INHERITANCE OF GRAIN AND FODDER YIELDS AND YIELD COMPONENTS IN COWPEA *(Vigna unguiculata* (L.) Walp).

BY

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(*MSc/AGRIC/06398/2008-2009)*

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NIGERIA

MARCH, 2012

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**DEPARTMENT OF PLANT SCIENCE
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NIGERIA**

MARCH, 2012

DECLARATION

I declare that the work in this thesis titled "Inheritance of grain and fodder yields and yield components in cowpea (*Vigna unguiculata* (L.)Walp.*)"* has been performed by me in the Department of Plant Science under the supervision of Dr M.F. Ishiyaku, Prof. M. Yeye and Dr U.S. Abdullahi. The information derived from literature has been duly acknowledged in the text and a list of references provided. No part of this thesis was previously presented for another degree or diploma at any university.

HASSANE FODI BALKISSA	_____	_____
STUDENT	Signature	Date

CERTIFICATION

This thesis titled "Inheritance of grain and fodder yields and yield components in cowpea (*Vigna unguiculata* (L.) Walp.)" meets the regulations governing the award of Master of Science (Plant Breeding) of Ahmadu Bello University, Zaria, and is approved for its contribution to knowledge and literary presentation.

Dr M.F. Ishiyaku, Chairman, Supervisory committee	_____ Signature	_____ Date
Prof. M. Yeye Member, Supervisory committee	_____ Signature	_____ Date
Dr U.S. Abdullahi, Member, Supervisory committee	_____ Signature	_____ Date
Dr I.S. Usman Head, Department of Plant Science,	_____ Signature	_____ Date
Prof A.A. Joshua, Dean, School of Postgraduate Studies	_____ Signature	_____ Date

DEDICATION

To Almighty Allah (S.W.T.) who taught man what he does not know, to whom my life and all I have belong. Also to my dear son Mohamed Zabeirou, who spent part of his childhood with me at school in this program; to my husband for his patience and encouragements, and also to my parents, Mr. and Mrs. Hassane Fodi.

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ABSTRACT

Studies were carried out on Two landraces Kanannado Brown and Biu Local (Fodder types) and IT98K-205-8 (grain type) to estimate the gene effects for grain and fodder yields and yield components in cowpea, using generation mean analysis. Six generations were developed (P_1, P_2, F_1, BC_1 P_1,BC_2 P_2 and F_2) and evaluated at Kadawa. Data collected were analyzed for: gene segregation, gene action governing the three key parameters (leaf-stem ratio, total biomass and dual trait) as well as heritability. Significant mean for leaf-stem ratio in the crosses Kanannado brown × IT93K-205-8 and in the Biu local × IT93K-205-8, and for dual trait in the cross Biu local × IT93K-205-8. All the backcrosses had significant better mean performance for all the parameters. This indicated that backcross breeding procedure may be important in the improvement of yield in cowpea. Different means obtained showed by the individuals in the population was an indication of the presence of considerable amount of genetic variability. Transgressive segregation for high and low leaf-stem ratio observed in the cross Kanannado brown × IT93K-205-8 suggests that genes were dispersed among the parents in this study. Polygenic inheritance for the three traits studied was confirmed by unimodality in the F_2 s coupled with the number of effective factors. Complementary gene effects as evidenced by skewness, epistatic effects were also found. Duplicate gene was predominantly involved in the inheritance. Correlation had been found to be high and significant (negative and positive) between dual trait and dry fodder yield; dry fodder yield and dry seed weight; dual trait and days to first flower, and also between days to first flower with dry seed yield. Also high heritability was obtained. These showed the importance of the above traits in selection to improve yield in cowpea.

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ABBRREVIATIONS AND SYMBOLS

a	Additive gene effect
aa	Additive by additive gene effect
ad	Additive by dominance gene effect
b.	Total biomass
BC_1P_1	Backcross to parent one
BC_2P_2	Backcross to parent two
CV.	Coefficient of variation
d	Dominance gene effect
dd	Dominance by dominance gene effect
F_1	First filial generation
F_2	Second filial generation
G.L.M	General Linear Model
h^2	Broad sense heritability
H_{BS}	Broad sense heritability
H_{NS}	Narrow Sense Heritability
Kan.	Kanannado brown
L-S ratio	Leaf-stem ratio
m	Mean
MP	Mid parent
N	Number of effective factors

r	Correlation
R	Range of F_2 segregation in the cross
SE	Standard Error
σ^2_G	Genetic variance
$\sigma^2 BC_1P_1$	Variance of backcross to parent one
$\sigma^2 BC_2P_2$	Variance of backcross to parent two
$\sigma^2 F_1$	Variance of first filial generation
$\sigma^2 F_2$	Variance of second filial generation
σ^2_P	Phenotypic variance
$\sigma^2 P_{1..}$	Variance of parent one
$\sigma^2 P_2$	Variance of parent two

CHAPTER ONE
INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp) is one of the most important pulse crops; native to Central Africa and belongs to the family *Fabaceae*; Cowpea is called vegetable meat due to high amount of protein in the grain with better biological value on dry weight basis (Withanage, 2005). Cowpea grain on dry weight basis contains 23.4 per cent protein, 1.8 per cent fat and 60.3 per cent carbohydrates and it is a rich source of calcium and iron (Gupta, 1988). Apart from this, cowpea forms excellent forage and it gives a heavy vegetative growth and covers the ground so well that it checks soil erosion. As a leguminous crop, it fixes about 70 – 240 kg per ha of nitrogen per year Cowpea is mainly grown in tropical and sub tropical regions of the world for vegetable and seed purpose and to a lesser extent as a fodder crop (Gupta, 1988). It is a versatile pulse crop because of its smothering nature, drought tolerant characters, soil restoring properties and multi-purpose uses. As a pulse crop, cowpea fits well into most of the cropping systems. It has been estimated that the total pulse requirement for consumption by 2010 was 43 million tons (FAO, 2010). Among the different pulses grown in the world, area of production of cowpeas is approximately 10.1 million hectares (FAO, 2010), global cowpea grain production is now approximately 4.99 million tons (FAO, 2010) with a productivity of 387 kg/ha (FAO, 2008). The largest areas under cultivation are in Central and West Africa. Nigeria and Niger Republic being the leaders with a global yield of 2.9 million tones. In Nigeria grain yield is estimated at 340 kg for northern part; which is lower compared to the average grain production from Food and Agriculture Organization (FAO) for West Africa which is 387 kg/ha (FAO, 2008)

In spite of the fact that cowpea yields are low, cowpea continues to be a popular crop

among farmers. This is because it can be grown even on marginal soil and can withstand any stress, the grains are consumed as food in many forms; young leaves, green pods and green seeds are used as vegetables; dry seeds are used in various food preparations (*'moi moi'* in Nigeria; '*kazolaki*', '*dankaida*', '*bairuwa*' in Niger Republic); It provides high protein to people especially children. The haulms are fed to livestock as nutritious fodder. It also has the unique ability to fix nitrogen even in very poor soils (Tarawali *et al.,* 1997*).*

Across developing world, there is an increasing emphasis on integrating crop and livestock production for sustainable agricultural system. In dry savannah of West and Central Africa, crop and livestock enterprises have integrated very closely (Adeyanju, 2008), livestock are kept by farmer in these regions, and therefore cowpea cropping is an integral part of the cropping system. The cowpea haulms are used to feed the livestock while the latter provide manure (Tarawali *et al., 1997).* Two types of cowpea varieties are usually intercropped in alternate rows with millet, maize and/or sorghum in West and Central Africa. A short duration cowpea variety (early maturity, 55-60 days) for grains and a long duration variety (late maturity 100-120 days) for fodder, but both are spreading type. The grain and fodder yield are poor due to low potential of the spreading variety and also due to early cessation of rains. According to Singh (2000), the grain cowpea and millet are harvested at the end of August or beginning of September while the late type is left in the field until the onset of the dry season (October-November).

Cowpea fodder is as important as the grain especially in dry savannah of West and Central Africa; farmers derive significant income from selling cowpea fodder to livestock

owners where in the dry season, the cost of fodder per kg is as much as that of grain (Singh *et al.,* 2000). The farmers wait until the cowpea leaves show sign of wilting before they cut the cowpea plant at the base and tie it into bundles with all leaves still intact; these bundles are kept on rooftops or on tree fork for drying and sold in the peak of dry season when prices are high. On dry-weight basis, the price of cowpea haulms ranges between 50 and 80% of the grain price, and therefore, haulms constitute an important source of income (Langyintuo *et al.,* 2003). In case where there are rains in October/November, the fodder type cowpea produce some grains as well. There is no evidence that any farmer can grow cowpea for fodder alone (Langyintuo *et al.,* 2003*).* This suggests that both grain and fodder are valuable therefore, the ratio of grain and the fodder is very important to support the crop-livestock integration system.

It has been known that high levels of genetic variation for the ratio of grain to fodder exist in cowpea (Roquib and Patnaik*, 1990*). The variation exist in form of traits such as number of primary branches per plant, plant height, pod weight, leaf weight, seed weight, threshing percentage, biomass, leaf to stem ratio and harvest index (Roquib and Patnaik, 1990). However, very little is known about inheritance of these important traits. There is therefore the need to understand the genetic control of such traits. This will facilitate development of a viable breeding strategy for improved cowpea varieties with high grain and fodder yield.

1.1 OBJECTIVES OF THE STUDY

The objectives of the study were:

i. To determine genetic basis of grain and fodder yields traits in cowpea.

ii. To estimate correlations between grain and fodder yields with other yield components

iii. To suggest breeding procedures that can aid selection and development of varieties with high grain and fodder yields.

CHAPTER TWO

LITERATURE REVIEW

Cowpea (*Vigna unguiculata* (L.) Walp.) is one of the most important leguminous crops, belonging to family *Fabaceae* and tribe *Phaseolae*. It primarily originated in West Africa (Rawal, 1975). With increased popular use of pulses in high fibre diets, the demand for cowpea can be expected to increase. Since, limited availability of high productive varieties with good plant types and lack of short duration varieties, are the major hindrance to increase the production.

2.1 HERITABILITY AND MODE OF INHERITANCE OF YIELD COMPONENTS

Cowpea is predominantly self-pollinating crop and studies so far show that it responds to yield improvement through selection (Singh *et al*., 1997). Research results have shown that yield of 1500-1800kg/ha are possible if improved varieties of cowpea are grown as a sole crop and adequately protected against diseases and insect/pests (Anon, 1975). With two third of the world total production (Moody, 1973), Nigeria is the largest producer of cowpea. The grain yield is estimated at 340kg/ha for northern parts; these are lower compared to the average grain production from Food and Agriculture Organization (FAO) for West Africa which is 387 kg/ha (FAO, 2008).

Yield is a very important trait in cowpea. In breeding to increase the inherent yielding ability of a crop, the selection criterion may be yield directly or indirectly through its components (Venkatesan *et al.,* 2003). Several researchers have investigated the genetic nature of traits important to yield, Adewale *et al.* (2006) studied genotypic variability and stability of grain yield components. They reported that genotypes differ significantly in grain yield, the pods per plant and fresh fodder yield equally differed significantly for the two year of work. Seeds per pod, 100 grain weight and pod length had fairly high relative genetic grain resulting from high genotypic coefficient of variation to phenotypic coefficient of variation ratio. Yield

improvement has been achieved through directional selection for yield contributing traits (Venkatesan *et al.,* 2003). Numbers of Pods, seed yield and 100 seed weight have been reported among the prominent grain yield determinants of cowpea (Saddique and Gupta, 1991).

Heritability is a function of character as well as the environment and the population. Thus heritability estimate applies to a character in a specific situation or condition (Zaria, 1988). In cowpea, many studies on heritability have been conducted for in all the components that contribute to yield. The results of many recent works indicate that the yield of both reproductive and the vegetative portion of cowpea plant are moderately to highly heritable under most environmental conditions. Most of the reports on genetic variability showed a wide range of variability for plant height with moderate to high heritability and high genetic advance, for varying number of genotypes and few reports for the segregating material. Patil and Patil (1986) reported moderate heritability and moderate genetic advance; Apte *et al.* (1987) also reported low heritability and low genetic advance for trait plant height. Nehru and Manjunath (2001) indicated low heritability (5.61%) with 6 % genetic advance. However, Selvi *et al.* (1994), revealed high heritability (99.89%).

Fery (1985), in a review of genetics of cowpea, remarked that reported heritability estimates were highly erratic but that the averages for the various characters were; 53.10% for number of pods per plant, 52.80% for number of seeds per pod, 45.55% for seeds per plant, 45.00% for yield per plant, 48.30% for days to flowering and 65.80% for seed size. The range for characters were: 7.00-98.90% for number of pods per plant, 9.60-98.90% for number of seeds per pods, 35.80-55.30% for number of seeds per plant, 12.00-80.80% for yield per plant, 3.80-94.30% for days to flowering and 3.80-98.90% for seed size. From a cowpea cross between small and large seeded parents, Drabo *et al.* (1984) reported that broad and narrow sense heritability estimates for seed size were 85.10 ± 5.30% and 75.40 ± 18.60%, respectively. Seed size was inherited quantitatively and small seed size was partially dominant to large seed size. Jatasara (1980) reported that most of the genes governing seed yield act additively. Saddique and Gupta (1991) also reported the importance of additive gene effect in conditioning both seed and number of clusters per plant. High parent heterosis of between 28 – 84% has been reported by Sangwan and Lodhi (1995). Reports on number of main branches indicated moderate to high heritability. A moderately high heritability with moderate value of genetic advance was reported by Mehta and Zaveri (1999) while, Rangaiah and Nehru (1998) reported low to moderate heritability estimates for number of branches with very low genetic advance in cowpea. Madhusudhan (1994) reported high heritable values of 96.21 per cent in F_1 materials, while Balraju 1997 reported that, low heritability (14.2%) for this trait. Many reports indicate low to high genetic advance ranging from 0.6 (Apte *et al.,* 1987) to 13.43 (Balraju, 1997). **Heritability estimates for pods number, seed yield and fresh fodder yield average 62%, 62% and 55%, respectively. Jatasta (1980) reported that most of the genes governing seed and green fodder yield act additively. However, he observed that non additive gene action was more important in conditioning dry**

fodder yield (Jatasara, 1979). Saddique and Gupta (1991) demonstrated that additive gene effects were important in conditioning seed yield and number of pods/plant.

In a heritability study of seed size in three crosses of chickpea (*Cicer arietinum*), it was reported that the narrow sense estimate of heritability in a cross, large × large, was 55.00% , in small × small, was 30.00% and large × large, was 85.00% (Anon., 1975). These high heritability values indicate that seed size is a highly heritable trait and that selection could improve the characters. Medhi *et al.* (1980) found high broad sense estimates of heritability for characters, seed size (99.43%, seeds yield per plant (99.19%), seed per pod (99.90%), effective branches per plant (89.23%) and clusters per plant (90.38%) in green gram (*Vigna radiata (L.)Wilczek).* They noted associations between high heritability estimates and high corresponding values of expected genetic advance for number of effective branches bearing pods, number of clusters per plant, seeds per pod, seed size and seed yield per plant. This is an indication of predominance of additive gene action and that mass selection for phenotypic value can be useful for improving these characters. On the other hand, the high heritability estimates for days to flowering (94.34%) and days to maturity (96.19%) in conjunction with the low expected genetic advance, they reported, indicate the predominance of non-additive gene effects. They concluded that judicious application of pure-line selection may prove effective in improving these two characters in green gram. Yassin (1973) reported that broad sense heritability estimates for three characters were, 28.70% (yield per plant), 54.70% (pods per plant) and 93.70% (seed size) in field beans (*Vicia faba* L.) .

Fodder yield in cowpea is the weight of the above ground parts excluding the seeds. Fodder yield has been studied by many different researchers. There is scarcity of information available in the literature regarding genetic control of fodder yield in cowpea. Some use stem–leaf while others used total biomass to measure fodder productivity in cowpea. Cowpea genotypes differ in their genetic potential for fodder yield. Roquib and Patnaik (1990) from study of 25 genotypes of this crop in India, reported significant phenotypic and genotypic variation for some fodder component traits. The highest significant genotypic variations were reported for plant height at maturity followed by green yield and terminal leaflet area. Fodder like grain yield can be measured through different component trait. The selection can be made for

the trait that is not only strongly associated with fodder yield but also can be easy to measure. Roquib and Patnaik (1988), reported results of genotypic and phenotypic correlation coefficient and path analysis for 10 fodder yield related traits in cowpea. The result indicated that green forage and dry matter yield may be improved by selecting for increases in root module numbers at 30 and 65 days after sowing, plant height, lateral and terminal leaflet area and leaf stem ratio. Roquib and Patnaik (1990) reported green forage yield of 4000-10000kg/ha and dry matter yield of 1000-3000kg/ha. Singh (1990) in a study to evaluate some dual-purpose cowpea varieties in Minjibir, Toumnia, and Samaru of the dry savannas of Nigeria reported a range of 658–1004 and 1458 – 4868 kg/ha for grain and fodder yields, respectively, for the cowpea line TVU12349. However, Jindal *et al.* (1989), reported that number of branches per plant is the most important component trait to consider in breeding for fodder yield and leafiness in cowpea. Sharma and Singhania (1992) reported a broad heritability estimate for stem-leaf ratio of 96%, but Roquib and Patnaik (1990) estimate for the same trait was only 9%. Thaware *et al.* (1991) demonstrated that broad heritability estimates for the components of green fodder yield, i.e. leaf yield (55%) and stem yield (62%) are smaller than broad heritability estimate for green fodder yield itself (67%). Their broad heritability for the leaf yield index (leaf weight/weight of total green forage x 100) was only 15%. Also Mendez and Hall (1996), reported that the heritability of harvest index was 38% and 58%. From a study of 80 genotypes of cowpea (*Vigna unguiculata* (L.) Walp.) grown during rainy season, Thaware *et al.* (1991) reported that green forage yield, leaf yield, stem yield and leaves per plant showed high heritability values of 66.6%, 55.9%, 62.2% and

38.3%, respectively. They also reported 57.4%, 61.2%, 51.7% and 30.7%, respectively, for genetic advance suggesting that great scope for improvement of these traits exist. In another report, Kannan *et al.* (2005) in a study of 60 genotypes of fodder cowpea reported high heritability and genetic advance for number of branches per plant, number of leaves per plant, dry weight of leaves, dry weight of stem, dry matter yield and plant height, indicating that these traits were controlled by additive genetic effects, providing better source population for developing high yielding fodder cowpea cultivars.

Mitra *et al*. (2001) in a study of gene action for fodder yield and its components in three diverse parents of cluster bean (*Cyanopsis tetagonoloba* (L.) taub.). Using generation mean analysis reported that green fodder yield per plant appeared to be influenced by both additive and non additive gene actions. They also reported that complementary gene interaction was predominantly involved in the inheritance of most characters.

Heterosis for fodder yield was reported by Ponmariammal and Das (1996). Highest heterosis (12%) over the high parent was recorded for the hybrid UPC9201 x CO5. Diallel analysis of six cowpea genotypes and their F_1 hybrids revealed additive gene action for most of the quantitative traits including green fodder and total dry matter (Jain and Lodhi(1980); Ponmariammal and Das (1996)).

2.2 CORRELATION OF YIELD AND ITS COMPONENTS

Correlation studies give the nature and magnitude of association of characters.

Therefore knowledge of correlation coefficients is very useful in plant breeding for indirect selection of characters that show low heritability and/or are difficult to measure (Cuatero and Cubero, 1952). Correlation studies are also helpful in formulating efficient breeding programme for multiple traits selection. Correlation coefficient measures the mutual association between various plant characters and gives reasonable indication for plant breeders to face selection on characters to improve economic yield and also plan more efficient breeding programmes (Shashidhar, 2007). In crops like cowpea, where production of hybrid is out of question and hybridization followed by selection is the main procedure for improvement, knowledge on correlation is an obligate necessity for achieving genetic improvement. The importance of correlation study in selection programme is appreciable when highly heritable characters are associated with important characters like yield which have low heritability.

Cuatero and Cubero (1952) and Singh *et al.* (1982) reported significant positive correlations between grain yield per plant and days to flowering (0.404), cessation of flowering (0.405), days to maturity (0.434), plant height (0.517), number of pods per plant (0.639), pod length (0.341), number of grains per pod (0.670) and seed size (0.433). They concluded that in cowpea, pods per plant, grains per pod and seed size were the important yield components. Highly significant positive correlations in cowpea between seed yield and pods per plant, seed seeds per pod and seed size in F_2 were reported by Virupakshappa *et al.* (1980). They pointed out that while the strength of correlations between seed yield and pods per plant of the backcross1 (BC_1) was more than of F_2, no correlation was found between seeds yield and seed size. The magnitude of correlation between seed yield and seed per pod remained the

same in all the three generations. The correlations between pods per plant and seed size and seeds per pod were not significant in any generation .The strength of association between seed size and seeds per pod varied with generation. While there were significant positive correlations in the F_2 and BC_2, the association was negligible. Seed yield per plant has been reported to be positively and significantly associated with number of pods per plant, seeds per pod and seed size (Tikka and Asawa, (1978); Hanchinal *et al*. (1979); Virupakshappa *et al*. (1980); Pandey *et al*. (1981); Dumbre *et al*. (1982); Murthy, (1982); Marangappanavar, (1984); Chowlkar and Borikar (1985); Chikkadevaiah, (1985); Obisensan, (1985); Natarajarathnam *et al*. (1986) and Gowda, (1996)). Patil and Shah (1982), observed that grain yield per plant had significant positive correlation with number of branches, pods and clusters per plant. Sawant (1994) opined that seed yield was significantly and positively correlated with branches per plant, inflorescence per plant, pods per plant, pod length, seeds per pod, 100 seed weight and harvest index. A study on correlation between seed yield per plant and its components in 75 accessions of cowpea was made by Altinbas and Sepetoglu (1993). Seed yield per plant was significantly correlated with pods per plant, seeds per pod and branches per plant. Both days to flowering and maturity had no influence on seed yield, while 100 seed weight was negatively and significantly associated with pods per plant and seeds per pod. Information on correlation among 13 characters in 15 genotypes assessed by Damarany (1994) revealed that number and weight of pods, seeds per pod, plant height and number of branches per plant had significant and positive correlations with seed yield.

CHAPTER THREE

MATERIALS AND METHODS

3.1 EXPERIMENTAL MATERIALS

Table 3.1: Origin and characteristics of experimental materials used in the study

Genotypes	Origin	Characteristics
Kanannado Brown	Nigeria	Landrace, fodder type, late maturing, spreading in growth habit, highly photosensitive varieties, black eyes.
Biu local	Nigeria	Landrace also, fodder spreading and late maturing, photosensitive varieties, medium seeds size with milky color and black eye.
IT98K-205-8	Institute for Agricultural Research (I.A.R) Samaru.	An elite Breeding line of I.A.R, Samaru, grain type, indeterminate growth, early maturing non-photosensitive ,semi erect, medium white seed, black helium, medium white seed, black helium.

3.2 EXPERIMENTAL SITE

The hybridization experiment was conducted in green house at the Institute for Agricultural Research (IAR) Samaru-Zaria ($11^{o}11'$N, $07^{o}38'$E) in the Northern Guinea Savannah ecological zone from March 2010 to February 2011. Samaru has an altitude of 686m above sea level. The soil type is sandy loam. The long term mean annual rainfall is 1058mm within 160 days (from May to end of September). The dry season period starts at about the middle of October and lasts to the end of April. The hottest months are those preceding rains (March and April) with temperatures above 27^{o}C. The evaluation trial was carried out from March to July 2011 at Kadawa Irrigation Research Station.

3.3 DEVELOPMENT OF THE GENETIC POPULATION

3.3.1 Hybridization

Hand emasculation technique was use to develop, F_1, F_2, and backcrosses populations in

the green house in 2010 from crosses Kanannado Brown x IT98K-205-8 and Biu local x IT98K-205-8; using bi-parental mating design. Hand crossing was used to develop the hybrids. Anthesis takes place just before or simultaneously with the opening of the papilanaceous corolla. Hence, flowers destined to open the following morning are ready for emasculation when the buds reached their maximum unopened size and have started to pale lightly from the deep rich green to early development. Emasculation using a finely pointed forceps was carried out during the cool periods of the day (early morning and evenings). The selected buds for emasculation were grasped firmly to avoid any stress at the attachment of the bud and raceme. Two thirds of the width of the unopened bud will be cut starting from the center. The cut segment was then turned off using the forceps. Thus the upper portion of the style, stigma and stamens were left free and exposed to facilitate removal of the ten anther sacs with the forceps already dipped in (75 – 90%) alcohol.

The flowers that were emasculated were crossed immediately. To expose the anther sacs in the pollinating flowers, the innermost petal of the matured open flowers were removed or were slipped downward. The mass of pollen on the hairy-neck style were used like a brush to deposit pollen grains immediately on the stigma. A small tag listing the cross and date was affixed on the peduncle beneath the pollinated bud for identification.

The following crosses were made to develop the various F_1 populations:

1. Kanannado brown x IT98K-205-8 Fodder x Grain
2. Biu Local x IT98K-205-8 Fodder x Grain

The backcrosses were developed by crossing each F_1 hybrid to its respective parents giving rise to two backcrosses (BC_1P_1 and BC_2P_2) for each F_1 hybrid.

The following backcrosses were developed:

1. (Kanannado brown x IT98K-205-8) x Kanannado brown BC_1P_1
2. (Kanannado brown x IT98K-205-8) x IT98K-205-8 BC_2P_2
3. (Biu Local x IT98K-205-8) x Biu Local BC_1P_1
4. (Biu Local x IT98K-205-8) x IT98K-205-8 BC_2P_2

The F_2 populations were generated by selfing the F_1 hybrids. Seeds harvested from the selfed F_1's were planted to raise F_2 plants and seeds. Pots were used for planting in the screen house. Six seeds were sown in the plastic pots filled with fresh top soil at a depth of 2.5cm. Seedling received water daily and insect pests and diseases were controlled by application of insecticides. Weed was controlled by hand pulling as often as necessary during the growing period of the crop. At maturity, pods were harvested, threshed, and placed in properly labeled seed packets.

3.3.2 Field Evaluation

The parents, F_1, F_2, and backcross generations were subjected to field evaluation (in 2011) under irrigation in one location at Kadawa research station. Randomized Complete Block Design (RCBD) with three replications for each cross was used. The field was ploughed and later harrowed to a tilt and plots were established. Each plot was consisted of one row for parents and F_1 (twenty plant stands/row); three rows for back cross (fifteen plants/row), and five rows for F_2 (twenty plants/row).The spacing was 150 cm (1.5m) inter row and 100cm (1m) intra row. One seed was sown per hill. Hoe weeding was done as often as was necessary starting from three weeks after planting and re-ridging at five weeks after planting. Insecticide (Decamethrin 2.5% W/V) was applied at the rate of 1.2l/ha on weekly basis from two weeks after planting to control diseases and fungicides

(benomyl 50%) were used to control fungal diseases. The insecticides and fungicides were mixed for the sprays. Fertilizers (NPK 15:15:15) at a rate of twenty five kg/ha were applied at five weeks after planting 5-10 cm away from the plant.

3.4 DATA COLLECTION

Data were taken on twenty plants from each parent and F_1, thirty plants from each of the backcrosses and fifty plants from the F_2 generations.

The following quantitative characters were measured and recorded:

- Number of primary branches: Total number of primary branches per plant.
- Plant height: height in centimeters of the plant from soil to the tip of the main branch, at flowering.
- Days to first flower: The number of days taken from sowing to first flower opening.
- Dry leaf weight at maturity**:** Weight in grammes of all the leaves per plant.
- Dry stem weight: Weight in grammes of the dry shoot excluding leaves of each plant.
- Leaf-stem ratio: Ratio of dried leaves to dried stems for each plant.
- Pod weight: Weight in grammes of all dry pods per plant.
- Grain weight: Total dry grain weight in grammes per plant.
- Fodder yield: Weight in grammes of dried leaves, chaff, and dried stem per plant.
- Total biomass: Weight in grammes of the dried leaves, dried pods and dried stems /plant.
- Threshing percentage: Total grain weight expressed as percentage of total biomass /plant
- Dual trait**:** Ratio of dried pods weight to total biomass.

3.5 STATISTICAL ANALYSES

Analysis of variance for the key parameters was conducted to determine the genetic basis of grain and fodder yields traits and to check whether the genotypic variation was significant before conducting genetic analysis using general linear model (GLM) procedure of the Statistical Analysis System (SAS) programme.

3.5.1 Generation Mean Analysis (GMA)

Generation mean analysis was performed separately for each crossing following the procedure described by Kang (1994). Generation means were calculated for each of the six generations. To determine the mode of inheritance of grain and fodder yields, the notation of Gamble's (1962) was used, where:

m= F_2 mean,

a= additive gene effects,

aa=additive x additive epistatic effects,

ad= additive x dominance epistatic gene effect, and

dd= dominance x dominance epistatic gene effects.

The model for generation, Y is : $Y = m + \alpha a + \beta d + \alpha 2aa + 2\alpha\beta ad + \beta 2dd$.

Where Y is the observed generation mean; m is F_2 mean; a is additive gene effects; d is dominance gene effects; aa is additive x additive epistatic gene effects; ad is additive x dominance epistatic gene effects; and dd is dominance x dominance epistatic gene effects.

α and β represent the coefficients for the genetic effects for the particular generation being estimated (Hayman 1958; Mather and Jinks 1982).

3.5.2 Number of Effective Factors

The following formula proposed by Lawrence and Frey (1976) was used to estimate the minimum number of effective factors (N)

$$N = R^2 / 8(\sigma^2 g)$$

Where: R is range of F_2 segregates in the cross.

$\sigma^2 g$ = Genetic variance; $\sigma^2_g = \sigma^2 F_2 - \sigma^2_E$

3.5.3 Heritability

In its broad sense, Heritability was calculated in accordance with the procedures outlined by Allard (1960). Heritability in the narrow sense was calculated in accordance with the procedures outlined by Warner (1952). Broad sense heritability was estimated as follows:

$$H_{BS} = \frac{\sigma^2 F_2 - (\sigma^2 P_1 + \sigma^2 P_2 + \sigma^2 F1)/3}{\sigma^2 F_2} x100 \quad \text{(Allard, 1960)}$$

Where $\sigma^2 F_2 = \sigma^2 G + \sigma^2 E$, $\sigma^2 F1 = \sigma^2 E3$, $\sigma^2 P_1 = \sigma^2 E_1$, $\sigma^2 P_2 = \sigma^2 E_2$ In these relationships:

H_{BS} = Broad sense heritability
$\sigma^2 F_2$ = Variance of F_2 population
$\sigma^2 P_1$ = Variance of parent$_1$
$\sigma^2 P_2$ = Variance of parent$_2$
$\sigma^2 F_1$ = Variance of Fist filial generation
$\sigma^2 E$ = Environmental variance

Narrow sense Heritability was estimated as follows:

$$H_{NS} = \frac{2\sigma^2 F_2 - (\sigma^2 BC_1 P_1 + \sigma^2 BC_2 P_2)}{\sigma^2 F_2} X100 \quad \text{(Warner, 1952)}$$

Where:

H_{Ns} = Narrow sense Heritability
$\sigma^2 F_2$ = Variance of F_2 population
$\sigma^2 BC_1 P_1$ = Variance of the backcross to parent$_1$
$\sigma^2 BC_2 P_2$ = Variance of the backcross to parent$_2$

Where:

$$\sigma^2 F_2 = \tfrac{1}{2} A + \tfrac{1}{4} D + E$$

$$\sigma^2 B_1 + \sigma^2 B_2 = \tfrac{1}{2} A + \tfrac{1}{2} D + E$$

$$2\sigma^2 F_2 - \sigma^2 B_1 - \sigma^2 B = A + \tfrac{1}{2} D + 2E - (\tfrac{1}{2} A + \tfrac{1}{2} D + 2E) = \tfrac{1}{2} A$$

A = Additive genetic variance

D = Dominance variance

E = Environmental variance

B_1 = Backcross to parent P_1

B_2 = backcross to parent P_2

F_2 = Second filial generation

Assumptions are:

(i) Independence of genotypic and environmental variances

(ii) Additivity of genetic effects over the various loci.

(iii) The F_2 and the two backcross variances are of comparable magnitude

3.5.4 Correlation

Phenotypic and genotypic correlation coefficients were worked out to determine the degree of association of characters with yield and also among the yield components, using statistical analysis system (SAS) programme.

CHAPTER FOUR

RESULTS

4.1 MEAN PERFORMANCE

Table 4.1, contains the summary of the mean values of the generations for leaf-stem ratio,

total biomass, and dual trait for both crosses Kanannado brown × IT98K-205-8 and Biu local × IT98K-205-8. The parameter leaf-stem ratio in the cross Kanannado brown × IT98K-205-8 indicates that F_1 was better that the second parent (P_2) and the mid parent (MP) and just below the higher parent; which indicates partial dominance of the better parent. The cross Biu local × IT98K-205-8 shows over dominance of the better parent for the same parameter (leaf-stem ratio), because F_1 mean value exceeded the higher parent value is also higher than the mid parent. The backcross to the second parent, Biu local (BC_2P_2), in cross two, results in significant high mean for leaf-stem ratio. For total biomass, F_1 mean in both crosses was higher than the mid parent but lower than the better yielding parent (P_1 in the cross Kanannado brown × IT98K-205-8 and P_2 in the cross Biu local × IT98K-205-8) which indicate partial dominance of the higher parent. Backcross to parent two (P_2) in the cross Biu local × IT98K-208-5 was higher significantly.

For dual trait, the F_1 was lower than the mid parent but higher than the lower yielding parent. This suggests partial dominance of higher yielding parent. Concerning the second cross (Biu local × IT98K-205-8), the F_1 mean was higher than the MP but lower than the better parent suggesting partial dominance of the higher parent. In the cross Kanannado Brown × IT98K-205-8 backcross to parent two (BC_2 P_2) showed highly significant dual trait mean. The F_2 mean value in cross one for leaf-stem ratio is higher than the F_1 mean for total biomass for the same cross, but the F_1 mean in total biomass for the same cross. In the cross Biu local × IT98K-205-8, the F_2 mean is lower than F_1 mean for leaf-stem ratio and for dual trait. For total biomass, F_2 mean was higher than the F_1 mean for dual trait.

Table 4.1: Mean performance of leaf-stem ratio, total biomass, and dual trait for the populations evaluated at Kadawa

	Kan. Brown x IT98K-205-8			Biu local x IT98K-205-8		
Generations	L-S ratio	Total b.	Dual trt.	L-S ratio	Total b.	Dual trt
P_1		45.69^{a}	529.48^{a}	37.77^{b}	205.15^{b}	0.14^{a}
0.06^{b}						
P_2		37.80^{ab}	205.15^{d}	40.11^{ab}	342.44^{a}	0.08^{c}
0.14^{a}						
F_1		44.81^{a}	480.33^{ab}	46.21^{a}	283.05^{ab}	0.12^{b}
0.07^{b}						
F_2		45.41^{ab}	407.25^{bc}	42.82^{ab}	310.42^{ab}	0.9^{b}
0.06^{b}						
BC_1P_1		42.11^{ab}	453.40^{abc}	46.80^{a}	298.96^{ab}	0.85^{l}
0.06^{b}						
BC_2P_2		38.80^{ab}	364.07^{c}	40.29^{ab}	363.92^{a}	0.09^{c}
0.08^{a}						
MP		41.74	367.31	38.94	273.79	0.11

0.1

Means in a column with different letters are significantly different at 0.05 level of probability.
MP: Mid-Parent value; trt: trait; b: biomass; L-S: leaves-stem

Table 4.2 showed grand mean, standard error of the mean (SE), range, and coefficient of variation (CV %) for all the F_2 populations for leaf-stem ratio, total biomass, and dual trait. There was variation within each parameter among the F_2 plants Table 4.2. Leaf-stem ratio per plant had grand means of 48.93 and 45.66 for crosses Kanannado Brown × IT98K-205-8 and Biu local × IT98K-205-8 respectively, SE ± 40.42 and 12.54 and ranged between 20 to 94, 21.15 to 90.11, and coefficient of variation of 82.60%,and 27.4% for the F_2 populations emanated. Table 4.2 for total biomass had grand mean (for the two crosses) of 507.07, and 296.44; ±SE of 56.27 and 141.46, and ranged between 55 to1755 and 95 to 799, with coefficient of variation of 97.11 and 47.71 respectively for the two F_2 both crosses in Table 4.1. Dual trait had grand means of 0.057, and 0.08; ±SE of 0.40 and 0.05, and ranged between 0.01 to 0.030, and 0.46 to 0.92, coefficient of variation of 81.9 and 64.99 for the two F_2 for the both crosses respectively. High coefficient of variation was however observed for leaf-stem ratio, total biomass, and dual trait for the Kanannado brown × IT98K-205-8 (82.60%; 97.11% and 81.9 %). Also high coefficient of variation was observed in the cross Biu local x IT98K-205-8 for dual trait (64.99%).

Table 4.2: Grand mean; standard error; range, and coefficient of variation of the F_2 populations for leaf-stem ratio, total biomass, and dual trait

Parameters		F_2 (Kanannado brown x IT98K-205-8)	F_2 (Biu Local x IT98K-205-8)
Leaf-stem ratio	Mean	48.93	45.66
	SE±	±40.42	±12.54
	Range	20-94.74	21.15-90.11
	CV (%)	82.60	27.40
Total biomass	Mean	507.60	296.44
	SE±	±56.27	±141.46
	Range	55-755	95-799
	CV (%)	97.11	47.71
Dual trait	Mean	0.57	0.08
	SE±	±0.04	±0.05
	Range	0.01-0.30	0.46-0.92
	CV (%)	81.9	64.9

4.2 MODE OF INHERITANCE

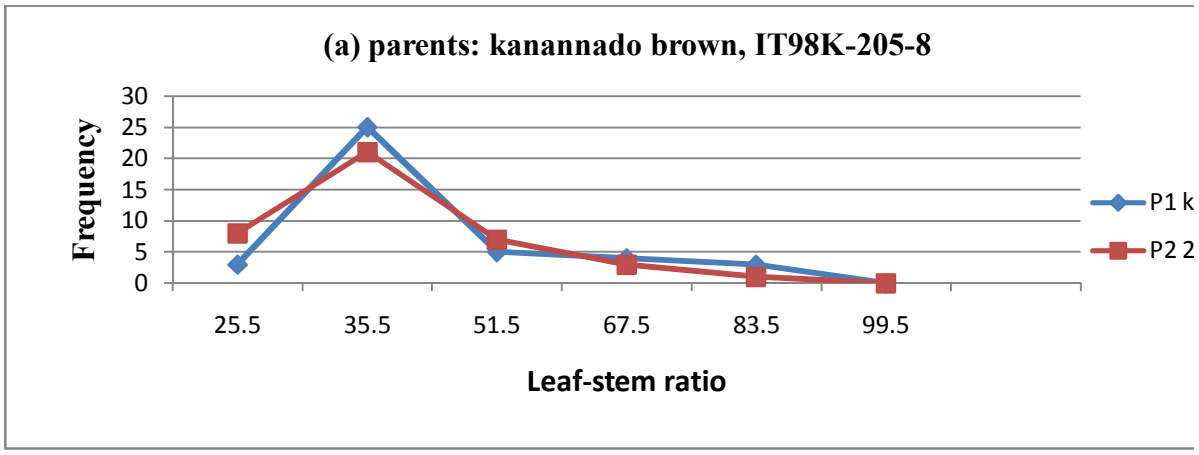
Frequency distribution per plant of leaf-stem ratio, the parental, F_1, F_2, and backcross generations are presented in Figure 4.1 (a) to 4.1(d) and Figure 4.4 (a) to 4.4 (d). The

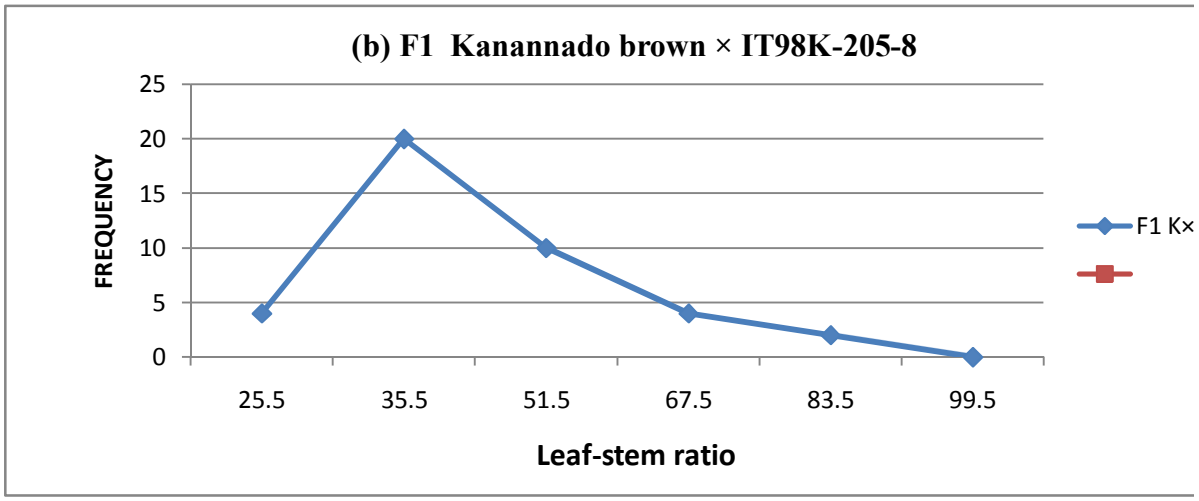
parents used in this study did not represent genotypic extremes for leaf-stem ratio as the mean of F_1 in cross Kanannado brown x IT98K-205-8 was observed to be higher than the lower parent (P_2) but lower than the better parent (P_1). In cross Biu Local x IT98K-205-8, the F_1 distribution exceeded even the better parent. Figure showed that the parents skewed positively, the same scenario was observed in the cross Biu Local x IT98K-205-8 for the parents which indeed overlap. Positive skewness was observed in the two F_1 for the same trait in both crosses. BC_1P_1 and BC_2P_2 plants were partially distributed across the range of both parents but were skewed towards the recurrent parent in the cross Kanannado brown × IT98K-205-8. In the cross Biu Local x IT98K-205-8 the backcross frequency Figure (4.2c) showed nearly normal distribution with little skewness towards the recurrent parent. On the hand, the distribution curve of the F_2 population in the cross Kanannado Brown × IT98K-205-8 showed normal distribution and spread normally with two tails in both sides; the curve is flat at the top and is unimodal with 67.5% per plant having the highest frequency. The unimodal distribution suggests polygenic control of the trait. Unimodal (67.1% per plant having the highest frequency) and skewness in F_2 distribution for the cross Biu local × IT98K-205-8 was apparent for the same trait (leaf-stem ratio).

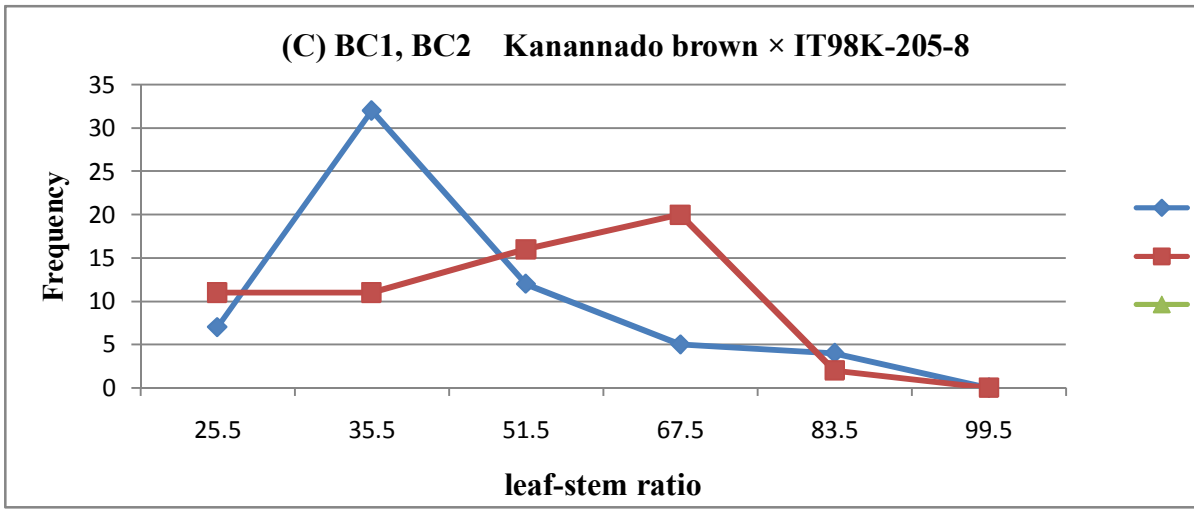
Figure 4.2 (a) to 4.3 (d) and Figure 4.5 (a) to 4.5 (d) are the frequency distributions of total biomass for the parents, F_1, F_2, and backcross generations. The parents of the cross Kanannado Br.× 205-8 overlapped and skewed positively with long tail at the right side. The F_1 which had a mean (480.33g) higher than the lower parent but lower than the better parent, showed a curve closely similar to the first parent (P_1: Kanannado brown) with skewness and long tail by the right. This showed partial dominance of the higher yielding

parent P_1 and $P_{2;}$ in the sense that their frequency distribution curves skewed at the right and overlapped. In the same cross for same trait, the F_2 distribution curve showed transgressive segregation. The curve spread towards the two extremes with one tail longer than the other. The lowest total biomass point frequency on the curve was 159.5g with unimodal 560g per plant having the highest frequency. In the cross Biu local × 205-8; the curves for total biomass behaved differently. The parents (Figure 4.5 (a) overlap at many points along the two curves and had tails which spread towards the right. The two backcrosses Figure 4.5(c) almost behave like their recurrent parents in the sense that they overlapped and met at many points along the curves. The F_2 frequency distribution Figure 4.5(d) of the cross Biu local × IT98K-205-8, is unimodal with 359.5g total biomass per plant and skewed positively. It transgressed the parent with total biomass yield ($P_{1=}$ 205.11g) this also suggest polygenic control of the character.

Figures 4.3(a) to 4.3 (d) and Figure 4.6 (a) to 4.6(d) show the frequency distribution curves of the parameter dual trait. Parents, F_1 , F_2, BC_1 P_1, and BC_2 P_2 of the crosses Kanannado Brown × 205-8, and Biu Local × 205-8. All the curves in both crosses skewed positively, the frequency distribution curves of the backcrosses (4.1 and 4.2) Figure 4.3(c) and Figure 4.6 (c), skewed towards the recurrent parents respective. The F_2 distributions were positively skewed and transgressed the lower yielding parent. They were also unimodal at 0.155 for the two F_2 in both crosses. This also suggests polygenic control of the character.


(a) parents: kanannado brown, IT98K-205-8
Frequency
30
25
20
15
10
5
0
25.5
35.5
51.5
67.5
83.5
99.5
Leaf-stem ratio
P1 k
P2 2


(b) F1 Kanannado brown × IT98K-205-8
FREQUENCY
25
20
15
10
5
0
25.5
35.5
51.5
67.5
83.5
99.5
Leaf-stem ratio
F1 K×


(C) BC1, BC2 Kanannado brown × IT98K-205-8
Frequency
35
30
25
20
15
10
5
0
25.5
35.5
51.5
67.5
83.5
99.5
leaf-stem ratio

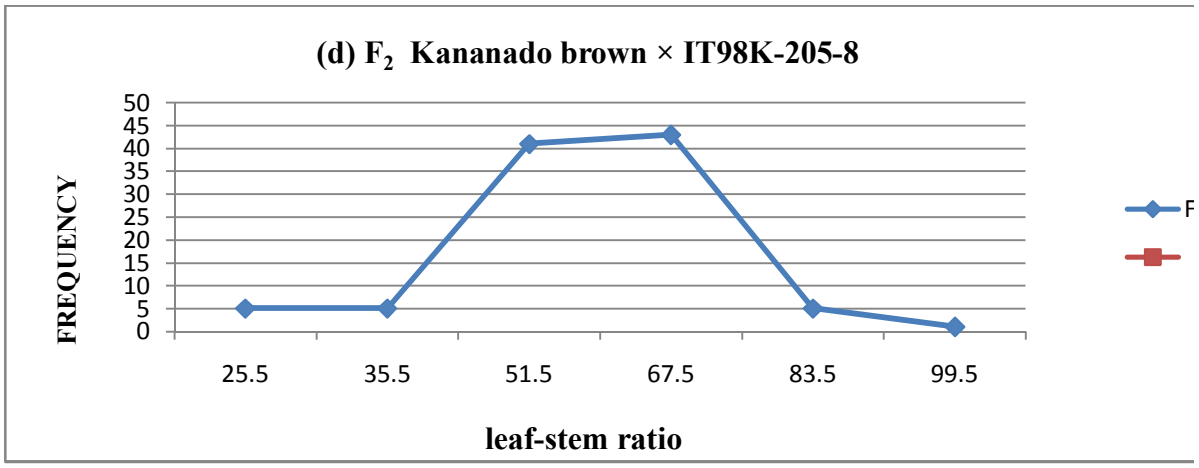
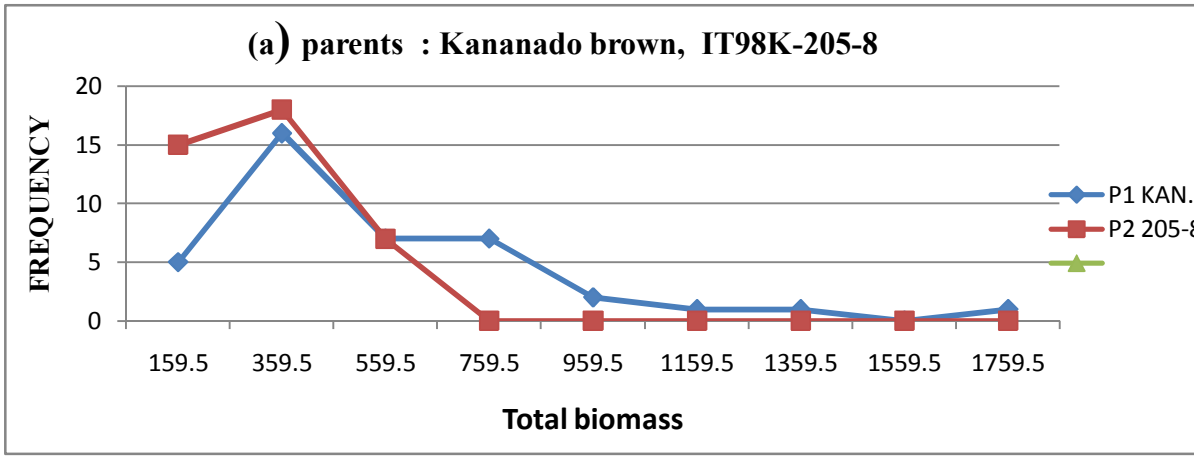
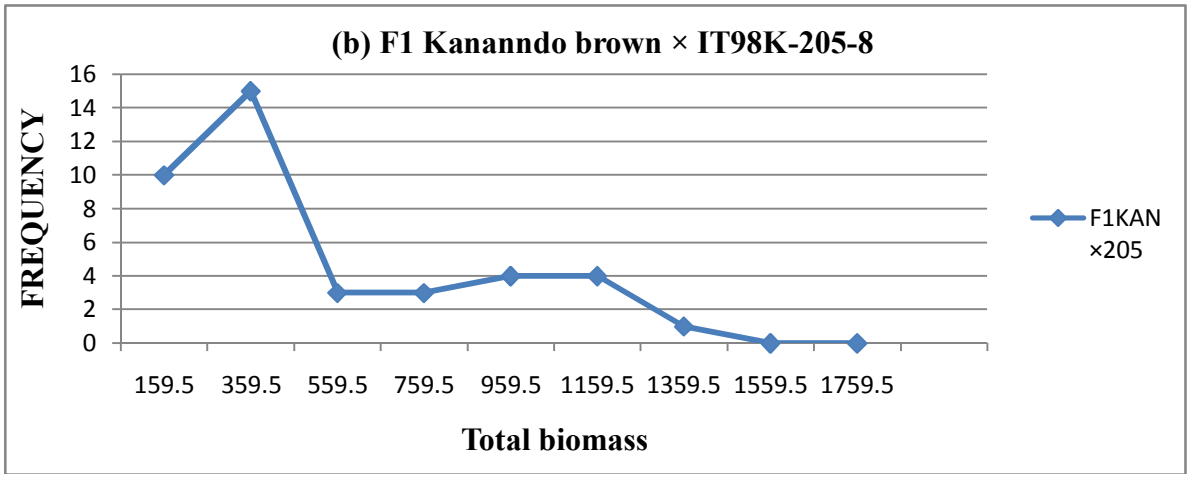
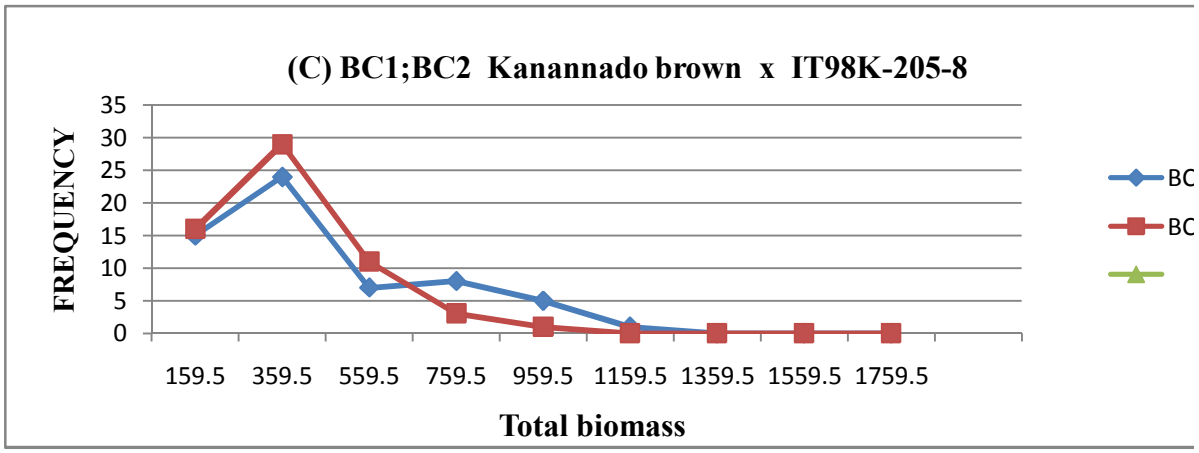


Figure 4.1: Frequency distribution of leaf-stem ratio for (a) parents, (b) F_1, (c) backcrosses and (d) F_2 populations for the cross Kanannado brown × IT98K-205-8 evaluated in the field at Kadawa, Nigeria in 2011.







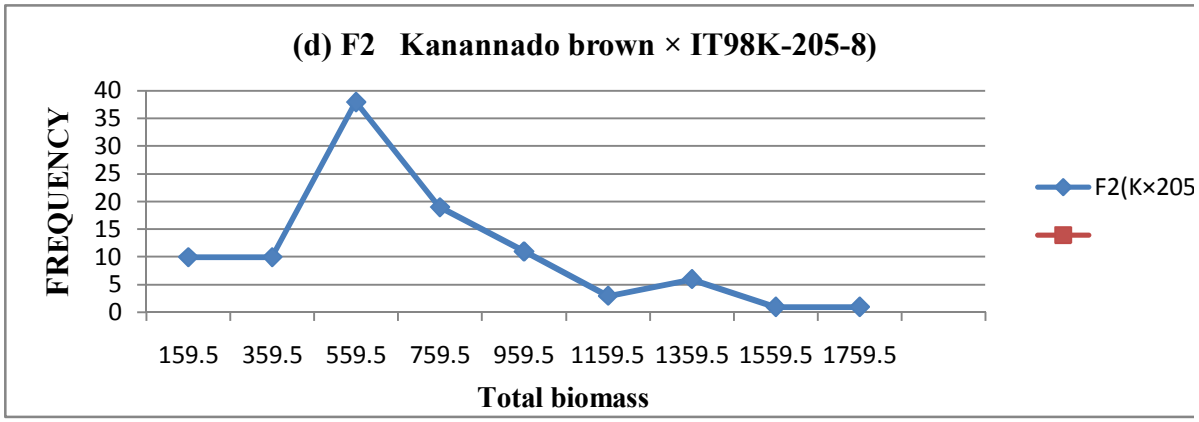
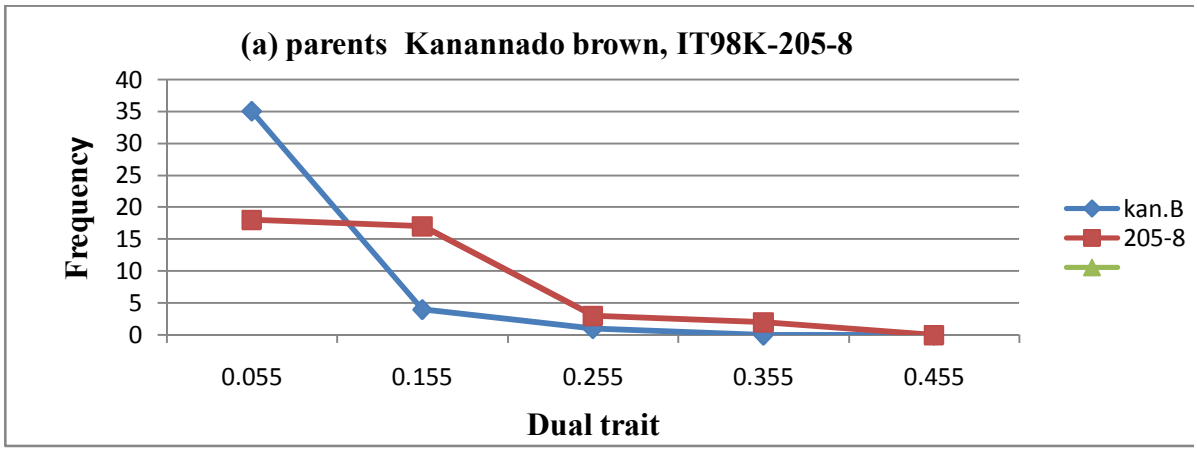
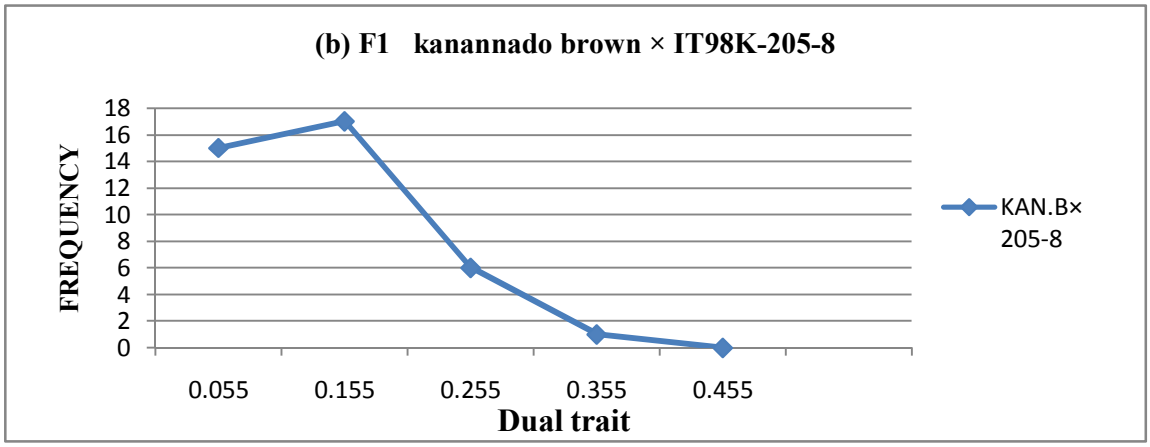
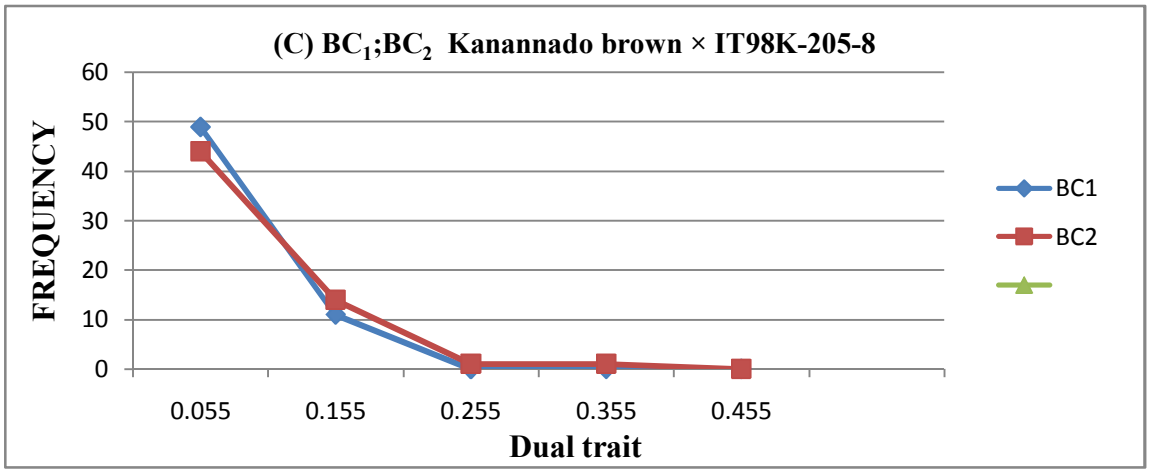


Figure 4.2: Frequency distribution of total biomass for (a) parents, (b) F_1, (c) backcrosses and (d) F_2 populations for the cross Kanannado brown × IT98K-205-8 evaluated in the field at Kadawa, Nigeria in 2011.


(a) parents Kanannado brown, IT98K-205-8
Frequency
40
35
30
25
20
15
10
5
0
0.055
0.155
0.255
0.355
0.455
Dual trait
kan.B
205-8


(b) F1 kanannado brown × IT98K-205-8
FREQUENCY
18
16
14
12
10
8
6
4
2
0
0.055
0.155
0.255
0.355
0.455
Dual trait
KAN.B×
205-8


(C) BC1;BC2 Kanannado brown × IT98K-205-8
FREQUENCY
60
50
40
30
20
10
0
0.055
0.155
0.255
0.355
0.455
Dual trait
BC1
BC2

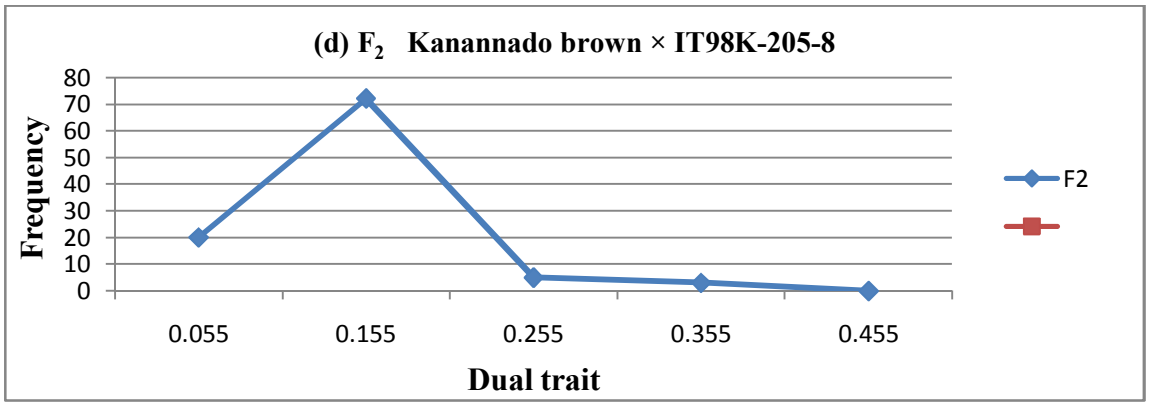
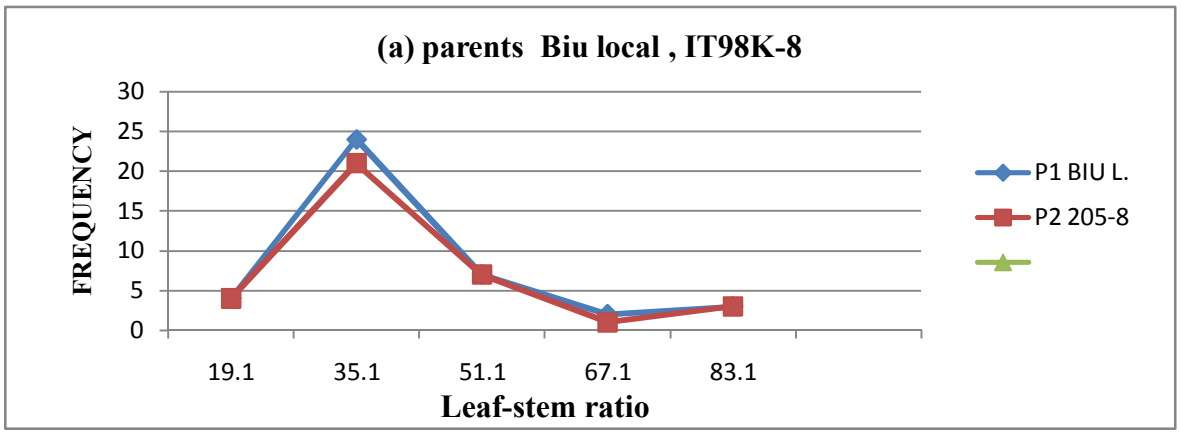
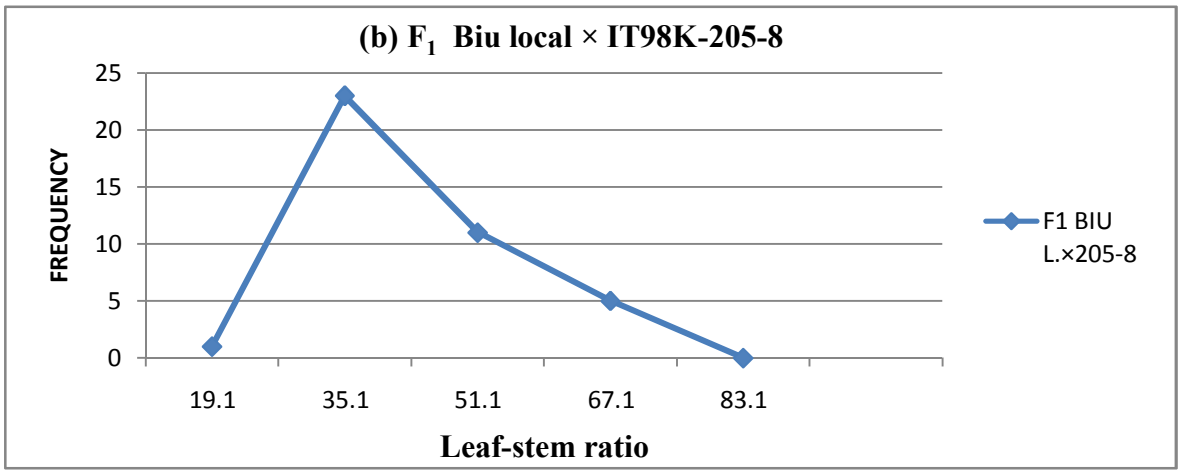
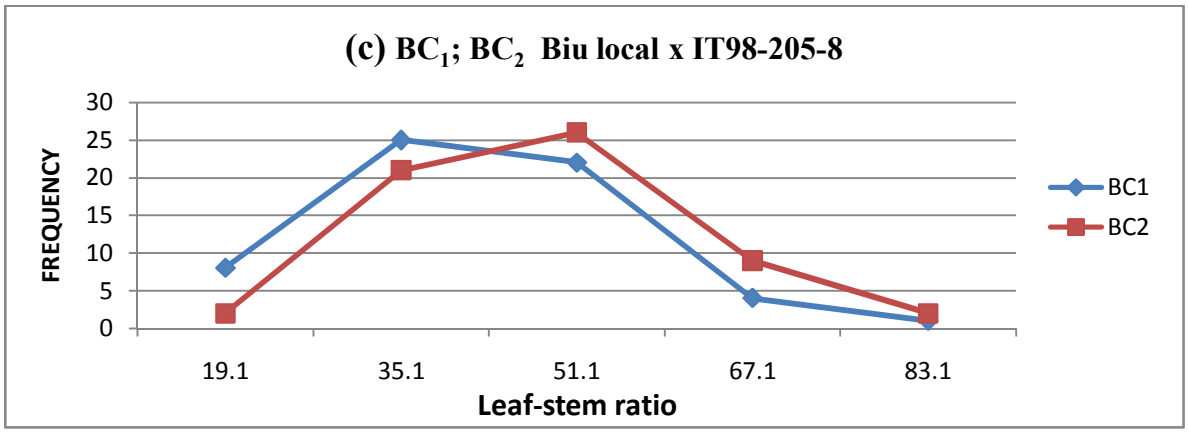


Figure 4.3: Frequency distribution of dual trait for (a) parents, (b) F_1, (c) backcrosses and (d) F_2 populations for the cross Kanannado brown × IT98K-205-8 evaluated in the field at Kadawa, Nigeria in 2011.







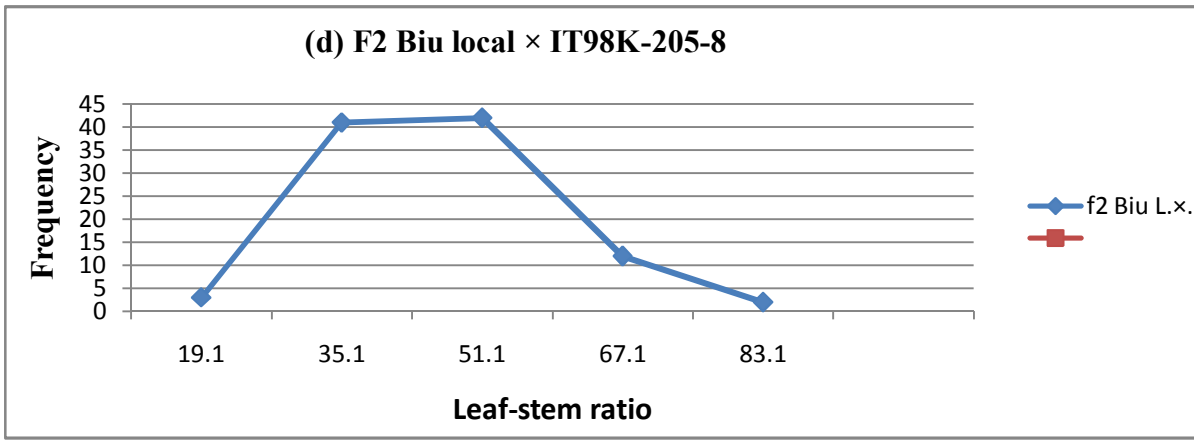
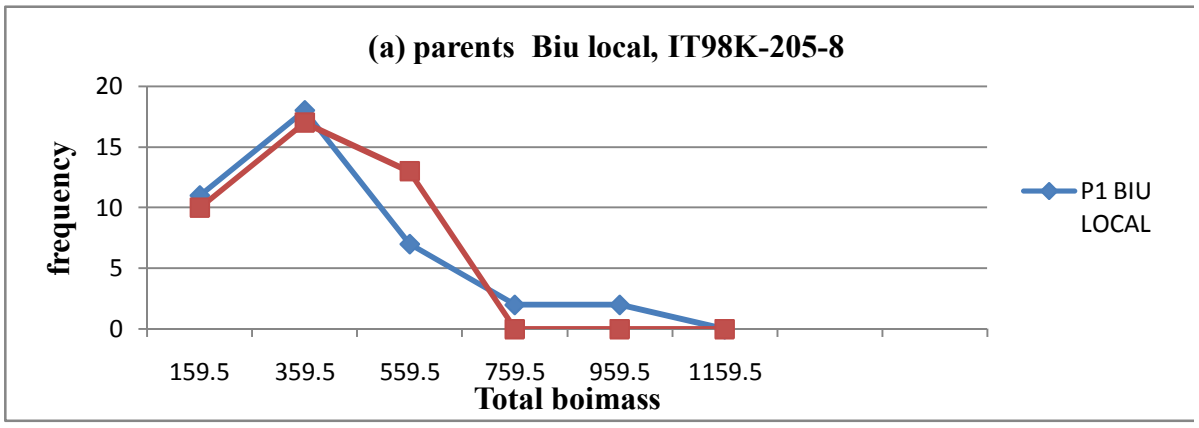
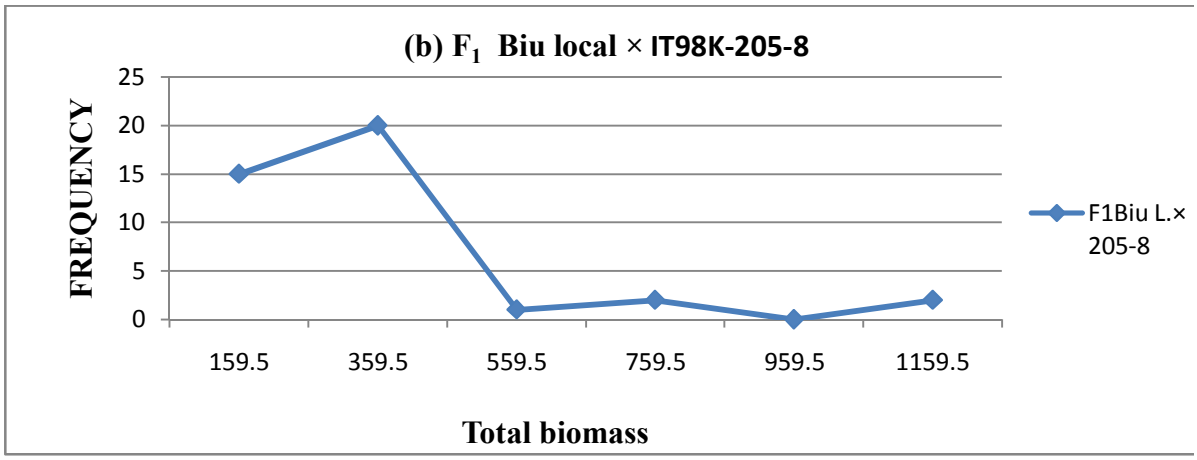
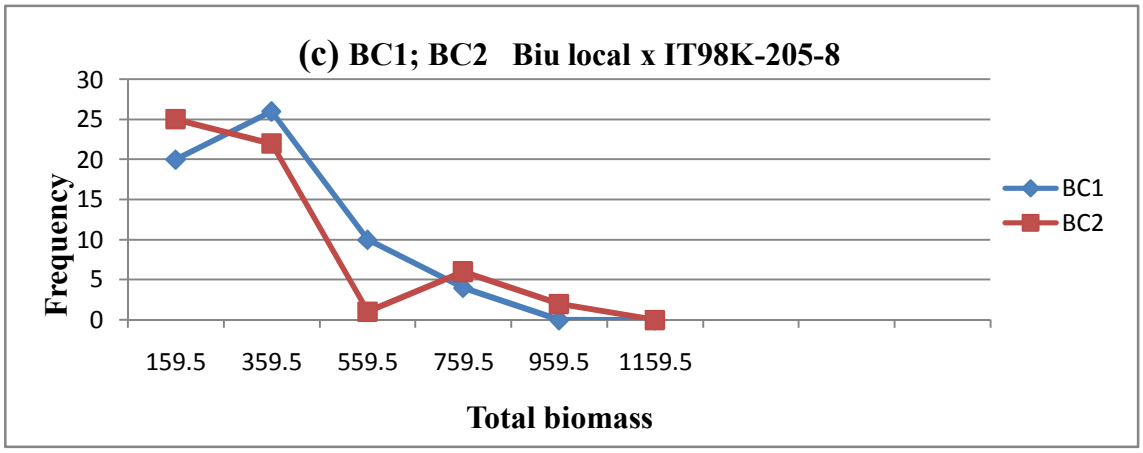


Figure 4.4: Frequency distribution of leaf-stem ratio for (a) parents, (b) F_1, (c) backcrosses and (d) F_2 populations for the cross Biu local × IT98K- 205-8 evaluated in the field at Kadawa, Nigeria in 2011.







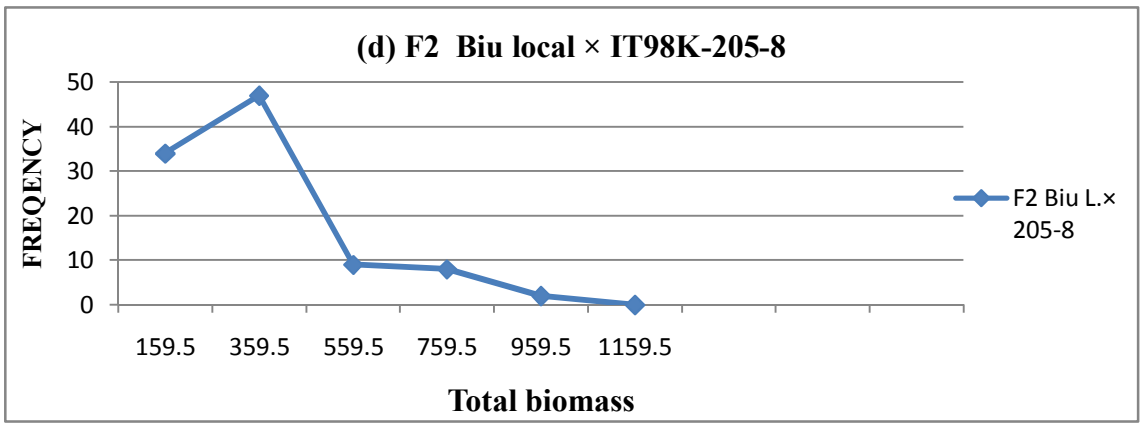
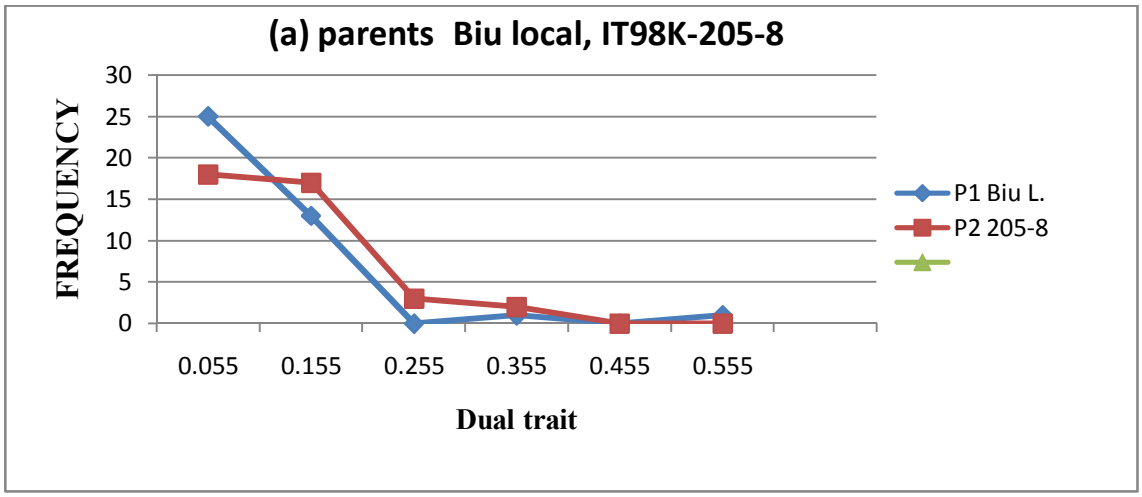
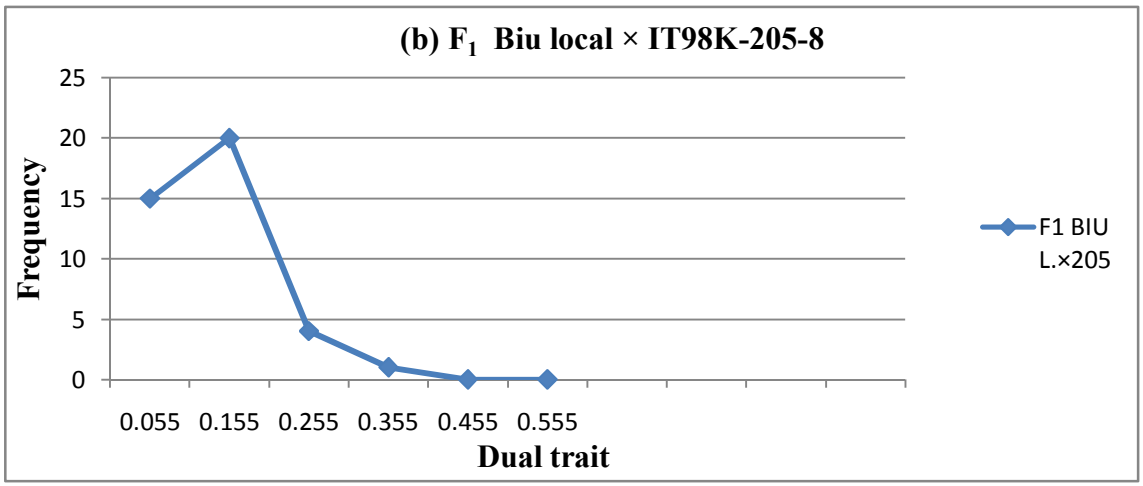
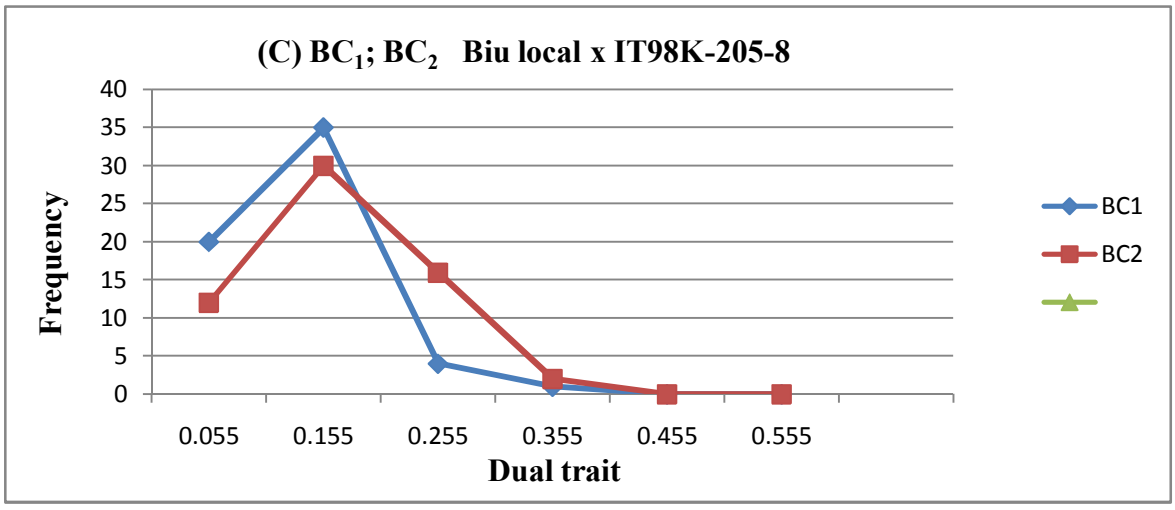


Figure 4.5: Frequency distribution of total biomass for (a) parents, (b) F_1, (c) backcrosses and (d) F_2 populations for the cross Biu local × IT98K-205-8 evaluated in the field at Kadawa, Nigeria in 2011


(a) parents Biu local, IT98K-205-8
FREQUENCY
30
25
20
15
10
5
0
0.055
0.155
0.255
0.355
0.455
0.555
Dual trait
P1 Biu L.
P2 205-8


(b) F1 Biu local × IT98K-205-8
Frequency
25
20
15
10
5
0
0.055
0.155
0.255
0.355
0.455
0.555
Dual trait
F1 BIU L.×205


(C) BC1; BC2 Biu local x IT98K-205-8
Frequency
40
35
30
25
20
15
10
5
0
0.055
0.155
0.255
0.355
0.455
0.555
Dual trait
BC1
BC2

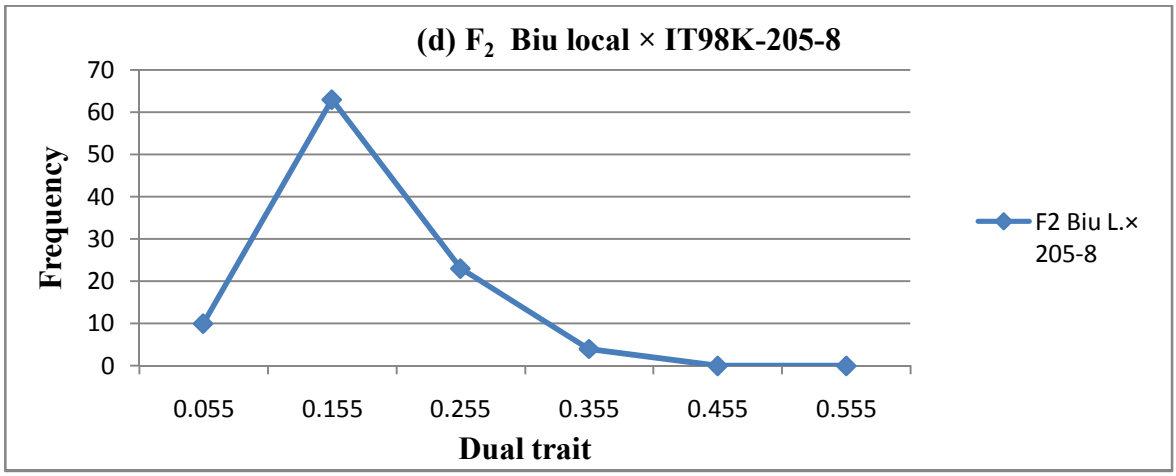


Figure 4.6: Frequency distribution of dual trait for (a) parents, (b) F_1, (c) backcrosses and (d) F_2 populations for the cross Biu local × IT98K-205-8 evaluated in the field at Kadawa, Nigeria in 2011.

4.3 GENETIC ANALYSES

Results of the different genetic analyses suggest polygenic control of this trait (yield). The generation mean analyses of leaf stem ratio, total biomass and dual trait showed the presence of epistatic gene action in both cross (table4.3 to 4.5).The estimation of the five parameters for the genetic analysis for leaf-stem ratio (table4.3) for the cross Kanannado brown × IT98-205-8, revealed that additive (a) gene effect was significant (5%), the dominance(d) and the dominance × dominance gene effects were highly significant ($P<0.01$).The dominance (d); the additive × additive (aa) and the additive × dominance (ad) gene effects acted in opposite direction suggestion duplicate action in the inheritance of leaf-stem ratio. In the same cross the dominance × dominance (dd) gene interaction was of a great magnitude suggesting its predominance in the inheritance of leaf-stem ratio. In the cross Biu local × IT98K-205-8, for the same parameter (leaf-stem ratio), results of the genetic analysis showed that only the additive × additive (aa) and additive × dominance (ad) were significant. The additive (a) and the dominance × dominance gene effects were negative suggesting epistasis interaction. The high relative magnitude of dominance (d)

gene effect suggest that dominance effect is predominant in the inheritance of the trait leaf-stem ratio in the cross Biu local × IT98-205-8.

Table 4.3: Estimates of gene effects for leaf-stem ratio for two cowpea crosses

Crosses	m	a	d	aa	ad	dd
Kanannado brown × IT98K-205-8	48.98*	3.94*	-49**	-20.36	-0.73	32**
	±4.02	±0.85	±14.42	±5.94	±383	±8.91
Biu local × IT98K-205-8	45.66*	-0.66	22.20	4.76*	14.16*	-9.78
	±12.6	±1.53	±18.49	±7.19	±5.58	±12.02

For total biomass (Table4.4) in the cross Kanannado brown × IT98K205-8, only additive (a) and additive × dominance (ad) gene effects were highly significant ($p<0.01$) while the additive × additive (aa) gene effect was significant at $p<0.05$. The dominance × dominance (dd) gene effect was the largest in magnitude followed by the additive (a) gene effect. The remaining three, dominance (d), additive × additive, and dominance × dominance (dd) gene effects were all negative suggesting duplicate gene interaction. The greater dominance × dominance (dd) gene effect over the additive (a) gene effect suggests it predominance in the inheritance of total biomass trait. For the second cross, Biu local × IT98K-205-8, the results (Table 4.4) showed additive (a) and additive × additive (aa) gene effects were significant (at 1% and 5% level of probability respectively). Their magnitudes were also almost the same. The dominance (d) gene effect was not significant but had the largest magnitude. The additive × dominance (ad) and the dominance × dominance (dd) gene effects were negative and not significant; the negative sign of the additive × dominance (ad) suggests dispersion of the gene for the traits. While the negative dominance × dominance (dd) suggested duplicate epistasis.

Table 4.4: Estimates of gene effects for total biomass for two cowpea crosses

Crosses	m	a	d	aa	ad	dd
Kanannado Brown ×IT-98K-205-8	507.07	162.39**	-282	-136.56*	-206.52**	251.05
	±56.89	±14.00	±146.27	±49.67	±52.97	±118.12
Biu local×IT98K-205-8	296.44*	68.20**	317.44	63.87*	-24.99	-242.24
	±14.13	±14.81	±31.24	±138.53	±95.42	±217.94

The genetic analysis for the parameter dual trait in the cross Kanannado brown × IT98K-205-8 was shown in table 4.5. It revealed that additive (a), and additive × dominance (ad) gene effects were highly significant ($P<0.01$), the additive (a) gene effect was indeed negative. The dominance (d), additive × additive (aa), dominance (dd) gene effects were negative but not significant but the dominance × dominance (dd) gene effect had the largest magnitude suggesting predominance of the epistatic gene effect in the parameter dual trait. In the cross Biu local × IT98K-205-8 (Ttable4.5), the additive × additive (aa) and dominance × dominance (dd) gene effects were highly significant and significant respectively.

The dominance × dominance gene interaction had the largest magnitude suggesting predominance of the dominance epistatic action in the inheritance of dual trait. Dominance (d) and additive × dominance (ad) gene interactions were behaving in the opposite ways suggesting dispersion of the genes for dual trait.

Table 4.5: Estimates of gene effects for dual trait for two cowpea crosses

Crosses	m	a	d	aa	ad	dd
Kanannado brown x IT98K-205	0.05*	-0.004**	-0.04	0.02	0.36**	0.46
	±0.04	±0.004	±0.22	±0.9	±0.05	±0.13
Biu local x IT98K-205-8	0.08	0.02	-0.19	0.05**	-0.02	0.98*
	±0.005	±0.01	±0.19	±0.07	±0.53	±0.12

4.4 HERITABILITY AND NUMBER OF EFFECTIVE FACTORS

Tables 4.7; 4.8 and 4.9 showed the estimates of heritability (broad and narrow) and number of effective factors of the F_2 segregating generations. The results (table 4.6) showed that effective factors was 10 and 7 for leaf-stem ratio in crosses Kanannado brown × IT98K-205-8; and Biu local × IT98K-205-8 respectively; it was 4.8 and 4.13 for total biomass and was 4.7 and 4.6 for dual trait. The results for broad sense heritability (Table 4.7 to 4.9) ranged from 52.75% to 74.02% for leaf-stem ratio; 53.52% to 54.71% for total biomass and 75% to 92% for dual trait in crosses Kanannado brown x IT98K-205-8 and Biu Local x IT98K-205-8 respectively. Narrow sense heritability ranged from 14.24% to 31.07%; 14.12% to 23.50% and 32.7% to 40.01% for leaf--stem ratio, total biomass and dual trait respectively in crosses Kanannado brown x IT98K-2058 and Biu local x IT98K-205-8.

Table 4.6: Estimates of Heritability and Number of Effective Factors for leaf-stem ratio in two cowpea crosses

Crosses	h^2 (%)	H_{NS} (%)	N
Kan. Brown × 205-8	42.72	31.07	10
Biu local × 205-8	74.02	14.27	7

h^2 = broad sense heritability; H_{NS} = Narrow sense heritability;
N = Number of Effective Factors; Kan.= Kanannado

Table 4.7: Estimates of Heritability and Number of Effective Factors for total biomass in two cowpea crosses

Crosses	h^2(%)	H_{NS}(%)	N
Kan. Brown × 205-8	54.71	23.50	8
Biu local × 205-8	53.52	14.12	13

h^2 = broad sense heritability; H_{NS} = Narrow sense heritability;
N = Number of Effective Factors; Kan. = Kanannado

Table 4.8: Estimates of Heritability and Number of Effective Factors for dual trait in two cowpea crosses

Crosses	h^2 (%)	H_{NS} (%)	N
Kan. Brown × 205-8	75	32.70	7
Biu local × 205-8	92	40.01	6

h^2 = broad sense heritability; H_{NS} = Narrow sense heritability;
N = Number of Effective Factors; Kan.= Kanannado

4.5 CORRELATION

Table 4.9 and 4.10 show genotypic and phenotypic correlation coefficients between four characters from both crosses. In both crosses, the results showed that in general, genotypic

correlations were higher than the corresponding phenotypic correlations for the traits studied. In the cross Kanannado brown × IT98K-205-8, dual trait correlate negatively with days to flowering but not significant. A high significant negative correlation was observed between dual trait and dry fodder yield. The phenotypic correlation with days to first flowering was negative and highly significant for dry fodder yield, the phenotypic correlation with dual trait was negative and significant; the correlation was, however, positive and not significant with seed weight.

Day to first flower was positively correlated with dry fodder yield and negatively with dry seed weight, the phenotypic correlation for seed weight was positive but were not significant. Dry fodder yield has a genotypically negative and highly significant correlated with dry seed weight, the phenotypic correlation was also negative and not significant. The correlations (phenotypic and genotypic) of dual trait with dry fodder yield, and dry fodder yield with dry seed weight were all negative, highly significant and of high magnitude; and also these values were closed or almost the same. For the cross Biu local × IT98K-205-8, the results showed that genotypic correlation were also higher than their corresponding phenotypic correlations. Dual trait correlated negatively with days to first flower and dry fodder yield, but positively with dry fodder yield and dry seed weight. Their corresponding phenotypic correlations were all negative and not significant. Days to first flower correlated positively with dry fodder yield and dry seed weight only the correlation with dry seed weight was significant with high genotypic correlation value. Dry fodder yield correlated positively with dry seed weight but the phenotypic correlation was negative and not significant.

Table 4.9: Genotypic (r_g) and Phenotypic (r_p) Correlations among four parameters in the cross Kanannado brown × IT98K-205-8

Character		Days to first flower	Dry folder yield	Dry Seed weight
Dual trait	r_g	-0.4562	-0.8397**	0.1534
	r_p	-0.4226	- 0.7956**	0.0794
Day to first Flowering	r_g		0.209	- 0.0352
	r_p		0.256	0.2198
Dry folder yield	r_g			- 0.9051**
	r_p			0.8178**

*=significant at 0.05 level (0.576) **= highly significant at 0.01 level (0.708); df= n-2

Table 4.10: Genotypic (r_g) and Phenotypic (r_p) Correlation among four parameters in the cross Biu local × IT98K-205-8

Character		Days to first flower	Dry folder yield	Dry seed weight
Dual trait	r_g	-0.8503**	-0.4122	0.2928
	r_p	-0.2937	-0.2342	-0.0917
Days to first Flowering	r_g		0.4060	0.9144**
	r_p		0.1694	0.2296
Dry folder Yield	r_g			0.4407
	r_p			-0.1084

*= significant at 0.05 level (0.576), ** = highly significant at 0.01 level (0.708); df= n-2

CHAPTER FIVE

DISCUSSION

The success of any crop improvement programme depends on the magnitude of genetic variability and the extent to which the desirable trait is heritable. The presence of genetic variability in breeding material has been emphasized by Falconer (1960), as basis for exercising central selection pressure. The major yield components in cowpea are number of pods per plant, seed weight per plant and seed size. Therefore improvement for such characters is one of the important objectives of cowpea breeding (Redder *et al*. 1984). The primary need of a plant breeder is an objective evaluation of the current material to decide which course of action to take in raising the next generation. The choice of parents have to be critical in terms of their *per se* performance and their behavior in transgressive breeding. The essential pre-requisite for hybridization is that the parents perfectly complement each other for most of the yield components; so that on hybridization such combination can generate the desired segregants accumulating the favorable alleles increasing expressing of these yield traits (Redder *et al*., 1984).

5.1 MEAN PERFORMANCE

The presence of heritable variation within different genotypes in an evaluation has always been used by geneticists and plant breeders. In this study, the degree of variation among the different populations such as parents and their generations for the three key parameters (leaf-stem ratio, total biomass and dual trait), strongly suggests genetic differences among them. These were in agreement with Wein and Summerfield (1980), Tyagi *et al*. (1978),

Sharma and Singhania (1992) in fodder cowpea, and Sharma (1999) in grain cowpea. Leaf-stem ratio showed partial dominance of better parents in the cross Kanannado brown × IT93K-205-8 and dominance in cross Biu local × IT93-K205-8, mean significant differences between the parents and their generations. This also showed high genetic variation among the parents used in this study, suggesting that genes segregate for the parameter leaf-stem ratio. Over-dominance and partial dominance patterning the same trait have been reported by Kheradnam *et al*. (1975). Ojomo (1974), speculated that heterotic response for yield was due to the effect of dominance or epistasis.

The total biomass (weight of above ground parts including seed weight) was highly significant within the both crosses, suggesting genetic variation for total biomass. This indicated that fodder type parents (Kanannado brown and Biu local) possess high fodder yielding genes, and high grain type parents (IT98K-205-8) possess the high grain yielding gene. Partial dominance for pods per plant which is included in total biomass has been reported by Mak and Yap (1977), Kheradnam *et al*. (1975). Aryeetey and Laing (1973) observed partial dominance of pods and additive gene effect for the same character. Dual trait was also statistically significant and the partial dominance of the high yielding parent over the lower parent, showed variation among the parent used in the study. Pods weight which was part of this character had been reported by Mathur (1995) on pods weight per plant was highly variable trait. However, low to moderate variability have been reported by Sharma (1999) for the same trait. Furthermore variability for seed yield has been reported by Mathur (1995).

5.2 GENETIC VARIABILITY

The frequency distribution of the parents and their F_1 hybrids confirmed the patterns shown by the family means. The F_{1s} distribution was skewed in all the three parameters used in this study. In all the cases it skewed towards either the high yielding parent depending on the trait (grain type or fodder type) confirming the dominance aspect. The normal and near normal (skewness) distribution of the F_2 populations in both crosses implies that fodder and grain yields were governed by polygenes. The tendency of the BC_1P_1 and BC_2P_2 frequency distributions towards their respective recurrent parents and their overlapping nature confirmed the presence of epistatic interactions. The two distributions of the backcross tended towards the same direction of higher fodder yielding parent (in the parameter leaf stem ratio and total biomass) in both crosses, confirming the high concentration of fodder yielding genes in the fodder type genotypes used in this study i.e. Kanannado brown and Biu local. Transgressive segregation for high and low seed yield (for dual trait) was observed in both crosses which included IT93K-205-8 (grain type) this suggests that grain yielding genes were dispersed among parents. This was in conformity with the works of Oseni *et al. (*1992) who reported that the role of pods per plant was apparent in the determination of seed yield, similarly Sawant (1994), observed that pods per plant had highest positive direct effect on seed yield.

Quantitative inheritance for fodder yield has been reported by Tyagi *et al*. (2000). In their study of the component analysis of green fodder yield in cowpea, they stated that fodder yield is a very complex trait influenced by many factors such as number of branches, days to flowering, leaf weight per plant, stem weight, leaf stem ratio etc. Grafius (1956) stated

that to develop high yielding genotypes, selection for yield alone will not be very effective unless due regards is given to fodder component because the higher the dry matter accumulation bring in by long days to flowering, the higher the fodder yield, the lower the grain yield.

5.3 HERITABILITY

Heritability refers to the ratio of the total genotypic to the phenotypic variation. Estimates of heritability are very important to the plant breeder because this parameter determines progress from selection. Two types of estimates are recognized, broad and narrow sense. Broad sense heritability is the ratio of total genetic variance to the phenotypic variance while narrow sense heritability is the ratio of additive genetic (heritable portion) variance to the phenotypic variance. In this study, two types of heritability (broad and narrow sense) were reported. The narrow sense heritability were generally low. The low heritability reported can be due to the fact that only one environment was used therefore estimate of the genotype × environment were not obtained. This had been reported to cause upward bias in the estimate of heritability (Obilana and Fakorede 1981). The low broad sense heritability observed for dual trait (42.75%) can be attributed to the predominance of epistatic gene action. Roquib and Patnaik (1990) also reported low broad sense heritability of 9%, 14% and 24% for leaf-stem ratio, green forage yield per plant and dry matter yield per plant respectively. On the other hand, high broad sense heritability estimates of 90%, 84.4%, 62%, and 95.5% have been reported for plant height, green fodder yield per plant, dry fodder yield per plant and leaf-stem ratio, respectively. This was in conformity with the high broad sense heritability for dual trait in this study which

was 92%; 75%; 74.02%; 54.71%, and 53.52% in the respective crosses. Similarly, high broad sense heritability has been reported by Thaware *et al*. (1991), Kohli (2002) in fodder cowpea, Kumar and Sangwan (2000), Nehru and Manjunath (2001) in grain cowpea.

The results for narrow sense heritability for total biomass in crosses Biu local × IT93K-205-8 and Kanannado x IT98K-205-8 ranged from 32.7% to 40.01% which is high compare to the values for others traits. High narrow sense heritability were reported from crosses of different sizes and seed weight per plant in chick pea (Anon., 1975).The high heritability values indicate that these traits are highly heritable and selection could improve the character.

5.4 GENETIC ANALYSES

Leaf-stem ratio was predominantly under duplicate gene action. The gene effect showed that dominance (d) gene effect was larger in magnitude in the two crosses than other epistatic gene effects. This suggests that the dominance effect was more important than the epistatic effect in the inheritance of leaf-stem ratio. This was in agreement with the findings of Pathmanathan *et al*. (1997) who reported that although both additive (a) and dominance (d) effects were larger and of more importance in the inheritance of leaf-stem ratio and pods weight. Total biomass was predominantly under duplicate gene effect for the two crosses. The epistatic effects, additive × additive (aa), dominance × dominance (dd) magnitude were large enough in the two crosses; this suggests that the contribution of the epistatic effects to the inheritance of total biomass is greater than that of additive but

lesser than that of dominance effect. On individual basis, epistatic effect, the dominance × dominance (dd) estimate was the largest for total biomass. The presence of dominance (d), epistatic and duplicate epistatic would tend to retard the pace of progress in incorporation of total biomass through generation selection.

Dual trait (which here comprises pods weight and total biomass) was also under polygenic gene action for the two crosses. The additive × dominance (ad), and dominance × dominance (dd) epistatic effects for the first cross (Kanannado brown × IT98-K-205-8) and additive × additive (aa) and dominance × dominance (dd) epistatic effects were of large magnitude and important. The implication was that the contribution of epistatic effects to the inheritance of dual trait, was more than additive (a) and dominance (d) gene effects. Even as Jatasara, (1980) in his work reported that most of gene governing yield (either seeds, fodder etc.) act additively. Mitra *et al*. (2001), using generation mean analysis reported that fodder, seeds, pods per plant appeared to be influenced by both additive and non additive gene action. They also reported that complementary gene action was predominantly involved in inheritance of most characters.

5.5 CORRELATION STUDIES

In genetic studies, two types of correlation between characters are recognized, genotypic and environmental. Correlation analysis gives a picture of association pattern of different yield related characters among themselves. Yield is a complex quantitative character governed by a large number of genes. For a rational approach towards improvement of the yields, selection has to be made for the component of the yield. Genetic correlation between different characters of plant often arises because of either linkage or pleiotropy. If

a negative association between characters is due to pleiotropic effects it would be very difficult to obtain the desired combinations, while if linkage is involved special breeding programmes are needed to break the linkage (Al-jibouri *et al*., 1958; Pandey and Gritton, 1975) The correlation pattern is expected to differ with material that is studied since it is a reflection of the genetic makeup of the population. Indirect selection of one trait to improve another is for the phenotypic correlations between characters of interest. But phenotypic and genotypic correlation may differ in magnitude and sign. One may be negative and the other positive or on the other hand one low and the other high. Selection for one of the character here would result in greater changes in the other character than would be expected if the genotypic correlation were assumed equal to the phenotypic correlation. This is for the assumption that differences indicated between genotypic and phenotypic correlations are true differences and not due to sampling variation alone (Johnson *et al*., 1955).

In general, the results in this study indicate that genotypic correlations were higher than phenotypic correlations with few exceptions. This is in agreement with the findings of Johnson *et al*. (1955); Doku (1970); Aryeetey and Laing (1973); Waldia *et al*. (1980); Yunus and Paroda (1980) and Sharma (1984) who reported strong inherent associations between characters. The negative highly significant association of dual trait with other characters in all the crosses implies that indirect selection will dry reduced the yield. Dual trait was highly correlated with dry fodder yield, dry fodder yield with dry seed weight also highly significant (in the first cross); the same trend was noticeable in the cross two: dual trait (pod weight/total biomass) with days to first flower, days to flowering with seed

weight (for second cross). These correlations agreed with those reported by Trehan *et al*. (1970), Virupakshappa *et al.* (1980) and Sigh *et al*. (1982), meaning that direct selection for these characters to improve yield would be effective. Many researchers reported positive, highly significant or not correlations partaining to yields and its components in cowpeas. Patil *et al.* (1989) reported that grain yield near highly correlated with pods per plant, seed weight, and days to flowering. Saddique and Gupta (1991) observed highly significant correlation of seed weight per plant and days to flowering. Oseni *et al*. (1992) revealed that there is a positive correlation with seed yield and days to flowering, and also positive correlation between days to flowering and other yield components such as dry and green fodder yield. Sawant (1994) found that seed yield was significantly and positively correlated with inflorescence per plant, and pods per plant. Tamiselvan and Das (1994) reported that pod weight, and seed weight, should be used as criterions in the development of high yielding genotypes in cowpeas. Singh and Singh (1957) reported that parameters such as seed weight and total biomass made greater directional contribution to seed yield in 45 cowpea genotypes. Rangaiah *et al*. (1999) reported that total biomass was positively and significantly correlated with all traits except plant height.

CHAPTER SIX

SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

6.1 SUMMARY

Studies were carried out at Institute for Agriculture Research green house, Samaru and Kadawa (under irrigation) in the years 2010 and 2011 to investigate inheritance of grain and fodder in cowpea. Three parental genotypes (Kanannado Brown; Biu Local and IT98K-205-8) were used, and the parents with their corresponding hybrids from two crosses (six generations per cross) were replicated three times in a randomized complete block design (RCBD) for evaluation. Kanannado brown in the cross Kanannado Brown x IT98K-205-8, scored high mean performance compared to Biu local in the cross Biu local x IT98K-205-8. IT98K-205-8 performed better in the cross Kanannado Brown x IT98K-205-8 than in the cross Biu local x IT98K-205-8 for the trait total biomass. For dual trait, IT93K-205-8 had significant mean performance in the cross Kanannado Brown x IT98K-205-8, than in cross Biu local x IT98K-205-8. Means of backcrosses progenies were high in both crosses for all traits studied. The F_2 distributions showed unimodality and transgressive segregation in both crosses for characters studied. Broad sense heritability estimates ranged from 52.75% to 74.02% for leaf-stem ratio; 53.52% to 54.71% for total biomass and 75% to 92% for dual trait in crosses Kanannado brown x IT98K-205-8 and Biu Local x IT98K-205-8 respectively. Narrow sense heritability ranged from 14.24% to 31.07%; 14.12% to 23.50% and 32.7% to 40.01% for leaf-stem ratio, total biomass and dual trait respectively in Kanannado brown x IT98K-205-8 and Biu local x IT98K-205-8. Number of effective factors was 10 and 7 for leaf-stem ratio in crosses Kanannado brown

× IT93K-205-8; and Biu local × IT93K-205-8 respectively; 8 and 13 for total biomass and 7 and 6 for dual trait. Results obtained on correlation studies, consistently showed high significant correlation between dual trait and dry fodder yield, dry fodder and dry seed weight in the cross Kanannado Brown x IT98K-205-8, Dual trait with days to first flower and also positive and highly significant correlation between days to flowering and dry seed **weight**.

6.2 CONCLUSIONS

From results partial dominance and over dominance were jointly and severally recorded in the traits studied. High variations were also found in the material used. Backcrossing was revealed to be a best Breeding procedure for developing cowpea varieties with high grain and fodder yields. Unimodality of F_2 distributions, coupled with number of effective factors showed that the inheritance is polygenic. Finally high heritabity (broad and narrow), and how the traits studied correlated showed that selection can be done on such trait in order to increase yields in cowpeas.

6.3 RECOMMENDATIONS

The use of varieties with high grain as well as fodder yields (commercially and in research) is expected to increase farmers' incomes and provide enough food and feed to livestock. For developing of high grain and fodder yielding varieties in cowpea, strongly recommending procedure is hybridization between parents of different genetic backgrounds (in terms of variations in grain and fodder yields), then the hybrids should be subsequently backcrossed to their respective parents.

6.4 FUTURE WORK

1. While using materials such as landraces (which in general are highly photosensitive), the photoperiodic aspect should be given due consideration so that the flowering period should be monitored.

2. While breeding for dual purpose (for grain and fodder yield) in cowpea grain types should be taken as the female parent.

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