

Genetic Variability and Heritability Studies in Cowpea Genotypes (*Vigna unguiculata*. L. Walp): A Review



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Abstract

Cowpea is a staple food crop and a primary source of protein in the diet of millions of people and it also provides fodder for livestock including income for households. The objective of this research is to review related researches conducted by researchers on genetic variability and heritability in cowpeas. Cowpea breeding programmes have studied extensively qualitative and quantitative genetic of the crop to better enhance its improvement. The knowledge on the nature and extent of genetic variability present in any crop species play an important role in designing a suitable breeding method. Genetic diversity is the foremost basic requirement for a successful breeding programme. Heritability is a biostatistic commonly used in plant breeding and genetic works that estimates how much variation in a phenotypic trait in a population is due to genetic variation among individual plant in that population. Furthermore, genetic advance is the improvement in the mean genotypic value of selected plant families over that of base population. It depends upon phenotypic variability, heritability and intensity of selection. The evaluation of cowpea germplasm, quantification of the magnitude of variability existing for different characters and classification into groups help in identifying potential distinct genotypes which are having contrasting characters, can be used to operate effective selection of genetically diverse genotypes for the improvement of yield. In this review paper, the research work carried on different aspect of genetic variability is discussed under the sub-heads: crop and botanical description of cowpea, variation of qualitative and quantitative traits, genetic variability, heritability and genetic advance, genetic divergence, D2 analysis and genetic diversity by using principal component axes.

Keywords: Cowpea; Genetic Variability; Genetic Diversity; Germplasm and Heritability; Crop improvement

Abbreviations: DNA: Deoxyribo Nucleic Acid; RNA: Reoxyribo Nucleic Acid; IITA: International Institute of Tropical Agriculture; SNP: Single Nucleotide Polymorphism; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; PCR: Polymerase Chain Reaction; MAB: Marker Assisted Breeding

Introduction

Cowpea belongs to the family *Fabaceae/Leguminosae* (Pea family), genus *Vigna* and the species *Vigna unguiculata* (L.) Walp. [1,2]. The first written reference of the word 'cowpea' appeared in 1798 in the United States. Studies suggest that most Southern region of Africa could be center of origin of *Vigna unguiculata* while domestication might have occurred near Ethiopia and West Africa. The name was most likely acquired due to their use as a fodder crop for cows. Cowpea is also known as bachapin bean, southern pea, black eyed cowpea, black eyed dolichos, poona pea, blackeyed pea, rope bean, black-eyed bean, red pea, china bean, marble pea, common cowpea, macassar bean, cowgram, cowpea, kafir bean, cultivated african cowpea, crowder bean, field pea, horse bean, yard long bean, asparagus bean and crowder pea [2-6]. Names in Indian languages [7] are in Bengali: Ghangra; Hindi: Chauli, Kulath; Kannada: Alasabde, Alasande; Malayalam: Perumpayar; Marathi: Chavali, Alasunda; Sanskrit: Rajamasah,

Mahamasah. Others are: Tamil: Kaattu Ulundu, Thattapayir; Telugu: Kaaraamanulu, Alasandalu. Black-eyed peas, a common name for a cowpea cultivar, are named due to the presence of a distinctive black spot on their hilum. There are seven varieties of cowpea which are named as blackeye or purple eye peas, brown eye peas, crowder peas, cream, white acre type, clay types and forage cultivars [2].

Cowpea is an important legume grown predominantly in the dry Savannah Agro ecologies of Sub Africa, Southern Africa and other developing countries of the world [8,9]. In addition to being a food crop, the crop plays a key role in sustainable farm, [10] and a stable for crop and primary source of protein for millions of people in developing countries [11,12]. Cowpea is one of the most important native food and forage legumes, and it is grown in Sub-Saharan Africa and some temperate regions of the world. The young leaves, green pods and green grains are used as vegetables,

and the dry grains are used in various preparations for both human food and livestock feed [13,14].

Genetic diversity is fundamental in plant breeding programs and in cowpea it has declined due to various biotic and abiotic factors [15]. 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 [16,17]. 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 [18]. Studies conducted using germplasm collections from the continents of north America, Asia and Africa revealed a narrow genetic base of cowpea [15]. 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-fertilization. Gbaguidi et al. [18], reported loss of genetic diversity of cowpea in Africa at a rate of 28 to 60% in some Agro-ecologies.

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. In cowpea, there is a high level of morphological diversity that is found within species with large variations in size, shape, and structure of the plant [19]. Quantitative traits include: number of branches per plant, days to 50% flowering, days to 50 maturities, number of pods per plant, pod length, pod width, seed weight, number of seeds/pods, and seed yield [17,20]. 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 are recently advocated for which may improve the efficiency of selection in plant breeding programs [17,21].

Genetic variability is the variation in alleles of genes or variation in deoxyribonucleic acid and reoxyribonucleic (DNA/RNA) sequences in the gene pool of a species or population. Genetic variability for agronomic traits is a key component of breeding programs for broadening the gene pool of both cowpea and other crops. [22] several possible factors including gene flow due to population migration, homologous combination or crossing over during meiosis, polyploidy (presence of more than two homologous chromosomes) and mutations might contribute

to genetic variability in the population [23]. Of these possibilities, mutations make the primary source of genetic variation [22,23]. Mutations affect a single nucleotide; whereby new alleles that are formed constitutes a common source of genetic variation. On the other hand, chromosomal mutations moved the alleles around either on a different locus on the same chromosome. Beedanagari et al. [23] and medline plus Genetic [22] reported that different chromosomes by homologous recombination or translocation results in genetic variation.

Genetic variability could be affected by these factors Viz: mutation, random mating between organisms, random fertilization, crossing over (or recombination) between chromatids of homologous chromosomes during meiosis and selection in both natural and artificial selection. Genetic variability has wide range of uses and that is quite beneficial. It utilizes the genetic variation between individuals within a plant species and combines the desired properties in to non-improved varieties. Plant breeding is dependent on genetic variation and new variation is fundamentally important for introduction of traits in breeding programs. Heritability refers to the extent to which genetic factors contribute to the observed variation in a particular trait within a population. In other words, it measures the proportion of the variability in a trait that can be attributed to genetic differences among individuals and it is often expressed as a percentage, ranging from 0% to 100% [24].

The concept of genetic heritability has several important uses and it is beneficial in cowpea study. Some of the uses and benefits of genetic heritability includes:

Understanding the causes of traits: Genetic heritability helps researchers and scientists understand the relative contributions of genetic and environmental factors to the observed variation in traits within a population. In agriculture and animal husbandry, heritability is used to guide selective breeding programs by understanding the heritability of desirable traits (such as crop yield, disease resistance), in which breeders can make informed decisions to enhance these traits over generations. Predictive Genetics: In certain cases, knowledge of the heritability of a trait can be used for predictive purposes. For example, if a trait has high heritability, it may be more reliably passed from one generation to the next, allowing for predictions about the likelihood of certain traits appearing in offspring. Heritability is also relevant in evolutionary biology and it help researchers understand how traits change over generations and how natural selection acts on genetic variation within a population amongst others [25].

Heritability is influenced by a combination of genetic and environmental factors [24]. Understanding the factors contributing to genetic heritability involves considering various elements that affect the variation in traits within a population. Thus, the extent of genetic heritability depends on the presence of genetic variation within a population. If there is little genetic diversity for a particular trait, it may limit the potential for that trait

to be heritable. Other factors include, the genetic architecture of a trait refers to the number of genes involved and their interactions; while others are influenced by numerous genes with smaller effects. The complexity of genetic architecture influences the heritability of a trait. Environmental factors play a significant role in the expression of genetic traits, gene-environment interaction, developmental stage, gene flow and migration [26]. Heritability is also influenced by a combination of genetic and environmental factors [27]. Several key factors can affect the estimation of heritability for a particular trait and some of the factors that play a role in determining genetic heritability are: Genetic variation, environmental variation, gene-environment interaction, gene-environment correlation, shared and non-shared environment.

Crop Description of Cowpea

There is a large morphological diversity found within the crop, and the growth conditions and grower preferences for each variety vary from region to region [28]. However, as the plant is primarily self-pollinating its genetic diversity within varieties is relatively low. Cowpeas can either be short and bushy (as short as 20 cm) or act like a vine by climbing supports or trailing along the ground (to a height of 2 m) as reported by Sheahan, [29] and National Research Council [30]. The tap root can penetrate to a depth of 2.4 m after eight weeks of sowing [31]. The size and shape of the leaves varies greatly, making this an important feature for classifying and distinguishing cowpea varieties [32]. Another distinguishing feature of cowpeas is the long 20-50 cm peduncles which hold the flowers and seed pods. One peduncle can support four or more seed pods [33]. Flower color varies through different shades of purple, pink, yellow and white and blue [30]. Seeds and seed pods from wild cowpeas are very small [33] while cultivated varieties can have pods between 10 and 110 cm long [34]. A pod can contain 6 - 13 seeds that are usually kidney shaped, although the seeds become more spherical the more restricted, they are within the pod [33]. Their texture and color are very diverse. They can have a smooth or rough coat and be speckled, mottled or blotchy. Colors include white, cream, green, red, brown and black or various combinations [33,35].

Genus Vigna: *Vigna* is a genus of flowering plants in the legume family called *Fabaceae*, subfamily: *Faboideae*, tribe: *Phaseoleae*, subtribe: *Phaseolinae*, with a pantropical distribution. It includes some well-known cultivated species, including many types of beans. *Vigna* are herbs or occasionally subshrubs. The leaves are pinnate, divided into 3 leaflets. The inflorescence is a raceme of yellow, blue, or purple pea flowers. The fruit is a legume pod of varying shape containing seeds. Familiar food species include the adzuki bean (*Vigna angularis*), the black gram (*Vigna mungo*), the cowpea (*Vigna unguiculata*) and the mung bean (*Vigna radiata*), which is used as a whole bean, a bean paste, or as bean sprouts. The genus is named after Domenico Vigna, a seventeenth-century Italian botanist and director of the Orto botanico di Pisa [36].

The genus *Vigna* has 5 subgenera [36]. These includes subgenus:

- i. Subgenus *Ceratotropis* [18 species].
- ii. Subgenus *Haydonia* [4 species].
- iii. Subgenus *Lasiospron* [7 species].
- iv. Subgenus *Vigna* [12 species] and
- v. Subgnus *Incertae Sedis* [19 species].

Taxonomy of the Subgenus *Vigna* [12 species] [36]: *Vigna ambacensis* Welw. ex Bak; *Vigna angivensis* Baker; *Vigna filicaulis* Hepper; *Vigna friesiorum* Harms; *Vigna gazensis* Baker f.; *Vigna hoesi* (Craib) Backer - Sarawak-bean; *Vigna luteola* (Jacq.) Benth. - Dalrymple *Vigna* and *Vigna membranacea* A. Rich. Others include: *Vigna monantha* Thulin; *Vigna racemosa* (G. Don) Hutch. and Dalziel; *Vigna subterranea* (L.) Verdc. - Bambara groundnut, Congo goober, hog-peanut, jugo bean, njugumawe (Swahili) (sometimes separated in *Voandzeia*; *Vigna unguiculata* (L.) Walp. - cowpea, crowder pea, Southern pea, Reeve's-pea, snake-bean.

- i. **Important Species of Cowpea** [36]: *Vigna unguiculata* (L.) Walp. - cowpea, crowder pea, Southern pea, Reeve's-pea, snake-bean
- ii. *Vigna unguiculata* ssp. *Cylindrica* - catjang.
- iii. *Vigna unguiculata* ssp. *Dekindtiana* -wild cowpea, African cowpea, Ethiopian cowpea.
- iv. *Vigna unguiculata* ssp. *Sesquipedalis* - yardlong bean, long-podded cowpea, asparagus bean, Chinese long bean, pea-bean.
- v. *Vigna unguiculata* ssp. *Unguiculata* - black-eyed pea, black-eyed bean.

Cowpea is a *Dicotyledonea* belonging to the order *Fabales*, family *Fabaceae*, subfamily *Faboideae*, tribe *Phaseoleae*, subtribe *Phaseolinae*, genus *Vigna*, and section *Catiang* [37,38]. *Vigna* is a pantropical genus with several species, whose exact number varies according to authors: 184 [39], 170 [40], between 170 and 150 [41], 150 [37], 154 [42], and about 84 (of which some 50 species are indigenous to Africa) [38]. In their revision of the genus *Vigna*, Marechal et al., [38] subdivided the genus described earlier by Verdcourt [37] into seven subgenera. In this classification, *V. unguiculata* (L.) Walpers and *V. nervosa* Markotter constitute the section *Catiang*, one of the six sections of the subgenus *Vigna*. Species of the section *Catiang* are characterized by spurred stipules below the attachment point of the leaf stalks and canoe-shaped keel with beak. The surface of their pollen grains reticulated with raised exine [43].

Interspecific crosses made between the two species have not been successful [44-46]. On the basis of a study on isoenzyme

variation in the genera *Phaseolus* and *Vigna*, Jaaska and Jaaska [47] proposed to raise the section *Catiant* to the rank of a subgenus. All cultivated cowpeas are grouped under *V. unguiculata* subspecies *unguiculata*, which is subdivided into four culti groups, namely *Unguiculata*, *Biflora*, *Sesquipedalis*, and *Textilis* [38,48,49]. The classification and nomenclature of the wild taxa within *V. unguiculata*, however, is complicated, and could sometimes be confusing. More than 20 epithet names have been used in the past to designate wild taxa within *V. unguiculata* species complex. An extensive work on characterization of over 400 wild *V. unguiculata* accessions was conducted at International Institute of Tropical Agriculture (IITA) [50,51].

Botanical Description of Cowpeas

The crop is an herbaceous warm-season annual that is similar in appearance to common bean except that leaves are generally darker green, shinier, and less pubescent. Cowpeas also are generally more robust in appearance than common beans with better developed root systems and thicker stems and branches. Plant growth habit can be erect, semi-erect, prostrate (trailing), or climbing depending mostly on genotype, although photoperiod

and growing conditions can also affect plant stature. Most cowpea accessions have indeterminate stem and branch apices. Early flowering cowpea genotypes can produce a crop of dry grain in 60 days, while longer season genotypes may require more than 150 days to mature depending on photoperiod. Flowers are borne on racemes on 15-40 mm peduncles that arise from the leaf axils. Two or three pods per peduncle are common, and often four or more pods are carried on a single peduncle if growing conditions are very favorable. The presence of these long peduncles is a distinguishing feature of cowpea, and this characteristic also facilitates hand harvesting [52]. Cultivated cowpea seed weighs between 8 and 32 mg and ranges from round to kidney shaped. Pods are cylindrical and may be curved or straight, with between 8 and 15 seeds per pod. The seed coat can be either smooth or wrinkled and of various colors including white, cream, green, buff, red, brown, and black. Seed may also be speckled or patterned. Seeds of well-known cowpea types (Figure 1), such as "blackeye pea" and "pinkeye," are white with a round irregular-shaped black or red pigmented area encircling the hilum, giving the seed the appearance of an eye [52].



Figure 1: Seed color - Black, Red, Brown, White, Green (Singh, 2016).

Emergence is epigeal (similar to common bean and lupin), where the cotyledons emerge from the ground during germination. This type of emergence makes cowpea more susceptible to seedling injury, since the plant does not regenerate buds below the cotyledonary node. The open display of flowers in and above the canopy and the presence of extra floral nectaries contribute to the attraction of insects. Cowpea primarily is self-pollinating, but

out-crossing rates as high as 5% have been recorded and care needs to be taken to avoid outcrossing during the production of breeder and foundation seed, or unacceptable levels of "off-types" will result. Cowpea is a short-day plant, and many cowpea accessions exhibit photoperiod sensitivity with respect to floral bud initiation and development, while others are day neutral [53,54]. For some genotypes, the degree of sensitivity to photoperiod (extent of delay

in flowering) is modified by temperature [53,55]. In West Africa, selection for differing degrees of photosensitivity or differences in juvenility has occurred in different climatic zones such that pod ripening coincides with the end of the rainy season in a given locale, regardless of planting date, which is often variable due to the variable onset of wet seasons [56]. This attribute allows pods to escape damage from excessive moisture and pathogens. Photoperiod sensitivity, when appropriately deployed in a breeding program, can be valuable to ensure crop maturity after wet seasons or before drought or cold weather limits crop growth. However, it may constrain the direct usefulness of an otherwise desirable cultivar to a small area of adaptation or even to a specific season within this restricted area.

Cultivated cowpeas have been divided into five cultivar groups based mainly on pod and seed characteristics [57,58]. Cultivar group Unguiculata is the largest and includes most medium and large seeded African grain and forage type cowpeas. Cultivar group Melanophthalmus includes “black eye pea”-type cowpea with large, somewhat elongated seeds with wrinkled seed coats and fragile pods [59]. Cowpea (*Vigna unguiculata*) plant is erect or scandent or trailing or twining herb. Stem 1.-2.5 m long glabrous or sometimes sparsely covered with 0.8-1.0 mm long white hairs. Leaves 3-foliolate, terminal leaflet ovate, lateral leaflets obliquely ovate. Stipule ovate to lanceolate, medifixed, 15-18 x 4-5 mm. Inflorescence 8-10 flowered; flowers bluish white or pale white or pink, 2.5-2.7 mm in diameter, calyx tuberculate. Pods subterete, sub-compressed and glabrous or puberulate, 16-18 x 0.9-1.0 cm, pale yellow when mature. Seeds rounded, 10-16 per pod, smooth, pale yellow, 10x5x7 mm, aril slightly developed [60].

Members of cultivar group Biflora (also known as “catjang”) are common in India and characterized by their relatively small smooth seeds borne in short pods that are held erect until maturity. Cultivar group Textilis is a rather rare form of cowpea with very long peduncles that were used in Africa as a source of fiber. Cultivar group Sesquipedialis (known as “yardlong bean,” “long bean,” “Asparagus bean,” or “snake bean”) is widely grown in Asia for production of its very long (40 to 100 cm) green pods that are used as “snap” beans. Despite the striking differences in morphological characteristics among the cultivar groups, there are no practical barriers to hybridization or recombination between members of the different groups. The plant ranges from erect, sub-erect, prostrate and are all annuals. The leaves are trifoliolate with entire leaflets. Flowers join in clusters of 2 - 4 flowers and are white, yellow or violet [3,4].

As the plant is primarily self-pollinating, its genetic diversity within varieties is relatively low. Cowpeas can either be short and bushy (as short as 20 cm) or act like a vine by climbing supports or trailing along the ground (to a height of 2 m). The taproot can penetrate to a depth of 2.4 m after eight weeks. The size and shape of the leaves vary greatly, making this an important feature for classifying and distinguishing cowpea varieties.

Another distinguishing feature of cowpeas is the long 20 - 50 cm peduncles, which hold the flowers and seed pods. One peduncle can support four or more seed pods. Flower color varies through different shades of purple, pink, yellow, and white and blue. Seeds and seed pods from wild cowpeas are very small, while cultivated varieties can have pods between 10 and 110 cm long. A pod can contain six to 13 seeds that are usually kidney-shaped, although the seeds become more spherical the more restrict they are within the pod. Their texture and color are very diverse. They can have a smooth or rough coat and be speckled, mottled, or blotchy. Colors include white, cream, green, red, brown, and black, or various combinations [61]. Cowpea, (*Vigna unguiculata*), also called black-eyed pea or southern pea, annual plant within the pea family (*Fabaceae*) grown for its edible legumes. Cowpeas are typically climbing or trailing vines that bear compound leaves with three leaflets. The white, purple, or pale-yellow flowers usually grow in pairs or threes at the ends of long stalks. The pods are long and cylindrical and can grow 20-30 cm long, depending on the cultivar. The plants are heat-adapted and drought-tolerant [5]. Growth habit ranges from erect, determinate, non-branching type to prostrate or climbing, indeterminate, with profuse branching. It has strong tap root system with several lateral roots. Stems are cylindrical and slightly ribbed, twisting, sometimes hollow and glabrous. Stems may be green or pigmented (purple). Leaves are alternate, trifoliolate, with one symmetrical terminal leaflet and two asymmetrical leaflets. Petioles are 3 - 25 cm long with a swollen pulvinus at the base.

Inflorescence is an un-branched axillary raceme bearing several flowers at the terminal end of peduncles. The peduncles vary from 5 to 60 cm in length and are slightly twisted and ribbed. Calyx is longitudinally ribbed, tubular with 2 - 15 mm long subequal lobes. The corolla is papilionaceous with an erect standard petal spreading at anthesis. The pigmentation pattern of corolla varies from white to solid mauve with yellow spots near the base of the standard petal. The wings are adherent to the boat-shaped keel, enclosing the androecium and gynoecium. The stamens are diadelphous (9+1). Anthers are bright yellow. Ovary is monocarpellary, unilocular with many ovules. Pods are pendent or vertically attached to the raceme axis. They are mostly linear, although curved and coiled shapes are also found. The length of pods may vary from less than 11 to more than 100 cm [62]. Herbaceous legume which is grown annually. Taproot and abundant lateral roots spreading in a soil. Stem smooth, striate, hairy, purple shades and length: 3 m. Leaf dark green, lanceolate-ovate, shiny to dull and 10 cm long.

Flower is bell shaped, dirty yellow, white, pale blue, pink, or purple. Seeds are kidney shaped, Length: 6 – 12 mm. Seed color is green, red, white, cream, black, and buff brown. Pod shape is slightly curved and cylindrical, length: 6 to 10 inch. Pod color is green, purple or yellow. Flavor/aroma is nutty. Varieties/Types are black eye or purple eye peas, brown eye peas, crowder peas, cream, white acre type, clay types, and forage cultivars [7]. Cowpea

is an herbaceous legume which grows annually in a warm climate with adequate rainfall. It is the crop which grows well in the warm season, temperate zones and humid tropic. It prefers well drained, sandy soils or sandy loams. The plant grows up to 24 inches in height. The flower has got the shape of bell in the color of white, pink, dirty yellow, purple or blue. The leaves are dark green and 10 cm long with smooth, rhomboid, pubescent and shiny to dull appearance. The leaves are dark green with smooth, rhomboid, pubescent and shiny to dull appearance. The stem is 3 m long with smooth, straight, slender hairy and some shades of purple. The plant has got no branches at all. The plant has the taproot with an expansion of lateral roots in the soil. The parts of the plant which are edible are roots, green leaves, immature pods, seeds and green seeds. The pod is yellow, green or purple, slightly curved and cylindrical with 6-10 inch long. Each pod possesses 6-13 seeds. The seeds are white, green, cream, buff, brown, red and black. It has got the shape of kidney with 6 - 12 mm in length. It has got the flavor of nuts and the seed has got the lifespan of 5 years [2].

Objective of the Research

The objective of this research is to review the findings,

inferences, observation and opinions on researches conducted variability and heritability studies in cowpeas.

Cowpea germplasm diversity and conservation

Several countries grow cowpea as a vegetable crop. The most preferred types are the yard long cowpeas with fleshy tender pods, but these varieties need staking to keep pods from touching the ground and rotting, which involves extra cost and thus restricts the area under cultivation. Hence bush-type vegetable cowpea is required [63]. Major cowpea germplasm collections are conserved at International Institute of Tropical Agriculture, Ibadan, Nigeria with 15,872 accessions from 90 countries, at Griffins Georgia, USA with 7146 accessions from 50 countries and at Riverside, California, USA with 4876 accessions from 45 countries [64]. These gene bank represent the largest repertoires of cowpea biodiversity. In addition to cultivated accessions, IITA holds about 1818 accessions of wild relatives made available to the International Community for Research, Food and Agriculture. Within the two types of cowpea varieties-grain type and fodder type-there is wide variation for seed type, seed size, seed color, (Figure 2) hilum color and plant type [12,64].



Figure 2: Genetic variability in seeds of cowpea.

Individual samples from 36 farmers’ fields have shown from 1 to 11 seed types in cowpeas of early grain-type and from 3 to 7 seed types in the late fodder-type cowpeas. The varieties have local names that often describe their characteristics. The genetic diversity within each group of varieties is probably maintained by the farmers, to ensure stability under the harsh environmental conditions in which cowpea is grown [65]. Genetic diversity is the

foremost basic requirement for a successful breeding programme. A quantitative assessment of the genetic divergence among the collection of different traits towards the genetic divergence provides essential and effective information to breeder in his hybridization programme and there by genetic improvement of yield [66]. Some examples of diversity trials carried out by researchers are as follows:

Cowpea Diversity Researches

Genetic diversity refers to the range of different inherited traits within a specie. In a species within high genetic diversity, there would be many individuals with a wide variety of different trait.

Forty cowpea genotypes were evaluated for 18 quantitative characters to estimate the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes were grouped into six clusters. The cluster strength varied from single genotype (Clusters III, IV and V) to 25 genotypes (Cluster I). Clusters IV and VI had high inter cluster distance. Clusters II, III and I had maximum 100-seed weight, number of seeds per pod and seed yield respectively. Cluster IV had maximum seedling vigor index, germination per cent, peduncle length, number of clusters per plant and number of primary branches. The genotypes from clusters IV and VI may be inter crossed to obtain high variation [67]. Genetic divergence using D^2 analysis was carried out in 50 diverse genotypes of cowpea. All the 50 genotypes were grouped into twelve clusters. Cluster I was largest comprising of twenty-seven genotypes followed by Cluster II with twelve genotypes, cluster IV with three genotypes, and cluster III, V, VI, VII and VIII, IX, X, XI, XII were represented each by single genotype. Intra-cluster D^2 values ranged from 0 to 38.06. The inter-cluster D^2 values ranged from 44.08 to 276.55. The maximum inter cluster distance was observed between VII and XII clusters followed by clusters IV and XII and cluster X and VII. The maximum contribution towards genetic divergence is by days to 50% flowering (25.22%); followed by plant height (12.24%) and biological yield per plant. Hence it can be concluded that the diverse parent belonging to different cluster should be involved in the hybridization programme based on their merits of characters. Beside this more number of germ plasm should be incorporated in hybridization programme [68].

Field experiments were conducted at the Agricultural Research Council-Roodeplaat Vegetable and Ornamental Plant Institute in South Africa, in 2011 and 2012, to estimate the level of phenotypic variability among a collection of 25 cowpea genotypes. Analysis of variance for the phenotypic traits revealed that differences among genotypes were highly significant for all traits. This indicated the high level of genetic variability among the cowpea genotypes studied. Genetic and phenotypic coefficient of variation, and broad-sense heritability were estimated for all phenotypic traits. The first five principal components showed 79.30% of the total variability among the genotypes. Pod length, leaf area, leaf area index and number of seeds per plant contributed mainly to PC1, while leaf number, plant height, dry biomass and fresh biomass contributed mainly to PC2. Cluster analysis of the phenotypic traits resulted in five distinct groups of genotypes. The phenotypic traits therefore provide a useful measure of genetic distances among the cowpea genotypes and will enable the identification of potential parental materials for future breeding efforts. Genotypes IT93K129-4, Fahari, Glenda and Veg cowpea Dakama Cream were associated with desirable grain yield characteristics

and are recommended as suitable parental lines for improvement of grain production. Genotypes 5431, Tatro mix, Kisumu mix and Okalulenu were identified to possess good vegetative traits and are also recommended for use as suitable parents when breeding for leafy vegetable or for fodder production as reported by Abe et al. [69].

The genetic diversity of cowpea was analyzed, and the population structure was estimated in a diverse set of 768 cultivated cowpea genotypes from the USDA GRIN cowpea collection, collected from 56 countries, by Xiong et al. [70] Genotyping by sequencing was used to discover single nucleotide polymorphism (SNP) in cowpea and the identified SNP alleles were used to estimate the level of genetic diversity, population structure, and phylogenetic relationships. Based on the model-based ancestry analysis, the phylogenetic tree, and the principal component analysis, three well-differentiated genetic populations were postulated from 768 worldwide cowpea genotypes. According to the phylogenetic analyses between each individual, region and country, we may trace the accession from off-original, back to the two candidate original areas (West and East of Africa) to predict the migration and domestication history during the cowpea dispersal and development. To our knowledge, this is the first report of the analysis of the genetic variation and relationship between globally cultivated cowpea genotypes. The results will help curators, researchers, and breeders to understand, utilize, conserve, and manage the collection for more efficient contribution to international cowpea research [70].

Genetic diversity in cultivated crops by Wamala et al. [71] indicated gene pool richness. The study was conducted by Masinde Muliro University to evaluate genetic diversity in 19 cowpea accessions from Kenya national gene bank of which the accessions clustered into two major groups. High divergence was observed between accessions from Ethiopia and Australia and those from Western Kenya. Upper Volta accessions were closely related to those from Western Kenya. Low variation was observed between accessions from Eastern and Rift Valley than those from Western and Coastal regions of Kenya. Diversity obtained in the study can further be exploited for the improvement of cowpea in Kenya as a measure of food security Joghande et al. [72].

A study was undertaken on 30 genotypes of cowpea by Joghande et al. [72] to understand the extent of genetic diversity through sixteen traits. Mahalanobis's D^2 analysis established the presence of wide genetic diversity among these genotypes that revealed six Clusters groups. The cluster I was largest and consisted of 21 genotypes; followed by cluster III of 5 genotypes and clusters II, IV, V and VI consisting of only one genotype each. Maximum inter cluster D^2 value was observed between VI (6987.85) and III (4806.87), indicating that the genotypes included in these clusters had maximum divergence. The diversity among the genotypes measured by inter-cluster distance was adequate for improvement of cowpea by hybridization and selection.

Ogbuagu and Ndem [73] evaluation and identification of genetic variation pattern in 30 cowpea accessions showed that, the first four principal components accounted for 93.75% of the total genetic divergence. Furthermore, cluster analysis revealed that, accessions were grouped not necessarily based on geographical location but genetics. Selection for high yielding accessions were grouped not necessarily based on geographical location but genetic. Selection for high yielding accessions should be done on cluster II as we recommend selection and hybridization of accessions from cluster I, II, and III for optimal benefits.

Genetic variation and morphological diversity by Viswanatha and Yogeesh [74] in 169 cowpea genotypes using Mahalanobi's D^2 analysis revealed that, the genotypes were grouped in to eight cluster of which maximum intra cluster distance was exhibited by cluster VI and minimum by cluster II, the inter cluster distance was maximum between cluster II and IV. The genotypes from cluster II and IV had high and low cluster means for majority of the characters.

Genetic variability study on 27 genotypes of cowpea by Ramesh et al. [75] using D^2 analysis grouped the genotypes in to six clusters. Cluster I, was the largest having 11 genotypes, whereas cluster IV was smallest with 1 genotype. The highest value D^2 distant help breeders in selection of the parental line for initiating any hybridization program. Thus, the lines from cluster v and cluster I gave the maximum variation, followed by the closeness made between the lines of cluster VI and IV between cluster V and cluster I and cluster III and IV. Nelia et al. [76] carried out a study to determine the extent of genetic diversity present among a collection of cowpea accessions from Zambia and Malawi using phenotypic traits and single nucleotide polymorphism (SNP). The SNP markers revealed gene diversity and polymorphism information content of 0.22 and 0.17 respectively, showing that, the tested cowpea accessions were genetically diverse.

Furthermore, the test genotypes were classified in to four genetic groups. Genetic divergence study of cowpea genotypes by Sanjeev et al. [77] revealed that all selected genotypes displayed marked divergence. Among the five clusters obtained, cluster I consisted 8 genotypes, cluster II had 3, cluster III had 11, cluster IV had 9 and cluster V had 2 genotypes. Shrikant et al. [78] genetic variability study in cowpea using Mahalanobi's D^2 statistics on 30 cowpeas and results grouped the genotypes in to four clusters and a maximum number of genotypes was observed in cluster I with 16 genotypes, followed by cluster II and III with 8 genotypes each and cluster IV with solitary genotype.

Genetic Variability Research in Cowpea

Cowpea Genetic Variability Researches

Genetic variability is the tendency of individual genetic characteristics in a population to vary from one another. It may also refer to the potential of a genotype to change or deviate when exposed to environmental or genetic factor. The presence

of considerable amount of variability in the basic genetic material ensures better chances of evolving desired plant types. A clear understanding of variability of various characters of the breeding materials is an asset to the plant breeder for selecting superior genotypes on the basis of their phenotypic expression. In this regards estimates of genotypic and phenotypic variance for various quantitative characters along with heritability and genetic advance expected by selection for yield and its components are useful in designing an effective breeding programme [79]. The estimates of heritability, phenotypic coefficient of variation, genotypic coefficient of variation and genetic advance are helpful to determine the method of selection to improve a particular plant population for a specific trait [80]. The magnitude and type of genetic variability help the breeder(s) to determine the selection criteria and breeding schemes to be used for improvement purposes as reported by Omoigui et al. [81].

The Genotypic Coefficient of Variation (GCV) is a statistical measure used in plant breeding to assess the extent of genetic variability in a population. It quantifies the percentage of variation in a trait that is attributed to genetic differences among individuals. In essence, it helps breeders evaluate the genetic potential for improvement in specific traits within a plant population. Phenotypic Coefficient of Variation (PCV) in the other hand, is a statistical measure used to assess the extent of variation in a trait within a population, considering both genetic and environmental factors. It represents the ratio of the phenotypic standard deviation to the phenotypic mean, expressed as a percentage. In essence, PCV quantifies the overall variability in a trait observed across all individuals in a population, including the influence of both genetic and environmental factors [82,83].

Furthermore, high GCV is an indication of the possible scope for improvement through selection procedure Chauhan [84] and Ravish et al. [80]. Similarly, high PCV is helpful to determine the method of selection to improve a particular plant population for a specific trait Omoigui, et al. [81] and Ariyo [85]. Several GCV and PCV revealed thus; Imandi and Depanshu [86] trial on genetic analysis on cowpea revealed high GCV and PCV for pod length (50.20% and 50.21%), plant height (40.78% and 40.80%), pods/plant (43.50% and 43.55%), seeds/plant (39.65% and 39.68%), and leaves/plant (35.95% and 37.79%).

Study on genetic variability in cowpea by Ramesh et al. [75] revealed high GCV and PCV for plant height (49.79% and 51.41%), pod yield/plant (49.59% and 50.81%), pod yield (46.16% and 48.35%), pods/plant (43.78% and 45.16%), nodes on main stem (39.31% and 41.17%), and branches/plant (36.27% and 38.83%). Abiola and Alaba [87] genetic variability study of 25 accessions of cowpea indicated high GCV and PCV for leaves/plant (347.20% and 403.44%), seeds/plant (87.13% and 89.09%), seed yield/plant (78.83% and 80.99%), pods/plant (73.63% and 75.74%), plant height (37.35% and 43.72%), peduncle length (38.42% and 40.03%), main branches (30.54% and 31.52%), and 100 seed weight (30.56% and 30.89%).

Study by Shivam et al. [88] on 12 divergence varieties of cowpea revealed high magnitude of GCV and PCV for economic yield (71.97% and 81.76% respectively), biological yield, (61.59% and 79.96% respectively), harvest index (19.78% and 35.53% respectively) and plant height (19.52% and 25.86% respectively). Hermes et al. [89] heritability, genetic gain and correlation study in cowpeas revealed high PCV and GCV for yield (34.42% and 22.81% respectively), 100 seed weight (22.69% and 22.47% respectively), pods/plant (18.36% and 13.60%), nodes on main stem (12.67% and 10.66%) and peduncle length (15.52% and 6.78%). Shrikant et al. [78] variability study in 30 genotypes of cowpea revealed high GCV and PCV for pods/plant, lignin content, test weight, and seeds/plant. Thus; these characters provide a good source of variation and hence are useful in crop improvement programme in cowpea. Tekle et al. [90] genetic variability study in Mung bean showed high estimates of GCV and PCV for terminal leaf length (14.23% and 25.5%), plant height (18.41% and 23.8%), branches/plant (15.83% and 23.5%), pods/cluster (11.30% and 28.7%) and pods/plant (17.02% and 35.9%).

Estimate of genetic parameters study of forty-two genotypes of cowpea by Hermes et al. [91] revealed that days to harvest recorded the high GCV and PCV (45.32 and 50.05 respectively), 100 seed weight (41.14 and 41.28 respectively), and pods/peduncle (29.22 and 30.59 respectively). Maletsema et al. [92], genetic variation studies in cowpea genotypes revealed high GCV and PCV were obtained in seed/plant (116.63 and 54.67 respectively), pod weight/plant (53.62 and 62.93 respectively), grain yield (43.85 and 46.87 respectively) and pod/plant (40.69 and 44.16 respectively). In a study of 10 cowpea accessions by Manggoel et al. [93] revealed high PCV and GCV for days to 50% flowering, flowers/plant, peduncles/plant, pods/plant, 100 seed weight and grain yield. Omoigui et al. [81] carried out a screen house experiment at Samaru Zaria in 1999 and 2000 dry seasons to estimate the genotypic variability of some reproductive traits and their heritability in 9 cowpea varieties. Results showed that, there was considerable variation among cultivars for duration of reproductive phase and rate of photosynthate partitioning this information showed that there is sufficient genetic variance to warrant selection for improvement in the cowpea genotypes studied.

Idahosa et al. [94] evaluated eight cowpea genotypes and the results indicated substantial variation for all characters studied namely: pod length, pod weight, seeds/pod and 100 seed weight. Abe et al. [69] in their genetic variability study in twenty-five cowpea revealed high level of variation among all the cowpea genotypes studied with respect to pod length, leaf area, leaf area index and number of seeds/plants. Others traits are: leaf number, plant height, dry biomass and fresh biomass. Ten (10) cowpea genotypes trials by Adeigbe et al. [95] for genetic variability and stability analysis study revealed that the genotypes differed significantly with respect to days to first flowering, plant height at 4 weeks, pod length, days to first ripening, peduncle length/

plant and branches/plant. Manggoel et al. [93] evaluated ten cowpea genotypes in a genetic variability study and results showed significant variability for days to 50% flowering, number of peduncles/plants, for days to flowers/plant, pods/plant, seeds/pod, pod length, and 100 seed weight. Nwosu et al. [96] genetic variability and heritability study in five cowpea genotypes, observed significant variances for all the 16 traits evaluated.

Archana and Rajesh [97] variability study revealed that all the genotypes differed significantly for all the traits; which include: plant weight, number of pods/plants, and numbers of branches / plant. These indicated preponderance of additive gene effect for the expression of these traits. Ogbaugu and Ndem [73] evaluation and identification of genetic estimates in thirty cowpea accessions of cowpea revealed that, number of seeds/pods, 100 seed weight, pod length, days to 50% maturity, seed yield, number of leaves/plants significantly contributed to genetic variability among the genotypes. Abe et al. [69] genetic variability study in twenty-five cowpea genotypes recorded high level of genetic variability among the cowpea for pod length, leaf area, leaf area index, and numbers of seeds/plants.

Ramnarayan et al. [98], variability study of fifteen diverse cowpea genotypes observed significant variance for all the traits in number of flowers/clusters, number of pods/plants, number of branches, pod weight and pod length depicting possible selection for improvement. Khanpara et al. [99], genetic variability and heritability studies in sixty vegetable cowpea analysis revealed significant differences among the genotypes for 12 characters in green pod yield/plant, pod weight, number of pods/plant and plant height. Antonio et al. [100], genetic variability and selection of early cowpea genotypes showed a wide variation for days for flowering, days to maturity, plant height, pod length, seeds/pod, grains/plant, 100 seed weight and total weight. Genetic variability study by Kwon-Ndung and Kwala [101] for 80 cowpea genotypes evaluated revealed significant differences among all entries studied. Joghande et al. [72], thirty cowpea genotypes were evaluated in genetic variability trial and observed significant differences among genotypes for branches/plant, pod yield/plot, pods/plant and seeds/pod. One hundred and eighty genotypes of cowpea were evaluated in a genetic variability and heritability study by Manju and Jayamani [102]. Results indicated that significant differences existed among the genotypes for number of pods/plants, number of clusters/plants, 100 seed weight and single plant yield.

Patel et al. [103], genetic variability and heritability study in cowpea evaluated 32 genotypes and the results observed distinct variations for days to 50% flowering, branches/plant, clusters/plant, pod length, seeds/pod, pods/plant, plant height at harvest and furthermore wide variation was also observed for green pod yield/plant and green pod yield/hectare. Genetic variability and heritability study for yield component of twenty-four cowpeas by Verma et al. [104], revealed wide range of variability for all the

traits except number of branches/plant and pod width. Reshma et al. [105] genetic variability and heritability study in cowpea evaluated 15 genotypes and the results revealed significant differences for all the traits, seed yield/plant, seed index, number of pods/plant and pod length and as well number of primary branches/plants.

Study on genetic variability in cowpea by Ramesh et al. [75] revealed significant differences among all the genotypes for plant height, number of branches/plants, days to first flowering, number of pods/clusters, pod length, pod yield/plant, number of seeds/pod and numbers of pods/plant. Imandi and Deepanshu [86], genetic analysis in twenty-seven cowpea genotypes showed significant variation for all the traits studied, which includes: number of seeds/plants, plant height, days to first flowering, leaves/plant and pod yield/plant. Magashi et al. [106] in a genetic variability study of some cowpea traits observed highly significant differences for plant height, number of days to 50% flowering, number of days to maturity, number of pods/plants, pod length, number of seeds/plant and number of branches/plants.

Nkhoma, et al. [76] in assessing the genetic diversity of cowpea genotypes, revealed wide differences among all the traits which includes: days to flowering, days to maturity, pod length, pods/plant, seeds/pod, seed size, 100 seed weight and grain yield. Chaudhary et al. [107], genetic variability analysis among thirty cowpea accessions showed highly significant differences in all the traits evaluated, which include: seed yield, number of pods/plants, seed yield/plant, number of seeds/plants, number of branches/plants, plant length, plant height and days to 50% flowering.

Ugale et al. [108] studied 21 cowpea genotypes for their genetic variability and the results revealed remarkable differences among all the genotypes with respect to plant height, number of primary branches/plants, days to 50% flowering, pods/plant, seed/pods, pod weight, pod length, pod width, seed weight, pod yield/plant and pod yield/hectare. Shivam et al. [88] study on genetic variability and heritability for twelve cowpea traits observed highly significant variations for all the traits evaluated, which include: pod yield/plant, plant height, days to 50% flowering and days to first fruit. Abiola and Alaba, [87] evaluated 25 cowpea genotypes on genetic variability analysis and revealed highly significant differences among all the genotypes in emergence percentage, plant height, number of main branches, number of leaves, days to first flowering, pods/plant, seeds/pod, seeds/plant, 100 seed weight, and seed yield/plant. Pandiyan et al. [109], genetic variability study in twenty-eight cowpea genotypes observed wide range of variability for various traits studied were: days to 50% flowering, plant height, number of pods/plants, number of clusters/plants, number of seeds/plant and seed weight.

Sanjeev et al. [77], genetic divergence study for yield and quality traits in cowpea observed marked differences among all the genotypes studied in the following traits: plant height, number

of branches/plants, days to 50% flowering, number of pods/clusters, plant length, pod diameter, number of positions /plants, 100 seed weight and pod yield/plant. Significant variation was recorded for all the traits evaluated in a genetic variability studies in cowpea by Santonu et al. [110] in the following traits: plant height at maturity, number of flowers in florescence, primary branches/plant, leaf area, pods/plant, pod weight, grains/pod, pod length, biological yield /plant, area of primary leaf, 100 grain weight and grain yield/plant. Hermes et al. [89], heritability, genetic gain and correlation study in thirty cowpea genotypes observed a wide significant difference for all the traits evaluated, which includes: days to first flowering, number of pods/plants, pods/peduncle, peduncle length, nodes on main stem, grain length, grain width and 100 seed weight and grain weight.

Tekle et al. [89], variability and genetic advance study in sixty cowpea genotypes analysis observed highly significant differences in days to 50% flowering, days to maturity, petiole length, leaf length, peduncle length, plant height, primary branches/plant, pod length, pods/cluster, pods/plant, seeds/pod, seed yield/plant, 100 seed weight, seed yield, biomass yield and harvest index. Shrikant et al. [78] studied 30 cowpea genotypes in a genetic variability trial, the results showed wide variations in all the traits i.e., days to 50% flowering, days to maturity, leaf length, leaf width and nodes/stem. Others include: number of main branches, pods/plant, pod length, seeds/pod and seed yield/plant. Genetic variability and advance study by Gaiwal et al. [111] in cowpea population revealed remarkable variation in all the traits for yield/plant, pods/plant, plant height, primary branches, days to maturity, pod length, 100 seed weight, and grain yield.

Sudhamani et al. [112], genetic parameter trial of some cowpea genotypes and results showed significant variation for all the character studies i.e. plant height, plant length, number of pods/plants, 100 seed weight, seed yield/plant, number of clusters/plants, number of branches/plants, number of pods/plant and number of pods/clusters. Genetic gain study by Hermes et al. [89], among 30 cowpea genotypes showed sharp variation on the traits evaluated which include: days to flowering, pods/plant, pods/peduncle, nodes on main stem, grain length, grain width, 100 seed weight and yield. Datthi et al. [113], study on genetic variability in thirty-three cowpea genotypes revealed distinct variation for all the traits (plant height, number of nodes, days to first pod formation, days to first flowering, peduncle/plant and pods/plant). Genetic variability study on yield traits on grain yield in forty-five cowpea genotypes by Kavyasshree et al. [114] showed sufficient variability for days to maturity, days to 50% flowering, pod length, 100 seed weight, seeds/pod and yield/plant.

Heritability and Genetic Advance in Cowpea

Lush [115] defined heritability in broadness as the ratio between genotypic variance to phenotypic variance. The genotypic variance includes the additive, dominance and the epistatic effects. He further defined narrow sense heritability as the ratio

of additive genetic variance to the phenotypic variance [116]. Although heritability value of a trait indicates the effectiveness of selection based on the phenotypic expression. The genetic gain that can be obtained for a particular trait through selection is the product of its heritability, phenotypic standard deviation and selection differential [117].

The genetic advance is more useful in predicting the actual value of selection as shown by Johnson et al. [118]. The concept of heritability which specify the proportion of the total variation among a species due to genetic component, combined with genetic advance are good parameters for determining gene action involved in the inheritance of any traits and by extension help in deciding the best breeding method to apply for improving such trait. High heritability indicates less environmental influence in the observed variation [119], while high heritability accompanied by high genetic advance is an indication of additive gene action for such trait making its most amenable to selection [120]. Singh et al. [121] observed significant mean squares for all traits revealing adequate variability among genotypes studied. Results revealed high phenotypic and genotypic coefficient of variation coupled with high heritability and genetic advance for plant height, stem weight, leaf weight, biological yield, dry matter yield and green fodder productivity; indicating predominance of additive gene effect in the expression of these traits.

Experiment carried out by Chattopadhyay et al. [122] found out all the eight characters under study differed significantly among the genotypes. Furthermore, high to moderate GCV and PCV values were found for pods/plant, pod yield/plant, pod weight, seeds/pod and pod length. Higher estimates of heritability and high genetic advance for pods/plant, pod yield/plant, pod weight, seeds/pod and pod length were observed. High heritability was also observed by Abe et al. [69] in 25 cowpea genotypes for the estimates of all phenotypic traits studied; such as days to 50% flowering, pods/plant, harvest index, seeds/pod, 100 seed weight, yield/pod, pod length, leaf area, leaf area index, number of seeds/plants, leaf number as well as plant height including fresh and dry biomass. Adewale et al. [123] conducted heritability study for grain yield in eleven cowpea components and revealed high heritability in days to 50% flowering, days to 95% maturity, seeds/pod, 100 seeds weight, grain yield, dry fodder yield and pod length. Adeigbe et al. [95], genetic variability trial among ten cowpea genotypes revealed high heritability for all the traits evaluated such as plant height at 4 weeks, days from planting to first ripe, days to first flowering, peduncle length/plant, pod length, peduncle/plant, branches/plant including number of pods/plants. These indicated that meaningful selection of genotypes is possible for cowpea improvement.

Genetic variability and heritability study of ten cowpea genotypes yield components showed high heritability for all the traits studied (days to 50% flowering, peduncle/plant, pods/plant, number of flower/plants, seeds/plant, plant length, 100 seed

weight, seeds/pod and grain yield). This indicated that there is possibility of cowpea improvement through selection [93]. Nwosu et al. [96] genetic variability, heritability, and genetic advance in six cowpea genotypes in two locations revealed high heritability and high genetic advance which attributed to high additive gene effect for clusters/plant, pods/plant, peduncle length, pod length, dry pod weight, 100 seed weight, seeds/pod and number of seeds/plants including seed yield/plant.

Archana and Rajesh [97] assessed 30 cowpea genotypes and recorded high heritability coupled with high genetic advance for plant height, number of pods/plants and numbers of branches/plant. Khanpara et al. [99] genetic variability and heritability trial in sixty vegetable cowpea and results revealed high heritability along with high genetic advance for branches/plant, plant height, pod length, pod width, number of pods/plants, pod weight, number of pods/clusters, 100 fresh seed weight, green pod and yield/plant. This showed that these traits are mainly governed by additive gene action and can response for further improvement. Genetic heritability study of 15 cowpea genotypes by Ramnarayan et al. [98] recorded high estimates of heritability and high genetic advance for flower clusters/plant, pods/plant, pod length, pod weight, pod yield/plant and yield/ha.

Kwon-Ndung and Kwala [101] heritability study in 80 cowpeas observed high heritability and genetic advance for days to flower initiation and termination, branches/plant, pods/plant, pod length, seeds/pod, 100 seed weight and grain yield. Viswanatha and Yogeesh [74] conducted genetic variation and heritability study in 169 cowpea genotypes and recorded high heritability and high genetic advance for days to 50% flowering, number of branches/plants, number of pods/plants, seeds/plant, pod length, seeds/pod and seed yield/plant. Joghande et al. [72], heritability study in 30 cowpea genotypes revealed high heritability and genetic advance for branches/plant, pod yield/plot, total number of pods/plants, seeds/pod, plant height, number of green pods/clusters, and seed yield/plot. Results indicated the possibility of effective selection for cowpea improvement. Manju and Jayamani [102], genetic variability and heritability study among 180 cowpea genotypes of cowpea revealed high heritability and genetic advance for plant height, number of racemes/plants, peduncle length, number of pods/plants, number of clusters/plants, pod length, 100 seed weight, and single plant yield/plant.

These traits could be utilized in breeding programs for the improvement of cowpea. Patel et al. [103], heritability study for thirty-two cowpea genotypes; observed high heritability and genetic advance for days to 50% flowering, branches/plant, pods/plant, plant height at harvest and green pod yield/plant, which indicated that phenotypic selection would be effective for genetic improvement in this trait. Verma et al. [104] genetic variability, heritability and genetic advance study for yield components of cowpea genotypes and revealed high heritability values for plant height, seed yield/plant, pods/plant, branches/plant, flowers/

cluster, pods/cluster and percent pod set. Other traits include: days to harvest, pod length, pod weight, seeds/pod, 100 seed weight and pod yield/plant. This indicates the presence of a weak or slight environmental influence and prevalence of additive gene action in gene expression.

Furthermore, Reshma et al. [105], evaluated 15 cowpea genotypes in a genetic variability, heritability and genetic advance study and found high heritability estimates for plant height, yield/plant, pods/plant, pod length and 100 seed weight thereby indicating effectiveness for improvement. Genetic heritability study in 27 cowpea genotypes by Ramesh et al. [75], revealed high heritability coupled with high genetic advance as percent of mean for pod yield/plant, plant height, pods/plant, number nodes on the main stem, first flowering nodes, branches/plant and peduncle length. Other traits include: pods/cluster, days to first picking, pod length, pod weight, seeds/pod and pod diameter. These indicated the preponderance of additive gene action governing the inheritance of these traits and it offers the best possibility of improvement of these traits through simple selection procedure.

Imandi and Deepanshu [86], genetic variability in 27 cowpea genotypes and revealed high estimates of heritability and high genetic advance for plant height at flowering and maturity, branches/plant, pods/plant, leaves/plant, number of nodes/plants, pod length and seeds/plant. Genetic variability and heritability study in 30 cowpea genotypes by Chaudhary et al. [107] recorded high heritability coupled with high genetic advance estimates for seed yield/plant, pods/plant, seeds/pod, pod length, seed yield/plant, test weight and leaf area/plant; which specifies that, these characters were govern by additive gene action of polygene and might be considered for simple selection criteria. Study by Ugale et al. [108] on high heritability and high genetic as percent mean among 21 cowpea genotypes was recorded for plant height, branches/plant, pods/plant, pod length and pod yield/ha. Shivam et al. [88] study on genetic variability and heritability for 12 genotypes of cowpea showed high heritability and high genetic advance for plant height, pods/plant, green and dry pod length, biological yield, seeds/pod, 100 seed weight and pod yield/plant.

Abiola and Alaba [87] evaluated 25 cowpea genotypes on genetic variability, heritability and genetic advance study and results revealed high heritability estimates for all the traits evaluated for plant height, number of branches, number of leaves, peduncle length, number of pods/plants, plant length, seeds/pod, seeds/plant, 100 seed weight and seed yield/plant. Pandiyan et al. [109] genetic variability and heritability study on 40 cowpea genotypes recorded high heritability and genetic advance estimates for plant height (43.88 and 5.14), number of pods/plants, (32.68 and 2.74) and number of seeds/pod (48.96 and 6.34). Santonu et al. [110] on genetic variability and heritability in 10 cowpea genotypes revealed high heritability and high genetic

advance as percent of mean for plant height, area of primary leaf, leaf area, pod length, pod weight, pods/plant, pod yield/plant and seed yield/plant. Heritability and genetic gain study by Hermes et al. [89], who evaluated 30 cowpea genotypes and observed high heritability and high genetic gain estimates for number of pods/plants, nodes on main stem, 100 seed weight, and grain yield.

Tekle et al., [89] worked on 60 mung bean genotypes and recorded high heritability estimates and genetic advance for peduncle length, plant height, primary branches/plant, seeds/pod, seed yield/plant and harvest index. Shrikant et al. [78] variability study in 30 genotypes of cowpea revealed high heritability and high genetic advance for days to 50% flowering, leaf width, nodes on main stem, branches/plant, pods/plant, pod length and seeds/pod. Gaiwal et al. [111] in their genetic variability study revealed high heritability and high genetic advance values for days to maturity, plant height, primary and secondary branches/plant, 100 seed weight and grain yield/plant. Hermes et al. [89] trial on 15 cowpea genotypes recorded high heritability and high genetic advance value for pods/plant, grain length and width, nodes on main stem, 100 seed weight and grain yield (kg). Ansh et al. [124] conducted genetic variability and heritability trial on 36 cowpea genotypes and obtained high heritability estimates and high genetic advance as percent mean for branches/plant, pods/plant, nodes/plant on main stem, pod length and 100 seed weight. Others includes pod yield/plant, pod yield/plot and pod yield/ha.

Traditional Breeding Methodologies and Limitations

Being self-pollinated, cowpea cultivar development has benefited from the breeding methodologies applicable to this group of crops. Many cultivars were obtained at the beginning of the breeding programs using mass selection and pure line approaches. Landraces collected from farm fields were evaluated and single plants found to be of good performance were selected. In the case of mass selection, seeds from these plants were bulked and grown to produce improved populations where further selections could be repeated several times. For pure-line breeding, the seeds from each selected plant were sown as progeny rows. Seeds of the best rows were evaluated in replicated yield trials and superior lines selected to constitute new improved cultivars.

Because of the limited genetic variability associated with these two breeding approaches, segregating populations were produced from single or multiple crosses between two or more lines. Depending on the aim of the breeding program, the segregating populations were handled in a number of ways. The pedigree method of breeding is used largely in many cowpea breeding programs. This method has proved suitable for the short-term objective of developing cultivars with new combinations of horticultural characteristics and disease resistance [125].

Another method that is commonly used in cowpea breeding programs is the backcross breeding method which has proved to be useful for transferring single resistance genes for specific production constraints into cowpea lines that have good yield performance or are preferred by farmers, but susceptible to or lacking this particular trait. To reduce the time and efforts for record keeping associated with pedigree method, breeders have also used bulk population method. In this method of breeding plants in the segregating populations are harvested in bulk through several generations under natural or artificial conditions. IITA often performs a combination of these conventional breeding methods. Fery [125] reported that a combination of backcross-pedigree breeding method has been used in some programs to transfer desired traits from relatively un adapted genetic backgrounds into well-adapted commercial cultivars.

Despite the progress achieved through traditional breeding methods, there are certain limitations associated with them. Sources of resistance to key production constraints such as insect pests, mainly the pod borer and pod sucking bugs, show low levels of expression in cowpea germplasm lines and cultivars. Unfortunately, a wild cowpea relative *Vigna vexillata* (L.) A. Rich which has good sources of resistance genes to these pests is not cross compatible with the cultivated lines. This has prevented the transfer of the resistance genes into cultivated cowpea. In addition, the traditional cowpea breeding approaches require up to a decade or more to develop improved cultivars largely due to the need to employ sequential and repeated phenotypic evaluations and performance trials [126]. These authors pointed out that in many cases, complex, specialized conditions, techniques and skills are needed to assess phenotypes for selection.

The disadvantages of traditional breeding are that it takes often many years [127] and effort is required and it may not produce the desired result (*cropimprovement.learn.genetic.utah.edu*). Some traits are tricky to manipulate by traditional breeding, for example drought resistance is influenced by variations in multiple genes, each of which may have a very small effect. Making a plant drought resistance requires generating offspring with certain gene combinations that may form only rarely [64,126,128].

With the advent of recent advances in biotechnology and genomics, cowpea improvement can be made more efficient [64]. Molecular marker - assisted breeding (biotechnology) is much more efficient than traditional breeding, because only the plants that carry the desired allele are grown and evaluated. Marker Assisted Breeding that entails Polymerase Chain Reaction (PCR); uses markers that are linked to traits or to estimates the genotypic effects instead of the phenotypic measurement alone. This method provides a powerful and potential cost and time saving avenues to increase the rates of genetic gain in plant breeding programmes [126].

Marker assisted breeding (MAB) is much faster than traditional breeding and it can be used for traits like drought tolerance that involves variations in multiple genes. However, it can still take

years. MAB looks a lot like Traditional Breeding, but instead of looking at the offspring's "phenotypic" - like disease resistance or drought tolerance, you look for short segment of DNA (or markers) from the offspring when seedlings are tender and using PCR to analyze at molecular level. Any seedlings that do not have desired marker(s) can be eliminated. There are still limitations to MAB because it is not practical in tree plants that takes longer time to mature and produce seeds [129-131].

Trans genetic Technology (TT)

TT is much more precise than either TB or MAB. It can be used to insert just the gene that you are interested in; while leaving all of the rest of the plant's genes intact. However, it does require a thorough up-front understanding of the gene that is being transferred; as well as testing of the product to ensure that it is functioning as intended. Since you are replacing just one gene, you do not have to back-cross to get rid of any extra undesired genes. And with no breeding required, this method works on plants like trees, which have very long reproductive cycles as well as between species that cannot interbreed naturally - even organisms other than plants. TT is faster than other methods, for it is helpful for staying ahead of pests.

Conclusion

Findings obtained from the analysis of variance Tables by the various researchers in this review work revealed highly significant differences in the following traits: pods/plant, branches/plant, plant height, pod length, 100 seed weight, seeds/pod, days to 50% flowering, pod weight, days to maturity and grain yield [77,87,93,106,107]. Furthermore, the following traits recorded high heritability and genetic advance; pods/plant, plant height, pod length, branches/plant, and 100 seed weight. Others includes seeds/pod, seed yield/plant, peduncle length, nodes on main stem including grain yield as recorded by the following researchers: Khanpara et al. [99], Joghande et al. [72], Kwon Ndung and Kwala [101], Ramesh et al. [75], Verma et al. [104], Abiola and Alaba [87] and Ansh et al. [124].

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