

# EFFECT OF SPACING ON GROWTH AND FORAGE YIELD OF TWO GENOTYPES OF LABLAB BEAN (Lablab purpureus(L.) sweet) IN SHAMBAT AREA, SUDAN

By

Hassan Ali Mansour Elhassan B.sc (Agric.) Honours Sudan University of Science and Technology December 2004

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> Supervisor: Dr. Abdelwahab Hassan abdalla

> > Agronomy Department Faculty of Agriculture University of Khartoum

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# **DEDICATION**

To whom pay the pain to sell our soul...

# ACKNOWLEDGEMENT

I would like to acknowledge my supervisor Dr. Abdelwahab Hassan Abdalla for his guidance and assistance.Also I would like to acknowledge my father and mother whom hold me every where and teach me the first ward. I have honor to express gratefull thanks to my love, my wife, Asma Abdalla Ahmed, for her continuous and unlimited support.

# EFFECT OF SPACING ON GROWTH AND FORAGE YIELD OF TWO GENOTYPES OF LABLAB BEAN (Lablab purpureus(L.) sweet) IN SHAMBAT AREA, SUDAN Hassan Ali Mansour Elhassan Thesis ( Master)

# ABSTRACT

An exepriment was carried out to investigate the effect of spacing on growth and yield on Lablab bean (Lablab purpureous.(L) sweet) as forage. The experiment was conducted at the Demonstration farm of the Faculty of Agriculture, University of Khartoum, Sudan, during Summer 2009 season. The treatment used were two genotype of lablab the brown (Commercial Cultivar) the white seed (DL07-11) and four seed spacings 10 cm, 20 cm, 30 cm and 40 cm. The treatment were randomly assigned to a split-plot design with three replicates. Parameters studied included: plant height, stem diameter, number of branches per plant, number of nodules per plant, fresh weight and dry weight. Results showed that the spacings increased stem diameter, number of branches per plant, fresh weight and dry weight increased with spacing. Also the genotype had effect on plant height, the  $V_2$  genotype affect fresh weight while  $V_1$ affect dry weight. The S<sub>4</sub> affect fresh and dry weight.

# كعلف(Lablab Bean)أثر مسافات الزراعة علي نمو وإنتاج اللوبيا حسن علي منصور الحسن أطروحة( ماجستير)

## المستخلص

أجريت تجربة لدراسة الثر مسافات الزراعة على نمو وانتاج اللوبيا (Lablab Bean) كعلف . أجريت التجربة في المزرعة التجريبيه بكلية الزراعة-جامعة الخرطوم، السودان خلال صيف 2009م . احتوت التجربة علي مقارنة بين صنفين من اللوبيا عفن: ذات البذور البنية ( عينة تجارية) وذات البذور البيضاء(DL07-11) واربعة مسافات زراعة :10 سم ،20سم ، 30سم ، 40سم. تم توزيع المعاملات عشوائيا علي تصميم القطع المنشقة في ثلاثة مكررات. المعايير التي ذرست شملت: طول النبات،سمك الساق،عدد الافرع الخضرية / النبات،العقد الجذريه / النبات ،الوزن الرطب والوزن الجاف . أظهرت النتائج ان معاملات مسافات الزراعة ادت الي زيادة معنوية في سمك الساق ،عدد الافرع الخضرية / النبات،العقد الجذريه / النبات معنوية في سمك الساق ،عدد الافرع الخضرية الوزن الرطب والوزن الجاف إزدادت مع زيادة مسافات الزراعة. كما كانت هناك فروق معنوية بين الاصناف في طول النبات حيث أن الصنف ذو البذور البيضاء أقل طولا اظهر الصنف 2V كفاءة اعلى نسبيا في الوزن الرطب والصنف ال كفاءة اعلي نسبيا في الوزن الجاف . اعطت المسافة و 40 سم كفاءة اعلى نسبيا في الوزن الرطب والوزن الرطب والوزن الحاف . اعلم المانف 20

# LIST OF CONTENT

| Subject                                 | Page |
|---|------|
| Dedication                              | i    |
| Acknowledgements                        | ii   |
| English abstract                        | iii  |
| Arabic abstract                         | iv   |
| List of contents                        | V    |
| List of tables                          | viii |
| CHAPTERONE:                             |      |
| Introduction                            | 1    |
| CHAPTERTWO:                             |      |
| Review of literature                    |      |
| 2.1 Introduction                        |      |
| 2.2 Classification                      |      |
| 2.3Description                          | 5    |
| 2.4Environmental requirements           |      |
| 2.4.1 Soil                              |      |
| 2.4.2 Moisture                          | 6    |
| 2.4.3 Temperature                       | 6    |
| 2.5 Reproductive development            | 6    |
| 2.6 Crop cultivars                      | 7    |
| 2.7 Lablab forage yield                 | 8    |
| 2.8 Fertilization                       | 9    |
| 2.9 Sowing date                         | 9    |
| 2.10 Irrigation and weeding             | 9    |
| 2.11 Harvesting                         | 10   |
| 2.12 Lablab seed production             | 10   |
| 2.13 Nutritive value                    | 11   |
| 2.14 Spacing                            | 12   |
| CHAPTER THREE: Materials and methods    | 14   |
| 3.1 Treatments                          | 14   |
| 3.2 Data collection                     | 15   |
| 3.2.1 Plant height                      |      |
| 3.2.2 Number of vegetative branch/plant | 15   |
| 3.2.3 Stem diameter                     | 16   |
| 3.2.4 Number of root nodules/plant      | 16   |
| 3.2.5 Fresh weight                      | 16   |
| 3.2.6 Dry weight                        | 16   |
| 3.3 Statistical analysis                | 16   |
| CHAPTER FOUR: Results                   | 17   |
| 4.1 Plant height                        | 17   |
| 4.2 Stem diameter.                      | 21   |
| 4.3 Number of branches/plant            | 24   |

| 4.5 Fresh weight.304.6 Dry weight.33CHAPTER FIVE: Discussion.355.1 Plant height.365.2 Stem diameter.365.3 Number of branches/plant.375.4 Number of root nodules/plant.375.5 Fresh weight.385.6 Dry weight38Summary AND Conclusions39REFERENCES40 | 4.4 Number of root nodules/plant |    |
|--|----------------------------------|----|
| 4.6 Dry weight.33CHAPTER FIVE: Discussion.355.1 Plant height.365.2 Stem diameter.365.3 Number of branches/plant.375.4 Number of root nodules/plant.375.5 Fresh weight.385.6 Dry weight38Summary AND Conclusions39REFERENCES.40                   | 4.5 Fresh weight                 |    |
| CHAPTER FIVE: Discussion.355.1 Plant height.365.2 Stem diameter.365.3 Number of branches/plant.375.4 Number of root nodules/plant.375.5 Fresh weight.385.6 Dry weight38Summary AND Conclusions39REFERENCES.40                                    | 4.6 Dry weight                   |    |
| 5.1 Plant height.365.2 Stem diameter.365.3 Number of branches/plant.375.4 Number of root nodules/plant.375.5 Fresh weight.385.6 Dry weight38Summary AND Conclusions39REFERENCES.40   | CHAPTER FIVE: Discussion         | 35 |
| 5.2 Stem diameter.365.3 Number of branches/plant.375.4 Number of root nodules/plant.375.5 Fresh weight.385.6 Dry weight38Summary AND Conclusions39REFERENCES.40  | 5.1 Plant height                 |    |
| 5.3 Number of branches/plant375.4 Number of root nodules/plant375.5 Fresh weight385.6 Dry weight   | 5.2 Stem diameter                |    |
| 5.4 Number of root nodules/plant.375.5 Fresh weight.385.6 Dry weight38Summary AND Conclusions39REFERENCES40  | 5.3 Number of branches/plant     |    |
| 5.5 Fresh weight   | 5.4 Number of root nodules/plant |    |
| 5.6 Dry weight   | 5.5 Fresh weight                 |    |
| Summary AND Conclusions  | 5.6 Dry weight                   |    |
| REFERENCES40   | Summary AND Conclusions          |    |
|  | REFERENCES                       | 40 |

# **LIST OF TABLES**

| Number of | LIST OF TABLES  | Page   |
|-----------|---|--------|
| table     |   | number |
| Table:1   | Mean squares from analysis of variance for plant height, estimated at   | 19     |
|           | 30, 40, 50, 60 and 70 days in two lablab – bean genotype grown at four  |        |
|           | spacing in 2009.  |        |
| Table:2   | Mean plant height (cm) of two genotype in different spacing.            | 20     |
| Table:3   | Mean square from analysis of variance of the data on stem diameter      | 22     |
|           | estimated at 30, 40, 50, 60 and 70 days, in two lablab – bean genotype  |        |
|           | grown at four spacings in 2009.   |        |
| Table:4   | Mean stem diameter (mm) of two genotype in different spacing.           | 23     |
|           |   |        |
| Table:5   | Mean square from analysis of variance for number of branch/plant        | 25     |
|           | estimated at 30, 40, 50, 60 and 70 days, in two lablab – bean genotype  |        |
|           | grown at four spacings in 2009  |        |
| Table:6   | Mean number of branch / plant of two genotype in different spacing.     | 26     |
| Table:7   | Mean square from analysis of variance for number of nodules /plant      | 28     |
|           | estimated at 30, 40, 50, 60 and 70 days, in two lablab – bean genotype  |        |
|           | grown at four spacings in 2009.   |        |
| Table:8   | Mean number of nodules / plant of two genotype in different spacing.    | 29     |
|           |   |        |
| Table:9   | Mean square from analysis of variance for fresh weight estimated at 30, | 31     |
|           | 40, 50, 60 and 70 days, in two lablab – bean genotype grown at four     |        |
|           | spacings in 2009.   |        |
| Table:10  | Mean fresh weight (g) of two genotype in different spacing.             | 32     |
| Table:11  | Mean square from analysis of variance for dry weight estimated at 30,   | 34     |
|           | 40, 50, 60 and 70 days, in two lablab – bean genotype grown at four     |        |
|           | spacings in 2009.   |        |
| Table:12  | Mean dry weight (g) of two genotype in different spacing.               | 35     |

# CHAPTER ONE INTRODUCTION

The total area of Sudan is about 250 million hectares. The area under fodder crop is estimated as 126000 hectares of which 46% is in Khartoum state. Normally, 80-90% of the area allocated to fodder crops is cultivated annually. Sudan is endowed with a large livestock population, mainly raised under traditional pastoral and agro-pastoral systems. The production of forage crops is very important for livestock in Sudan.This due to the fact that animals have a social value which leads to the build up of their population to reach about 132 millions of cattle, sheep, goats and camels (Ministry of Animal Resources, 2003).

Forage is necessary for dairy farms, most of the animals in Sudan depend on rangeland as a source of feed, for maintenance and production. Due to over grazing in rangelands, and low forage quantity and quality the performance of animals is poor.

In Sudan the major forage crops belong to two plant families, namely the grass family which include Abu Sbein *(sorghum bicolor)*, Sudan grass *(S. Sudanese)* the hybrid pioneer *(sorghum bicolor \times S. Sudanese)*, maize *(Zea mays)* and the legume forage crops, which include alfalfa *(Meddiago sativa)*, blue pea *(Clitoria ternatea L)*, Lablab *(Lablab purpureus)*. Sustainability of agriculture depends on its ability to restore soil fertility to a level enabling continuous productivity of sufficient land to meet subsistence for food(Skerman *et al* ,1988). Native and introduced forage legumes have the potential to improve wild life (Gee *et al* ;1994).

The ideal legumes would be the ones, which not only have fast and higher growth but also enhanced levels of drought tolerance for longer survival time during the dry period (Ewansiha and Singh, 2006).

The importance of legumes as food crops lies primarily in their high protein content that averages 20-25%, because of their nitrogen fixing ability, which is beneficial to other crops grown with or after them. Ibrahim *et al.* (1996) showed that lablab is better than other crops in yield and quality. In Australia lablab bean(*lablab purpurus*) has replaced cowpea in some areas because it has longer growing season providing a good grazing further into winter and high resistance to disease and insect attack (Pilotte , 1969).

The crop, either green or hay or silage, is used as a feed for livestock. Lablab bean has many advantages over other leguminous forage crop such as cowpea (Wilden ,1974). The origin of lablab bean (*Lablab purpures* in Africa, (Kenya) but the crop is widely grown in the tropic of Africa, India, Australia the Caribbean, Central America, Middle East, Pacific Ocean and South America (Ishag, 1994). Due to its potential for use as vegetative cover, soil improvement, ability to fix nitrogen and control weeds, lablab bean is an old established crop in the Sudan and inter-planted with sorghum or maize along the Nile in the northern states (Ahmed, 1978). It used to be grown in Gezira Scheme as part of the rotation with cotton, as soil improving crop. The green fodder yield of the crop ranged between 15.5-24.6 t/ha and the total grain yield ranged from 514-1378 Kg/ha in Gazira Scheme (Ishag, 1994).

To increase forage yield and improve quality to cope with high demand of the livestock feed, proper cultural practices such as seed rate, time of sowing, spacing and irrigation must be determined. The objective of this study was to assess the effect of spacing on growth and yield of Lablab bean as a forage crop.

# CHAPTER TWO LITERATURE REVIEW

### **2.1 Introduction:**

Livestock in the Sudan is mostly raised under nomadic condition with traditional methods of management and natural grazing. Recent drought and desertification resulted in detrimental effects on the rangelands.

The plant family *Leguminosae* is second only to *Geraminesae* in importance. Members of the family have a world –wide distribution, with greatest variety occurring in the tropics and subtropics. The family holds promise for human kind in supplying the vastly increasing vegetable proteins for human nutrition especially in low-income countries.

Leguminous plants are of an important contribution to pasture, and they are valued for their ability to grow in a symbiotic relationship with nitrogen fixing bacteria and also for their drought resistance. (Humphreys,1978). Nutritionally, legumes (e.g. Clover, Lucerne, and Lablab bean) are frequently superior to grasses in protein and mineral content (particularly calcium ,phosphorus and magnesium) but their nutritive value falls with age (Reid *et al.*, 1973).

Legumes are useful to bridge the gap in feed supply in areas where livestock depend on poor quality crop residues during the dry seasons (Said and Tolera, 1993).

#### **2.2 Classification of Lablab bean:**

#### Lablab purpureus (L.) Sweet

Synonyms – Dolichus lablab

The most common names e.g. Rongai dolichos, lablab bean (Australia), Lubia (Sudan), poor mans bean, Tonga bean (England), batao (Philippines), Indian bean (India), bonavest bean and hyacinth bean (Brazil). The origin of lablab bean is Africa (Kenya) but the crop is widely cultivated in Africa, India,Australia, the Carbbean,Central America and some other countries particularly in Africa e.g Egypt, Sudan(Ishag, 1994).

#### **2.3 Description**

Lablab bean is a summer growing, rampant and vigorously twining herbaceous, annual or short-lived perennial. Stems are robust 3.6 m, leaves are trifoliate, and leaflets are broad ovate. Petioles are long and slender, flower are white in Rongai or blue or purple. Pods are 4.5 cm long containing two to four seeds.(Bakur, 2001).

# 2.4 Environmental requirements

#### 2.4.1 Soil:

Lablab bean grows on a wide range of soils from deep sand to heavy clays, good drainage with pH range from 4.5-7.5. Low salinity tolerance causes leaf chlorosis, reduces growth and may cause plant death. Lablab does not always nodulate well with native strains of Rhizobia; it is recommended to be inoculated with a appropriate lablab Rhizobium strain (Ibrahim, 2007).

#### 2.4.2 Moisture:

Lablab is adapted to annual rainfall regimes from 650-3000mm, but it can grow where rainfall is less than 500 mm; it is drought tolerant when established, but can withstand prolonged dry period. The plant is capable of extracting soil water from at least 2 meters depth even in heavy clay textured soils and will tolerate short periods of flooding but it is intolerant to poor drainage and prolonged inundation (Ibrahim,2007).

### 2.4.3 Temperature

The plant tolerates high temperature, but the average daily temperature for growth is  $18-30^{\circ}$ C; it can also grow in low temperatures (down to 3 °C) for short periods. The plant is susceptible to frost (Ibrahim, 2007).

## **2.5 Reproductive Development**

Lablab bean is a short-day plant, with early and late flowering types with some land races flowering as early as 55 days after sowing. The plant is self pollinated with some out-crossing, but observations suggested that this is usually minimal.Being an annual or weak perennial, lablab flowers and sets seed in the first season of growth. Three harvests are possible from annual types but the crop will not stand heavy grazing. As forage, the crop should be utilized before flowering (Ibrahim, 2007).

# 2.6 Crop cultivars

Lablab bean is characterized by many taxonomic variations. About

- 39- 50 varieties are recognized based on according to (Duke, 1981):
  - Variability of the size , shape and colour of pods (green, white , purple or purpled margins), fleshy or fibrous .
  - 2. Size , shape or colour of seeds (white to yellow to black or reddish purple).
  - 3. Flower characteristics, size of corolla.
  - 4. Colour of leaves

Little work has been done on improving this crop in Sudan. Numerous trials at the Gazira Research Station for more than 25 years produced no strain good enough to replace the main selected type originally grown at the beginning of the scheme (Pursglove, 1969). In the Sudan four lablab cultivars namely Brazilian, High Worth, Local and Rongai , gave the best yield of both forage and grain , and proved to be well adapted .The local varieties produced the lowest forage and grain yields (Ishag,1994).

#### 2.7 Lablab Forage Yield

In the United States, lablab fodder yield ranges from 2 to 10 t/ha (Duke, 1981). However, Skerman *et al.*, (1988) reported 25 t/ha of green material after four to six months in Colombia. In Brazil 40 t/ha were obtained for pure stand and 35 t/ha for mixed maize and lablab (Mohammed, 1999). Magoon and Mehra.,(1974) reported fresh fodder yields of 2.3 to 7.5 t/ha in the first cutting and 2.2 t/ha in the second cutting in India. In Australia, the highest dry matter yield of lablab under irrigation ranged from 6.7 to 14 t/ha (Mulldoon, 1985). However, English (1986) reported that with good growing conditions lablab produced 8 t/ha (D.M).

In Sudan, the average productivity is about 2.6 t/ha dry matter (Abu-Gada *et al*, 1981; Mustafa *et al.*, 1999). However, Osman and Osman (1981) reported from 1.47 to 2.46 t/ha dry matter in saline soil in Soba.

Once established, lablab bean is highly drought resistant often staying green during the dry season. Dry matter yield per hectare varies with rainfall, soil conditions and time of seeding, but work in Australia suggested that 4000 kg of DM per ha with maximum leaf production of two tons DM per ha is not unusual. The ratio of leaf to stem varies with cutting and curing procedures, from 30:70 to 45:55, respectively (Ibrahim, 2007).

#### 2.8 Fertilization

Nutrient use efficiency is an important factor determining fertilizer needs. For example N use efficiency is only 30-50%, thus about two-three times of N fertilizer has to be applied in relation to its uptake by a crop. While it is common to grow lablab without fertilizer application, sowing in sandy soils often requires application of nitrogen, phosphorus and sulphur and it benefits from application of lime in very acid soils (Ibrahim, 2007).

## 2.9 Sowing date

Generally, lablab bean can be sown all over the year in the Sudan Although the productivity is reduced in winter., the best time for sowing ranges from March to October (Mustafa *et al*, 1999). It was observed that the best productivity was in July sowing (Ahmed, 1978). Nevertheless, in Gezira sowing date is in September to avoid cotton leaf curl virus, which is haboured by lablab bean (Abu-Agada *et al.*, 1981and Mustafa *et al.*, 1999).

## **2.10 Irrigation and weeding:**

In the northern states the summer growing lablab bean is irrigated every 14 days, but Damira sown lablab bean needs to be irrigated every 8 days. In Khartoum Atate the irrigation is applied every 10 days (Mustafa *et al*, 1999).Lablab needs one weeding after three to six weeks after sowing followed by another weeding after each cut .The crop once established , will continue to grow and cover up all the interspaces and thus has smothering effect on weeds (Ckakravaraty and Ramartan , 1971).

# 2.11 Harvesting:

Forage harvesting date, especially lablab bean, depends on the growing season. Therefore, the production decreases in winter (Mustafa *et al.*, 1999). During summer when lablab growth is rapid, cutting is done after two months after sowing. First grazing is 7 to 10 weeks after sowing. Subsequent grazing are 6 to 9 weekly intervals (Philotts, 1969). Lablab bean gives three cuttings over season. These cuttings are taken at the height of 12-20cm above soil surface (Kakravarty and Ramartan, 1971).

# 2.12 Lablab seed production:

Lablab produces seeds in winter. Seeds begin to ripen about 8 weeks after first flower appear (English, 1986). It was recommended that seed should be harvested when 80% of pods were dry (Gonzalez and Mendoza, 1996). The production is reduced by half if the crop is utilized for grazing or cutting (Kakravarty and Ramartan, 1971). The yield is greatly affected by the degree of weed control, plant population and soil fertility hence it is very variable (English, 1986) About 400 t/ha of seeds produced annually in Queensland of which more than 70% is cv. Rongai (English et al., 1999). Seed yield ranges from 1.8t/ha to 2.2t/ha. (English, 1986).

#### **2.13 Nutritive value:**

There is a wide variation in the dry matter yield and CP concentration of lablab bean forage depending on location and stage of harvesting. In Australia, woods,(1983) reported that lablab produced herbage yield of 8.6 t/ha at flowering which was comprised of 3.6 t/ha leaf containing 231 g/kg CP and 5 t/ha of stem containing 69 g/kg CP. In Zimbabwe, sun-dried lablab at 8 week growth (pre-an thesis) contained 250, 370, 89, 7.2 and 1.1 g/kg of CP, NDF, acid detergent lignin (ADL), Ca, and P, respectively, with a DM degradation of 842 g/kg (Mupangwa et al., 1997). Abule et al (1995) showed that CP,NDF, Ca and P concentrations of sun-dried lablab were 186, 420, 14 and 1.9 g/kg respectively. Agana and Tshwenyane (2003) reported that, the crude fiber were 41.8%, 61.8%and 43% for leaf, stem and lablab hay, respectively. Umunna et al.(1995) found the crude fiber of lablab hay was 43%, whereas Murphy and Colucci (1999) found that 27.8% as average of crude protein of whole plant and the mean crude protein content of lablab herbage was 17% with a range of 10% to 22% on a dry matter basis. Nyambati (2002) showed that the concentration of the niterogen,

lignin and polyphenol of various residue of lablab bean was 16.7, 10.2, and 11.3g/kg N, 99, 109 and 108g/kg lignin and 15, 8 and 5g/kg ployphenol of leaf, stem and roots respectively.

Lablab contain other anti-nutritional factors such as polyphenols, tannins, trypsin inhibitors activity, cyanogenic glycosides and hemage lutanating activities (Rajaram and Jonardhanan,1991). Tannins in forage legumes have both negative and positive effects on their nutritive value. Tannins in high concentrations reduce intake, digestibility of proteins and carbohydrates (Reed *et al.*, 1990 and Tanner *et al.*, 1990). Tannins in low to moderate concentration, especially condensed tannins, prevent bloat and increase the flow of non-ammonia N and essential amino acids from the rumen (Woodward and Reed, 1997).

## 2.14 Spacing

Spacing is an important factor governing plant population and ultimately the yield. The effect of spacing on seed yield component is needed to design management system. Cultivated row of 50 to 60 cm apart required 40 to 50 kg of seeds ha-<sup>1</sup>. Drill planting rows 15 to 50 cm apart is used where weeds are not serious competitors of bean and 90 to 100 kg of seeds are planted (Francis, 1976).

Results of experiment in the Sudan and other parts of the world showed that narrow and close spacing between plants produced highest yield (Ahmed, 1985). The optimum plant spacing varies with the growth habit of the variety under consideration. Seed yield per unit area is relatively constant over a wide range of plant population for indeterminate or pole cultivars, but decreases at similar plant populations for the determinate or bush cultivars (Westerman and Grather ,1977).

Eltohami *et al*, (2005) reported that plant population have increased leaf area index, total dry matter and grain yield.

# CHAPTER THREE MATERIALS AND METHODS

An experiment was conducted for one season 2009 in order to study the effect of spacing on growth and yield of Lablab bean *(Lablab purpureus* (L) sweet) as a forage crop. The Experiment was carried out in the experimental farm of the F aculty of Agriculture at Shambat, Sudan (Latitude 15°40'N and longitude 32° 32'E).The climate of the study area is semi-arid with hot summer. Part of which is rainy during the period of July to September.The annual rainfall is about 160 mm which varies greatly in intensity and distribution with the peak in August. The mean maximum temperature is about 39°C during summer season. Relative humidity is low (19-29%) especially in the long dry period (October to May) (Oliver, 1965). The soil is heavy clay with about 54% clay and low infiltration rate. The soil pH is 8.5(Saeed ,1968).

#### **3.1 Treatments:**

Two lablab genotypes; namely brown- seeded (V1), which is commercial cultivar and DLO7-11 (V2), white-seeded inbred line were used in this study. The seeds of these genotypes were provided by Dr. A.H. Abd alla, Department of Agronomy, Faculty of Agric. UK. The treatments comperised four spacings (10,20,30 and 40 cm). Before planting the land was disc ploughed, harrowed, leveled then ridged at 70 cm apart .The experiment area was divided into plots. Each main plot was divided into 4 sub-plots with an area of  $4 \times 5m$  for each sub-plot in which 5 ridges. The experiment was laid out in a split-plot design with three replications.The main plots were assigned to genotypes and the sub-plot to the spacing treatments.

The seeds were sown on 24th March 2009. Three seeds were planted in each hole and then thinned to two plants per holes two weeks after planting. Irrigation was applied weekly. Plots were hand weeded when necessary.

#### **3.2 Data collection:**

For data collection a random sample of ten plants were taken from the three middle ridges in each plot. Measurements were taken every ten days, starting one month after sowing until the end of experiment. The plants were pulled out, cleaned and taken to the laboratory for determination of fresh weight and dry weight.

**3.2.1 Plant height (cm):** It was measured from the base of the plant to the tip of the top leaf.

**3.2.2 Number of vegetative branches/ plant:** The branches in the plants of the sample were counted for number of branches / plant.

**3.2.3 Stem diameter (mm):** It was measured using Vernia, on the ten randomly selected plants then the mean stem diameter was obtained.

**3.2.4 Number of root nodules/plant:** It was determined on a random sample of five plants then the mean number of nodules/plant was obtained.

**3.2.5 Fresh weight (g):** In the Laboratory, the sample of plants were washed with tap-water for cleaning then weighted using a sensitive balance to determine fresh weight.

**3.2.6 Dry weight (g):** The sample plants used for fresh weight was air dried for three weeks then oven dried at 60°C for about 72 hours till a constant weight was reached and the mean dry weight was obtained.

#### **3.3 Statistical analysis:**

The collected data, at each occasion, were subjected to analysis of variance then the means were compared according to the procedure described by Gomez and Gomez (1984).

# **CHAPTER FOUR**

# RESULTS

# 4.1 Plant height (cm):

At 30 days, analysis of variance (Table 1) showed that there were significant differences between the two genotypes in plant height. However, there were no significant differences among the spacings. Also the genotype x spacing interaction was not significant. The mean plant height for  $V_1$  was 22.04cm, which was significantly greater than recorded for  $V_2$ . For spacing the overall mean plant height was 17.7cm.

At 40 days, analysis of variance (Table 1) showed that there were no significant differences between the genotypes. Also, there were no significant differences a mong the spacings and the genotypes x spacing interaction was not significant. The overall mean plant height was 48.86 cm.

At 50 days, analysis of variance (Table 1 ) showed that there were no significant differences between the genotypes. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean plant height was 88.71 cm.

At 60 days, analysis of variance (Table 1 ) showed that there were no significant differences between the genotypes. Also there were no significant differences among the spacings. And the genotypes x spacing interaction. The overall mean plant height was 114.9cm.

At 70 days, analysis of variance (Table 1 ) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings.And the genotypes x spacing interaction.. The overall mean plant height was 124.78 cm. **Table (1):**Mean squares from analysis of variance for plant height, estimated at 30, 40, 50, 60 and 70days in two lablab – bean genotype grown at four spacing in 2009.

|             | Mean | Mean Square |            |           |           |           |  |  |  |
|-------------|------|-------------|------------|-----------|-----------|-----------|--|--|--|
| Sources of  | D.F  | 30          | 40         | 50        | 60        | 70        |  |  |  |
| variation   |      |             |            |           |           |           |  |  |  |
| Block       | 2    | 21.85 ns    | 82.83 ns   | 145.67ns  | 112.96 ns | 218.28 ns |  |  |  |
| Genotype    | 1    | 451.62*     | 2280.13 ns | 264.07 ns | 329.67 ns | 159.39 ns |  |  |  |
| (G)         |      |             |            |           |           |           |  |  |  |
| Error (a)   | 2    | 23.12       | 187.70     | 126.47    | 155.68    | 222.95    |  |  |  |
| Spacing (S) | 3    | 2.82 ns     | 54.45 ns   | 79.96 ns  | 220.16 ns | 246.22 ns |  |  |  |
| GxS         | 3    | 7.13 ns     | 17.59 ns   | 56.53 ns  | 59.12ns   | 47.60 ns  |  |  |  |
| Error (b)   | 12   | 6.40        | 28.30      | 90.21     | 10149.63  | 165.62    |  |  |  |
| Total       | 23   |             |            |           |           |           |  |  |  |

ns = non significant

\*. \*\* = significant at (p<0.05and 0.01), respectively.

| Genotype       | 30 days |        |        |        |               |
|----------------|---------|--------|--------|--------|---------------|
|                | 10 cm   | 20 cm  | 30 cm  | 40 cm  | Genotype mean |
| $V_1$          | 22.24   | 21.32  | 22.42  | 22.18  | 22.04         |
| $V_2$          | 11.37   | 15.6   | 12.9   | 13.57  | 13.36         |
| Spacing mean   | 16.8    | 18.46  | 17.66  | 17.87  | 17.70         |
| LSD 0.05       | 3.18    |        |        |        | 8.45          |
|                | 40 days |        |        |        |               |
|                | 10 cm   | 20 cm  | 30 cm  | 40 cm  | Genotype mean |
| $\mathbf{V}_1$ | 57.3    | 57.06  | 58.82  | 61.22  | 58.6          |
| $V_2$          | 34.32   | 40.4   | 36.97  | 44.77  | 39.12         |
| Spacing mean   | 45.81   | 48.73  | 47.89  | 52.99  | 48.86         |
| LSD 0.05       | 6.69    |        | ·      |        | 24.07         |
|                | 50 days |        |        |        |               |
|                | 10 cm   | 20 cm  | 30 cm  | 40 cm  | Genotype mean |
| $\mathbf{V}_1$ | 95.03   | 88.8   | 86.27  | 98.0   | 92.03         |
| $V_2$          | 83.32   | 79.78  | 88.55  | 89.92  | 85.39         |
| Spacing mean   | 89.18   | 84.29  | 87.41  | 93.96  | 88.71         |
| LSD 0.05       | 11.95   |        |        |        | 19.75         |
|                | 60 days |        |        |        |               |
|                | 10 cm   | 20 cm  | 30 cm  | 40 cm  | Genotype mean |
| $\mathbf{V}_1$ | 109.5   | 110.93 | 103.26 | 121.43 | 111.28        |
| $V_2$          | 114.56  | 113.58 | 119.93 | 126.7  | 118.69        |
| Spacing mean   | 112.03  | 112.25 | 111.59 | 124.06 | 114.99        |
| LSD 0.05       | 126.74  |        | ·      |        | 21.92         |
|                | 70 days |        |        |        |               |
|                | 10 cm   | 20 cm  | 30 cm  | 40 cm  | Genotype mean |
| $\mathbf{V}_1$ | 117.83  | 123.26 | 114.8  | 132.86 | 122.18        |
| V <sub>2</sub> | 123.36  | 122.81 | 127.56 | 135.63 | 127.34        |
| Spacing mean   | 120.59  | 123.03 | 121.18 | 134.24 | 124.76        |
| LSD 0.05       | 16.2    |        |        |        | 26.2          |

 Table (2): Mean plant height (cm) of two genotype in different spacing:

#### 4.2 Stem diameter (mm):

At 30 days, analysis of variance (Table 3) showed that there were no significant differences between the tow genotypes. Also, there were no significant differences among the spacings and the genotype x spacing interaction. The overall mean stem diameter was 4.31 mm.

At 40 days, analysis of variance (Table 3) showed that there were no significant differences between the genotypes. Also there were no significant differences between the spacings and the genotype x spacing interaction was not significant. The overall mean plant height was 5.44 mm.

At 50 days, analysis of variance (Table 3) showed that there were significant differences between the spacings. However, there were no significant differences among the genotype. Also the genotype x spacing interaction was not significant. The mean stem diameter for  $S_4$  was 7.92 mm, which was significantly greater than mean stem diameter 7.42 mm of  $S_2$ , 7.39 mm of  $S_3$ , and 6.86 mm of  $S_1$ . For genotypes the overall mean stem diameter was 7.39 mm.

At 60 days, analysis of variance (Table 3) showed that there were no significant differences between the genotypes. Also, there were no significant differences among the spacings and the genotype x spacing interaction.The overall mean stem diameter was 8.84 mm.

At 70 days, analysis of variance (Table 3) showed that there were significant differences among the spacings. However, there were no significant differences between the genotypes. Also, the genotype x spacing interaction was not significant. The mean stem diameter for  $S_4$  was 10.79 mm, which was significantly greater than mean stem diameter 9.67 mm of  $S_{2,9.61}$  mm of  $S_3$  and 8.94 mm of  $S_1$  .For genotype the overall mean stem diameter was 9.75 mm.

**Table (3)**:Mean square from analysis of variance of the data on stem diameter estimated at 30, 40, 50, 60 and 70days, in two lablab – bean genotype grown at four spacings in 2009.

|             | Mean Square |         |         |         |         |         |  |  |
|-------------|-------------|---------|---------|---------|---------|---------|--|--|
| Sources of  | D.F         | 30      | 40      | 50      | 60      | 70      |  |  |
| variation   |             |         |         |         |         |         |  |  |
| Block       | 2           | 0.72 ns | 0.81 ns | 0.34 ns | 0.02 ns | 0.10 ns |  |  |
| Genotype    | 1           | 0.30 ns | 0.13ns  | 0.35 ns | 0.11 ns | 0.35 ns |  |  |
| (G)         |             |         |         |         |         |         |  |  |
| Error (a)   | 2           | 0.17    | 0.44    | 0.13    | 0.20    | 0.10    |  |  |
| Spacing (S) | 3           | 0.11 ns | 0.57 ns | 1.22 *  | 1.61ns  | 3.52 *  |  |  |
| GxS         | 3           | 0.06 ns | 0.06 ns | 0.09 ns | 0.12 ns | 0.53 ns |  |  |
| Error (b)   | 12          | 0.11    | 0.17    | 0.28    | 0.58    | 0.76    |  |  |
| Total       | 23          |         |         |         |         |         |  |  |

ns = non significant

\*. \*\* = significant at (p<0.05and 0.01), respectively.

| spacing.       |         |       |       |       |               |  |
|----------------|---------|-------|-------|-------|---------------|--|
| Genotype       | 30 days |       |       |       |               |  |
|                | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |  |
| $V_1$          | 4.22    | 4.44  | 4.54  | 4.47  | 4.42          |  |
| $V_2$          | 4.0     | 4.43  | 4.07  | 4.29  | 4.19          |  |
| Spacing mean   | 4.11    | 4.43  | 4.30  | 4.38  | 4.31          |  |
| LSD 0.05       | 0.43    |       |       |       | 0.73          |  |
|                | 40 days |       |       |       |               |  |
|                | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |  |
| $V_1$          | 5.80    | 6.11  | 6.27  | 6.41  | 6.14          |  |
| $V_2$          | 5.52    | 6.15  | 5.89  | 6.42  | 5.99          |  |
| Spacing mean   | 5.66    | 6.13  | 6.08  | 6.41  | 6.07          |  |
| LSD 0.05       | 0.52    |       |       | ·     | 1.17          |  |
|                | 50 days |       |       |       |               |  |
|                | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |  |
| $V_1$          | 6.98    | 7.53  | 7.67  | 7.95  | 7.53          |  |
| $V_2$          | 6.74    | 7.31  | 7.11  | 7.9   | 7.26          |  |
| Spacing mean   | 6.86    | 7.42  | 7.39  | 7.92  | 7.39          |  |
| LSD 0.05       | 0.67    |       |       | ·     | 0.65          |  |
|                | 60 days |       |       |       |               |  |
|                | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |  |
| $V_1$          | 8.11    | 8.99  | 9.13  | 9.43  | 8.91          |  |
| $V_2$          | 8.25    | 8.75  | 8.64  | 9.47  | 8.77          |  |
| Spacing mean   | 8.18    | 8.87  | 8.88  | 9.45  | 8.84          |  |
| LSD 0.05       | 0.42    |       |       |       | 0.79          |  |
|                | 70 days |       |       |       |               |  |
|                | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |  |
| $V_1$          | 8.81    | 10.19 | 9.79  | 10.71 | 9.87          |  |
| V <sub>2</sub> | 9.07    | 9.15  | 9.44  | 10.87 | 9.63          |  |
| Spacing mean   | 8.94    | 9.67  | 9.61  | 10.79 | 9.75          |  |
| LSD 0.05       | 1.1     |       |       |       | 0.56          |  |

Table (4): Mean stem diameter (mm) of two genotype in different spacing:

### 4.3 Number of branches/plant:

At 30 days, analysis of variance (Table 5) showed that there were no significant differences between the genotypes. Also, there were no significant differences among the spacings and the genotype x spacing interaction. The overall mean number of branches was 3.08.

At 40 days, analysis of variance (Table 5) showed that there were significant differences among the spacings and the genotypes x spacing interaction. However, there were no significant differences between the genotypes. The mean number of branches for  $S_4$  was 4.42, which was significantly greater than 4.12 of  $S_2$ , 4.09 of  $S_3$  and 3.79 of  $S_1$ . For genotypes the overall mean number of branches was 4.11.

At 50 days, analysis of variance (Table 5) showed that there were significant differences among the spacings. However, there were no significant differences between the genotypes. Also, the genotype x spacing interaction was not significant. The mean number of branches for  $S_4$  was 5.99, which was significantly greater than 5.74 of  $S_3$ , 5.29 of  $S_2$  and 5.26 of the  $S_1$ . For genotype the overall mean number of branches was 5.57.

At 60 days, analysis of variance (Table 5) showed that there were significant differences among the spacings. However, there were no significant differences between the genotype; Also the genotype x spacing interaction was not significant. The mean number of branches for  $S_4$  was 7.45, which was significantly greater than 7.19 of  $S_3$ , 6.51 of  $S_2$  and 6.51 of  $S_1$  .For genotype the overall mean number of branches was 6.92.

At 70 days, analysis of variance (Table 5) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The mean overall mean number of branches was 7.84.

**Table (5):** Mean square from analysis of variance for number of branch/plant estimated at 30, 40, 50, 60 and 70days, in two lablab – bean genotype grown at four spacings in 2009.

|             | Mean Square |         |        |          |         |         |  |  |
|-------------|-------------|---------|--------|----------|---------|---------|--|--|
| Sources of  | D.F         | 30      | 40     | 50       | 60      | 70      |  |  |
| variation   |             |         |        |          |         |         |  |  |
| Block       | 2           | 1.88 ns | 2.02 * | 1. 54 ns | 0.20 ns | 0.30 ns |  |  |
| Genotype    | 1           | 0.96 ns | 0.37ns | 0.12 ns  | 0.01ns  | 0.28 ns |  |  |
| (G)         |             |         |        |          |         |         |  |  |
| Error (a)   | 2           | 0.21    | 0.09   | 0.16     | 0.52    | 0.47    |  |  |
| Spacing (S) | 3           | 0.02 ns | 0.38 * | 0.72 *   | 1.36 *  | 1.35 ns |  |  |
| GxS         | 3           | 0.05 ns | 0.18 * | 0.013 ns | 0.03ns  | 0.18ns  |  |  |
| Error (b)   | 12          | 0.08    | 0.01   | 0.067    | 0.27    | 0.47    |  |  |
| Total       | 23          |         |        |          |         |         |  |  |

ns = non significant

\*. \*\* = significant at (p<0.05and 0.01), respectively.

| Genotype              | 30 days |       |       |       |               |
|-----------------------|---------|-------|-------|-------|---------------|
| ~ ~ ~                 | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| <b>V</b> <sub>1</sub> | 3.1     | 3.23  | 3.5   | 3.3   | 3.28          |
| V <sub>2</sub>        | 2.9     | 2.93  | 2.83  | 2.87  | 3.88          |
| Spacing mean          | 3.0     | 3.08  | 3.16  | 3.08  | 3.58          |
| LSD 0.05              | 0.37    |       |       |       | 0.82          |
|                       | 40 days |       |       |       | ·             |
|                       | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| $\mathbf{V}_1$        | 3.97    | 4.17  | 4.27  | 4.53  | 4.24          |
| V <sub>2</sub>        | 3.6     | 4.07  | 3.9   | 4.3   | 3.97          |
| Spacing mean          | 3.79    | 4.12  | 4.09  | 4.42  | 4.11          |
| LSD 0.05              | 0.15    |       |       |       | 0.53          |
|                       | 50 days |       |       |       |               |
|                       | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| $\mathbf{V}_1$        | 5.3     | 5.43  | 5.77  | 6.07  | 5.64          |
| V <sub>2</sub>        | 5.23    | 5.16  | 5.7   | 5.9   | 5.49          |
| Spacing mean          | 5.26    | 5.29  | 5.74  | 5.99  | 5.57          |
| LSD 0.05              | 0.33    |       |       |       | 0.72          |
|                       | 60 days |       |       |       |               |
|                       | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| V <sub>1</sub>        | 6.6     | 6.6   | 7.16  | 7.4   | 6.94          |
| V <sub>2</sub>        | 6.43    | 6.43  | 7.23  | 7.5   | 6.89          |
| Spacing mean          | 6.51    | 6.51  | 7.19  | 7.45  | 6.92          |
| LSD 0.05              | 0.65    |       |       |       | 1.28          |
|                       | 70 days |       |       |       |               |
|                       | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| $V_1$                 | 7.56    | 7.86  | 8.06  | 8.3   | 7.94          |
| V <sub>2</sub>        | 7.03    | 7.36  | 8.1   | 8.43  | 7.73          |
| Spacing mean          | 7.29    | 7.61  | 8.08  | 8.36  | 7.84          |
| LSD 0.05              | 0.87    |       |       |       | 1.2           |

**Table (6):** Mean number of branch / plant of two genotype in different spacing:

#### 4.4 Number of root nodules/plant:

At 30 days, analysis of variance (Table 7) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean number of nodules was 3.22.

At 40 days, analysis of variance (Table 7) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean number of nodules was 5.77.

At 50 days, analysis of variance (Table 7) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean number of nodules was 3.97.

At 60 days, analysis of variance (Table 7) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean number of nodules was 4.83.

At 70 days, analysis of variance (Table 7) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean number of nodules

was 3.87.

**Table (7):**Mean square from analysis of variance for number of nodules /plant estimated at 30, 40, 50, 60 and 70days, in two lablab – bean genotype grown at four spacings in 2009.

|             | Mean So | Mean Square |         |          |          |          |  |  |  |
|-------------|---------|-------------|---------|----------|----------|----------|--|--|--|
| Sources of  | D.F     | 30          | 40      | 50       | 60       | 70       |  |  |  |
| variation   |         |             |         |          |          |          |  |  |  |
| Block       | 2       | 1.14 ns     | 0.36 ns | 1.37ns   | 2.08ns   | 5.011 ns |  |  |  |
| Genotype    | 1       | 0.04 ns     | 0.001ns | 23.60 ns | 0.006 ns | 2.041 ns |  |  |  |
| (G)         |         |             |         |          |          |          |  |  |  |
| Error (a)   | 2       | 2.84        | 2.23    | 1.62     | 8.82     | 1.22     |  |  |  |
| Spacing (S) | 3       | 3.05 ns     | 5.51 ns | 0.52ns   | 0.50 ns  | 1.21 ns  |  |  |  |
| GxS         | 3       | 1.21 ns     | 2.96 ns | 5.52 ns  | 1.96ns   | 0.22ns   |  |  |  |
| Error (b)   | 12      | 4.11        | 3.44    | 3.95     | 6.31     | 2.09     |  |  |  |
| Total       | 23      |             |         |          |          |          |  |  |  |

ns = non significant

\*. \*\* = significant at (p<0.05and 0.01), respectively.

| Genotype              | 30 days |       |       |       |               |
|-----------------------|---------|-------|-------|-------|---------------|
|                       | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| $V_1$                 | 2.7     | 4.4   | 1.9   | 4.0   | 3.25          |
| V <sub>2</sub>        | 2.8     | 3.7   | 3.1   | 3.2   | 3.2           |
| Spacing mean          | 2.75    | 4.05  | 2.5   | 3.6   | 3.23          |
| LSD 0.05              | 2.55    | •     | •     | -     | 2.96          |
|                       | 40 days |       |       |       |               |
|                       | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| <b>V</b> <sub>1</sub> | 7.5     | 5.9   | 5.2   | 4.5   | 5.77          |
| V <sub>2</sub>        | 6.6     | 4.4   | 6.7   | 5.4   | 5.77          |
| Spacing mean          | 7.05    | 5.15  | 5.95  | 4.95  | 5.77          |
| LSD 0.05              | 2.34    |       |       |       | 2.62          |
|                       | 50 days |       |       |       |               |
|                       | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| V <sub>1</sub>        | 3.8     | 4.13  | 2.46  | 1.6   | 2.99          |
| V <sub>2</sub>        | 4.6     | 4.3   | 4.8   | 6.13  | 4.95          |
| Spacing mean          | 4.2     | 4.21  | 3.63  | 3.86  | 3.97          |
| LSD 0.05              | 2.50    |       | ·     |       | 2.24          |
|                       | 60 days |       |       |       |               |
|                       | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| $V_1$                 | 5.73    | 4.26  | 4.26  | 3.66  | 4.47          |
| V <sub>2</sub>        | 4.53    | 4.26  | 4.26  | 7.73  | 5.19          |
| Spacing mean          | 5.13    | 4.26  | 4.26  | 5.69  | 4.83          |
| LSD 0.05              | 3.16    | •     | •     | -     | 5.21          |
|                       | 70 days |       |       |       |               |
|                       | 10 cm   | 20 cm | 30 cm | 40 cm | Genotype mean |
| <b>V</b> <sub>1</sub> | 4.13    | 4.53  | 3.6   | 4.33  | 4.14          |
| <b>V</b> <sub>2</sub> | 4.13    | 3.8   | 2.8   | 3.53  | 3.56          |
| Spacing mean          | 4.13    | 4.16  | 3.2   | 3.93  | 3.85          |
| LSD 0.05              | 1.8     |       |       |       | 1.9           |

 Table (8):
 Mean number of nodules / plant of two genotype in different spacing:

## 4.5 Fresh weight (g):

At 30 days, analysis of variance (Table 9) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean fresh weight was 15.39 g. At 40 days, analysis of variance (Table 9) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean fresh weight was 64.69g. At 50 days, analysis of variance (Table 9) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean fresh weight was101.15g. At 60 days, analysis of variance (Table 9) showed that there were significant differences among the spacings. However, there were no significant differences between genotype, Also the genotype x spacing interaction was not significant. The mean fresh weight for S<sub>4</sub> was 174.01 g, which was significantly greater than 129.06 g of  $S_3$ , 111.13 g of  $S_1$  and 106.15g of  $S_2$ . For genotype the overall mean fresh weight was 129.98 g. At 70 days, analysis of variance (Table 9) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean fresh weight was 216.52g.

**Table (9):** Mean square from analysis of variance for fresh weight estimated at 30, 40, 50, 60 and 70days, in two lablab – bean genotype grown at four spacings in 2009.

|             | Mean | Mean Square |           |            |           |            |  |  |  |
|-------------|------|-------------|-----------|------------|-----------|------------|--|--|--|
| Sources of  | D.F  | 30          | 40        | 50         | 60        | 70         |  |  |  |
| variation   |      |             |           |            |           |            |  |  |  |
| Block       | 2    | 16.32ns     | 752.59 ns | 850.02ns   | 450.64 ns | 318.01 ns  |  |  |  |
| Genotype    | 1    | 34.32 ns    | 25.01 ns  | 0.92 ns    | 651.63ns  | 7830.09 ns |  |  |  |
| (G)         |      |             |           |            |           |            |  |  |  |
| Error (a)   | 2    | 37.20       | 114.48    | 251.68     | 569.58    | 1429.96    |  |  |  |
| Spacing (S) | 3    | 21.26ns     | 269.30 ns | 1733.57 ns | 5729.08*  | 10553.84ns |  |  |  |
| G x S       | 3    | 7.74ns      | 226.74 ns | 304.94ns   | 149.19 ns | 406.64ns   |  |  |  |
| Error (b)   | 12   | 9.20        | 252.96    | 8931.79    | 1016.65   | 3254.26    |  |  |  |
| Total       | 23   |             |           |            |           |            |  |  |  |

ns = non significant

\*. \*\* = significant at (p<0.05and 0.01), respectively.

| Genotype     | 30 days      |        |        |        |               |  |  |  |
|--------------|--------------|--------|--------|--------|---------------|--|--|--|
|              | 10 cm        | 20 cm  | 30 cm  | 40 cm  | Genotype mean |  |  |  |
| $V_1$        | 16.17        | 14.8   | 15.8   | 19.5   | 16.57         |  |  |  |
| $V_2$        | 11.8         | 15.7   | 12.6   | 16.7   | 14.2          |  |  |  |
| Spacing mean | 13.9         | 15.25  | 14.2   | 18.1   | 15.39         |  |  |  |
| LSD 0.05     | 10.72 5.39   |        |        |        |               |  |  |  |
|              | 40 days      |        |        |        |               |  |  |  |
|              | 10 cm        | 20 cm  | 30 cm  | 40 cm  | Genotype mean |  |  |  |
| $V_1$        | 65.1         | 58.8   | 63.4   | 75.6   | 65.73         |  |  |  |
| $V_2$        | 50.1         | 73.5   | 60.1   | 70.9   | 63.65         |  |  |  |
| Spacing mean | 57.6         | 66.15  | 61.75  | 73.25  | 64.69         |  |  |  |
| LSD 0.05     | 20.01        | ·      |        | 18.79  |               |  |  |  |
|              | 50 days      |        |        |        |               |  |  |  |
|              | 10 cm        | 20 cm  | 30 cm  | 40 cm  | Genotype mean |  |  |  |
| $V_1$        | 87.86        | 90.96  | 105.9  | 120.66 | 101.34        |  |  |  |
| $V_2$        | 78.13        | 106.93 | 91.26  | 127.5  | 100.95        |  |  |  |
| Spacing mean | 82.99        | 98.61  | 98.58  | 124.08 | 101.15        |  |  |  |
| LSD 0.05     | 118.89 27.87 |        |        |        |               |  |  |  |
|              | 60 days      |        |        |        |               |  |  |  |
|              | 10 cm        | 20 cm  | 30 cm  | 40 cm  | Genotype mean |  |  |  |
| $V_1$        | 103.83       | 100.8  | 120.06 | 176.3  | 125.24        |  |  |  |
| $V_2$        | 118.43       | 111.5  | 138.06 | 171.73 | 134.93        |  |  |  |
| Spacing mean | 111.13       | 106.15 | 129.06 | 174.01 | 130.09        |  |  |  |
| LSD 0.05     | 40.1 41.9    |        |        |        |               |  |  |  |
|              | 70 days      |        |        |        |               |  |  |  |
|              | 10 cm        | 20 cm  | 30 cm  | 40 cm  | Genotype mean |  |  |  |
| $V_1$        | 206.66       | 204.0  | 233.0  | 291.33 | 233.74        |  |  |  |
| $V_2$        | 144.0        | 188.33 | 211.33 | 253.5  | 199.29        |  |  |  |
| Spacing mean | 175.33       | 196.16 | 222.16 | 272.41 | 216.52        |  |  |  |
| LSD 0.05     | 71.77        | 66.43  |        |        |               |  |  |  |

 Table (10): Mean fresh weight (g) of two genotype in different spacing:

## 4.6 Dry weight (g):

At 30 days, analysis of variance (Table 11) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean dry weight was 2.42 g.

At 40 days, analysis of variance (Table 11) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean dry weight was 11.23 g.

At 50 days, analysis of variance (Table 11) showed that there were no significant differences between the genotype. Also there were no significant differences among the spacings and the genotype x spacing interaction was not significant. The overall mean dry weight was 19.89 g.

At 60 days, analysis of variance (Table 11) showed that there were significant differences among the spacings. However, there were no significant differences between the genotype. Also the genotype x spacing interaction was not significant. The mean dry weight for  $S_4$  was 35.23 g, which was significantly greater than dry weight 27.31 g of  $S_3$ , 21.58 g of  $S_1$  and 20.71 of  $S_2$ . For varieties the overall mean dry weight weight was 26.2 g.

At 70 days, analysis of variance (Table 11) showed that there were significant differences among the spacings. However, there were no significant differences among the genotype. Also the genotype x spacing interaction was not significant. The mean dry weight for  $S_4$  was 54.33 g, which was significantly greater than 47.01 g of  $S_3$ , 40.88 g of  $S_2$  and 35.35 g of  $S_1$ . For genotype the overall mean dry weight was 44.39 g.

**Table (11):**Mean square from analysis of variance for dry weight estimated at 30, 40, 50, 60 and 70days, in two lablab – bean genotype grown at four spacings in 2009.

|           | Mean Square |         |          |          |          |           |
|-----------|-------------|---------|----------|----------|----------|-----------|
| Sources   | D.F         | 30      | 40       | 50       | 60       | 70        |
| of        |             |         |          |          |          |           |
| variation |             |         |          |          |          |           |
| Block     | 2           | 1.005ns | 18.34 ns | 15.64 ns | 45.51 ns | 1.16 ns   |
| Genotype  | 1           | 2.04 ns | 11.76 ns | 15.52 ns | 2.87 ns  | 479.72 ns |
| (G)       |             |         |          |          |          |           |
| Error (a) | 2           | 1.22    | 5.78     | 21.63    | 53.52    | 91.46     |
| Spacing   | 3           | 0.41ns  | 10.13 ns | 44.69 ns | 268.45*  | 399.57**  |
| (S)       |             |         |          |          |          |           |
| G x S     | 3           | 0.37 ns | 7.63 ns  | 9.56ns   | 29.94 ns | 12.10 ns  |
| Error (b) | 12          | 0.38    | 8.40     | 50.50    | 51.02    | 23.04     |
| Total     | 23          |         |          |          |          |           |

ns = non significant

\*. \*\* = significant at (p<0.05and 0.01), respectively.

| Genotype              | 30 days   |       |       |       |               |  |  |  |
|-----------------------|-----------|-------|-------|-------|---------------|--|--|--|
|                       | 10 cm     | 20 cm | 30 cm | 40 cm | Genotype mean |  |  |  |
| $V_1$                 | 2.8       | 2.4   | 2.7   | 2.9   | 2.7           |  |  |  |
| $V_2$                 | 1.7       | 2.3   | 1.8   | 2.7   | 2.13          |  |  |  |
| Spacing mean          | 2.25      | 2.35  | 2.25  | 2.8   | 2.43          |  |  |  |
| LSD 0.05              | 0.78 1.95 |       |       |       |               |  |  |  |
|                       | 40 days   |       |       |       |               |  |  |  |
|                       | 10 cm     | 20 cm | 30 cm | 40 cm | Genotype mean |  |  |  |
| <b>V</b> <sub>1</sub> | 11.13     | 10.26 | 12.3  | 14.0  | 11.92         |  |  |  |
| V <sub>2</sub>        | 8.1       | 12.2  | 10.2  | 11.6  | 10.53         |  |  |  |
| Spacing mean          | 9.6       | 11.23 | 11.25 | 12.8  | 11.23         |  |  |  |
| LSD 0.05              | 3.65      |       |       | 4.22  |               |  |  |  |
|                       | 50 days   |       |       |       |               |  |  |  |
|                       | 10 cm     | 20 cm | 30 cm | 40 cm | Genotype mean |  |  |  |
| <b>V</b> <sub>1</sub> | 18.3      | 19.0  | 21.5  | 24.0  | 20.7          |  |  |  |
| V <sub>2</sub>        | 14.8      | 20.9  | 18.1  | 22.5  | 19.08         |  |  |  |
| Spacing mean          | 16.55     | 19.95 | 19.8  | 23.25 | 19.89         |  |  |  |
| LSD 0.05              | 8.94      |       |       | -     | 8.17          |  |  |  |
|                       | 60 days   |       |       |       |               |  |  |  |
|                       | 10 cm     | 20 cm | 30 cm | 40 cm | Genotype mean |  |  |  |
| <b>V</b> <sub>1</sub> | 20.53     | 19.83 | 26.96 | 38.9  | 26.55         |  |  |  |
| V <sub>2</sub>        | 22.63     | 21.6  | 27.66 | 31.56 | 25.86         |  |  |  |
| Spacing mean          | 21.58     | 20.71 | 27.31 | 35.23 | 26.21         |  |  |  |
| LSD 0.05              | 8.9 12.85 |       |       |       |               |  |  |  |
|                       | 70 days   |       |       |       |               |  |  |  |
|                       | 10 cm     | 20 cm | 30 cm | 40 cm | Genotype mean |  |  |  |
| $V_1$                 | 41.1      | 43.53 | 51.83 | 59.1  | 48.89         |  |  |  |
| V <sub>2</sub>        | 29.6      | 38.23 | 42.56 | 49.56 | 39.89         |  |  |  |
| Spacing mean          | 35.35     | 40.88 | 47.01 | 54.33 | 44.39         |  |  |  |
| LSD 0.05              | 6.04      |       | 16.8  |       |               |  |  |  |

 Table (12):
 Mean dry weight (g) of two genotype in different spacing:

# **CHAPTER FIVE**

# DISCUSSION

**5.1 Plant height(cm):** The spacing treatments did not affect plant height of the two lines. This result agreed with Idris(2002) who recorded that plant spacing treatments did not affect the plant height of faba bean at all sampling periods agreed with Ahmed(2008) who found that plant spacing treatments had non significant effect on plant height of groundnut and not agreed with Singh and Singh.(1992) who reported that the increase in plant density caused an increase in plant height. This may be explained by the fact that the growth habit of the crop was indeterminate, and the plants were taller than the determinate ones irrespective of plant spacing. The genotype had significance effect on the plant height. This may be due to the genotypic factors.

**5.2 Stem diameter(mm):** The effect of spacing on stem diameter was significant. Increasing stem diameter with increasing in the spacing. This result is in agreement with Omer(2008)who reported that plant population affected stem thickness, where, a decrease of ratoon plant population, increased stem diameter. This may be due to the lesser competition. The genotype had no significance effect on stem diameter.

**5.3 Number of branches/plant:** The results showed that the spacing had significance effect on the number of branches per plant, the wide spacing had higher number of branches. This result agreed with Pilbem and Hebbleth (1990) who reported that the total number of branches per plant declined as plant population density increased. Also agreed with Franclin *et al.* (1985), who stated that the branching is a function of genotype interaction with a host of physical and biological environmental factors, and was not in agreement with Idris(2002) who showed that the spacing treatments did not affect the number of branches per plant.

**5.4 Number of root nodules/plant:** The results showed that the spacing did not affect the number of nodules per plant. Also genotype and the interaction between the two factors was not affected. This result agreed with Ahmed (2008) who found that the number of nodules was not affected by plant spacing treatments. This may be due to the losses of nodules in the ground restrictions .

**5.5 Fresh weight(g):** The results showed that the spacing treatments affected fresh weight significantly. This result was in agreement with Mohamed (1984) who indicated that weight per plant was greater with wider than with closer distance between plant within the row, it also agreed with Mohamed (2002) who reported that hay yield increased with increasing inter-row and intera-row spacing and disagreed with Hamad

Elneel (2004) who recorded that high significant effect in closer plant spacing 15 cm gave greater shoot biomass than 30 cm and 45 cm in cowpea. This may be due to the fact that widely spaced plants suffer less from competition than closely spaced plants and thus expected to grow and yield better.

**5.6 Dry weight(g):** The results showed that the spacing treatments affected dry weight significantly. This result agreed with Ageeb et al. (1984) who recorded that increasing plant density was found to decrease plant. Also the total dry matter per in agreement with Mohamed,(2002)who showed that dry weight increased with the increased in the intera-row spacing and the result was agreed with Mohamed and Hago(1990)who found that shoot dry weight was affected by plant spacing. The widest spacing of 30cm gave significantly greater shoot dry weight than 20cm and 10cm plant spacing. This may be reffering to the low competition between plant at wide spacing.

# **Summary and Conclusions**

The experiment was carried out to investigate the effect of spacing on growth and yield on lablab bean. The treatments comperised four spacings (10,20,30 and 40 cm). The design used was split-plot design with three replications.

1- Result showed that genotype had limited effect on plant height and fresh weight.

2- The effect of spacing is limited according to the results which is not affected all the parameters measured .

3- The interaction between the treatments was not significant in all parameters, except number of branch/plant at 40 days.

4- Further studies are needed regarding to the influence of different factors, genotypes, environment and the spacing. To investigate the effect of spacing/plant density on lablab bean as legume fodder crop which has many roles.

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