GENETIC STUDIES ON SEED COAT TEXTURE AND COOKING TIME IN SOME VARIETIES OF COWPEA (*Vigna unguiculata* (L.) Walp.)

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CERTIFICATION

This is to certify that this thesis has been examined and approved for the award of the degree of **DOCTOR OF PHILOSOPHY in CYTOGENETICS AND PLANT BREEDING.**

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DECLARATION

I hereby declare that this work is the product of my own research efforts; undertaken under the supervision of Professor O.P. Ifenkwe and has not been presented elsewhere for the award of a degree or certificate. All sources have been duly distinguished and appropriately acknowledged.

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DEDICATION

This work is dedicated to my late mother Mrs. Evelyn Samuel Mashi who nurtured me through life with a love such as transcends all that is imaginable.

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ABSTRACT

Genetic studies on seed coat texture and cooking time in some varieties of cowpea (*Vigna unguiculata* (L.) Walp.) were carried out between August 14, 2000 and November 20, 2002 and August 2, 2001 and December 3, 2003 respectively. The experiments were carried out at the research and teaching farm, Federal University of Technology, Yola, Adamawa State. Randomized complete block design with five replications was used for the two experiments. Appropriate crosses were made among eight cowpea varieties with four types of seed coat texture in order to study inheritance pattern of seed coat texture. Seed coat texture was observed to be controlled by two gene pairs with various forms of gene interactions such as dominance and recessive epistasis. Complete dominance of smooth seed coat texture over wrinkle, rough and loose seed coat textures was observed. Wrinkle seed coat texture plants also show complete dominance over rough and loose seeded plants. Recessive epistasis was observed in the cross between rough seed coat texture and loose seed coat texture. The genes that controlled smooth, wrinkle, rough and loose seed coat textures were all nuclear and cytoplasmic genes had no effect on seed coat texture. The progenies of reciprocal crosses between two long and one short cooking time varieties that were found to be significantly different among the eight cowpea varieties were evaluated in a field study to determine the mode of inheritance of cooking time in cowpea. The generation mean analysis adopting the additive-dominance model was not adequate for explaining the mode of inheritance of cooking time in cross TVu 39 (long cooking time) x TVu 14195 (short cooking time) and TVu 803 (long cooking time) x TVu 14195 (short cooking time) due to the

involvement of non-allelic interactions in the inheritance of seed cooking time, but adequate for cross TVu 39 (long cooking time) x TVu 803 (long cooking time). However, the six-parameter model with epistatic gene interactions was adequate for explaining the inheritance of seed cooking time. Frequency distribution of F_2 and backcross populations shows that the trait is quantitatively inherited. Two dominant alleles operating at different loci controlled cooking time trait in the cowpea varieties studied. Although gene action was predominantly dominance, additive and all epistatic gene effects were also significant. Short cooking time was dominant over long cooking time. The genes that controlled cooking time were all nuclear and cytoplasmic genes had no effect. There was transgressive segregation in cooking time and this may suggest that a new variety having very short cooking time could be selected at advanced generation. Broad and narrow sense heritability estimates were high (89%-95% and 58%-85% respectively). Genetic advance under selection with 5% selection intensity was 4.69 and 3.77 minutes for cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 respectively, suggesting that progress could be made in breeding for short cooking time. The large genotype effect of cooking time coupled with the high heritability suggests that selection based on the trait itself may allow for progress in breeding.

CHAPTER ONE

INTRODUCTION

1.1 BACKGROUND INFORMATION

Cowpeas are grown extensively throughout the lowland tropics of Africa in a broad belt along the Southern fringes of the Sahara and in Eastern Africa from Ethiopia to South Africa. They are mainly confined to the hot semi-arid to sub-humid areas with significant production in Nigeria (which alone produces about 61% of the World production), Niger, Burkinafaso, Uganda and Senegal (Rachie and Roberts, 1974). The crop is also extensively cultivated in India, Southeastern Asia, Australia, the Caribbean lowland and coastal areas of South and Central America and in the Southern regions of the United States. In Nigeria, cowpea is the most important and widely grown grain legume (Fatokun and Singh, 1987). Cowpeas are widely consumed in different forms in Nigeria and other West African countries. Various types of products are traditionally produced by soaking, dehulling, grinding, boiling or frying (Akinyele *et al.,* 1986).

Cowpea contributes 60-70KgN/ha in the soil due to its nitrogen fixing properties and also serves as a residue, which benefits the succeeding crops. It is also a shade tolerant and, therefore, compatible as an intercrop with a number of cereals and root crops, as well as with cotton, sugarcane and several plantation crops. Coupled with these attributes, its quick growth and rapid ground cover have made cowpea an essential component of sustainable subsistence agriculture in marginal lands and drier regions of the tropics, where rainfall is scanty and soils are sandy with little organic matter (Singh *et al*., 1997).

1.2 CONCEPT/STATEMENT OF PROBLEM

Insect pests, diseases, nematodes, parasitic weeds and drought are major production constraints, which lead to reduced yield. However, the International Institute of Tropical Agriculture (IITA), Ibadan has made a lot of progress in cowpea breeding and a range of varieties has been developed and distributed to over 60 countries combining diverse plant type and maturity with resistance to several diseases, insect pest and parasitic weeds with high yield potentials. However, only few of these varieties have the desired combination of seed size, colour, seed coat texture and short cooking time, which are important for consumers' acceptability in West Africa (Ojomo, 1968; Dovlo *et al*., 1976; IITA, 1980a).

In West Africa the most preferred types of cowpeas are large white or brown seeds with rough seed coat whereas in East Africa medium brown or red seeds with smooth seed coat are preferred. In Nigeria white rough seed coat texture cowpea seeds with short cooking time are preferred (Cuso and Zoaka, 1974 and Ojomo and Cheda, 1972). However, in some Latin American Countries, particularly Cuba and parts of the Caribbean, red to black colour with various categories of seed texture is preferred (IITA, 1983). Dovlo *et al*. (1976) reported that the preference of cowpea grain with rough seed coat in Nigeria is because of their ease of dehulling and greater swelling capacity, which are used for processed food such as "akara" and "moimoin". Hussain *et al*. (1984) reported that the choice of cowpeas varieties by Nigerian women is guided predominantly by the cooking time, swelling capacity, taste and colour.

Cooking time is an aspect of quality that affects consumers' acceptability of any newly released variety (Myaka and Lwaitama, 1993). With many varieties prolonged time is required to cook cowpeas to a point at which they are palatable,

render protein and starch digestible and detoxify anti-nutrients. This has contributed to the decline in the consumption and acceptability of many improved cowpea varieties released by research institutions. Firewood is the main fuel source used for cooking which is increasingly becoming scarce and expensive. Also the alternative source of fuel (kerosene) used in most homes has become increasingly very expensive and beyond the reach of many households in Nigeria. Thus prolonged cooking is viewed as a major problem of many varieties due to lack of convenience, fuel cost and loss of nutrition (Burr *et al*., 1968, Dovlo *et al*., 1976, Molina *et al*., 1976; Kakadam *et al*., 1981; Myaka and Lwaitama, 1993 and Bressani, 1985).

The long cooking time required to prepare bean dishes compared to other foods stuff and the fact that the use of open wood fires in African homes are not fuel efficient, exacts a high cost in human and physical resources. Also excessive cutting of trees for fuel use has resulted in a rapid rate of deforestation in Africa (Sirven, 1981).

1.3 JUSTIFICATION

Singh *et al.* (1997) reported cowpea as a single crop species whose varietal requirements in terms of plant type, seed type, cropping system, maturity and use pattern are extremely diverse from region to region, thus making breeding programmes for cowpea more complex than for other crops. Consequently these varying preferences show the need to develop varieties with different characteristics, as no single variety can be suitable for all regions.

Nielsen *et al*. (1993) have reported significant genetic variability for cooking time for 100 improved cowpea breeding lines developed at IITA, indicating the possibility of shortening cooking time by genetic improvement thereby developing

acceptable cowpea cultivar. Therefore, the development of cowpea cultivars with short cooking time might help conserve fuel wood and other energy sources. This research, therefore, aims at further assessing the possibility of developing cowpea genotypes with acceptable seed coat texture and short cooking time.

1.4 GENERAL OBJECTIVES AND RESEARCH SCOPE

In view of the importance of cowpea as food legume and the consumer preference of certain seed coat texture and short cooking time there is need to understand the pattern of inheritance of these traits. Therefore, the general objective of this study is to carry out genetic studies on seed coat textures and cooking time in some varieties of cowpea.

The specific objectives are:

1. To determined the mode of inheritance of seed coat texture in some varieties of cowpea.
2. To determined the mode of inheritance of cooking time in some varieties of cowpea.
3. To determined, if any, the types of gene interactions influencing the expression of these traits.

CHAPTER TWO

LITERATURE REVIEW

2.1 ORIGIN OF COWPEA

Cowpea is one of the most ancient of human food sources and has probably been used as a crop since Neolithic times (Chevalier, 1944). Because of scanty archeological evidence the centre of origin of cowpea is controversial. Thus the subject is still being discussed. Theories on cowpea centre of origin have been formulated based on the degree of diversity in the crop, on linguistic data and on the distribution patterns of its wild progenitors (Zohary, 1973). The wide distribution and early cultivation of cowpea in Asia led to the suggestion that cowpea has an ancient origin, and Asia could be the centre of origin (Purseglove, 1976). But this suggestion could not be supported because its wild progenitors were not found in that area (Ng and Marechal, 1985).

However, Flight (1970) reported that the oldest archeological evidence of cowpea was found in Africa in the Kintampo rockshelter remains in Central Ghana dating about 1450 – 1000 BC.

Several authors have reported different probable centres of domestication of cowpea in Africa. Faris (1963; 1965) concluded that cowpea arose from the domestication of *Vigna unguiculata* subspecies *dekindtiana* forms in West Africa. Steele (1972) noted that there is greater variability in subspecies *dekindtiana* (the probable progenitor of cowpea in Ethiopia than West Africa and suggested that domestication could actually have occurred in Ethiopia and dissemination went westwards across Africa and eastwards across the Indian-sub continent. Rawal (1975) suggested that cowpea was domesticated in the sub-humid and semi-arid regions of West Africa.

Rachie and Roberts (1974), Marechal *et al*. (1978) and Steele and Mehra (1980) also support West Africa as the center of origin of cowpea. Rachie and Rawal (1976) suggested Nigeria as the probable center of origin where a profusion of wild and weedy species abounds in both the savanna and forest zones of the country. More recent studies by Padulosi and Ng (1997) have suggested South Africa, as the center of cowpea origin because of the maximum diversity in wild *Vigna* in the region.

Despite its uncertain origin, it is known that cowpea was not introduced into the new World until the late 17th century and probably reached the Southern states of the United States of America (USA) in the early 18th century (Wright, 1907).

2.2 TAXONOMY

Cowpea belongs to the genus *Vigna* which comprises a large number of species whose exact estimation varies according to authors between 150 and 170 (Summerfield *et al*., 1974); 150, (Vercourt, 1970), 154 (Steele, 1972) and 84, out of which some 50 species are indigenous to Africa (Marechal *et.al*., 1978).

D'Urzo *et al*. (1990) reported that the presence of species of diverse origin characterized by great ecological and morphological diversity has made the taxonomy of the genus controversial. Marechal *et al*. (1978) further reported that many species names found in the literature are actually just synonyms.

The genus *Vigna* was sub-divided by Vercourt (1970) into eight sub genera: *Vigna, Sigmoidotropis,Cochliasanthus,Plectotropis,Ceratotropis,Dolichovigna, Macrorhynchus and Haydonia*. This classification was modified by Marechal *et al*. (1978) to seven sub-genera: *Vigna, Sigmoidotropis, Plectotropis, Macrorhyncha,Ceratotropis, Haydonia and Lasiocarpa.* The African sub genus *Vigna* with nine sections according to Vercourt now has six sections with varying

numbers of species: *Vigna* (20spp.),*Comosae* (2 spp.),*Macrodontae* (2spp.), *Reticulatae* (9spp.), *Liebrechtsia* (1sp.) and *Catiang* (2spp). Cowpea, *Vigna unguiculata*, belongs to the order Fabales, section *Catiang*, sub-genus *Vigna*, genus *Vigna*, tribe Phaseoleae, and sub family Faboideae of the family Fabaceae. The species consists of one cultivated sub-species *unguiculata* and three wild sub species (Marechal *et al*., 1981). The wild species include sub species *dekindtiana* (variety *dekindtiana*, var. *mensensis*, var*. pubescens* and var. *protracta*), sub species *tenuis* and sub species *stenophylla*.

2.3 CYTOLOGY

Darlington and Wylie (1955) reported a somatic chromosome number of 2n=22 in *Vigna unguiculata* (L.) Walp. The same chromosome number was found later by Faris (1964) and Frahm-Lelived (1965). Rachie and Roberts (1974) reported some cowpea varieties and their closely related weedy and wild relatives to have 2n= 24 chromosome number. However 2n=22 is the more common condition.

2.4 MORPHOLOGY

Vigna unguiculata (L.) Walp is an annual herbaceous leguminous crop with cylindrical and glabrous, twisting and coloured (green or purple) stem. Buds in the leaf axils may develop into a slender branch or a flower bearing peduncle. Different cultivars of cowpea show a range of growth habit from erect, semi-erect, spreading to climbing and twinning. The height of the plant varies from dwarf (15cm) to tall (over 100cm) depending on the growth habit. The first pair of leaves is unifoliate and opposite while the second and subsequent leaves are alternate, trifoliate with one terminal and two lateral leaflets. The plant bears a slender

taproot with fibrous lateral roots. Petioles vary in length from three to 25cm (Rachie and Rawal, 1976). The shapes of the leaves are mostly hastate, ovate, lanceolate, sub-hastate and rhombic. Flowers and pods arise at the terminal end of peduncles. Flowers have the typical leguminous standard, keel and wings. Usually 2-6 flowers are found per peduncle. They are borne singly or in multiples. Flower is complete and colour varies through many shades of purple to yellow and white, depending on the concentration of anthocyanin pigment present.

The stamens are diadelphous (9 forming a tube of filaments and 1 free). The ovary is straight with a bent style, which is hairy along the inner side and a globular, glandular stigma. Flowers are self-pollinated but a low percentage of out crossing may occur depending on season and varieties of pollen vectors (Rachie and Roberts, 1974). Fruits are dehiscent pods, which usually shatter when dry. The shape and length of pod varies. It is pendulous, mostly linear although curved and coiled forms occur. The pod is green at early stage and when maturing it becomes usually yellow, light brown, pink or purple. The pod length may vary from less than 11cm to more than 100cm (Rachie and Rawal, 1976). Seeds of cowpea cultivar vary considerably in colour (such as brown, purple, white and speckled), shape (reniform or kidney shaped, ovoid, rhomboid etc.) and are of different sizes ranging between 0.4cm to 1.2 cm in length and 0.3cm to 1.0cm in width. Seedcoat texture can be smooth, rough, wrinkle and loose (Ebong, 1970 and IITA, 1974).

2.5 PRODUCTION

Cowpea (*Vigna unguiculata*) (L.) Walp is an important food legume and a versatile crop cultivated between 35^{o}N to 30^{o}S of the equator covering Asia and Oceania, the Middle East, Southern USA, and Central and South America (Fery,

1985; 1990; Mishra *et al*., 1985; Singh and N'tare, 1985; Perrino *et al*., 1992, 1993). Cowpea being a drought-tolerant crop with better growth in warm climates is most popular in the semi arid regions of the tropics where other food legumes do not perform as well. It is shade-tolerant and, therefore, compatible as an inter crop with a number of cereals and root crops as well as with cotton, sugar cane and several plantation crops. Coupled with these attributes, its quick growth and rapid ground cover have made cowpea an essential component of sustainable subsistence agriculture in marginal lands and drier regions of the tropics where rainfall is scanty, and soils are sandy with little organic matter.

Information from Food and Agriculture Organization (FAO) and scientists in several countries indicates that cowpea is now cultivated on at least 12.5 million hectares, with an annual production of over 3 million tonnes worldwide. Central and West Africa accounts for over 64% of the area (with about 8 million hectares), with significant production from the drier regions of Northern Nigeria (about 4 million ha, with 1.7 million tonnes) and Southern Niger (about 3 million ha, with 0.3 million tonnes), Central and South America (2.4 million hectares) with about 1.9 million ha, with 0.7 million tonnes production in Northeastern Brazil, Asia (1.3 million hectares) and about 0.8 million hectares in East and Southern Africa (Singh *et al*. , 1997).

Ojomo (1967) observed that in Nigeria, 50-127mm of rainfall per month is required from seedling to flowering after which less rainfall and more sunshine are required for seed ripening. Although there are two growing seasons in the southern parts, better quality seeds are usually produced from the late Season crop than from early ones. Ebong (1965) noted that in parts of the drier north, there is a sufficiently long season extending between June and November, during which adequate rains for increased vegetative vigour and sufficient sunlight for the

hastening of maturity are available. Thus, more cowpea is produced in the North than in the South. These conditions according to Ebong (1965) encourage the production of high quality seeds. Singh *et al*. (1987) reported that the best cowpea yields are obtained in well-drained sandy loam to clay loam soils between pH 6 to 7.

2.6 UTILIZATION

Cowpea (*Vigna unguiculata* (L.) Walp) is a broadly adapted and highly variable crop legume cultivated around the world primarily as a pulse but also as a vegetable, a cover crop and for fodder. Cowpea leaves, green pods and dry grains are consumed as human food (Steele, 1972). The green leaves as well as dry haulms are fed to livestock particularly in the dry season when animal feed is scarce. Cowpea haulms, which contain about 20% protein, are highly valued feed as much as grain on a dry weight basis. Thus cowpea promotes crop - livestock integration leading to better nutrient cycling and enhanced income generation. In addition, because of its tolerance to drought and soil acidity and its ability to fix aerial nitrogen as well as its fast growth habit in warm climates, it contributes to improving the soil in the desert marginal areas of the tropics (Quinn, 1997).

Furthermore, the spreading indeterminate or semi-determinate bushy growth of cowpea provides ground cover, thus suppressing weeds and providing some protection against soil erosion. After harvest of the cereals inter-cropped with cowpea, the late season varieties of cowpea respond to improved light and grow out to cover the land. Trading in fresh produce and processed cowpea foods provide both rural and urban opportunities for providing cash, particularly for women. Farmers cut and store cowpea fodder for subsequent sale at the peak of

the dry season thus providing cash and also improving their annual income by as much as 25% (Quinn, 1997).

2.7 PRODUCTION CONSTRAINTS

Insect pests, diseases, parasitic weeds, drought, poor soil fertility are major constraints in cowpea production. Eighty five insect species have been identified which attack cowpea (Booker, 1965). However, aphids, thrips, pod borers, pod bugs and bruchids are the major insect pests causing up to 100% yield loss and seed damage (Singh and Jackai, 1985).

Over 35 major diseases caused by viruses, bacteria, fungi and nematodes (Emechebe and Shoyinka, 1985; Singh and Reddy, 1986) attack cowpea.

The occurrence, severity and yield loss due to each disease and mixed *infections* vary from place to place but some diseases occur and cause significant damage across the cowpea growing regions of the world (Emechebe and Florini, 1997). Two bacterial diseases, bacterial pustule (*Xanthomonas* spp.) and bacterial blight (*Xanthomonas vignicola*), cause severe damage to cowpea worldwide. *Cercospora* leafspot, brown blotch, *Septoria* leaf spot and scab are the most common fungal diseases (Abadassi *et al*., 1987).

About 55 species of nematodes have been reported on cowpea of which *Meloidogyne incognita* is the most damaging and widespread species (Singh and Reddy, 1986). *Striga gesnerioides* (wild) Vatke and *Alectra vogelii* (Benth.) are two parasitic weeds which cause substantial yield reduction in cowpea particularly in the semi-arid regions of West and Central Africa (Aggarwal, 1985, 1991; Singh and Emechebe, 1990; Singh *et al*., 1993; Atokpe *et al.,* 1993, 1995).

2.8 COWPEA GENETICS

The genus *Vigna* has great potential for improvement since gene exchange has proved successful between some wild and cultivated forms (Rawal, 1975; Evans, 1976; Marechal *et al*., 1978). The cowpea is ideal for genetic research and plant breeding. It is a diploid with a relatively short cycle. Its large flowers and untwisted keels make it easy to emasculate and pollinate. Genetic research in cowpea has been a subject of immense interest since the beginning of the 1900s. Genetic information is needed to devise or select efficient breeding procedure, which could lead to the development of improved and high yielding cowpea varieties suitable for different ecological zones and cropping systems.

2.8.1 Seed Coat Texture

Seed coat texture is the degree of fineness of the seed coat (skin). For wide adoption in West Africa, new cowpea varieties must have features desired by consumers as well as farmers. Seed coat texture is one of these features. Ebong (1970) identified three categories of seed coat texture in cowpea (smooth, rough and wrinkle) while IITA (1974) identified four categories (smooth, rough, wrinkle and loose). Cowpeas with large white or brown grains with rough seed coat are preferred throughout West Africa, whereas in East Africa they prefer medium brown or red seeds with smooth seed coat. But in some Latin American countries, particularly Cuba and part of Caribbean, black colour with various categories of seed coat texture are preferred (IITA, 1983).

The preference of cowpea grain with rough seed coat in Nigeria is because of their ease of dehulling and greater swelling capacity. Such grain is used for the processed food such as akara and moimoin (Dovlo *et al*., 1976). Ojomo and Cheda (1972) reported that cowpea varieties with smooth and wrinkled seed coat

have thicker testa than those with rough seed coat, which in turn affects the rate of water absorption. Cultivar with comparatively thick, smooth seed coats have a slow initial rate of water absorption, whereas thin seed coat cultivar have high initial rate and dehull better after soaking (Sefa-Dedeh *et al*., 1979). Akinyele *et al*. (1986) did not observe significant difference in the swelling capacity between smooth and wrinkled seed coat varieties.

2.8.2 Inheritance of Seed Coat Texture

Genetic studies on the inheritance of seed coat texture in cowpea have been few and in most cases only two categories of testa textures (smooth and rough) are involved. Ene (1973); Rawal (1975); Franckowiak (1973) and Drabo (1981) found smooth testa was dominant to rough. Franckowiak (1973) reported rough testa to be controlled by at least two recessive genes. Ene (1973) and Drabo (1981) did not find any rough testa in the segregating F_2 population of plants from a cross involving a smooth and rough parents.

2.8.3 Cookability

The term cookability as applied to legumes seeds refers to the condition by which they achieve a degree of tenderness during cooking acceptable to consumers (Moscoso *et al.*, 1984). With many improved varieties prolonged time is required to cook cowpeas to a point at which they are palatable, render protein and starch digestible and detoxify anti nutrient factors. This has resulted to non-acceptance of these varieties by consumers in Africa and Latin America, where cowpea is a dietary staple of low and middle income families (Bressani, 1985).

In Africa cowpeas are cooked over an open fire built on the ground (Poulsen, 1978). However, the long cooking time required for cowpeas compared

to other foodstuffs and the fact that open wood fires are not fuel efficient, exacts a high cost in human and physical resources. The cost is reflected in an excessive use of fuel wood and labour required for gathering the wood and tending the fire throughout the cooking period. The important contribution of cowpeas to human nutrition and the large amount of fuel wood required to prepare them for consumption illustrate a strong link between nutritional well- being and fuel supply in Africa.

Eckholm *et al*., 1984 reported wood as the most widely used household fuel in the developing world. Deforestation has occurred at a rapid rate in Africa because of excessive cutting of trees for fuel use (Sirven, 1981). The development of cowpea cultivars with shorter cooking time than the cultivar currently grown for consumption might help conserve fuel wood. Shorter cooking time also save time.

Akinyele *et al*. (1986) established a positive correlation between cooking time and protein in cooked bean. Prolonged cooking increases the percentage of leached solid and destroys the heat labile vitamins. Thus, fast cooking does not only improve the acceptability of cowpeas but could also give the grain a higher nutrient retention by reducing the amount of leached solids.

2.8.4 Inheritance of Cooking Time

There is a dearth of information on the mode of inheritance of cooking time in cowpea. However Nielsen *et al*. (1993) reported significant genetic variability in cooking time for 100 improved cowpea-breeding lines developed at IITA, Ibadan. Nielsen *et al*. (1993) reported a value of 0.76 broad sense heritability for cooking time in cowpea *Vigna unguiculata* L. Walp. Elia *et al*. (1997) reported a high value of 0.9 narrow sense heritability for the same trait in *Phaseolus vulgaris* in

Tanzania. While Jacinto-Hernandez *et al*. (2003) reported a value of 0.74 narrow sense heritability for the same trait in *Phaseolus vulgaris* in Mexico.

Elia *et al.* (1997) observed that cooking time trait were governed by genes with partial dominance of short cooking time over long cooking time in Andean dry beans *Phaseolus vulgaris*. He also reported cytoplasmic influences on the trait expression while Jacinto-Hernandez *et al.* (2003) reported that two genes controlled cooking time trait in *Phaseolus vulgaris* with short cooking time dominant over long cooking time.

Akinyele *et al.* (1986) did not find any significant difference in cooking time between smooth and wrinkled seed coat varieties. Demooy and Demooy (1990) reported longer cooking time for small seeded cultivars than large seeded ones. Myaka and Lwaitama (1993) reported a highly significant and negative correlation between protein content and cooking time in three improved cowpea cultivars and one local cultivar in Tanzania.

2.8.5 Heritability

One of the most important factors in formulating effective breeding plans for improving crops and livestock is knowledge of the contribution made by genes to the variability of a trait (Akoroda, 1981; Stansfield, 1988).

The ratio of total genetic variance to total phenotypic variance is termed broad sense heritability whereas the ratio of additive genetic variance to phenotypic variance is narrow sense heritability (Falconer, 1989). Technique for estimating heritability in crop plants fall into three main categories namely; parent-offspring regression, variance components from an analysis of variance and approximation of non-heritable variance from genetically uniform populations to estimate total genetic variance (Warner, 1952).

Warner (1952) reported that none of these techniques is completely satisfactory from the viewpoint of the plant breeder. He thus provided a method that uses only within population variance for an early generation estimation of heritability.

Mammud and Kramer (1951) concluded that heritability estimates based on regression were higher than those based on variance components. The procedure involves regressing the mean value of characteristics in the progeny upon the value for the same characteristic in the parent. However regression on mid-parent gives better precision than regression on one parent (Falconer, 1989).

2.8.6 Maternal Effect

Literature on maternal effect especially on the mechanism of unilateral crosses in cowpea and wild *Vigna* is scanty. Maternal effects have, however, been genetically evaluated and analysed in animals as well as plants that show normal reciprocal cross differences (Hayman, 1954a; Hayman, 1954b; Jinks *et al*., 1972; Mather and Jinks, 1982; Falconer, 1989). Maternal effects arise where the mother makes a contribution to the phenotype of her progeny above that which results from the genes she contributes to the zygote. Maternal effect results in the production of difference between reciprocal crosses, which are showed between the offspring of both sexes in all the generations where they occur. Maternal effects also lead to a greater resemblance of the progeny to the maternal parent. In hermaphroditic species maternal effects can be detected by making crosses reciprocally between pairs of individuals irrespective of whether they are homozygous or heterozygous. However, the breeding history of the individual should be known in order to make a useful biometrical analysis and interpretation (Mather and Jinks, 1982).

Jinks *et al*. (1972) discussed in detail the analysis and interpretation of differences between reciprocal crosses using *Nicotiana rustica* varieties. He noted that reciprocal differences could either be transient when there are differences in the maternal environment, or persistent, which arise through unequal contributions of cytoplasmic determinants from the female and male gametes to the zygote.

Maternal effects are controlled by nuclear genes of the mother and are different from extranuclear inheritance. Extranuclear contents of the egg, however, reflect the influences of the mother's genotype and thus the pattern of inheritance becomes like that of extranuclear inheritance (Gardner and Snustard, 1981). Sometimes, the early growth and development of the zygote is so much influenced by the surrounding maternal tissue that the progeny very much resemble the female parent. However, by rising subsequent generations, maternal effect, extrachromosomal inheritance or maternal inheritance is suspected where a significant difference is detected in reciprocal crosses (Sinha and Sinha, 1980). But unlike maternal effect, the differences caused in maternal inheritance do not usually disappear after one generation.

2.9 GENETIC ANALYSIS

Data obtained from the inheritance of seed coat texture studies, being a qualitative trait, was subjected to Chi-square analysis to test for the goodness of fit to the proposed segregation ratio. This test gives the proportion of times a particular degree of deviation is likely to occur by chance (Harrison, 1970).

Many biometrical genetic models and designs have been used in the study of inheritance of quantitative characters in plants and animals. Generation mean analysis utilizing the procedures of A, B and C scaling tests (Mather, 1949) and joint scaling tests using weighted least square procedures (Cavalli, 1952) as well

as the six parameter models for estimating epistatic genetic interactions (Jinks and Jones, 1958; Hayman, 1954a, 1954b) are some important models in genetic analysis of quantitative traits.

Generation Means Analysis (GMA) was used to observe the mode of inheritance of cooking time and the pattern of segregation in F_2 populations. Generation mean analysis deals with the relative effects estimated from the means of different generations (Hallauer and Miranda, 1981). The primary function of this is to obtain some specific information about a specific pair of lines. The estimates of genetic effects in quantitative traits would be different for different pairs of lines, depending on the relative frequency of opposing and reinforcing effects for the pair of lines studied.

Mather (1949), Singh and Chaudhary (1985) presented several generation comparisons to test for additiveness of genetic effects, for estimation of additive variance and dominance variance. If the scale of measurement deviated from additivity, he suggested a transformation to make the effect additive. The generation model has been extended to include the estimation of epistatic effects.

The additive- dominance model of GMA was adopted in the analysis of genetic expectations. Drabo *et al*. (1984) and Aliyu and Akoroda (2000) used the additive-dominance model of GMA to study the mode of inheritance of seed size in cowpea, while Agwaranze (1992) and Aliyu (2001) adopted the additive – dominance model of GMA to study the mode of inheritance of pubescence in *Vigna vexillata* and *Vigna rhomboidea* respectively. The adequacy of the model in explaining the inheritance pattern was examined by two tests:

a. The scaling tests of Mather (Mather, 1949)

b. The joint scaling tests of Cavalli (Cavalli, 1952)

Generation means was also analysed using the six-parameter model of Jinks and Jones (1958).

Broad sense heritability was estimated by the formula outlined by Mammud and Kramer (1951) while narrow sense heritability was estimated by the formulae and notations outlined by Mather and Jinks (1971).

The numbers of effective factors differentiating the parents were estimated according to Burns (1976).

The variance and standard errors of means for each generation were obtained from individual plant data.

A t-test for unpaired observations and unequal variances (Steel and Torrie, 1980) was used to determine the significance of the reciprocal differences.

Total correlation coefficient was estimated using the formula outlined by Steel and Torrie (1980).

CHAPTER THREE

MATERIALS AND METHODS

The experiments were carried out at the research and teaching farm, Federal University of Technology, Yola, Adamawa State. Yola is located on 9^{o} 14'N latitude and 12^{o} 32'E longitude. It is 200m above sea level and is located within the Sudan Savanna ecological zone of Nigeria.

The site had maize the previous year. The land was ploughed with a disc plough.

Eight cowpea varieties were obtained from the Genetic Resources Unit (GRU) of the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. The accession number, pedigree, origin, seed coat texture and maturity of each variety is given in Table 1. Each variety was selfed for two generations. This was done to check whether the varieties were homozygous or not. The selfing was done in the screen house and plastic pots each measuring 24cm at the top and 17.5 cm at the base with 22.5 cm in height were used. There were two plants per pot and three pots were used for each variety. Garden soil was used. The seeds were sown on August 14, 2000 and the plants were watered whenever necessary.

After the test for homozygosity was completed, the eight varieties were used to initiate two different experiments, which are described below.

3.1 EXPERIMENT 1. INHERITANCE OF SEED COAT TEXTURE IN SOME VARIETIES OF COWPEA.

Plastic pots measuring 24cm at the top and 17.5cm at the base with 22.5 cm height were filled with garden soil. The pots were kept in a screen house. Seeds of TVu 14195, TVu 13677, TVu 16514, TVu 39 and TVu 899 were sown two seeds per pot on April 1, 2001. Seeds of TVu 803, TVu 3741 and TVu 3743 were sown on April 25, 2001.

Table 1. Origin, Pedigree and some Characteristics of the Cowpea varieties Used.

Accessions	Cultivar Name or Pedigree	Origin	Seed Coat Texture	Maturity
TVu 14195	IT84S-2246-4	Nigeria	Wrinkle	Early
TVu 13677	IT82D-716	Nigeria	Wrinkle	Early
TVu 16514	IT90K-59	Nigeria	Rough	Early
TVu 803	Kanannado	Nigeria	Rough	Late
TVu 3741	KR81	Nigeria	Loose	Late
TVu 3743	KR83	Nigeria	Loose	Late
TVu 39	NO.19	Tanzania	Smooth	Early
TVu 899	Kanannado	Nigeria	Smooth	Early

Source: IITA, Ibadan

The different types of crosses made within the screen among cowpea varieties having different seed coat textures were as follows:

S/N	Crosses	No. of Flower Pollinated	Pod Set
1	TVu 39 (Smooth) x TVu 899 (Smooth)	22	12
2	TVu 899 (Smooth) x TVu 39 (Smooth)	21	11
3	TVu 39 (Smooth) x TVu 803 (Rough)	20	11
4	TVu 803 (Rough) x TVu 39 (Smooth)	18	8
5	TVu 39 (Smooth) x TVu 13677 (Wrinkle)	21	10
6	TVu 13677 (Wrinkle) x TVu 39 (Smooth)	21	9
7	TVu 39 (Smooth) x TVu 3741 (Loose)	22	9
8	TVu 3741 (Loose) x TVu 39 (Smooth)	20	9
9	TVu 14195 (Wrinkle) x TVu 13677 (Wrinkle)	17	11
10	TVu 13677 (Wrinkle) x TVu 14195 (Wrinkle)	19	12
11	TVu 14195 (Wrinkle) x TVu 803 (Rough)	20	11
12	TVu 803 (Rough) x TVu 14195 (Wrinkle)	22	11
13	TVu 14195 (Wrinkle) x TVu 3741 (Loose)	18	8
14	TVu 3741 (Loose) x TVu 14195 (Wrinkle)	18	8
15	TVu 3741 (Loose) x TVu 3743 (Loose)	16	10
16	TVu 3743 (Loose) x TVu 3741 (Loose)	16	9
17	TVu 3741 (Loose) x TVu 803 (Rough)	17	8
18	TVu 803 (Rough) x TVu 3741 (Loose)	19	11
19	TVu 803 (Rough) x TVu 16514 (Rough)	21	11
20	TVu 16514 (Rough) x TVu 803 (Rough)	17	9

The crossing procedure used by Rachie *et al*. (1975) was followed which consists of emasculation, in the evening of the plants flower buds which will open the following morning and to be used as female parent and applying pollen of the

male parent directly to the stigma of the emasculated parent the same evening or the following morning. Emasculation was done with sharply pointed forceps sterilized with alcohol between crosses to prevent contamination by unwanted pollen. The flower chosen as a source of pollen was held between the thumb and the forefinger with the standard and wing folded back to expose the pollen. This was then used as 'brush' to apply sufficient pollen to the emasculated flower. Tags (listing the cross and date) were affixed to the raceme or peduncle beneath the pollinated bud to identify the cross and date of cross.

After the F_1 seeds were produced, four F_1 seeds from each cross as well as a few parental seeds were sown again in the screen house and crossed with both parents to produce the backcross seeds while two F_1 seeds from each cross was selfed to produce F_2 seeds. These were sown on August 25, 2001 and harvested on November 18, 2001. Then the parents (8 genotypes), F_1 (20 genotypes), F_2 (20 genotypes), backcross one (20 genotypes) and backcross two (20 genotypes) were sown in the field on August 2, 2002 at the teaching and research farm, Federal University of Technology, Yola, Adamawa State. Randomized complete block design with five replicates was used.

The spacings within and between rows were 60 cm and 100 cm, respectively. Each replicate consisted of one 6 m row for the parents and the F_1, six rows for the F_2 and three 6 m row for the backcrosses. The parents and the F_1 had one seed per hill while the F_2 and the backcrosses had two seeds per hill. Two days after sowing a mixture of Galex 500 EC and Gramoxone at the rates of three and one litre per hectare were applied to control growth of weeds. Hand weeding was carried out at three and six weeks after sowing.

To control insect pests Sherpa plus was sprayed to the plants two weeks after emergence at the rate of one litre per hectare. Thereafter, Sherpa plus was applied weekly starting from flowering until the pods were fully matured.

Visual observation was used to classify seed coat texture of seeds into smooth, loose, wrinkle and rough (Plates 1-5).

3.2 EXPERIMENT 2. INHERITANCE OF COOKING TIME IN SOME VARIETIES OF COWPEA.

Seeds of eight cowpea varieties (the same varieties as those used in experiment one) were sown in the field on August 2, 2001 at the teaching and research farm, Federal University of Technology, Yola, Adamawa State. There was 60 cm spacing within a row and 100 cm between rows. There were two rows per plot. Randomized complete block design with five replications was used. Cultural practices were similar as experiment one.

When the pods were fully matured the mean seed cooking time (min) was determined from 25 seeds collected randomly from ten plants from each parent on a per plant basis for all replications.

The cooking time was recorded at IITA, Ibadan Nigeria and cookability of the cowpea seeds was evaluated using a Matson Bean Cooker (Matson, 1946). The twenty-five unsoaked seeds of each plant were placed into each of the 25 cylindrical holes of the Matson Cooker and stainless rod weighing 100g with piercing tips was placed in contact with the surface of each seed. The Matson Cooker together with the beans and the iron rod were placed in a two litre beaker containing tap water. The beaker was placed on a hot plate adjusted at 100^{o}C temperature. The cowpea sample was considered to be 100% cooked when the stainless rods had pierced all the twenty-five seeds.

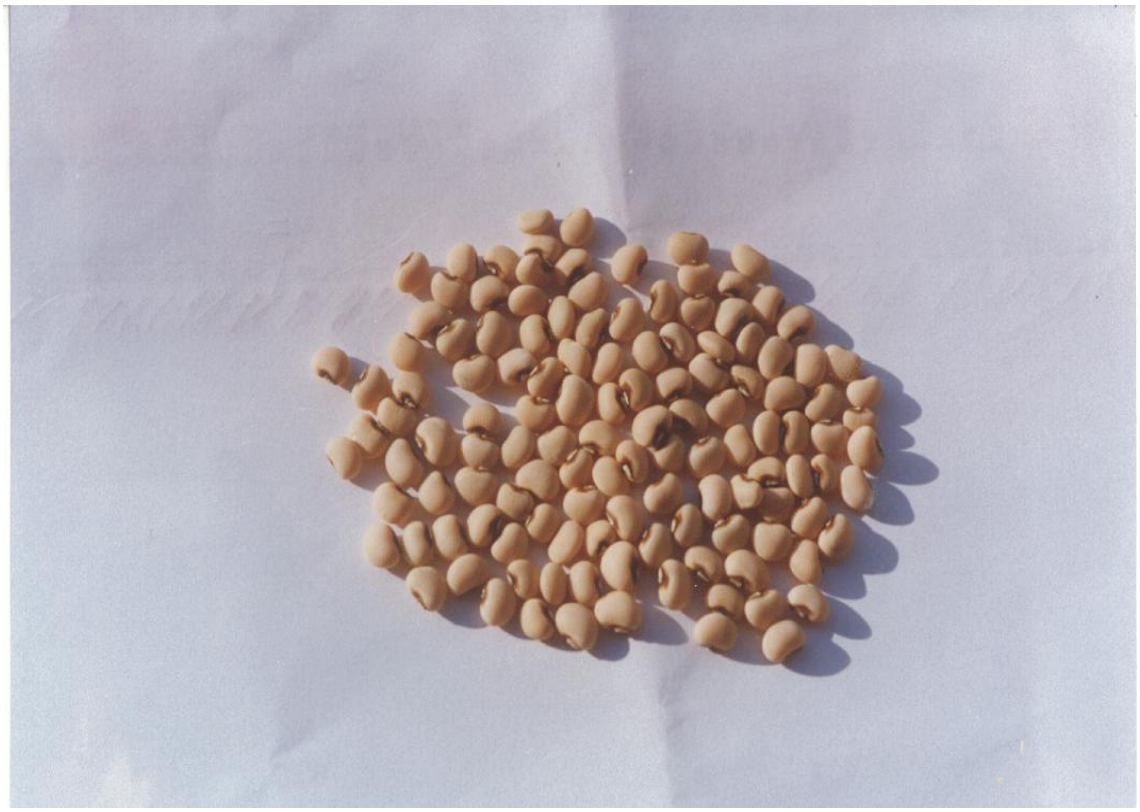

Plate 1: Seeds of TVu 899 with Smooth Seed Coat Texture (mag. x 1½)

Plate 2: Seeds of TVu 39 with Smooth Seed Coat Texture (mag. x 1½)

Plate 3: Seeds of TVu 3741 with Loose Seed Coat Texture (mag. X 1½)

Plate 4: Seeds of TVu 14195 with Wrinkle Seed Coat Texture (mag. x 1½)

Plate 5: Seeds of TVu 803 with Rough Seed Coat Texture (mag. x 1½).

After analysis of variance for cooking time was completed, three varieties were selected for crossing. The selected varieties include: TVu 39, TVu 803 and TVu 14195 and seeds of these cowpea varieties took 46.8, 45.5 and 28.2 min to cook, respectively. Seeds of these parents were sown on December 2, 2001. Crossing procedure, pot size, and soil type used were similar to those used in experiment one. The different types of crosses made are given below. The F_1 plants were backcrossed to both parents. Six F_1 and parental seeds were sown on April 4, 2002 in similar pots and soil type as before.

In August 18, 2003 seeds of the following genotypes were sown in the field at the teaching and research farm, Federal University of Technology, Yola, Adamawa State.

S/N	Genotypes
1	TVu 39
2	TVu 14195
3	TVu 39 x TVu 14195 (F_1)
4	TVu 14195 x TVu 39 (F_1) reciprocal
5	(TVu 39 x TVu 14195) x TVu 39 backcross one
6	(TVu 39 x TVu 14195) x TVu 14195 backcross two
7	(TVu 14195 x TVu 39) x TVu 39 reciprocal backcross one
8	(TVu 14195 x TVu 39) x TVu 14195 reciprocal backcross two
9	TVu 39 x TVu 14195 (F_2)
10	TVu 14195 x TVu 39 (F_2) reciprocal
11	TVu 803
12	TVu 803 x TVu 14195 (F_1)
13	TVu 14195 x TVu 803 (F_1) reciprocal
14	(TVu 803 x TVu 14195) x TVu 803 backcross one

15 (TVu 803 x TVu 14195) x TVu 14195 backcross two

16 (TVu 14195 x TVu 803) x TVu 803 reciprocal backcross one

17 (TVu 803 x TVu 14195) x TVu 14195 reciprocal backcross two

18 TVu 803 x TVu 14195 (F_2)

19 TVu 14195 x TVu 803 (F_2) reciprocal

20 TVu 39 x TVu 803 (F_1)

21 TVu 803 x TVu 39 (F_1) reciprocal

22 TVu 39 x TVu 803 (F_2)

23 TVu 803 x TVu 39 (F_2)

24 (TVu 39 x TVu 803) x TVu 39 backcross one

25 (TVu 803 x TVu 39) x TVu 39 reciprocal backcross one

26 (TVu 39 x TVu 803) x TVu 803 reciprocal backcross two

27 (TVu 803 x TVu 39) x TVu 803 reciprocal backcross two

The above 27 genotypes were evaluated in three groups according to parents used in the crosses. Thus each group consisted of eight genotypes viz: F_1, RF_1, F_2, RF_2, BC_1, RBC_1, BC_2, RBC_2 and the two parents. Each group was laid out separately using randomized complete block design with five replications. The plot sizes for each replication were one 6 m long row for the parents and F_1s, five rows for F_2s and three rows for the backcross generations. The F_1s had one seed per hill while the parents and F_2s had two seeds per hill for the three crosses. Cross TVu 39 x TVu 14195 had two seeds per hill for the backcrosses while cross TVu 803 x TVu 14195 and TVu 39 x TVu 803 had one seed per hill. Location of the experiment, spacing and cultural practices were similar as in experiment one.

When the pods were fully matured the mean seed cooking time (min) was determined from 25 seeds collected randomly from 10 plants for the parents, five plants for the F_1s and on all F_2s and backcross populations on a per plant basis for

all replications. The cookability of the cowpea seeds were evaluated using Matson Bean Cooker as earlier described. Cowpea with cooking time less than 37.5 min in cross TVu 39 x TVu 14195 and less than 36.8 in cross TVu 803 x TVu14195 were classified as short cooking time. Cowpea above those values was classified as long cooking time.

3.3 GENETIC AND STATISTICAL ANALYSIS

Data for the inheritance of seed coat texture were subjected to Chi-square analysis to test for the goodness of fit to the proposed segregation ratio.

The generations mean analysis (GMA) was undertaken to observe the mode of inheritance of cooking time in the crosses and the pattern of segregation in F_2 population. The additive – dominance model was adopted in the analysis of genetic expectations. The adequacy of the model in explaining the inheritance pattern was examined by two tests:

1. The scaling tests of Mather (Mather, 1949).
2. The joint scaling tests of Cavalli (Cavalli, 1952).

Mather's scaling test (Mather, 1949) involves testing the parameters A, B and C for their deviation from zero using the relationships below. If the model is adequate parameters A, B and C will each equals to zero within the limits of sampling error.

$A = 2\bar{B}_1 - \bar{P}_1 - \bar{F}_1 \qquad \delta^2 A = 4\delta^2 \bar{B}_1 + \delta^2 \bar{P}_1 + \delta^2 \bar{F}_1$

$B = 2\bar{B}_2 - \bar{P}_2 - \bar{F}_1 \qquad \delta^2 B = 4\delta^2 \bar{B}_2 + \delta^2 \bar{P}_2 + \delta^2 \bar{F}_1$

$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}2 \qquad \delta^2 C = 16\delta^2 \bar{F}_2 + 4\delta^2 \bar{F}_1 + \delta^2 \bar{P}_1 + \delta^2 \bar{P}_2$

where $\bar{B}_1$, $\bar{B}_2$, $\bar{P}_1$, $\bar{P}_2$, $\bar{F}_1$ and $\bar{F}_2$ are the generation means.

The standard errors (S.E) of A, B and C are the square roots of the corresponding variance.

S.E (A) =$\sqrt{\delta^2 A}$

S.E (B) = $\sqrt{\delta^2 B}$

S.E (C) = $\sqrt{\delta^2 C}$

The appropriate test of significance is:

tA = A/ S.E (A)

tB = B/ S.E (B)

tC = C/S.E (C)

Where tA, tB and tC are the calculated t values. The degree of freedom of $\delta^2 A$, $\delta^2 B$ and $\delta^2 C$ are found as the sum of the degrees of freedom of the sampling variance of the generation mean.

A more general method of testing the expected relationship between generation means on the additive – dominance model is a procedure known as the joint scaling test (using weighted least square procedure) proposed by Cavalli in 1952. It consists of estimating parameter m, (mid parent value) and origin of scale, [d] (additive) and [h] (dominance) from means of available types of generations followed by a comparison of the observed generation means with expected values derived from the estimates of the three parameters. The joint scaling test is flexible such that if one generation is missing, it can test, the remaining ones, provided the available generations are not less than three.

The genetic component m, [d] and [h] were estimated by the equation:

$M = J^{-1}S$

Where M is the estimate of the parameters m, [d] and [h]

S is the matrix of scores

J is the information matrix

J^{-1} is the inverse of the information matrix and is a variance-covariance matrix

$$M = \begin{matrix} m \\ [d] \\ [h] \end{matrix} \quad \begin{matrix} \Sigma\,[\text{coeff.m} \times \text{Yi} \times \text{wt.}] \\ S = \Sigma\,[\text{coeff.d} \times \text{Yi} \times \text{Wt.}] \\ \Sigma\,[\text{coeff.h} \times \text{Yi} \times \text{Wt.}] \end{matrix}$$

$$J = \begin{matrix} \Sigma[\text{coeff.m}^2 \times \text{wt.}] & \Sigma\,[\text{coeff.m} \times \text{coeff.d} \times \text{wt.}] & \Sigma\,[\text{coeff.m} \times \text{coeff.hx wt.}] \\ & \Sigma\,[\text{coeff.d}^2 \times \text{wt.}] & \Sigma\,[\text{coeff.d} \times \text{h} \times \text{wt}] \\ & & \Sigma\,[\text{coeff.h}^2 \text{xwt.}] \end{matrix}$$

The coefficient (coeff.) of m, [d], and [h], (Table 2) are the same as given by Mather and Jinks (1971) in components of variation for each generation. The weights (wt) are the reciprocal of the squared standard errors of the observed generation means. The standard error of each of the estimates m, d, h is obtained as under root of the diagonal element of the inverse matrix.

The predicted generation means have been calculated as follows:-

$P_1 = m + d$

$P_2 = m - d$

$F_1 = m + h$

$F_2 = m + 1/2\ h$

$B_1 = m + 1/2\ d + 1/2\ h$

$B_2 = m - 1/2\ d + 1/2\ h$

where m, d, and h are the estimated parameters. The calculated χ^2 has been computed by squaring the deviation of the observed from the expected value for each type of family, multiplying by the corresponding weight and summing the products over all six types of families.

None adequacy or failure of an additive-dominance model between generation means is an indication that more complexes factor (non-allelic interaction or epistasis) are involved in the inheritance (Mather and Jinks, 1982). When this happens, Mather and Jinks (1982) suggested a transformation on the original data

Table 2. Generations means (Yi), Weight (wt) and Coefficient of m,[d],[h].

Generation	Observed	Weight wt	Coefficient of Parameters		
	Yi		[m]	[d]	[h]
$\bar{P}_1$	Y_1	$\frac{1}{(S.E)^2}$	1	1	0
$\bar{P}_2$	Y_2	"	1	-1	0
$\bar{F}_1$	Y_3	"	1	0	1
$\bar{F}_2$	Y_4	"	1	0	0.5
$\bar{B}_1$	Y_5	"	1	0.5	0.5
$\bar{B}_2$	Y_6	"	1	-0.5	0.5

to the log scale to normalize the distributions in the non-segregating populations; this was done on cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195.

Failure of the model after transformation confirms the presence of non-allelic interaction and subsequent analysis of the data must be based on a model that incorporates epistatic gene interactions.

Brebaker (1964) reported that the presence of epistasis or non-allelic interaction is a complication in the analysis of quantitative traits. Epistasis biases the variances of the populations and the complexity of the bias permits no generalization (Mather and Jinks, 1971).

A perfect fit solution formula (six-parameter model) by Jinks and Jones (1958) was fitted into the two crosses to allow for non-allelic interactions as suggested by Mather and Jinks (1982). The genetic parameters estimated by the six parameter model (Jinks and Jones, 1958) include the mid parent (m) which is the mean of the inbred population derived from the cross between P_1 and P_2, additive genetic effect ([d]), dominance effect ([h]), additive x additive (homozygote x homozygote) ([i]) interaction, additive x dominance (homozygote x heterozygote) ([j]) interaction and dominance x dominance (heterozygote x heterozygote)([l]) gene interaction.

P_1 is the parent with the higher cooking time while P_2 is the parent with lower cooking time. F_1 is the first filial generation of a cross between P_1 and P_2, while F_2 is the progeny of selfed F_1 plants. BC_1 is the progeny of a cross between F_1 and the higher parent, while BC_2 is that between F_1 and the lower parent.

$$m = 1/2\,\bar{P}_1 + 1/2\,\bar{P}_2 + 4\bar{F}_2 - 2\bar{B}_1 - 2\bar{B}_2$$

$$[d] = 1/2\,\bar{P}_1 - 1/2\,\bar{P}_2$$

$$[h] = 6\bar{B}_1 + 6\bar{B}_2 - 8\bar{F}_2 - \bar{F}_1 - 3/2\bar{P}_1 - 1/2\,\bar{P}_2$$

$$[i] = 2\bar{B}_1 + 2\bar{B}_1 - 4\bar{F}_2$$

$$[j] = 2\bar{B}_1 - \bar{P}_1 - 2\bar{B}_1 + \bar{P}_2$$

$$[l] = \bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\bar{B}_1 - 4\bar{B}_2$$

The variance of these estimates is the weighted sums of the variance of generation means.

$$\sigma^2 m = 1/4\ \sigma\bar{P}_1 + 1/4\ \sigma^2\bar{P}_2 + 16\sigma^2\bar{F}_2 + 4\sigma^2\bar{B}_1$$

$$\sigma^2[d] = 1/4\ \sigma^2\ \bar{P}_1 + 1/2\ \sigma^2\bar{P}_2$$

$$\sigma^2[h] = 36\sigma^2\bar{B}_1 + 36\sigma^2\bar{B}_2 + 64\sigma^2\bar{F}_2 + \sigma^2\bar{F}_{1+} 9/4\sigma\bar{P}_1 + 9/4\sigma\bar{P}_2$$

$$\sigma^2[i] = 4\sigma^2\bar{B}_1 + 4\sigma^2\bar{B}_2 + 16\sigma^2\bar{F}_2$$

$$\sigma^2[j] = 4\sigma^2\bar{B}_1 + \sigma^2\bar{P}_1 + 4\sigma^2\bar{B}_2 + \sigma^2\bar{P}_2$$

$$\sigma^2[l] = \sigma^2\bar{P}_1 + \sigma^2\bar{P}^2 + 4\sigma^2\bar{F}_1 + 16\sigma^2\bar{F}_2 + 16\sigma^2\bar{B}_1 + 16\sigma^2\bar{B}_2$$

The standard errors of these estimates are square root of their respective variance e.g.

$$S[d] = \sqrt{V[d]}$$

The significance of each parameter can be tested by dividing the parameter by their standard error.

Reciprocal differences in the various generations have been evaluated as follows:

$$d = Yij - Yji$$

where d is the reciprocal difference between Yij and Yji, which are the generation, means of crosses between i and j and j and i genotype respectively. A t-test for unpaired observations and unequal variances (Steel and Torrie, 1980) was used to determine the significance of the reciprocal differences.

$$t\ (cal.) = \frac{d}{\sqrt{(S.E.\ Yij)^2 + (S.E.Yji)^2}}$$

$$t' = \frac{(S.E.Yij)^2\, t_1 + (S.E.Yji)^2\, t_2}{(S.E.Yij)^2 + (S.E.Yji)^2}$$

where t (cal.) is the calculated t, t' is the theoretical t (it lies between t_1 and t_2). S.E. Yji and S.E. Yij are the standard errors of the mean for Yij and Yji respectively. t_1 and t_2 are the values of student's t for the degrees of freedom of Yij and Yji, respectively. If t (cal.) is greater than t' for a given level of significance, then Yij and Yji are significantly different. If t calculated is less than t', than Yij and Yji are not significantly different.

Total correlation coefficient was estimated using the formula outlined by Steel and Torrie (1980):-

$$r\ XY = \frac{\sum_{i=1}^{n} XY}{\sqrt{\sum_{i=1}^{n} X^2}\ \sum_{i=1}^{n} Y^2}$$

Where r XY is the correlation coefficient between the 2 characters X and Y.

$\sum_{i=1}^{n} XY$ is the corrected sum of cross products of traits X and Y

$\sum_{i=1}^{n} X^2$ is the corrected sum of squares of traits X

$\sum_{i=1}^{n} Y2$ is the corrected sum of squares of traits Y.

n = is the number of pairs of observations for X and Y.

Broad sense heritability was estimated by the formula outlined by Mahmud and Kramer (1951).

Narrow sense heritability was estimated by the formulae and notations outlined by Mather and Jinks (1971).

Genetic advance under selection was calculated by the methods of Allard (1960).

Number of effective factor (genes) was estimated according to Wright's formula (Burns, 1976). The formula is presented on appendix 1.

The underlying assumption for the estimates of the effective factors (genes) includes:

a) Absence of non-allelic interaction

b) Absence of linkage

c) One parent supplies only plus factors and the other only minus factor

d) Each allele at all loci has an equal additive effect (Mather and Jinks, 1982).

CHAPTER FOUR

RESULTS

4.1 INHERITANCE OF SEED COAT TEXTURE IN SOME VARIETIES OF COWPEA.

Cross 1: TVu 39 (smooth) x TVu 899 (smooth)

The inheritance of seed coat texture using the cross combination smooth x smooth was studied in the cross involving TVu 39 and TVu 899. All the fifty plants of TVu 39 and TVu 899 were smooth. All the F_1, backcross and F_2 plants were smooth (Table 3). Reciprocal crosses yielded the same phenotypes in about the same proportion (Table 4). When the reciprocal crosses were combined (Table 5), all the 100 plants of TVu 39 and TVu 899 were smooth. The 46 F_1 plants, 55 backcrossed plants and 1196 F_2 plants were all smooth.

Cross 2: TVu 39 (smooth) x TVu 803 (rough)

The inheritance of seed coat texture in cowpea using the above cross was studied in a reciprocal cross involving TVu 39 (smooth) and TVu 803 (rough).
The parental lines bred true. The F_1 plants derived from the cross between smooth x rough and between its reciprocal rough x smooth plants had smooth seed coat texture. Segregation in the F_2 and reciprocal F_2 gave a 3 smooth: 1 rough ratio (Tables 6 and 7). Backcross F_1 plants involving rough parent gave a close fit to 1:1 ratio of smooth and rough plants, while backcross of the F_1 involving smooth parent gave all smooth plants (Tables 6 and 7).

Combined reciprocal crosses yielded 35 smooth seed coat plants in the F_1, 863 and 299 smooth and rough seed plants respectively in the F_2 (which closely fit a 3 smooth: 1 rough ratio); 284 smooth and 256 rough seed plants (fitting a 1 smooth: 1 rough ratio) in the backcross of the F_1 to the rough parent and 240

Table 3. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 899 (smooth) Cross.

Generation	Observed number of plants						χ^2
	smooth	rough	wrinkle	loose	total	expected ratio	
TVu 39	50	0	0	0	50		
TVu 899	50	0	0	0	50		
TVu 39 x TVu 899(F_1)	21	0	0	0	21		
TVu 39 x TVu 899 x TVu 39	11	0	0	0	11		
TVu 39 x TVu 899 x TVu 899	15	0	0	0	15		
TVu 39 x TVu 899(F_2)	600	0	0	0	600		

Table 4. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 899 (smooth) Cross (Reciprocal).

Generation	Observed number of plants						χ^2
	smooth	rough	wrinkle	loose	total	expected ratio	
TVu 39	50	0	0	0	50		
TVu 899	50	0	0	0	50		
TVu 899 x TVu 39 (F_1)	25	0	0	0	25		
TVu 899 x TVu 39 x TVu 39	14	0	0	0	14		
TVu 899 x TVu 39 x TVu 899	15	0	0	0	15		
TVu 899 x TVu 39 (F_2)	596	0	0	0	596		

Table 5. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 899 (smooth) Cross (Combined).

Generation	Observed number of plants					expected ratio	χ^2
	smooth	rough	wrinkle	loose	total		
TVu 39	100	0	0	0	100		
TVu 899	100	0	0	0	100		
F_1	46	0	0	0	46		
BC_1	25	0	0	0	25		
BC_2	30	0	0	0	30		
F_2	1196	0	0	0	1196		

Table 6. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 803 (rough) Cross.

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 39	50	0	0	0	50		
TVu 803	0	50	0	0	50		
TVu 39 x TVu 803 (F_1)	15	0	0	0	15		
TVu 39 x TVu 803 x TVu 39	120	0	0	0	120		
TVu 39 x TVu 803 x TVu 803	140	130	0	0	270	1:1	0.3700
TVu 39 x TVu 803 (F_2)	430	151	0	0	581	3:1	0.3000

Not significant at 0.05 probability level.

Table 7. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 803 (rough) Cross (Reciprocal).

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 39	50	0	0	0	50		
TVu 803	0	50	0	0	50		
TVu 803 x TVu 39 (F_1)	20	0	0	0	20		
TVu 803 x TVu 39 x TVu 39	120	0	0	0	120		
TVu 803 x TVu 39 x TVu 803	144	126	0	0	270	1:1	1.2000
TVu 803 x TVu 39 (F_2)	433	148	0	0	581	3:1	0.0690

Not significant at 0.05 probability level.

smooth seed coat texture plants in the backcross of the F_1 to the smooth parent (Table 8).

Cross 3: TVu 39 (smooth) x TVu 13677 (wrinkle)

The segregation pattern in the study of the inheritance of seed coat texture using smooth seed coat texture variety TVu 39 and wrinkle seed coat texture variety TVu 13677 is presented in Table 9. All the parental lines bred true. The F_1 plants derived from the cross involving the two parents had smooth seed coat texture. The F_2, segregated into 456 smooth and 144 wrinkle (which closely fits a 3 smooth: 1 wrinkle ratio) [Table 9]. Reciprocal crosses yielded the same phenotypes in about the same proportion (Table 10). Combined reciprocal crosses yielded 39 smooth seeds plants in the F_1, 904 smooth and 296 wrinkle seed plants in the F_2 (which closely fit a 3 smooth: 1 wrinkle ratio), 209 smooth and 183 wrinkle plants (fitting a 1 smooth: 1 wrinkle ratio) in the backcross of the F_1 to the wrinkle parents and 208 smooth plants in the backcross of the F_1 to the smooth parents (Table 11). These results confirm the dominance of smooth seed coat texture and the observation that segregation occurred in only one gene.

Cross 4: TVu 39 (smooth) x TVu 3741 (loose)

The segregation pattern in the study of the inheritance of seed coat texture using smooth seed coat and loose seed coat varieties is presented in Table 12. The inheritance pattern was studied in cross TVu 39 x TVu 3741. All the parental lines bred true. The F_1 plants derived from the cross involving the two parents had smooth seed coat texture. The F_2, segregated into 440 smooth and 160 loose (which closely fits a 3 smooth: 1 loose ratio) [Table 12]. Reciprocal crosses yielded the same phenotypes in about the same proportion (Table 13). When the

Table 8. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 803 (rough) Cross (Combined).

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 39	100	0	0	0	100		
TVu 803	0	100	0	0	100		
F_1	35	0	0	0	35		
BC_1	240	0	0	0	240		
BC_2	284	256	0	0	540	1:1	1.4519
F_2	863	299	0	0	1162	3:1	0.3316

Not significant at 0.05 probability level.

Table 9. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 13677 (wrinkle) Cross.

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 39	50	0	0	0	50		
TVu 13677	0	0	50	0	50		
TVu 39 x TVu 13677 (F_1)	19	0	0	0	19		
TVu 39 x TVu 13677 x TVu 39	88	0	0	0	88		
TVu 39 x TVu 13677 x TVu 13677	107	0	85	0	192	1:1	2.5200
TVu 39 x TVu 13677 (F_2)	456	0	144	0	600	3:1	0.3200

Not significant at 0.05 probability level.

Table 10. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 13677 (wrinkle) Cross (Reciprocal).

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 39	50	0	0	0	50		
TVu 13677	0	0	50	0	50		
TVu 13677 x TVu 39 (F_1)	20	0	0	0	20		
TVu 13677 x TVu 39 x TVu 39	120	0	0	0	120		
TVu 13677 x TVu 39 x TVu 13677	102	0	98	0	200	1:1	0.0080
TVu 13677 x TVu 39 (F_2)	448	0	152	0	600	3:1	0.2756

Not significant at 0.05 probability level.

Table 11. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 13677 (wrinkle) Cross (Combined).

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 39	100	0	0	0	100		
TVu 13677	0	0	100	0	100		
F_1	39	0	0	0	39		
BC_1	208	0	0	0	208		
BC_2	209	0	183	0	392	1:1	1.7245
F_2	904	0	296	0	1200	3:1	0.0711

Not significant at 0.05 probability level.

Table 12. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 3741 (loose) Cross.

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 39	50	0	0	0	50		
TVu 3741	0	0	0	50	50		
TVu 39 x TVu 3741 (F_1)	13	0	0	0	13		
TVu 39 x TVu 3741 x TVu 39	110	0	0	0	110		
TVu 39 x TVu 3741 x TVu 3741	109	0	0	87	196	1:1	2.4700
TVu 39 x TVu 3741 (F_2)	440	0	0	160	600	3:1	0.8900

Not significant at 0.05 probability level.

Table 13. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 3741 (loose) Cross (Reciprocal).

Generation	Observed number of plants				total	expected ratio	χ^2
	smooth	rough	wrinkle	loose			
TVu 39	50	0	0	0	50		
TVu 3741	0	0	0	50	50		
TVu 3741 x TVu 39 (F_1)	15	0	0	0	15		
TVu 3741 x TVu 39 x TVu 39	120	0	0	0	120		
TVu 3741 x TVu 39 x TVu 3741	106	0	0	90	196	1:1	1.3061
TVu 3741 x TVu 39 (F_2)	444	0	0	15	600	3:1	0.3270

Not significant at 0.05 probability level.

reciprocals were combined (Table 14), all the 28 F_1 plants were smooth. In the F_2, 884 and 316 plants had smooth and loose seed coat texture respectively, which closely fit a 3 smooth: 1 loose ratio. Backcross of the F_1 to loose parent yielded 215 smooth and 177 loose seeded plants fitting a 1 smooth: 1 loose ratio. All the 230 plants obtained from backcross of the F_1 to the smooth parent were smooth (Table 14). These results confirm the dominance of smooth seed coat texture and the observation that segregation occurred in only one gene.

Cross 5: TVu 14195 (wrinkle) x TVu 13677 (wrinkle)

Inheritance of seed coat texture using the above cross combination was studied in cross TVu 14195 x TVu 13677. All the parental, F_1, reciprocal F_1, F_2, reciprocal F_2 and reciprocal backcrossed had wrinkle seed coat texture plants, showing no segregation (Tables 15 and 16). In the combined reciprocal crosses there were: 40 wrinkled F_1 seed plants, 1075 wrinkled F_2 plants and 70 wrinkled backcross plants (Table 17).

Cross 6: TVu 14195 (wrinkle) x TVu 803 (rough)

The segregation pattern in a cross involving TVu 14195 (wrinkle) and TVu 803 (rough) and its reciprocal is presented in Tables 18 and 19. All the parental lines bred true. The F_1 of all the crosses had wrinkle seed coat texture. The F_2 of the crosses segregated in a 3: 1 ratio of wrinkle and rough respectively (Tables 18 and 19).

Backcross of the F_1 to the rough parent gave a 1:1 ratio of wrinkle and rough seed coat texture plants while backcross of the F_1 to the wrinkle parent gave all wrinkle seeded plants (Tables 18 and 19).

Table 14. Segregation Pattern for Seed Coat Texture in TVu 39 (smooth) x TVu 3741 (loose) Cross (Combined).

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 39	100	0	0	0	100		
TVu 3741	0	0	0	100	100		
F_1	28	0	0	0	28		
BC_1	230	0	0	0	230		
BC_2	215	0	0	177	392	1:1	3.6837
F_2	884	0	0	316	1200	3:1	1.1377

Not significant at 0.05 probability level.

Table 15. Segregation Pattern for Seed Coat Texture in TVu 14195 (wrinkle) x TVu 13677 (wrinkle) Cross.

Generation	Observed number of plants					expected ratio	χ^2
	smooth	rough	wrinkle	loose	total		
TVu 14195	0	0	50	0	50		
TVu 13677	0	0	50	0	50		
TVu 14195 x TVu 13677 (F_1)	0	0	18	0	18		
TVu 14195 x TVu 13677 x TVu 14195	0	0	20	0	20		
TVu 14195 x TVu 13677 x TVu 13677	0	0	20	0	20		
TVu 14195 x TVu 13677 (F_2)	0	0	535	0	535		

Table 16. Segregation Pattern for Seed Coat Texture in TVu 14195 (wrinkle) x TVu 13677 (wrinkle) Cross (Reciprocal).

Generation	Observed number of plants					expected ratio	χ^2
	smooth	rough	wrinkle	loose	total		
TVu 14195	0	0	50	0	50		
TVu 13677	0	0	50	0	50		
TVu 13677 x TVu 14195 (F_1)	0	0	22	0	22		
TVu 13677 x TVu 14195 x TVu 14195	0	0	20	0	20		
TVu 13677 x TVu 14195 x TVu 13677	0	0	15	0	15		
TVu 13677 x TVu 14195 (F_2)	0	0	540	0	540		

Table 17. Segregation Pattern for Seed Coat Texture in TVu 14195 (wrinkle) x TVu 13677 (wrinkle) Cross (Combined).

Generation	Observed number of plants					expected ratio	χ^2
	smooth	rough	wrinkle	loose	total		
TVu 14195	0	0	100	0	100		
TVu13677	0	0	100	0	100		
F_1	0	0	40	0	40		
BC_1	0	0	35	0	35		
BC_2	0	0	35	0	35		
F_2	0	0	1075	0	1075		

Table 18. Segregation Pattern for Seed Coat Texture in TVu 14195 (wrinkle) x TVu 803 (rough) Cross.

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 14195	0	0	50	0	50		
TVu 803	0	50	0	0	50		
TVu 14195 x TVu 803 (F_1)	0	0	26	0	26		
TVu 14195 x TVu 803 x TVu 14195	0	0	58	0	58		
TVu 14195 x TVu 803 x TVu 803	0	70	79	0	149	1:1	1.3600
TVu 14195 x TVu 803 (F_2)	0	123	328	0	451	3:1	1.2400

Not significant at 0.05 probability level.

Table 19. Segregation Pattern for Seed Coat Texture in TVu 14195 (wrinkle) x TVu 803(rough) Cross (Reciprocal).

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 14195	0	0	50	0	50		
TVu 803	0	50	0	0	50		
TVu 803 x TVu 14195 (F_1)	0	0	26	0	26		
TVu 803 x TVu 14195 x TVu 1419	0	0	60	0	60		
TVu 803 x TVu 14195 x TVu 803	0	71	79	0	150	1:1	0.4267
TVu 803 x TVu 14195 (F_2)	0	121	329	0	450	3:1	0.8563

Not significant at 0.05 probability level.

Combined reciprocal crosses gave 52 wrinkle F_1 plants, 657 wrinkle and 244 rough seeded plants fitting closely a 3 wrinkle: 1 rough ratio in the F_2. Back crossing F_1 plants to the rough parent gave 141 rough and 158 wrinkle fitting closely a 1 wrinkle: 1 rough ratio, while backcross F_1 plants to the wrinkle gave all 118 wrinkled seed texture plants (Table 20).

Cross 7: TVu 14195 (wrinkle) x TVu 3741 (loose)

The inheritance of seed coat texture using the above combination was studied in the cross TVu 14195 (wrinkle) x TVu 3741 (loose). All the parental lines bred true. The F_1 plants of the cross had wrinkle seeds. Segregation in the F_2 gave a close fit to 3 wrinkle: 1 loose ratio. Backcross F_1 plants involving loose parent segregated into 1 wrinkle: 1 loose ratio, while backcross F_1 plants involving the wrinkle parent gave all wrinkle seeded plants.

Reciprocal crosses yielded the same phenotypes in about the same proportion (Table 22). Combined reciprocals gave 62 wrinkle F_1 plants, 766 wrinkle and 245 loose plants (fitting closely a 3 wrinkle: 1 loose ratio) in the F_2. Backcross F_1 plants involving the loose parent had 42 wrinkle and 34 loose plants (fitting closely a 1 wrinkle: 1 loose ratio), while backcross F_1 plants involving the smooth parents had all 182 wrinkle seeds (Table 23).

Cross 8: TVu 3741 (loose) x TVu 3743 (loose)

Inheritance of seed coat texture using the above cross combination was studied in the cross TVu 3741 (loose seeded) x TVu 3743 (loose seeded). All the 50 plants of TVu 3741 and 50 plants of TVu 3743 were loose seeded (Table 24). All the 22 F_1 plants, 588 F_2 plants and 30 backcross plants were loose seeded (Table 24), showing no segregation. Reciprocal crosses yielded the same

Table 20. Segregation Pattern for Seed Coat Texture in TVu 14195 (wrinkle) x TVu 803 (rough) Cross (Combined).

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 14195	0	0	100	0	100		
TVu 803	0	100	0	0	100		
F_1	0	0	52	0	52		
BC_1	0	0	118	0	118		
BC_2	0	141	158	0	299	1:1	0.9666
F_2	0	244	657	0	901	3:1	2.0810

Not significant at 0.05 probability level.

Table 21. Segregation Pattern for Seed Coat Texture in TVu 14195 (wrinkle) x TVu 3741 (loose) Cross.

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 14195	0	0	50	0	50		
TVu 3741	0	0	0	50	50		
TVu 14195 x TVu 3741 (F_1)	0	0	32	0	32		
TVu 14195 x TVu 3741 x TVu 14195	0	0	92	0	92		
TVu 14195 x TVu 3741 x TVu 3741	0	0	22	16	38	1:1	0.9500
TVu 14195 x TVu 3741 (F_2)	0	0	388	123	511	3:1	0.2400

Not significant at 0.05 probability level.

Table 22. Segregation Pattern for Seed Coat Texture in TVu 14195 (wrinkle) x TVu 3741 (loose) Cross (Reciprocal).

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 14195	0	0	50	0	50		
TVu 3741	0	0	0	50	50		
TVu 3741 x TVu 14195 (F_1)	0	0	30	0	30		
TVu 3741 x TVu 14195 x TVu 14195	0	0	90	0	90		
TVu 3741 x TVu 14195 x TVu 3741	0	0	20	18	38	1:1	0.1053
TVu 3741 x TVu 14195 (F_2)	0	0	378	122	500	3:1	0.0960

Not significant at 0.05 probability level.

Table 23. Segregation Pattern for Seed Coat Texture in TVu 14195 (wrinkle) x TVu 3741 (loose) Cross (Combined).

Generation	Observed number of plants						
	smooth	rough	wrinkle	loose	total	expected ratio	χ^2
TVu 14195	0	0	100	0	100		
TVu 3741	0	0	0	100	100		
F_1	0	0	62	0	62		
BC_1	0	0	182	0	182		
BC_2	0	0	42	34	76	1:1	0.8421
F_2	0	0	766	245	1011	3:1	0.3168

Not significant at 0.05 probability level.

Table 24. Segregation Pattern for Seed Coat Texture in TVu 3741 (loose) x TVu 3743 (loose) Cross.

Generation	Observed number of plants						χ^2
	smooth	rough	wrinkle	loose	total	expected ratio	
TVu 3741	0	0	0	50	50		
TVu 3743	0	0	0	50	50		
TVu 3741 x TVu 3743 (F_1)	0	0	0	22	22		
TVu 3741 x TVu 3743 x TVu 3741	0	0	0	15	15		
TVu 3741 x TVu 3743 x TVu 3743	0	0	0	15	15		
TVu 3741 x TVu 3743 (F_2)	0	0	0	588	588		

phenotype in about the same proportion (Table 25). The pooled over of the reciprocal crosses gave 47 F_1 plants, 1129 F_2 plants and 62 backcross plants (Table 26). These results indicate that no segregation occurred in all the lines used.

Cross 9: TVu 3741 (loose) x TVu 803 (rough)

The segregation pattern in the study of the inheritance of seed coat texture using loose and rough seeded varieties is presented in Table 27. The inheritance pattern was studied in one cross and its reciprocal TVu 3741 x TVu 803. All the parental lines bred true. The F_1 plants had smooth seeded plants, which does not resemble any of the parental lines and also indicates the dominance of smooth over loose and rough seeded plants. Segregation in the F_2 gave a 9 smooth: 3 loose: 4 rough ratio (Tables 27 and 28), indicating two gene interaction in the expression of seed coat texture in cowpea. The F_1 backcross plants involving the loose seeded parent gave 36 loose and 30 smooth seeded plants (closely fitting a 1 loose: 1 smooth ratio (Table 27), while the F_1 backcross plants involving the rough seeded parents gave 26 smooth and 20 rough plants closely fitting a 1 smooth: 1 rough ratio. Thus confirming the dominance of smooth over rough and loose seed coat texture and digenic inheritance of the trait.

Pooled over of the reciprocal crosses yielded 42 smooth F_1 plants, 644 smooth, 211 loose and 302 rough seeded plants in the F_2 (which closely fit a 9 smooth: 3 loose: 4 rough ratio) [Table 29], confirming the dominance of smooth and digenic inheritance of the trait.

Table 25. Segregation Pattern for Seed Coat Texture in TVu 3741 (loose) x TVu 3743 (loose) Cross (Reciprocal).

Generation	Observed number of plants					χ^2
	smooth	rough	wrinkle	loose	total expected ratio	
TVu 3741	0	0	0	50	50	
TVu 3743	0	0	0	50	50	
TVu 3743 x TVu 3741 (F_1)	0	0	0	25	25	
TVu 3743 x TVu 3741 x TVu 3741	0	0	0	20	20	
TVu 3743 x TVu 3741 x TVu 3743	0	0	0	12	12	
TVu 3743 x TVu 3741 (F_2)	0	0	0	541	541	

Table 26. Segregation Pattern for Seed Coat Texture in TVu 3741 (loose) x TVu 3743 (loose) Cross (Combined).

Generation	Observed number of plants						χ^2
	smooth	rough	wrinkle	loose	total	expected ratio	
TVu 3741	0	0	0	100	100		
TVu 3743	0	0	0	100	100		
F_1	0	0	0	47	47		
BC_1	0	0	0	35	35		
BC_2	0	0	0	27	27		
F_2	0	0	0	1129	1129		

Table 27. Segregation Pattern for Seed Coat Texture in TVu 3741 (loose) x TVu 803 (rough) Cross.

Generation	Observed number of plants						
	smooth	loose	wrinkle	rough	total	expected ratio	χ^2
TVu 3741	0	50	0	0	50		
TVu 803	0	0	0	50	50		
TVu 3741 x TVu 803 (F_1)	17	0	0	0	17		
TVu 3741 x TVu 803 x TVu 3741	30	36	0	0	66	1:1	0.5400
TVu 3741 x TVu 803 x TVu 803	26	0	0	20	46	1:1	0.7800
TVu 3741 x TVu 803 (F_2)	310	101	0	146	557	9:3:4	0.4753

Not significant at 0.05 probability level.

Table 28. Segregation Pattern for Seed Coat Texture in TVu 3741 (loose) x TVu 803 (rough) Cross (Reciprocal).

Generation	Observed number of plants						
	smooth	loose	wrinkle	rough	total	expected ratio	χ^2
TVu 3741	0	50	0	0	50		
TVu 803	0	0	0	50	50		
TVu 803 x TVu 3741 (F_1)	25	0	0	0	25		
TVu 803 x TVu 3741 x TVu 3741	28	32	0	0	60	1:1	0.2667
TVu 803 x TVu 3741 x TVu 803	29	0	0	21	50	1:1	1.2800
TVu 803 x TVu 3741 (F_2)	334	110	0	156	600	9:3:4	0.3319

Not significant at 0.05 probability level.

Table 29. Segregation Pattern for Seed Coat Texture in TVu 3741 (loose) x TVu 803 (rough) Cross (Combined).

Generation	Observed number of plants						
	smooth	loose	wrinkle	rough	total	expected ratio	χ^2
TVu 3741	0	100	0	0	100		
TVu 803	0	0	0	100	100		
F_1	42	0	0	0	42		
BC_1	58	68	0	0	126	1:1	0.7937
BC_2	55	0	0	41	96	1:1	2.0400
F_2	644	211	0	302	1157	9:3:4	0.7958

Not significant at 0.05 probability level.

Cross 10: TVu 803 (rough) x TVu 16514 (rough)

Inheritance of seed coat texture using the above cross combination was studied in cross TVu 803 and TVu 16514. All the parental, F_1, F_2, reciprocal F_1, F_2 and backcross plants in all the crosses had rough seed coat texture (Tables 30 and 31). Pooled over of the reciprocal crosses, there were: 43 F_1 plants, 1150 F_2 plants and 80 backcross plants with rough seed coat texture (Table 32).

Table 30. Segregation Pattern for Seed Coat Texture in TVu 803 (rough) x TVu 16514 (rough) Cross.

Generation	Observed number of plants					expected ratio	χ^2
	smooth	rough	wrinkle	loose	total		
TVu 803	0	50	0	0	50		
TVu 16514	0	50	0	0	50		
TVu 803 x TVu 16514 (F_1)	0	25	0	0	25		
TVu 803 x TVu 16514 x TVu 803	0	17	0	0	17		
TVu 803 x TVu 16514 x TVu 16514	0	21	0	0	21		
TVu 803 x TVu 16514 (F_2)	0	590	0	0	590		

Table 31. Segregation Pattern for Seed Coat Texture in TVu 803 (rough) x TVu 16514 (rough) Cross (Reciprocal).

Generation	Observed number of plants					χ^2
	smooth	rough	wrinkle	loose	total	expected ratio
TVu 803	0	50	0	0	50	
TVu 16514	0	50	0	0	50	
TVu 803 x TVu 16514 (F_1)	0	18	0	0	25	
TVu 803 x TVu 16514 x TVu 803	0	20	0	0	20	
TVu 803 x TVu 16514 x TVu 16514	0	22	0	0	22	
TVu 803 x TVu 16514 (F_2)	0	560	0	0	560	

Table 32. Segregation Pattern for Seed Coat Texture in TVu 803 (rough) x TVu 16514 (rough) Cross (Combined).

Generation	Observed number of plants					expected ratio	χ^2
	smooth	rough	wrinkle	loose	total		
TVu 803	0	100	0	0	100		
TVu 16514	0	100	0	0	100		
F_1	0	43	0	0	43		
BC_1	0	37	0	0	37		
BC_2	0	33	0	0	33		
F_2	0	1150	0	0	1150		

4.2 INHERITANCE OF COOKING TIME IN SOME VARIETIES OF COWPEA.

4.2.1 Evaluation of Cooking Time in the Eight Cowpea Varieties

Analysis of variance indicated significant differences among the eight cowpea varieties for cooking time trait at P=0.05. TVu 39 and TVu 803 had the longest cooking time of 46.8 and 45.5 min respectively while TVu 14195 had the shortest cooking time of 28.2 min (Table 33). Based on these results, TVu 39, TVu 803 and TVu 14195 were chosen to study the mode of inheritance of cooking time trait.

4.2.2 Generation Mean Analysis (GMA)

Cross 1: TVu 39 (long cooking time) x TVu 14195 (short cooking time)

The mean, standard error and genetic variance of the six basic generations of the above cross combination and their reciprocals (original and $\log_{10}$) are presented in Tables 34 and 35. The mean of the F_1 is less than the mid-parent value but higher than the mean of the parent with short cooking time (Tables 34 and 35). This may suggest dominance of short cooking time over long cooking time. The F_2 mean was higher than F_1 mean. The differences between the means of the reciprocal crosses were not significant; so the values of the reciprocals were pooled for subsequent computations (Tables 34 and 35).

Mather's (1949) A, B and C scaling test were significantly different from zero at P=0.05 (Table 36). The values of A, B and C were large and negative.

Table 33. Mean Cooking Time (min) in seeds of eight Cowpea Varieties.

Accessions	Cooking Time
TVu 14195	28.2h
TVu 899	35.0fg
TVu 13677	36.8ef
TVu 3741	39.0de
TVu 16514	40.2cd
TVu 3743	42.4c
TVu 803	45.5ab
TVu 39	46.8a

Means followed by the same letter(s) are not significantly different at P = 0.05 (Duncan's Multiple-Range Test).

Table 34. Mean Seed Cooking Time (min), Standard Errors and Genetic Variances in TVu 39 x TVu 14195 F_1, RF_1, F_2, RF_2, BC_1, RBC_1 BC_2 and RBC_2 Crosses.

Generations	Number of Plants	Mean	Genetic variance
TVu 39	50	46.8 ± 0.1513	1.1449
TVu 14195	50	28.2 ± 0.0929	0.4316
F_1	25	29.2 ± 0.1020	0.2600
RF_1	25	29.3 ± 0.1040	0.2704
F_2	455	29.9 ± 0.1510	10.3797
RF_2	455	29.8 ± 0.1496	10.1784
BC_1	280	34.0 ± 0.1143	3.6584
RBC_1	280	34.1 ± 0.1105	3.4170
BC_2	280	27.9 ± 0.0752	1.5851
RBC_2	280	28.0 ± 0.0933	2.4417

R = Reciprocal
BC_1 = Progeny of a cross between F_1 and the higher parent
BC_2 = Progeny of a cross between F_1 and the lower parent

Table 35. Mean Seed Cooking Time (min), Standard Errors and Genetic Variances in TVu 39 x TVu 14195 (Log_{10}) F_1, RF_1, F_2, RF_2, BC_1, RBC_1 BC_2 and RBC_2 Crosses.

Generations	Number of Plants	Mean	Genetic variance
TVu 39	50	1.6701 ± 0.0014	0.0001
TVu 14195	50	1.4506 ± 0.0014	0.0001
F_1	25	1.4653 ± 0.0015	0.0001
RF_1	25	1.4674 ± 0.0015	0.0001
F_2	455	1.4724 ± 0.0021	0.0021
RF_2	455	1.4724 ± 0.0021	0.0021
BC_1	280	1.5308 ± 0.0015	0.0006
RBC_1	280	1.5318 ± 0.0014	0.0006
BC_2	280	1.4452 ± 0.0011	0.0004
RBC_2	280	1.4468 ± 0.0014	0.0005

R = Reciprocal
BC_1 = Progeny of a cross between F_1 and the higher parent
BC_2 = Progeny of a cross between F_1 and the lower parent

Table 36. A, B and C Scaling and Joint Scaling Tests of Cross TVu 39 x TVu 14195.

Scaling test (Mather, 1949)	
A	-7.9920* ± 0.2897
B	-1.5840* ± 0.2187
C	-14.0860* ± 0.6599
Joint scaling test (Cavalli, 1952)	
Mid-parent m	35.9570* ± 0.1003
Additive, [d]	8.3619* ± 0.0938
Dominance [h]	-7.9696* ± 0.1637
χ^2 3df	985.1097*

χ^2 = Chi–square for testing the adequacy of the model
* = Significantly different from zero at the 0.05 probability level

In the joint scaling test of Cavalli (1952), the Chi-square test value was high and significantly different from zero (Table 36), perhaps suggesting the occurrence of epistasis or the presence of non-allelic interaction in the inheritance of cooking time. The dominance [h] component was negative and the magnitude of [h] and additive component [d] was more or less the same.

When the original data were transformed to log $_{10}$, Mather's (1949) A, B and C scaling test and the joint scaling test of Cavalli (1952) were also significantly different from zero which provide overwhelming evidence of the failure of the additive-dominance model (Table 37).

The perfect fit solution that detects and estimates the magnitude of effects of non-allelic interaction (Jinks and Jones, 1958) was applied (Table 38). The [d] and [h] components were significantly different from zero. The magnitude of [h] was greater than that of [d]. The additive x additive [i], additive x dominance [j] and dominance x dominance [l] types of non-allelic interaction were all significantly different from zero. The component [j] and [h] was negative while [l] component was positive (Tables 38). Heritability was high (Table 39).

When the transformed data (log_{10}) was subjected to the six-parameter model of Model of Jinks and Jones (1958), the component [d], [h], [i], [j] and [l] were significantly different from zero (Tables 38). Component [h] and [j] were negative while component [l] was positive. Heritability was also high (Table 40).

Cross 2: TVu 803 (long cooking time) x TVu 14195 (short cooking time)

The mean, standard error and genetic variance of the six basic generations of the above cross combination and their reciprocals (original and log_{10}) are presented in Tables 41 and 42.

Table 37. A, B and C Scaling and Joint Scaling Tests of Cross TVu 39 and TVu 14195 (Log_{10}).

Scaling test (Mather, 1949)		
A		-0.0739* ± 0.0037
B		-0.0250* ± 0.0035
C		-0.1638* ± 0.0099
Joint scaling test (Cavalli, 1952)		
Mid-parent	m	1.5521* ± 0.0009
Additive,	[d]	0.1046* ± 0.0009
Dominance	[h]	-0.1049* ± 0.0017
χ^2 3df		633.2488*

χ^2 = Chi–square for testing the adequacy of the model
* = Significantly different from zero at the 0.05 probability level

Table 38. Estimate of Genetic Components, additive [d], dominance [h] and epistatic ([i], [j] and [l]) interactions for Cooking Time in the Cross TVu 39 x TVu 14195, Determined from the Six Parameter Model.

Components	Original scale	Log $_{10}$
m	33.0050* ± 0.6700	1.4954* ± 0.0098
[d]	9.2850* ± 0.0887	0.1098* ± 0.0003
[h]	-8.8010* ± 1.4975	-0.0628* ± 0.0217
[i]	4.5100* ± 0.6641	0.0650* ± 0.0098
[j]	-6.4100* ± 0.3330	-0.0489* ± 0.0044
[l]	5.0660* ± 0.8678	0.0338* ± 0.0126

* = Significant at 0.05 probability level.
[i] = [d] x [d], [j] = [d] x [h] , [l] = [h] x [h] interactions

Table 39. Percentage Heritability of Cooking Time in the Two Crosses (Original Data).

Cross	Heritability (%)	
	Broad sense (Hb)	Narrow sense (Hn)
TVu 39 x TVu14195	93.2	71.0
TVu 803 x TVu 14195	89.1	58.0

Table 40. Percentage Heritability of Cooking Time in the Two Crosses (Log_{10}).

Cross	Heritability (%)	
	Broad sense (Hb)	Narrow sense (Hn)
TVu 39 x TVu14195	95.2	84.7
TVu 803 x TVu 14195	91.7	70.7

Table 41. Mean Seed Cooking Time (min), Standard Errors and Genetic Variances in TVu 803 x TVu 14195 F_1, RF_1, F_2, RF_2, BC_1, RBC_1 BC_2 and RBC_2 Crosses.

Generations	Number of Plants	Mean	Genetic variance
TVu 803	50	45.5 ± 0.2369	2.8070
TVu 14195	50	28.2 ± 0.2303	0.4316
F_1	25	29.6 ± 0.1766	0.7800
RF_1	25	29.4 ± 0.1746	0.7624
F_2	455	30.8 ± 0.1489	10.0850
RF_2	455	30.7 ± 0.1484	10.0169
BC_1	140	34.5 ± 0.1879	4.9404
RBC_1	140	34.45 ± 0.1767	4.3723
BC_2	140	28.1 ± 0.1526	3.2608
RBC_2	140	28.1 ± 0.1566	3.4324

R = Reciprocal
BC_1 = Progeny of a cross between F_1 and the higher parent
BC_2 = Progeny of a cross between F_1 and the lower parent

Table 42. Mean Seed Cooking Time (min), Standard Errors and Genetic Variances in Cross TVu 803 x TVu 14195(Log_{10}) F_1, RF_1, F_2, RF_2, BC_1, RBC_1 BC_2 and RBC_2 Crosses.

Generations	Number of Plants	Mean	Genetic variance
TVu 803	50	1.6576 ± 0.0031	0.0002
TVu 14195	50	1.4506 ± 0.0014	0.0001
F_1	25	1.4711 ± 0.0026	0.0002
RF_1	25	1.4688 ± 0.0026	0.0002
F_2	455	1.4861 ± 0.0020	0.0017
RF_2	455	1.4856 ± 0.0020	0.0017
BC_1	140	1.5373 ± 0.0024	0.0008
RBC_1	140	1.5344 ± 0.0023	0.0007
BC_2	140	1.4478 ± 0.0022	0.0007
RBC_2	140	1.4489 ± 0.0023	0.0007

R = Reciprocal
BC_1 = Progeny of a cross between F_1 and the higher parent
BC_2 = Progeny of a cross between F_1 and the lower parent

The mean of the F_1 is less than the mid-parent value but higher than the mean of the parent with short cooking time (Tables 41 and 42). This may suggest dominance of short cooking time over long cooking time. The F_2 mean was higher than F_1 mean. The differences between the means of the reciprocal crosses were not significant; so the values of the reciprocals were pooled for subsequent computations (Tables 41 and 42).

Mather's (1949) A, B and C scaling test were significantly different from zero at P=0.05 (Table 43). The values of A, B and C were large and negative.

In the joint scaling test of Cavalli (1952), the Chi-square test value was high and significantly different from zero (Table 43), perhaps suggesting the occurrence of epistasis or the presence of non-allelic interaction in the inheritance of cooking time. The dominance [h] component was negative and the magnitude of [h] and additive component [d] was more or less the same.

When the original data were transformed to $\log_{10}$, Mather's (1949) A, B and C scaling test and the joint scaling test of Cavalli (1952) were also significantly different from zero which provide overwhelming evidence of the failure of the additive-dominance model (Table 44).

The perfect fit solution that detects and estimates the magnitude of effects of non-allelic interaction (Jinks and Jones, 1958) was applied (Table 45). The [d] and [h] components were significantly different from zero. The magnitude of [h] was greater than that of [d]. The additive x additive [i], additive x dominance [j] and dominance x dominance [l] types of non-allelic interaction were all significantly different from zero. The component [j] and [h] was negative while [l] component was positive (Tables 45). Heritability was high (Table 39).

When the transformed data ($\log_{10}$) was subjected to the six-parameter model of Jinks and Jones (1958), the components [d], [h], [I], [j] and [l] were

Table 43. A, B and C Scaling and Joint Scaling Tests of Cross TVu 803 x TVu 14195.

Scaling test (Mather, 1949)	
A	-6.0243* ± 0.4689
B	-1.4857* ± 0.3675
C	-9.7424* ± 0.7360
Joint scaling test (Cavalli, 1952)	
Mid-parent m	35.6545* ± 0.1655
Additive, [d]	7.9251* ± 0.1594
Dominance [h]	-7.4752* ± 0.1496
χ^2 3df	248.6356*

χ^2 = Chi–square for testing the adequacy of the model
* = Significantly different from zero at the 0.05 probability level

Table 44. A, B and C Scaling and Joint Scaling Tests of Cross TVu 803 x TVu 14195 (Log_{10}).

Scaling test (Mather, 1949)	
A	-0.0539* ± 0.0059
B	-0.0239* ± 0.0054
C	-0.1047* ± 0.0100
Joint scaling test (Cavalli, 1952)	
Mid-parent m	1.5450* ± 0.0015
Additive, [d]	0.0965* ± 0.0015
Dominance [h]	-0.0931* ± 0.0029
χ^2 3df	248.6356*

χ^2 = Chi–square for testing the adequacy of the model
* = Significantly different from zero at the 0.05 probability level

Table 45. Estimate of Genetic Components, additive [d], dominance [h] and epistatic ([i], [j] and [l]) interactions for Cooking Time in the Cross TVu 803 x TVu 14195, Determined from the Six Parameter Model.

Components	Original scale	Log_{10}
m	34.6280* ± 0.7736	1.5271* ± 0.0104
[d]	8.6300* ± 0.1272	0.1035* ± 0.0013
[h]	-10.3852* ± 1.9100	-0.1079* ± 0.0257
[i]	2.2324* ± 0.7631	0.0270* ± 0.0103
[j]	-4.5386* ± 0.5416	-0.0300* ± 0.0070
[l]	5.2776* ± 1.2067	0.0507* ± 0.0164

* = Significant at 0.05 probability level.
[i] = [d] x [d], [j] = [d] x [h] , [l] = [h] x [h] interactions

significantly different from zero (Tables 45). Component [h] and [j] were negative while component [l] was positive. Heritability was also high (Table 40).

Frequency distribution for the six generations for the two cross and $\log_{10}$ transformed data is presented in Figures 1-4. The distribution in the F_2 is continuous. It can be observed from the two crosses that the spread of F_2 distribution is greater than that of the parents and F_1 generation. The F_1 distributions were skewed toward the short cooking time parents, as were the F_2s. The BC_2 is skewed to the left while BC_1 is skewed to the right. There were transgressive segregants for the parent with short cooking time in both crosses and only few individuals in F_2 distribution reached the lower size limit of the parent with long cooking time.

The Chi-square tests for some fixed (Mendelian) ratio for F_2 (both original and $\log_{10}$ scale) in both crosses indicated lack of fit to the 3:1 and 9:7 ratio and a good fit to the 15:1 ratios (Table 46). The Chi-square values for BC_1 and BC_2 were significant (Table 46), indicating lack of fit to the 1:1 ratio. Application of Wright's formula suggested that the parents differed by four genes for this trait in both crosses.

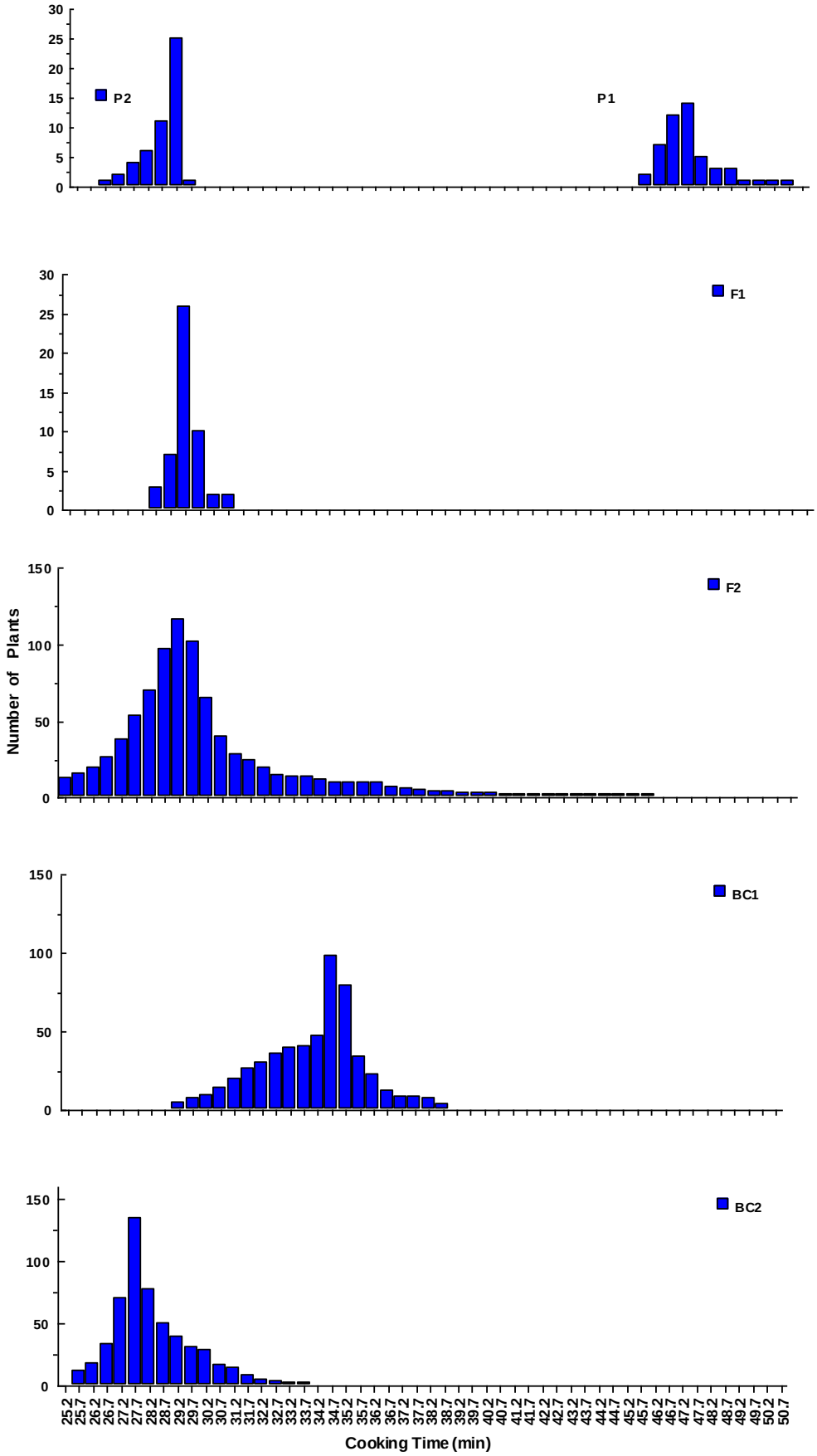

Fig. 1. Frequencies of Cooking Time of Parental (P1 and P2), F1, F2 and Backcross (BC1 and BC2) Generations of the Cross TVu 39 (P1) and TVu 14195 (P2)

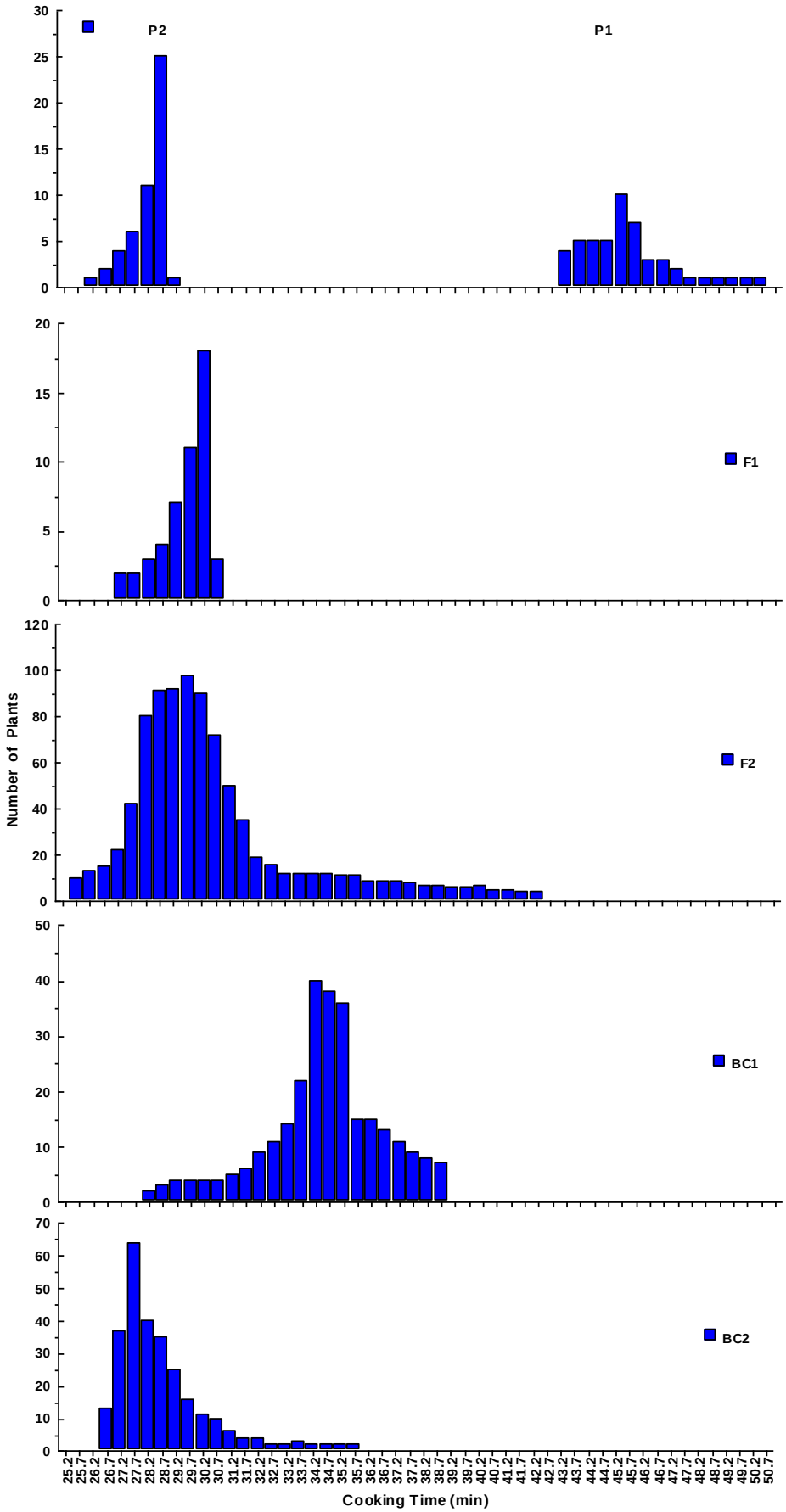

Fig. 2. Frequencies of Cooking Time of Parental (P1 and P2), F1, F2 and Backcross (BC1 and BC2) Generations of the Cross TVu 803 (P1) and TVu 14195 (P2)

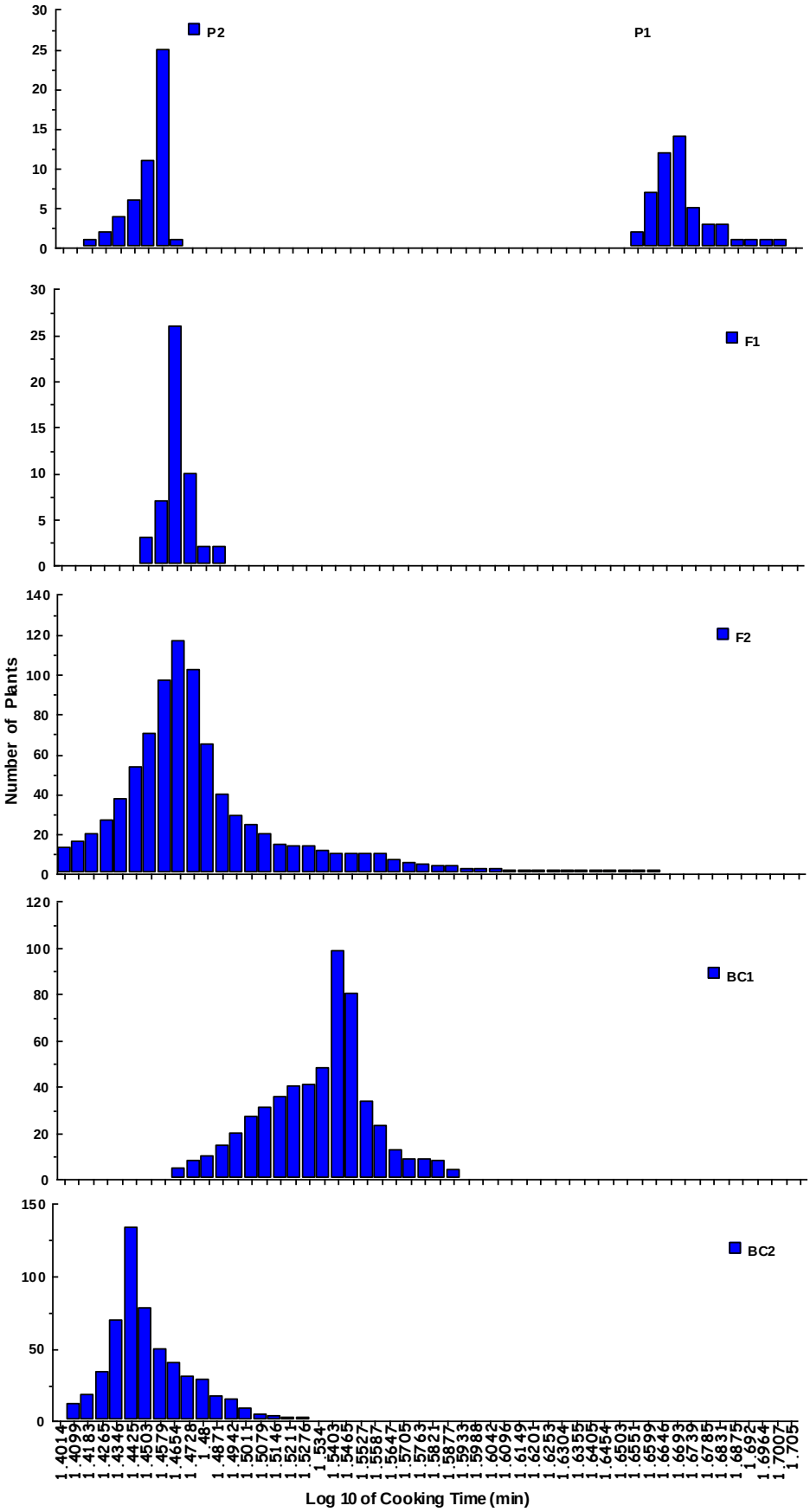

Fig.3. Frequencies of Cooking Time of Parental (P1and P2), F1, F2 and Backcross (BC1 and BC2) Generations of the Cross TVu 39 (P1) and TVu 14195 (P2) [Log10]

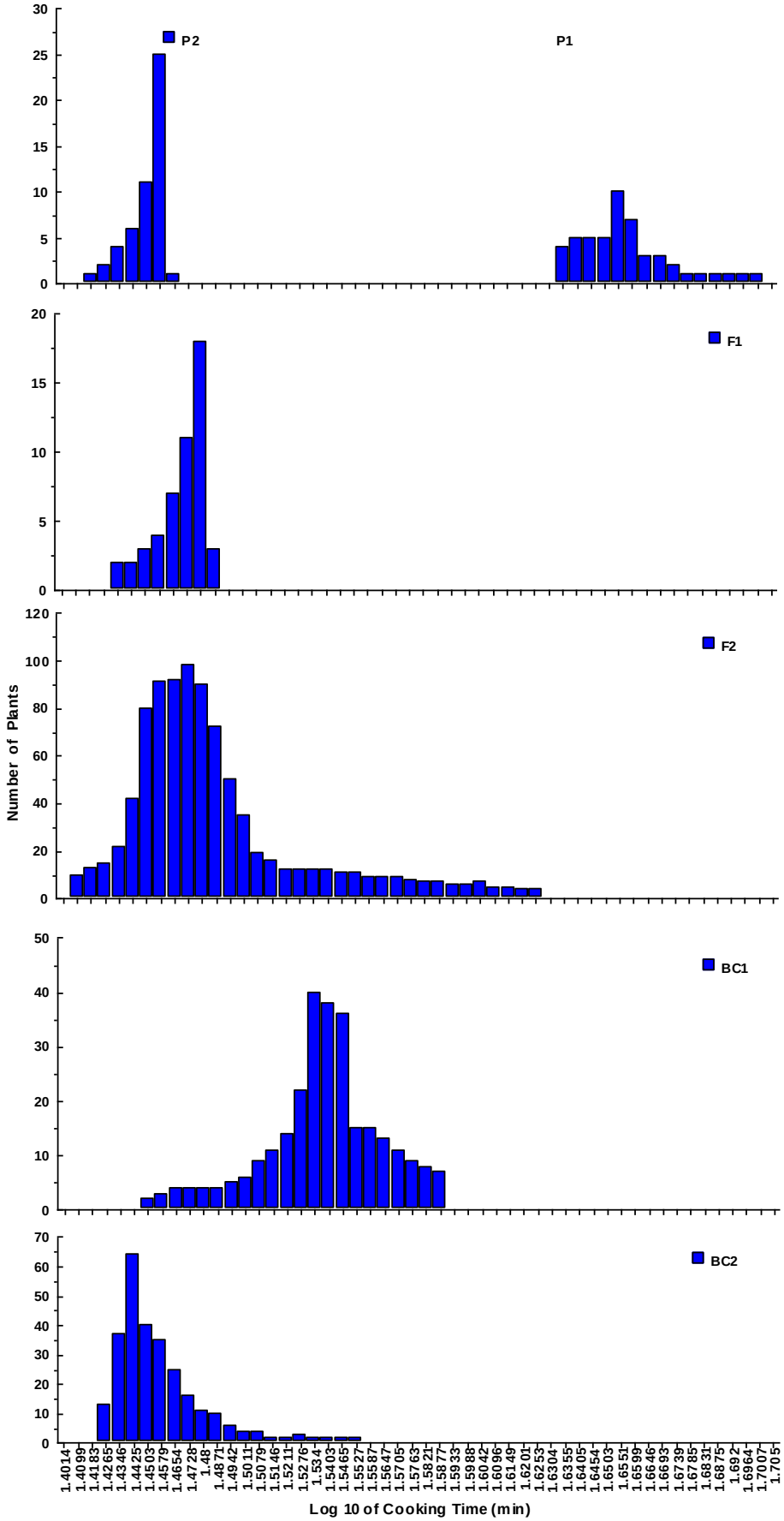

Fig.4. Frequencies of Cooking Time of Parental (P1and P2), F1, F2 and Backcross (BC1and BC2) Generations of the Cross TVu 803 (P1) and TVu 14195 (P2) [Log10]

Table 46. Chi-square (χ^2), the Observed (O) and Expected (E) Values for Different Ratio of Cooking Time.

Generation	Ratio		TVu 39 x TVu 14195				TVu 803 x TVu 14195			
			short		long		short		long	
F_2	3:1	O	866	:	44	O	842	:	68	
		E	682.5	:	227.5	E	682.5	:	227.5	
		χ^2	197.35*			χ^2	149.1*			
	9:7	O	866	:	44	O	842	:	68	
		E	511.88	:	398.13	E	511.88	:	398.13	
		χ^2	559.97*			χ^2	486.64*			
	15:1	O	866	:	44	O	842	:	68	
		E	853.13	:	56.88	E	853.13	:	56.88	
		χ^2	3.11ns			χ^2	2.32ns			
BC_1	1:1	O	539	:	21	O	245	:	35	
		E	280	:	280	E	140	:	140	
		χ^2	479.15*			χ^2	157.5*			
BC_2	1:1	O	560	:	0	O	280	:	0	
		E	280	:	0	E	140	:	140	
		χ^2	560.00*			χ^2	280.00*			

* = Significantly different from zero at P = 0.05
ns = Not significantly different from zero at P = 0.05

Cross 3: TVu 39 (long cooking time) x TVu 803 (long cooking time)

The mean, standard error and genetic variance of the six basic generation of the above cross combination (original and $\log_{10}$) are presented in Tables 47 and 48. The mean F_1 value was midway between the two parents indicating the absence of dominance and the mean values of F_1, F_2, BC_1 and BC_2 were more or less equal. The differences between the means of the reciprocal crosses were small and non-significant, so the reciprocals were pooled for subsequent computations (Tables 47 and 48).

The Mather's (1949) A, B and C scaling test were not significantly different from zero in both the original and $\log_{10}$ scale (Tables 49 and 50). There was also no correlation between generation means and variance (Table 51).

In the joint scaling test of Cavalli (1952), the estimate of m and [d] was significantly different from zero in both the original and $\log_{10}$ transformed data. [h] was not significantly different from zero. The magnitude of [d] was five times that of [h]. The component [h] was negative on both scales. However, the Chi-square value was not significantly different from zero on both scales (Tables 51 and 50).

When the data was subjected to two-parameter model by removing the dominance component so that more precise estimate of [d] is obtained, [d] was significant on both scales. The magnitude of [d] was slightly higher than in the 3-parameter model on the original data but same on the transformed data. The standard error was lower in both cases compared to the 3-parameter model (Table 52). However, the Chi-square value was not significantly different from zero (Table 52).

When the six-parameter model that detects and estimates the magnitude of effects of non-allelic interaction (Jinks and Jones, 1958) was applied to the cross,

Table 47. Mean Seed Cooking Time (min), Standard Errors and Genetic Variances in TVu 39 x TVu 803 F_1, RF_1, F_2, RF_2, BC_1, RBC_1 BC_2 and RBC_2 Crosses.

Generations	Number of Plants	Mean	Genetic variance
TVu 39	50	46.8 ± 0.1513	1.1449
TVu 803	50	45.5 ± 0.2369	2.8070
F_1	25	46.0 ± 0.1811	0.8200
RF_1	25	46.0 ± 0.1764	0.7776
F_2	455	46.1 ± 0.0672	2.0555
RF_2	455	46.1 ± 0.0712	2.3044
BC_1	140	46.4 ± 0.1215	2.0676
RBC_1	140	46.5 ± 0.1177	1.9404
BC_2	140	45.8 ± 0.1340	2.5140
RBC_2	140	45.9 ± 0.1356	2.5755

R = Reciprocal
BC_1 = Progeny of a cross between F_1 and the higher parent
BC_2 = Progeny of a cross between F_1 and the lower parent

Table 48. Mean Seed Cooking Time (min), Standard Errors and Genetic Variances in TVu 39 x TVu 803(Log_{10}) F_1, RF_1, F_2, RF_2, BC_1, RBC_1 BC_2 and RBC_2 Crosses.

Generations	Number of Plants	Mean	Genetic variance
TVu 39	50	1.6701 ± 0.0014	0.0001
TVu 803	50	1.6576 ± 0.0031	0.0002
F_1	25	1.6627 ± 0.0017	0.0001
RF_1	25	1.6628 ± 0.0017	0.0001
F_2	455	1.6635 ± 0.0006	0.0002
RF_2	455	1.6634 ± 0.0007	0.0002
BC_1	140	1.6663 ± 0.0011	0.0002
RBC_1	140	1.6667 ± 0.0011	0.0002
BC_2	140	1.6601 ± 0.0013	0.0002
RBC_2	140	1.6616 ± 0.0013	0.0002

R = Reciprocal
BC_1 = Progeny of a cross between F_1 and the higher parent
BC_2 = Progeny of a cross between F_1 and the lower parent

Table 49. A, B and C Scaling and Joint Scaling Tests of Cross TVu 39 x TVu 803.

Scaling test (Mather, 1949)	
A	$0.0257^{ns} \pm 0.3351$
B	$0.1534^{ns} \pm 0.4011$
C	$0.0702^{ns} \pm 0.5326$
Joint scaling test (Cavalli, 1952)	
Mid-parent m	46.1690* ± 0.1144
Additive, [d]	0.6288* ± 0.1091
Dominance [h]	$-0.1381^{ns} \pm 0.2175$
χ^2 3df	0.4543^{ns}

ns = Not significantly different from zero at 0.05 level of probability
* = Significantly different from zero at the 0.05 probability level

Table 50. A, B and C Scaling and Joint Scaling Tests of Cross TVu 39 x TVu 803(Log_{10}).

Scaling test (Mather, 1949)	
A	$0.0002^{ns} \pm 0.0033$
B	$0.0014^{ns} \pm 0.0037$
C	$0.0006^{ns} \pm 0.0051$
Joint scaling test (Cavalli, 1952)	
Mid-parent m	$1.6637^{*} \pm 0.0012$
Additive, [d]	$0.0062^{*} \pm 0.0012$
Dominance [h]	$-0.0012^{ns} \pm 0.0023$
χ^2 3df	0.4543^{ns}

ns = Not significantly different from zero at 0.05 level of probability
* = Significantly different from zero at the 0.05 probability level

Table 51. Correlation between Generation Means and Variances for the Three Crosses.

Cross	Correlation	
	Original scale	Log_{10}
TVu 39 x TVu14195	-0.15^{ns}	-0.23^{ns}
TVu 803 x TVu 14195	0.04^{ns}	-0.18^{ns}
TVu 39 x TVu 803	-0.55^{ns}	-0.55^{ns}

ns = Not significant at the 0.05 level of probability

Table 52. Estimate of Additive Component [d] for Cooking Time in the Cross TVu 39 x TVu 803 as Determined from the 2- Parameter Model.

Components	Original scale	Log_{10}
m	46.1040 ± 0.0491	1.6636 ± 0.0005
[d]	0.6465* ± 0.1053	0.0062* ± 0.0011
χ^2 3df	0.8194ns	0.6923ns

* = Significant at 0.05 probability level.
ns = Not significant at the 0.05 level of probability

only the additive component [d] was significantly different from zero in both the original and transformed data (Table 53). The estimates of the interaction parameters are either smaller than their standard errors or not significantly larger than them (Table 53).

The frequency distribution of F_2, BC_1 and BC_2 populations on both the original and $\log_{10}$ scale is shown in Figures 5-6. The distribution is continuous and approaches a symmetrical curve. The F_1 plants lie in between the two parents. In the F_2 distribution, parental extremes were recovered. There was no evidence of transgressive segregation for cooking time.

Table 53. Estimate of Genetic Components, additive [d], dominance [h] and epistatic ([i], [j] and [l]) Interactions for Cooking Time in the Cross TVu 39 x TVu 803, Determined from the Six Parameter Model.

Components	Original scale	Log $_{10}$
m	46.2522* ± 0.4722	1.6605* ± 0.0045
[d]	0.6550* ± 0.1405	0.0063* ± 0.0013
[h]	-0.3566^{ns} ±1.2959	-0.0039^{ns} ± 0.0122
[i]	-0.1072^{ns} ± 0.4508	-0.0012^{ns} ± 0.0043
[j]	-0.0028^{ns} ± 0.4585	-0.0001^{ns} ± 0.0043
[l]	0.1044^{ns} ± 0.8983	0.0015^{ns} ± 0.0085

* = Significant at 0.05 probability level.
ns = Not significantly different from zero at 0.05 probability level
[i] = [d] x [d], [j] = [d] x [h] , [l] = [h] x [h] interactions

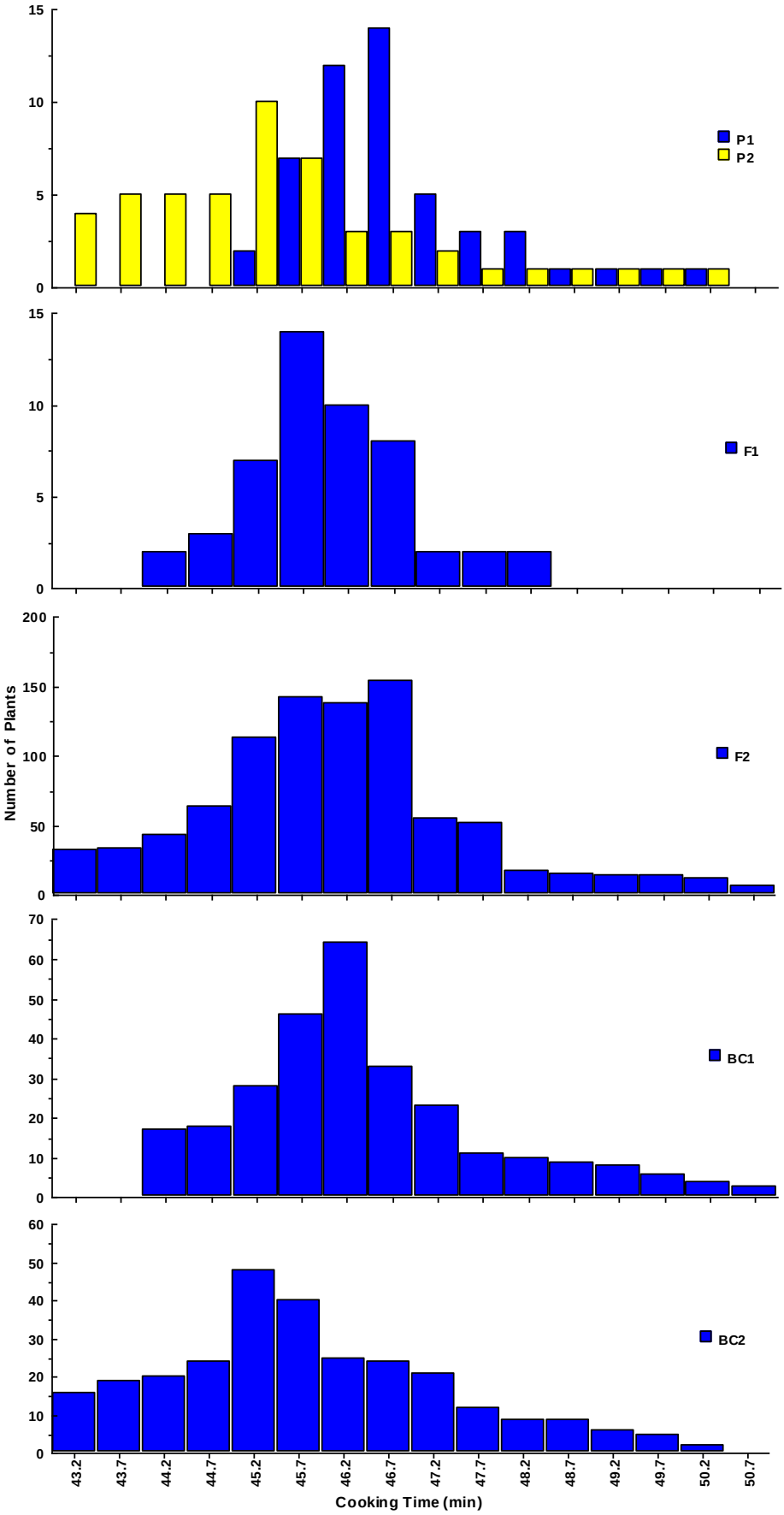

Fig. 5. Frequencies of CookingTime of Parental (P1 and P2), F1, F2 and Backcross (BC1 and BC2) Generations of the Cross TVu 39 (P1) and TVu 803 (P2)

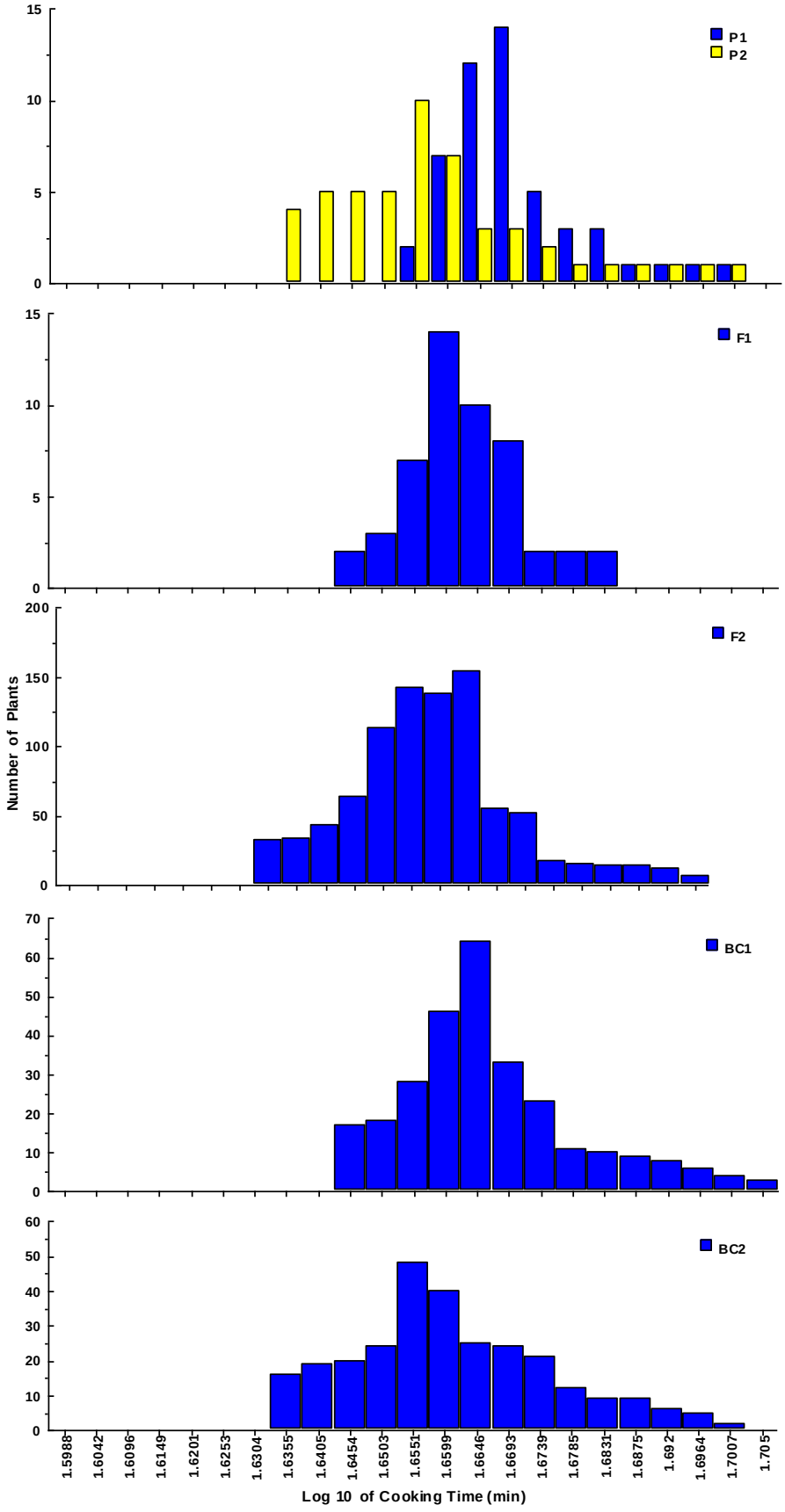

Fig.6. Frequencies of Cooking Time of Parental (P1 and P2), F1, F2 and Backcross (BC1 and BC2) Generations of the Cross TVu 39 (P1) and TVu 803 (P2) [Log10]

CHAPTER FIVE

DISCUSSION

Inheritance of seed coat texture and cooking time traits of some cowpea varieties were studied during this research. Attempts were made to determine the number of genes controlling each trait and to explain the interactions among these genes. Different patterns of inheritance were observed between the two traits studied.

5.1 INHERITANCE OF SEED COAT TEXTURE IN SOME VARIETIES OF COWPEA.

Genetic analysis of seed coat texture was carried out on crosses involving eight accessions of cowpea, *Vigna unguiculata* (L.) Walp. Four types of seed coat texture were used in this study: smooth, rough, wrinkle and loose. Two gene pairs were observed to control seed coat texture. A similar result was suggested by Drabo (1981), who reported that probably two or more genes control seed coat texture in cowpea. This observation disagrees with the report of Yilwa (2001) who reported the trait to be controlled by one gene. This could be because Yilwa (2001) research was based on only two types of seed coat texture (smooth and rough).

The gene controlling smooth, wrinkle, rough and loose seed coat textures were most likely the same in crosses involving smooth and smooth, wrinkle and wrinkle, rough and rough and loose and loose parents respectively due to lack of segregation in the F_1, back cross and F_2 populations.

The fact that reciprocal crosses were not significantly different suggest that the genes that controlled smooth, wrinkle, rough and loose seed coat textures were all nuclear and cytoplasmic genes had no effect on seed coat texture.

It was further observed that several types of gene interactions were involved in the expression of various seed coat textures. Dominance was observed in crosses involving smooth and rough, smooth and wrinkle and smooth and loose seeded plants. Smooth seeded plants were observed to be completely dominant over rough (Tables 6 and 7), wrinkle (Tables 9 and 10), and loose (Tables 12 and 13) seeded plants. The report of dominance of smooth texture over rough texture and monogenic inheritance of smooth seed coat texture over rough seed coat texture were suggested by Rajendra *et al*. (1979), Drabo (1981) and Yilwa (2001).

Even though seed coat texture appeared to be controlled by two genes, only one gene appears to segregate, therefore 3 smooth: 1 rough, 3 smooth: 1 wrinkle and 3 smooth: 1 loose ratio was obtained from segregating F_2 population. Back cross of F_1 plants involving wrinkle, rough and loose parents segregated into 1smooth: 1wrinkle, 1smooth: 1rough and 1smooth: 1loose ratio respectively while back cross F_1 plants involving the smooth parents gave all smooth seeded plants. These results confirm the dominance of smooth seed coat texture over wrinkle, rough, loose, and monogenic inheritance of the trait.

Dominance was also observed in crosses involving wrinkle and rough, wrinkle and loose seed plants. Wrinkle seed texture plants was observed to be completely dominant over rough (Tables 18 and 19) and loose (Tables 20 and 21). The F_2 yielded a 3 wrinkle: 1 rough and 3 wrinkle: 1 loose seeded plants, suggesting that segregation occurs in only one gene. Back cross F_1 plants involving rough and loose parents segregated into 1wrinkle: 1rough and 1wrinkle: 1loose ratio respectively while back cross F_1 plants involving the wrinkle parent

gave all wrinkle seeded plants, confirming the dominance of wrinkle over rough, loose, and monogenic inheritance of the traits.

This study reveals that dominant genes control smooth and wrinkled seed coat texture; the wrinkled seed coat texture is only expressed in the absence of the gene controlling smooth seed coat texture because of dominance of smooth over wrinkle.

Recessive epistasis (Modifying gene interaction) was observed in the cross between rough seed texture and loose seed texture plants. Modifying gene interaction refers to the interaction between gene pairs to produce a particular effect different from that observed in either of the parents. The cross between rough and loose texture plants gave smooth seed coat texture plants in the F_1, which is quite outside the range of the parents seed coat texture (rough and loose) and segregation in the F_2 gave 9 smooth: 3 loose: 4 rough ratio (Tables 27 and 28), suggesting that a modifying gene effect exists between two genes controlling seed coat texture in cowpea.

5.2 INHERITANCE OF COOKING TIME IN SOME VARIETIES OF COWPEA.

In the inheritance of cooking time study, eight varieties of *Vigna unguiculata* (L.) Walp were evaluated for cooking time to determine the existing genetic variability. Genotypic differences for cooking time trait were significant. Cooking time ranged from 28.2 to 46.8 minutes. Thus, there is sufficient genetic variability for cooking time trait within the cowpea germplasm studied for a sustained breeding programme.

In the generation mean analysis (GMA) Mather (1949) A, B, and C scaling test and the joint scaling test of Cavalli (1952) were significantly different from zero and this was true both on the original and log $_{10}$ transformed data for cross TVu 39

x TVu 14195 and TVu 803 x TVu 14195 indicating the unsuitability of the additive - dominance model for these sets of data and further suggesting the occurrence of epistasis or non-allelic interaction in the inheritance of cooking time trait in cowpea (Tables 36, 37 ,43 and 44).

However the A, B, and C scaling test and the joint scaling test were not significantly different from zero both on the original and log $_{10}$ transformed data for cross TVu 39 x TVu 803, which indicates that the additive-dominance model adequately explains the mode of inheritance of cooking time in this cross (Tables 49 and 50). The lack of correlation between the means of the generations and their variances (Table 51) further confirms the suitability of the model (Mansur *et al*., 1993).

The better estimate of the additive effect, together with the lower standard errors of the estimates on the 2-parameter model of the generation mean analysis (Table 52) as well as the non significance of the dominance effect confirms that the inheritance of cooking time in cross TVu 39 x TVu 803 is governed by mainly additive gene effects and that a 2-parameter model consisting of only m and [d] components could have been sufficient for the analysis. However, analysis on the 3–parameter model should be a preliminary step as it affords the opportunity to observe the whole pattern of genetic effects involved in the inheritance.

The perfect fit solution (Jinks and Jones, 1958) that detects and estimates the magnitude of effects of non-allelic interaction indicated that the additive [d], dominance [h] gene effects, additive x additive [i], additive x dominance [j] and dominance x dominance [l] epistatic interactions were significantly different from zero for cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 both on the original and log $_{10}$ transformed data (Tables 39 and 45). In cross TVu 39 x TVu 803 only the additive gene effects were significant (Table 53) further confirming the

adequacy of the additive-dominance model for this cross combination. The relative values of [d] and [h] was more or less equal in cross TVu 39 x TVu 14195 (Table 39) but the magnitude of [h] was a bit higher than that of [d] in cross TVu 803 x TVu 14195 (Table 45)

The magnitude of the parameter m, [d] and [h] in the additive-dominance model differed from those based on the model, which included non-allelic interaction (by perfect fit estimation). This situation is expected when additive – dominance model has failed. Furthermore, once we allow the presence of non-allelic interaction, the mid point is no longer the origin; therefore 'm' no longer corresponds to the original definition of 'm' as the mid point (Mather and Jinks, 1982).

Component [h] was significantly negative and [i] was significantly positive suggesting a duplicate type of non-allelic interaction. This signifies that the genes for long cooking time and short cooking time are allelic to each other.

The frequency distribution of the F_2 and backcross populations in the three crosses both on the original and log $_{10}$ transformed data resulted in continuous variations that were wider than those of the parents or F_1. This is due to the fact that the spread of the parents and F_1 is caused only by the environment since the parents were homozygous and the F_1 are uniformly heterozygous. The spread of the F_2 on the other hand, is partly caused by the environment and partly caused by the segregation of genes. This is an indication that cooking time trait is quantitatively inherited. The transgressive segregants in the F_2 and backcross populations of cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 suggest the role of modifiers. The F_2 segregation pattern is unimodel as is expected from crosses where no discrete classes could be differentiated. The unimodel distribution is in two categories: (a) continuous distribution with trangressive

segregation to the lower as in cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 (b) continuous distribution within parental limits as in cross TVu 39 x TVu 803. It means that in addition to the major genes controlling cooking time trait, many genes with relatively smaller and cumulative effects are present in every parent to account for the large range in variation of cooking time found in the F_2 progenies. Many genes control the F_2 phenotypes, each having only a small effect on the expression of the character. The resulting segregation is typically that of quantitative characters. However, the skewness of the F_2 distribution in favour of the short cooking time parents suggest that the trait is governed by dominant genes.

Attempt to partition the distribution in the F_2 and backcross populations of cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 to some simple Mendelian ratios of one or two genes model was unsuccessful for a 3:1 and 9:7 ratio due to the significant difference between the observed and expected values in F_2 and backcross populations, but successful for the 15:1 ratio due to lack of significant difference between the observed and expected values in the F_2. This suggests that the inheritance of cooking time in cowpea is governed by two dominant alleles interacting at two loci, which signifies duplicate dominant epistasis interaction in the inheritance of cooking time in cowpea. This is a situation where the dominant allele at either locus can override the homozygous recessive at the other locus.

Although the estimate of number of effective factors (genes) according to Wright's formula (Burns, 1976) suggested that four genes control cooking time in cowpea, this estimate may be biased by epistasis because the underlying assumption for the estimates of the effective factors (genes) include the absence of non-allelic (epistasis) interaction, absence of linkage, one parent supplies only plus factors and the other only minus factors and each allele at all loci has an

equal additive effect (Lawrence and Jinks, 1973 and Mather and Jinks , 1982). Therefore, the estimate of effective factor (genes) is at best only a useful guide to the genetic basis of seed cooking time.

From the above observations and the fact that the F_1 means in cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 were less than the mid-parent value and F_2 distribution was skewed towards the lower parent, it is suggested that short cooking time is dominant to long cooking time although additive gene effect, [i], [j], and [l] epistatic interaction also played a major role in the inheritance of cooking time in the two crosses. In addition, the inheritance pattern was the same in the two crosses. This result is in agreement with the work of Jacinto-Hernandez *et al*. (2003) who reported the dominance of short cooking time in *Phaseolus vulgaris* L. in Mexico.

The fact that there was no evidence of trangressive segregation in the F_2 in cross TVu 39 x TVu 803 and no significant differences between the means of the two parents, F_1, F_2, BC_1, and BC_2 generations of this cross (Figs 5 and 6) suggest that the same genes controlled this trait in both parents.

The presences of transgressive segregants in the F_2 in cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 may suggest that a new variety having very short cooking time could be selected at advanced generation.

There was no significant difference between reciprocal crosses. So the cytoplasmic influences on the trait expression as reported by Elia *et al*. (1997) in Andean dry bean *Phaseolus vulgaris* L. was not observed in this study. This means that the genes controlling cooking time trait were all nuclear and cytoplasmic genes had no effect in the inheritance of cooking time.

The estimate of heritability in the broad sense ranged from 89% to 95% (Table 46). Nielsen *et al.* (1993) reported a value of 76% for the same trait in

cowpea. Narrow sense heritability range from 58% to 85%. The estimate of narrow sense heritability includes both additive and additive x additive epistatic effects and is therefore an upper limit (Drabo *et al*., 1984). According to Stanfield (1988), traits with narrow sense heritability higher than 50% are considered to have a high heritability. The value reported here is lower than the value of 90% reported by Elia *et al*. (1997) for the same trait in *Phaseolus vulgaris* L. in Tanzania, but higher than the value of 74% reported by Jacinto-Hernandez *et al*. (2003) for the same trait in *Phaseolus vulgaris* L. in Mexico.

Assuming that 5% of the F_2 plants with the shortest cooking time were selected for further propagation; the expected genetic advance will be 4.69 and 3.77 minutes for cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 respectively.

5.3 CONCLUSION

The study revealed that Seed coat texture trait in cowpea appeared to be controlled by two gene pairs, with various forms of gene interactions such as dominance and recessive epistasis (modifying gene effects). Dominance of smooth seed coat texture over wrinkle, rough and loose seed coat texture was indicated. Wrinkle seed coat texture plants were also observed to be completely dominant over rough and loose seeded plants. The wrinkle seed coat texture is only expressed in the absence of the gene controlling smooth seed coat texture because of the dominance of smooth over wrinkle. Interaction between genes controlling loose and rough seed coat texture plants exhibit modifying gene effect by giving smooth seed plants in both F_1 and F_2 generations. The genes that controlled smooth, wrinkle, rough and loose seed coat textures were all nuclear and cytoplasmic genes had no effect on seed coat texture.

Significant genotypic variability was observed for cooking time trait in the eight-cowpea varieties evaluated for the study of the inheritance of cooking time. Two dominance alleles interacting at different loci were observed to govern cooking time trait in cowpea. Dominance of short cooking time over long cooking time was observed. Long cooking time was observed to be expressed only when it is homozygous recessive at both loci. Gene action was predominantly dominance but additive, additive x additive, additive x dominance and dominance x dominance epistatic effects were also significant.

Heritability both on broad and narrow sense was high. Assuming that 5% of the F_2 plants with the shortest cooking time were selected for further propagation; the expected genetic advance was 4.69 and 3.77 min for cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 respectively.

The presences of transgressive segregants in the F_2 in cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 may suggest that a new variety having very short cooking time could be selected at advanced generation.

The non-significant difference between reciprocal crosses suggests that the genes controlling cooking time trait were all nuclear and cytoplasmic genes had no effect in the inheritance of cooking time.

The large genotype effect of cooking time coupled with the high heritability for this trait suggest that selection based on the trait itself may allow for progress in breeding. This will lead to the development of fast cooking time cowpea cultivar acceptable to consumers, which might help conserve fuel wood.

Summary of Findings

The genetics effects and mode of inheritance of seed coat texture and cooking time traits in some varieties of cowpea were investigated in order to provide information that could be useful to breeders for developing breeding strategies for acceptable cowpea varieties. Different patterns of inheritance were observed between the two traits studied.

Genetic analysis of seed coat texture was carried out on crosses involving eight accessions of cowpea. Four types of seed coat texture were used in the study. Seed coat texture trait appeared to be controlled by two gene pairs, with various forms of gene interactions such as dominance and modifying gene effects. Dominance of smooth seed coat texture over wrinkle, rough and loose seed coat texture was indicated. Wrinkle seed coat texture plants were also observed to be completely dominant over rough and loose seeded plants. The wrinkle seed coat texture is only expressed in the absence of the gene controlling smooth seed coat texture because of the dominance of smooth over wrinkle. Interaction between genes controlling loose and rough seed coat texture plants exhibit modifying gene effect by giving smooth seed plants in both F_1 and F_2 generations. The genes that controlled smooth, wrinkle, rough and loose seed coat textures were all nuclear and cytoplasmic genes had no effect on seed coat texture.

Significant variability was observed for cooking time trait in the eight-cowpea varieties evaluated for the study of the inheritance of cooking time. Generation mean analysis of the six basic generations showed the inadequacy of the additive-dominance model in the inheritance of cooking time in the varieties of cowpea studied due to the presence of non- allelic (epistasis) interactions. Two dominance alleles interacting at different loci were observed to govern cooking time trait in cowpea.

Dominance of short cooking time over long cooking time was observed. Long cooking time was observed to be expressed only when it is homozygous recessive at both loci. Gene action was predominantly dominance but additive, additive x additive, additive x dominance and dominance x dominance epistatic effects were also significant.

The presences of transgressive segregants in the F_2 in cross TVu 39 x TVu 14195 and TVu 803 x TVu 14195 may suggest that a new variety having very short cooking time could be selected at advanced generation.

The non-significant difference between reciprocal crosses suggests that the genes controlling cooking time trait were all nuclear and cytoplasmic genes had no effect in the inheritance of cooking time.

Broad and narrow sense heritability estimates were quite high signifying that cooking time trait is heritable.

Contribution to Knowledge

Genetic studies on seed coat texture and cooking time in some varieties of cowpea (*Vigna unguiculata* (L.) Walp was carried out with the aim to provide information for cowpea breeder for understanding the genetic effects involved in the inheritance of these traits for the formulation of better breeding plans in order to produce acceptable cowpea varieties. The following were established:

- Two dominant genes control seed coat texture in the varieties of cowpea studied. This differed from the reports of Rajendra *et al*. (1979) and Yilwa (2001) who reported monogenicity (one gene) for the trait.
- Smooth seed coat texture was observed to be completely dominant over wrinkle and loose seed coat texture plants.
- Wrinkle seed coat texture was completely dominant over rough and loose seed coat texture plants.
- Recessive epistasis (modifying gene effects) exist in a cross involving loose and rough seed coat texture plants which gave smooth texture plants, a trait not previously expressed by either parents in both the F_1 and F_2.
- The genes that controlled smooth, wrinkle, rough and loose seed coat textures were all nuclear and cytoplasmic genes had no effect on seed coat texture.
- Genetic studies on cooking time trait in cowpea have rarely been reported previously.
- The generation mean analysis adopting the additive-dominance model could not explained the mode of inheritance of cooking time in the cowpea varieties used due to involvement of non-allelic interaction (epistasis) in the inheritance of cooking time. The six parameter model was adequate.

- Two dominant alleles interacting at different loci were observed to govern cooking time.
- Short cooking time was dominant over long cooking time.
- Gene action was predominantly dominance, but additive, additive x additive, additive x dominance and dominance x dominance effects were also significant.
- The genes that controlled short cooking time and long cooking time are allelic and all nuclear and cytoplasmic genes had no effect on cooking time.
- There were transgressive segregation in cooking time and this may suggest that a new variety having very short cooking time could be selected at advanced generations.
- The estimate of heritability in the broad sense ranged from 89% to 95% while Nielsen *et al.* (1993) reported a value of 76%.
- Narrow sense heritability ranged from 58%-85%.

Since evaluation of cooking time in cowpea is expensive and time consuming there is need for further study by identifying Random Amplified Polymorphic DNA (RAPD) markers associated with the trait as a method of indirect selection and estimate genetic parameters of cooking time in cowpea. This might increase selection efficiency.

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Appendix. Formulae Used in Calculation of Various Parameters.

1. Chi-square (χ^2) Test

The general formula for is as follows:

$$\chi^2 = \sum \frac{(Ob - Ex)^2}{Ex}$$

Where:

Ob is the observed value for each of two or more classes.

Ex is the corresponding expected value.

The degree of freedom (df) of the estimate is equal to the number of observed classes minus one.

2. Broad sense heritability estimate (Hb)

$$Hb = \frac{\sigma^2F_2 - \sqrt{\sigma^2P_1 \times \sigma^2P_2}}{\sigma^2F_2}$$

where σ^2F_2, σ^2P_1, σ^2P_2 are variances of the generations.

3. Narrow sense heritability estimate (Hn)

$(Hn) = 1/2\ D_R/1/2D_R + 1/4\ H_R + E$, where

D_R, H_R are the additive and dominance variances respectively and

$E = \sigma^2P_1, + \sigma^2P_2 + \sigma^2F_1 /3$, is the environmental variance.

4. Expected Genetic advance under selection (Gs).

$Gs = (k)(\sigma A)(H)$

Where:

K = Selection differential

σA= Phenotypic standard deviation

H = Heritability coefficient

Appendix Continued.

5. Estimate of number of effective factor (genes) according to Wright's formula

$$n = \frac{R^2}{8(\sigma^2 F_2 - \sigma^2 F_1)}$$

where n = Number of genes

R = Difference in mean values of parents.

$\sigma^2 F_2$ = Variance of F_2

$\sigma^2 F_1$ = Variance of F_1