the genetic diversity and finger-printing of germplasm. Modern biotechnology techniques led to the development of an improved consensus genetic linkage map used to identify QTLs of additional traits. In order to take advantage of these developments, single nucleotide polymorphism (SNP) genotyping is being streamlined to establish an efficient workflow. Cowpea linkage maps of AFLP and SSR markers have been used to identify QTLs for resistance to flower bud thrips (Boukar et al., 2016). Reverse genetics strategies such as TILLING allow the recovery of potentially useful alleles that do not produce phenotypic differences alone but do so when combined with others (Bado et al., 2011). 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 which may improve the efficiency of selection in plant breeding programmes (Araus and Cairns, 2014).

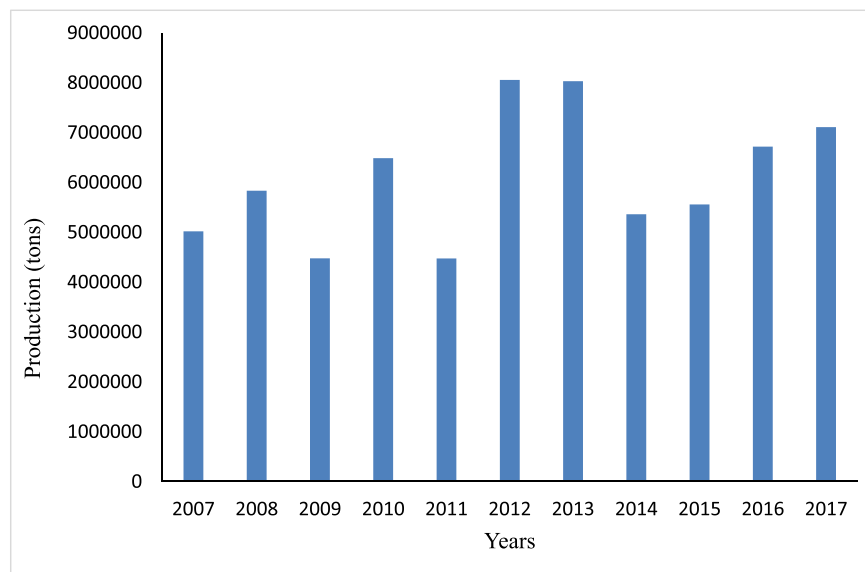


Fig. 3. Overall annual cowpea production (tons) in Africa over the past 10 years. Source (FAOSTAT, 2017).

#### 4. Breeding cowpea

Cowpea is a self-pollinating plant and the breeding methods that have been widely and successfully used for its improvement are: pure line selection, mass selection, pedigree, backcross and single seed descent. Different national and international research organizations notably the IITA has been actively developing improved cowpea cultivars with high yields, early maturity, pest and disease resistance (Boukar et al., 2018; Omoigui et al., 2012). The needs for agronomic traits differ from one region to another. For example, in the tropical regions, earliness, erect growth habit, resistance to biotic stresses (insect pests, pathogens, weeds), drought tolerance, high and stable seed yield, high harvest index, and appropriate seed quality were outlined as required cowpea agronomic traits (Abadassi, 2015; Boukar et al., 2018). According to Singh et al. (2016), pure Line, pedigree and recurrent selection could be followed in cowpea improvement using different crosses for utilizing additive, dominance, additive x additive, additive x dominance and dominance x dominance effects for different traits. Most breeding programmes use conventional and molecular breeding tools to harness cowpea genetic variation for breeding. Hall (2012) discussed the need for breeding for water-use efficiency, deeper rooting, and heat tolerance. One of the most efficient ways to study and breed cowpea for adaptation to drought is by optimal cycle lengths determination. This is suitable for cowpeas growing under rain-fed conditions in semi-arid zones through a hydrologic budget analysis method outlined by Hall (2012). Boukar et al. (2016) reported on linkage maps used to identify quantitative trait locus (QTLs) for desirable traits in cowpea. QTLs are important in identifying molecular markers (such as SNPs or AFLPs) that correlate with an observed trait in breeding. Once the genetic markers that define the QTL have been identified, breeders can use them to select individuals with desired QTL. Some advanced breeding programme in Africa make use of Effective Field-based High-throughput Phenotyping Platforms (HTPPs) which are robust plant breeding selection programmes (Araus and Cairns, 2014).

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 ethyl methanesulphonate (EMS) (Horn and Shimelis, 2013; Jain, 2005; Maluszynski et al., 2000). This has led to the development and release of improved cowpea cultivars in Africa, Asia, and Latin America with different agronomic traits of interest. The

application of induced mutation breeding techniques in cowpea has increased in most countries across Africa as a faster way to enhance genetic variation (Goyal and Khan, 2010; Singh et al., 2013). Induced mutation fit well in cowpea genetic enhancement as most cowpea breeding initiatives aim at broadening the genetic bases of the crop to adapt to various cropping systems and agro-ecologies, and also in the development of consumer-preferred varieties (Lima et al., 2011; Singh et al., 2003). Despite all the previous efforts, there is still a big gap in cowpea improvement in order to increase productivity. Therefore, it is recommended for future and current cowpea breeding efforts to be geared towards traits such as earliness, erect growth habit, resistance to insect pests, pathogens and weeds, drought tolerance, high and stable seed yield, high harvest index, and appropriate seed quality (Abadassi, 2015). Introduction of new value added cowpea products into the market would significantly raise revenues from cowpea production. Following is a summary of different breeding methods used in cowpea improvement programmes for many years.

##### 4.1. Pure-line selection

The concept of this selection method was proposed by the Danish botanist Johanssen in 1903 based on his studies on Princess bean (*Phaseolus vulgaris*). This method is suitable for highly self-fertilizing crop species (Boukar et al., 2018) such as wheat, barley, sorghum, peas, cowpea etc. Pure Line selection involves a selection of promising individuals from segregating populations after systematic crossing or induced mutagenesis. Selected individuals are harvested individually and continuously selfed and selected to develop and release pure Line cultivars. Ayo-Vaughan et al. (2013), reported the preponderance of additive genetic variance in their studies suggesting that these traits could be exploited and new genotypes developed by using the conventional breeding methods such as pure Line selections. Pure line selection was used to improve nodulation ability in pigeon pea (Ayo-Vaughan et al., 2013).

##### 4.2. Pedigree breeding

Unlike pure Line breeding, pedigree method maintains detailed records 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<sub>2</sub> plant from which it had descended. It is commonly applied in selection of desirable plants from the segregating populations



of self-pollinated crops (Huynh et al., 2016). Pedigree method following crossing between two parental lines has been used for improving some specific traits lacking in an already established variety. Ayo-Vaughan et al. (2013) used pedigree selection in their studies on evaluating the combining ability and genetic components for pod and seed traits. 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 (Annicchiarico et al., 2011).

#### 4.3. Bulk population breeding

Bulk population method is also known as mass selection or population breeding. It was used in wheat to develop high yielding and winter type varieties (Ibrahim and Barrett, 2001). This method involves genetic advancement in a population grown in bulk plot from F1 to F5 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 F6 or later generation (Bakhsh et al., 2005). Bulk selection method is useful to increase the frequency of desirable types through positive mass selection. It is suitable for studies on the advancement of genes and genotypes in populations and it offers greater chances of isolation of transgressive segregants than pedigree method. This method was successfully used in selecting mutant cowpea genotypes in Namibia cowpea breeding program (Horn et al., 2016).

#### 4.4. Backcross breeding

Backcross breeding was used to transfer disease and pest resistance genes, and to introduce genetic variability in crop plants (Schrauf et al., 2003). It is used to transfer few genes into an established cultivar of self- or cross-fertilizing crop. Backcrossing leads to increased homozygosity allowing selection of desirable genotype in homozygous and desirable genetic backgrounds. Hall (1990) conducted backcrosses

in improving cowpea for heat tolerance. The use of new resistance genes from the wild have steadily increased since many breeders have exploited wild relatives for incorporating resistance to diseases for over a century through backcross breeding (Hajjar and Hodgkin, 2007).

#### 4.5. Single seed descent selection method

Single-seed-descent selection method was used by Urrea and Singh (1994) in an interracial population of common bean to identify superior genotypes. This selection procedure was suggested to advance segregating generations from hybridization to homozygosity through single seed selection (Snape, 1976; Snape and Riggs, 1975). A single seed method was preferred in the screening for the presence of the dehydrin protein using an immunoblot assay of a chip taken from a cowpea cotyledon (Hall, 2004). In this method, only a single seed collected from each of the F2 plant is kept and bulked to grow the F3 generation. This process continues up to the F5 and F6 generations (Schrauf et al., 2003) whereby a desired level of homozygosity is achieved. In the F6, large number of single plants are selected and their progeny grown separately. In the F7 and F8 best performing lines are selected for preliminary and national yield trials.

#### 4.6. Mutation breeding

Mutations are the ultimate source of genetic variation and raw material for plant breeding programmes. 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 guides the researcher in the

choice of the ideal dose depending on the plant materials and desired outcome (Horn and Shimelis, 2013). Induced mutations provide considerable genetic variation within a reasonably short period 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).

A number of 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 since the 1950s. Maluszynski (2001) outlined some of the major successes 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 of different crops were released in Asia, the highest number in the world, while only 48 mutant varieties of different crops were released in Africa (Maluszynski, 2001). The Mutant Varieties Database (MVD) of FAO and IAEA maintained a list of 2252 crop cultivars developed through artificial mutations (Nielen, 2004). The cultivars were released across 59 countries worldwide, mainly in continental Asia (1142 cultivars), Europe (847) and North America (160) (Maluszynski, 2001). Some of the released mutant varieties released between 1981 and 2018, 15 were cowpea. This figure could have increased because countries such as Egypt, China and Namibia reported the release of mutant cowpea but are not reflected on the current FAO/IAEA database (<https://mvd.iaea.org>). Recent developments in the field of induced mutagenesis technology have shown successful improvement of 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). Once the desired varieties have been identified, it is required to undergo multi-location testing for assessing Genotype by environment interaction (GxE).

### 5. Genotype by environment interaction

Genotype by environment interaction (GxE) is a differential response of genotypes when grown across environments. Multi-environmental trials (METs) are required to quantify the magnitude of GxE interaction and to recommend varieties with narrow or broader adaption (Ramburan et al., 2012). GxE trials are valuable for cultivar recommendation or for the final stages of selection of elite breeding material. Data generated through GxE 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 GxE 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 a change in the 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 the inconsistent performance of test genotypes across locations (Annicchiarico et al., 2010; Jalata, 2011).

GxE interaction has the advantage to crop improvement that targets broad adaptation, but it can also represent opportunities to genetic improvement for specific sites (Annicchiarico et al., 2010). Shiringani and Shimelis (2011) determined the relative yield response and stability among selected improved cowpea genotypes to make recommendation for wide or specific adaptation through GxE analysis and results showed significant interactions among genotypes, planting dates and locations for seed yield. Research on the occurrence and molecular mechanisms of phenotypic plasticity and GxE in plant

populations was carried out by Des Marais et al. (2013), and revealed that GxE was often caused by changes in the magnitude of genetic effects in response to the environment, and associated with diverse genetic factors and molecular variants. GxE interactions may present a barrier to crop improvement because it can contribute to the temporal and spatial instability of crop yields. The advantage of GxE interactions, is the 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). Varieties that are found to be good for a certain environment are selected by farmers through participatory varietal selection involving the end users. In Namibia thirty-four newly developed mutant genotypes and three local checks were evaluated under multi-location trials

in order to determine the GxE among the genotypes. The study was able to discriminate genotypes and grouped them into different agro ecological zones. Four promising mutant genotypes ShL3P74, HhR3P4, ShR9P5 and ShL2P4 showed wide adaptation and good grain yield, some of which have been released in Namibia (Horn et al., 2018).

## 6. Participatory rural appraisal (PRA) and participatory variety selection (PVS)

Participatory rural appraisal (PRA) is an approach used in the agricultural system to involve rural communities for their knowledge and opinions on the specific matter with the aims to incorporate their knowledge and opinions in the planning and management of developmental projects or programmes. Participatory rural appraisal can be achieved through mapping and modelling, transect walks, matrix scoring, seasonal calendars, trend and change analysis, well-being and wealth ranking and grouping, and analytical diagramming (Chambers, 1994). PRA applications include natural resources management, agriculture, poverty and social programmes, and health and food security (Chambers, 1994). PRA was successfully used to empower citizen using knowledge about their local biophysical and social environment and its associated problems, raising awareness of how to help solve these problems (Solano Lara et al., 2018). It is reported that PRA helps the community in raising their problems to the relevant authority in order to work towards their solution (Solano Lara et al., 2018). Studies reported that the communities' knowledge about their environment and a close relationship with the land and the natural world is much greater. PRA techniques have been successfully used to identify farmers' perceived production constraints, preferred crop varieties and traits for the deployment of production packages and suitable crop variety (Rusinamhodzi and Delve, 2011). Depending on the breeding goal and the environment, farmers contribute significantly at different stages of crop cultivar design, development, release and adoption. Therefore, PRA should be the first step for any developmental project or activities done to benefit communities.

On the other hand, participatory variety selection is an approach used to provide choices of varieties to the farmers for increasing production in their diversity of socioeconomic and agro-ecological condition (Belay et al., 2006). Participatory variety selection (PVS) is a more rapid and cost effective way of identifying farmer preferred cultivars (Hoffmann et al., 2007). Various researchers (Rusinamhodzi and Delve, 2011; Hoffmann et al., 2007; vom Brocke et al., 2010) 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 (Rusinamhodzi and Delve, 2011). PVS is used 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

(vom Brocke et al., 2010). 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 Hoffmann et al. (2007) 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 region and develop cultivar with wide adaptation is encouraged.

## 7. Conclusions

Cowpea is the major food crop and a source of cheap protein for most resource poor households in SSA, including Namibia. This literature review showed the gap in global research efforts directed at improving cowpea, one of the orphan crops globally. Concerted research and development efforts are 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 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 programmes contributed significantly in developing improved cowpea germplasm and generation of scientific knowledge. These programmes 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 the SAA, cowpea improvement is not advanced leaving the major work to the IITA. Therefore, there is an urgent requirement for different cowpea breeding programmes focusing on developing varieties with short maturity, drought, pest and disease tolerance. Most farmers face yield losses due to parasitic weeds (*Striga gesnerioides* and *Alectra vogelii*) and insect pests. Farmers reported to have lost their cowpea germplasm overtime. This requires the creation of genetic pool of the crop for cultivar development incorporating farmers' preferred traits.

## Acknowledgements

The study was supported by the Ministry of Agriculture, Water and Forestry (MAWF) Namibia, and the International Atomic Energy Agency (IAEA).

## References

- Abadassi, J., 2015. Cowpea (*Vigna unguiculata* (L.) Walp.) agronomic traits needed in tropical zone. *Int. J. Pure app. Biosci.* 3, 158–165.
- Aboki, E., Yuguda, R., 2013. Determinant of profitability in cowpea production in Takum local government area of Taraba state. *Nigeria. J. Agric. Sci.* 4, 33–37.
- Adejumo, T.O., Florini, D.A., Ikotun, T., 2001. Screening of cowpea cultivars for resistance to leaf smut. *Crop Prot.* 20, 303–309.
- Agbicodo, E.M., Fatokun, C.A., Muranaka, S., Visser, R.G.F., van der Linden, C.G., 2009. Breeding drought tolerant cowpea: constraints, accomplishments, and future prospects. *Euphytica*. 167, 353–370.
- Agbogidi, O., 2010. Screening six cultivars of cowpea (*Vigna unguiculata* L.) walp for adaptation to soil contaminated with spent engine oil. *J. Environ. Chem. Ecotoxicol.* 2, 103–109.
- Annicchiarico, P., Iannucci, A., 2008. Breeding strategy for faba bean in southern Europe based on cultivar responses across climatically contrasting environments. *Crop Sci.* 48, 983–991.
- Annicchiarico, P., Harzic, N., Carroni, A.M., 2010. Adaptation, diversity, and exploitation of global white lupin (*Lupinus albus* L.) landrace genetic resources. *Field Crop Res.* 119, 114–124.
- Annicchiarico, P., Pecetti, L., Abdelguerfi, A., Bouizgaren, A., Carroni, A.M., Hayek, T., Bouzina, M.M.H., Mezni, M., 2011. Adaptation of landrace and variety germplasm and selection strategies for lucerne in the Mediterranean basin. *Field Crop Res.* 120, 283–291.
- Araus, J.L., Cairns, J.E., 2014. Field high-throughput phenotyping: the new crop breeding frontier. *Trends Plant Sci.* 19, 52–61.

- Ayo-Vaughan, M.A., Ariyo, O.J., Alake, C.O., 2013. Combining ability and genetic components for pod and seed traits in cowpea Lines. *Ital. J. Agron.* 8, 73–78.
- Bado, S., Matijević, M., Till, B.J., Jankowicz-Cieslak, J., Huynh, O.A., 2011. Reverse-genetics by TILLING expands through the plant kingdom. *Emir. J. Food Agric.* 23, 290–300.
- Bailey, J.A., Nash, C., O'Connell, R.J., Skipp, R.A., 1990. Infection process and host specificity of a *Colletotrichum* species causing anthracnose disease of cowpea, *Vigna unguiculata*. *Mycol. Res.* 94, 810–814.
- Bakhsh, A., Arshad, M., Iqbal, S., 2005. Development of chickpea blight resistant variety (Dasht) using combination of bulk population and pedigree breeding method. *Pak. J. Bot.* 37, 325–335.
- Barrera-Figueroa, B.E., Gao, L., Diop, N.N., Wu, Z., Ehlers, J.D., Roberts, P.A., Close, T.J., Zhu, J.K., Liu, R., 2011. Identification and comparative analysis of drought-associated microRNAs in two cowpea genotypes. *BMC Plant Biol.* 11, 127. <https://doi.org/10.1186/1471-2229-11-127>.
- Belay, G., Tefera, H., Tadesse, B., Metaferia, G., Jarra, D., Tadesse, T., 2006. Participatory variety selection in the Ethiopian cereal tef (*Eragrostis tef*). *Exp. Agric.* 42, 91–101.
- Boukar, O., Fatokun, C.A., Huynh, B.L., Roberts, P.A., Close, T.J., 2016. Genomic tools in cowpea breeding programs: status and perspectives. *Front. Plant Sci.* 7, 757. <https://doi.org/10.3389/fpls.2016.00757>.
- Boukar, O., Belko, N., Chamarithi, S., Togola, A., Batieno, J., Owusu, E., Haruna, M., Diallo, S., Umar, M.L., Olufajo, O., 2018. Cowpea (*Vigna unguiculata*): genetics, genomics and breeding. *Plant Breed.* 138, 415–424.
- Chambers, R., 1994. The origins and practice of participatory rural appraisal. *World Dev.* 22, 953–969.
- Christopher, P.K., Vernon, K.H., James, B., Peter, M., 2018. Screening for resistance mechanisms in cowpea genotypes on *Alectra vogelii*. *Am. J. Plant Sci.* 9, 1362–1379.
- Daryanto, S., Wang, L., Jacinthe, P.A., 2015. Global synthesis of drought effects on food legume production. *PLoS One* 10, e0127401.
- Des Marais, D.L., Hernandez, K.M., Juenger, T.E., 2013. Genotype-by-environment interaction and plasticity: exploring genomic responses of plants to the abiotic environment. *Annu. Rev. Ecol. Syst.* 44, 5–29.
- Dugie, I., Omoigui, L., Ekeleme, F., Kamara, A., Ajeigbe, H., 2009. Farmers' Guide to Cowpea Production in West Africa. IITA, Ibadan, Nigeria, p. 20.
- Fakayode, B.S., Omotesho, A.O., Adebayo, T.Z., 2014. An economic survey of cowpea (*Vigna unguiculata*) storage practices in Kwara State, Nigeria. *Bangladesh J. Agric. Res.* 39, 47–57.
- Fang, J., Chao, C.C., Roberts, P., Ehlers, J., 2007. Genetic diversity of cowpea [*Vigna unguiculata* (L.) Walp.] in four West African and USA breeding programs as determined by AFLP analysis. *Genet. Resour. Crop. Evol.* 54, 1197–1209.
- FAOSTAT, 2017. Available online: <http://www.fao.org/faostat/en/#data.QC> (accessed on January 2018).
- Gbaguidi, A.A., Dansi, A., Loko, L.Y., Dansi, M., Sanni, A., 2013. Diversity and agronomic performances of the cowpea (*Vigna unguiculata* Walp.) landraces in southern Benin. *Int. res. J. Agric. Sci. Soil Sci.* 3, 121–133.
- Gbaye, O.A., Holloway, G.J., 2011. Varietal effects of cowpea, *Vigna unguiculata*, on tolerance to malathion in *Callosobruchus maculatus* (Coleoptera: Bruchidae). *J. Stored Prod. Res.* 47, 365–371.
- Gheysen, G., Mitchum, M.G., 2011. How nematodes manipulate plant development pathways for infection. *Curr. Opin. Plant Biol.* 14, 415–421.
- Girija, M., Dhanavel, D., 2009. Mutagenic effectiveness and efficiency of gamma rays, ethyl methane sulphonate and their combined treatments in cowpea (*Vigna unguiculata* L. Walp.). *Global J. Mol. Sci.* 4, 68–75.
- Govindaraj, M., Vetriventhan, M., Srinivasan, M., 2015. Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. *Genet. Res. Int.* 2015, 431487. <https://doi.org/10.1155/2015/431487>.
- Goyal, S., Khan, S., 2010. Induced mutagenesis in Urd bean (*Vigna mungo* L. Hepper): a review. *Int. J. Bot.* 6, 194–206.
- Gurmu, F., Mohammed, H., Alemaw, G., 2009. Genotype × environment interactions and stability of soybean for grain yield and nutrition quality. *Afr. Crop. Sci. J.* 17, 87–99.
- Haegeman, A., Mantelin, S., Jones, J.T., Gheysen, G., 2012. Functional roles of effectors of plant-parasitic nematodes. *Genet.* 492, 19–31.
- Hajjar, R., Hodgkin, T., 2007. The use of wild relatives in crop improvement: a survey of developments over the last 20 years. *Euphytica* 156, 1–13.
- Hall, A., 1990. Breeding for heat tolerance an approach based on whole-plant physiology. *HortScience* 25, 17–19.
- Hall, A.E., 2004. Breeding for adaptation to drought and heat in cowpea. *Eur. J. Agron.* 21, 447–454.
- Hall, A., 2012. Phenotyping cowpeas for adaptation to drought. *Front. Physiol.* 3, 155 (10.3389/fphys.2012.00155).
- Hoffmann, V., Probst, K., Christinck, A., 2007. Farmers and researchers: how can collaborative advantages be created in participatory research and technology development? *Agric. Hum. Values* 24, 355–368.
- Horn, L., Shimelis, H., 2013. Radio-sensitivity of selected cowpea (*Vigna unguiculata*) genotypes to varying gamma irradiation doses. *Sci. Res. Essays* 8, 1991–1997.
- Horn, L., Shimelis, H., Laing, M., 2015. Participatory appraisal of production constraints, preferred traits and farming system of cowpea in the northern Namibia: implications for breeding. *Legume Res. J.* 38, 691–700.
- Horn, L.N., Ghebrehiwot, H.M., Shimelis, H.A., 2016. Selection of novel cowpea genotypes derived through gamma irradiation. *Front. Plant Sci.* 7, 262.
- Horn, L., Shimelis, H., Sarsu, F., Mwadzigeni, L., Laing, M.D., 2018. Genotype-by-environment interaction for grain yield among novel cowpea (*Vigna unguiculata* L.) selections derived by gamma irradiation. *Crop J.* 6, 306–313.
- Huynh, B.L., Matthews, W.C., Ehlers, J.D., Lucas, M.R., Santos, J.R., Ndeve, A., Close, T.J., Roberts, P.A., 2016. A major QTL corresponding to the Rk locus for resistance to root-knot nematodes in cowpea (*Vigna unguiculata* L. Walp.). *Theor. Appl. Gen.* 129, 87–95.
- Ibrahim, Kamal, Barrett, James, 2001. Evolutionary changes in Cambridge composite cross five of barley. In: Cooper, H., Spillane, C., Hodgkin, T. (Eds.), Broadening the genetic base of crop production. CAB, UK.
- Ibro, G., Sorgho, M.C., Idris, A.A., Moussa, B., Baributsa, D., Lowenberg-DeBoer, J., 2014. Adoption of cowpea hermetic storage by women in Nigeria, Niger and Burkina Faso. *J. Stored Prod. Res.* 58, 87–96.
- Jain, S.M., 2005. Major mutation-assisted plant breeding programs supported by FAO/IAEA. *Plant Cell Tissue Organ Cult.* 82, 113–123.
- Jalata, Z., 2011. GGE-biplot analysis of multi-environment yield trials of barley (*Hordeum vulgare* L.) genotypes in Southeastern Ethiopia highlands. *IJPBCS* 5, 59–75.
- Kabambe, V.H., Tembo, Y.L.B., Kazira, E., 2013. Awareness of the parasitic weed *Alectra vogelii* (Benth.) amongst extension officers in three districts in Malawi. *Am. J. Exp. Agric.* 3, 432–442.
- Kabambe, V., Mazuma, E., Bokosi, J., Kazira, E., 2014. Release of cowpea Line IT99K-494-6 for yield and resistance to the parasitic weed, *Alectra vogelii* Benth. in Malawi. *African J. Plant Sci.* 8, 196–203.
- Karanja, J., Ngululu, S., Wambua, J., Gatheru, M., 2013. Response of cowpea genotypes to *Alectra vogelii* parasitism in Kenya. *Afr. J. Biotechnol.* 12, 6591–6598.
- Kimiti, J.M., Odee, D.W., 2010. Integrated soil fertility management enhances population and effectiveness of indigenous cowpea rhizobia in semi-arid eastern Kenya. *Appl. Soil Ecol.* 45, 304–309.
- Lima, K.D.S.C., Souza, L.B.E., Godoy, R.L.D.O., França, T.C.C., Lima, A.L.D.S., 2011. Effect of gamma irradiation and cooking on cowpea bean grains (*Vigna unguiculata* L. Walp.). *Radiat. Phys. Chem.* 80, 983–989.
- Maluszynski, M., 2001. Officially released mutant varieties—the FAO/IAEA Database. *Plant Cell Tissue Organ Cult.* 65, 175–177.
- Maluszynski, M., Nichterlein, K., Zanten, L.V., Ahloowalia, B., 2000. Officially Released Mutant Varieties-The FAO/IAEA Database.
- Mbeyagala, E.K., Mukasa, B.S., Tukamuhabwa, P., Bisikwa, J., 2014. Evaluation of cowpea genotypes for virus resistance under natural conditions in Uganda. *J. Agric. Sci. (Toronto)* 6, 176–187.
- Mohammed, Y.A., Chen, C., McPhee, K., Miller, P., McVay, K., Eckhoff, J., Lamb, P., Miller, J., Khan, Q., Bohannon, B., Knox, M., Holmes, J., 2016. Yield performance and stability of dry pea and lentil genotypes in semi-arid cereal dominated cropping systems. *Field Crop Res.* 188, 31–40.
- Molosiwa, O.O., Gwafila, C., Makore, J., Chite, S.M., 2016. Phenotypic variation in cowpea (*Vigna unguiculata* [L.] Walp.) germplasm collection from Botswana. *Int. J. Biodivers. Conserv.* 8, 153–163.
- Ngakou, A., Tamò, M., Parh, I.A., Nwaga, D., Ntonifor, N.N., Korie, S., Nebane, C.L.N., 2008. Management of cowpea flower thrips, *Megalurothrips sjostedti* (Thysanoptera, Thripidae), in Cameroon. *Crop Prot.* 27, 481–488.
- Nielsen, S., 2004. FAO/IAEA Mutant Variety Database. Mutation Plant Breeding, IAEA/FAO Vienna.
- Noubissietchiagam, J.B., Bell, J.M., Guissaibirwe, S., Gonne, S., Youmbi, E., 2010. Varietal response of cowpea (*Vigna unguiculata* (L.) Walp.) to *Striga gesnerioides* (Willd.) Vatke race SC5 infestation. *Notulae Botanicae, Horti Agrobotanici, Cluj-Napoca* 38, 33–41.
- Oliveira, J.T.A., Andrade, N.C., Martins-Miranda, A.S., Soares, A.A., Gondim, D.M.F., Araújo-Filho, J.H., Freire-Filho, F.R., Vasconcelos, I.M., 2012. Differential expression of antioxidant enzymes and PR-proteins in compatible and incompatible interactions of cowpea (*Vigna unguiculata*) and the root-knot nematode *Meloidogyne incognita*. *Plant Physiol. Biochem.* 51, 145–152.
- Omoigui, L., Kamara, A., Ishiyaku, M., Boukar, O., 2012. Comparative responses of cowpea breeding lines to *Striga* and *Alectra* in the dry savanna of northeast Nigeria. *Afr. J. Agric. Res.* 7, 747–754.
- Pujari, J.D., Yakkundimath, R., Byadgi, A.S., 2015. Image processing based detection of fungal diseases in plants. *Procedia Comput. Sci.* 46, 1802–1808.
- Ramburan, S., Zhou, M., Labuschagne, M.T., 2012. Investigating test site similarity, trait relations and causes of genotype × environment interactions of sugarcane in the Midlands region of South Africa. *Field Crop Res.* 129, 71–80.
- Rugare, J.T., Mabasa, S., Tsekenedza, S., 2013. Response of cowpea (*Vigna unguiculata* L.) genotypes to witch weed (*Alectra vogelii* Benth.) infection. *Asian J. Agric. Res. Develop.* 3, 667–673.
- Rusinamhodzi, L., Delve, R.J., 2011. Participatory variety selection of pulses under different soil and pest management practices in Kadoma District, Zimbabwe. In: Bationo, A., Waswa, B., Okeyo, M.J., Maina, F., Kihara, M.J. (Eds.), Innovations as Key to the Green Revolution in Africa: Exploring the Scientific Facts. Springer Netherlands, Dordrecht, pp. 1015–1022.
- Schrauf, G., Blanco, M., Cornaglia, P., Deregibus, V., Madia, M., Pacheco, M., Padilla, J., García, A., Quarín, C., 2003. Ergot resistance in plants of *Paspalum dilatatum* incorporated by hybridisation with *Paspalum urvillei*. *Tropical Grasslands* 37, 182–186.
- Shiringani, R., Shimelis, H., 2011. Yield response and stability among cowpea genotypes at three planting dates and test environments. *Afr. J. Agric. Res.* 6, 3259–3263.
- Singh, B.B., Ajeigbe, H.A., Tarawali, S.A., Fernandez-Rivera, S., Abubakar, M., 2003. Improving the production and utilization of cowpea as food and fodder. *Field Crop Res.* 84, 169–177.
- Singh, D.P., Sharma, S.P., Lal, M., Ranwah, B.R., Sharma, V., 2013. Induction of genetic variability for polygenic traits through physical and chemical mutagens in cowpea *Vigna unguiculata* (L.) Walp. *Legum. Res.* 36, 10–14.
- Singh, A., Singh, Y., Sharma, A., Visen, A., Singh, M.K., Singh, S., 2016. Genetic analysis of quantitative traits in cowpea [*Vigna unguiculata* (L.) Walp.] using six parameter genetic model. *Legume Res. J.* 39, 502–509.
- Snape, J., 1976. A theoretical comparison of diploidised haploid and single seed descent populations. *Heredity* 36, 275–277.



- Snape, J., Riggs, T., 1975. Genetical consequences of single seed descent in the breeding of self-pollinating crops. *Heredity* 35, 211–219.
- Solano Lara, C., Fernández Crispín, A., López Téllez, M.C., 2018. Participatory rural appraisal as an educational tool to empower sustainable community processes. *J. Clean. Prod.* 172, 4254–4262.
- Stejskal, V., Kosina, P., Kanyomeka, L., 2006. Arthropod pests and their natural enemies in stored crops in northern Namibia. *J. Pest. Sci.* 79, 51–55.
- Taiwo, L.B., Taiwo, M.A., Shoyinka, S.A., Jegede, S.E., Okogun, J.A., Oyatokun, O.S., Adebayo, G.G., 2014. Interactive effects of virus and Rhizobium inocula on nodulation, growth and yield of cowpea. *Int. J. Plant Physiol. Biochem.* 6, 34–39.
- Timko, M.P., Ehlers, J.D., Roberts, P.A., 2007. *Cowpea. Pulses, Sugar and Tuber Crops*. Springer, pp. 49–67.
- Tshilenge-Lukanda, L., Funny-Biola, C., Tshiyoyi-Mpunga, A., Mudibu, J., Ngoie-Lubwika, M., Mukendi-Tshibingu, R., Kalonji-Mbuyi, A., 2012. Radio-sensitivity of some groundnut (*Arachis hypogaea* L.) genotypes to gamma irradiation: indices for use as improvement. *Brit J. Biotechnol.* 3, 169–178.
- Urrea, C.A., Singh, S.P., 1994. Comparison of mass, F<sub>2</sub>-derived family, and single-seed-descent selection methods in an interracial population of common bean. *Can. J. Plant Sci.* 74, 461–464.
- Viswanatha, K.P., Pallavi, M.S., Khan, P.H., 2011. Sources of resistance to cowpea (*Vigna unguiculata* L.) bacterial leaf blight disease. Plant growth-promoting rhizobacteria (PGPR) for sustainable agriculture. Proceedings of the 2nd Asian PGPR Conference, Beijing, China, 21–24 August 2011, pp. 465–472.
- vom Brocke, K., Trouche, G., Weltzien, E., Barro-Kondombo, C.P., Gozé, E., Chantreau, J., 2010. Participatory variety development for sorghum in Burkina Faso: farmers' selection and farmers' criteria. *Field Crop Res.* 119, 183–194.
- Waddington, S.R., Li, X., Dixon, J., Hyman, G., de Vicente, M.C., 2010. Getting the focus right: production constraints for six major food crops in Asian and African farming systems. *Food Security* 2, 27–48.