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Characterization of Indigenous Goats Type using Morphological Characters and Body Measurements in Sinana District, Bale Zone, South East Ethiopia

By Gelana Jeda & Belete Asefa

Maddawalabu University

Abstract- The study was conducted on Characterization of Indigenous Goats Type Using Morphological Characters and Body Measurements in Sinana district, Bale zone, South East Ethiopia, with objectives of on-farm characterization of Indigenous Goats type using linear body measurement and qualitative physical characteristics and investigating the prediction of live weight using body measurement for Indigenous Goats type. For this study, purposive sampling and simple random sampling methods were used for selection of kebeles and experimental goats, respectively. About 120 animals were sampled for body measurements and qualitative characters. Statistical analysis system software was applied for analyzing of data. Goats type in the study area were characterized as red dominant coat color (35.83%), concave head profile (37.5%), no wattle (100%), have no toggles (86.67%), have no ruff (75%), horned (100%) of about (75%) were straight horn shape.

Keywords: *body measurements; morphological characterization; indigenous goats type; sinana district.*

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Characterization of Indigenous Goats Type using Morphological Characters and Body Measurements in Sinana District, Bale Zone, South East Ethiopia

Gelana Jeda ^α & Belete Asefa ^σ

Abstract- The study was conducted on Characterization of Indigenous Goats Type Using Morphological Characters and Body Measurements in Sinana district, Bale zone, South East Ethiopia, with objectives of on-farm characterization of Indigenous Goats type using linear body measurement and qualitative physical characteristics and investigating the prediction of live weight using body measurement for Indigenous Goats type. For this study, purposive sampling and simple random sampling methods were used for selection of kebeles and experimental goats, respectively. About 120 animals were sampled for body measurements and qualitative characters. Statistical analysis system software was applied for analyzing of data. Goats type in the study area were characterized as red dominant coat color (35.83%), concave head profile (37.5%), no wattle (100%), have no toggles (86.67%), have no ruff (75%), horned (100%) of about (75%) were straight horn shape. The strong correlation between body weight and linear body measurement is observed between body weight and chest girth with correlation coefficient of ($r=0.78$). Overall mean of body weight, body length, chest girth, height at wither, rump height, rump length, head length, and ear length were 25 kg, 59.02 cm, 74.99 cm, 61.64 cm, 66.65 cm, 14.72 cm, 11.20 cm 12.72 cm and 25.08 cm, respectively. Body weight of goats were easily estimated from heart girth with equation of $BW = -3.36 + 0.38HG$ as under field condition addition of more variable in the model is not economical.

Keywords: body measurements; morphological characterization; indigenous goats type; sinana district.

1. INTRODUCTION

Ethiopia is endowed with abundant livestock resources of varied and diversified genetic pools with specific adaptations to a wide range of agro-ecologies. Farm animals as a whole are an integral part of the country's agricultural system and are raised both in the highland and lowland areas. Similarly, the habitats of the indigenous goat breeds extend from the arid lowlands (the pastoral and agro-pastoral production system) to the humid highlands (mixed farming systems) covering even the extreme tsetse-infested areas of the country (Workneh, 1992). Goats in Ethiopia

are generally considered associated more with warm and dry areas of the lowlands. However, their broad feeding habits and multipurpose production functions appear to have well served the interests of highland farmers. Utilities of the goat and its products in Ethiopia vary with the traditional farming practices across the agro-ecological zones. But in all cases, goats are raised under low input management and they serve multiple output and input functions (Worknek, 1992; Alemayehu, 1994). The small body size, broad feeding habits, adaptation to unfavorable environmental conditions and their short reproductive cycle provide for goats comparative advantage over cattle and sheep to suit the circumstances of especially the poorer mixed crop-livestock production environments of the highlands. These attributes make it easier to adjust goat flock size to match the available resources, facilitate the integration of livestock production into small scale production systems (low capital, low risk) and enable flexible production (Peters, 1987; Devendra, 1992).

The number of goats in Ethiopia is estimated at 21.71 million. Out of these, about 69 percent are females and 31 percent are males (CSA, 2012). These goat populations are phenotypic ally classified into 11 distinct major breed types or populations and five additional sub-types (Workneh, 1992; Alemayehu, 1993; Nigatu, 1994; FARM-Africa, 1996; IBC, 2004). However, genetic/molecular characterization revealed only the presence of eight distinctively different breed types or populations in the country (Tesfaye, 2004). According to this author, the eight distinct genetic entities include Arsi Bale, Gumuz, Keffa, Woyto-Guji, Abergelle, Afar, highland goats (previously separated as Central and North-West highland) and the goats from the previously known as Hararghe highland, Short-eared Somali and Long-eared Somali).

The report of FARM Africa(1996) shows that the goat breed distributed in the Bale zone is Arsi Bale goat breed. Again the report of Belete (2013) shows that Somali goat breed is distributed in lowlands of bale zone including Madda Walabu, Sawena and Rayitu districts. The previous characterization done so far in bale zone does not cover all parts of bale zone,

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particularly in the study area. Again there is a probability of mixing up of goats type with surrounding area. Thus, characterization of the breed is required for improving the productivity of the breed, to limit the existing constraints and for the conservation of indigenous animal genetic resources.

Breed characterization has been recognized as the first approach to the sustainable use of animal genetic resource (Lanari *et al.*, 2003). Characterization of local genetic resources depends on the knowledge of the variation of morphological traits, which have played a very fundamental role in classification of live stock based on size and shape (Ferra *et al.*, 2010; Agga *et al.*, 2010; Leng *et al.*, 2010). The most common measure of animal performance is live weight which provides reliable and informative measure for selection, feeding requirements, health management, and decision on selling price (Thiruvankanden, 2005). Larger sized animals usually produce more meat than smaller animals (ESGPI, 2009).

Measurements of various body conformations are of value in judging quantitative characteristics of meat and are helpful in developing suitable selection criteria. Moreover, the relative ease in measuring linear dimensions they can be used as an indirect way to estimate live weight (Tesfaye, 2008). Prediction of body measurements in sheep remains very important for avoiding the errors of visual determination of animal weights in areas where weighing balance cannot be assessed (Halima *et al.*, 2012). In general, the information obtained in this study will be useful for designing appropriate breeding and selection schemes for indigenous Goats improvement and sustainable conservation. Therefore, the present study was conducted with the following objectives:

- To make on-farm Phenotypic characterization of Indigenous Goats type using linear body measurement and qualitative physical characteristics in Sinana District

II. MATERIAL AND METHODS

a) Selection of the Study Site

A rapid field survey was conducted by the researcher in study district to locate appropriate sites for on farm phenotypic characterization of goats. Three Kebele from the district was selected purposively, based on the goat's population potential. For body linear measurements and qualitative characters a total of 120 animals, 40 animals per Kebeles was measured. Goats were classified based on sex and age. Each class of goats were sampled from one household once to incorporate diversity of goats in the sample. Sampling was continued until measurement of 120 mature goats have been obtained.

b) Qualitative traits data collection

Visual observation was made and morphological features will be recorded based on breed morphological characteristics descriptor list of FAO (2011) for phenotypic characterization of goat. Each animal was identified by its sex, dentition and sampling site. Dentition record was included, as this was the only reliable means to estimate the approximate age of an animal.

c) Quantitative trait data collection

Morph metric measurements were made on the quantitative traits of breed using measuring tape. The measurements were made on animals that will be classified based on sex and age group. Animal's age classification was made using dentition technique supplemented with owner's information. The linear body measurement was made using plastic tape, while body weight of animals was measured using suspended spring or Slater weighing scale having 50 kg capacity with 0.2 kg precision.

d) Data Analysis

Quantitative and qualitative data generated from field survey and on farm linear body measurement was recorded on Microsoft excel spread sheet and analyzed using statistical analysis system (SAS 2008). Simple descriptive statistics was compile the observed categorical variables and chi-square test was used to test independence of the categorical variables separately for both male and female.

For adult animals, sex and age group of the goats was fitted as independent variables while body weight and linear body measurement was fitted as dependent variables. A general linear model procedure (PROC GLM) of the Statistical Analysis System (SAS 9.2, 2008) was used for quantitative variables to detect statistical differences among sample goat's populations. Least square means with their corresponding standard errors was calculated for each body trait over sex, dentition. When analysis of variance declared significant difference, least square means has been separated using Tukey-Kramer test. The model employed for analyses of body weight and other linear body measurements was:

$$Y_{ijk} = \mu + A_i + D_j + e_{ijk}$$

Where:

Y_{ijk} = the observed k (body weight or linear body measurements) in the i^{th} age group and j^{th} Sex,

μ = Overall mean,

A_i = the effect of i^{th} age group ($i = 1PPI, 2PPI, 3PPI$ and $4PPI$),

D_j = the effect of j^{th} Sex ($j=1$ (Female) and 2 (male))

e_{ijk} = random residual error.

Correlations of live body weight with different body measurement under consideration was computed for each sex using Pearson correlation coefficient.

Stepwise regression procedure of SAS (2008) was used to regress body weight for both male and female within each age group using PROC REG procedure of SAS in order to determine the best-fitted regression equation for the prediction of live body weight. Best fitting models was selected based on coefficient of determination (R^2), mean square error, the mallows C parameters C (p). The following models was be used for the estimation of body weight from LBMs.

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_n X_n + e_j$$

Where:

y = the response variable (live body weight)

β_0 = the intercept

X_1, \dots, X_n are the explanatory variables (chest girth, body length, height at wither and rump height)

β_1, \dots, β_n are regression coefficients of the variables X_1, \dots, X_n

e_j = random error

III. RESULT AND DISCUSSIONS

a) Qualitative traits of goats

Qualitative trait of study area are summarized in table 4,1. Out of the total sampled goat population in the study area (120 goats) 48.3 plain 35 spotted and 16.67 were patchy coat color. In the study area the dominant coat color types were red (35.83%), black (19.19%), black plus red (19.16%), red plus white (17.5%), and black plus white (8.34%). The sample population has concave and convex head profile (37.5%), and flat (25%) and 100% of the population has no wattle. Majority of goats in the study area have no toggles (86.67%). About 75% goats in the study area have ruff which is common for both male and female goats. 100% of goats have horns and had straight (75%) and curved (25%) shape. Regarding horn orientation: backward (83.33%), (8.33%) up ward and lateral (8.34%). The most dominant ear form were lateral (64.17%) flowed by down ward (19.17%) and erect (16.99%) were observed in goat population. The hair type dominated in the study area were smooth (54.16%) flowed by curl (45.84%).

Table 1 : qualitative traits of goats in the study area

Character	Attribute	female		Male		Over all
		N	%	N	%	N(%)
Coat color pattern	plain	43	35.83	15	12.5	58(48.33)
	spotted	32	26.67	10	8.33	42(35)
	patched	15	12.5	5	4.17	20(16.67)
	X square					0.05
Coat color type	black	17	14.17	6	5.00	23(19.16)
	Red	31	25.83	12	10.00	43(35.83)
	Black and white	8	6.67	2	1.67	10(8.33)
	Black and red	19	15.83	4	3.33	23(19.16)
	Red and white	15	12.5	6	5.00	21(17.5)
	X square					1.19
Horn shape	Straight	75	62.5	15	12.5	90(75)
	Curved	25	20.83	5	4.17	30(25)
	Spiral	0	0	0	0	0(0)
	X square					0.00
Horn orientation	Back ward	75	62.5	25	20.83	100(83.33)
	Up ward	7	5.83	3	2.50	10(8.33)
	Lateral	8	6.67	2	1.67	10(8.33)
	X square					0.27
Ear form	Lateral	57	47.50	20	16.67	77(64.16)
	Down ward	17	14.17	6	5.00	23(19.16)
	Erect	16	13.33	4	3.33	20(16.66)
	X square					0.32
Ruff	Present	73	60.83	17	14.67	90(75)
	Absent	26	21.67	4	3.33	30(25)
	X square					1.35
Toggle	Present	12	10	4	3.33	16(13.33)
	Absent	78	65	26	21.67	104(86.67)
	X square					0.00
hair type	Smooth	46	38.33	19	15.83	65(54.16)
	Curl	44	36.67	11	9.17	55(45.83)
	X square					1.35

head profile	Flat	22	18.33	8	6.67	30(25)
	Concave	34	28.33	11	9.17	45(37.5)
	Convex	34	28.33	11	9.17	45(37.5)
	X square					



Figure 1 : Typical goats type in the study area

b) Correlation between Body Weight and Linear Body Measurements

The Pearson coefficient of correlation among various body measurements of goats in the study area are presented in the following table. The correlation of body weight with that of LBM ranges from weak to moderate correlation for both male and female (Table 2). The strong correlation between body weight and linear body measurement is observed between body weight and chest girth with correlation coefficient of ($r=0.78$). The finding was in line with the finding of Halima *et al.* (2012) where there were high correlation between body weight and chest girth ($r=0.89$) and body weight and body length ($r=0.73$) for west Amhara region goat population and Belete *et al.* (2013) for bale zone goat population of got types the correlation between body weight and chest girth ($r=0.75$). The strong correlation between body weight and chest girth indicates that body weight was easily estimated from chest girth. This was in agreement with the finding of (Adeyinka and Mohammed, 2006). However, the accuracy of prediction was improved when other significant and positive correlation was added in multiple regression analysis.

The correlation coefficient between body measurement and body weight were positive and

significant for all traits under consideration in the study area. In this finding chest girth and wither height have high correlation with body weight. This was in agreement with the report of Mahilet (2012) for Hararghae high land goats, Grum (2010) for short-eared Somali goat. Similarly, the report of Halima *et al.* (2012) indicates that there were higher association between body weight and chest girth ($r=0.89$) and between body weight and body length ($r=0.73$).

The positive correlation between body weight and linear body measurements indicates that an increase in any one of the body measurement would result in a corresponding increase in live body weight. Further, the accuracy of prediction was ameliorated when traits are combined in multiple regressions. The strong relationship existing between body weight and body measurement suggests that either or the combination of these morphological traits could be used to estimate live weight in goats fairly well in the situation where weighbridge or scales are not available. The association may also be useful as selection criteria since positive correlation of traits suggest that the traits may be under the same genetic influences.

Table 2 : Correlation coefficient between body weight and other linear body measurement of goat in study area

	HG	WH	BL	BW	HL	HRL	EL	RL	RH
HG		0.35*	0.64*	0.78*	0.65*	0.15*	0.11*	0.26*	0.20*
WH	0.35*		0.59*	0.72*	0.72*	0.01*	0.11*	0.28*	0.04*
BL	0.64*	0.59*		0.56*	0.67*	0.31*	0.02*	0.50*	0.09*
BW	0.78*	0.72*	0.56*		0.42*	0.11*	0.21*	0.24*	0.34*
HL	0.65*	0.72*	0.67*	0.42*		-0.03ns	-0.06ns	0.36*	0.03*
HRL	0.15*	0.01 ns	0.31*	0.11*	-0.03ns		0.15*	0.17*	0.08*
EL	0.11*	0.11*	0.02ns	0.21*	-0.06ns	0.07ns		0.60*	0.10*
RL	0.26*	0.28*	0.50*	0.24*	0.360*	0.18*	0.60*		0.09*
RH	0.20*	0.04ns	0.09*	0.34*	0.03ns	0.01ns	0.10*	0.09*	

c) Live Body Weight and Linear Measurements

Least square mean and standard error for sex and age effect on body weight and linear body measurements are presented in (Table 3). In this study area females have higher body weight and other linear body measurements ($p < 0.05$) than males counterpart. The present finding was in contrast with the report of Aladeet *et al.* (2008); Sowande *et al.* (2009); Samakulaet *et al.* (2010); and Okbeku *et al.* (2011) where female have higher body weight and other body measurements than male counterpart. On the other hand the finding is in agreement with the report of Alemayehuet *et al.* (2012) for Abergelle goat and Adeyinke (2006) where males have higher body weight than female counterpart. The difference in live body weight between male and female across different age classes indicates that these parameters are sex and age dependent. Increase in live body weight and other linear body measurements with advance age were in line with the report of (Otoikhian *et al.*, 2008). In the study area location, sex and age differences were apparent for various body measurements. The finding was in agreement with the report of (Belete *et al.*, 2013; Grum, 2010; Halima *et al.*, 2012; Mahilet, 2012).

The average value for body weight and other linear body measurement obtained from this study was comparable with other literatures. In the study area overall mean of body weight, body length, chest girth, height at wither, rump height, rump length, head length, and ear length were 25 kg, 59.02 cm, 74.99 cm, 61.64 cm, 66.65 cm, 14.72 cm, 11.20 cm 12.72 cm and 25.08 cm, respectively. The present finding for body weight of goat is lower than that of Belete *et al.* (2013) for goat types in bale zone (29.52kg).

Age effect: Age differences were obvious for most of linear body measurements ($p < 0.05$). The linear body measurements increased as animal advances with age (1PPI to 4PPI). This was in consonance with the report of (Otoikhian *et al.*, 2008). All body measurements were increased as age group increase from 1PPI to 4PPI.

Sex effect: The result revealed that sex is an important source of variation for live body weight and linear body measurements at all age groups. In the study area female have higher body weight than male ($p < 0.05$). Most of linear body measurements were not significant ($p > 0.05$) between sexes except body weight, body length and height at withers.

Table 3 : Least square mean of quantitative traits of goats in study area (Mean \pm SE)

		BW(Mean \pm SE)	BL(Mean \pm SE)	WH(Mean \pm SE)	HG(Mean \pm SE)	HL(Mean \pm SE)
Over all		25 \pm 3.6	59.0 \pm 7.2	61.1 \pm 3.8	74.9 \pm 7.3	11.2 \pm 1.6
CV		13.41	12.35	7.56	9.35	16.77
R square		0.13	0.04	0.04	0.13	0.002
SEX	*		ns	*	*	Ns
FEMAL		24.4 \pm 0.35b	58.1 \pm 0.7a	61.7 \pm 0.4b	73.4 \pm 0.7a	11.16 \pm 0.2a
MALE		27.5 \pm 0.78a	61.73 \pm 0.4a	59.36 \pm 0.8a	79.56 \pm 1.29b	11.33 \pm 0.3a
AGE	Ns		*	*	*	*
1PPI		24.13 \pm 0.78 ^a	58.68 \pm 0.68 ^{ab}	62.86 \pm 0.98 ^a	72.36 \pm 1.5 ^b	10.63 \pm 0.34 ^b
2PPI		25.51 \pm .46 ^a	59.73 \pm 0.9 ^a	62.95 \pm 0.45 ^a	76.85 \pm 0.9 ^a	12.13 \pm 0.2 ^a
3PPI		25.11 \pm 0.8 ^a	54.56 \pm 1.7 ^b	55.72 \pm 0.9 ^c	72.72 \pm 1.7 ^b	10.05 \pm 0.38 ^b
4PPI		25.57 \pm 0.8 ^a	61.36 \pm 1.6 ^a	58.47 \pm 0.8 ^b	74.21 \pm 1.5 ^{ab}	10.00 \pm 0.37 ^b
		HRL	EL	RL	RH	
OVER ALL MEAN		1.3 \pm 0.4	12.7 \pm 0.8	14.3 \pm 1.1	66.6 \pm 5.3	
CV		28.03	6.98	8.2	8.1	
R SQUARE		0.0004	0.07	0.03	0.004	
SEX	ns		ns	Ns	Ns	
MALE		1.34 \pm 0.04a	12.59 \pm 0.09a	14.19 \pm 0.12a	66.44 \pm 0.57a	
FEMALE		1.33 \pm 0.6a	13.13 \pm 0.16a	14.67 \pm 0.21a	67.23 \pm 0.98a	
AGE	ns		*	*	*	
1PPI		1.3 \pm 0.07 ^a	12.9 \pm 0.18 ^{ab}	14.2 \pm 0.2 ^a	68.1 \pm 1.14 ^a	
2PPI		1.3 \pm 0.04 ^a	12.93 \pm 0.1 ^a	14.6 \pm 0.14 ^a	66.68 \pm 0.68 ^{ab}	
3PPI		1.2 \pm 0.08 ^a	12.11 \pm 0.2 ^c	13.2 \pm 0.25 ^b	64.55 \pm 1.3 ^b	
4PPI		1.36 \pm 0.08 ^a	12.42 \pm 0.2 ^{bc}	14.62 \pm 0.14 ^a	66.8 \pm 1.2 ^{ab}	

d) Regression Analysis

Multiple linear regression models for predicting the body weight of goats from linear body measurements were presented in (Tables 4). It indicates that the trend of increment in R^2 value as the number of variable increase. R^2 is widely used to determine how well regression fits as the coefficient of determination. All

body measurements were fitted into the model and through elimination procedures, the optimum model was identified. Chest girth, rump height and ear length were the best fitted model for goats in the study area.

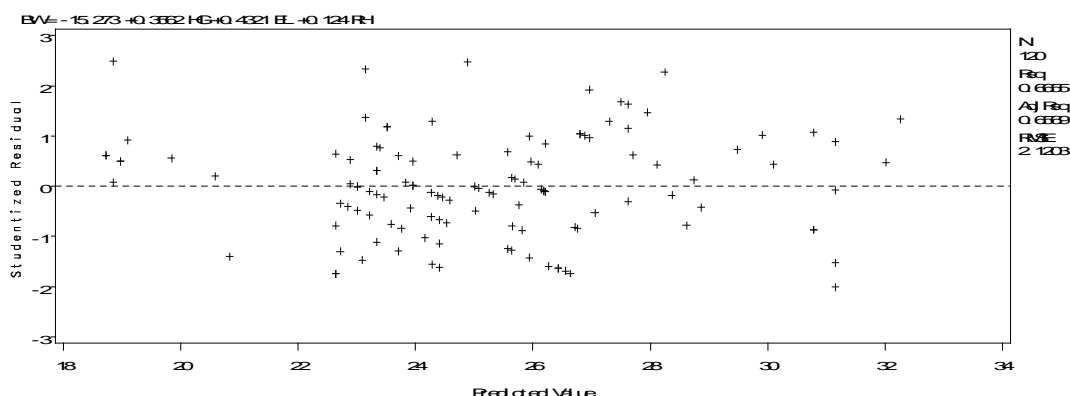
Chest girth was more reliable in predicting body weight than other linear body measurements. The better association of body weight with chest girth was possibly

due to relatively larger contribution to body weight of chest girth, which consists of bones, muscles and viscera(Thiruvankadan,2005). Using many body measurements to predict the live weight is not handy in goat breeding, the less body parameters used, the easiest result obtained (Pesman and Yardmic, 2008). The result of stepwise regression analysis indicates that other measurement to the chest girth would result

in significance improvement in accuracy of prediction in overall assessment even though the extra gain was small, which was in agreement with the report of (Afolayan *et al.*, 2006). Under field condition addition of more variable in the model is not economical. Therefore, under this study body weight of goat is easily estimated from heart girth with equation of $BW = -3.36 + 0.38HG$.

Table 4 : Multiple linear regression analysis of live body weight on different LBMs of goats in the study area

Model	I	B1	B2	B3	R square	CP
CG	-3.36	0.38	-	-	0.618	33.84
CG+RH	-10.608	0.36	0.13	-	0.65	21.66
CG+RH+EL	-15.27	0.36	0.43	0.14	0.66	19.08



V. CONCLUSION

Goats in the study area have some distinct physical character and other linear body measurements. Most of the measured body measurements of the goats were lowered as compared by different author with respect to comparable sex and age groups. This may be due to poor management aspect of goats in the study area. Phenotypic characterization of indigenous goats types in their existing production system is the prerequisite before making some breed improvement programs. The present study will put some base line information regarding goat type and their characteristics.

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Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits in Bread Wheat (*Triticum Aestivum* L.) Genotypes

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Abstract- Sixty four wheat genotypes were tested in 8x8 simple lattice design at Ginchi, West Shewa in 2012/13 cropping season. The overall objective was to study the extent of genetic variability, heritability and genetic advance. Analysis of variance revealed that there was a significant difference among the sixty four genotypes for all the characters studied. The phenotypic coefficients of variation (PCV) values were higher than genotypic coefficients of variation (GCV) values for all the traits studied. Medium phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were recorded for plant height, number of kernels per spike, thousand kernels weight, grain yield per plot, biomass yield per plot and harvest index. Medium phenotypic coefficients of variation (PCV) and low genotypic coefficients of variation (GCV) values were displayed for days to heading.

Keywords: PCV, GCV, heritability, genetic advance.

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Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits in Bread Wheat (*Triticum Aestivum* L.) Genotypes

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Abstract- Sixty four wheat genotypes were tested in 8x8 simple lattice design at Ginchi, West Shewa in 2012/13 cropping season. The overall objective was to study the extent of genetic variability, heritability and genetic advance. Analysis of variance revealed that there was a significant difference among the sixty four genotypes for all the characters studied. The phenotypic coefficients of variation (PCV) values were higher than genotypic coefficients of variation (GCV) values for all the traits studied. Medium phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were recorded for plant height, number of kernels per spike, thousand kernels weight, grain yield per plot, biomass yield per plot and harvest index. Medium phenotypic coefficients of variation (PCV) and low genotypic coefficients of variation (GCV) values were displayed for days to heading. Low phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) values were recorded for days to maturity, spike length, number of spikelets per spike and hectoliter weight (test weight), which suggests the limitation of selection for these traits. High heritability values were observed in all the characters studied. The expected genetic advance as a percent of mean ranged from 7.4 to 25.93 %. Characters with a high genetic advance as a percent of mean allow the improvement of this character through selection.

Keywords: PCV, GCV, heritability, genetic advance.

I. INTRODUCTION

Bread wheat (*Triticum aestivum* L. em Thell. 2n=6x=42), a self-pollinating annual plant in the true grass family *Gramineae* (*Poaceae*), is largest cereal crop extensively grown as staple food sources in the world (Mollasadeghi *et al.*, 2012). It is one of the most important export and strategic cereal crop in the world and in Ethiopia in terms of production and utilization (Ranjana and Kumar, 2013). It has been described as the 'King of cereals' because of the largest hectare it occupies, high productivity and the observable position it holds in the international food

grain trade (Shashikala, 2006). The Food and Agriculture Organization of the United Nations (FAO) gracefully project the worldwide acclaim sticking with wheat as human food and the International Maize and Wheat Improvement Center (CMMYT) have chosen a wheat spike symbol in their logo with the description "Let there be bread." It is a major source of energy, protein and dietary fiber in human nutrition (Rizwana *et al.*, 2010).

In Ethiopia, wheat is grown at an altitude ranging from 1500 to 3000 meters above sea level, between 6-16° N latitude and 35-42° E longitude. The most suitable agro- ecological zones, however, fall between 1900 and 2700 masl (Tefera, 2012). The major wheat producing areas in Ethiopia are located in Oromiya (Arsi, Bale, Shewa, Ilubabor, and Western Hareghe), in SNNPR (Hadiya, Sidamo, Silite, Guraghe, Kambata), Tigray, Amhara (Northern Gondar and Gojam zones) (Zerihun *et al.*, 2012). Wheat is the third most important small cereal crops in Ethiopia in terms of cultivated land, food value and number of smallholders engaged in production after Tef (*Eragrostis tef* L.) and Maize (*Zea mays* L.).

For a successful breeding program, the presence of genetic variability plays a vital role. It is true that the more diverse plants, the greater chance of exploiting high heterotic crosses or to generate productive recombinants and broad variability in segregating generations during genetic improvement (Mohammadi and Prasanna, 2003; Verma *et al.*, 2013). Rauf *et al.* (2012) stated that precise knowledge about germplasm diversity and genetic relationship among breeding materials is a pre-requisite for crop improvement programs as it helps in the development of superior recombinants. Genetic diversity is essential to meet the diversified goals of plant breeding such as breeding for increasing yield, wider adaptation, desirable quality, pest and disease resistance (Ferdous *et al.*, 2011).

Genetic divergence analysis estimates the extent of diversity existed among selected genotypes (Mondal, 2001). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Hailegiorgis *et al.*, 2011).

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To make an effective selection for grain yield, understanding the genetic variability, heritability and genetic advance as percent of mean as well as the association of grain yield with yield contributing characters is important. In addition, to evolve superior genotype for further hybridization and selection it is important to get precise information on the nature and degree of genetic diversity present in wheat collections from principal areas of cultivation. Existence of genetic diversity is very essential to meet the present and future crop breeding challenges. It is a prerequisite for the development of improved cultivars with wider adaptability and broad genetic base (Hailu, 2011). Currently, large numbers of bread wheat accessions were introduced from CIMMYT through bread wheat improvement program of Ethiopian Agricultural Research Institute (EIAR). So far, little or no information is generated about genetic variability, divergence and character associations between yield and yield contributing characters in these exotic bread wheat genotypes in Ethiopia. Hence, the present study was undertaken with the objectives of to estimate the extent of variability, heritability and genetic advance.

II. MATERIALS AND METHODS

a) Description of the study area

The experiment was conducted at Ginchi, West Shewa in 2012/13 cropping season. Ginchi Agricultural

Research Sub Center is located at an altitude of 2240 meters above sea level, 84 kilometers (kms) to the West of Addis Ababa, and at a Latitude and Longitude of 09°03'N and 38°15'E, respectively. It is the center where the cereal crops like Teff, barley and wheat are grown. The maximum and minimum temperatures of the area are 24.72°C and 8.76°C, respectively, whereas the mean annual rainfall is 1080.4mm. The major soil types are black (Vertisol) and clay loam with pH of 6.4, which is heavy clay with 0.91-1.32% organic matter (HARC, Soil Analysis and Plant Physiology Team, 2012).

b) Experimental Materials

A total of sixty four bread wheat (*Triticum aestivum L.*) genotypes that include three standard checks and sixty one exotic bread wheat accessions introduced from CIMMYT were included in this study. The accessions were obtained kindly from HARC. The three released cultivars Digelu, Alidoro and Meraro were used as a standard checks. They were selected based on their agronomic performances and suitability to the growing conditions (Table 1).

The details of the genotypes used in the experiment are given in Table 2.

Table 1 : List of genotypes used in the study

Entry	PedigreeSeed source	Entry	Pedigree	Seed source
1	CIMMYTOB/2	CIMMYT 33	CIMMYTOB/65	CIMMYT
2	CIMMYTOB/7	CIMMYT 34	CIMMYTOB/66	CIMMYT
3	CIMMYTOB/14	CIMMYT 35	CIMMYTOB/67	CIMMYT
4	CIMMYTOB/22	CIMMYT 36	CIMMYTOB/68	CIMMYT
5	CIMMYTOB/23	CIMMYT 37	CIMMYTOB/70	CIMMYT
6	CIMMYTOB/24	CIMMYT 38	CIMMYTOB/71	CIMMYT
7	CIMMYTOB/25	CIMMYT 39	CIMMYTOB/75	CIMMYT
8	CIMMYTOB/27	CIMMYT 40	CIMMYTOB/76	CIMMYT
9	CIMMYTOB/29	CIMMYT 41	CIMMYTOB/77	CIMMYT
10	CIMMYTOB/32	CIMMYT 42	CIMMYTOB/78	CIMMYT
11	CIMMYTOB/33	CIMMYT 43	CIMMYTOB/79	CIMMYT
12	CIMMYTOB/35	CIMMYT 44	CIMMYTOB/80	CIMMYT
13	CIMMYTOB/39	CIMMYT 45	CIMMYTADT/1	CIMMYT
14	CIMMYTOB/40	CIMMYT 46	CIMMYTADT/2	CIMMYT
15	CIMMYTOB/41	CIMMYT 47	CIMMYTADT/3	CIMMYT
16	CIMMYTOB/44	CIMMYT 48	CIMMYTADT/4	CIMMYT
17	CIMMYTOB/45	CIMMYT 49	CIMMYTADT/5	CIMMYT
18	CIMMYTOB/48	CIMMYT 50	CIMMYTADT/6	CIMMYT
19	CIMMYTOB/49	CIMMYT 51	CIMMYTADT/7	CIMMYT
20	CIMMYTOB/50	CIMMYT 52	CIMMYTADT/8	CIMMYT
21	CIMMYTOB/51	CIMMYT 53	CIMMYTADT/9	CIMMYT
22	CIMMYTOB/52	CIMMYT 54	CIMMYTADT/11	CIMMYT
23	CIMMYTOB/53	CIMMYT 55	CIMMYTADT/13	CIMMYT
24	CIMMYTOB/54	CIMMYT 56	CIMMYTADT/15	CIMMYT
25	CIMMYTOB/57	CIMMYT 57	CIMMYTADT/16	CIMMYT
26	CIMMYTOB/58	CIMMYT 58	CIMMYTADT/17	CIMMYT
27	CIMMYTOB/59	CIMMYT 59	CIMMYTADT/19	CIMMYT
28	CIMMYTOB/60	CIMMYT 60	CIMMYTADT/20	CIMMYT
29	CIMMYTOB/61	CIMMYT 61	CIMMYTADT/21	CIMMYT
30	CIMMYTOB/62	CIMMYT 62	ALIDORO	HARC
31	CIMMYTOB/63	CIMMYT 63	MERARO	KARC
32	CIMMYTOB/64	CIMMYT 64	DIGELU	KARC

c) *Experimental Design and Trial Management*

The experiment was carried out in 8x8 Simple Lattice Design at random. The genotypes were grown under uniform rain fed conditions. The plot size was six rows of 2.5 m length with 0.2 m row spacing i.e. 1.2 m x 2.5 m = 3m² (standard plot size for variety trial). Planting was done by hand drilling on July 06, 2012. Seed rate was 150 kg/ha (45g/plot). Recommended fertilizer rate of 100/100 kg/ha N/P₂O₅ in the forms of Urea and DAP was applied to each plot in the shallow furrow depths and mixed with soil at the same time during sowing. For data collection, the middle four rows were used (2m² area). The central four rows were harvested for grain yield and biomass yield from each plot leaving boarder rows to avoid boarder effects. All other agronomic practices were undertaken uniformly to the entire plot as recommended for wheat production in the area during the growing season to raise a healthy crop.

d) *Description of Data Collected*

The data on the following attributes was collected on the basis of the central four rows in each plot per replication.

Days to 50% heading (DH): The numbers of days from sowing to 50% of plants have started heading.

Days to 75% maturity (DM): The numbers of days from date of sowing to a stage at which 75% of the plants have reached physiological maturity or 75% of the spikes on the plots turned golden yellow color.

Grain filling period: The grain filling period in days was computed by subtracting the number of days to heading from the number of days to maturity.

Thousand Kernels weight (TKW): The weight (g) of 1000 kernels from randomly sampled seeds per plot measured by using sensitive balance. It was the weight (gm) of 1000 kernel estimated by counting 1000 seeds randomly drawn from the grain yield of each plot.

Grain yield per plot (GYP): The grain yield per plot was measured in grams using sensitive balance after moisture of the seed is adjusted to 12.5%. Total dry weight of grains harvested from the middle four rows out of six rows was taken as grain yield per plot and expressed as grams per plot.

Biomass yield per plot (BMYP): It was recorded by weighing the total above ground yield harvested from the four central rows of each experimental plot at the time of harvest.

Harvest index (%): It was estimated by dividing grain yield per plot to biological yield per plot. It is ratio of grain yield to the above ground biomass yield.

Hectoliter weight (HLW): It is grain weight of one hectoliter volume random sample of wheat grain for each experimental plot expressed by (kg/ha).

Plant height (cm): The average height (cm) of ten randomly taken plants at the maturity time from the

middle four rows of each plot of the replication was measured from the ground level to the top of the spike excluding the awn.

Number of productive tillers per plant: The numbers of tillers per plant bearing productive heads were counted at the time of harvest and average was recorded for the ten randomly taken plants from the middle four rows.

Spike length (cm): The average spike length of ten randomly taken plants from the base of the main spike to the top of the last spikelet excluding awns was recorded in centimeter from four central rows of each plot.

Number of spikelets per spike: Total numbers of spikelets on main spike of all ten plants from four central rows were counted at the time of maturity and average was recorded.

Number of kernels per spike (NKPS): Total number of grains in the main spike were counted at the time of harvest from ten randomly taken plants and expressed as average and recorded from four central rows of each plot.

e) *Statistical Analysis*

i. *Analysis of variance (ANOVA)*

The data collected for each quantitative trait were subjected to analysis of variance (ANOVA) for simple lattice design. Analysis of variance was done using Proc lattice and Proc GLM procedures of SAS version 9.2, (SAS Institute, 2008) after testing the ANOVA assumptions.

The Mathematical Model for Simple Lattice Design is:

$$Y_{ijr} = \mu + A_r + G_{ij} + B_{ir} + B_{jr} + e_{ijr},$$

where Y_{ijr} = the value observed for the plot in the r^{th} replication containing the genotype G_{ij} , μ = grand mean, G_{ij} = genotype effect in the i^{th} row & j^{th} column, A_r = replication effect, B_{ir} = i^{th} block effect, B_{jr} = j^{th} block effect, e_{ijr} = the plot residual effect*

ii. *Analysis of genetic parameters*

a. *Estimation of phenotypic and genotypic coefficient of variation*

The phenotypic and genotypic variances and coefficients of variation were estimated according to the method suggested by (Singh and Chaudhary, 1999) as follows:

Environmental variance (σ^2_e)

$$\sigma^2_e = MSe$$

Genotypic variance (σ^2_g)

$$\sigma^2_g = \frac{MSg - MSe}{r}$$

Where, r = number replication, MSg = mean square due to accessions and MSe = mean square of error (Environmental variance).
Phenotypic variance (σ^2p)

$$\sigma^2P = \sigma^2g + \sigma^2e$$

Where, σ^2g = genotypic variance and σ^2e = mean square of error (Environmental variance).
Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2P}}{\bar{X}} * 100$$

Where, σ^2P = phenotypic variance and \bar{X} = mean of the character being evaluated.
Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2g}}{\bar{X}} * 100$$

Where, σ^2g = genotypic variance and \bar{X} = mean of the character.

iii. Heritability (in the broad sense)

Heritability in the broad sense for quantitative characters was computed using the formula suggested by (Allard, 1999) as:

$$H = \frac{\sigma^2g}{\sigma^2P} \times 100$$

Where, H = heritability in the broad sense, σ^2g = genotypic variance and σ^2P = phenotypic variance.

iv. Genetic advance expected (GA)

The genetic advance expected under selection assuming selection intensity of the superior 5% of the plants was estimated in accordance with the methods illustrated by (Allard, 1999):

$$GA = K * \sigma_p * H$$

Where, GA = expected genetic advance, H = heritability in the broad sense, K = the selection differential and σ_p = is phenotypic standard deviation on mean basis.

The Genetic advance as % of mean (GAM) was computed as:

$$GAM = \frac{GA}{\bar{X}} * 100$$

Where, GAM = genetic advance as percent of mean, GA = genetic advance under selection and \bar{X} = mean of the population in which selection was employed.

III. RESULTS AND DISCUSSION

a) Analysis of variance (ANOVA)

Mean squares of the 13 characters from analysis of variance (ANOVA) are presented in (Table 2).

Highly significant differences among genotypes ($P < 0.01$) were observed for seven characters (days to heading, number of productive tillers per plant, spike length, number of spikelets per spike, 1000 kernel weight, grain yield plot⁻¹ and hectoliter weight or test weight), significant at ($p < 0.05$) for the rest six characters; namely, days to 75% maturity, grain filling period, plant height, number of kernels spike⁻¹, biomass yield and harvest index. This result indicating that there is variability among the genotypes studied and would respond positively to selection.

Several researchers reported significant differences among wheat genotypes studied. Shashikala (2006) reported significant differences among 169 genotypes for 11 morphological traits such as days to 50% heading, days to 75% maturity, plant height, spike length, peduncle length, number of tillers per m², number of spikelets per spike, 1000 grain weight, protein content and grain yield per plot. Similarly, works of Kumar *et al.* (2009) and Monpara (2011) showed that significant differences among 30 genotypes of bread wheat for 8 quantitative characters and among 21 genotypes of bread wheat for 11 quantitative characters respectively. Kalimullah *et al.* (2012) reported that grains per spike, number of tillers per plant, 1000 grain weight, spike density and grain yield per plant showed highly significant differences between forty one bread wheat genotypes were studied. Thus, it indicated that there was sufficient variability in the material used for their study, which provides ample scope for selecting superior and desired genotypes by the plant breeders for further improvement.

b) Range and mean values

Range and mean values for the 13 characters is presented in Table 3.. The mean grain yield ranged from 500 to 1182 gram per plot. 43.75% of the genotypes gave above the grand mean. Phenological characters, days to 50% heading and days to maturity ranged from 53 (CIMMYTADT/3) to 82 CIMMYTOB/27) and 111 (CIMMYTOB/50, CIMMYTADT/2 CIMMYTADT/3) to 131(CIMMYTOB/27), respectively. Grain filling period is an important trait in wheat that ultimately affects the overall grain yield by increasing grain weight. It ranged from 43 (CIMMYTOB/39) to 72(CIMMYTADT/17) with a mean value of 56.27 days, which is slightly higher than our commercial varieties Alidoro, Meraro and Digelu 51, 52 and 55 days respectively. A significant number of lines (90.625%) took 50-72 days to fill the grains.

Table 2 : Analysis of variance (Mean squares) for the 13 characters of 64 bread wheat genotypes grown at Ginchi (2012/13)

Characters	Replication (df=1)	Genotype (df=63)	Intra Block Error (df=49)	CV (%)	Efficiency Relative to RCBD
Days to 50% heading (days)	8.51	86.99**	9.22	10.62	107.38
Days to 75% maturity (days)	2.53	37.75*	5.42	4.04	100.49
Grain filling period (days)	13.78	47.30*	5.58	10.16	100.72
Plant height (cm)	29.5488	248.40*	22.48	11.94	101.24
Number of productive tillers per plant	0.0183	0.68**	0.1563	10.58	105.37
Spike length (cm)	0.71252	1.0870**	0.1043	8.84	109.36
Number of spikelets per spike	3.30	2.5444**	0.2479	6.87	102.31
Number of kernels per spike	25.9200	50.4459*	8.8261	16.20	111.15
1000 kernels weight (g)	0.131328	43.2103**	3.722	12.628	103.52
Biomass yield per plot (g)	22578	160197*	9604	19.50	115.26
Harvest index (%)	18.9036	37.2436*	6.1859	18.09	103.12
Hectoliter weight (kg/hL)	6.7070	18.4252**	3.4176	13.75	116.27
Grain yield per plot(g)	1287.78	22864**	4066	2.07	120.90

df=Degrees of freedom

*=significant at 5% probability level and **=highly significant at 1% probability level

CV= Coefficient of Variation, RCBD=Randomized Complete Block Design

The mean plant height was 97.51cm with a range of 79.5 cm (CIMMYTOB/32) to 129 cm (CIMMYTOB/35). Number of productive tillers plant⁻¹ showed a wide variation, which ranged from 4.8 (CIMMYTADT/13) to 8.63 (CIMMYTOB/33) and mean value for this trait was 6.19. A range of 6.85 cm (CIMMYTOB/40) to 11.2 cm (the standard check, ALIDORO) with the mean value of 8.73 cm was observed for spike length. Number of spikelets spike⁻¹ ranged from 14.8 (CIMMYTADT/3) to 21 (one of the standard check, ALIDORO) with the mean value of 17.38. Number of kernels per spike ranged from 23 (CIMMYTOB/80) to 52 (CIMMYTADT/17) with a mean of 38.38.

The average 1000-kernel weight was 38.46g and it ranged from 28.3 g (CIMMYTOB/7) to 49g (CIMMYTOB/70). Genotypes CIMMYTOB/22 and CIMMYTOB/25 were yielding as low as 500 g/plot to as high as 1182 g/plot respectively, with over all mean of 742 grams plot⁻¹. The range for biological yield varied between 1100 grams plot⁻¹ for genotype CIMMYTOB/54 to 3500 grams plot⁻¹ for CIMMYTOB/25 among the 64 genotypes studied with over all mean of 2056 grams plot⁻¹. A wide range was observed for this character with the minimum value being 25% and the highest 58% in respect of genotype CIMMYTADT/6 and CIMMYTOB/54, respectively. The mean harvest index was noted to be 36%.

The average hectoliter weight was 80.06 kg/hL and it ranged from 76.10 kg/hL (CIMMYTOB/7) to 83.1 kg/ha (DIGELU, one of the three standard checks). Generally, the range of variation was wide for all the characters studied. Similarly, Radhu *et al.* (1995) observed high range of variation for yield, 1000-kernel weight, plant height and days to flowering, Maqbool *et*

al. (2010) reported wide range of variation for plant height, grain filling period, number of spikeletes per spike, biological yield per plot, grain yield and 1000-kernel weight. Moreover, Sajjad *et al* (2011) reported large variation for grain yield, 1000 kernels weight and number of kernels per spike. From the result it was obtained that those characters with the higher range of values were also had higher mean values and vice versa. Such considerable range of variations provided a good opportunity for yield improvement. Thus, high variability for thirteen traits in 64 bread wheat genotypes used for this study implied that there was reasonably sufficient variability, which provides ample scope for selecting superior and desired genotypes by the plant breeders for further improvement.

c) Variability components and coefficients of variation

Estimates of phenotypic variance (σ^2_p), genotypic variance (σ^2_g), phenotypic (PCV) and genotypic coefficients of variation (GCV) are given in Table 3. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged from 3.8% (days to maturity) to

Table 3 : Table 3 Estimate of ranges, mean, phenotypic (σ^2_p) and genotypic (σ^2_g) component of variances, broad sense heritability and genetic advance as percent of mean for 13 characters of bread wheat genotypes tested at Ginchi (2012/13)

Character	Mean	Range		σ^2_p	σ^2_g	PCV (%)	GCV (%)	H^2_{BS} (%)	GA (k =2.063)	GAM (k=2.063)
		Min.	Max.							
DH	65.55	53	82	48.1	38.90	10.6	9.50	81.00	11.60	17.70
DM	122.2	111	131	21.58	16.20	3.8	3.30	75.10	9.06	7.40
GFP	56.27	43	72	26.44	20.90	9.14	8.10	79.05	8.40	14.90
PH	97.51	79.5	129	135.6	112.96	11.94	10.90	83.30	20.01	20.52
NTPP	6.19	4.8	8.63	0.43	0.264	10.64	8.30	61.40	0.83	13.4
SL	8.73	6.85	11.2	0.596	0.497	8.84	8.10	83.34	1.33	15.20
NSPS	17.38	14.8	21	1.40	1.20	6.81	6.30	85.72	2.64	15.20
NKPS	38.38	23	52	29.6	18.31	14.18	11.15	62.00	6.95	18.13
TKW	38.46	28.3	49	23.5	19.75	12.60	11.56	84.04	8.40	21.90
GY	742	500	1182	13465	9399	15.64	13.07	69.80	167.00	22.52
BMV	2056	1100	3500	84900	75297	14.17	13.35	88.70	533.00	25.93
HI	36	25	58	21.71	15.53	12.95	10.95	71.53	6.88	19.11
HLW	80.06	76.1	83.1	10.92	7.51	4.3	3.43	68.77	4.69	5.86

σ^2_p =Phenotypic variation, σ^2_g =Genotypic variation, PCV=Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation, H^2_{BS} = Broad sense heritability, GA=genetic advance, and GAM=Genetic advance as percent of mean

15.64% (grain yield plot⁻¹) and 3.3% (days to maturity) to 13.35% (biomass yield plot⁻¹), respectively. Generally, the PCV values were higher than GCV values for all the traits studied that reflect the influence of environment on the expression of all the traits. The maximum phenotypic variance value of 84900 grams plot⁻¹ was noted for the trait biomass yield and 13465 grams plot⁻¹ for grain yield. Similarly, the genotypic variances for these characters were also high indicating that the genotype could be reflected by the phenotype and the effectiveness of selection based on the phenotypic performance for these characters.

Deshmukh *et al.* (1986) classified PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above) values. Based on this delineation, characters which showed moderate phenotypic and genotypic coefficients of variation were plant height, number of kernels per spike, thousand kernels weight, grain yield, biomass yield and harvest index. This indicated that selection may be effective based on these characters and their phenotypic expression would be good indication of the genotypic potential. Days to 50% heading and number of productive tillers per plant were found to be medium for PCV while low for GCV. The rest of the characters grouped under low phenotypic and genotypic coefficients of variation, indicating less scope of selection as they were under the influence of environment. The result obtained was in accordance with the findings Shashikala (2006) reported for 1000 kernels weight and grain yield per plot, Kalim *et al.* (2011) and Wani *et al.* (2011) for yield/plant, 1000 grains weight, number of kernels per spike in bread wheat. Monpara (2011) obtained moderate PCV with low GCV for grain filling period in 21 bread wheat genotypes. Ali

et al. (2012) reported moderate PCV and GCV for grain yield per plot in 20 bread wheat genotypes. Degewione *et al.* (2013) reported moderate PCV and GCV for 1000 grain weight, plant height and days to heading in twenty six bread wheat genotypes.

d) Heritability and genetic advance

Although the genotypic coefficient of variation revealed the extent of genetic variability present in the genotypes for various traits, it does not provide full scope to assess the variation that is heritable. The genotypic coefficient of variation along with heritability estimates provide reliable estimates of the amount of genetic advance to be expected through phenotypic selection (Burton, 1952). Heritability (H^2_{BS}), genetic advance (GA) and genetic advance as percent of mean (GAM) estimates for characters under study are indicated in Table 3. Robinson *et al.* (1949) classified heritability values as high (>60%), moderate (30-60%) and values less than 30% low. Accordingly, the results of the present study indicated that high heritability values were observed in all the characters studied. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. Rahim *et al.* (2010) noticed higher heritability value for plant height, days to 50 per cent flowering, number of productive tillers per meter length, grain yield per plot, and number of grains per spike. Further, Salem *et al.* (2008), Ali *et al.* (2008) and Khan *et al.* (2010) recorded high heritability estimates for grain yield, number of kernels per main spike, plant height and thousand kernel weights and number of tillers per plant.

The expected genetic advance expressed as a percentage of the mean by selecting the top 5% (high grain yield) of the bread wheat advanced genotypes, ranged from 5.86% for hectoliter weight to 25.93% for biomass yield plot⁻¹ (Table 3), indicating that selecting the top 5% of the base population could result in an advance of 5.86 to 25.93 percent over the respective population mean. Falconer and Mackay (1996) classified genetic advance as percent of mean as low (0-10%), moderate (10-20%) and high (20% and above). Genetic advance as percentage of mean was maximum for biomass yield plot⁻¹ (25.93%) followed by grain yield plot⁻¹ (22.52%), thousand kernels weight (21.90%) and plant height. Similarly, genetic advance was maximum for biomass yield plot⁻¹ (533grams), followed by grain yield plot⁻¹ (167grams) and plant height (20.01cm). Degewione *et al.* (2013) obtained similar results in twenty six bread wheat genotypes. Johnson and Hernandez (1980) reported that high heritability and high genetic advance as percentage of mean provide better information than each parameter alone. High heritability and genetic advance as percent of mean were found in biomass yield, plant height, thousand kernels weight and grain yield plot⁻¹; indicated that these characters could be useful basis of selection.

Genetic advance as percentage of mean was maximum for biomass yield plot⁻¹ (25.93%) followed by grain yield plot⁻¹ (22.52%) and thousand kernels weight (21.90%). Similarly, genetic advance was maximum for biomass yield plot⁻¹ (533grams), followed by grain yield plot⁻¹ (167grams) and plant height (20.01cm). Accordingly, days to heading, grain filling period, number of productive tillers per plant, spike length, number of spikelets per spike, number of kernels per spike and harvest index showed moderate genetic advance as percent of mean; whereas days to maturity and hectoliter weight showed low genetic advance as percent of mean.

Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson *et al.*, 1955). The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1999).

High heritability associated with high genetic advance were observed for plant height (83.3%, 20.52%), 1000 grain weight (84.04%, 21.9%), grain yield per plot (69.8%, 22.52%) and biomass yield per plot (88.7%, 25.93%), respectively. These are simply inherited traits indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. The results are in accordance with reports of earlier work done by

Munir *et al* (2007) reported high heritability with high genetic advance for plant height and number of spikelets per spike and Kalimullah *et al.* (2012) was reported similar findings for plant height, biomass yield per plot and 1000 grain weight, which supports the present results.

In general, traits such as plant height, thousand kernels weight, grain yield per plot and biomass yield per plot had high heritability and high genetic advance as percent of the mean. Selection based on these characters will result in the improvement of the performance of the genotypes for the traits.

IV. CONCLUSION

This study generally indicated that there was genetic variability among the genotypes. Thus, there is enormous opportunity in the improvement bread wheat genotypes. Therefore, the information generated from this study needs to be used by breeders who are interested in different traits. However, the present result is only an indication and we cannot reach a definite conclusion. Therefore, since the experiment was carried out at one location in one season, it is advisable to continue with this study over several years and locations.

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Review on: Effect of using Recombinant Bovine Somatotropin(rbST) Hormone on Dairy Cattle Production

By Dereje Shibru

Gambella University

Summary- Recombinant bovine somatotropin(rbST) administration to dairy cows increases milk production and improves the efficiency of milk synthesis, though management factors have been identified as major source of variation in dairy cows responses. Milk nutrient density is unaffected by rbST supplementation and no significant differences in milk composition between cows treated and not treated. The magnitude of reproductive responses of dairy cows to rbST is variable where there exists an increase in days to first estrus and twinning rates, increases days-open and services per conception.

The use of rBST may have significant welfare consequences since unnaturally high milk yield production exist. This is reflected in different forms, among these, challenge of maintaining body condition of cows treated with rBST at the end of lactation, relative risk of mastitis due to increased milk yield and an increased incidence of lameness in cows. Reproductive problems in dairy cows have become very common as consequence of using rBST's, resulting with large numbers of cows being culled.

Keywords: *rbST, milk yield, reproductive, animal and human welfare, environment.*

GJSFR-D Classification : FOR Code: 860299



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rBST is biologically inactive in humans and its residues in food products have no physiological effect, but its injection to cow results in an increase in quantities of IGF-I and becomes one of the leading suspects involved in the development and spread of cancers. There is also suspect of increased human risk for development of anti microbial resistance in exposure to milk antibiotic residues from the use of rbST caused mastitis. This could be managed by practices in use by the dairy industry.

The use of rbST reduces the resource used and environmental impact per unit of milk production. That is why increased animal performance is suggested as one of the most effective mitigation strategies to decrease greenhouse gas (GHG) and ammonia (NH₃) emissions from livestock production per unit of product produced.

Keywords: rbST, milk yield, reproductive, animal and human welfare, environment.

I. INTRODUCTION

Bovine Somatotropin(BST) is a natural peptide hormone produced in pituitary gland of cows. It is produced in small quantities and used in regulating metabolic processes. Circulating concentrations of BST are positively correlated with the level of milk production (EFSA, 2015). In the early stages

of a calf's development, it acts as a growth hormone and has a great impact on mammary gland development and subsequent milk-producing capacity in dairy heifers (Soliman and EL-Barody, 2013). During lactation, it serves to mobilize body fat to use for energy and diverts feed energy more toward milk production than for tissue synthesis. The reason of using BST is its potential to increase the efficiency of milk production. Potentially 10- 25% (AHI, 1987) more milk and 10-15% increase in feed efficiency can be from each cow with a cost of implementation of less than 5%. It was discovered in the 1920 and originally called bovine growth hormone (BGH). Experiments in the 1930s revealed that its extraction from the pituitary gland of one cow and injection into another cow, could increase milk production in the recipient cow. In the late 1970s, Dale Bauman, an animal scientist successfully transferred the gene responsible for BGH production in cows to a bacterium. The resulting product was called recombinant bovine growth hormone (rBGH), to avoid the stigma associated with hormones, the industry agreed to change its name to bovine somatotropin (BST). Thus, its synthetic analog would be called recombinant bovine somatotropin (rBST). Simple multiplication of the bacterium meant that it could easily be produced in commercial quantities at a very reasonable cost. Though several pharmaceutical and non pharmaceutical companies became very interested in the product production, monsanto was the first firm to receive approval of FDA to release its products (<http://www.agecon.ucdavis.edu/Faculty/Bees/Butler.html>). Monsanto licensed Genentech's patent (Keith, 1990) and marketed their products as "Posilac"(Dohoo *et al.*, 2003). Though rBST is used to increase milk yield, it also associates animal health and welfare concerns related with increased production. Therefore, the objective of this paper is:-

- To review the effect of rBST on productive and reproductive performance of dairy cows
- To assess the effect of rBST on animal health and welfare concerns of dairy cows .
- To review the effect of rBST on environment and human health concerns.

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II. SOURCES OF BST/BGH AND ITS BIOTECHNOLOGY PRODUCTION

Recombinant-DNA technology has allowed for the commercial production of rbST which is biologically equivalent to natural pituitary-derived bST and has the same amino acid sequence plus one extra amino acid (the essential amino acid methionine) at one end. The genes responsible for production of BST in bovine tissue cells cause the pituitary cells to produce the biological product BST. These genes were isolated and inserted in to specific bacteria as part of a plasmid, with gene splicing. As these altered bacteria replicate, the new genes are also replicated and passed along to all new bacteria (Crooker, 1993). The presence of these genes causes the bacterial cell to become a little "manufacturing plant" which produces BST in large quantities. Eventually the bacterial cells are killed and removed, leaving the purified BST.

III. HOW DOES RBST WORK AND WHEN IS IT USED

In lactating dairy cows, somatotropin is a major regulator of milk production. In biological terms it is referred to as a homoerotic control and acts to coordinate metabolism, thereby allowing more nutrients to be used for milk production. This coordination involves most organs and tissues in the body and includes the metabolism of all nutrients. The bST can act directly on tissues or act indirectly by causing the release of IGF-I (Chase *et al.*, 1998). Indeed, IGF-I levels were increased during rbST administration to lactating cows (Molento *et al.*, 2002). The biological effects of IGF-I are further regulated by specific IGF-binding protein that control access of IGF-I to target tissues and by the abundance of the type-I IGF receptor at the target tissues (McGuire *et al.*, 1992). In this respect, Vanderkool *et al.* (1995) showed that rbST similarly increased serum concentrations of somatotropin in cows and they also increased serum IGF-I, liver IGF-I mRNA and serum IGF-binding protein-3, but serum IGF-binding protein-2, number of free binding sites for IGF-I in mammary tissues were decreased. The supplemented rbST working in conjunction with the animal's naturally circulating somatotropin results in an increase in milk production in dairy cattle (Bauman, 1999). Rapidity of onset and cessation of the increased milk yield response suggested that activity rather than number of secretory cells was affected by exogenous bST (Gluckman and Brier, 1987). Total RNA is an index of cell metabolic activity (Butler and Cohn, 2013). Binelli *et al.* (1995) showed that the total RNA, RNA concentrations, RNA accumulation and the RNA to DNA ratio increased in the mammary tissues of cows treated with rbST. Increased metabolic activity of mammary tissue, which is likely

effected via bST-mediated insulin-like growth factor-I (IGF-I) could promote local production of vasodilators, which, in turn, would result in an increased percentage of cardiac output perfusing the mammary gland (Davis and Collier, 1985). This increase in mammary blood flow would contribute to a partitioning of nutrients to the mammary gland (Pee1 and Bamnan, 1987) and to an increase in milk component synthesis and secretion, because many key enzymes, notably lactose synthetase, inherently operate below their respective maximum velocity (OKronfeld, 1982). Therefore, mammary cell activity can be increased by exogenous bST, further increases in milk yield requires increase and retention of cell numbers (Tucker, 1987). Involvement of bST, directly or indirectly via growth factors, is likely in regulation of mammary secretory cell proliferation and maintenance (Forsyth, 1989; McFadden *et al.*, 1990 and Politis, *et al.*, 1990). In its administration cows produce more milk and utilize nutrients more efficiently. The net effect is commonly referred to as an improvement in "productive efficiency". Productive efficiency is highest for a dairy producer's best cow and indeed, genetically superior cows make more somatotropin and have greater production efficiency.

The period of rbST supplementation is done in synchrony with a cow's natural lactation cycle. A cow's peak milk yield occurs about eight weeks after the calf is born and thereafter daily milk production gradually declines through the remainder of the lactation cycle. Also small response was found when lactating animals are injected rbST in early lactation prior to peak yield. In addition, bST increases milk yield by 10% when administered in early to mid-lactation and by 40% in late lactation (Bauman and Vernon, 1993). Finding in Thailand, reported that, bST increased lactation performance by 22% during early lactation (Chaiyabutr *et al.*, 2009). Hence, the use of rbST is initiated during the 9th or 10th week of lactation and continues until the end of lactation. From a producer prospective the use of rbST makes all cows more like the best cows in the herd. Milk responses have been observed in all cows regardless of genetic merit and for all breeds of dairy cattle.

IV. EFFECT OF RBST ON PRODUCTIVE PERFORMANCE OF COWS

a) Milk yield of cows treated with rbST

Use of rbST treatments has increased milk production in all dairy breeds examined, including Bos indicus cows (Phipps *et al.*, 1991). Though management factors have been identified as major source of variation in the magnitude of dairy cows responses to rbST (Bauman, 1992). These factors include dosage of rbST, injection interval and genetic potential and environmental conditions. According to Phillips (1996) cows that are better managed are known to have a

greater response to rbST than poorly managed. In addition to management factors bovine somatotropin (bST) is a major regulator of milk production through coordinating the metabolism of body tissues to use more nutrients for milk synthesis (Etherton and Bauman, 1998). Indeed, a characteristic of healthy, high producing cows is a greater pituitary secretion of somatotropin (Burton *et al.*, 1994). In addition to the innate production of somatotropin, for lactating dairy cows, the optimal dose of rbST administration as a galactopoietics agent is between 25 and 50 mg/day (Downer *et al.*, 1993; Phillips, 1996). Similar study by Bauman (1992) reported that the production response increases with increasing dose of BST up to a maximum response at 30-40 mg/day. Given an adequate dosage, increasing the milk yield in response to rbST was maintained by following the rbST administration in daily and every 7, 14 or 28 days (Zinn *et al.*, 1993; Chalupa *et al.*, 1996). Low doses of rbST (10.2 mg/day) in the transition period resulted in higher postpartum body weight, quicker recovery of body condition during lactation and significantly more milk during treatment (Gulay *et al.*, 2003). The magnitude of milk yield response to rbST were reported to be increased by 7, 19, 21 and 24% with 5, 10, 15 and 20 mg/day (West *et al.*, 1990); 7 and 9% with 10.3 and 25 mg/14 days (Zhao *et al.*, 1992); 9, 14 and 12% with 11.4, 22.8 and 22.9/28 days (Laurent *et al.*, 1992) 0, 12 and 25% with 7.1, 14.3 and 21.4 mg/7 days (Zinn *et al.*, 1993), 18% with 250 mg/14 days (Ocampo *et al.*, 1995), 12.2 and 20.0% with 250 and 500 mg/14 days (Abdel-Rahman *et al.*, 2010) and 22% with 500 mg/14 days (Thammacharoen *et al.*, 2011). Although, rbST daily injection may produce better response (Bauman, 1992), administration of sustained release formulations of rbST are more practical (Fernandez *et al.*, 1995). However, the increase in milk yield with sustained-release formulations of rbST within a single injection interval will vary (Zinn *et al.*, 1993). That is, following each injection, the milk yield will increase to a peak, approximately at the mid-point of the injection interval and then decline until the next injection (Phillips, 1996).

Bauman *et al.* (1999) reported that rbST administration to dairy cows increases milk production and improves the efficiency of milk synthesis. In agreement with this Chilliard (1988a,b) also reported that rbST use significantly increases milk yield in dairy cattle. Its supplementation prolongs an increased level of milk production and is, therefore, a management tool for dairy producers that makes all cows produce milk more like the farmer's most efficient cow does (NRC, 1994; Etherton and Bauman, 1998). According to Phipps *et al.* (1991) report rbST administration significantly increased milk yield in Jersey (+2.9 kg per day), Friesian (+ 3.6 kg per day) and Holstein (+ 2.7 kg per day) cows. Moallem *et al.* (2000) finding strengthen similarly that daily milk yield (DMY) was significantly

increased by bST of two different doses of treatment. The commercial preparation in use in the USA is a slow release formulation in which 500 mg are administered every 2 weeks. Similarly administration of rbST increase milk yield in cows, buffaloes and goats (Helal and Lasheen, 2008 as cited by Prasad and Singh, 2010). According to Etherton and Bauman, (1998) in dairy cattle, an increased milk yield after rbST administration is found in all parity dairy cows; however the magnitude of the increase in milk production differs to be due to stage of lactation. Opposing this Abdelrahman *et al.* (2010) reported that primiparous cows showed tiny increases with either 250 and 500 mg, because of not having a well-developed udder, whereas multiparous cows showed significant increases especially cows received 500mg of bST.

b) Milk composition of cows treated with rbST

Milk nutrient density is unaffected by rbST supplementation, thus the quantity of milk required to produce 500,000 t of Cheddar cheese was unchanged compared with that required from populations without rbST supplementation (Barbano *et al.*, 1988). There are no significant differences in milk composition from cows treated with BST and from cows which were not treated as finding of different study summarized in Table 1 showed. All cows produce BST and all milk contains BST. According to Collier and Bauman (2014) and Campose *et al.* (2001) use of rbST has no significant effect on the micro and macro composition of milk. Flavor of the milk is also not affected. Similar studies by Vicini *et al.* (2008) and O'Donnell *et al.* (2010) reported that comparison of retail milks found no meaningful differences in composition of milks labeled as rbST-free or organic (unlabeled). Consumers are not able to pick out the milk from cows treated with BST as compared to milk from control cows. Moreover, the manufacturing qualities of milk are not influenced by rbST, including cheese-making properties such as yield, composition and sensory characteristics of resulting cheeses.

Natural variations occur between cows, but these cannot be related to which treatment the cow received. Phipps *et al.* (1991) reported that milk composition in *Bos indicus* and its crossbreds was unaffected by the administration of bST. Factors such as genetics, diet, breed of cow, age, stage of lactation, environment, season and milking practices such as milking interval and frequency of milking cause the variability observed in milk quality and composition; however, these factors would have equal effects in rbST supplemented and non-supplemented cows (NRC, 1994 and Bauman, 1992). Contrary to this, results was reported that there was increase for milk fat, somatic cell counts, IGF1 levels and decrease for milk protein percentage was reported (Chilliard *et al.*, 1998; Baer *et al.*, 1989 and Kindstedt *et al.*, 1991).

Table 1 : Comparing milk yield and Composition of cows untreated and treated with rbST

Species	Group treatment	Milk yield (L/day)	Protein (%)	Fat (%)	Lactose (%)	References
Cattle	Control	23.5	3.65	4.29	9.00	Kim and Kim, 2012
	rbST	27.7	3.30	3.84	8.89	
Cattle	Control	20.7	3.16	3.50	4.51	Campos <i>et al.</i> , 2001
	rbST	22.6	3.16	3.52	4.49	
Cattle	Control	15.6	3.27	3.67	–	Macrina, Tozer and Kensinger, 2011
	rbST	17.9	3.28	3.65	–	
cattle	Control	41.9	2.86	3.65	–	Rivera <i>et al.</i> , 2010
	rbST	45.4	2.81	3.30	–	
cattle	Control	36.1	2.90	3.82	–	Liboni <i>et al.</i> , 2008
	rbST	37.6	2.83	3.78	–	
cattle	Control	12.9	3.45	3.94	4.90	Chaiyabutr <i>et al.</i> , 2007, 2008
	rbST	14.6	3.51	4.24	4.62	

NOTES: rBST = recombinant Bovine somatotrophin, – not reported

V. EFFECT ON REPRODUCTIVE PERFORMANCE

As the Phillips (1996) result indicated, the magnitude of reproductive responses of dairy cows to rbST is variable. High doses of rbST treatment (20.6 mg/day) decreased conception rates, increased days open by 28-30%, days to first estrus and twinning rates

and there was a trend for increased services per conception (Burton *et al.*, 1990). In addition, increases in days open were observed in cows in which rbST treatment was initiated early in lactation, but not when treatment started at mid or late lactation (McGuffey *et al.*, 1991).

Table 2 : Reproductive performance of primiparous & multiparous cows given 250 & 500 mg

Parameter	Primi parous			Multi parous		
	Control	250mg	500mg	Control	250mg	500mg
Days-open (month)	3±0.43	3.5±0.41	3.2±0.32	2.8±0.42	4.4±0.5	4.8±0.52
Conception rate (%)	60	80	90	50	60	80

Abdel-Rahman *et al.*, 2010

According to Abdel-Rahman *et al.* (2010) results effect of administration of bST (250 and 500 mg) on some parameters related to breeding and conception revealed that, the days-open of treated cows have no significant changes in between primiparous group, but there were apparent increase in average days open in multiparous cows (Table 2). Concerning conception rate (%), it revealed an increase in cows given both 250 and 500 mg bST in both groups than control cows. Although rbST increased days-open in multiparous cows, (possibly due to increased milk production), it simultaneously improved conception rate(%). Flores *et al.* (2008) reported that rbST increased growth hormone (GH) in beef cattle and hypothesized that rbST would alter other metabolic hormones and might influence ovarian follicles in postpartum. Meantime, somatotropin treatment increased concentrations of IGF-I in postpartum cows and is at least partly responsible for the increase in diameter of the largest follicle in anestrus post partum cow. Bell *et al.* (2008) results were in agreement with this conclusion. While Silvia *et al.* (2002) reported that rbST had no effect on reproductive performances, which agrees with results of different studies found no differences in days open, services per conception and days to first estrus at 500 mg/14 day (Weller *et al.*, 1990; Pell *et al.*, 1992) or at 56-

700 mg/14 day (Downer *et al.*, 1993). On the contrary, Dohoo *et al.* (2003) mentioned that bST altered the reproductive performance of treated cows. Similar finding by Flores *et al.* (2007) reported that rbST at 500 mg/14 day in Brahman cows increased the first-service conception rate during the first 30 days of breeding and pregnancy rates during the first 3 days of breeding.

VI. EFFECTS OF RECOMBINANT BOVINE SOMATOTROPIN ON ANIMAL HEALTH AND WELFARE

The use of rBST may have significant welfare consequences since unnaturally high milk yields are associated with poorer body condition and increased rates of mastitis, lameness, and reproductive problems (SCAHAW, 1999).

a) Diminished Body Condition

Body Condition (BC) is a term used to describe a cow's energy reserves, which, when excessively depleted, can have welfare implications (SCAHAW, 1999). According to Grandin (2001) the indiscriminant use of recombinant bovine somatotropin and genetic selection for increased milk production are the two reasons for body condition scores of dairy cows decline.

Similar review by an expert panel of Canadian Veterinary Medical Association (CVMA) on the use of rBST reported that using the nutritional management programs that are common on the majority of commercial dairy herds, it would be a challenge to maintain body condition in cows treated with rBST," despite the fact that there is very good nutritional management (CVMA, 1998). Most research papers showed poorer body condition in cows treated with BST mostly at the end of lactation than the control animals. The difference between BC of treated and control animals varied between 0.2 and 0.5 points (Wells, 1995; Chilliard, 1988; Phipps, 1990). Similarly Studer (1998) suggests that high producing cows which are thin, and whose body condition score declines by 0.5 to 1.0 during lactation, often experience anoestrus. On the other hand, rBST treated cows might have an increased voluntary feed intake starting 4-6 weeks after the onset of the treatment (Oldenbroek and Gansen, 1990). Contrary to the BC of cows, the body weight of rBST treated animal has been recorded as approximately 40 kg higher than control animals at the end of the lactation. However, body composition changed and this effect may be largely due to an increase in body water (Oldenbroek, 1990; Wells, 1995; Chilliard, 1991)

b) Mastitis

Mastitis is an inflammation of the mammary gland, characterized by increased somatic cell counts (SCC) in the milk and by pathological change in the mammary tissue. The disease is usually caused by pathogenic micro-organisms entering the gland through the teat duct. Many different bacteria cause mastitis, some being considered as specific udder pathogens, others being merely opportunistic organisms that cause disease when there is an increased susceptibility of the udder for some reason. Among the common bacteria causing clinical mastitis are *Staphylococcus aureus*, *Streptococcus* spp., *E. coli*, as well as other pathogens (Bramley, 1992; Wilesmith *et al.*, 1986). Major factors affecting the incidence of mastitis are related to environmental conditions and management practices (Hogan and Smith, 2012). There is also a small increase in mastitis incidence, expressed on a per cow basis, as milk production increases and the FDA reported that the use of rbST was also associated with an increase in the relative risk of mastitis. Similar finding was also reported by Soliman and EL-Barody (2013) that the incidence of mastitis in rbST-treated cows is due more to increased milk yield than to any direct effects of rbST. Similarly meta-analyses by Dohoo *et al.* (2003) reported that nearly 25% increase in the risk of clinical mastitis resulted due to rBST using.

Research trials prior to registration of rbST for commercial use indicated that there may be a slight increase in somatic cell count (SCC) with its use, which can be a reflection of milk quality or mammary health

status (FDA, Veterinary Medicine Advisory Committee, 1993).

Milk somatic cell count (SCC) is a measure of milk quality and a reflection of mammary health. Macrophages is one type of Leukocytes mostly predominant somatic cell found in the milk of healthy cows, but neutrophils, lymphocytes and epithelial cells are also present (van Schaik *et al.*, 2002). Somatic cells from an infected quarter of the udder, predominately contains much greater number of neutrophils, macrophages and lymphocytes present in milk (van Schaik *et al.*, 2002). Therefore, SCC values provide insight related to milk quality and subclinical mastitis. To ensure high-quality dairy products, Bulk tank somatic cell count (BTSCC) is monitored in milk shipments using standards outlined in the U.S. Pasteurized Milk Ordinance (APHIS Veterinary Service, Centers for Epidemiology and Animal Health, 2011). The legal maximum BTSCC for Grade A milk shipments is 750,000 cells/mL. Maximum allowable BTSCC for other countries include 400,000 cells/mL in the European Union, Australia, New Zealand, and Canada and a maximum BTSCC of 1,000,000 cells/mL for Brazil (Norman *et al.*, 2011). The overall pattern of the average SCC in U.S milk supply has declined steadily since 2001. More recent data indicate a continued decline of BTSCC averaged 224,000 cells/mL in 2010 and 206,000 cells/mL in 2011 (Norman *et al.*, 2013). Therefore, SCC for the U.S. dairy herd has not increased over the interval of rBST use. Rather, SCC has declined over the last decade indicating an improvement in milk quality and mammary health. Van Schaik *et al.* (2002) demonstrated that high SCC is a generic predictor of poor milk quality. Herds with 200,000 cells per mL of milk or less had the lowest incidence of antibiotic residues. Therefore, the inference from SCC data over the period of 15 years is that the potential human threat from milk antibiotic residues has declined dramatically. Contrary to this the CVMA and the European Commission's Scientific Committee on Animal Health and Animal Welfare (SCAHAW) found that rBST use increases the risk of both mastitis and lameness (Grandin, 2001 and CVMA, 1998). As CVMA, (1998) reports rBST use may increase the frequency of clinical mastitis by approximately 25% and prolong recovery. It is concluded that BST causes a substantial increase in the risk of mastitis on most farms and this risk, with associated poor welfare, would not occur if BST were not used (Grandin, 2001).

c) Recombinant Bovine somatotropin (rBST) use increases lameness rates

Given the pain associated with foot and leg problems, "welfare will be seriously and adversely affected as a consequence of the BST treatment" and the CVMA did not feel that existing dairy cattle management techniques would be able to control or eliminate the increased risk of lameness (CVMA, 1998).

Studies found that the risk of lameness approximately 50% higher for rBST-injected cows (CVMA, 1998) while SCAHAW found a 220% increase in foot problems with injected cows suffering twice as long (Grandin, 2001). In agreement with this Cole *et al.* (1992) and Zhao *et al.* (1992) reported that there was increased incidence of lameness in rbST-treated cows. Dohoo *et al.* (2003) meta-analyses review reported that 55% increased risk of developing clinical signs of lameness as a result of using rBST.

d) *Recombinant bovine somatotropin use may introduce reproductive problems*

Rates of pregnancy drop in rBST-injected cows, which may be a sign of how “severely affected by metabolic demands” cows are, and the frequency of multiple births increases substantially, which can lead to further welfare problems (Grandin, 2001). SCAHAW conclusion on the effects of rBST on reproductive problems is failure to conceive which an indicator of poor welfare is. Similar study reported that reproductive problems in dairy cows have become very common resulting with large numbers of cows being culled because of failure to get in calf (Esslemont and Kossaibati, 1997). Dohoo *et al.* (2003) meta-analyses reported supporting results where 40% reduction in fertility of cow as a result of using rBST's. Contrary to this idea Soliman and EL-Barody (2013) reported that rbST did not adversely affect reproduction and the observed decreases in reproductive performance in rbST-treated cows may be attributed more to the increases in milk yield than to direct effect of rbST. Studies showing that milk yield is positively correlated with the extent of fertility problems have come from a range of different countries (Pryce *et al.*, 1998).

The increased metabolic activity associated with BST-induced galactopoiesis also involves an increase in heat production by the body, which challenges thermoregulatory processes. As Elvinger *et al.* (1992) reported that, of 18 cows receiving BST and subjected to heat stress, two cows died and four suffered from ataxia, whereas no such responses were observed in 16 control cows. Therefore rBST may also lower the ability of cows to cope with heat, increasing the risk of heat stress.

In general, rBST-treated cows are culled at a higher rate than non treated cows, which likely demonstrates poorer welfare overall (Grandin, 2001). Cows have a natural lifespan of about 20 years, but the stress caused by the conditions on farms renders cows worthless to the dairy industry by the age of 4 or 5 years (USDA, 2007). According to USDA (2007) report, 26.3% of permanently culling in dairy cows from the United States dairy herd was due to reproductive problems. Both the CVMA and SCAHAW recommend against using rBST for welfare reasons which would not occur if it were not used. The conclusion which should be drawn

is that avoidable actions which result in poor welfare, such as BST usage, should not be permitted (Grandin, 2001). Contrary to this other studies did not reveal a high culling incidence of BST treated animals compared with control animals (Oldenbroek, 1990).

e) *The Human Health Concerns of rBST*

i. *Effect of Insulin-like growth factor-1 in milk of cows supplemented with rBST*

FDA scientists have reviewed and concluded that rBSH is biologically inactive in humans and therefore, residues of rBSH in food products would have no physiological effect even if absorbed intact from the gastrointestinal tract.

Insulin-like growth factor-I (IGF-1) is a secondary hormone produced by mammals in response to levels of natural (synthetic) growth hormones. IGF-1 circulates in the blood of mammals, miraculously coordinating cellular growth and function. Added synthetic growth hormone's presence stimulates more production of IGF1, which circulates to the milk duct tissues, where a tremendous concentration of IGF-1 receptors exist. IGF-1 is structurally identical in both cows and humans. The injection of rBGH into animals could temporarily increase quantities of IGF-1 in milk; however, these increased levels are within the naturally occurring range of IGF-I found in untreated milk or human breast milk. For instance, the daily IGF-1 level in human saliva and other digestive secretions is equal to the amount of IGF-1 in 270 glasses of cows' milk (JECF, 1998). Therefore, there is no evidence that this amount of IGF-I would pose a health hazard (Juskevich and Guyer, 1990; FAO/WHO Expert Committee on Food Additives, 1998 and Elwood, 2008). Contrary to this IGF-1 is not destroyed by normal pasteurization and if cow's milk sourced IGF-1 entered the human blood stream; the IGF-1 would be active in humans. However, FDA scientists argued that digestive acids in the human gut would break down any IGF-1 consumed through milk. On the other hand, Collier and Bauman (2014) agreed on ideas that oral consumption of IGF-I by humans has little or no biological activity and concentrations of IGF-1 in digestive tract fluids of humans far exceed any IGF-1 consumed when drinking milk. Subsequent research has widely discounted FDA's mistaken notion that stomach acids denature milk-borne IGF-1. Opposing with FAD result, in 1995, the Journal of Endocrinology cited work by researchers in Australia who demonstrated that milk proteins protect IGF-1 from digestion. Therefore, IGF-1 became one of the leading suspects involved in the development and spread of cancers. The IGF-1 hormone already exists in humans; it is usually bound to protein and thus has less of an effect than unbound IGF-1 in milk. Therefore, IGF-1 is biologically active in humans and behaves as a cancer accelerator being associated with breast, prostate and colon cancers (<http://www.ejnet.org/bgh/nogood.h>

tml). IGF-1 promotes cell division. As cells divide, at some point they are instructed (by their genes, in combination with hormone signals) to stop dividing or they are instructed to die so that the creation of new cells is matched by the death of cells and no net growth occurs; this is called "programmed cell death." If "programmed cell death" is prevented and then cells don't die at the right time, causing out of control growth of cells, which is another way of saying cancer. Cancer is uncontrolled cell division (<http://www.ejnet.org/bgh/nogood.html>).

ii. The risk of Antibiotic resistance

The increased incidence of mastitis experienced by treated cows, which indirectly inducing increased antibiotic use on cows and a resulting dangerous level of antibiotic residue in milk, as well increased pus content in the milk. Though, it is known that major factors affecting the incidence of mastitis are related to environmental conditions and management practices (Hogan and Smith, 2012). There is also a small increase in mastitis incidence, as milk production increases and hence, the use of rbST was also associated with an increase in the relative risk of mastitis. In 1998 the 50th JECFA conference evaluated and concluded that "the use of rbST will not result in a higher risk to human health due to the use of antibiotics to treat mastitis and that the increased potential for drug residues in milk could be managed by practices currently in use by the dairy industry and by following label directions for use (JECFA, 1998). The pattern of percent of bulk milk tank trucks testing positive for antibiotic residues has steadily declined since 1996 and in 2012 was less than one-fifth of the level detected in 1995 (0.100% in 1995 vs. 0.017% in 2012). Therefore, there is no evidence of increased human risk for exposure to milk antibiotic residues from the use of rbST. Similarly EFSA (2015) report also confirmed that, assuming that the appropriate withdrawal times for antimicrobial treatments are respected, the use of rBSTs would not result in a higher risk to human health due to the use of antibiotics to treat mastitis and that the increased potential for the presence of drug residues in milk could be managed by practices currently in use by the dairy industry and by following the drug manufacturers' directions for use'.

VII. THE EFFECT OF RBST SUPPLEMENTATION ON ENVIRONMENTAL IMPACT

The use of rbST to improve productivity within the lactating cow herd allows for a reduction in resource use and environmental impact per unit of milk (Capper *et al.*, 2008, Dunlap *et al.*, 2000 and Johnson *et al.*, 1992). Capper *et al.* (2008) evaluated a dairy herd of one million lactating cows supplemented with rbST and calculated the environmental impacts associated with producing the same amount of milk in a herd not

supplemented with rbST. The herd supplemented with rbST required 11.8% fewer animals (including lactating cows, dry cows, and heifers), used 8.5% less feed, 8.1% less cropping land and 8.1% less water. Moreover, the rbST herd produced 9% less nitrogen and 9.5% phosphorus in excreta and 8.1% fewer greenhouse gases (Capper *et al.*, 2008). These are substantial environmental gains achieved through maximizing production efficiency in dairy cattle.

This technology alters nutrient partitioning, which results in an increase in daily milk yield of an average of 4.5 kg per cow (Capper *et al.*, 2008). This increase affects environmental sustainability through the dilution of maintenance concept, the net effect being that rbST use reduces the amount of land required to produce a unit of milk by 9.2%, water use by 10.4%, and the carbon footprint by 9.1% (Capper *et al.*, 2008). On an industry basis, rbST supplementation of 1 million cows would therefore reduce the dairy industry's carbon footprint by the annual equivalent of removing about 400,000 cars from the road. The mitigating effect of rbST use on environmental impact has also been noted by other investigators (Bauman, 1992 and Jonker *et al.*, 2002), including Johnson *et al.* (1992), who suggested that large-scale use of rbST would reduce methane emissions by approximately 9%. Nonetheless, the political and social acceptability of rbST use within dairy production has been a contentious issue in several countries (Brinckman, 2000).

Use of rBST allows each cow to produce an average of approximately 15 percent additional milk. This means, six cows supplemented with rBST can produce the same amount of milk as seven unsupplemented cows and that represents one cow less producing manure, consuming feed and water, using electricity for milking and requiring human efforts for husbandry. In fact, the use of rBST in just 15 percent of the U.S dairy cow population reduces the carbon footprint of milk production equal to taking approximately 390,000 cars off the road each year or planting approximately 290 million trees annually (Capper, 2008). Increased animal performance is suggested as one of the most effective mitigation strategies to decrease greenhouse gas (GHG) and ammonia (NH₃) emissions from livestock production per unit of product produced (Stackhouse *et al.*, 2012).

The use of rBST is a management tool that improves agricultural sustainability and reduces the carbon footprint per gallon of milk (Capper, 2008). All food production has an environmental impact. However, FAO estimates that in the next 50 years, the world food production must be increased by 100 percent to provide adequate nutrition for the increasing global population. Thus, innovative food production practices like rbST that increase the efficiency of food production while mitigating the environmental impact will be of even greater

importance in the future for the global production (FAO, 2011).

VIII. CONCLUSION

The rBST has increased milk production in dairy animals. It increases cardiac output and heart rate and this is associated with an increase in the rate of mammary blood flow. Mammary metabolic activity is increased, involving greater substrate uptake and synthesis of milk components. Resulting in milk yields increase by about 10%-15%, little effects on the milk composition, processing properties and taste.

rbST treatment have adverse effect on reproduction such as drop in pregnancy rate, the number of days open (failure to conceive) increased in primi-parous cows. It is also a cause for multiple births. This all lead to poor welfare or an indicator of poor welfare.

BST usage increases the risk of clinical mastitis above the risk in non-treated cows. The duration of treatment for clinical mastitis was longer in rbST-treated than in non-treated cows. The welfare of most cows with mastitis is poor, the extent of poor welfare being dependent on the severity of the condition. Which may result in over usage of antibiotics resulting in its residue in milk to be human health concerns of anti microbial resistance?

There is an increased incidence of foot and leg disorders associated with the long term administration of BST which will result in pain and other suffering in these animals. Hence welfare will be seriously affected as a consequence of the BST treatment.

The use of rbST reduces the resource used and environmental impact per unit of milk production. That is why increased animal performance is suggested as one of the most effective mitigation strategies to decrease green house gas (GHG) and ammonia (NH₃) emissions from livestock production per unit of product produced.

The human demand for animal protein will double by the year 2050 whereas resources like water and arable land is limited to produce extensively. On the other hand, livestock production emits carbonaceous and nitrogenous compounds that contribute to air and water pollution as well as climate change. Therefore, it is advisable to be aware of using rbST to enhance efficient utilization of resource and reduce environmental impact.

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Genesis and Classification of Soils on a Toposequence Underlain by Mica Schist in Ife Area, Southwestern Nigeria

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Abstract- The study was conducted to establish the morphological, physical and chemical properties of soils on a toposequence underlain by mica schist in Ife Area, identify the pedogenic processes that produced the soils and establish the taxonomic and fertility capability classes of the soils. The toposequence was delineated into five physiographic units and soil profile pits were established, described and sampled at each unit. The soil samples collected from each of the genetic horizon were subjected to routine analyses following the procedures in methods of soil analysis. Taxonomic and fertility capability classification of the soils were carried out.

Keywords: *genesis, classification, toposequence, mica schist.*

GJSFR-D Classification : *FOR Code: 050399*



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Genesis and Classification of Soils on a Toposequence Underlain by Mica Schist in Ife Area, Southwestern Nigeria

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Abstract- The study was conducted to establish the morphological, physical and chemical properties of soils on a toposequence underlain by mica schist in Ife Area, identify the pedogenic processes that produced the soils and establish the taxonomic and fertility capability classes of the soils. The toposequence was delineated into five physiographic units and soil profile pits were established, described and sampled at each unit. The soil samples collected from each of the genetic horizon were subjected to routine analyses following the procedures in methods of soil analysis. Taxonomic and fertility capability classification of the soils were carried out.

The colour and texture of the soils change in response to changes in slope position and drainage condition along the toposequence. The soil's colour ranged from reddish brown to dusky red (5YR 3/2- 2.5YR 3/2) in the surface and yellowish red (5YR 4/8) to reddish yellow (7.5YR 6/6) in the subsoil at the higher position of the toposequence while it range from dark brown (7.5YR 4/2) to dusky red (2.5YR 3/2) in the surface and red (2.5YR 4/ 6) to reddish yellow (7.5YR 6/6) in the subsoil at the lower position. Texturally, the soils varied from sandy clay loam in the surface to sandy clay in the subsoil all through the pedons sampled. The soils were moderately acidic to neutral (pH 5.2 – 6.7) at the surface and strongly acidic to moderately acidic (pH 4.4 - 5.7) in the subsurface. They were characterized by low exchangeable bases which were in the order Ca> Mg> K> Na irrespective of slope position with low to moderate organic matter content. The soils were classified as Typic Kanhaplustults and Aquic Haplustults (USDA soil taxonomy) Plinthic Luvisols, Gleyic Luvisols and Eutric Luvisols (FAO-UNESCO). The agronomic constraints of the soils were acidic reactions, low nutrient reserve and gleying, hence dominant FCC unit of soils in the study area was SC *keh*.

The soils studied were highly-weathered, low in inherent fertility and with acidic solum. Therefore, sustainable use of the soils requires careful management to prevent rapid physical and chemical degradation.

Keywords: genesis, classification, toposequence, mica schist.

1. INTRODUCTION

Nigerian agriculture and indeed African agriculture has not succeeded in meeting the continuously changing needs of the citizenry (Chukwu *et al.*,

2013). Persistent food insecurity and failure of agriculture to supply adequate quantities of raw materials to industries are stark realities. These are attributed to many factors, among which is soil resource illiteracy (Wang *et al.*, 2001).

Researchers have identified poor knowledge of soil as a major problem hindering agricultural development in some parts of Nigeria (Chukwu *et al.*, 2013). This is not a surprise as similar observations had been made in most parts of Africa (Ololade *et al.*, 2010). Some of the reasons for this situation are related to lack of soil survey reports of most rural communities and Local Government Areas (LGAs) where food and fibre production take place. Further, the scales of most national soil surveys are so coarse (at reconnaissance level) that pedological information about rural communities where majority of the agricultural produce are coming from is virtually non-existent (Lawal *et al.*, 2010).

Soils vary considerably in their physical, chemical and mineralogical characteristics which are related to their geological history. The continued lack of required knowledge on the nutrient management as related to available pedological information of nutrient depleted soils are not only exacerbating soil degradation, but also jeopardizing agricultural sustainability in these regions (Ayoub, 1999; Sheldrick *et al.*, 2002). Similarly, in these communities, soils where most agricultural research and production take place are not characterized. All these reasons and perhaps more contribute to the widespread problems of soil resource illiteracy which in turn hinders effective agricultural development between areas with similar and/or different soils (Chukwu *et al.*, 2013).

Soil is a product of interaction between climate, parent material, relief and organisms over a period of time. While climate (Maynard *et al.*, 2004) and organisms (Quideau *et al.*, 2001) actively influence soil formation, topography indirectly affects the rate of pedogenesis and distribution of soils (Wang *et al.*, 2001). The effect of topography on soil genesis had long been recognized (Pregitzer *et al.*, 2000). It had been established that soils vary in vertical and lateral directions and that such variations follow systematic changes (Wilding and Dress, 1983). Graham *et al.* (1990) proposed a conceptual model relating slope

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processes to pedogenesis in which transported parent material interrupts the orderly progression of soil development in residual parent material. It was then suggested that genesis and distribution of soils are best understood when studied in landscape context rather than at the level of individual pedons or classification units (Graham *et al.*, 1990). Nye (1966), Smyth and Montgomery (1962), Murdoch and Ojo-Atere (1976) and Ojanuga (1979) had earlier noted that the study of soil distribution along slope was the corner stone of most soil classification in the basement complex area of SW Nigeria.

However, most pedological soil studies in Ife Area had been restricted to the granite gneiss bedrock areas while studies on the pedogenesis in mica schist predominant zones have not received the desired research attention. Yet, the two rock types cover well above 70% of the basement complex area in Ife Area. Therefore, characterization and classification of soils in the land forms of mica schist bedrock are necessary to generate baseline data on the soils with particular reference to Ife area of SW Nigeria. The specific objectives of this study were to establish the morphological, physical and chemical properties of soils on a toposequence underlain by mica schist in Ife area and establish the taxonomic and fertility capability classes of the various soil types along the toposequence.

II. MATERIALS AND METHOD

a) The study area

The study area is located approximately between latitudes 7° 32' N and 7° 33' N and longitudes 4° 39' E and 4° 40' E, which is about 2.5 km away from Kajola village, a suburb of the Obafemi Awolowo University (O.A.U.) Teaching and Research Farm (T&R-F) Ile-Ife and is located within the schist belt of southwestern Nigeria (Rahaman, 1988).

b) Climate

Kajola area is in the same ecological zone (tropical rainforest) as Ile-Ife with hot, humid tropical climate having distinct dry and bimodal rainy seasons. The mean annual rainfall is about 1,527mm and the mean monthly air temperature is approximately 31°C. The wet season starts from mid-March to late October, and the bimodal rainfall pattern has peak periods in June/July and September/October. The dry season runs from early November to early March. The influence of the north-east trade wind, which loses all its moisture as it passes over the Sahara desert towards the equator, is felt in the study area as 'harmattan' (cold dry wind) between late December and early January (FMANR, 1990).

Atmospheric temperature is moderately high throughout the year, with a low range between the monthly mean minimum and maximum temperatures.

The peak of the maximum is usually between February and March (34.3- 33.8°C) just before the onset of rains while the lowest minimum temperatures are between July and August (27.1 - 27.9°C) during the peak periods of rainfall. The area also records the following average monthly data: humidity 73.8%, and sunshine 6.6 hours. The wind speed was 114.6 km d⁻¹ while potential evaporation is 4.36 mm d⁻¹ (Meteorological data bank, T&R-F, O.A.U., Ile-Ife, 2010). The mean monthly soil temperature at 50 cm depth in Ile-Ife, for June, July and August is 27.7°C and for December, January and February is 29.4°C. Since these differ by less than 5°C, the soil temperature regime in the study area is isohyperthermic (Soil Survey Staff, 2006).

c) Vegetation and land use

The native vegetation of the study area was originally rainforest characterized by very tall, big trees and thick shrubs. However, as a result of human interferences, the vegetation now consists of admixture of bush regrowth, arable crop farms and tree crop plantations. The crest (summit) and the shoulder are presently being used for arable crop cultivation (cassava (*Manihot spp.*); yam (*Discorea spp.*); maize (*Zea mays*) and scattered banana/ plantain (*Musa spp.*). The upper slope area was cultivated to cocoa (*Theobroma cacao*), but was unkept and gradually transforming into secondary forest. The mid slope area was under bush fallow with mostly *Chromolaena odorata* and scattered oil palm (*Elaeis guinensis*). The lower slope supported cocoa plantation inter-planted with cassava (*Manihot spp.*) and banana/plantain (*Musa spp.*), while plantain/banana (*Musa spp.*) and cocoa (*Theobroma cacao*) were grown in the valley bottom area.

d) Field study

Guided by the geological map of the study area produced by the Department of Geology, O.A.U. Ile-Ife, a toposequence underlain by mica schist was selected for the study. The toposequence is slightly undulating with relatively flat top and is approximately 2.5 km southeast of Kajola village. The toposequence is approximately 500 m long from the valley bottom to the crest with an elevation of 295.9 m above mean sea level (amsl) at the crest and 268.6 m amsl at the valley bottom. The other physiographic positions were clearly identified and the upper slope, sedentary and hill-wash areas were 293.6 m, 283.5 m and 276.9 m amsl respectively.

Five soil profile pits were established along the toposequence at different physiographic positions. All the pedons were described following the procedures in the guidelines for soil profile description (FAO, 2001) and horizon designations of the Soil Survey Staff (2006). Soil samples were collected from each of the identified genetic horizons for physical and chemical analyses in the laboratory. Undisturbed core soil samples were collected and used for bulk density determination.

e) *Laboratory analyses*

The soil samples were air dried, gently crushed in ceramic mortar with pestle and passed through 2mm sieve to separate materials that were greater than 2mm. The fraction that was less than 2mm was used for the laboratory analyses other than the bulk density determination.

f) *Physical analyses*

The bulk density was determined by the core method. The particle size distribution was evaluated by the modified Bouyoucos hydrometer method (Bouyoucos, 1951) using 5% w/v sodium hexameta-phosphate (calgon) as the dispersing agent. Particle fractionation into very coarse sand (VCS), coarse sand (CS), medium sand (MS), fine sand (FS) and very fine sand (VFS) was carried out with the use of a set of sieves (1.0, 0.5, 0.25, 0.100 and 0.05 mm) representing 1000, 500, 250, 100 and 50 μ m respectively arranged in decreasing order of sieve sizes as listed (Buol *et al.*, 1997). Each of the sand fractions was weighed and preserved.

g) *Chemical analyses*

The soil pH was determined both in distilled water and 1.0 M KCl (1:1 soil: solution ratio) using glass electrode pH meter (Kent model 720) (Thomas, 1982) and was also carried out in duplicate. Delta pH computed is defined as the difference between pH in KCl and H₂O. The exchangeable bases (Ca, Mg, K and Na) were extracted with 1.0 M ammonium acetate (NH₄OAC) solution at pH 7.0 (Thomas and Throp, 1985). Calcium, Ca²⁺, sodium, Na⁺, and potassium, K⁺ ions in the extract were determined with the use of flame photometer (Gallenkamp Model FH 500), while magnesium (Mg²⁺) ion in the extract was determined by titration which was carried out by extracting the soil with neutral ammonium acetate solution (Soil Survey Staff, 2006).

The exchangeable acidity was determined by extraction with 1.0 M KCl solution and titrated with NaOH and HCl solutions to measure total acidity (Al³⁺ and H⁺) concentrations respectively (McLean, 1965). Effective cation exchange capacity (ECEC) was computed as the summation of NH₄OAC extractable bases (Ca²⁺, Mg²⁺, Na⁺ and K⁺) and KCl extractable aluminium (Al³⁺) (Soil Survey Staff, 2006). The organic carbon was determined by the Walkley Black method (Allison, 1965), and the available phosphorous by Bray No. 1 method.

h) *Fertility capability classification (FCC)*

The results of the laboratory analyses and field morphological properties of the pedons identified in the study area were used for fertility capability classification. The conversion data used in evaluating the soils are as outlined by Sanchez (2002), which consists of three categorical levels, 'type' (texture of plough layer or top

20 cm), 'substrata type' (texture of sub soils), and 'modifiers' (soil properties or conditions which act as constraints to crop performance). Class designations from the three categorical levels were combined to form FCC unit. Thus the soils were classified according to whether a characteristic was present or not.

i) *Statistical analyses*

Correlation coefficients and simple regression analysis between the selected soil properties were calculated. All statistical analyses were carried out using SAS 9.1 version (2002-2004) software programme.

III. RESULTS AND DISCUSSION

a) *Soil morphology and landform relationship*

Locational map showing the topographical sequence of the soil series identified in the study area is presented in Figure 1 and the summary of the important morphological characteristics of the soil types identified on the landscape positions on the toposequence is presented in Table 1. The soils along the toposequence are derived from fined-grained biotite gneisses and schist and are very extensive in southwestern Nigeria, the parent rocks are very easily weathered and give rise to very deep soils. The colour and texture of the soils change in response to changes in slope position and drainage condition down to the valley bottom. The bright yellowish and dark brown to red colours of soils in the higher topographical sites was an indication of good drainage (Periaswamy and Ashaye, 1982).

b) *Physical properties of the soils*

Table 2 shows the particle size distribution and bulk density data of the soils along the toposequence under study. The gravel content varied from 8 to 68 \pm 17.38%, with Pedons from the summit, upper and middle slopes having relatively high values of 22 to 68 \pm 14.94% while the lower slope and valley bottom Pedons have lower values, 8 to 32 \pm 7.26%. The gravel content generally increased from the A-horizon to B-horizon and then decreased significantly from B to C-horizon, except at the lithologic break. However, in pedons at the lower slope position, there were no particular patterns of gravel distribution. This gravel accumulation had been found to be a characteristic property of soils formed in the upland portion of the landscapes derived from granitic gneiss metamorphic rock complex of central western Nigeria (Smyth and Montgomery, 1962; Okusami and Oyediran, 1985). These have not constituted an obstacle to root proliferation since roots are found beyond the gravel horizons.

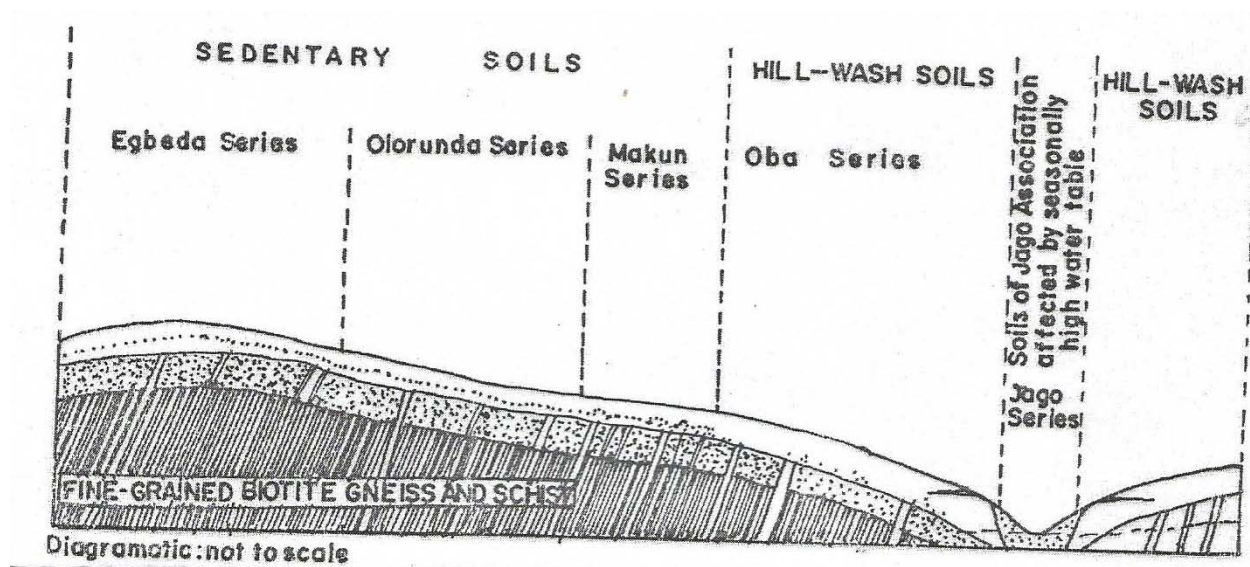


Fig. 1 : Topographical Sequence of soil Series in the Study Area (After Smyth and Montgomery, 1962)

Table 2 : Field morphological discription of the soils studied

Horizon	Depth (cm)	Colour Moist	Texture ¹	Structure ^x	Consistence ^y	Concretions ^b	Boundary ^z	Notes
Ap	0-18	5YR 3/2	SL	2mcsbk	Nstnplvfr	Profile 01 Egbeda series	cs	Abundant very fine, fine, and few medium roots
AB	18-24	10YR 4/4	SCL	2msbk	Nplfrnst		cs	Abundant fine and medium roots
B	24-51	2.5YR 4/4	SC	2msbk	Sstfrspl		gw	Few fine and medium roots
BC	51-70	5YR 4/8	SC	3psbk	Sstsplfr		cs	Very few fine roots
Ap	0-18	5YR 3/3	SCL	cmsbk	Sstsplfr	Profile 02 Olorunda series	cs	Abundant fine, medium to coarse roots
AB	18-28	2.5YR 4/4	SCL	2mcr	Sstsplfr		ds	Common fine and very fine and few medium roots
B21	28-72	2.5YR 4/8	SC	1msbk	Nstnplfr		s	Frequent fine roots
B22	72-132	2.5YR 4/4	SC	2msbk	Sstspl		cs	Few gravels
BC1	132-185	5YR 4/6	SC	3csbk	Fmstpl	Profile 03 Makun series	ds	Thick cutans of clay and iron oxides on ped
BC2	185-210	5YR 6/6	SC	3msbk	Vfr		-	Few mottles, frequent pieces of weathered rock, devoid of roots.
Ap	0-18	5YR 4/2	SCL	2msbk	Nstnplfr		cs	Common coarse fine to medium roots
BA	18-33	2.5YR 4/2, (5YR 5/6)	CL	2mlsbk	Sstspl		ds	Abundant very fine and few coarse and medium roots
B21	33-65	2.5YR 4/6	SC	2msbk	Frstpl	Profile 04 Oba series	Ds	Common medium and coarse roots
B22	65-120	(5YR 5/6)	SC	2msbk	Sstsplfr		Ds	Medium to fine prominent mottles, Weathered quartz stones with few patchy cutans
BC	120-200	5YR 4/6	SC	2msbk	Sstsplfr		-	Frequent quartz materials. Devoid of roots
Ap	0-20	7.5YR 4/2	SCL	2fcr	Vfrnstnpl		cs	Common medium frequent fine and few coarse roots
BA	20-40	5YR 4/6	SCL	2msbk	Frststpl	Profile 05 Jago series	cs	Few medium, common fine and few very fine roots
B1	40-71	2.5YR 4/6	SC	2msbk	Frststpl		ds	Few patchy cutans, common fine and medium roots
2BtC1	71-115	2.5YR 4/8	SC	2msbk	Vstpl		gs	Few patchy cutans with stonelines, few medium to fine roots
2BC2	115-170	5YR 5/8	SC	2msbk	Frstpl		-	Few roots with frequent black hard concretions present.
Ap	0-18	2.5YR 3/2	SCL	2mcr	Sstnp	Jago series	gw	Common medium frequent fine roots
AB	18-40	2.5YR 4/4, (5YR 6/1)	SC	2msbk	Sstspl		gw	Common medium frequent fine roots
B	40-60	2.5YR 4/6	SC	1msbk	Fmstpl		gw	Frequent medium and few fine roots
Btg	60-75	7.5YR 6/6	SC	2f	Fmstvpl		-	Common medium roots merging into a water saturated layers

Texture: SC= Sandy Clay, SL= Sandy Loam, SCL=Sandy Clay Loam, L= Loamy, LS= Loamy Sand, C=clay, CL= Clay Loam;

^x Structure: 1 = weak, 2 = moderate, 3 = strong, cr = crumb, sbk = subangular blocky, abk = angular blocky, p= platy, vf= very fine, f= fine, m = medium, c = coarse;

^y Consistence: m = moist, w = wet, vfr = very friable, fr = friable, fm = firm, vfm = very firm, nst = non sticky, sst = slightly sticky, vst = very sticky, st =

The soil texture varied from sandy loam to sandy clay loam for surface horizons except in Pedon 05 which has clay texture. The B and C-horizons have clay loam texture except in Pedons 03 and 04 that were more clayey in the B and BC horizons. The sand content ranged from 29 to 67 \pm 12.83% and decreased with increasing depth except at certain depths where the BC-horizon contained more of sand as in Pedons 03 and 04. An outstanding feature of these soils irrespective of their location on the topography is their low to moderate silt content at the surface. The silt content ranged from 11 to 25 \pm 3.31%, although the value fluctuated within all the pedons with increasing depth. Generally, the silt content is low, a characteristic which the soils shared with most Nigerian soils (Ojanuga *et al.*, 1981).

The clay values ranged from 18 to 59 \pm 13.98% in the Bt horizons. The clay content increased generally

with increasing depth to a maximum (probably due to illuviation/ eluviation interplay or possibly clay migration) and then decreased in the BC horizons. Similar trend was observed by Ojanuga (1978) in soils of Ife and Ondo areas of southwestern Nigeria. Generally, soils in the middle and lower slope positions have higher clay content than those of the valley bottom position. For Pedons 02, 03, and 04, the particle size distribution of the sub-soil horizon of the soils suggests that the B-horizons were influenced more by eluviation – illuviation processes. The high clay content in the deeper horizons of some of the soils coupled with some morphological properties such as the colour, texture, consistence and plasticity in the profile description formed the basis for the recognition of argillic horizons in some of the soils (Fasina *et al.*, 2005).

Table 2 : Physical properties of the soils along the toposequence

Horizon	Depth (cm)	>2000mm (% of the whole soil)	Very coarse sand (1000- 2000 μ m)	coarse sand(500- 1000 μ m)	Medium Sand (250- 500 μ m)	Fine Sand (50- 100 μ m)	Very fine sand (0.05-0.50 μ m)	Total sand	Silt	Clay	Bulk density g/cm ³	Textural class
← % →												
Profile 01 Egbeda series												
Ap	0-18	35	10	13	10	9	7	49	21	30	1.06	Sandy loam
AB	18-24	61	10	12	10	8	7	47	25	28	1.54	Sandy clay loam
B	24-51	68	7	8	7	5	4	31	11	58	1.62	Sandy clay
BC	51-70	50	7	7	6	5	4	29	13	58	1.59	Sandy clay
Profile 02 Olorunda series												
Ap	0-18	41	10	13	12	10	10	55	17	28	1.01	Sandy clay loam
AB	18-28	68	10	12	11	10	8	51	11	38	1.57	Sandy clay loam
B21	28-72	64	10	8	7	7	6	39	13	48	1.63	sandy clay
B22	72-132	56	11	4	7	7	5	33	13	54	1.68	sandy clay
BC1	132-185	33	9	7	7	7	6	35	17	48	1.73	Sandy clay
BC2	185-210	22	9	9	9	8	8	43	15	42	1.48	Sandy clay
Profile 03 Makun series												
Ap	0-18	43	12	13	11	11	9	55	17	28	1.34	Sandy clay loam
BA	18-33	42	11	12	10	10	8	51	15	34	1.42	Clay loam
B21	33-65	39	12	8	7	4	3	34	13	53	1.45	Sandy clay
B22	65-120	47	12	6	6	4	2	30	11	59	1.65	Sandy clay
BC	120-200	23	11	8	10	5	5	39	15	46	1.40	Sandy clay
Profile 04 Oba series												
Ap	0-20	8	11	15	13	11	8	57	15	28	1.54	Sandy clay loam
BA	20-40	32	10	12	7	7	2	39	13	48	1.48	Sandy clay loam
B1	40-71	25	8	11	5	5	3	31	11	58	1.30	Sandy Clay
2BtC1	71-115	27	8	11	4	5	3	31	13	56	1.71	Sandy Clay
2BC2	115-170	15	10	13	7	7	2	39	13	48	1.40	Sandy clay
Profile 05 Jago series												
Ap	0-18	26	16	15	14	13	10	67	15	18	0.74	
AB	18-40	19	14	13	13	13	12	65	13	22	1.21	Sandy clay
B	40-60	18	14	17	15	12	10	67	11	22	1.31	Sandy clay
Btg	60-75	24	13	14	13	13	12	65	15	20	1.13	Sandy clay

The bulk density ranged from 0.74 g cm^{-3} in the Ap horizons to 1.7 g cm^{-3} in the Bt horizons. Generally, the bulk density value increased with increasing depth to a maximum and then decline with increasing soil depth. The exception to this trend was observed in Pedon 04 with their values fluctuating. However the higher values at depth have not created any hindrance to plant root penetration as evidenced by deep rooting of plants into greater depth in Pedon 02. A positive correlation exists between bulk density and clay that indicated the contribution of clay to soil bulk density with increasing depth.

c) Chemical properties of the soils

Tables 3 show the chemical properties of the pedons studied. The soils studied fall within the neutral to very strongly acid class (Ojanuga, 1978; Landon, 1991; Soil Survey Staff, 2003), with pH (H_2O) values ranging from 5.6 to 7.0. The pH decreased with soil depth except in Pedon 03. The pH (1M KCl) ranged from 4.4 to 5.7. The value also decreased with soil depth except in Pedon 03 where no definite pattern was observed. Generally, the surface horizons of the pedons were medium to slightly acid (pH 5.2 - 5.7), while B and C-horizon were strong to very strong acid with pH values ranging from 4.4 - 5.7. The acid nature of the soil can be ascribed to high rate of leaching of bases which is prevalent in the humid tropics, and the acidic nature of the parent rock (granite-gneiss). The higher pH values observed at the soil surface horizons according to Fasina *et al.* (2005) might be due to liming effect of bush burning and bio cycling of nutrients. The pH in 1M KCl was lower than the pH in water (H_2O), thus the difference in soil pH values between the pH in KCl and H_2O (as expressed by $\Delta\text{pH} = \text{pH}(\text{KCl}) - \text{pH}(\text{H}_2\text{O})$) were all negative ranging from -0.9 to -1.5. This suggests the dominance of silicate clay minerals over oxides (Van Raij and Michael, 1972).

Generally, there was higher accumulation of bases in the surface horizons $6.59 - 12.57 \text{ cmol}(+)\text{kg}^{-1}$ of the soil, and the total exchangeable bases decreased with soil depth except in some cases owing to nutrient biocycling (Ajiboye and Ogunwale, 2010), and could also be due to differential weathering that had taken place or as a result of plant uptake and leaching losses. Like in most tropical soils, the exchangeable sites of the soils studied were dominated by exchangeable calcium and magnesium. Exchangeable sodium (Na^+) and potassium (K^+) are low (Table 3) with values ranging from 0.08 to $0.26 \text{ cmol}(+)\text{kg}^{-1}$ and 0.15 to $0.30 \text{ cmol}(+)\text{kg}^{-1}$ soil for Na^+ and K^+ respectively. These low values indicated that the soils under investigation developed from materials that are either low in K^+ and Na^+ content or have been exhausted by plant uptake or leaching due to their mobility within the soil. The higher values obtained at the surface horizon of the pedons could be attributed to higher organic matter content

(Ano, 1991). However, the values fluctuated irregularly down the soil profile. Exchangeable acidity values ranged from 0.3 to $1.0 \text{ cmol}(+) \text{ kg}^{-1}$ soil (Table 3). All the pedons examined showed little variation in the exchangeable acidity (Al^{3+} and H^+) and the values were almost uniform with soil depth. Exchangeable Al^{3+} accounted for a greater percentage (54.14%) of the total acidity. Effective cations exchange capacity (CEC) was generally low with values ranging from 3.73 to $14.26 \text{ cmol}(+) \text{ kg}^{-1}$ soil. There were higher values in the surface horizons of all the soils examined than in the sub-soil, probably due to the influence of organic carbon on the exchange sites of the soils. However, in those profiles where higher values were noticed in the sub-soil as in Pedons 02 (B22) and 03 (BC) with more of clay content (Table 2), this could be due to the process of pedoturbation either by fauna or flora.



Table 3 : Chemical properties of the soils

Horizon	Depth (cm)	pH (H ₂ O)	pH KCl	ΔpH	OM %	P Ppm	Ca ²⁺	Mg ²⁺	Exchangeable Bases		Exchangeable Acidity		Sum of Bases	ECEC	Base saturation (%)	Aluminium Sat. (%)	
									Mg ²⁺	Na ⁺	K ⁺	Al ³⁺	H ⁺				
Profile 01 Egbeda series																	
Ap	0-18	6.9	6.0	-0.9	2.55	11.2	7.2	4.86		0.21		0.30	0.4	0.2	12.57	12.97	97
AB	18-24	6.8	5.4	-1.4	1.61	7.4	6.6	4.86		0.26		0.26	0.2	0.3	11.98	12.18	98
B	24-51	6.5	5.0	-1.5	1.21	3.4	6.7	4.10		0.25		0.30	0.3	0.3	11.30	11.60	97
BC	51-70	6.0	4.6	-1.4	1.07	3.2	5.8	3.20		0.20		0.24	0.7	0.3	9.44	10.10	93
Profile 02 Olorunda series																	
Ap	0-18	6.5	5.3	-1.2	1.68	6.3	5.3	4.86		0.19		0.24	0.4	0.2	10.58	10.98	96
AB	18-28	6.4	5.0	-1.4	1.14	8.2	4.9	4.05		0.19		0.22	0.4	0.3	9.35	9.75	96
B21	28-72	6.2	5.0	-1.2	0.87	4.1	5.5	1.62		0.21		0.28	0.1	0.4	7.69	7.79	99
B22	72-132	6.1	5.0	-1.1	0.67	3.3	5.3	5.67		0.19		0.26	0.4	0.3	11.42	11.82	97
BC1	132-185	5.9	4.9	-1.0	0.60	3.0	5.3	4.05		0.20		0.26	0.1	0.3	9.81	9.91	99
BC2	185-210	5.6	4.8	-0.8	0.07	2.6	5.0	4.86		0.17		0.26	0.2	0.2	10.29	10.49	98
Profile 03 Makun series																	
Ap	0-18	6.8	5.6	-1.2	1.54	8.4	4.0	7.29		0.14		0.22	0.4	0.3	11.64	12.04	97
BA	18-33	6.7	5.5	-1.2	0.94	10.5	4.9	4.05		0.19		0.24	0.3	0.3	9.38	9.68	97
B21	33-65	6.6	5.5	-1.1	0.94	7.0	5.3	1.62		0.21		0.30	0.2	0.2	7.44	7.64	97
B22	65-120	6.4	5.5	-0.9	0.87	5.8	4.1	6.48		0.14		0.20	0.2	0.3	10.91	11.11	98
BC	120-200	6.7	5.7	-1.0	0.40	3.2	3.1	10.53		0.11		0.22	0.3	0.2	13.96	14.26	95
Profile 04 Oba series																	
Ap	0-20	6.4	5.2	-1.2	1.74	7.7	4.7	4.05		0.23		0.24	0.2	9.22	0.9	9.92	93
BA	20-40	6.2	4.8	-1.4	0.93	8.4	3.2	5.67		0.12		0.22	0.2	9.21	0.3	9.31	99
BC1	40-71	6.0	4.8	-1.2	0.67	5.8	2.2	5.67		0.08		0.24	0.2	8.19	0.3	8.29	99
2BtC1	71-115	5.8	4.6	-1.2	0.60	6.2	2.1	4.05		0.10		0.24	0.3	6.49	0.4	6.59	99
2BC2	115-170	5.6	4.4	-1.2	0.40	4.5	2.8	3.24		0.16		0.26	0.2	6.46	0.3	6.56	99
Profile 05 Jago series																	
Ap	0-18	7.0	6.7	-1.3	1.74	6.9	1.5	4.86		0.08		0.15	0.2	6.59	0.6	6.99	94
AB	18-40	6.6	5.2	-1.4	0.74	8.9	1.9	4.86		0.08		0.24	0.3	7.08	0.6	7.38	96
B	40-60	6.5	5.0	-1.5	0.40	5.4	0.6	2.43		0.08		0.22	0.2	3.33	0.6	3.73	89
Btg	60-75	6.3	5.0	-1.3	0.13	5.2	1.5	2.43		0.08		0.21	0.2	4.22	0.6	4.62	91

The organic matter content of the surface horizons of the pedons ranged from 1.54 to 2.55% (Table 3) and decreased with soil depth. The sub-surface horizons were generally lower in organic matter than the surface horizons of all the pedons examined. The reasons for this may be due to the fact that the surface horizons are the points where decomposition and humification of organic materials take place. The organic matter content of the entire soils studied was generally low, mostly less than 2% except in the surface horizon of Pedon 01. The low organic matter obtained may be partly due to the effect of high temperature and relative humidity which favour rapid mineralization of organic matter (Fashina *et al.*, 2005). It might also not be unconnected with the degradative effect of cultivation and other land use and management activities. Available phosphorous content of the soils varied from 2.6 to 11.2 ppm in all the horizons in the profiles with the highest values at the surface horizons. The relatively high concentration of the available P and organic carbon in the surface horizons may imply significant organic or biocycled P in the soils and also an indication that organic matter contributes significantly to the available phosphorus in these soils. The available P values are considered low at some horizons as they were below or only slightly above the 10 ppm critical limit recommended for most commonly cultivated crops in the area (Uponi and Adeoye, 2000; Aduayi *et al.*, 2002; Obigbesan, 2009). The values generally decreased with depth, though the pattern is irregular in all the pedons examined. The low value of available P might be due to the fixation of phosphorus by iron and aluminum sesquioxides under well drained and acidic conditions of the soils (Onyekwere *et al.*, 2001). Further, Jubrin *et al.* (2000) noted that deficiency of P may occur in soils due to its strong adsorption by the soil colloids. Pedons 04 and 05 exhibit an unusually high concentration of available P in the sub surface horizons 8.4 and 8.9 ppm respectively (Table 3). This could probably be due to the effect of farming activities especially decomposed cocoa pod residue because the pedons are located within a cocoa farm or deposition of P in the valley bottom soils of the toposequence through erosion.

d) Classification of the soils studied

i. Local system

The following factors were taken into considerations in the classification of the soils under examination; nature of the bedrock, the form of parent material, physiographic position, soil colour, presence or absence of mottles, soil texture and general profile morphology. Pedon 01 of the toposequence is confined to the hill top and is formed over hard rock material. The pedon is dark reddish brown to yellowish red in colour with clayey texture, frequent ironstone concretions. The fine texture contains appreciable number of rounded

edge gravels with sub angular blocky structure. They were therefore, classified as Egbeda series. Pedon 02 is confined to the upper slope position of the toposequence. The soils were dark reddish brown to reddish yellow in colour with gravelly clay texture. They contain variable content of iron stones and fragments of iron pan in some horizon together with few continuous thick cutans probably of clay and iron oxides on peds. It was therefore, classified as Olorunda series.

Pedon 03 occupied the middle slope at intermediate to low levels in the topography. The soils are dark reddish grey to yellowish red in colour and have a sandy clayey texture close to the soil surface and mostly structureless. They are majorly devoid of mottles and consist of few gravel size iron concretions at some points within the profile. In view of its position on the toposequence, they were classified as Makun series (Smyth and Montgomery, 1962).

Pedon 04 occupied gently sloping section of the lower slope area of the toposequence. The soils were dark brown to yellowish red in colour and clayey textured close to the surface with almost uniform morphology. The profile is well drained with evidence of lithologic break at a portion in the pit. This suggests that colluvial materials were washed from higher sites. They are essentially devoid of stones and gravels to a certain depth. The residual materials are gravelly clay in texture with moderate medium subangular blocky structure. The colour ranges from (2.5YR 4/8 moist) red to yellowish red (5YR 5/8 moist). They were therefore, classified as Oba series (Smyth and Montgomery, 1962). Pedon 05 was at the valley bottom of the toposequence, the soils are poorly drained with gravelly clay loam texture and dusky red to reddish yellow colour. The profile was saturated at 75-cm from the soil surface. The pedon contained gley mottles and were therefore classified as Jago series.

ii. Taxonomic classification

All the pedons observed showed increasing trend in clay content with soil depth to a certain level, a kind of trend that was indicative of argillic horizon. Low level of fertility as observed from the organic matter content and other soil mineral composition to the extent that they cannot be used to grow crops economically unless fertilizers are used to supply nutrients (Soil Survey Staff, 2003). These are the two most important differentiating characteristics of the Ultisols. The pedons studied are mineral soils with ochric epipedon, low in organic matter, high in colour values and chromas. The soils are dry for more than 90 cumulative days but less than 180 (Table 1). The upland soils of southwestern Nigeria is primarily under ustic moisture regime (Periaswamy and Ashaye, 1982), therefore, the soils are in Ustults suborder. Pedon 05 qualifies as Aquults because of the hydromorphic properties right from the soil surface and the gleyed subsurface horizons. The

presence of Kandic horizons are established in most pedons because they meet the following requirements: coarse textured surface horizon over vertically continuous sub-surface horizons; ECEC values within the sub-surface B-horizons that are less than 12cmol(+)/kgclay (Table 3); a regular decrease in organic carbon contents with increasing soil depth (Table 3) (Soil Survey Staff, 2003).

Soils of Pedons 01, 02, 03 and 04 have no evidence of hydromorphic properties within 150 cm of the mineral soil surface but have clay distribution such that the percentage clay decreased from its maximum by 20% or more within 150 cm of the mineral soil surface. These soils therefore, classify as Typic Kanhaplustults, they have ECEC of less than 12 cmol/kg soil. Soils of pedon 05 show evidence of redox depletion within 75 cm of the mineral soil surface and therefore, qualify as Aquic Haplustults. In the FAO-UNESCO soil legend, all the pedons under consideration qualify as Luvisols because of the presence of argillic horizon and humus surface horizon that is separated from the mineral horizon (Bruand *et al.*, 2004), a horizon eluviated of clay minerals and a horizon of at least 5 cm thick with

illuvial clays (Bruand *et al.*, 2004). The soils of pedon 03 and 04 classify as Plinthic Luvisols because of the presence of indurated coherent plinthite within 100 cm of the soil mineral surface. Soil of pedon 05 classifies as Gleyic Luvisols because of evidence of gleyic properties within 100 cm of the soil surface. The soils of pedon 01 and 02 classify as Eutric Luvisols because of the high base saturation (IUSS, 2006).

e) Fertility capability classes of the soils

The fertility capability classification (FCC) is a technical system for grouping soils which have similar agronomic limitations and management problems in terms of the nutrient supply capacity of the soils (Buol *et al.*, 1997; Sanchez, 2002). The result (Table 6) showed that the dominant FCC unit of soils in the study area was SC *keh*, that is sandy clay texture with low nutrient reserve, low cations exchange capacity and acidic soils. However, they all have similar agronomic constraints. The study revealed that the general fertility constraints of the soils were acidic reaction (h), low potassium reserve (k) and gleying (g) at the valley bottom area.

Table 6 : Fertility capability classification (FCC) units of the soils studied

Pedon	Top soil	Sub soil	Condition Modifier				FCC Units
			g	K	E	h	
1	S	C	-	+	+	+	SCkeh
2	S	C	-	+	+	+	SCkeh
3	S	C	-	+	+	+	SCkeh
4	S	C	-	+	+	+	SCkeh
5	S	C	+	+	+	+	SCgkeh

Keys:

S = Sandy, C = Clayey, h = acidic reaction, e = low cations exchange, k=low nutrient reserve, g = gleying, + = present, and - = absent

IV. CONCLUSION

The study was designed to examine the morphological, physical and chemical properties of the soils formed in mica schist in the study area along a given Toposequence with a view to classifying them. The toposequence was delineated into different physiographic units namely the crest, the upper slope, mid-slope/ sedentary, hillwash and valley bottom and soil profiles were established, described and sampled at each unit. The soil samples were subjected to routine analyses. The morphology, physical and chemical characteristics alongside the taxonomic and fertility capability classifications of the soils were determined to generate valuable information about the soils' properties, understand their mode of formation/ genesis, their management requirements and agronomic constraints.

In conclusion, topography invariably influenced the pedogenetic processes leading to formation of

different soil types on the landscape. This study, therefore, provided evidence for the need to adopt different management practices to suit each soil type at the different physiographic positions as evidenced by the taxonomic and fertility capability classes.

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Evaluation of Red Common Bean (*Phaseolus Vulgaris* L.) Genotypes for Yield and Yield Traits in Borecha District of Sidama Zone, Southern Ethiopia

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Abstract- Eight red common bean varieties were evaluated in Borecha district of Sidama Zone using Randomized complete block design replicated in four villages. Phenotypic traits such as yield and yield component was measured and evaluated. Significant ($P < 0.05$) to highly significant ($P < 0.01$) were observed in days to 50% flowering, days to 95% physiological maturity, plant height, Biomass, grain yield, pod length, pod per plant, 100 seed weight, seed per pod and branch per plant. Genotypes yield stability across the villages was estimated by Additive Main Effects and Multiplicative Interaction Analysis (AMMI). The genotype named 'Nasir' is stable variety across the villages (environment). However, Dimtu and Hawassa dume was stable and out performed at village 1 & 3 even if high environment interaction was observed on village 4.

Keywords: common bean, yield, stability, environment, interaction.

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Abstract- Eight red common bean varieties were evaluated in Borecha district of Sidama Zone using Randomized complete block design replicated in four villages. Phenotypic traits such as yield and yield component was measured and evaluated. Significant ($P < 0.05$) to highly significant ($P < 0.01$) were observed in days to 50% flowering, days to 95% physiological maturity, plant height, Biomass, grain yield, pod length, pod per plant, 100 seed weight, seed per pod and branch per plant. Genotypes yield stability across the villages was estimated by Additive Main Effects and Multiplicative Interaction Analysis (AMMI). The genotype named 'Nasir' is stable variety across the villages (environment). However, Dimtu and Hawassa dume was stable and out performed at village 1 & 3 even if high environment interaction was observed on village 4.

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I. INTRODUCTION

Common bean is the most important crop for soil health due its excellent biological nitrogen fixation and food security crops for its source of starch, protein, dietary fiber, minerals and vitamins (Broughton, 2003). It is also an important source of income for the farmers and an export commodity that generates foreign currency for the country. It ranks third as an export commodity in Ethiopia, contributing about 9.5 % of total export value from agriculture (FAOSTAT, 2010). In Ethiopia Production ranges 100-200 thousand tons per year with yield highly dependent on rain fall. Given current trends of climate change and bean consumption as well as demand in increase of bean market, the productivity of local variety is limited due to biotic and a biotic factor. For instance, 'Red woliata' Borecha district popular common bean landraces have passed many generations of natural and human selection for end-use quality and found to be low yielding and susceptible to pest (farmer's personnel communication). The average national yield of common bean in Ethiopia is estimated at 1300kg/ha on

smallholder farms in contrast to a production potential of 3000 to 4000kg/ha in research field (Darkwa *et al.*, 2016). The yield gap is partly due to lack of information for farmers to use improved genotypes released from research centers.

As reported by Katungi *et al.* (2009) through Ethiopian national bean breeding program number of common bean varieties had been released since 1970s and 2009. However, a few varieties (i.e. Mexican 142 and Red wolaita) released in early 1970s still dominate the area allocated for common bean production in Ethiopia. For instance, Mexican 142 occupy 50 percent of area allocated to common bean in the central rift valley, while Red wolaita accounts for about 70 percent of area allocated for common bean production in Southern Nation and Nationalities peoples Regional state.

According to this report, the improved varieties of 1990s (i.e Awash one, Awash melka) provided farmers with little incentive to switch from Mexican 142 to new varieties. They were either inferior to Mexican 142 in important market traits (e.g Awash melka) or not significantly different (e.g Awash one). The study further indicates that within the more recently released varieties and evaluated by a significant number of farmers, Argene (also referred to as AR04GY released in 2005) demonstrate a high potential to replace Mexican 142 because it is equally as good as Mexican 142 in terms of market traits while outperforms it in terms of yield.

Hence, the best way to minimize the yield gap is to conduct on farm evaluation of improved genotype so that the yield is enhanced and smallholder farmers get the full benefit. Therefore, the present study is conducted to evaluate on farm performance of red common bean for yield and yield traits potential and to identify the best yielding variety to be used by Kayyo seed producer cooperative in Borecha district.

II. MATERIALS AND METHODS

a) Descriptions of Experimental site

The experiment was conducted in four villages of Borecha district namely Sidamo chala, Shello Belela, Shello Abore and Hanja Goro in 2010/2011 cropping season. The altitude of the site lies within the range of

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1710 to 1900 m asl. Centre of the village is located at 06° 56.454'N and 38°15.175'E. The average annual rainfall is 700mm and annual temperature is 17.6-22.5°C (LSB, 2010).

b) *Experimental design and trial management*

Pre released common bean varieties were planted on four *village* of Borecha *district*. The trial consists of seven improved genotypes and one locally popular variety as a control. The experimental design used was RCB design; where seed producers' villages were used as replications. Before planting, the land was oxen ploughed three times. At each *village* seven genotypes with their local control were grown on plot size of 324m² by dividing the plots in to six rows for each variety (with 40 cm between rows and 10 cm plant spacing). Two seeds were sown per hole and 10 days after emergency it was thinned. DAP was applied with rate of 100kg per hectare and weeding was carried out three times.

c) *Common bean Traits measurement*

i. *Traits measurement from plot basis*

Understated plot based traits were measurements from the two central rows.

1. Days to flowering: Days from planting up to the time when 50% of plants bear flower.
2. Days to physiological maturity: Days from planting up to the time when 95% of plants matured.
3. Hundred seed weight: weight of 100 seeds in gram drawn randomly from the bulk of seeds of each plot when seed moisture content was adjusted to 10.5%.
4. Biomass yield: determined by weighing the total sun dried above ground biomass of plants in the two middle rows per plot.
5. Grain yield: grain yield in kilogram of plants from the three middle rows adjusted to 10.5% moisture level
6. Harvest index: Calculated as the ratio of grain yield to above ground biomass measured at physiological maturity.

ii. *Common bean traits measurement from single plant basis*

Plant based traits were measurements from six randomly sampled plants of the two middle rows on each plot.

1. Number of branches per plant: The numbers of primary branches of six randomly taken plants from each of the two middle rows excluding the main plant were counted at maturity and the average was taken per plot.
2. Pod length: pod length from base to tip of four random pods from each of ten random plants per plot was measured and expressed as average of ten plants per plot.
3. Pods per plant: Average number of mature pods, counted at harvest on 6 randomly taken plants.

4. Number of Seeds per pod: Average number of seeds per pod, counted at harvest on 6 randomly taken plants, in five randomly taken pods per plant.
5. Plant height (cm): Length of the central axis of the stem, measured from the soil surface up to the tip of the stem
6. Hundred Seed weight: the weight of 100 seeds in gram per plant was taken at moisture of 10.5%.

d) *Statistical Analysis*

Combined analysis of variance over each village was done as per Gomez and Gomez, (2004) using PROC GLM SAS software version 9.0 (SAS, 2002). The villages (as replication) and varieties were used as fixed variables, therefore fixed model was used. Mean separation was done by Duncan Multiple range test (DMRT) at probability level 0.05. Correlation analysis was carried out to determine association of yield to its components. Phenotypic correlation was computed by PROC CORR of SAS software.

e) *Stability analysis for grain yield*

Stability statistics for the grain yield were computed by SAS GLM procedures using a program written by Hussein *et al.*, (2000). Angles between environment vectors were used to judge correlations (similarities/dissimilarities) between pairs of environments (Yan and Kang, 2003). It is important to identify and select genotypes with consistent (stable) performance across diverse environments (broad adaptation). The results can be graphed in a useful bi-plot that shows both main and interaction effects for both genotypes and environments (Guach and Zobel, 1998).

III. RESULT AND DISCUSSION

a) *Phenological parameters and Growth Parameters*

A very highly significant difference was observed between varieties for days to flowering and physiological maturity (Table 1). Varieties Dinkinash, Omo-95, Nasir, Hawassa dume, Dimtu and Red woliata flowered later than Melka dima and Ibado (Table 2). Kassu, (2009) and Daniel, (2007) made similar observation on different common bean varieties. The observed difference in days to flowering and maturity were due to varieties difference in genotypic makeup, as common bean show variability in growth habit, seed characteristics, maturity and adaptation.

Table 1 : Variation of red common bean genotypes for crop phenology and growth parameters

Traits	Source of Variation			CV
	Replication (df=3)	MSv(df=7)	MSe (df=21)	
Days to flowering (no. days)	43.91***	28.57***	1.79	2.92
Days to maturity (no. days)	11.19 ^{ns}	67.74***	6.05	2.70
Plant height (cm)	1021.56 ***	643.55***	142.62	21.92
Pod length (cm)	1.23**	2.80***	0.25	4.91
Branch per plant	0.31 ^{ns}	0.54*	0.16	10.79

df =degree of freedom, MSv =mean square of variety, MSe=Mean square of error

CV= coefficient of variation

There was a very highly significant genotypic difference in plant height and pod length (Table 1). The mean values of plant height ranged from 45.30 for Ibado to 83.12cm for Omo-95 (Table 2). Kassu, (2009) observed the same result for Omo-95 for plant height. The highest plant height observed for Omo-95 was due to the climbing nature of the variety. Significant association ($r=0.437^*$) of plant height was observed with number of pods per plant (Table 5). The highest pod length (12.00) was recorded for Ibado and the lowest (9.09) for Nasir. The differences in plant height and pod length between varieties were due to genotype and environment.

Significant difference was observed between varieties for branch per plant (Table 1). The result was in contrast of Amanullah and Asim (2011), who reported insignificant variation between common bean germplasm collected from Pakistan. Significant difference observed across location (replication across villages) for days to flowering, plant height and pod length was due to variability in growing environment. Insignificant difference between replication for days to flowering might be due to offset of rainfall in the villages at the same time.

Table 2 : Means of common bean genotypes for crop phenology and growth parameters

Varieties	Days to flowering	Days to maturity	plant height	Pod length	Branch per plant
Melka dima	41.00e	88.25cd	45.74b	10.84b	4.00ab
Dinkinash	45.0dc	93.75b	57.81b	10.00bc	3.16c
Omo-95	48.00ab	87.00d	83.12a	10.03bc	3.78abc
Nasir	46.00bc	88.25cd	47.24b	9.09d	3.50
Ibado	43.25d	98.75a	45.30b	12.00a	3.83ab
Hawassa dume	47.00abc	91.00cb	48.60b	10.21bc	4.16a
Dimtu	48.00ab	87.50cd	49.15b	10.02a	4.21a
Redwoliata ¹	48.75a	93.75b	58.80b	10.16bc	3.44
CV	2.92	2.70	21.92	4.91	10.79

1= control cv=coefficient of variation

b) Yield and yield components

Significant difference was number of pods per plant was observed among common bean varieties (Table 3). Dimtu and Hawassa dume produce highest mean number of pods per plant while the lowest was produced by Red woliata (Table 4). The observed difference in number of pod per plant was probably due to their genetic potential. Difference in productivity is primarily associated with number of pods per plant as observed from their significant correlation ($r=0.667^{**}$) and ($r=0.646^{**}$) for biomass yield, grain yield respectively (Table 5). Similarly, Daniel (2007) observed significant correlation between common bean cultivars at Awassa and Tefera (2006) observed differences in number of pods per plant among haricot bean cultivars at Eastern Ethiopia. Seed number per pod was highly

significant among varieties and insignificant across location (Table 3). The range was from 4.85 for Melka dima and 6.60 for Omo-95. Hundred seed weight was negatively correlated ($r=-0.617^{**}$) with number of seed per pod (Table 5). Thus there is evidence that selection for a larger number of seeds per pod increase grain yield and decrease seed size.

Varieties showed significant difference in 100 seed weight (Table 3). The highest hundred seed weight of 42 and 40.60 g was recorded from Ibado and Melka dima respectively. Lowest hundred seed weight was recorded from Dinkinash (18.40 g), Omo-95 (18.55 g) and Red woliata (control) (19.13 g). The highest difference was observed was due to maximum seed size nature of the varieties which was actually influenced by growth environment (Gallagher *et al.*, 1975).

Table 3 : Mean square values for yield components, grain yield, biomass yield, and harvest index

Traits	location (df=3)	MSv(df=7)	MSe (df=21)	CV
Pod per plant	362.43**	116.30**	47.34	23.90
Seed per pod	0.47 ^{ns}	1.38 **	0.37	10.03
100 seed weight (g)	16.26*	371.92**	4.09	7.73
Biomass yield (kg)	8137196.01**	16412925.96**	2483466.6	33.00
Grain yield (kg)	3277475.52**	2074856.63**	473941.22	32.80
Harvest index	6.62 ^{ns}	2.27 ^{ns}	0.40	26.74

df =degree of freedom, MSv =mean square of variety, MSe=Mean square of error

CV= coefficient of variation

Biomass: Significant differences have been observed for shoot biomass accumulation among common bean varieties (Table 3). Highest biomass yield was obtained from Hawassa dume (6770.83kg/ha) while the lowest (2317.70 kg/ha) was from Red woliata (Table 4). Similar observation was made by Daniel, (2007) in which Red woliata was resulted in lower biomass than Awash-1 at Awassa. There was a positive and significant correlation of biomass yield with grain yield ($r=0.834^{**}$), plant height ($r=0.375^{*}$), pod per plant ($r=0.667^{**}$) and branch per plant ($r=0.441^{*}$) (Table 5). Shoot biomass accumulation was considered as important trait to attain high seed yield in grain legumes (Saxena *et al.*, 1990).

Grain yield: Significant cultivar differences were observed for grain yield (Table 3). Highest grain yield of (3098.95kg/ha) and (3046.87kg/ha) was obtained from Hawassa dume and Dimtu respectively. Whereas the lowest mean grain yield (1093.74 kg/ha) was obtained from local check Red woliata (Table 4). In larger extent biomass yield, plant height, pods per plant, and branch per plant were determined the differences in yielding levels of tested genotypes. There was positive and significant correlation of grain yield with biomass yield ($r=0.834^{**}$), plant height ($r=0.375^{*}$), pod per plant ($r=0.667^{**}$) and branch per plant ($r=0.441^{*}$) (Table 5). Greater productivity of the varieties may have been partly associated with growing environment. In contrast to Kebera *et al.*, (2006), positive correlation coefficients were obtained for grain yield with pod per plant ($r=0.667^{**}$) and branch per plant ($r=0.589^{**}$); however, pod length, hundred seed weight and seed per pod did not show association with grain yield (Table 5). Several authors also observed lack of association between grain yield and hundred seed weight of different crops (Riggs *et al.*, 1981; Waddington *et al.*, 1987; White and Izquierdo, 1991; Tarekegne, 1994; Teklu, 1998).

Harvest index: Differences in harvest index were insignificant among varieties (Table 3). The mean harvest index of Melka dima and Hawassa dume was high (0.50 and 0.53) respectively (Table 4), which was probably associated with greater shedding of leaves aggravated by high temperature, occurred around maturity before harvesting. Likewise, higher harvest index value of 0.59 for chickpeas (Saxena *et al.*, 1983)

was reported as the result of greater loss of leaves before measurements. However, harvest index was insignificant between genotypes which were the same with finding of Daniel, (2007). Harvest index was positively correlated with biomass and insignificantly correlated with grain yield (Table 5). Similarly, Laing *et al.*, (1984) on haricot bean, Salado-Navarro *et al.*, (1993) on soybean and Teklu (1998) on teff found positive correlation between grain yield and biomass yield but no correlation between grain yield and harvest index. In contrast, no relation between grain yield and biomass yield and positive association between grain yield and harvest index were reported on bread wheat (Tarekegne, 1994). Other authors also reported grain yield to have positive association with both biomass yield and harvest index (Riggs *et al.*, 1981; Waddington *et al.*, 1987; Perry and D' Antuono, 1989). Hence, the result reported herein indicated that grain yield improvement resulted from biomass production rather than the harvest index. These findings suggest that the characters showing positive correlation could effectively utilized in crop improvement program and develop new common bean genotypes.

Table 4 : Means of genotypes for yield components, grain yield, biomass yield and Harvest index

Varieties	Pod per Plant	Seed per pod	100 seed weight	Biomass yield	Grain yield	Harvest index
Melka dima	25.98bc	4.85b	40.60a	3880.20bc	1943.55bc	0.50ab
Dinkinash	26.60bc	6.20a	18.40c	3802.08bc	1432.29bc	0.38ab
Omo-95	30.84abc	6.60a	18.55c	5677.08ab	1718.75bc	0.30b
Nasir	25.23bc	6.13a	23.20b	4322.91bc	2031.24bc	0.47ab
lbado	26.04bc	5.59ab	42.00a	5442.70ab	2421.87ab	0.44ab
Hawassa dume	35.45ab	6.43a	22.47b	6770.83a	3098.95a	0.46ab
Dimtu	37.78a	6.27a	24.90b	5781.25ab	3046.87a	0.53a
Red woliata ¹	22.37c	6.55a	19.13c	2317.70c	1093.74c	0.47ab
CV	23.90	10.03	7.73	33	32.80	26.74

¹ = control CV=coefficient of variation

Table 5 : Correlation (r) analysis between common bean traits

	BM	GY	HI	PH	PL	PPP	HSW	SPP	PPP	DF
BM										
GY	0.834**									
HI	-0.263	0.248								
PH	0.375*	0.030	-0.365*							
PL	0.287	0.244	-0.002	0.149						
PPP	0.667**	0.646**	0.047	0.437*	0.189					
HSW	0.105	0.209	0.075	-0.313	0.627**	-0.059				
SPP	0.287	0.156	-0.185	0.423*	-0.223	0.346	-0.617**			
BPP	0.441*	0.589**	0.143	-0.080	0.207	0.437*	0.145	-0.002		
DF	0.043	0.100	0.059	0.164	-0.473**	0.034	-0.579**	0.420*	0.171	
DM	0.14	0.014	0.078	-0.067	0.562**	-0.093	0.232	0.008	-0.100	-0.155

BM=Biomass, GY=Grain Yield, HI=Harvests Index, PH=Plant height, PL= Pod Length, PPP=Pod per plant, HSW=Hundred seed weight, SPP= Seed per Pod, BPP=Branch Per plant, DF=Days to flowering, DM=Days to maturity, *, **, ***, significant, highly significant and very highly significant respectively

c) Grain Yield Stability

Since the presence of genotype environment interaction (GEI) effects hinder the identification and recommendation of genotypes over wide environments, performing stability analysis to identify stable genotypes based on the traits of interest is crucial. Several statistical models including uni-variate and multivariate have been developed to evaluate genotype stability. This paper concentrates on the most popular one, the AMMI model. Grain yield stability analysis was conducted for eight genotypes of common bean.

Variability in yield and interaction principal components (IPCA 1) of environments and genotypes are presented on (Figure 1). According to this IPCA 1, two environments (village) Shello Balela and Hanja Goro are high yielding environments that were favorable for the for common bean production. The remaining two environments, Shelo Abore and Sidamo Chala were the lowest yielding environments that were the least favorable to the tested genotypes.

Highest yield was obtained from Hawassa dume and Dimtu at village 1, 3 and 4. Variety located near to origin of the plot was less responsive than the vertex variety (Figure 1). Accordingly, Nasir is stable variety in all villages. Red woliata and Melka dima are

found outside the vertex which indicates unstable of the nature varieties. Villages 1 and 3 near to the origin and relatively exhibit low interaction with varieties. Such environment is good for variety selection with average adaptation. Villages 2 and 4 show high interaction with varieties which is not good for variety selection.

Variety located near to origin of the plot is stable and less responsive than the vertex variety (Figure 1). Genotype named 'Nasir' is found near to the vertex, so that it is the stable variety in all villages. Red woliata and melka dima are found outside the vertex which indicates unstable nature of the varieties. Villages 1 and 3 near to the origin and relatively exhibit low interaction. These environments are good for variety selection with average adaptation. Villages 2 and 4 show high interaction with varieties which is not good for variety selection.

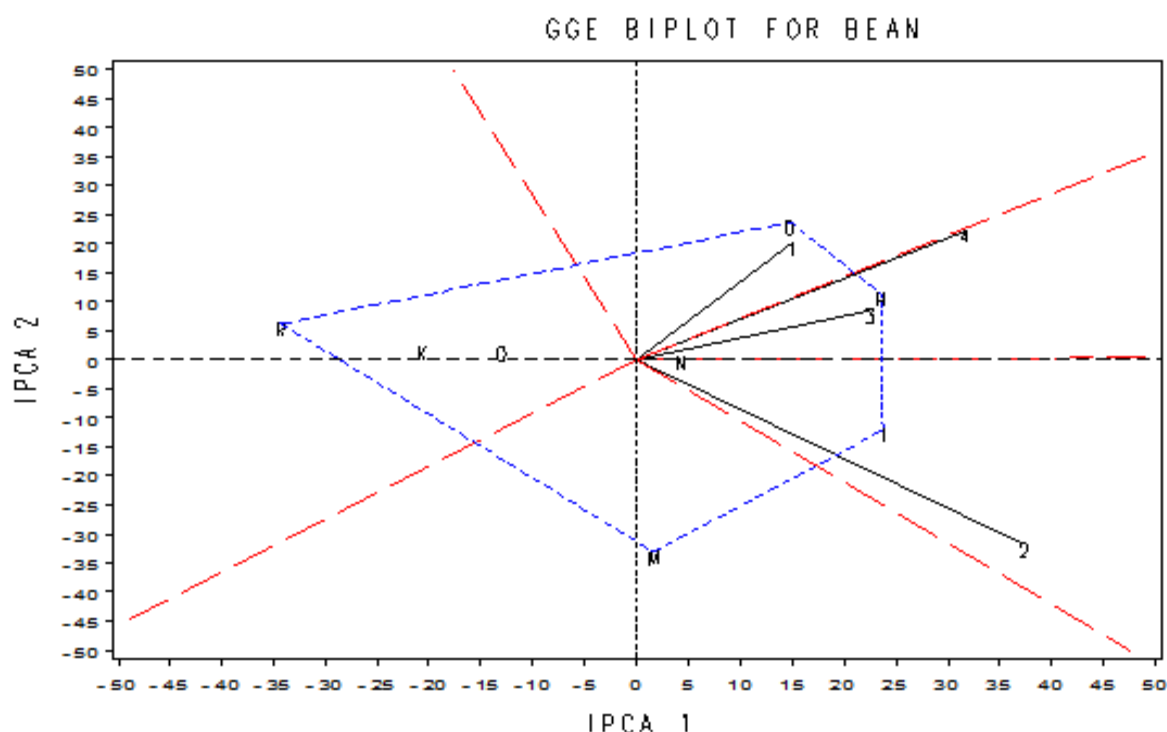


Figure 1 : Grain Yield biplot of 8 genotypes and four environments

1– 4 are the four villagess; D – Dimtu, H- Hawassa Dume, I – Ibado, N – Nasir M – Melkadima, K – Dinknesh, O – Omo95, R – Red Wolayita)

IV. CONCLUSION AND RECOMMENDATION

A significant genotype difference was observed for days to flowering and days to physiological maturity. Hawassa dume, Dimtu and Melka dima were matured than other genotypes. The analysis also indicated a significant difference regarding plant height and pod length. The mean values of varieties for plant height ranged from 45.30 for Dimtu to 83.13 cm for Omo-95. The maximum pod length 12.0 was recorded for Ibado while the minimum 9.03 cm was for Nasir. Significant different was observed among genotypes for branch per plant. Positive correlation was observed between branch per plant and pod per plant ($r=0.437^*$), biomass yield ($r=0.441^*$) and grain yield ($r=0.589^{**}$) indicating greater impact of branch per plant on yield and yield components. These finding suggest that the characters showing positive correlation could effectively be utilized in crop improvement program and develop new common bean varieties.

Significant different among genotypes were observed for number of pods per plant, 100 seed weight, biomass yield and grain yield. Highest pod number per plant was obtained from Dimtu and Hawassa dume. Following the same trend, relatively highest grain yield was obtained from Hawassa dume (3098.95kg/ha) and Dimtu (3046.87kg/ha). The lowest pod per plant and grain yield (1093.74 kg/ha) was obtained from Red woliata (local check). However, best yield performance alone could not be enough to

recommend varieties across environments. Since significant genotype environment interaction effects were observed for most of the traits studied, there should be stability analysis to identify the most stable varieties across the test environments and unstable varieties for narrow adaptation. There for stability analysis is conducted for grain yield which is major traits of interest for common bean users using the most popular stability analysis; AMMI. Accordingly, one variety called Nasir was identified as stable for grain yield. The two top yielding varieties, Hawassa dume and Dimtu were found to be unstable and could be recommended for narrow adaptation (village 1, 2 & 3)

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Prevalence of Ovine Pasturellosis and In-Vivo Evaluation of the Level of Protective Antibody Titer before and after Ovine Pasteurellosis Vaccination in Bonga Sheep

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Abstract- Cross-sectional study for determining the prevalence of Ovine pasturellosis, in-vivo evaluation of the level of protective antibody titer before and after vaccination against the disease and proofing the farmers and animal health experts complaint of its cause on small ruminant production despite annual vaccination program against the disease in Adiyo district of Boka-Shuta and Buta Kebelle, Kaffa Zone. The study was conducted from July 2012 to June 2013 and the study kebelles were purposively selected based on sheep production potential, the disease's report and farmers' complaint on the vaccine's inefficacy for protecting the sheep against the disease. For these, the study was designed to answer the above stated objectives with two consecutive phases, viz. prevalence study followed by in-vivo antibody titer evaluation. For prevalence study, 192 blood samples were needed and calculated, but for more accuracy 200 samples were collected randomly from previously unvaccinated sheep population (in less than 1 year) against ovine pasturellosis disease.

Keywords: antibody titer, in-vivo evaluation, ovine pasteurellosis, prevalence, sheep, vaccination.

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Prevalence of Ovine Pasturellosis and In-Vivo Evaluation of the Level of Protective Antibody Titer before and after Ovine Pasteurellosis Vaccination in Bonga Sheep

Fisseha Mengstie ^α, Hailemariam Gizaw ^σ & Desiye Tesfaye ^ρ

Abstract- Cross-sectional study for determining the prevalence of Ovine pasturellosis, in-vivo evaluation of the level of protective antibody titer before and after vaccination against the disease and proofing the farmers and animal health experts complaint of its cause on small ruminant production despite annual vaccination program against the disease in Adiyo district of Boka-Shuta and Buta Kebelle, Kaffa Zone. The study was conducted from July 2012 to June 2013 and the study kebelles were purposively selected based on sheep production potential, the disease's report and farmers' complaint on the vaccine's inefficacy for protecting the sheep against the disease. For these, the study was designed to answer the above stated objectives with two consecutive phases, viz. prevalence study followed by in-vivo antibody titer evaluation. For prevalence study, 192 blood samples were needed and calculated, but for more accuracy 200 samples were collected randomly from previously unvaccinated sheep population (in less than 1 year) against ovine pasturellosis disease. For in-vivo evaluation, 52 blood samples were randomly collected from selected sheep population after they were vaccinated against ovine pasturellosis disease with *P. multocida* biotype A-vaccine by grouping them based on history of vaccination status (not vaccinated in less than 1 year against ovine pasturellosis disease) and age group (greater than 6 months of age). Sample collection, preservation and transportation were performed according to the recommended standard procedures. Laboratory analysis, Indirect haemagglutination Inhibition Test was employed at National Veterinary Institute (NVI), Ethiopia for both studies. Thus, out of 200 serum samples, 175 (87.5%) were positive. However, there were no statistical significant difference ($p \geq 0.05$) between study areas, age and sex of the animals. Regarding in-vivo evaluation of the level of protective antibody titer, it was found 87.5% before vaccination and 98.1% after vaccination. However, there was no statistically significant difference in between the study areas. In conclusion, Ovine pasturellosis was the major diseases of sheep in the study areas and the monovalent killed *P. multocida* biotype A-vaccine applied against ovine pasturellosis in the field was found effective in developing protective antibody in the vaccinated population. However, the complaint of the farmers and animal health

experts on the inefficacy of the applied vaccine despite annual vaccination program could be due to the presence of *M. haemolytica* serotypes which could not be cross-protected. And also, there were no research work on the serotypes present in the study areas. Therefore, comprehensive serological identification of involved serotypes for causing ovine pasturellosis should be performed, which could give the opportunity to know the exact antigenic structure present and indicate the use of multivalent vaccines combination against the disease in the study areas.

Keywords: antibody titer, in-vivo evaluation, ovine pasturellosis, prevalence, sheep, vaccination.

I. INTRODUCTION

Ethiopia lies within the tropical latitude of Africa and has an extremely diverse topography, a wide range of climatic features and a multitude of agro-ecological zone which makes the country suitable for different agricultural production system. This contributed to the existence of a large diversity of farm animal genetic resource in the country (Anon, 2004). Sheep constitute the second major component of livestock in Ethiopia and they play a significant role in the nation's economy. Meat and milk are major sources of protein, and hides, live animals, and carcasses account for a significant proportion of exports. The increased demand for sheep meat, cash income and food security has increased their importance in the country (Alemu and Merkel, 2008). Despite the large livestock population of Ethiopia the economic benefits remain marginal due to prevailing diseases, poor nutrition, poor animal production systems, reproductive inefficiency, management constraint and general lack of Veterinary core (Anon, 1992).

In Ethiopia, Sheep and goats contribute 25% of the meat domestically consumed with a production surplus mainly being exported as live animals (Alemayehu and Fletcher, 1991; Tibbo, 2006). Both species also contribute 50% of the domestic needs in wool, about 40% of skins and 92% of the value of hides and skin exported (ILCA, 1993). The total income share of small ruminants tends to be inversely related to size of land-holding, suggesting that small ruminants are of particular importance for landless people. In some

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settings where, agriculture (crop production) provides only seasonal employment, rearing small ruminants would provide employment and income as a subsidiary occupation (Coppock *et al.*, 2006).

Indigenous small ruminants constitute greater percentage of ruminant population in Africa (Lebbie *et al.*, 1994). These flocks of animals are commonly found in the rural areas where they are owned and managed under extensive system (Otchere, 1986). Small ruminants play an important role in the lives of most people especially rural farmers who livelihood entirely depend on them. They provide source of animal protein through their meat and milk (Fajemisin, 1991). Notwithstanding, they fetch a source of income when sold to meet some other family needs as well as play a vital social roles during ceremonies and festivals.

The importance of small ruminants (ie sheep and goats) to the socio-economic well being of people in developing countries in the tropics in terms of nutrition, income and intangible benefits (eg savings, insurance against emergencies, cultural and ceremonial purposes) cannot be overemphasized (Kosgey, 2004). Sheep and goats are important livestock species in developing countries because of their ability to convert forages, and crop and household residues into meat, fibre, skin and milk.

For an improved animal protein intake, there is need for improvement in the production of meat and other protein sources from the livestock industry. Sheep and goats offer a great potential in this respect due to their relative ease of breeding, management, ability to subsist on forages, hardiness, adaptation to a wide range of ecological zones and distribution among others. In recent times, sheep and goats production is becoming popular even among urban dwellers as result of the aforementioned merits (Umunna *et al.*, 2014).

Small ruminant management is seriously hindered by diseases in the tropics. Diseases are very important to farmers and affect the production of small ruminants in several ways. It increases cost of production, lowers production level, reduces the quality and quantity of animal products and generally causes great loss to the farmer (Abdullahi *et al.*, 2013). Respiratory diseases caused by concurrent infections have been identified as the leading health problem of small ruminants which accounts for up to 54% of the overall mortality of sheep in Ethiopian central highlands (Mukasa-Mugerwa *et al.*, 2000). Mannheimia haemolytica (formerly called Pasteurella haemolytica) and Pasteurella multocida are known to be the most prominent pathogens causing great economic losses in the domestic animal industry (Highlander, 2001; Confer, 1993). Pasteurellosis is a complex disease that develops when the immune system of the animal is compromised by stress factors mainly environmental stresses including inclement weather, feed shortage usually

assisted by inadequate management and husbandry practices (Bekele *et al.*, 1992).

As Kaffa Zones, pasteurellosis is considered to be the major sheep health problem and there have been a report on high rates of mortality and morbidity associated with the disease. And also, despite annual vaccination programs against pasteurellosis with the only commercially available Killed *P. multocida* biotype A containing vaccine (National Veterinary Institute, Ovine pasteurella vaccine) in the study areas, high mortality and morbidity continued to be observed and complaint by farmers and veterinarians. So far in the study area, it was the only vaccine type given to the farmer's sheep and was available in the market during the time of the research study. Therefore the present study was designed with the objectives of determining the prevalence of Ovine pasteurellosis, In-vivo evaluation of the level of protective antibody titer before and after vaccination with commercially available ovine pasteurellosis vaccine and proofing the farmers and animal health experts complaint of its cause on small ruminant production despite annual vaccination program against the disease in Adiyo district of Boka-Shuta and Buta Kebelle, Kaffa Zone.

II. MATERIALS AND METHODS

a) Study area, Study Design and Study Population

Cross-sectional study for determining the prevalence of Ovine pasteurellosis, In-vivo evaluation of the level of protective antibody titer before and after vaccination with commercially available ovine pasteurellosis vaccine and Proofing the farmers and animal health experts complaint of its cause on small ruminant production despite annual vaccination program against the disease in Adiyo district of Boka-Shuta and Buta kebele, Kaffa Zone, Southern Nations Nationalities and Peoples regional state was conducted from July 2012 to June 2013. The study kebelles were purposively selected based on sheep production potential, the disease's report and farmers' complaint on the vaccine's inefficacy for protecting the sheep against ovine pasteurellosis disease.

The study animals were Bonga sheep breed of both sex and all age group. Bonga sheep breed is geographically distributed and reared in Keffa, Sheka and Bench zones of Southern State and have physical feature and performance levels of Long fat tail with straight tapering end (98.4%); hair sheep; large size; predominantly plain brown (57.9%); both sexes are polled (Gizaw *et al.*, 2011).

b) Sample Size determination

The sample size was calculated based on 2013 prevalence's reported by Maru *et al.*, (25%) in Haramaya district with 5% desired absolute precision at 95% confidence level using the formula recommended by Thrusfield (2005). Thus, 192 blood samples were

needed to calculate the prevalence rate of the population.

The study had two consecutive phases, i.e, prevalence determination and in-vivo antibody titer evaluation. For these, blood sample collection was performed prior to vaccination (to determine the prevalence of ovine pasturellosis) and post vaccination (to evaluate the effectiveness of ovine pasturellosis vaccine). The time interval for sampling of the study animals between before and after vaccination was 20 day.

c) Blood Sampling and Laboratory analysis

i. Prevalence Determination

A total of 200 blood samples were collected from sheep of previously unvaccinated against ovine pasturellosis disease (at least a history of less than 1 year) according to standard procedures from the animal's jugular vein using plain vacutainer tubes and sterile needles and allowed to clot for 1-2 h at room temperature, stored horizontally overnight at 4°C and finally, the serum was separated from the clot. The separated serum was labeled and transported to National Veterinary institute (NVI) laboratory using cold chain and it was kept under refrigeration (-20 °C) until tested to determine the level of Sero-positivity. The type of laboratory test employed was Indirect haemagglutination Inhibition Test.

ii. In-vivo Antibody Titer Evaluation

Among the sixteen Bonga sheep breed improvement Community sites (cooperatives), Boka-Shuta site was selected for the study. The type of vaccine used was Ovine pasteurolosis (*P. multocida* biotype A) which is currently produced by National Veterinary Institute, Ethiopia and marketed for field vaccination against ovine pasturellosis disease. The study animals, fifty two sheep of both sex were randomly selected by grouping them based on their history of vaccination status (not vaccinated in less than 1 year against ovine pasturellosis disease) and age group (greater than 6 months of age). The selected sheep were vaccinated with *P. multocida* biotype A vaccine. The vaccine was administered through sub-cutaneous (SC) route around lateral cervical vertebrae. Then after, blood samples were collected from the animal's jugular vein using plain vacutainer tubes and sterile needles and allowed to clot for 1-2 h at room temperature, stored horizontally overnight at 4°C and finally, the serum was separated from the clot. The separated serum was labeled and transported to National Veterinary institute (NVI) laboratory using cold chain to identify the level of specified antibody in their serum.

The type of laboratory test employed was indirect haemagglutination (IHA) test. IHA test was conducted according to the procedures of OIE (2004). The source of *Pasteurella multocida* serotypes of

biotype A was CIRAD-EMVT, France. A titer greater than or equal to 1:16 was taken as positive.

d) Data Management and Analysis

All data was first entered and managed using Microsoft Excel spread sheet and analyzed using STATA version 11. Descriptive statistics was employed to determine the prevalence while Chi-square (χ^2) test was used to measure the effect of predisposing factors. A significance level ($p < 0.05$) and confidence level (95%) was set to determine the presence or absence of statistically significant difference between the given parameters.

II. RESULTS AND DISCUSSIONS

a) Prevalence of Ovine pasturellosis

Out of 200 serum samples, 175 (87.5%) was positive for ovine pasturellosis. The prevalence in between the study areas, age and sex had not statistical significant difference ($p \geq 0.05$) (Table 1).

The present finding is higher than the report of 31.1% by Aschalew (1998) in Debre Birhan and 83% by Sisay and Zerihun (2003) in Wollo area. Ayelet et al (2004) reported higher prevalence of respiratory problems in July (64%) in central highlands of Ethiopia which had a positive correlation with rainfall pattern, suggesting that climatic conditions play a role.

The higher prevalence in this study could be related to various forms of stress factors as predisposing factors include environmental (heat, cold, wind, chill, crowding), managemental and/or infectious factors also reported by different Authors (Thompson *et al.*, 1977; Frank, 1989; Carroll and Forsberg 2007). Another finding by Mengstie (2014) indicated that, there were 81% prevalence of ovine pasturellosis and in Autmen and summer as explained by the farmers in the same study area predisposed to different stress factors.



Table 1 : Prevalence and Distribution of Ovine Pasturellosis in Selected Community based Bonga Sheep Breed Improvement Site

Variables		Number of sample	Prevalence of ovine pasturellosis	Sig.
Study Area	Boka-Shuta	100	87(87.0)	Ns*
	Buta	100	88(88.0)	
Age	Adult	112	97(86.6)	Ns
	Young	88	78(88.6)	
Sex	Female	148	130(87.8)	Ns
	Male	52	45(86.5)	
Total			175(87.5)	

*Not significant

b) *In-vivo Antibody Titer Evaluation of Ovine Pasteurellosis Vaccine*

The level of protective antibody titer against ovine pasteurellosis before vaccination was 87.5 %, while after vaccination the antibody titer in response to *Pasteurella multocida* Bio-type A Vaccine was 98.1%. (Table 2 and Fig 1). There was no significant difference in level of antibody titer across sex and age ($p > 0.05$). Similar observations were reported by Ferede et al (2013) when the level of protective antibody ($> 1:16$) was increased from 32.5% (before vaccination) to 87.5% (after vaccination) which were vaccinated with *P. multocida* Bio-type A vaccine in northwest Ethiopian sheep and the author suggested that, the higher protective antibody titer recorded in the vaccinated

population could be due to the result of *P. multocida* Bio-type A vaccine, which induced higher level of invivo antibody production.

In the present finding, however, despite annual vaccination programs against pasteurellosis using Killed *P. multocida* biotype A containing vaccine (National Veterinary Institute, Ovine pasteurella vaccine) in the study areas, high mortality and morbidity continued to be observed and complaint by farmers and animal health experts and these could be best explained by Ayelet et al (2004) studied in central highlands of Ethiopia, as incompleteness of the available vaccine for pasteurellosis which does not include all species and serotypes for *Pasteurella haemolytica* could not completely protect sheep from pasteurellosis.

Table 2 : Comparative Evaluation of Antibody Titer of Ovine Pasteurellosis Before and After Vaccination in response to *Pasteurella multocida* Bio-type A Vaccination

Variables	Study Area	Before vaccination (N= 200)		After vaccination (N= 52)		Sig.
		Positive ($\geq 1:16$) (%)	Negative ($\leq 1:16$) (%)	Positive ($\geq 1:16$) (%)	Negative ($\leq 1:16$) (%)	
Study area	Boka-shuta	87(87.0)	13(13.0)	25(49.0)	1(100)	0.313
	Buta	88(88.0)	12(12.0)	26(51.0)	0(0.0)	
Age	Adult	97(86.6)	15(13.4)	36(70.6)	1(100)	0.520
	Young	78(88.6)	10(11.6)	15(29.4)	0(0.0)	
Sex	Female	130(87.8)	18(12.2)	36(70.6)	1(100)	0.520
	Male	45(86.5)	12(13.5)	15(29.4)	0(0.0)	
Total		175(87.5)	25(12.5)	51(98.1)	1(1.9)	

*Not significant

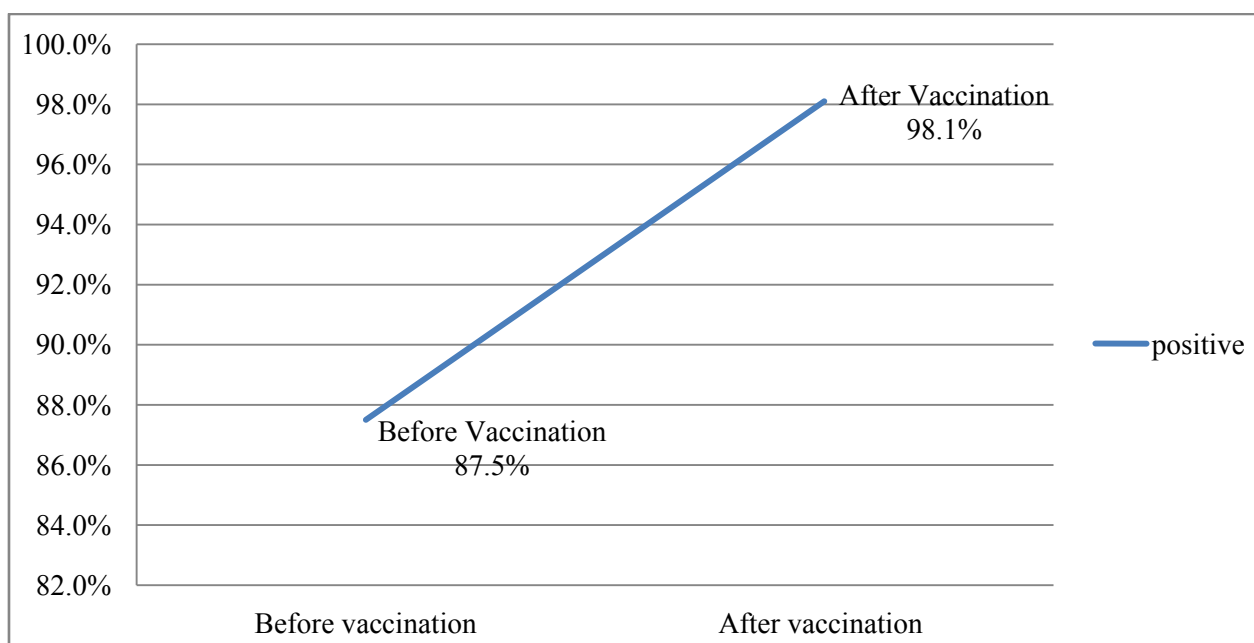


Figure 1 : Comparative Evaluation of Antibody Titer of Ovine Pasteurellosis Before and After Vaccination in response to *Pasteurella multocida* Bio-type A Vaccination

III. CONCLUSION AND RECOMMENDATION

Ovine pasteurellosis was the major diseases of sheep in the study areas and the monovalent killed *P. multocida* biotype A-vaccine applied against ovine pasteurellosis in the field was found effective in developing protective antibody in the vaccinated population. However, the complaint of the farmers and animal health experts on the inefficacy of the applied vaccine despite annual vaccination program could be due to the presence of *M. haemolytica* serotypes which could not be cross-protected. And also, there were no research work on the serotypes present in the study areas. Therefore, comprehensive serological identification of involved serotypes for causing ovine pasteurellosis should be performed, which could give the opportunity to know the exact antigenic structure present and indicate the use of multivalent vaccines combination against the disease in the study areas.

IV. ACKNOWLEDGMENTS

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- Make a decision if each premise is supported, discarded, or if you cannot make a conclusion with assurance. Do not just dismiss a study or part of a study as "uncertain."
- Research papers are not acknowledged if the work is imperfect. Draw what conclusions you can based upon the results that you have, and take care of the study as a finished work
- You may propose future guidelines, such as how the experiment might be personalized to accomplish a new idea.
- Give details all of your remarks as much as possible, focus on mechanisms.
- Make a decision if the tentative design sufficiently addressed the theory, and whether or not it was correctly restricted.
- Try to present substitute explanations if sensible alternatives be present.
- One research will not counter an overall question, so maintain the large picture in mind, where do you go next? The best studies unlock new avenues of study. What questions remain?
- Recommendations for detailed papers will offer supplementary suggestions.

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- When you refer to information, differentiate data generated by your own studies from available information
- Submit to work done by specific persons (including you) in past tense.
- Submit to generally acknowledged facts and main beliefs in present tense.



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References	Complete and correct format, well organized	Beside the point, Incomplete	Wrong format and structuring



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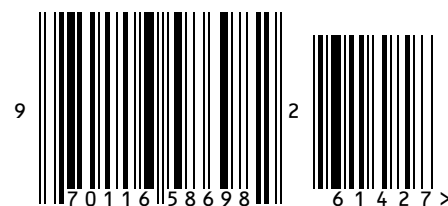
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