DIVERSITY AND GENOTYPE X ENVIRONMENT INTERACTION OF BEAN LANDRACES IN BUKOBA AND MISSENYI DISTRICTS OF TANZANIA

BY

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A DISSERTATION SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF CROP SCIENCE OF SOKOINE UNIVERSIY OF AGRICULTURE.

MOROGORO, TANZANIA.

2010

ABSTRACT

A field experiment was conducted during the 2008/09 short rain season in three major agro-ecological zones of Bukoba and Missenyi districts, Tanzania. The agroecological zones were characterized as follows based on the amount of rainfall: high (≥1500 mm), medium (1200 mm) and low (800 mm). Objectives of the study were to investigate the diversity of bean landraces in the areas, assess the effect of environment on genotypes performance, determine relationship among plant characteristics and their contribution to seed yield. Thirty eight bean landraces were collected from farmers in the two districts and evaluated in three locations: ARI- Maruku, Kyema and Byamutemba in high, medium and low rainfall zone, respectively. A Randomised Complete Block Design was used with three replications. Data collected were: days to 50% flowering, days to 90% maturity, plant height, number of pods per plant, number of seed per pods, 100 seed weight, grain yield and disease reaction. Data analysis revealed significant variations among genotypes for all characters investigated and significant genotypes x environment interactions for yield and yield components. Environmental factors reduced seed yield by 76% and by 39% in low and high rainfall zones, respectively, compared to the medium rainfall zone. Kamoshi gave significantly higher seed yield across locations. Seed yield had positive highly significant correlations with pods per plant and seeds per pod. Path coefficient analysis showed that, seeds per pod contributed most to seed yield. Stability parameters estimates indicated that genotypes had significantly different seed yield performance across environments, suggesting for multi-location testing for seed yield. However, Kamoshi had seed yield stability across the environments. The study findings suggest existence of diversity among the bean landraces and that their responses differ with environments. Future studies should focus on genotyping of the landraces to determine the extent of their diversity and performance in diverse production environments.

DECLARATION

I, LEONARD GEORGE MUKANDALA, do hereby declare to the Senate of Sokoine University of Agriculture, that this dissertation is my original work and that it has neither been submitted nor being concurrently submitted for degree award in any other institution.

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(Supervisor)

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ACKNOWLEDGEMENTS

I am very grateful to many people whom through their generous support and encouragements have made the accomplishment of this dissertation possible. In the due course, I have accumulated many debts, only a part of which I have space to acknowledge them here.

First, I must express my special gratitude to my supervisors Professors Susan Nchimbi-Msolla and Akwilin J.P. Tarimo for their special interest in my work and for their profound scientific advice throughout the process from initial proposal preparation to the writing of this manuscript. Both were generous with their time and ideas.

Indeed, I wish to express my gratitude to the officer in-charge, ARI – Maruku, Dr. Jackson Nkuba for his great support and for his readiness to help in times of social difficulties when deemed necessary. Dr. Freddy Baijukya deserves my special thanks for taking some hours of his time to read and for insightful and scientific suggestions. My gratitude also goes to Mr. S. Mkulila and Mrs C. Shumbusho (ARI- Maruku) for their assistance in data collection. Many thanks to ARI- Maruku staff for friendship and moral support.

I would also like to extend my sincere thanks to all members of staff and postgraduate students in the Department of crop Science and Production, Sokoine University of Agriculture who in one way or another have contributed to my achievement.

I would like to thanks the government of Tanzania, in particular the Ministry of Agriculture as my employer for granting me the study leave and for providing funds to support my postgraduate study.

My profound gratitude is due to my dear wife Loise Atieno for her constant encouragement and forbearance while I had to spend some months away from home. "I had to leave you with family responsibilities during the entire period of my study. Indeed, you have been an effective mother and father to our children; Kelvin, Emmy, Linda and Lewis (Dad) in my absence."

It is regrettable that both my parents could not live to see what their education foundation laid has achieved. I hope they would have been as happy as am I. Without their guidance, I would not be what I am today. To them, I dedicate this dissertation.

Finally, since it is impracticable to acknowledge adequately all the assistance I received from various people during the whole process of this work, I would like collectively to thank all those I have inadvertently omitted to whom this acknowledgement is due.

DEDICATION

This dissertation is dedicated to my parents; George Mugela and Mariakevina Nakilijja for the good foundation they laid for my education. To my junior brother Eleneus Bwanika who passed away during the writing of this dissertation, may God rest his soul in peace.

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LIST OF SYMBOLS AND ABBREVIATIONS

ALS	-	Angular leaf Spot
AMMI	-	Additive Main effect Multiplicative Interaction
ANOVA	-	Analysis of Variance
ARI	-	Agriculture Research Institute
C	-	Carbon
Ca	-	Calcium
CEC	-	Cation Exchange Capacity
CIAT	-	*Centro International Agricultura Tropical*
CIDA	-	Canadian International Development Agency
DAP	-	Days after planting
Df	-	Degree of freedom
DMRT	-	Duncan's Multiple Range Test
EMS	-	Error Mean Square
FAO	-	Food and Agriculture Organisation of United Nations
FEC	-	Farmers Extension Centre
HRZ	-	High rainfall Zone
K	-	Potassium
Kg/ha	-	Kilograms/hectare
LRZ	-	Low rainfall zone
LSD	-	Least Significant Difference
MAFS	-	Ministry of Agriculture and Food Security
MC	-	Moisture content
Mg	-	Magnesium
MRZ	-	Medium rainfall zone

MSTAT-C	-	Michigan State University Computer Software
Na	-	Sodium
NARS	-	National Agriculture Research Stations
NBS	-	National Bureau of Standards
^{0}C	-	Celcius centigrade
OC	-	Organic Carbon
P	-	Phosphorous
P≤	-	Probability less than
PABRA	-	Pan Africa Bean Research Alliance
RCBD	-	Randomised Complete Block Design
SUA	-	Sokoine University of Agriculture

CHAPTER ONE

1.0 INTRODUCTION

The common bean (*Phaseoulus vulgsris* L) is an important food and cash crop in the Eastern and Great lakes Region of Africa. The crop is a major source of protein as well as carbohydrate in this region where it is ranked the second most important source of dietary protein after maize. For this reason, throughout Africa, the common bean is termed as "poor man's meat (CIAT, 2005). In Tanzania, common beans contribute about 65% of dietary protein derived from pulses for human consumption (Mugenzi *et al*., 2002). It is mostly eaten with rice, '*ugali'* (maize meal) and banana.

Production of common beans in Tanzania is higher than any other pulses estimated at 300 000 tonnes annually, representing 82% of the total pulse production (NBS, 2006). It is one of the crops, which is grown under diverse farming systems and agro-climatic conditions. Small-scale farmers grow beans primarily to meet their domestic food demands. It is estimated that over 75% of rural households in Tanzania depend on beans for daily subsistence (CIAT, 2008). Kagera region has the largest planted area (about 160 000 ha) of beans in the country, representing 20% of the total area under beans (NBS, 2006). Moreover, the region has a higher bean diversity compared to other areas in the country (Mugenzi *et al*., 2002 and CIAT, 2008).

Over the millennia, the farmers have been growing mixtures of beans as an insurance against drought, diseases, and pest attacks. This process has produced limitless genetic array of beans with different colors, textures, and sizes to meet the growing conditions and taste preferences of many different consumers.

Small-scale farmers grow a variety of bean landraces ranging from small to large seeded (Nkuba, 2002; CIAT, 2005 and CIAT, 2008).

Landraces are commonly used as planting materials because they have some traits that are preferred by small-scale farmers (e.g. taste) and they are well adapted in both the crop production system and the social-economic situation of these farmers (Oscar, 2004). Genetic diversity among and within landraces make them a valuable resource as potential donors of genes for the development and maintenance of modern crop varieties, and for direct use by farmers (Soleri and Smith, 1995 and Oscar *et al.*, 2004).

Over 100 bean landraces are reported to be grown in Kagera region (CIAT, 2008). Bean germplasm studies conducted in Kagera region show that Bukoba and Missenyi Districts are endowed with broad variability of bean landraces (Mukandala, 1998 and William, 2002). In the two districts, beans are grown in three distinct agro-ecological zones differing in soil types and rainfall amounts. When cultivars are subjected to different environments, their performance, relative to each other may not be the same (Fehr, 1987). The variation in adaptation limits some farmers who would be interested to grow certain bean varieties in a particular area but restricted by instability of bean yields across environments (FAO, 2002 and Mwale *et al.*, 2008). Thus, it is important to determine the performance of bean germplasm in different environments and recommend genotypes in suitable environment. Hence, the genotypes with wide adaptability if available can be utilized.

The differences in performance among cultivars under different environments necessitate the need to evaluate genotypes under different environmental conditions as a basis for making informed recommendations to farmers in different geographical areas. At the same time, several landraces with superior genes are being eroded and it is feared that such

valuable material may be lost or become extinct in due course. Despite the current threat to bean diversity in the area, the information on genetic value of the bean landraces commonly cultivated by small-scale farmers in Bukoba and Missenyi districts remains scanty.

Current studies on the performance of bean landraces in Kagera region were limited to the high rainfall zone above 1500 mm annual rainfall (Bosch *et al.,* 1995 and William, 2002). The information about their performance under other environments (e.g. different cropping systems and agro-ecological zones) is not known. The overall objective of this study was to identify superior traits and genotypes among the bean landraces currently grown in Bukoba and Missenyi districts, and their environmental interaction.

Specific objectives of this study were:

(i) To determine the phenotypic variations among bean landraces currently grown by farmers in Bukoba and Missenyi districts,

(ii) To determine the relationship among yield and yield components of the bean landraces and their contribution to grain yield; and,

(iii) To assess the interaction of the bean genotypes and environment with regard to yield and yield components.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Genotype x Environment Interaction

Genotype x environment (GE) interactions is important sources of variation in crop breeding programs (Reza and Ahamed, 2009). Dixon and Nukenine (2000) defined Genotype x environment (GE) interaction as the change in a cultivar's performance over environments, resulting from differential response to various edaphic, climatic and biotic factors.

Allard and Bardshaw (1964) have categorised environmental factors which lead to GE interactions as predictable and unpredictable. Predictable interactions include permanent characters of the environment, namely climatic conditions, soil type as well as those environmental characteristics that fluctuate in a systematic manner (e.g. day length). Predictable factors also include environments, which can be manipulated by human beings, such as soil improvement by fertilization, planting date, plant population, intercropping and any other agronomic practices. Unpredictable factors, which lead to GE, are weather change; rainfall distribution and its amount, temperature fluctuations and radiation. The contribution of predictable environmental fluctuations to genotype x location interactions can be reduced by allocating specific cultivars to specific environments (Allard and Bardshaw, 1964).

Unpredictable environmental variations are more difficult to estimate and often lead to large genotype x year and genotype x year x location interactions (Allard and Bardshaw, 1964).

Selection of stable cultivars that perform consistently across environments can reduce the magnitude of these interactions. Moreover, better understanding of GE interactions in beans can lead to more efficient allocation of resources in multi-environment cultivar testing program and release well adapted varieties for different production environments.

2.2 Genotype x Environment Interaction Studies in Crops

Genotype x Environment interaction is a common phenomenon in agricultural research (Bondari, 2003). Differences between genotypic values may increase or decrease from one environment to another which might cause genotypes to even rank differently between environments, The association between environment and phenotype expression constitute the GE interaction.

In 6-multilocation trials of bean landraces carried out for 2 years by De Ron *et al.* (2004) indicated that 51 landraces out of 55 were adapted to specific environments and only four of them had broad geographical adaptability with similar performance under different conditions. Environmental influences also showed considerable influences on the performance of maize genotypes across locations (Ngowi, 2002).

A study on cowpeas by Ndiaga (2001) showed that environmental conditions could influence the outcome of selection if yield and harvest index (HI) are used as selection criteria.

In a study to determine the effect of drought on the seed yield components of common beans it was found that water stress played an important role in phenotypic expression of seed yield components (pod number per plant, seed number per pod and 100-seed weight).

Pod number per plant, seed number per pod and 100-seed weight was also significantly reduced in all populations by water stress. Water stress reduced seed yield by 80%, pods number per plant by 60%, seeds per pod by 26%, 100-seed weight by 13% (Szilagyi, 2003).

In another study evaluating bean landraces variations, the agro-ecological zones where the landraces were collected and the experiment- sites had a great influence on expression of traits. Interactions among these factors were also significant for 100-seed weight, leaf surface area and phonological traits had significant difference (Oscar, 2004).

The performance of bean genotypes in copping system was also compared with respect to developmental plant characteristics, seed yield and yield components, and food quality traits. A significant bean genotype x cropping system interaction was found for the time to flowering and seed yield, and there were significant differences among cropping systems for pods per plant, seed length and seed coat proportion. Intercropping with field maize reduced bean yield by 55% and intercropping with sweet maize reduced bean yield by 44% (Santalla *et al*., 2001).

A recent study conducted to analyse the genotype x environment interaction in 9 month old cassava clones showed that environmental factors namely; soils, rainfall, temperature and humidity had a great influence on the stability of starch yield.

2.1.2 Importance of GE interactions in plant breeding

The performance of bean lines brought forth in breeding programs or of cultivars (landraces) in use can be affected by environmental variability. In any breeding

programme therefore, efforts are made in developing cultivars, which can perform better under diverse environmental conditions.

Decreasing the variances of a cultivar mean improves the probability of detecting significant differences among cultivars (Gebuyehu and Habtu, 2003). Moreover, knowledge of the size of the variance components associated with GE interactions can be used in conjunction with combination of years, locations and replications, to determine the most efficient allocation of resources for cultivar testing (Rasmusson and Lambert, 1961). Different attempts have been made to solve the problems created by GE interactions (Comstock and Moll, 1963). Most of the estimates, however, only provide information on their existence and magnitude, but give no measurements of the individual genotypes with the environment, and therefore no measurements of stability of individual cultivars (Gebuyehu and Habtu, 2003). GE limits progress of crop improvement beyond the breeder's station. Thus, a breeder needs to understand and estimate the effect of GE in order to develop a suitable variety for specific purposes, different geographical area, and effective allocation of resource and at variable production levels. For example, common bean is grown under diverse environments differing in rainfall, temperatures, soil types as well as variation in seasonal changes. The knowledge of Genotype x location interaction is of interest in identifying potential needs for unique cultivars in different geographical area or agro-ecological zones.

The association of the environment and phenotypic expression of a genotype constitute the GE interaction. The GE interaction determines if a genotype is widely adapted for an entire range of environmental conditions or separate genotypes must be selected for different sub-environments. When GE interaction occurs, factors present in the environment (temperature, rainfall, etc.), as well as the genetic

constitution of an individual (genotype), influence the phenotypic expression of a trait. The impact of an environmental factor on different genotypes may vary implying that productivity of a crop may also vary from one environment to another (Bondari, 2003). Breeding plans may focus on the GE interaction to select the best genotype for a target population of environments. When the GE is large, this implies that testing cultivars in several environments becomes unavoidable to a breeder. Reducing the number of testing sites would imply rejecting some cultivars, which would have otherwise performed better (superior cultivars) in different environments (Bondari, 2003). On the other hand, absence of significant interactions involving genotypes (GE) simplifies the nature of testing programme for cultivar development as well as cultivar selection by a producer.

This means cultivars with the best performance in one location in one season would always be the superior in other locations and seasons. Statistically, GE interactions occur if the performance of genotypes varies significantly across environments. Assuming two genotypes (G1 and G2) tested in two environments (E1 and E2), Fig. 1, indicates the presence of GE interaction since G1 is phenotypically superior to G2 in Environment 1 (E1) but inferior to G2 in E2. Graphical illustrations of different Genotype x environment interactions (Fig. 1, 2 and 3).

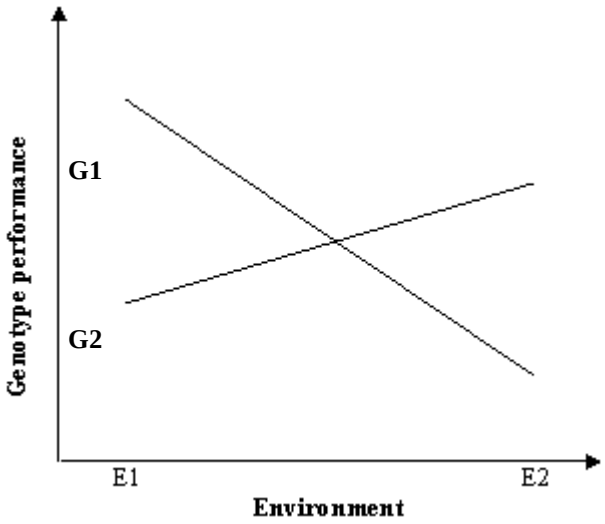


Figure 1: Genotype interaction at two locations resulting in change in ranking

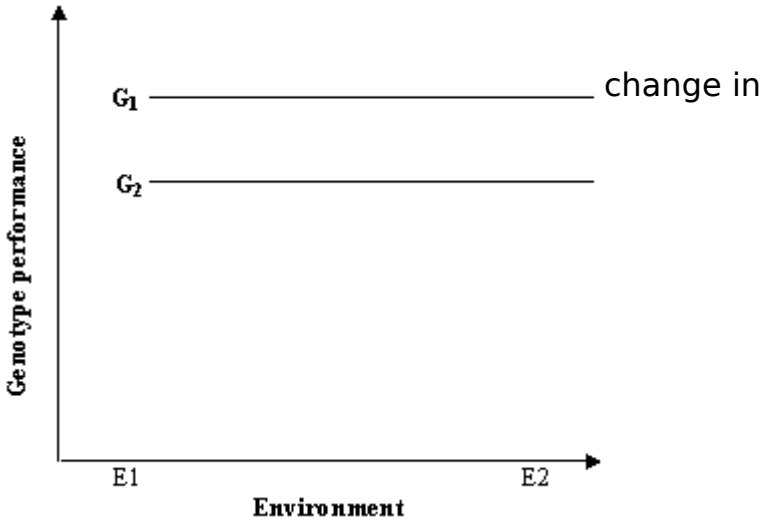


Figure 2: Absence of genotype environment interaction in two environments

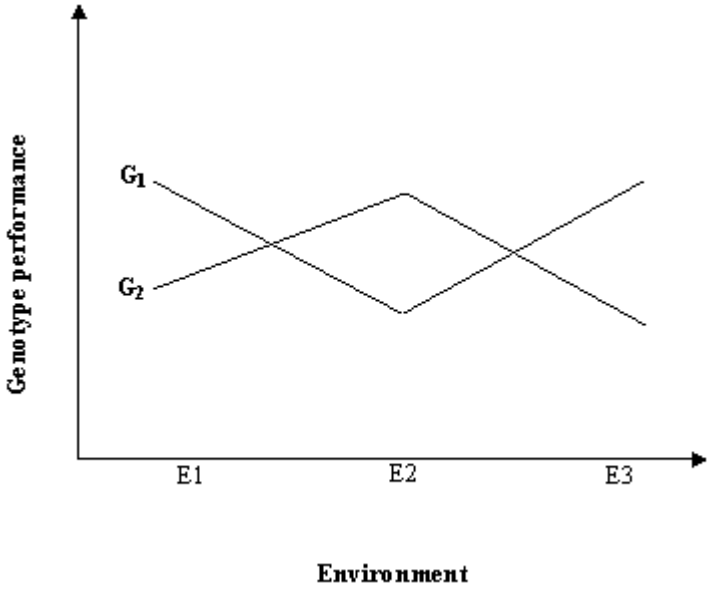


Figure 3: Genotype interaction at three locations with different ranking at each.

Fig. 2, the phenotypic difference between G1 and G2 remains the same in the two environments, which implies that, no interaction between the genotype and the environment. Considering 3 environmental conditions (E1, E2, and E3) and 2 genotypes (G1 and G2), interpretation of the results could be more complicated. Fig. 3 shows one type of GE interactions for this situation where G1 is superior in performance to G2 in E1 and E3, but is inferior to G2 when exposed to E2. Error: Reference source not found

Agricultural researches have demonstrated that a genotype resulting in a good phenotype in one environment might not necessarily result in a good phenotype in another environment. Practically the situation is more

complicated and usually involves many genotypes and environments and that a number of possible types of interactions must be considered.

2.1.3 Analysis of genotype by environment interaction

Phenotypic performance is a result of genetic and non-genetic influences (Comstock and Moll, 1963). Thus, expressing phenotypic value (P) as a function of the genotype (G) and the environment (E), the equation, P = G + E indicates the situation when environmental factors influence each genotype equally.

However, when environment influences some genotypes more than others, the phenotypic relationship changes to P = G + E + IGE and the expression includes the GE interaction term IGE. The variance (V) of the effects follows V(P) =V(G) + V(E) + 2 Cov(GE) showing that variance components analyses could be used to partition the phenotypic variance into its genotypic, environment chambers and random allocation of genotypes to environmental conditions). Genotype environment covariance (Cov) occurs when better genotypes are provided with better environments.

For a simple analysis of variance of a randomized complete block design the model:

$Yijk = \mu + Gi + Ej + GEij + Bjk + gijk$ can be applied where: μ is the mean, *Gi* is the effect of the *ith* genotype, *Ej* is the effect of the jth environment, *GEij* is the interaction of the ith genotype with the jth environment, Bjk is the effect of the *kth* replication in the *jth*

environment, and *gijk* is the random error environmental, and their interaction components

One way to determine the importance of V(G) or V(E) is to experimentally minimize one of the two effects (minimizing V(G) by using identical Genotypes or minimizing V (E) by using controlled environment chambers and random allocation of genotypes to environmental conditions).

The additive main effect and multiplicative interaction (AMMI) analysis has shown to be effective in understanding complex GE interactions where complex data sets are difficult to understand with ordinary analysis of variance (ANOVA), (Crosa *et al.*, 1990). The AMMI model is a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure. AMMI biplot analysis is considered to be an effective tool to diagnose GE interaction patterns graphically.

In AMMI, the additive portion is separated from interaction by analysis of variance (Yuksel *et al.*, 2002). Regression analysis has also been widely used in comparing and measuring genotypic performances of common bean cultivars (Reza and Ahamed, 2009).

2.1.4 Relevance of GE interaction in crop production

The extent to which it might be possible for new varieties to contribute changes in yield variability will differ among locations or farmers (Bondari, 2003; Ngeve *et al.*, 2005; CIAT, 2008). The problem of stability is acute particularly under condition of rain fed agriculture in semi arid and semi humid tropic In these environments, reducing crop failure

through GE interaction will be as important as increasing the yield potential (Izge *et al.,* 2006).

Thus breeding of improved varieties, better adapted to variable environments and stable performance is of paramount scientific importance (Yahaya and Mohammed, 2006 and Sholihin, 2009). In many circumstances improved varieties remain the most cost-effective means of increasing yield and reducing risks of crop failure (CIAT, 2008).

2.3 Relationship between Yield and its Components

To achieve significant progress in breeding programmes, it is essential also to know the relationship between yield and its components (Assady *et al.*, 2005). The correlation between yield and yield components has been widely studied.

In a study on the relationship between different traits in common beans, Assady *et al.* (2005) reported that days to flowering had highest and significant positive correlation with seed yield while 100 seed weight had the significant but negative correlation with seed yield.

Path coefficient analysis method permits the partitioning of the correlation coefficient into its components, one component being the path coefficient that measures the direct effect of a predictor variable upon its response variable; the second component being the indirect effect(s) of a predictor variable on the response variable through another predictor variable (Dewery and Lu, 1959; Ganesamurthy and Seshadri, 2004). In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Ganesamurthy and Seshadri, 2004).

The total correlation between an independent factor A and dependent factor E is described direct on E (a) plus indirect effect of B, C and D on E (e x b, f x c, g x d), where e, f, g are the simple correlations between A and B, C and D respectively; and b, c, d are the direct effects between E and B, C respectively (Fig. 4).

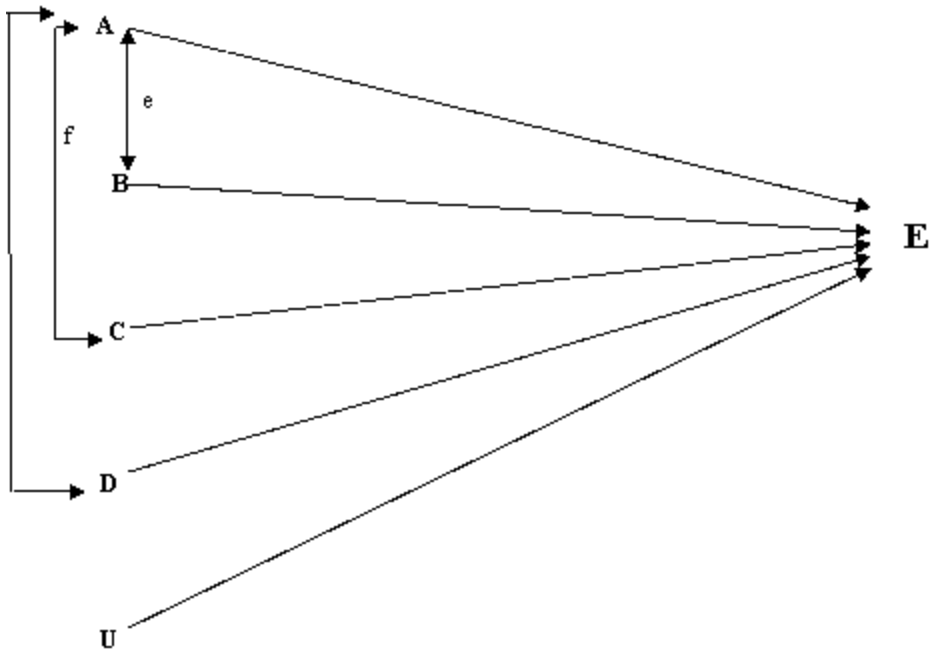


Figure 4: Correlation between independent variable A and dependent factor E and the indirect effects

2.4 Diversity of Common Bean

The bean diversity is considerably large. There are about 65 000 accessions of *Phaseolus* beans in major germplasm banks in the world of which more than 90% are *P.vulgaris* (Oscar, 2004). The Centro Internacional de Agricultura Tropical (CIAT), the largest in the world contain about 40 000 accessions of which 26 500 are the cultivated *Phaseolus vulgaris*. About 1300 are wild types and the rest are distant relatives of the common bean (CIAT, 2005). However, much of the variability in these sources has yet to be utilized for common bean improvement (Oscar, 2004). As much as 90% of the genetic variability available in the primary gene pool and related species (mostly of tropical and subtropical origins) remains underutilized or not utilized at all. Problems of adaptation associated with introduced germplasm and the lack of long-term sustained public funding might have hindered extensive use of this *Phaseolus* bean germplasm (Rao, 2001).

The cultivated forms of common beans usually known as landraces are often highly variable genotypically and in appearance (Phenotypically) but they can be distinguished by farmers and normally they have local names (Brown, 2000). They have particular characteristics (taste, early or late maturing, etc.) and adaptation to local production environments (Harian, 1992). Bean varietal diversity is high in Kagera bean producing areas (Bukoba and Missenyi districts), where white, brown and red coloured small seeded cultivars and yellow, red and tan coloured medium to large seed cultivars are the most common (Plate 1).

Plate 1: Diversity of bean landraces of Bukoba and Missenyi districts in seed shape, colour and size

The genetic diversity of landraces is considered to be the most economically valuable of global biodiversity and consequently of paramount importance for future world production (Wood and Lenne, 1997).

It is not known whether the diversity of bean landraces that are stored in ex-situ is affected by the condition under which they are maintained and multiplied (Oscar, 2004) Thus, efforts must be made to address their conservation and utilization.

2.4.1 Genetic diversity

A genotype or genetic make up of an organism is also defined by Falconer and Mackay (1996) as the combination of alleles at a single autosomal locus in a diploid organism. Genetic diversity is a measure of the possible choices of information provided by a gene. Different choices (alleles) may exist for that gene (i.e. a pink allele, a purple allele, a white allele). When all or nearly all the members of a population have the same allele at a gene, that population is said to have low genetic diversity at that gene (Julian, 2004).

If many variants exist for a gene sequence, that population has high genetic diversity at that gene. If genetic diversity becomes low at many genes of a species, that species becomes increasingly at risk. High genetic diversity has a greater chance to survive. The genetic diversity of a species is always open to change. The variants that survive in the next generation can contribute to species diversity in the future (Julian, 2004).

Genetic diversity is important to the applied crop breeding, because it may reduce vulnerability to pests and, at the same time, accelerate breeding progress for an agronomic trait such as yield.

2.4.2 Phenotypic diversity

Landraces of common bean are remarkably diverse in plant and seed morphology and agroecological adaptation (Beebe *et al*., 2000). The phenotypic diversity observed has genotypic as well environmental contribution (Comstock and Moll, 1963, and Bondari, 2003). Thus, genotypes express themselves differentially in different environments. Morphological diversity is also found in plant growth habit (determinate bush, indeterminate upright bush, indeterminate semi-vinery prostrate and indeterminate

climbing). Common beans differ in seed coat colour and seed size, ranging from small seeded to large seeded types (CIAT, 2001).

2.4.3 Determination of diversity

Traditional methods of estimating diversity among groups of plants have relied largely on morphological characters, which still play a central role in the ANOVA in crop species and their relatives (Newbury and Ford-Lloyd, 1997). Because of the strong environmental influence on morphological traits, mainly the quantitative traits, new techniques, which analyze diversity at biochemical or molecular level, have been developed (Falconer and Mackay, 1996). Molecular techniques are more expensive than most morphological approaches to the study of genetic or species diversity and consequently they should be used only where other techniques are less powerful or not feasible (Newbury and Ford-Lloyd, 1997). Thus, phenotypic differences are still a viable method, which could be used instead. Theoretically, phenotypic diversity should approximate genetic diversity.

As the number of phenotypic traits increases in a comparison of breeding pools, the number of genes involved in the control of phenotypic traits should increase accordingly and, thereby, improve the utility of phenotypic diversity in predicting genotypic diversity. Employing this concept Johns *et al.* (1997) used morphological, developmental, and physiological traits to create distance measures and examine genetic diversity in large collections of crop genotypes.

2.4.4 Diversity in bean growth Environment

Common bean are adapted to a wide range of soils. They are not sensitive to soil type as long as it is reasonably fertile, well drained and free from conditions that interfere with germination and plant emergence, such as saline soils (NDSU, 1997).

High temperatures (> 30^0C) can result into dropping of buds and flowers. Beans are a warm season crop with the optimum average growing temperatures ranging between 18 and 24^0C (NDSU, 1997). The crop requires moderate amount of water (3 - 6 cm).

The water requirement is essential during early stage of growth and water demand is critical at pod filling stage (during and soon after flowering). At this stage, moisture availability should not be less than 60% field capacity. During the crop maturation and harvesting, dry weather is desirable, as wet condition may lower the seed quality and market value (Free, 1993).

The common bean is generally considered to be a short-season crop with most varieties maturing in a range from 85 to 110 days from emergence to harvest ripe. Dry bean is not tolerant to frost or to long periods of exposure to near-freezing temperatures at any stage of growth (NDSU, 1997).

The diversity of edaphic and climatic condition where the common bean is cultivated as well as the highly specific local preferences for a particular grain type or colour complicates the genetic improvement of the crop (Rao, 2001).

However, there has been significant progress in improving the genetic adaptation of common bean to major biotic and abiotic stresses. Nevertheless, improving the genetic potential in terms of yield when a cultivar is grown in environments to which it is not adapted has been limited (Rao, 2001). Previous studies indicate that both morphological and physiological characteristics of bean plant have a significant role to play in determining yield (Oscsar, 2004). In a study to determine association among common bean traits, it was found that days to flower and days to maturity were negatively correlated with

yield, while days to maturity was positively correlated with seed weight and seed per pod positively correlated with yield (Rono, 1993). In another similar evaluation of bean accessions for phenological and physiological characteristics variations, it was found that the rate of growth, biomass and pod-filling duration were positively correlated with yield (Scully and Wallace, 1990). The knowledge of the relationships among yield components and among those components and yield as well environments are of paramount importance in crop improvement.

2.5 Production Constraints

The common bean is constrained by both abiotic and biotic problems in production (CIAT, 2008). Among abiotic constraints are low soil fertility, particularly deficiency of nitrogen, phosphorus, and zinc, as well as toxicities of aluminum and manganese (Oscar, 2004**).**

Ins**ect pests and diseases are also major bean production constraints. A wide range of insect pests and nematodes may attack the bean crop. The most common diseases include: angular leaf spot (*Phaeoisariopsis griseoloa*), anthracnose (*Colletotricum lindemuthianum*), common bacterial blight (*Xanthomonas axonopodis*.)** bean leaf rust (*Uromyces appendiculatus*) and Root rot (***Pythium spp*** **and** ***Fusarium spp*** **). Insect pests may attack all parts of the bean plant from roots, stems, to pods and seeds, hence resulting in significant yield loss. One of the major bean insect pest in East Africa is the bean fly or bean stem maggot (Hillocks *et al*., 2006).**

Drought is among the most widely distributed and endemic abiotic problems affecting bean production in many regions of the world, especially in most parts of East Africa. A complete crop failure under dry conditions in these regions is usually common (Szilagyi *et al.*, 2003; CIAT, 2008). Small-scale farmers do not usually have capital to solve edaphic

limitations through inputs (Broughton *et al*., 2003 as cited by Oscar, 2004). Thus, to maximize and sustain common bean production, it is essential to develop cultivars that are adapted to low-input sustainable farming systems (Baijukya *et al.*, 2004). Some farmers are concern about poor adaptation of some improved new varieties to intercropping system (CIAT, 2008).

There is a need therefore, to develop varieties capable of yielding high under diverse conditions due to varying environmental stresses and cropping systems (FAO, 2002 and Yahaya and Mohammed, 2006). This would probably need sustained, comprehensive, and integrated genetic improvement programmes in which favorable gene from cultivated and wild populations of common bean pools are accumulated in superior cultivars.

However, bean production problems due to predictable environmental fluctuations to genotype (GE) can be minimized by using cultivars adapted to specific environments (Allard and Bradshaw, 1964).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Collection of Landraces

The collection of landraces was carried out in three major bean growing areas of Bukoba and Missenyi Districts; namely high, medium and low rainfall zones. One representative

ward was selected in each zone. The selection of the ward was done based on its potential as bean producer and diversity.

For each landrace 0.5 kg of seeds were collected either from individual volunteer farmers or traders. Each bean landraces had its own passport data sheet to be recorded (Appendix 1). Each landrace was collected once. No re- collection of the same landrace/genotype was done in other zones. The collection was carried out between 20 August and 15 0ctober 2008. Thirty-eight (38) bean landraces representing the currently grown bean landraces in the three agro-ecological zones were collected (Table 1).

3.2 Description of the Study Site

The study was carried out in Bukoba and Missenyi districts of Kagera region in Tanzania. The two districts (formerly both were under Bukoba district) are located on the west shore of lake Victoria (1^0 - $1^0$30`S and 31^0 - 32^0 E) at an average of 1 200 m above sea level.

Based on the rainfall, parent materials and soils, the two districts are comprised of three major agro-ecological zones; the high, medium and low rainfall zones (Lorkeers, 1995). The high, medium and low rainfall zones represent areas which receive the average annual rainfall above 1500 mm, 1200 mm and below 800 mm, respectively (Appendix 2).

Table 1: Local name, source and colour of bean landraces evaluated in the present study

Entry Number	Genotype Local name	Zone collected	Phenotypic Seed colour
L05	Kinyobwa	LRZ	Light brown
L07	Kamenyamigo	LRZ	Red
L10	Kapiki	LRZ	D/green
L12	Komba omalemu	LRZ	D/brown
L16	Kwesikumo	LRZ	Brown
L18	Ruhondera Empango	LRZ	Brown
L20	Ex- Byamutemba	LRZ	D/brown

L21	Ruhuku	LRZ	Maroon
L25	Kayinja	LRZ	Red
L28	Maliyainda	LRZ	Maroon
L30	Lushara	LRZ	Brown
L34	Rozikoko	LRZ	Reddish
M02	Kyababikira	MRZ	D/red
M17	Shona eigunia	MRZ	Brown
M23	Ruhodera	MRZ	Grey
M24	Kapili	MRZ	Black
M27	Shereka ebineno	MRZ	Whitish
M29	Kanyabufuru	MRZ	D/ green
M33	Raja/Tikyakuponza	MRZ	Grey
H03	Canada	HRZ	Red
H04	Kabale	HRZ	Pure white
H01	Kamoshi	HRZ	Brown
H06	Kirangiti	HRZ	D/brown
H08	Kawanja	HRZ	White
H09	Kisapuli	HRZ	Maroon
H11	Batenda olwakyo	HRZ	White
H13	Kankulye mbaruke	HRZ	Red
H14	Chumbanoroza	HRZ	Maroon
H15	Karili	HRZ	Black
H19	Ruterana abatani	HRZ	Whitish purple
H22	Turaemishako	HRZ	Gey
H26	Tema ekibira	HRZ	White
H31	Kitunutunu	HRZ	Yellow
H32	Kashehe	HRZ	Brown
H35	Groli eikwera	HRZ	Cream
H36	Groli	HRZ	Light red
H37	Kyaburundi	HRZ	Brown
H38	Kashukari	HRZ	Brown

H, M and L before the number indicates the zone where the landrace was collected
HRZ = High rainfall zone; MRZ = Medium rainfall zone; LRZ = Low rainfall zone

In the high rainfall zone, the experimental site was located at Maruku Agricultural Research Institute. In the medium rainfall zone, the experimental site was located at Kyema village. In the low rainfall zone, the experimental site was located at Byamutemba village. The experimental sites were selected to represent respective zone according to Lorkeers (1995). Important soil characteristics for each zone are summarized in Appendix 4 - 6. The agro-ecological zones and the site in each zone where the experiment was conducted are indicated in Fig. 5.

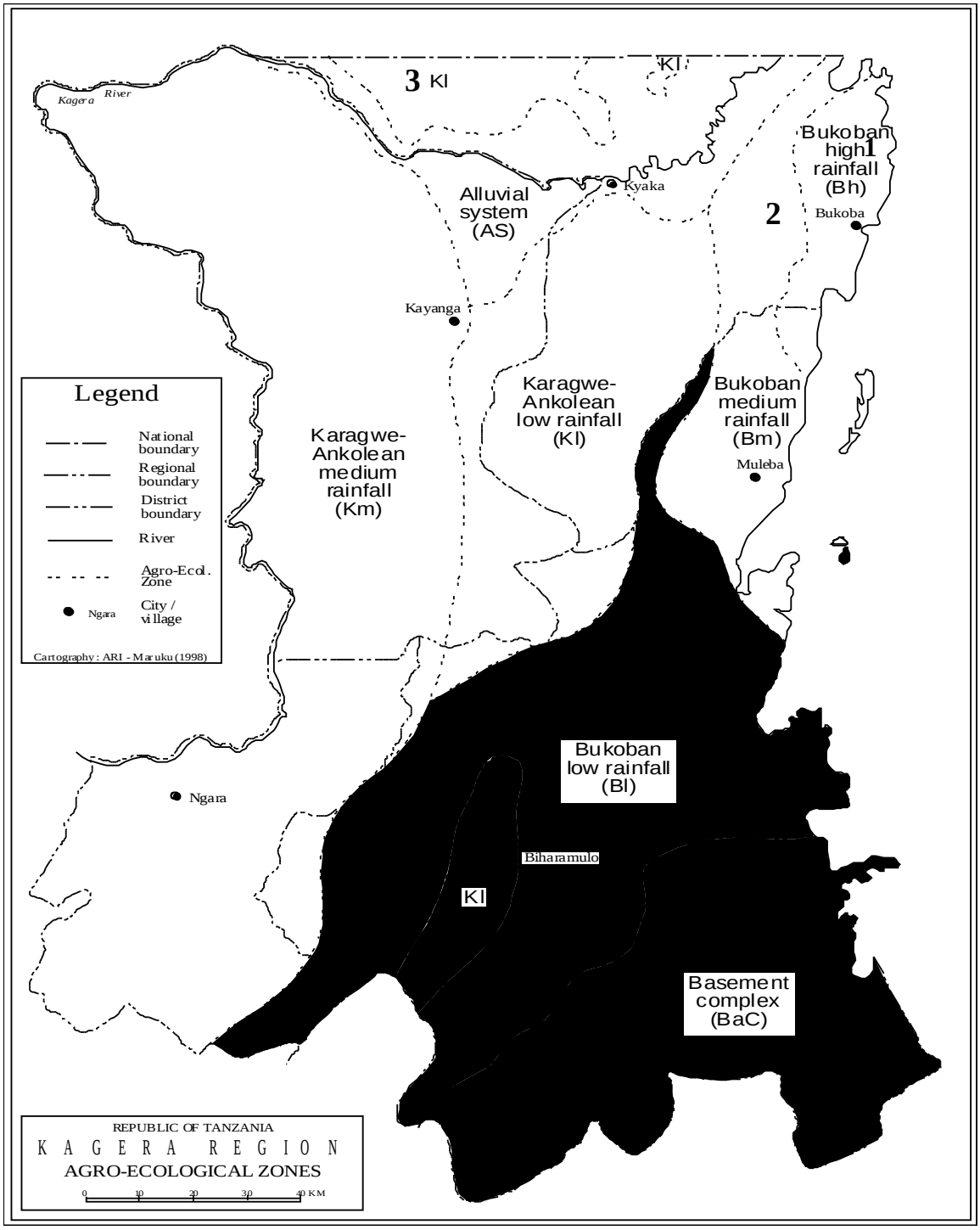
3.3 Soil Sampling and Analysis

A composite topsoil (0 - 0.3 m) sample was collected at each site before sowing. The soil samples collected from the three sites were air- dried and ground to pass through 2 mm sieve. Then, the soil samples were analysed at ARI- Ukiriguru soil laboratory for texture (hydrometer method), pH (H_2O) (1:25 w/v), organic C (OC, Walkley and Black), total N (macro-Kjeldahl), available P (Bray and Kurtz) and exchangeable K (1 M HH_4Oc at 7.0 pH). The methods of analysis were as described in detail by Page *et al*. (1992).

3.4 Experimental Establishment, Design and Management

3.4.1 Land preparation

All the three sites in the agro-ecological zones were established on fields, which had been planted with a similar crop (maize) during the previous season with the aim of minimizing variation in nutrients between sites due to the previous planted crop. Land preparation was done by hand hoe at all experimental sites. Sowing was done manually by dibbling.



1= Maruku 2 = Kyema 3 = Byamutemba

Figure 5: Agro ecological zones (high, medium and low rainfall) and locations of experimental sites (Maruku, Kyema and Byamutemba) in Bukoba and Missenyi districts, Kagera Region, Tanzania.

Source: Lorkeers (1995)

3.4.2 Experimental Design

A randomized complete block design (RCBD) was used with three replications at each of the sites. Each site was considered as an individual environment (differing in altitude, rainfall amounts, soil characteristics and other climatic factors).

All the collected landraces (38) were used in the evaluation. At Maruku (01^0 24' S; 31^0 46' E) and Kyema (01^0 29' S; 031^0 43' E) sites, sowing was done on 20 and 27 October 2008, respectively. At Byamutemba site (01^0 07 S; 31^0 23' E), sowing was done on 24 November 2008 due to differences in the time of onset of seasonal rainfall. Plot size was 3 m^2 consisting of single row plot of 6 m length. Plants were spaced at 0.5 m by 0.20 m between rows and within row, respectively. Two seeds were planted per hole and no thinning was carried out.

3.4.3 Experimental Management

At sowing, fertilizer was applied at the rate of 30 kg N ha^{-1} and 22 kg P ha^{-1} in all experimental plots. At each of the sites weeding was done as desired to avoid crop-weed competition. Two weeding operations using hand hoe were done at Maruku and Kyema sites whereas three weeding operations were done at Byamutemba due to high and fast weed infestation during the experimental period.

Due to low pest infestation levels at all experimental sites neither insect pests nor disease control measures were done. Harvesting and threshing was also done by hand. Sun drying was used for drying the grain to the desired moisture content of 15%. In all the three agro-ecological zones (sites), the experiment was established under rain fed-condition.

3.5 Data Collection

- **Days to 50% flowering**

This was collected by counting the number of days from planting to when 50% of the plants in the plot flowered.

- **Plant height**

This was obtained as an average of 5 plants sampled at maturity, measured from the cotyledonary scar to tip of plant in centimeters.

- **Number of pods per Plant**

Number of pods per plant was obtained by counting the number of pods from 10 plants in each plot and the taking the average number of pods per plant.

- **Pod length**

Pod length was determined by using a tape to measure the pod length and was recorded as an average of length in centimeters of the largest fully expanded immature pods sampled from 10 randomly selected normal plants in each plot.

- **Number of seed per pod**

This was obtained by counting the total number of seeds in 10 sampled pods and number of seeds per pod was determined by the average number of seeds.

- **Days to maturity**

This was recorded by counting number of days from planting to when 90% of the pods reached maturity in each plot.

- **Seed moisture content**

Seed moisture content (MC) was recorded from a sample of dried mixed seed harvested from each plot. MC was measured using Dickey-john grain tester.

- **Seed weight**

This was obtained by weighing 100 seeds of dry shelled seeds taken at harvest from each plot at 15 % MC using a sensitive balance (Sartorius 2354).

- **Grain Yield (kg/ha)**

This was calculated from the weight of dry seeds harvested from each entire plot area at 15 % moisture content using the following formula:

Yield (kg/ha) = (WSH/1000) x10, 000/AH

Where:

WSH = weight of seed harvested

AH = area harvested (m)

- **Disease score**

The response to infection by bean rust and angular leaf spot of the genotypes was recorded after flowering using a nine category disease severity scale (1-9 as described by CIAT (2005).

Where; 1= no disease, 2 = very low susceptibility, 3 = low susceptibility, 4 = medium to low susceptibility, 5 = medium susceptibility 6 = medium to high susceptibility, 7 = high susceptibility, 8 = very high susceptibility and 9 = extremely high susceptibility

- **Rainfall (mm) and Temperature (^{0}C)**

Rainfall and temperature data at each experimental site were recorded from the nearest weather recording stations in each agro ecological zone. The data were recorded during the entire duration of the experiment.

At the Maruku site, the rain gauge was located at ARI- Maruku, whereas at Kyema site it was located at Kyema Farmer Extension Centre (FEC) and Byamutemba sites the rain gauge was located at Kyaka Primary School.

3.6 Data Analysis

3.6.1 Analysis of variance (ANOVA)

Data collected were subjected to analysis of variance (ANOVA) using MSTAT-C statistical package (Michigan State University, 1986) and the treatment means separated, where applicable, using standard error, Fisher's Least Significant Differences (LSD) or Duncan Multiple Range (DMRT) tests.

Single site analysis

Data collected from each site were analysed independently for each location using a model of analyses of variance for single location experiments as described by Gomez and Gomez (1984) for randomized complete block design (RCBD). The statistical model used for single site analysis was as follow:

$$Y_{ijk} = \mu + B_i + T_{ij} + e_{ijk}$$

Where:

Y_{ijk} = Response

μ = General effect

B_i = Block effect

T_{ij} = Treatment effect

e_{ijk} = Random experimental error.

Combined analysis

Combined analyses of variance across sites were performed to determine the extent of genotype x environment interaction. The following statistical model was used:

$$Y_{ijk} = \mu + G_i + E_j + G_{ij} + e_{ijk}$$

Where:

Y_{ijk} = Yield of ith genotype of the kth replicate of the jth environment

μ = grand mean

G_i = the mean of ith genotype

E_j = the mean of jth environment

G_{ij} = the interaction effect of the ith genotype of the jth environment

e_{ijk} = random experimental error.

3.6.2 Estimate of variance components for bean traits studied

Using the table for a combined analysis of variance, components of variance for the main effects of genotype and location interactions were calculated and estimated using the method described by Johnson *et al.* (1955), in ANOVA for a one year at two or more location experiment. The error mean squares (EMS) were used to calculate variances for genotype, environment and their interaction (GE). The analysis of variance was used to estimate the components of variance as indicated in Table 2.

Table 2: Analysis of Variance used to estimate variance components the bean traits

Source of Variation (SV)	Degree of freedom (df)	MS	Expected Mean of Square (EMS)
Location	n-1 (2)	Ml	$\delta_e^2 + r\delta_e^2 ge + g\,\delta^2\, r/e + rg\,\delta_e^2$
Replication in location	n(r-1) (6)	M1	$\delta_e^2 + g\,\delta^2\, r/e$
Genotype	g-1 (37)	M_g	$\delta_e^2 + r(\delta^2_{gl} + \delta^2_{gly}) + rl(\delta^2_g + \delta^2_{gy})$
Genotypes x Location	(g-1)(n -1)	M_{gl}	$\delta_g^2 + r(\delta^2 gl + \delta^2_{gly})$
Error	e(r-1)(g-1)	M_e	δ_e^2

From the analysis of variance (ANOVA) table above, variance components were calculated from linear functions of Mean Squares (MS) as follows:

δ^2_e = Error Mean Square (M_e)

δge = mean square GxE (M_{gl}) – error mean square(M_e) /replication (r)

= $(M_{gl} - M_e)/r$

δ_g^2 = genotypes mean square (M_g) - mean square GxE (M_{gl}) / replication (r) x number of locations (e).

= $(M_g - M_{gl})/re$

Where:

δ^2_e = environmental variance

δ_g^2 = genotype variance within genotypes

r = number of replications

e = number of environments/locations (l)

g = number of genotypes

Phenotypic variance ($\delta^2 ph$) within genotypes means evaluated in r – replications and e – environments were then calculated using the following formula:

$\delta^2 ph = \delta_g^2 + \delta ge + \delta_e^2/er$

Where:

$\delta^2 ph$ = phenotypic variance

δ_g^2 = genotypic variance

δge = genotype variance due to environment interaction

δ_e^2 = error variance

e = number of environments/locations

r = number of replications

Phenotypic and genotypic variances calculated were used to compute the broad sense habitability (Hanson *et al*., 1956).

Broad sense heritability (h^2) was calculated as the percentage proportion of the total variance ($\delta^2 ph$) which is due to genetic effects (δ_g^2) as follows:

$h^2 = \delta_g^2 / \delta^2 ph \times 100$

Where: h^2 = heritability in broad sense

δ_g^2 = genetic variance

$\delta^2 ph$ = phenotypic variance

3.6.3 Correlation analysis

Correlation coefficients were calculated using MSTAT-C program for each location and across locations (by combined analysis) in order to determine the relationship among examined traits and seed yield

3.6.4 Path coefficient analysis

Path coefficient analysis was done according to Dewery and Lu (1959) for assessing the direct and indirect effects of each of the selected traits on grain yield. Path coefficient

analysis developed by Wright (1921), is an important step further in identifying potential or promising components and minimizing number of characters needed for selection. It is a standardized partial regression analysis and deals with closed system of variables that are linearly related.

Path coefficient analysis was used to partition the total correlation into direct and indirect effects of different selected components (traits) to judge the relative extent and direction of influence on grain yield. The relationship among correlation coefficients and path coefficients were calculated.

The method involves a series of simultaneous equations for substituting the simple coefficients for measuring the mutual associations of variables (r_{ij}) obtained using the diagram in Fig. 6. Calculations for the r_{ij} were derived from the formulae (r_{16} to r_{56}). The last equation was used to calculate the residual factor (PX_6)

r_{ij} = simple correlations for measuring the mutual association of variables

P**x** = path coefficient for measuring direct influence between variables

rP = indirect effects of variables to each other through another variable

Direct effects of components/traits (PX_{iy}) were derived from the following formula:

$$PX_{iy} = b_{iy} + S_{xi}/S_y$$

Where:

PX_{iy} = direct effect of the independent variables X_l on the dependent variable
biy = regression coefficient of variable X_l
S_x = Standard deviation of X_l
S_y Standard deviation of y
1 = (1, 2, 3, 4,……..9)

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Figure 6: Path diagram used to partition correlation into direct and indirect effects among yield components and grain yield

Source: Dewery and Lu (1956).

Where:

1 = 50% flowering

2 = Plant height

3 = pod per plant

4 = seed/pod

5 = 100 seed weight

6 = grain yield

The following simultaneous equations derived from the diagram above (Fig. 6.) were used to compute simple correlations for measuring the mutual association of variables (r_{ij}'s) and direct effect of the independent variables X on the dependent variable (PX_{iy}):

$r_{16} = P_{16} + r_{12}P_{26} + r_{13}P_{36} + r_{14}P_{46} + r_{15}P_{56}$

$r_{26} = r_{12}P_{16} + P_{26} + r_{23}P_{36} + r_{24}P_{46} + r_{25}P_{56}$

$r_{36} = r_{13}P_{16} + r_{23}P_{26} + P_{36} + r_{34}P_{46} + r_{35}P_{56}$

$r_{46} = r_{14}P_{16} + r_{24}P_{26} + r_{34}P_{36} + P_{46} + r_{45}P_{56}$

$l = P^2X_6 + P^2_{16} + P^2_{26} + P^2_{36} + P^2_{46} + P^2_{56} + 2P_{16}r_{12}P_{26} + 2P_{16}r_{13}P_{36} + 2P_{16}r_{14}P_{46} + 2P_{16}r_{15}P_{56} + 2P_{26}r_{23}P_{36} + 2P_{26}r_{24}P_{46} + 2P_{26}r_{25}P_{56} + 2P_{36}r_{34}P_{46} + 2P_{36}r_{35}P_{56} + 2P_{46}r_{45}P_{56}$

Where r(s) are correlation coefficients and the P(s) are the direct effects. Px is the residual effect.

3.6.5 Regression and stability analysis

3.6.5.1 Regression analysis

The assessment of variety performance across environments conducted using a linear regression method by Eberhart and Russel (1966) as shown below:

Regression model: $Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}(S^2 d)$

Where:

Y_{ij} = Variety mean the i^{th} variety at j^{th} environment

(e.g. variety = 1, 2, 3, 4, ……...v variety; environment = 1, 2, 3 ….n)

μ_i = the i^{th} variety mean over all environment

β_i = the regression coefficient that measures the response of the i^{th} variety to varying environment.

I_j = the environmental index obtained as means of all varieties at the j^{th} environment, minus grand mean

$\delta_{ij}(S^2 d)$ = the deviation from regression of the i^{th} variety at the j^{th} environment

3.6.5.2 Stability analysis

The method developed by Eberhat and Russel (1966) was also used to characterize the genotypic stability of the bean landraces evaluated in this study. Desirable stable genotype was characterized by having regression coefficient (b) equal a unit (1.00), with minimum deviation from regression ($S^2d = 0$) and with yields greater than location means.

CHAPTER FOUR

4.0 RESULTS

4.1 Climatic Conditions and Soils

The environments used in this study represented the three agro-ecological zones (High, medium and low rainfall) where the common bean is grown in Bukoba and Missenyi districts. Variations were observed in rainfall, temperature and soil characteristics as indicated in Appendices 2 – 6.

4.1.1 Rainfall

The rainfall pattern and monthly precipitation during the growing season are presented in Fig. 7. The average annual rainfall for each agro-ecological zone is also presented in Appendix 2. The rainfall data indicate that, Maruku site received the highest amount of rainfall followed by Kyema while Byamutemba received the least amount of rainfall of all the three sites.

The highest amount of rainfall at Maruku and Kyema was recorded in January 2009 whereas at Byamutemba site the highest was recorded in November 2008. At Kyema rainfall was relatively good in amount and distribution.

4.1.2 Temperature

The maximum and minimum monthly temperatures across the three sites during the experimental period of 2008/09 short rains season are indicated in Appendix 3. Temperatures across the three sites were moderate for crop growth (NDSU, 1997). Temperatures (Minimum and maximum) ranged from 16 to 28 ^{0}C. The difference in mean temperatures across the three sites during the experimental period was generally negligible.

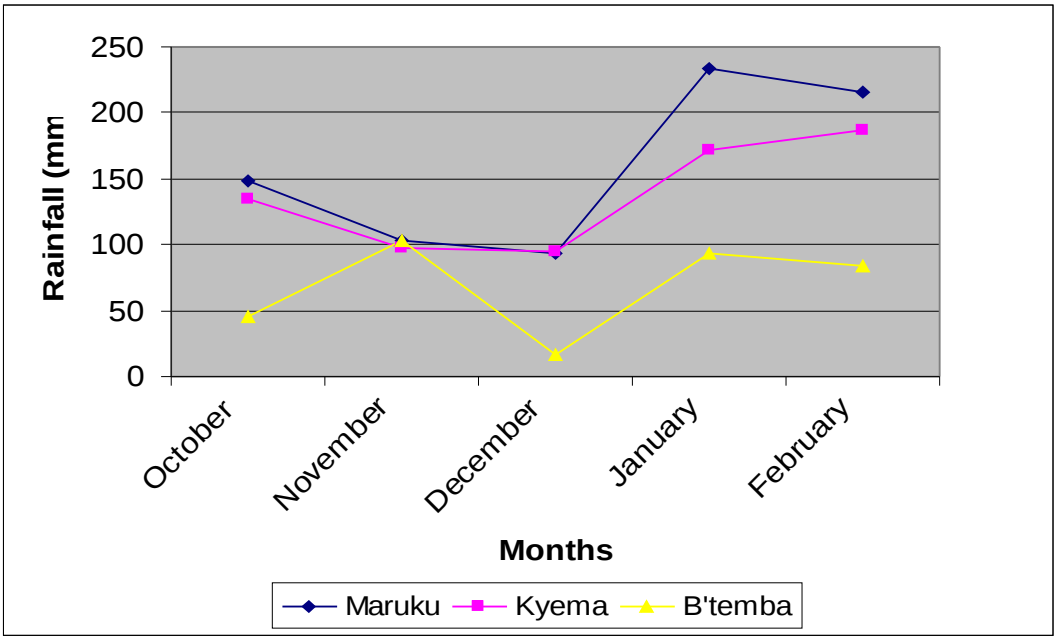

Figure 7: Rainfall pattern and amount across sites during the experimental period 2008/09 short rains season.

4.1.3 Soils

There were differences in soil characteristics across the three experimental sites (growing environments). Two sites (Kyema and Byamutemba) had sandy clay soils, while Maruku site had sandy clay loam. Soil pH varied among sites. Maruku had strongly acidic soils whereas Kyema and Byamutamba had medium acidic and slightly acidic soils, respectively.

All three sites, however, had similar status of organic carbon (OC), total N and available Ca. The three sites had medium OC, low total Nitrogen (N) and very low available Calcium (Ca). Soils at Maruku had low cation exchange capacity (CEC) while at Kyema and Byamutemba soils had medium CEC. At both Maruku and Kyema sites, the available magnesium (Mg) and Phosphorous (P) were medium and high, respectively. The available P at Byamutemba site was medium while the available Mg was low (Appendices 4 - 6).

4.2 Phenological Characteristics

4.2.1 Days to 50% flowering

There were significant (P≤ 0.05) differences in reaching 50% flowering among the bean genotypes evaluated (Table 3). However, this was not consistent across sites. The overall mean for 50% flowering at Kyema and Byamutemba was 37 days while at Maruku it was 38 days.

The results from combined analysis over the three locations indicated that there were no significant locations x genotype interactions among genotypes in days to achieve 50% flowering (Appendix 7). The mean days to 50% flowering ranged between 34 and 41 days after planting for Kybabikira and Kamoshi, respectively.

4.2.2 Days to 90% maturity

There were significantly (P≤ 0.05) different variations in attaining 90% physiological maturity among the bean genotypes evaluated (Table 3). The overall mean for 90% maturity at Kyema was 70 days whereas at Byamutemba it was 75 days and at Maruku was 76 days. The latest maturing genotype in High (Maruku) and Low (Byamutemba) rainfall zones was Shereka ebineno whereas in the medium (Kyema) rainfall zone, Karili was the late maturing genotype. Kwesikumo and ex-Byamutemba had the lowest overall mean for the number of days (66) to attain 90% maturity and Kawanja had the highest mean of 81 days.

Table 3: Phenolgical characteristics of 38 bean genotypes evaluated 2008/09 season

Local name of genotype/ landrace	Days to 50%flowering				Days to 90 % physiological maturity			
	Maruku	Kyema	Byamu temba	Mean	Maruku	Kyema	Byamu temba	Mean
Kamoshi	42	40	41	41	75	70	84	77
Kyababikira	34	36	35	35	67	68	70	68
Canada	37	36	34	36	80	68	82	77
Kabale	37	37	34	36	74	70	74	73
Kinyobwa	38	35	37	37	67	58	72	66
Kirangiti	36	35	37	36	72	72	70	71
Kamenyamigo	37	36	35	36	78	68	81	76
Kawanja	42	40	40	41	84	76	83	81
Kisapuli	37	35	36	36	74	69	73	72
Kapiki	40	38	37	38	68	77	59	68
Batenda olwakyo	36	38	35	36	84	72	82	79
Komba omalemu	40	40	40	40	71	72	75	74
Kankulye mbaruke	36	37	35	36	79	78	78	78
Chumbanoroza	41	41	40	41	85	68	81	78
Karili	42	41	38	40	85	73	74	77
Kwesikumo	36	35	36	36	68	72	59	66
Shona eigunia	39	37	39	38	86	65	76	76
Ruhondera								
Empango	36	33	35	35	77	65	77	73
Ruterana abatani	42	39	40	40	78	80	79	79
Ex-Byamutemba	35	34	35	35	65	67	66	66
Ruhuku	39	40	38	39	81	73	76	77
Turaemishako	36	35	34	35	67	67	75	70
Ruhodera	34	33	34	34	75	72	77	75
Kapili	39	38	39	39	83	70	79	77
Kayinja	39	38	38	38	69	68	74	70
Tema ekibira	39	40	39	39	84	76	72	77
Shereka ebineno	44	36	42	41	78	77	79	78
Maliyainda	39	36	38	38	78	67	81	75
Kanyabufuru	37	36	35	36	76	71	69	72
Lushara	38	36	37	37	76	69	73	73
Kitunutunu	39	41	38	39	87	69	74	77
Kashehe	41	37	40	39	74	73	74	74
Raja/Tikyakuponza	36	36	35	36	67	59	76	67
Rozikoko	37	34	36	36	78	67	77	74
Groli eikwera	35	34	33	34	74	67	76	72
Groli	37	35	37	36	75	70	70	72
Kyaburundi	36	35	35	35	75	68	77	73
Kashukari	38	37	37	37	79	68	76	74
Mean	38	37	37	37	76	70	75	74
SE (±)	1.44	0.80	0.81		2.68	0.67	2.84	
CV (%)	6.55	3.74	3.80		0.63	1.66	6.56	
LSD (P<0.05)	4.06	2.24	2.28		0.78	1.90	8.01	

4.4 Yield and Yield Components

4.4.1 Plant height

There were significant (P≤ 0.05) differences in plant height among the 38 genotypes evaluated at all locations (Table 4, 5 and 6). Results from combined analysis showed that there were significant differences (P≤ 0.05) in plant height among the evaluated genotypes (Table 7).

At Maruku, the mean plant height was 49.4 cm with a height range from 26 cm for Kwesikumo to 83 cm for Canada. At the Kyema site Turemishako was the tallest plant (80.9 cm) followed by Kanyabufuru (79 cm); whereas at Byamutemba, Canada with 102cm was the tallest genotype. At the three sites, Kwesikumo was the shortest genotype (25.7 cm). Kyema had the highest overall mean (52.9 cm) plant height followed by Maruku (49.4 cm), whereas Byamutemba had the lowest plant height (45.6 cm).

Combined analysis results indicated that the tallest genotype across locations was Canada (74.2 cm) followed closely by Chumbanoroza (73.3 cm). Combined analysis indicated that genotype x environment interaction on plant height was highly significant (Appendix 7).

Table 4: Yield and yield components of the genotypes (bean landraces) evaluated at Maruku in high rainfall zone (HRZ) during 2008/09 short rains season

Local name of genotype/landrace	Plant height (cm)	Pod length (cm)	Pods/ Plant	Seeds/ Pod	100 seed Weight (g)	Yield (kg/ha)
Kamoshi	54.5	8.8	8.7	5.5	20.0	1 131
Kyababikira	46.5	11.8	6.3	4.3	47.7	870
Canada	83.3	10.2	7.3	3.9	39.3	1 124
Kabale	31.8	9.4	9.0	3.9	18.0	637
Kinyobwa	33.0	9.5	5.0	5.5	45.0	682
Kirangiti	31.7	12.1	6.0	3.7	48.0	945
Kamenyamigo	56.7	10.7	5.3	3.9	39.0	776
Kawanja	52.1	8.3	7.7	4.8	16.3	664
Kisapuli	48.3	8.6	6.7	4.5	31.7	726
Kapiki	27.9	8.2	5.7	4.3	32.3	815
Batenda olwakyo	42.5	8.7	7.7	4.4	17.0	570
Komba omalemu	38.3	8.0	6.0	4.1	20.7	621
Kankulye mbaruke	46.2	8.7	8.7	4.3	27.0	809
Chumbanoroza	66.1	10.2	7.7	5.3	22.0	1 047
Karili	40.7	7.8	7.7	4.7	16.3	474
Kwesikumo	25.7	9.0	4.7	4.2	30.0	560
Shona eigunia	60.9	8.8	6.3	4.9	19.7	693
Ruhondera Empango	55.5	8.9	4.7	3.3	35.0	607
Ruterana abatani	48.2	9.2	7.0	4.6	21.0	869
Ex- Byamutemba	31.3	11.3	5.3	3.3	33.7	697
Ruhuku	44.9	10.3	8.0	5.9	24.0	1 083
Turaemishako	54.5	8.7	5.0	3.7	35.3	750
Ruhodera	43.2	7.9	5.0	3.7	24.0	763
Kapili	53.6	7.7	7.7	4.3	18.0	581
Kayinja	31.3	9.7	6.3	3.5	41.7	868
Tema ekibira	60.9	9.1	12.0	5.0	21.3	1 067
Shereka ebineno	43.5	8.9	10.0	4.9	20.0	830
Maliyainda	71.0	9.1	7.7	4.6	18.0	961
Kanyabufuru	70.9	7.6	6.7	4.3	16.0	667
Lushara	62.0	9.9	7.3	3.7	36.0	642
Kitunutunu	43.1	9.9	6.0	5.7	22.3	950
Kashehe	59.8	8.8	6.3	4.6	17.3	579
Raja/Tikyakuponza	65.0	11.3	7.7	3.5	44.0	937
Rozikoko	55.9	10.0	5.3	3.3	39.7	667
Groli eikwera	43.3	10.1	4.3	4.1	39.3	668
Groli	40.1	8.7	5.7	3.8	42.0	870
Kyaburundi	56.9	9.5	7.3	4.3	34.3	1 244
Kashukari	54.5	10.6	8.3	6.1	24.7	1 123
Mean	49.36	9.37	6.84	4.33	28.73	804
SE (±)	9.38	0.48	1.05	0.39	2.10	135.80
CV (%)	32.9	8.8	26.6	15.4	12.66	29.22
LSD (P<0.05)	26.44	1.343	2.959	1.086	5.91	382

Table 5: Yield and yield components of genotypes (bean landraces) evaluated at Kyema in medium rainfall zone (MRZ) during 2008/09 short rain season

Local name of genotype/landrace	Plant height (cm)	Pod length (cm)	Pods/ plant	Seeds/ Pod	100 SW (g)	Yield (kg/ha)
Kamoshi	70.8	8.9	7.7	6.0	22.3	2 631
Kyababikira	39.3	10.3	11.7	9.1	37.3	1 524
Canada	41.1	8.1	9.9	4.8	32.6	993
Kabale	35.1	8.3	7.2	3.9	20.4	720
Kinyobwa	35.6	8.9	7.5	6.7	38.0	679
Kirangiti	40.0	11.4	9.7	4.6	41.0	1 902
Kamenyamigo	72.7	8..4	4.7	4.4	35.5	720
Kawanja	38.6	8.2	8.5	4.8	20.0	1 257
Kisapuli	44.1	11.1	9.9	5.7	35.7	1 510
Kapiki	33.4	9.6	8.0	5.4	25.3	1 241
Batenda olwakyo	67.8	10.6	9.1	6.6	19.7	1 038
Komba omalemu	39.8	9.2	7.9	5.0	25.8	2 092
Kankulye mbaruke	71.9	8.2	11.0	4.1	22.8	1 085
Chumbanoroza	76.1	8.3	9.6	4.2	18.0	1 259
Karili	42.6	7.9	7.5	4.5	21.5	718
Kwesikumo	30.7	8.2	12.0	5.0	31.2	1 188
Shona eigunia	47.0	11.0	11.0	5.6	19.4	2 092
Ruhondera Empango	40.0	9.2	8.6	5.1	18.9	1 458
Ruterana abatani	45.2	8.9	12.0	5.0	18.6	2 152
Ex- Byamutemba	34.0	9.6	7.7	4.7	36.6	860
Ruhuku	49.2	9.6	8.2	5.9	25.9	1 342
Turaemishako	80.9	10.9	7.5	5.9	32.8	663
Ruhodera	39.9	9.3	9.0	5.6	26.3	595
Kapili	65.3	8.1	7.0	4.5	20.3	851
Kayinja	33.6	9.0	7.2	4.0	33.5	1 813
Tema ekibira	65.0	10.2	10.8	4.8	26.3	1 676
Shereka ebineno	53.4	14.7	8.4	5.7	21.3	1 273
Maliyainda	76.9	8.3	6.6	3.2	30.8	418
Kanyabufuru	79.1	10.8	10.4	4.9	38.0	874
Lushara	75.0	11.1	7.6	4.7	36.8	104
Kitunutunu	43.6	9.2	11.6	5.6	31.3	2 593
Kashehe	66.1	9.6	7.6	4.3	19.5	904
Raja/Tikyakuponza	41.8	11.7	8.5	4.2	36.8	1 235
Rozikoko	43.5	8.6	5.1	4.9	32.7	580
Groli eikwera	64.9	9.1	9.8	4.5	33.8	1 270
Groli	36.3	8.7	7.8	4.2	34.2	1 624
Kyaburundi	77.8	8.7	14.7	7.0	34.5	2 239
Kashukari	44.7	8.9	5.7	5.0	25.6	1 665
Mean	52.2	9.45	8.83	5.1	28.45	1 310
SE (±)	1.56	0.32	0.33	0.19	0.74	89.15
CV (%)	5.19	5.86	6.36	6.57	4.5	11.8
LSD (P<0.05)	4.41	0.904	0.914	0.55	2.08	251

Table 6: Yield and yield components of genotypes (bean landraces) evaluated at Byamutemba in low rainfall zone (LRZ) during 2008/09 short rain season

Local name of genotype/landrace	Plant height (cm)	Pod length (cm)	Pods/ plant	Seeds/ pod	100 SW (g)	Yield (kg/ha)
Kamoshi	53.3	9.4	6.5	5.5	19.0	834
Kyababikira	27.7	7.3	2.1	3.6	25.0	213
Canada	103.5	9.4	3.0	3.5	38.7	530
Kabale	41.5	7.4	3.6	3.7	17.3	261
Kinyobwa	33.6	7.5	5.0	4.6	29.3	338
Kirangiti	31.7	7.5	2.4	3.5	37.0	165
Kamenyamigo	58.6	9.6	2.5	3.0	41.0	328
Kawanja	39.3	7.4	3.5	3.5	18.7	254
Kisapuli	65.5	7.6	3.0	3.2	34.0	254
Kapiki	19.1	7.6	2.3	3.6	23.7	165
Batenda olwakyo	48.2	7.9	4.3	3.7	21.7	313
Komba omalemu	30.7	7.1	4.0	4.7	20.3	353
Kankulye mbaruke	43.7	7.7	3.5	4.1	18.7	373
Chumbanoroza	77.8	8.5	3.7	4.1	20.3	333
Karili	38.1	6.6	4.1	4.8	20.7	300
Kwesikumo	20.1	6.6	2.3	3.4	25.3	280
Shona eigunia	58.0	8.7	3.1	4.8	20.7	499
Ruhondera Empango	56.6	7.4	1.9	3.1	33.3	252
Ruterana abatani	55.5	9.0	6.7	5.6	19.3	680
Ex- Byamutemba	22.5	7.3	1.8	3.7	34.0	217
Ruhuku	56.2	8.4	2.7	5.4	27.3	399
Turaemishako	65.1	7.3	3.1	3.7	34.7	307
Ruhodera	27.1	5.7	1.4	2.9	27.0	132
Kapili	42.7	8.3	2.9	5.2	23.7	321
Kayinja	38.2	7.4	1.6	3.5	36.7	341
Tema ekibira	26.7	6.3	4.3	3.9	20.7	220
Shereka ebineno	38.0	7.8	3.5	3.6	19.0	282
Maliyainda	52.0	9.1	2.9	3.4	26.3	313
Kanyabufuru	20.3	6.0	1.5	3.2	24.7	180
Lushara	44.8	8.0	3.1	3.4	28.3	280
Kitunutunu	43.3	8.2	4.0	4.7	24.7	301
Kashehe	43.9	8.5	3.9	3.6	24.0	323
Raja/Tikyakuponza	62.3	9.4	2.1	3.2	37.3	177
Rozikoko	44.3	8.4	2.1	3.8	42.7	289
Groli eikwera	37.6	7.1	1.5	3.3	32.3	177
Groli	34.7	6.8	2.3	3.4	32.7	213
Kyaburundi	87.6	8.4	3.5	4.1	29.3	340
Kashukari	42.9	8.5	2.1	4.5	24.0	337
Grand mean	45.61	7.8	3.1	3.9	27.2	310
SE (±)	8.70	0.53	0.92	0.49	2.91	72.48
CV (%)	33.03	11.7	51.09	21.50	18.56	41.50
LSD (P<0.05)	24.51	1.49	2.58	1.37	8.20	0.204

Table 7: Combined yield and yield components of the genotype (bean landraces) evaluated at three locations (Maruku, Kyema and Byamutemba) during 2008/09 short rains season

Local name of genotype/landrace	Plant height (cm)	Pods/ Plant	Seeds/ Pod	100 seed weight (g)	Yield (kg/ha)
Kamoshi	59.6	8	6	20.4	1 532
Kyababikira	37.8	7	6	34.6	869
Canada	74.2	7	4	38.6	882
Kabale	36.1	7	4	18.5	540
Kinyobwa	34.1	6	5	37.4	566
Kirangiti	34.5	7	4	42.0	100
Kamenyamigo	62.7	4	4	38.5	607
Kawanja	43.3	7	3	18.3	725
Kisapuli	52.7	7	4	33.8	830
Kapiki	36.3	5	4	27.1	730
Batenda olwakyo	52.9	7	5	19.4	640
Komba omalemu	36.3	6	5	22.3	1 022
Kankulye mbaruke	53.9	8	4	22.8	722
Chumbanoroza	73.3	7	5	20.3	879
Karili	40.5	6	5	19.5	497
Kwesikumo	25.5	6	4	28.8	675
Shona eigunia	55.0	7	5	20.1	1 094
Ruhondera Empango	50.8	5	4	28.9	772
Ruterana abatani	49.6	9	5	19.7	1 233
Ex- Byamutemba	29.3	5	4	34.8	590.
Ruhuku	50.1	6	6	25.7	941
Turaemishako	66.8	5	4	34.3	573
Ruhodera	36.8	5	4	25.8	497
Kapili	53.9	6	5	20.7	584
Kayinja	34.4	5	4	37.3	1 007
Tema ekibira	50.9	9	5	22.8	988
Shereka ebineno	45.0	7	5	20.1	795
Maliyainda	66.5	6	4	25.0	564
Kanyabufuru	56.8	6	4	26.2	573
Lushara	60.6	6	4	33.7	654
Kitunutunu	43.3	7	5	26.0	1 281
Kashehe	56.6	6	4	20.3	601
Raja/Tikyakuponza	56.4	6	4	39.4	782
Rozikoko	47.9	4	4	38.1	511
Groli eikwera	48.6	5	4	35.1	705
Groli	37.0	5	4	36.3	902
Kyaburundi	74.1	9	5	32.7	1 274
Kashukari	47.4	5	5	24.7	1 041
Overall mean	49.0	6	4	28.1	808
CV (%)	26.2	23	14.6	13.0	22.01
LSD (P<0.05)	11.95	1.317	0.604	3.405	165

4.4.2 Pod length

Results from both single site and combined analysis indicated that pod length differed significantly (P≤ 0.05) among genotypes within and across locations. At Maruku, pod length ranged from 7.7 cm for Kapili to 11.8 cm for Kyababikira. At Kyema ranged from 7.9 cm for Karili to 14.7 cm for Shereka ebineno whereas at Byamutemba pod lengh was between 5.7 cm for Ruhondera and 9.6 cm for Kamenyamigo. The mean pod lengths at the three sites were 9.3 cm, 11.0 cm and 7.8 cm at Maruku, Kyema and Byamutemba, respectively. Combined analysis showed that genotype x environment interaction on pod length was not significant.

4.4.3 Pods per plant

Pods per plant varied significantly (P≤ 0.05) among genotypes and across locations (Tables 4 - 6). At Maruku Temaekibira recorded the highest number of pods per plant (12) and the lowest number (4) were recorded from Groli eikwera. At Kyema, Kyaburundi had the highest mean number of pods per plant (15) with Kamenyamigo recording the lowest number (5) per plant. At Byamutemba, Ruterana abatani had the highest mean pod number (7) while the lowest mean pods (1) per plant was from Ruhondera. Kyema had the highest overall mean of number of pods per plant (9) followed by Maruku (7) and Byamutemba had the lowest (3).

Combined analysis (Table 7) indicated that the genotype Tema ekibira had the highest number of pods per plant of 9 although it was not different from Rutera abatani and Kyaburundi which had the same number (9) of pods per plant. The lowest mean number of pods per plant was from Kamenyamigo and Rozikoko, each with 4 pods per plant. The overall mean number of pods per plant from the combined analysis was 6.

Combined analysis also indicated highly significant genotype x environment interaction on number of pod per plant (Appendix 7), implying that environments had some effect on this characteristic.

4.4.4 Seeds per pod

Significant differences (P≤ 0.05) were recorded among bean genotypes for the numbers of seeds per pod across sites (Tables 4 - 7). At Maruku, the number of seeds per pod ranged from 3 for Rozikoko to 6 for Kashukari with overall mean of 4 seeds per pod. At Kyema the range was between 3 for Maliyainda and 9 seeds per pod for Kyababikira with overall mean of 5. At Byamutemba the number of seeds per pod ranged from 3 for Raja to 6 for Ruterana abatani with overall mean 4 seeds per pod.

Combined analysis results indicated highly significant genotype x environment interaction on number of seeds per pod (Appendix 7) implying that the number of seeds per pod produced at each site was highly influenced by environmental differences. Combined analysis results also indicated that Ruhuku had the highest mean number of seeds per pod 6, although it was not significantly (P≤ 0.05) different from Kamoshi, Kyababikira, Kituntunu, Kashukari and Kyaburundi. The lowest number of seeds per pod was obtained from Ruhondera empango and Groli (Table 7).

4.4.5 100- seed weight

The weight of 100 seeds varied significantly (P≤ 0.05) among the bean genotypes and experimental sites (Table. 4, 5 and 6). At Maruku, 100 seed weight ranged from 16 to 48 g. Kirigiti had the highest 100 seed weight at Maruku and the lowest was obtained from Chumbanoloza. The site mean 100 seed weight was 28.7 g.

The 100 seed weight at Kyema had a range from 41 g for Kiringiti to 18 g for chumbanoloza, with the overall site mean of 28.5 g. At Byamutemba, the highest 100 seed weight (42.7 g) was from Rozikoko and the lowest (17.3) was from Kabale. The site mean was 27.2 g.

The combined analysis results indicated that 100 seed weight ranged from 18 to 42 g. Kiringiti and Kawanja had the highest and lowest 100 seed weight respectively. The 100 seed weight from Kiringiti was significantly ($P \leq 0.05$) higher across locations.

Combined analysis means squares (Appendix 7) indicated significant ($P \leq 0.001$) environment x genotype interactions on seed weight. This interaction showed that the genotypes responded differently to seed weight in each of the environment.

4.4.6 Seed yield

There was a significant ($P \leq 0.05$) difference in seed yield among the evaluated genotypes both within and across sites (Table 4, 5, 6, and 7).

At Maruku site, seed yield ranged from 474 kg/ha to 1240 kg/ha. The highest yielding genotype was Kyaburundi and the lowest was Karili. The site mean seed yield was 804 kg /ha.

At Kyema, Kamoshi was significantly ($P \leq 0.05$) the best yielder with seed yield of 2630 kg/ha. The lowest yielder was Maliyainda which produced 418 kg/ha. At Byamutemba, Kamoshi gave significantly ($P \leq 0.05$) higher seed yield (834 kg/ha) than all the other genotype evaluated. The poorest yielder at Byamutemba was Ruhondera which produced only 132 kg/ha.

Among the three sites, Kyema had the best seed yields with overall mean of 1310 kg/ha followed by Maruku with 804 kg/ha, and the poorest site was Byamutemba with only 310 kg/ha (Fig. 8).

Combined analysis results (Table 7) indicated that genotype Kamoshi had significantly (P≤ 0.05) highest grain yield across locations among all the genotypes evaluated. The yield ranged from 497 to 1532 kg/ha. The poorest yielding genotype was Ruhomdera. Combined analysis also showed that there was significant (P≤ 0.001) genotype x environment interaction on seed yield (Appendix 7).

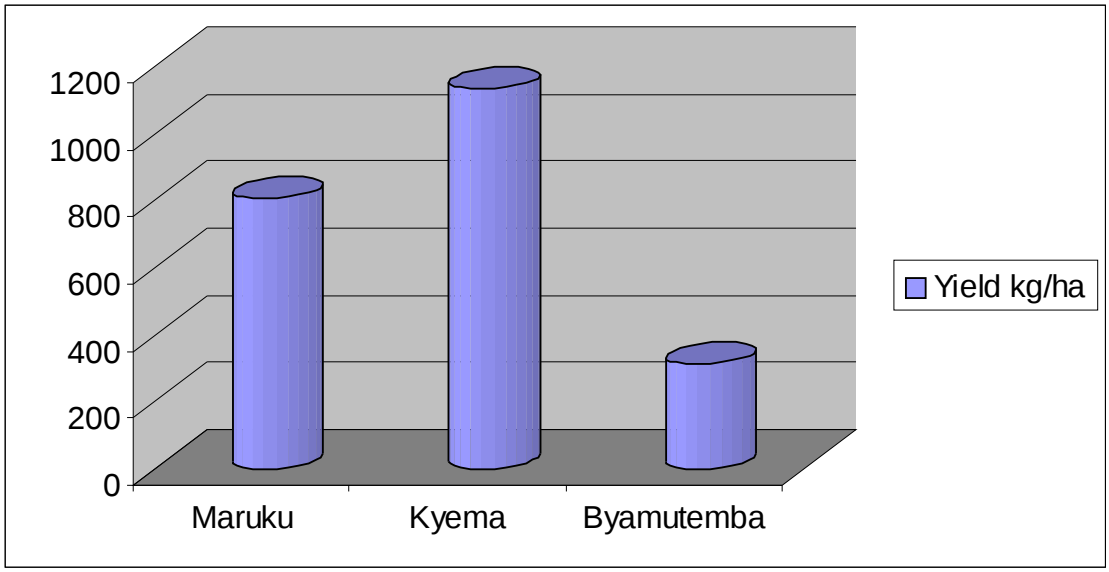

Figure 8: Mean seed yield of genotypes evaluated at Maruku, Kyema and Byamutemba in high, medium and low rainfall environments, respectively in Bukoba and Missenyi Districts during 2008/09 short rain season.

4.5 Disease Reactions

Bean leaf rust (*Uromyces appendiculatus*) and Angular leaf spot *(Phaeisariopsis griseola)* were the most important diseases which were observed and the genotypes were scored for them. The results of reaction of different genotypes at each site/location are presented in Table 8. The mean disease scores at all locations were generally low probably indicating low disease pressure during the season. Overall, disease severity (both leaf rust and ALS) at all locations had an overall mean score of less 3 according to CIAT disease severity scale used (1- 9) as described by *Phaseolus vulgaris* descriptors.

4.5.1 Bean leaf rust

The evaluated genotypes varied significantly ($P \leq 0.05$) in susceptibility to bean leaf rust disease. The disease score ranged from 1 to 5 with overall mean of 2.4. Genotypes Kashukari, Kitunutunu, Chumbanoroza and Ruhuku had higher mean disease score (equal or greater than 4.0) across the trial sites (Table 8). There was no significant difference at $P \leq 0.05$ (Appendix 8) on genotype x environment interaction with regard to leaf rust reaction, implying that genotypes reacted similarly to leaf rust at all the three locations (Maruku, Kyema and Byamutemba).

Table 8: Reaction of 38 bean genotypes to Bean rust and ALS at the three locations

Local name of Genotype	Bean Rust				Angular leaf Spot (ALS)			
	MRK	KYM	BMB	Mean	MRK	KYM	BTB	Mean
Kamoshi	1.0	1.3	1.3	1.2	2.3	2.3	2.7	2.4
Kyababikira	1.7	2.0	1.3	1.7	3.3	3.3	3.0	3.2
Canada	1.3	1.3	1.7	1.4	2.3	2.7	3.0	2.7
Kabale	3.3	3.0	3.3	3.2	2.7	2.7	3.0	2.8
Kinyobwa	1.7	1.7	2.0	1.8	4.0	3.7	3.7	3.8
Kirangiti	1.7	1.7	1.3	1.6	2.7	2.3	3.0	2.7
Kamenyamigo	1.3	2.0	2.0	1.8	2.7	2.3	2.7	2.6
Kawanja	2.0	2.0	1.7	1.9	4.3	4.0	4.0	4.1
Kisapuli	1.3	1.3	1.3	1.3	2.3	2.3	2.3	2.3
Kapiki	1.3	1.3	1.3	1.3	2.7	2.7	1.3	2.2
Batenda olwakyo	2.7	2.3	2.7	2.6	3.0	3.0	3.0	3.0
Komba omalemu	1.7	2.0	2.0	1.9	2.7	2.7	2.7	2.7
Kankulye mbaruke	3.7	3.7	2.7	3.3	2.7	2.3	2.7	2.6
Chumbanoroza	5.0	4.7	4.3	4.7	3.7	3.3	4.0	3.7
Karili	1.7	1.3	1.7	1.6	2.7	2.7	2.0	2.4
Kwesikumo	1.0	1.0	1.3	1.1	3.3	3.3	2.7	3.1
Shona eigunia	5.0	5.0	4.3	4.8	2.0	2.3	1.7	2.0
Ruhondera Empango	2.0	2.0	1.7	1.9	2.3	2.7	3.0	2.7
Ruterana abatani	2.7	2.7	2.3	2.6	2.0	2.3	2.7	2.3
Ex- Byamutemba	3.3	3.0	2.7	3.0	2.7	2.7	2.7	2.7
Ruhuku	4.0	4.0	4.7	4.2	2.0	2.7	3.0	2.6
Turaemishako	2.7	2.7	2.7	2.7	2.3	2.3	2.3	2.3
Ruhodera	2.0	2.0	1.3	1.8	3.0	3.0	2.3	2.8
Kapili	1.7	2.0	1.7	1.8	3.3	3.3	2.3	3.0
Kayinja	1.0	1.0	1.0	1.0	1.7	2.0	1.7	1.8
Tema ekibira	2.0	2.0	2.7	2.2	2.3	3.0	2.3	2.5
Shereka ebineno	1.7	2.3	1.7	1.9	2.7	2.7	3.0	2.8
Maliyainda	4.0	4.3	3.0	3.8	2.7	2.3	2.0	2.3
Kanyabufuru	3.3	3.7	2.7	3.2	2.7	2.3	2.3	2.4
Lushara	1.3	1.7	1.7	1.6	3.3	3.3	2.7	3.1
Kitunutunu	5.7	4.3	4.0	4.7	2.3	2.3	2.3	2.3
Kashehe	1.7	1.7	1.7	1.7	3.0	3.0	2.7	2.9
Raja/Tikyakuponza	1.7	2.0	2.0	1.9	2.7	2.3	3.0	2.7
Rozikoko	3.7	3.0	4.0	3.6	2.3	2.3	2.3	2.3
Groli eikwera	2.0	2.7	2.3	2.3	3.0	2.7	2.3	2.7
Groli	2.3	2.0	2.3	2.2	2.7	2.7	2.7	2.7
Kyaburundi	1.0	1.0	1.0	1.0	3.7	3.7	3.0	3.5
Kashukari	4.3	4.3	4.3	4.3	2.0	2.7	2.0	2.2
Overall mean	2.4	2.4	2.3	2.4	2.7	2.8	2.6	2.7
SE (±)	0.59	0.59	0.37		0.40	0.41	0.46	
CV (%	42.37	42.01	27.79		25.02	25.83	30.17	
LSD (P<0.05)	1.66	1.66	1.04		1.11	1.15	1.29	

MRK = Maruku KYM = Kyema BTB = Byamutemba

4.5.2 Angular leaf spot (ALS)

There were significant (P≤ 0.05) differences among different genotypic reactions to ALS (Table 8). Genotypes Kawanja had the highest score (4.00) across the locations, indicating relatively high level of susceptibility to ALS. The ALS mean scores ranged from 1.8 to 4.0 with the overall mean of 2.7 across locations. Combined analysis revealed that the genotype x environment interaction on ALS was not significant (P≤ 0.05).

4.6 Estimate of Variance Components

The variance components and genetic parameters for yield and yield components of 38 bean landraces/genotypes combined over three locations (Maruku, Kyema and Byamutemba) are presented in Table 9. The estimated genetic variances (δ^2_g) among variables studied were smaller than the corresponding phenotypic variances (δ^2_{ph}). The interaction variance (δ^2_{gl}) was more important for yield and plant height than in the other characters/traits studied.

The heritability (h^2) estimates and expected genetic advance were high for days to 50% flowering, 100 seed weight and plant height. The highest heritability was observed for days to 50% flowering (91.1%) whereas the highest expected genetic advance was recorded for 100 seed weight (37.7%). Pods per plant had the lowest heritability and expected genetic advance of 20.2 % and 8.67%, respectively.

Table 9: Variance components of 38-bean landrace (genotypes) evaluated at three locations during 2008/2009 short rains season.

Character	δ^2_g	δ^2_{gl}	δ^2_e	δ^2_{ph}	h^2 (%)	E G A (%)
Yield	3.17	25.67	0.03	11.72	27.0	20.0
100 seed weight	48.11	42.22	13.4	63.67	75.6	37.7
Seed/Pod	0.19	1.21	0.42	0.64	29.3	9.27
Pod/plant	0.47	5.01	2.06	2.30	20.2	8.67
Plant height	123.65	230.65	165.47	218.92	56.5	30.01
Days to 50% flowering	4.12	0.03	3.36	4.52	91.1	9.14

Where:

δ^2_g = component of variance due to genotypes

δ^2_{gl} = component of variance due to environment/location

δ^2_e = component of variance due to the error term

δ^2_{ph} = phenotypic variance

h^2 = heritability (Broad sense

E G A = Expected genetic advance

4.7 Relationship between Yield and Yield Components

4.7.1 Simple correlations of yield and yield components

At all the three locations seed yield was significant and positively correlated with pods per plant with correlation coefficients (r) equal to 0.37, 0.50 and 0.63 at Maruku, Kyama and Byamutemba respectively (Table 10 and Appendix 9 -11). The number of days to flowering was significantly and positively correlated with seed yield at Kyema and Byamutemba whereas at Maruku it was not.

Number of seeds per pod was found to have significant and positive correlation with seed yield at all the three locations (Table 10). Correlations of different character combination at each of the three sites indicate significant positive correlations for days to 50% flowering

and days to maturity, pods per plant and plant height. Significant ((P≤ 0.05) and negative correlation was found between seed weight and grain yield at Byamutemba (r = – 0.227).

Table 10: Summarized correlation Coefficients of different character combinations across locations

Character combinations	Location		
	Maruku	**Kyema**	**Byamutemba**
50% flowering vs pod / plant	0.289*	0.0059	0.355**
50% flowering vs 90% maturity	0.337**	0.385**	0.213*
50% flowering vs seed yield	- 0.021	0.261*	0.361**
Plant height vs pods/plant	0.246*	0.046	0.573***
Plant height vs seed yield	0.183	-0.1125	0.486**
Pods /plant vs seed yield	0.366**	0.499**	0.627***
Seeds/pod vs seed yield	0.321**	0.282*	0.464**
100 seed weight vs seed yield	0.192	0.086	-0.227*

* = significant at 0.05, ** = significant at 0.01 and *** = significant at 0.001.

The combined analysis revealed that there was highly significant (P≤ 0.001) correlation between yield and yield components (Table 11). The results from combined simple correlation indicated that seed yield have a positive and highly significant (P≤ 0.001) correlation with pods per plant (r = 0.741). Seed yield was also found to have significant (P≤ 0.001) positive and highly correlation with seed per pod (r = 0.50).

Positive and significant association between grain yield was also found with plant height (r = 0.16), pod length (r = 0.18) and weak positive association with days to 50% flowering and 100 seed weight.

The combined simple correlation also revealed significant correlations among yield components. Pods per plant was found to have highly significant (P≤ 0.001) and positive correlation with seed per pod (r = 0.55), days to 50% flowering had significant (P≤ 0.01) negative correlation with 100 seed weight. Days to 90% maturity had significant (P≤ 0.05)

negative correlation with seed weight. Plant height and pod per plant had highly significant (P≤ 0.001) and positive correlation (r = 0.22).

Table 11: Combined simple correlations among yield and yield components of 38-bean genotypes/landraces for the three locations (Maruku, Kyema and Byamutemba).

	1	2	3	4	5	6	7	8
1. Days to 50% flower								
2. Plant height	0.022							
3. Pods /plant	0.135	0.217**						
4. Pod Length	-0.001	0.1149*	0.162*					
5. Days to 90% Maturity	0.323	0.2571	-0.038	-0.015				
6. Seed/ Pod	0.1602*	0.1252	0.547***	0.077	-0.006			
7. 100 grain seed wt.	-0.4030**	0.0065	-0.107	0.070	-0.357*	-0.199		
8. Seed yield	0.1023	0.1550*	0.742***	0.178*	-0.143	0.502***	0.038	

* = significant at 0.05, ** = significant at 0.01 and *** = significant at 0.001.

4.7.2 Direct and indirect relationship of yield components with yield

A simple correlation does not provide the contribution of the characters toward the yield. The genotypic correlations were portioned into direct and indirect effects through path coefficient analysis (Table 12). From the table, diagonal figures (bolded) show the direct effect of respective yield component to the final seed yield. The effects/contribution of different yield components (the direct and indirect) on seed yield is diagrammatically presented in Fig. 9.

Table 12: Path coefficient analysis of direct (diagonal bolded) and indirect effects of various characters of bean landraces combined across three locations 2008/09 short rain season

	DTF	PLH	PPP	POL	SPP	HSW
DTF	**0.0520**	-0.0004	0.0887	-0.0005	0.0262	-0.0644
PLH	0.0011	**-0.0160**	0.1426	0.0054	0.0205	0.0011

PPP	0.0070	-0.0035	**0.6570**	0.0079	0.0897	-0.0170
POL	-0.0005	-0.0018	0.1064	**0.0490**	0.0126	0.0111
SPP	0.0083	-0.0020	0.3594	0.0038	**0.1640**	-0.0316
HSW	-0.0210	-0.0001	-0.0703	0.0034	-0.0326	**0.1590**

DTF - Days to 50% flowering PLH - Plant height PPP - Pods /Plant

HSW - 100 seed weight POL - Pod length SPP - Seeds/pod

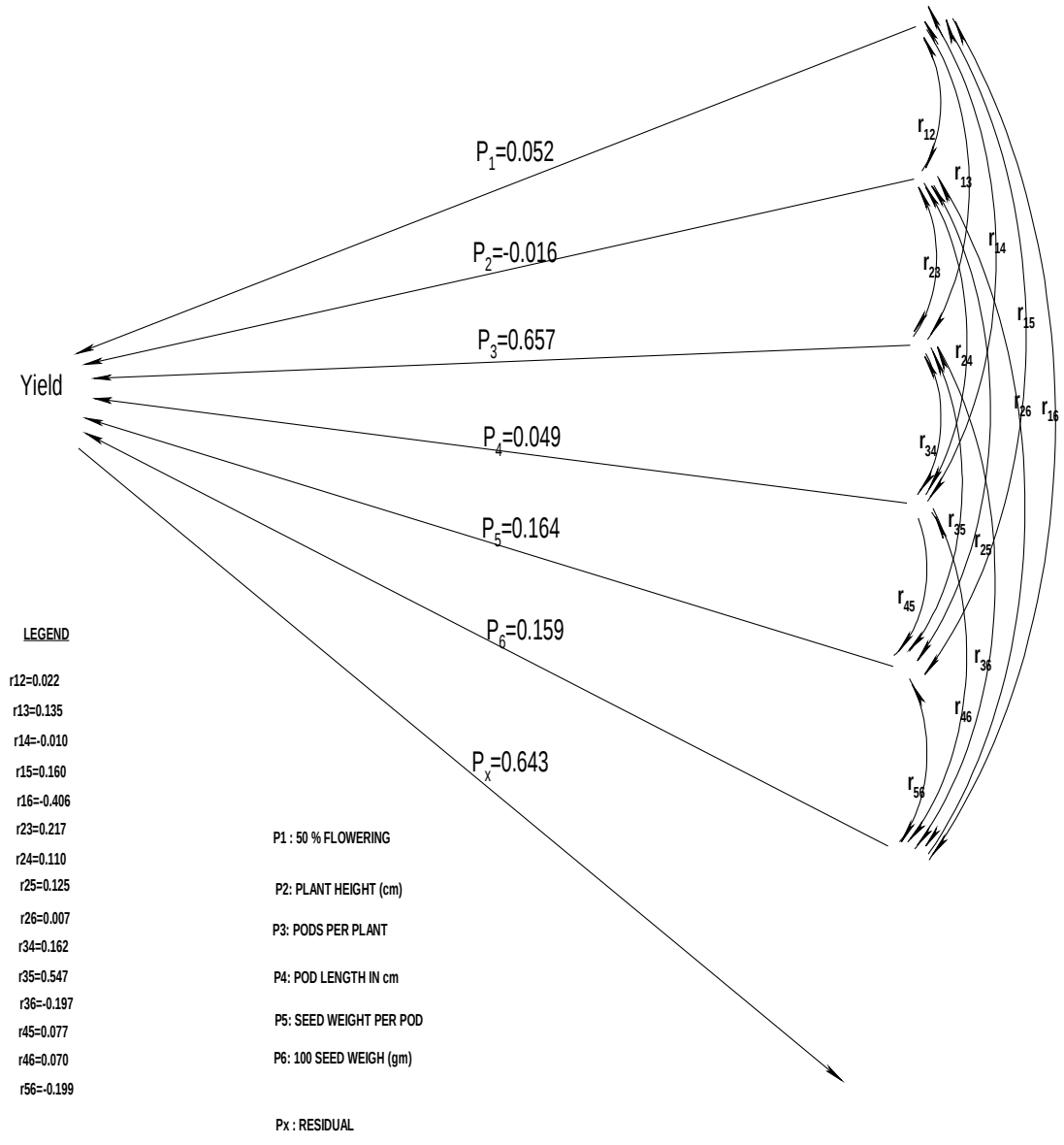

Figure 9: Path diagram showing direct and indirect effects coefficients of different yield components on seed yield.

The path analysis results revealed that number of pod per plant had the highest and positive direct effect (0.67) followed seeds per pod (0.16). The remaining traits that are 50% flowering, pod length and 100 seed weight had weak positive direct effect, except for plant height which had weak direct effect but negative (Table 12). Most of the traits/characters indicated weak indirect effects on grain yield except for number of seeds per pod in which through number of pods per plant exerted relatively higher indirect influence on yield (Fig. 9).

The calculated residual (PX6) had a value of 0.6427. This means that the characters evaluated are not the only factors contributing to the final total grain yield of the bean genotypes

4.6 Stability of Genotypes

4.6.1 Estimate of stability and stability parameters

The mean squares from combined analysis of yield and yield components studied are presented in Appendix vii. The results indicated significance difference ($P \leq 0.05$) for genotype x environment interaction for days to 50% flowering, plant height, pod per plant, seeds per pod, 100 seed weight and seed yield. This implied that environments differed and that the genotypes were responding differently. This indicated the need for estimation of genotypic stability across the environments.

The mean seed yield and stability parameter namely, regression coefficient (b), mean square deviation (S^2d) and coefficient of determination (R^2) for 38 genotype evaluated in the three environments are presented in Table 13.

Table 13: Estimate of phenotypic stability parameters for seed yield for 38 common bean genotypes grown under three diverse environments during 2008/09 short rains season.

Genotype /landracelocal name	Mean grain Yield (kg/ha)	b	S^2d	R^2
Kamoshi	1 532	0.48	0.03	0.87
Kyababikira	869	0.76**	0.00	0.99
Canada	882	1.18	1.17	0.54
Kabale	540	1.91	0.49	0.87
Kinyobwa	566	2.12	1.68	0.74
Kirangiti	1 004	0.57*	0.03	0.99
Kamenyamigo	607	1.64	1.51	0.64
Kawanja	725	0.99*	0.01	0.99
Kisapuli	830	0.78	0.01	0.98
Kapiki	740	0.91	0.01	0.99
Batenda olwakyo	640	1.34	0.04	0.97
Komba omalemu	1 022	0.51	0.07	0.79
Kankulye mbaruke	722	1.38	0.04	0.99
Chumbanoroza	879	0.98	0.10	0.90
Karili	497	2.37	0.04	0.99
Kwesikumo	675	1.05	0.05	0.96
Shona eigunia	1 094	0.53	0.04	0.84
Ruhondera Empango	772	0.78	0.03	0.95
Ruterana abatani	1 233	0.57	0.06	0.85
Ex- Byamutemba	591	1.43	0.18	0.92
Ruhuku	941	1.00	0.06	0.94
Turaemishako	573	1.66	1.96	0.57
Ruhodera	497	1.07	1.18	0.49
Kapili	584	1.89**	0.00	0.99
Kayinja	1 007	0.66	0.01	0.98
Tema ekibira	988	0.68	0.01	0.99
Shereka ebineno	795	1.00	0.01	0.99
Maliyainda	564	0.21	2.02	0.02
Kanyabufuru	573	1.36	0.00	0.94
Lushara	654	-0.59	2.97	0.11
Kitunutunu	1 281	0.41	0.01	0.94
Kashehe	601	1.71	0.01	0.99
Raja/Tikyakuponza	782	0.89	0.05	0.93
Rozikoko	511	1,84	2.97	0.53
Groli eikwera	705	0.91*	0.03	0.99
Groli	902	0.70	0.01	0.99
Kyaburundi	1 274	0.53	0.00	0.99
Kashukari	1 041	0.74	0.01	0.98
Overall mean	808			
LSD (P<0.05**)**	165			

* and ** = significantly at P≤ 0.05 level and P≤ 0.01 respectively.

Wider ranges of regression coefficient values were observed from stability analysis among genotypes for seed yield. The b values ranged from 0.2 to 2.4 and S^2d values between 0 and 2.97, indicating wider variation among genotypic performance across the three locations.

Genotypes Canada, Chumbanoloza and Ruhuku had b values equal or nearly equal to a unit, minimum deviation (S^2d) from regression and seed yield above the overall mean indicating that they performed consistently across the three locations. However, most genotypes had b value less than unity or more than unity and deviation from regression (S^2d) > 0 implying differences in performance of individual genotypes at each location. Overall mean seed yield for all the evaluated genotype across locations was 808 kg/ha, with the highest individual genotypes mean seed yield of 1532 kg/ha.

CHAPTER FIVE

5.0 DISCUSSIONS

5.1 Diversity among Genotypes

Genetic diversity is important for applied crop breeding. This is because diversity may reduce vulnerability to pests and, at the same time, accelerate breeding progress for an agronomic trait such as yield. The analysis of variance in this from this study revealed significant differences among genotypes for all the characters studied. These characters included, phenological traits, plant height, pod length, number of pods per plant, seeds per pod, 100-seed weight and grain yield. The genotypes diversity was also reflected in qualitative traits. There was great variation in seed coat colour and seed shape among the genotypes (Table 1).

These suggest that the bean landraces had considerable diversity. Harian (1992) reported that cultivated forms of common beans known as landraces are often highly variable genotypically and in appearance (Phenotypically). Similar findings of high bean varietal diversity in Bukoba and Missenyi were reported by Mushi (1994) and William (2002).

At Byamutemba drought stress (16.2 mm monthly rainfall) during flower and pod setting (Appendix 3) significantly reduced yield for all 38 genotypes. This suggests that there was no difference in drought resistance/tolerance among the evaluated landraces/genotypes. Szilagyi (2003) reported similar results on the influence of drought on seed yield and yield components in common bean.

The development of superior materials or genotypes depends largely on the availability and the magnitude of genetic variability in the basic materials. Thus, the observed bean

diversity in Bukoba and Missenyi districts suggests that there is good scope for bean improvement and the bean landraces could be used as source of genetic materials. This is in agreement with Wood and Lenne (1997) who suggested that the genetic diversity among landraces is the most valuable biodiversity for future production improvement.

However, the genetic diversity of a crop is not always static. It is shaped by several factors namely population, environment where it is grown and human management (Oscar, 2004). Hence, one can expect the variation obtained during this study to change continuously over time and thus the present results obtained is probably just a representative of the level of variation in the currently grown bean landraces in the study area (Bukoba and Missenyi districts).

5.2 Yield and Yield Components

High rainfall at the Maruku site during flowering and maturation periods resulted into shedding of flower and poor seed quality respectively. Moreover, extend drought at Byamutemba resulted into poor crop development from early growth to later stages. Rainfall differences among the three sites had a profound influence on environmental variation and ultimately on individual genotype performance.

Genotype x environment interactions were highly significant ($P \leq 0.001$) for plant height, number of pods per plant, number of seeds per pod and grain yield, indicating differential genotypic responses of yield and yield components across environment. Thus, the four traits varied from location to location, implying that selection for these traits has to be done at each location.

This observation also indicates that the relative ranking of genotype differ across locations and this can make evaluation and selection of genotypes more complicated and difficult. Similar results of environmental influences on common bean performance were reported by Bondari (2003), De Ron *et al.* (2004) and Oscar (2004). Genotypes x environment interactions among maize genotypes have also been reported by Ngowi (2002).

Days to 50% flowering varied significantly ($P \leq 0.05$) among genotypes within locations. However, genotype x environment interactions for flowering duration was not significant across locations. This implies that the differences among genotypes for duration to flowering were caused by genotypic differences. These results suggest that duration to flowering is highly heritable, and thus less affected by the environments.

The significant variation among genotypes within location on plant height, pods per plant, and seeds per pod and grain yield was due to genetic differences among the landraces (Harian, 1992).

The variations of genotypes across the locations on these variables could be attributed to a larger extent to differences in available moisture as indicated by amount of rainfall recorded at each location during the experimental period (Appendix 2).

Soil characteristic differences (Appendices 4 – 6) among the locations could have also influenced plant characters such as height of the genotype at each location. Both soil characteristics and available moisture have a great influence on soil nutrient uptake during plant growth, resulting into differential plant height.

Plant heights were significantly reduced in the low rainfall zone (Byamutemba) as compared with the medium (Kyema) and high rainfall (Maruku) zones. According to NDSU (1997) the crop requires moderate amount of water (3 - 6 cm) particularly during early stages of growth and the demand becomes critical at pod filling stage (during and soon after flowering). At this stage, moisture availability should not be less than 60% field capacity.

This situation may have greatly influenced the seed yield obtained at Byamutemba and Maruku sites where there was moisture deficit and too much water stress, respectively. Similar results on the influence of moisture stress on common bean seed yield and yield components were also reported by Szilagyi (2003) and Mwale *et al*. (2008).

There was highly significant ($P \leq 0.001$) genotype x environment interaction for seed yield among the genotypes. The presence of genotype x environment interaction generally altered genotypic ranking for seed yield in different environments (Dixon and Nukenine, 2000). The relative magnitude of the environmental effect was much greater than for the genotypic effect. Seed yield varied from one location to another, indicating that final selection for seed yield has to be done at each location. Similar results in pearl millet hybrids have also been reported by Yahaya *et al.* (2006).

In general, most of the genotypes produced higher seed yield in the medium rainfall (Kyema) than in the other two zones (Fig. 8). Seed yield was lowest in the low rainfall zone (Byamutemba). Thus, Kyema was the most productive site for seed yield implying that the medium rainfall (with average annual rainfall 1200 mm) could probably be the best zone for production of common bean in Bukoba and Missenyi districts. On average the

seed yield was reduced by 52% in high (Maruku) and 81% in low (Byamutemba) rainfall zones as compared to medium (Kyema) rainfall zone.

5.3 Disease Resistance

About 71% and 76% of the 38 bean genotypes (landraces) evaluated at all three sites (Maruku, Kyema and Byamutemba during the short rains season of 2008/09 showed low reaction to bean leaf rust and angular leaf spot respectively (with score rating < 3). These results could imply that probably during the short rains season weather conditions were not favourable for development of diseases and therefore the plants escaped from the diseases. However, some significant variations of disease reaction among genotypes in the three sites suggest possible differences in levels of disease susceptibility regardless of disease pressure (Michael, 2005). For instance, at all the sites, genotypes Kashukari, Kitunutunu, Chumbanoroza and Ruhuku showed high disease rating scores for leaf rust implying that these genotypes could be less resistant to the disease. This also indicates that, these genotypes could be easily susceptible to disease even under low disease pressure in the field (Meronuck *et al.,* 2009).

Genotype Kawanja scored the highest mean for ALS disease (4.1) across the three locations, indicating that this genotype could be probably highly susceptible to angular leaf spot. For both diseases (rust and ALS), genotype x environment interaction for disease reaction was not significant ($P \leq 0.05$), implying that the location had no major influence on the genotype reaction to the diseases.

Similar results on ALS were reported by Michael (2005) in snap beans where several varieties that were included in both the growth room and field trials reacted similarly to *P. griseola* in both environments. This suggests that probably a single location could be

enough for screening bean genotype for both rust and ALS. However, the temperatures (minimum and maximum) across the three experimental sites were more or less the same (Appendix 3) throughout the growing season, could have possibly influenced equal disease reaction across the sites. The average minimum and maximum temperatures were16.5^{0}C and 27^{0}C respectively. However, according to Mandes and Bergamin (2008) temperature and leaf wetness have great influence on infection of bean rust, and because of that it is unlikely to occur at high temperatures (> 25°C) and short leaf wetness periods (< 7 hrs). Nevertheless, further testing of the landraces is needed to determine their reactions to leaf rust and ALS in diverse environmental conditions namely rainfall, temperatures, relative humidity and soils because all these factors have a greater influence on bean growth and disease development (Ngeve *et al.*, 2005; Mandes and Bergamin, 2008).

5.4 Relationship between Traits

Yield is a polygenically controlled complex character because it is determined by a number of character components which are also quantitatively inherited (Ganesamurthy and Seshandri, 2004).

Therefore, the knowledge of the association between yield and its components and among the components themselves is of immense practical value in crop improvement through selection.

5.4.1 Simple correlation

Significant positive correlations were observed for pods per plant and grain yield in all locations implying that pods per plant contribute positively to seed yield regardless of the growing environment. Highly significant correlations revealed from combined analysis between yield and pods per plant and between yield and seed per pod imply that the more

pods and seeds per pod the plant have the more the grain yield is expected. Highly significant positive correlation was also observed between pod per plant and seed per pod indicates that plants with more number of pods tend also to have more number of seeds. Significant negative correlation observed in combine analysis over location for days to 50 % flowering and 100 seed weight which implies that lager seeded bean genotypes take lesser days to attain flowering than the small seeded bean genotypes. Combined analysis revealed that 100 seed weight had significant negative correlation with grain yield. Assady *et al.*, 2005 reported also that days to flowering had highest significance positive correlation with seed yield and 100 seed weight had the significant negative correlation with seed yield.

Highly significant and positive correlation observed between yield and pods per plant and seed per pod implying that these traits had an important role to play in the final grain yield. Similarly the high significant indicated between pods per plant and plant height signifies that plant height is important for increased number of pods per plant which will ultimately contribute to the final grain yield. Previous studies have also reported similar association of yield and yield component in various crops Szilagyi (2003); Ganesamurthy and Seshandri (2004) and Izge *et al.* (2006).

5.4.2 Path coefficient analysis

Simple correlation does not provide the actual contribution of the characters towards the yield. Hence, path coefficient was used to determine the contribution of the traits to the final grain yield. Path coefficient analysis showed pod per pod had the highest contribution to the final grain yield of common beans followed by seed per pod.

From the study results it is expected that the bean genotype which has high number of pods per plant will produce more seed grain and consequently more grain yield. Important indirect contribution was indicated by seed per pod through pods per plant. The remaining traits evaluated had weak direct and indirect effect on grain yield. The direct effect of seed per pods revealed in this study implies that with other traits held constant increasing seeds per pod will significantly increase grain yield.

However, a more stable indirect effect plays a more important part and masks the direct influence (Dewery and Lu, 1959). In addition, the residual (indicated by P_X6 in the path diagram) value was 0.643, indicating that there are other factors which contribute to grain yield which were not included in this model.

Hence, this call for involvement of as many traits as possible in path analysis in order to determine the relative contribution or of different traits for the improvement of grain yields of common beans.

5.5 Estimate of Variance Components

Estimation of variance components is important in deciding the criteria for evaluation and testing procedure in crop improvement. The portioning of variance components gives an estimate of relative importance of different factors involved in determining the phenotypic expression by assessing the influence of environment on heredity.

From this study it was indicated that the estimates of genetic variance (δ^2g) were smaller compared to the corresponding phenotypic variance (δ^2ph) implying that there was an environmental influence in determining phenotypic expression. However, when estimates of genetic variance are high for a particular trait, heritability estimate is also expected to be

high indicating less involvement of environmental influence. High phenotypic variances for the trait (yield and pods per plant in this case) imply that environmental factors played a major role on the phenotypic expression of the trait. The genotypes x location interaction variance (δ^2gl) were higher for yield, seeds per pod, pods per plant and plant heights compared to the corresponding genotypic variances.

These interaction variances explain the differences in performance of genotypes in different environment and their degree as opposed to genetic variance for various traits. High broad sense heritability values were observed in days to 50% flowering, 100 seed weight and plant height. High heritability values for 100 seed weight and plant height in common beans have previously been reported by Szilagyi (2003). Other authors have reported high heritability for grain yield other traits such as 100 seed weight, seeds per pod and pods per plant (Ndiaga, 2001; Ganesamurthy and Seshadri, 2004).

The impact of an environmental factor on different genotypes may vary implying that the productivity of a crop may also vary from one environment to the next (Bondari, 2003). Therefore bean improvement plans may focus on the GE interaction to select the best genotype for a target population of environments.

Absence of genotype x location interaction simplifies the work for multi-location trials to the breeder and allows for blanket recommendation to be made. This means that, a test at one location is enough for recommendation for wider environments. Heritability (h^2) is an approximate measure of the expression of character or trait to the progeny.

Johnson *et al.* (1955) defined expected genetic advance as proportionate change of selected group of population of genetically viable individuals through successive selection cycles

over environments. This means that genetically controlled traits will always attain the expected genetic gain much earlier as compared to traits that are under control of environment. Thus, heritability and genetic advance are important aspects to be considered during selection in breeding programme.

From this study, most of the traits had low heritability (grain yield, seeds per pod and pods per plant) and low genetic advance. Different genetic advance for different traits call for different breeding methods to be used in bean improvement strategies.

The low genetic advance observed in all studied traits of common beans means that in order to make improvement of these traits, several cycles of selection would be necessary and the final selection could be done during late stages.

5.6 Genotypes Yield Stability

A genotype is regarded to be stable when it performs consistently, at high or low yield levels across a wide range of environments (Annichiarico, 2002). Genotype stability across locations and years or seasons is an important aspect that should be considered in crop improvement. Some cultivars are well adapted to a particular environment whereas other cultivars are widely adapted under diverse environmental conditions.

A desirable cultivar is one that does not only yield well in its area of initial selection, but also maintain the high yielding ability over wide range of environments within the area of production (Yahaya *et al.,* 2006). In Elberthart and Russel (1966) model, b (regression coefficient) is considered as parameter of response and S^2d (deviation from regression) as a measure of possibility of cultivar reaction to environments or stability. Regression coefficient equal to a unit and S^2d equal to zero indicate wider stability across

environments. If b > 1 and S^2d= 0 may be suitable for favourable environment and if, b < and S^2d = 0 may be suitable for poor environment.

From the results (Table 12) the S^2d did not differ significantly from zero indicating the stability of these genotypes. This may imply that these genotypes (landraces) have been cultivated in these areas for a long time and through selection farmers have adopted the most adaptable landraces in their environments. High coefficient of determination (R^2) obtained revealed that environmental variation among the evaluated genotypes can be highly predicted by the linear regression model used. The genotypes with b < 1, minimum S^2d from zero and higher mean grain yield. Kamoshi, Rutera abatani, Kitununtunu and Kyaburundi could be suitable in poor environments. These genotypes could be very suitable under small-scale farmers who entirely depend on natural environments with poor soils and unreliable rainfall. On the other hand, genotypes with b >1 and with good yield performance namely Kinyobwa, Kamenyamigo, Roziko, Turaemishako, Kapili and Kasheshe may be grown in favourable environment thus, may be suitable for farmers who can afford better growing environments or in areas with favourable natural conditions (e.g. soil fertility and moisture). Genotypes Canada, Chumbanoloza and Ruhuku had equal or nearly unity, minimum deviation (S^2d) from regression and grain yield above the overall mean indicating wider environmental stability and adaptation. Hence, these genotypes may be suitable across wider environments and may be useful for different farmer categories. Regression coefficient (b) ranged from 0.21 to 2.32 showing that the performance of some genotypes were to stable over locations, implying the need for genotype selection for specific environmental conditions.

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATIONS

6.1 Conclusions

From this study, the following conclusions can be drawn:

(i) High genetic diversity exists among the common bean landraces grown in Bukoba and Missenyi districts. The differences among varieties were greater than between locations, although the results were obtained from relatively small samples of common bean landraces which were tested in few environments in one season. Genotypes varied significantly in plant height, number of pods per plant, seed size, and phonological characteristics.

(ii) Environmental conditions, such as amount of rainfall differences played an important role in phenotypic expression of grain yield and yield components (plant height, pods per plant and seeds per pod) of common bean genotypes evaluated. Plant heights, pod number per plant, number of seed per pod and grain yield were significantly reduced in most of the genotypes in the low rainfall environment at Byamutemba, which suggests that variability for low moisture tolerance in common bean is low. Thus, all the genotypes were more or less equally affected by moisture stress.

(iii) This study has revealed that the medium rainfall was the most productive zone for common beans. However, this could be justified by repeated experiment over several locations and years.

(iv) Genotype x environment interaction for diseases recorded (rust and ALS) was not statistically significant during the short rain season (2008/09). Most of the genotypes evaluated showed low reaction to bean rust and ALS, which suggests for further disease screening study for the two diseases

(v) Combined correlation analysis over locations indicated that pods per plant and seeds per pod were highly correlated with grain yield, implying that these two traits should be considered when breeding for yield increase in common beans.

(vi) Path coefficient analysis revealed that pods per plant had a greater direct contribution toward grain yield of common bean genotypes. This suggests that pods per plant with even moderate heritability should be taken into account during selection for higher grain yields in common beans.

(vii) Genotypes Canada, Chumbanoloza and Ruhuku yielded consistently above the mean across the three locations with b value nearly equal to unit, S^2d minimum and not significantly different from zero may be considered stable and widely adapted under different environments

6.2 Recommendations

(i) There is the need for further studies over more seasons and locations in different agro-ecological zones in order to verify the results obtained in this study.

(ii) An exploratory study should be conducted to collect and characterize more common bean landraces which are presently grown by farmers in Bukoba and Missenyi districts in order to determine the level of bean genetic diversity and its potential for future breeding programmes.

(iii) There is the need in future studies to screen for disease reaction in presence of common bean disease(s) through artificial infection of disease pathogens.

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APPENDICES

Appendix 1: Collection data sheet for bean landraces

Collector's name …….	Name of farmer/donor……..
Date of collection …….	Sample number ….……
Country of collection…….	Amount collected (Seeds or kg)……..
District……	Agro-ecological zone …….
Location :Village ……..	Latitude …….
Nearest town/city……. Km ……..	Longitude of collection site ……
	Altitude of collection site ……
Collection source (farmer, local market)…	Local vernacular name(s) ……
Seed colour ……..	Susceptibility to:
Type of sample (1= pure landraces and, 2=	*Diseases (1=low, 2=.medium 3=high)
mixture landraces)…….	*Pests(1=low, 2=.medium 3=high)
	*Drought (1=low, 2=.medium 3=high)
	* Specify if known
Remarks ……	

Appendix 2: Average annual rainfall and actual monthly rainfall during the experimental period 2008/09 short rain season

Annual/Monthly (mm)	High rainfall zone (Maruku)	Medium Rainfall zone (Kyema)	Low rainfall zone (Byamutemba)
Annual rainfall	1500	1200	800
October 08	148.9	134.9	45.7
November 08	102.5	97.3	102.6
December 08	94.0	95.0	16.2
January 09	233.4	171.9	94.0
February 09	216.1	186.2	83.2

Appendix 3: Monthly temperature at Maruku, Kyema and Byamutemba during experimental period 2008/09 sort rain season

Month	Maximum Temperature(^{0}C)			Minimum Temperature (^{0}C)		
	Maruku	Kyema	Byamutemba	Maruku	Kyema	Byamutemba
October 08	27.6	27.9	28.5	16.5	17.0	16.3
November	27.8	28.1	27.3	15.8	16.3	16.8
December	27.0	27.4	26.9	16.4	16.9	17.1
January 09	27.2	28.3	26.7	16.2	15.8	15.2
February	26.9	27.2	28.6	16.6	16.8	16.6
March	26.7	26.9	26.4	17.2	17.0	16.9
Mean	27.2	27.6	27.4	16.5	16.6	16.5

Appendix 4: Physical and chemical soil characteristics at Maruku site

Parameter		Remarks
Clay (%)	34.0	
Silt (%)	12.0	
Total sand (%)	54.0	
Texture class	Sandy clay loam	
pH (H_2O) 1:2.5	5.5	Strong acidic
Organic C (%)	2.2	Medium
Total N (%)	0.5	Low
CEC NH_4OAc (cmol/kg)	10.4	Low
Available K	0.1	Very low
Available Ca	0.2	Very low
Available Mg	1.1	Medium
Available P (mg /kg)	22.0	High

Appendix 5: Physical and chemical soil characteristics at Kyema site

Parameter		Remarks
Clay (%)	37.0	
Silt (%)	8.0	
Total sand (%)	55.0	
Texture class	**Sandy clay**	
pH (H_2O) 1:2.5	5.8	Medium acidic
Organic C (%)	2.1	Medium
Total N (%)	0.7	Low
CEC NH_4OAc (cmol/kg)	15.1	Medium
Available K	0.2	Low
Available Ca	0.1	Low
Available Mg	1.3	Medium
Available P (mg /kg)	18.6	High

Appendix 6: Physical and chemical soil characteristics at Byamutemba Site

Parameter		Remarks
Clay (%)	42.0	
Silt (%)	28.0	
Total sand (%)	30.0	
Texture class	Sandy Clay	
pH (H_2O) 1:2.5	6.1	Slightly
Organic C (%)	2.3	Medium
Total N (%)	0.2	Low
CEC NH_4OAc (cmol/kg)	16.3	Medium
Available K	1.3	Very high
Available Ca	0.3	Very low

Available Mg	1.0	Low
Available P (mg /kg)	12.6	Medium

Appendix 7: Mean Square from combined analysis of variance for different traits of the evaluated bean genotype at three locations during 2008/short rain season in Bukoba and Missenyi District

Source of Variations	Df	Days to 50% flower	Plant height (cm)	Pod length (cm)	Pods/plant (number)	Seed /pod (number)	100 seed weight (g)	Grain yield (kg/ha)
Environment (E)	2	55.34	1298.23	281.06	961.91	41.85	78.540	28492650.45**
Replication (R/E)	6	6.34	1725.97	21.31	3.35	0.620	26.80**	306149.48
Genotype (G)	37	40.65***	1508.97***	50.78	11.16***	3.23***	488.61***	569704.23**
G x E	74	3.59	396.11***	45.25	6.99**	1.64***	55.654	288162.02***
Error	222	3.36	165.47	42.22	2.01	0.42	13.430	31611.38

Appendix 8: Mean Square for the two diseases' scores (ALS and Bean rust) from combined ANOVA results

Source of Variations	df	Angular leaf spot (ALS)	Bean Leaf rust
Environment (E)	2	0.459	0.430
Replication (R/E)	6	0.240	1.602
Genotype (G)	37	2.038**	10.994**
Genotype x Environment (G x E)	74	0.282	0.316
Error	222	0.534	0.828

Appendix 9: Simple correlations among yield and yield components of 38-bean genotypes/landraces at Maruku site

	1	2	3	4	5	6	7	8
1. Days to 50% flower	1.00							
2. Plant height	-0.01745	1.00						
3. Pods/plant	0.28932	0.245699	1.00					
4. Pod length	-0.24461	0.093652	-0.05351	1.00				
5. Days to 90% maturity	0.336886	0.266701	0.021003	-0.25263	1.00			
6. Seed/pod	0.35329	0.111446	0.332964	0.030459	0.459722	1.00		
7. 100 grain seed wt.	-0.40939	-0.08223	-0.30773	0.54935	-0.58848	-0.4529	1.00	
8. Grain yield	-0.02132	0.183309	0.365697	0.221064	0.055774	0.320857	0.192048	1.00

Appendix 10: Simple correlations among yield and yield components of 38-bean genotypes/landraces at Kyema site

	1	2	3	4	5	6	7	8
1. Days to 50% flower	1.00							
2.Plant height	0.110603	1.00						
3. Pods/plant	0.005882	0.04606	1.00					
4. Pod length	-0.00115	0.087457	0.043799	1.00				
5. Days to 90% maturity	0.385128	0.045266	0.201807	0.09577	1.00			
6. Seed/pod	-0.13081	-0.0583	0.392	-0.0329	-0.08285	1.00		
7. 100 grain seed wt.	-0.43405	-0.05578	0.010789	0.022654	-0.45027	0.128641	100	
8. Grain yield	0.261012	-0.1125	0.498729	0.038882	0.141064	0.281766	0.08594	100

Appendix 11: Simple correlations among yield and yield components of 38-bean genotypes/landraces at Byamutemba site

	1	2	3	4	5	6	7	8
1. Days to 50% flowering	1.00							
2. Plant height	-0.00052	1.00						
3.Number of pods per plant	0.355187	0.217268	1.00					
4.Pod length	0.206174	0.577631	0.102372	1.00				
5.Days to 90% maturity	0.212985	0.530265	0.330576	0.364287	1.00			
6.Numberof seed per pod	0.412991	0.1533237	0.465965	0.209237	0.184054	1.00		
7.100 grain seed wt.	-0.43865	0.131455	-0.42804	0.161117	-14223	-0.38723	1.00	
8.Grain yield	0.361334	0.48644	0.6272	0.467441	0.419544	0.488665	-0.22697	1.00

Appendix 12: Path coefficient analysis

CORRELATION MATRIX TABLE

1.0000	0.0220	0.1350	-0.0100	0.1600	-0.4030	0.1020	LINE 1
0.0220	1.0000	0.2170	0.1100	0.1250	0.0070	0.1550	LINE 2
0.1350	0.2170	1.0000	0.1620	0.5470	-0.1070	0.7410	LINE 3
-0.0100	0.1100	0.1620	1.0000	0.0770	0.0700	0.1770	LINE 4
0.1600	0.1250	0.5470	0.0770	1.0000	-0.1990	0.5020	LINE 5
-0.4050	0.0070	-0.1070	0.0700	0.1990	1.0000	0.0380	LINE 6

Simultaneous equations:

1ST EQUATION COEFFICIENTS

P1= 1 P2= .022 P3= .135 P4=- .01 P5= .16 P6= - .403 Y- 102

2ND EQUATION COEFFICIENTS

P1= .022 P2= 1 P3= .217 P4= .11 P5= .125 P6= .007 Y= .714

3RD EQUATION COEFFICIENTS

P1= .135 P2= .217 P3= 1 P4= .162 P5= .547 P6= - .107 Y= .741

4TH EQUATION COEFFICIENTS

P1= .01 P2= .11 P3= .162 P4= 1 P5= .077 P6= .07 Y= 177

5TH EQUATION COEFFICIENT

P1= .16 P2= .11 P3= .162 P4= .077 P5= 1 P6= .199 Y= .502

6TH EQUATION COEFFICIENTS

P1= -.405 P2= .007 P3= -.107 P4= .07 P5= -.199 P6= 1 Y= .038

.052 .002704 .002704

-.016 ..000256 .00296

.159 .025281 .48917

Solution to the 6 simultaneous Equations

X 1 OR P1 = .052

X 2 OR P2 = .016

X 3 OR P3 = .657

X 4 OR P4 = .049

X 5 OR P5 = 164

X 6 OR P6 = .159

CALCULATED RESIDUAL ‘P’ = .6427822