ESTIMATE OF HERITABILITY OF GROWTH RATE IN RABBIT

BY

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DEPARTMENT OF ANIMAL SCIENCE
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CERTIFICATION

This is to certify that this project work was carried out by Grace Woyin-Imomoemi CLEMENT (Miss) from the Department of Animal Science, Faculty of Agriculture, University of Benin, Benin City, Nigeria, under the supervision of Professor A. M. Orheruata.

Professor A. M. Orheruata (Supervisor)	Date
Professor J. A. Imasuen (Head of Department)	Date

DEDICATION

This work is dedicated to God Almighty for his infinite mercy and my parents Mr.Clement Udoh Sam and Inspector Akpoboloukeme Christopher.

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I want to give all glory and thanks to God Almighty for guiding me throughout the years and giving me the strength to go through my academic years in the University of Benin.

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ABSTRACT

This project was carried out to determine the Estimate of Heritability of Growth Rate in Rabbits" which endeavors to interpret the genetic basis governing the growth performance of rabbits, an important trait in the context of animal agriculture. The experiment was carried out at the rabbitry section of the University of Benin Farm Project, Benin City, Edo state, Nigeria. A total of twenty rabbits (fifteen females and five males), of which five belong to one breed, were used for this experiment. The breeds used were New Zealand White, Chinchilla, Hyla and Dutch. The rabbits, which were 3 months of age, were kept for a duration of 18 weeks. Data collected were on Litter size at Birth, at two weeks and at weaning, Litter weight at Birth, at two weeks and at weaning were collected. encompassing a diverse population of rabbits, we aimed to quantify the heritability of growth rates, thereby discerning the relative influence of genetic factors. The data obtained was subjected to statistical analysis using GENSTAT, 12th edition and Heritability estimate was obtained by first Solving for variance components (due to sire, due to standard error and phenotype) using the result obtained from the analysis.

The result of the quantitative genetic components of litter size and growth rate were extensively analyzed, yielding noteworthy insights. Heritability estimates for litter size at birth and two weeks revealed substantial values (0.64 and 0.74, respectively), demonstrating significant genetic influence. Litter size at weaning exhibited a heritability estimate of 0.57, further emphasizing the genetic component in this trait. In contrast, the heritability estimate for weight gain, particularly litter weight at birth, two weeks, and weaning, ranged from 0.02 to 0.37, indicating a comparatively lower genetic influence.

The study shows that for litter size at birth and two weeks, there are high heritability estimates, suggesting that a significant portion of the variability in these traits can be attributed to genetic factors. This implies that selective breeding based on these traits could be effective in improving them. On the other hand, the heritability estimates for weight gain are lower, indicating that genetic factors play a relatively smaller role in determining this trait.

This research contributes valuable insights for breeding and for efficient and sustainable rabbit farming practices.

CHAPTER ONE

INTRODUCTION

Heritability is a term that describes how much of a trait's variation can be attributed to genetic factors. This concept holds significant importance in genetics and finds applications in various fields, including agriculture, animal breeding, and human genetics (Falconer *et al*., 1996). It represents the proportion of the variation in a trait that is influenced by genetic factors. Essentially, it indicates to what extent differences in a specific trait among individuals can be linked to differences in their genetic composition. This value typically falls between 0 and 1, where 0 suggests that the trait is primarily influenced by environmental factors, while 1 implies that genetic factors are the primary influencers (Mark *et al*., 2014). In genetics, heritability is a central measure for quantifying the extent to which genetic differences contribute to the observed variability in a trait. Commonly, methods for estimating heritability are based on random-effect models, largely for computational efficiency. The consideration of using a fixed-effect model has received relatively limited attention in the literature (Mai *et al*., 2021).It's important to note that heritability pertains to populations and does not indicate the genetic contribution to an individual's specific phenotype. These estimates are derived from the diversity of a trait observed within a population and may not necessarily apply to individual cases (Lynch & Walsh, 1998).

In the context of agriculture, heritability plays an important role in Genetic Improvement. This process involves the development of plant and animal varieties tailored to specific conditions or possessing desirable traits like increased yield, disease resistance, or improved quality. Heritability aids in the identification of the genetic factors contributing to these traits, enabling the selection of individuals with those traits for breeding purposes (Collard *et al*., 2008).

Genetic enhancement is crucial in animal production, aiming to cultivate breeds with advantageous traits like heightened meat or milk output, disease resilience, improved reproductive capabilities and high growth rate. The essential role of heritability in animal breeding programs lies in its capacity to pinpoint animals possessing sought-after traits, thus designating them as parents for successive generations (Hayes *et al*., 2010).

In devising breeding strategies for augmenting animal performance, heritability holds a crucial position. An important aspect of it is 'selection', the process of electing parents for the forthcoming generation, upon which progress hinges. For this selection to be efficacious, it is important that the population exhibits diversity in their genetic constitution concerning the specific trait in question (Subrat, 2000). Essentially, it is the genetically influenced variation that can be leveraged for a sustained enhancement of production attributes in a population. If the majority of variation within the population lacks a genetic basis, it cannot be utilized for enduring improvements.The refinement of livestock production and efficiency owes much to advancements in nutrition, animal health, and breeding, particularly genetics. Genetic enhancement continues to be a cornerstone in the advancement of livestock agriculture, amplifying the efficacy and sustainability of production across all livestock species (Blythe *et al.*, 2020). It remains a potent avenue for advancing the Nigerian livestock industry. (Ibe 1998) emphasized that a comprehensive grasp of fundamental genetics and animal breeding concepts, including genetic parameters of economically significant traits, is a prerequisite for animal genetic enhancement. These parameters, such as heritability, repeatability, and genetic and phenotypic correlations, are ratios of (co)variances and are essential for evaluating the genetic makeup of livestock populations, thereby facilitating upgrades and enhancements.

To ensure a sustained rabbit production and development of the sector, rabbit breeds and breeding practices should be explored. It is important to explore rabbit breeds and breeding practices. Growth rate stands as an important trait influencing the overall productivity and profitability of rabbit farming enterprises. This study shows various means to enhance rabbit production, particularly in relation to their growth rate, by using heritability estimates, which plays a vital role in selecting and breeding animals for heightened growth performance. The magnitude of heritability for important economic traits in rabbit production empowers breeders and farmers to make informed decisions regarding selection methods that lead to swift genetic advancement. Traits boasting high heritability may be enhanced through individual selection, whereas those with lower heritability can be genetically improved through family selection. (Obasi and Ibe 2008) propose that traits with lower heritability can also be elevated through harnessing heterosis via crossbreeding and non-genetically through refining environmental conditions.

Accurate knowledge of genetic parameters, particularly heritability (h2), is instrumental in deploying artificial selection, ultimately culminating in genetic enhancement via fitting breeding strategies . Information on heritability estimates proves invaluable in animal breeding as a means of forecasting potential responses to selection or progress(Kassahun D *et al.*,2022). Given the interdependence of production traits, consideration of these relationships is pertinent in selecting appropriate methodologies. Reported heritability estimates for various maternal and/or production traits in rabbits exhibit substantial variation. These heritability estimates serve as a compass in predicting advancements or setbacks in different traits that may result from diverse practices.

1.2 JUSTIFICATION

The rabbit farming industry is a significant contributor to global meat production. Understanding the genetic basis of growth rate is essential for maximizing profitability and meeting the growing demand for high-quality meat products

Knowledge of heritability allows breeders to make informed selection decisions, focusing on rabbits with superior growth potential. This accelerates genetic progress and leads to more efficient production systems Efficient growth translates to optimized resource utilization, reducing the environmental impact of rabbit farming. This aligns with broader sustainability goals and ensures long-term viability of the industry

Rabbits with enhanced growth rates make the industry more competitive by meeting consumer demands for larger, high-quality meat products. This gives breeders a competitive edge in the market. Rapid, uniform growth reduces susceptibility to health issues associated with slower growth rates. Prioritizing heritable growth traits promotes overall well-being and health in rabbit populations . Estimating heritability contributes to a broader understanding of genetic principles and informs future research in animal breeding and genetics. This knowledge has far-reaching implications for various fields of biology.

1.3 OBJECTIVES OF THE STUDY

The general objective of this study was to determine heritability estimates of growth rate in rabbit production in different breeds of rabbits raised at University of Benin Farm Project.

The specific objectives of this study were to:

1. Determine the variance components for growth traits in rabbits.
2. Estimate of heritability for growth in rabbit production.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 RABBIT FARMING

A significant portion of the global population relies on animal-based protein, yet its production diminishes amid escalating human population demands (McIntire *et al*., 1992). This has spurred the quest for cost-effective, easily accessible protein alternatives that pose minimal competition to humans (Akinmutimi, 2007).

Domestic Rabbits (Oryctolagus cuniculus) represent a significant source of meat production world wide therefore become a viable option, because of their proverbial prolificacy, early maturity, fast growth rate, high genetic selection potential, high feed conversion efficiency and economic utilization of space (Lebas, 1997; Hassan *et al*., 2012).

Rabbits have the potential to be one of the more profitable species to raise.They do not require large amounts of space compared with most other livestock species, and they are generally non demanding animals even if they are very susceptible to disease.(Nathaniel E. U., 2004).

The rabbit is a species that undergoes induced ovulation, with sexually mature does possessing numerous follicles (Harkness and Wagner, 1983). When mating occurs, copulation triggers a hormonal response leading to ovulation approximately 10 hours later (Paufler, 1985). The doe can theoretically be bred 24 hours after giving birth and has a gestation period ranging from 28 to 32 days, allowing for up to 11 litters per year. Rabbit breeds are distinctly identified based on observable traits such as body size, shape, and coat color (Lebas *et al*., 1997). This classification system has been adopted by the American Rabbit Breeders Association, which officially recognizes 47 distinct rabbit breeds, although only a handful are raised in Nigeria (MOLD, 2010).

2.2 RABBIT BREEDS AND CHARACTERISTICS

Among the most prevalent rabbit breeds in West Africa are the New Zealand White, Californian, Chinchilla, French Lop, Dutch, Checkered Giant, Flemish Giant, Angora, and Rex. They are further categorized by size: small breeds weighing about 1.4 – 2 kg at maturity, medium-sized breeds weighing 4 – 5.4 kg, and large breeds weighing 6.4 – 7.3 kg (USDA, 1972). New Zealand White and Californian White fall into the medium-sized category. They are highly favored for meat production due to their favorable growth characteristics and a high meat-to-bone ratio (Oseni, 2008; Mailafia *et al*., 2010). The New Zealand White is also esteemed as a dam breed due to its exceptional maternal genetic traits, particularly in terms of litter size, milk production, and overall mothering ability (Lebas *et al*., 1997; McNitt *et al*., 2000). These positive attributes have been cultivated through specific selection for enhanced reproductive performance (King, 1978; Owen, 1981). However, rabbit breeding studies in the U.S.A. have reported that the New Zealand White generally lags behind crosses in terms of post-weaning fryer growth, feed utilization, and carcass lean yield traits (Ozimba and Lukefahr, 1991; Lukefahr *et al*., 1992). Other popular meat breeds, such as Flemish Giant, French Ear Lop, and Checkered Giant, owe their popularity to their substantial size. Conversely, smaller breeds like Chinchilla, Dutch, and Angora are predominantly kept as pets (Moreki, 2007).

2.3 THE RABBIT INDUSTRY AND GENETIC SELECTION

The rabbit industry plays an important role throughout the agricultural sector in some European countries, such as Spain, Italy, France, Hungary, Portugal, Germany, Belgium, Poland and Malta (Cullere *et al*, 2018). In recent years, the rabbit industry is currently facing a critical period, mainly due to the increase in feeding, management costs and a constant decline in rabbit meat consumption. Hence, farmers and researchers have been looking for promising strategies to improve the current situation, one of them being the optimization of genetic selection by using genomic information. Genetic selection can improve productive and reproductive traits, such as meat characteristics, reducing feeding and management costs, which makes rabbit more appealing for consumers, and hence, will aid the rabbit industry (Cullere *et al*, 2018) . Reproductive traits, especially litter size, are those with relevant economic weight in the rabbit industry (Cartuche *et al*, 2014).

2.3 GROWTH RATE IN RABBIT PRODUCTION

To ensure the continuous production of rabbits and the advancement of this industry, it is imperative to delve into rabbit breeds and breeding techniques. The rate of growth stands as a key factor influencing the overall efficiency and profitability of rabbit farming operations.

Growth rate in rabbit production refers to the rate at which rabbits increase in size or weight over a specific period of time. It's a crucial metric in evaluating the overall performance and productivity of a rabbit farming operation. A higher growth rate implies that rabbits are gaining weight efficiently, which can lead to increased meat production. This parameter is influenced by various factors including genetics, nutrition, management practices, and environmental conditions. Efficiently managing and optimizing growth rates is essential for a successful and profitable rabbit farming venture.Genetic parameters have been estimated for production and functional rabbit traits (Drouilhet *et al*., 2013; Matics *et al*., 2014; Korteby, 2016; Nguyen *et al*., 2017). These traits have shown sufficient genetic variation and heritability to allow improvement through selection

In this study, we estimate major strategies for enhancing rabbit production, particularly focusing on their growth rate through heritability which plays a crucial role in the selection and breeding of animals for improved growth performance. Growth rate has been identified as the most crucial trait for the rabbit industry. Recording growth rate is more convenient and cost-effective than monitoring feed conversion rate, and it demonstrates a positive genetic correlation with it (Piles *et al*., 2004). This is why commercial rabbit breeding schemes are structured around three-way crossings. Two carefully chosen lines, emphasizing litter size either at birth or weaning, are crossed to yield a commercial doe (Baselga *et al*., 1989), which is then paired with a terminal sire from another selected line, emphasizing growth rate post-weaning or body weight at a point close to market age (Rochambeau *et al*., 1989). The objective of crossing the maternal lines is to leverage the anticipated positive heterosis in reproductive traits, the potential synergies among the lines, and the dilution of accumulated inbreeding within the lines (Baselga, 2004).

2.4 HERITABILITY ESTIMATE IN RABBIT PRODUCTION

Genetic progress in the selection programs depends mainly on the heritability of the selected trait and on the selection intensity. In this section, a review of quantitative genetic components for litter size and growth traits will be carried out. For litter size at birth, the estimates of the heritability show in general low values (0.05 to 0.20 and 0.11 on average) and tended to decrease slight from birth to slaughter (0.00 to 0.13 and 0.08 on average for number born alive, 0.02 to 0.12 and 0.07 on average for litter size at weaning, and 0.06 to 0.08 and 0.07 on average for litter size at slaughter, see Table 1). The estimates of the ratios of permanent environmental variance to the phenotypic variance are also rather low for litter size at birth. In agreement to heritability, the estimated values decrease from birth (0.11 on average) to market time (0.08 on average). These findings are an indication of the high effect of environmental influence on litter size and the low repeatability. Regarding genetic correlations between litter size traits, the estimates present positive and high values, ranging from +0.96 to +0.99 for litter size at birth and number born alive, and from +0.60 to +0.98 for number born alive and litter size at weaning. (Ragab and Baselga, 2010)

Table 1 ***Heritability (h^2) and permanent effect (p^2) of litter size at birth (LS), number of kits born alive (NBA), number of kits at weaning (NW) and number of rabbits at slaughter (NS).***

LS		NBA		NW		NS		LINE/BREED
h2	p2	h2	p2	h2	p2	h2	p2	
0.20	0.25			0.09	0.12			New Zealand White
0.10	0.07	0.70	0.09	0.07	0.07	0.07	0.06	Line selected by OR and LS
0.10	0.09							Environmental Variance of LS
0.11	0.08	0.10	0.09	0.09	0.07			Line A
0.08	0.12	0.05	0.09	0.02	0.07			Line H
		0.09	0.10	0.08	0.08			Line LP
		0.09	0.11	0.07	0.13			Line R
0.18	0.09	0.07	0.10	0.05	0.08	0.05	0.07	Line V
0.13	0.05	0.05	0.09	0.02	0.06			ITELV2006 line
		0.05	0.09					Pannon White
0.13	0.10	0.00	0.06					Pooled Poured Breed
0.05	0.09	0.03	0.09					Brazilian Synthetic Line
0.12	0.06	0.09	0.07					Pannon Ka
0.05	0.11	0.07	0.11					Pannon Large
0.07	0.10	0.07	0.09					Pannon White
0.11	0.09	0.08	0.08	0.06	0.06	0.03		Line Prat
0.09	0.21	0.12	0.20	0.09	0.16	0.07	0.12	Local line
0.19	0.19			0.08	0.19			Danish While

(Ragab and Baselga, 2010)

Present widely range of values (0.03 to 0.48 for weaning weight and 0.06 to 0.67 for slaughter weight); that can be related to different weaning age, from 28 days in semi intensive management to 42 days of age in extensive management, and different slaughter time, from 9 week in Spain to 13 weeks of age in Italy (see review by (Blasco et.al, 2018). Contrarily, the estimates of heritability for growth rate show a narrow range (0.12 to 0.34) and moderate average value (0.22).

2.5 HERITABILITY AND BREEDING PROGRAMMES

Heritability is a concept that measures the extent to which differences among individuals in a particular trait can be attributed to genetic factors. This concept has been widely used in selective breeding programmes to improve the genetic quality of livestock and crops. Selective breeding programmes aim to increase the frequency of desirable genetic variants in a population and reduce the frequency of undesirable variants (Garrick, 2014). The elements required in a breeding programme depend on the choice of the general breeding strategy. Thus, the first decision is which of the three main genetic improvement strategies should be applied: selection between breeds, selection within breeds or lines, or cross-breeding (Simm, 1998).

- Selection between breeds, the most radical option, is the substitution of a genetically inferior breed by a superior one. This can be done at once (when as in poultry the cost is not prohibitive) or gradually by repeated backcrossing with the superior breed (in large animals).
- Cross-breeding, the second fastest method, capitalizes on heterosis and complementarity between breeds' characteristics. Conventional cross-breeding systems (rotational systems). The inter mating of animals of newly developed composites has been suggested as an alternative form of cross-breeding.
- The third method, within-breed selection, gives the slowest genetic improvement, especially if the generation interval is long. However, this improvement is permanent and cumulative, which is not the case for cross-breeding programmes.

Gradual genetic improvement is the most sustainable form of improvement, as it gives the stakeholders time to adapt the production system to the intended change. When the traits of interest are numerous and/or some of them are antagonistic, different lines may be created, and maintained by within-line selection. These lines can then be crossed to produce commercial animals. This strategy is used in pig and poultry breeding. Setting up a breeding programme involves the definition of a breeding goal (Groen, 2000) and the design of a scheme that is able to deliver genetic progress in line with this goal. In practice, it involves the management of people and resources as well as the application of the principles of genetics and animal breeding (Falconer, 2017). Each aspect of the breeding programmes involves many processes, individuals and sometimes institutions. Success depends on how well the available resources are harnessed and managed to achieve the goals of the stakeholders. The stakeholders of a breeding programme are all those who are affected, in one way or another, by its success. These include the end users of the products of the programmes (i.e., livestock producers), commercial companies and others who directly or indirectly invest in the scheme, government departments, breed societies, and those employed to implement the programmes. Other stakeholders include ancillary beneficiaries such as suppliers, distributors, and sellers of byproducts of the scheme. Most programmes have a pyramidal structure (Simm, 1998), with varying number of tiers depending on the sophistication of the programmes. At the apex of the pyramid is the nucleus where selection and breeding of the elite pedigree animals is concentrated. The multiplication of stock happens in the middle tiers. This is required when the number of nucleus animals is insufficient to satisfy the demands of commercial farmers. The activities that constitute a breeding programmes can be summarized in eight major steps (Simm, 1998) which includes, choice of breeding goal, choice of selection criteria, design of the breeding scheme, recording of the animals, genetic evaluation of the animals,selection and breeding, progress monitoring and dissemination of genetic improvement.

2.6 THE USE OF HERITABILITY IN SELECTIVE BREEDING PROGRAMMES:

Heritability estimates can provide valuable information for selective breeding programmes. Traits with high heritability estimates are more likely to respond to selective breeding, as the variation in the trait is primarily due to genetic factors. Traits with low heritability estimates may still be selected for, but the response to selection will be slower, as the variation in the trait is primarily due to environmental factors. In general, traits with moderate to high heritability estimates are most suitable for selective breeding (Hickey *et al* 2018.,). Heritability has an important role for selection of polygenic traits. The final object of selection is to choose those animals with the best breeding values to become parents of the next generation. To do this, we need good information about the heritable traits of animals for selection. Because the only information available for selection is phenotypic information of the animals, so heritability is very meaningful. When the trait is highly heritable, selection is more important than crossbreeding and management, but when the trait is lowly heritable selection is no more appropriate rather than crossbreeding and management of the animals (Wendy *et al*., 2011). It provides a measure of genetic variation, that is, the variation upon which all the possibilities of changing the genetic composition of the population through selection depend. In other words, knowledge of its magnitude gives the idea about the scope for effecting genetic improvement through selection. (Subrat, 2000)

Selective breeding programmes often use a combination of pedigree and performance data to estimate the heritability of a trait. Pedigree data is used to identify the relatedness among individuals in a population, while performance data is used to measure the trait of interest in each individual. The heritability of a trait can then be estimated using statistical models that account for the relatedness among individuals and the environmental effects on the trait (Matukumalli *et al*., 2009).When the more desirable animals are chosen as parents of the next generation, the predicted change is the result of heritable fraction of the superiority of the parents over the average of the population from which they were chosen (Yamgar, 2017). Therefore, the expected change in the mean of the next generation will be predicted by this equation:

$\Delta M = h2 \times SD$

Where,

¬ h2 Heritability

¬ ΔM is the expected change in the mean of the next generation

¬ SD is the selection differential of the selected parents

Heritability also gives a measure of the accuracy with which the selection for a genotype can be made from a phenotype of the individual or a group of individuals. In general, the percentage of h2 dictates the choice of selection method and breeding system. High h2 estimates indicate that additive gene action is more important for that trait, and selective breeding i.e., mating of the best to the best animal should produce more desirable progeny. Low estimates, on the other hand, indicate that probably non-additive gene actions such as over dominance, dominance, and epitaxy are important and are not heritable (Subrat, 2000).

Advantages of using Heritability in breeding programmes:

Increased efficiency: Selective breeding programmes that target traits with high heritability estimates can produce significant improvements in the genetic quality of a population in a relatively short period.

Precision: Heritability estimates provide an objective measure of the genetic contribution to a trait, allowing breeders to make more informed decisions about which individuals to select for breeding.

Increased genetic diversity: By selecting for desirable traits with high heritability, breeders can increase the frequency of beneficial genetic variants in a population, leading to increased genetic diversity. (Gatabalew *et al*., 2019)

2.7 METHODS OF ESTIMATING HERITABILITY

Heritability estimates typically rely on the assumptions of large, randomly mating populations without factors like mutation, migration, selection, and genetic drift. These estimation methods are primarily designed for diploids with regular meiosis. It's also important to consider gender-specific variations in recombination when estimating heritability (Sakamoto *et al.*, 2000).There are generally two types of methods employed for estimating heritability. The first method utilizes regression and correlation to gauge heritability, while the second method entails the use of Analysis of Variance (ANOVA) and the estimation of variance components for heritability assessment. These different approaches for estimating heritability can be outlined as follows (Friars and Smith, 2010):

(i) Regression Between Parents and Offspring: This approach quantifies the extent to which a particular trait is passed from parent to offspring and is calculated using the formula: [$y = a + bx$]

Where x and y represent the mean values of the trait for parents and offspring respectively, a is the intercept, and b is the regression coefficient. The heritability is equivalent to the regression coefficient, i.e., $h^2 = b$, when mean values from both parents are used. However, when offspring are compared with only one parent, the heritability is $h^2 = 2b$.

(ii) Hierarchical Matings

, also referred to as the North Carolina mating design I, assesses the origin of variation within a population. It is calculated using the following formula:

$Y_{ijk} = m + S_i + D_{ij} + e_{ijk}$

Here, Y_{ijk} represents the measurement of a trait in the kth offspring of the jth dam (female parent) bred with the ith sire (male parent). The variables are defined as:

μ = the overall mean of the population,

S_i = the effect of the i-th sire,

D_{ij} = the effect of the j-th dam bred with the i-th sire, and

e_{ijk} = the combined impact of environmental factors and genetic segregation on the kth progeny of the jth dam bred with the ith sire.

(iii) Factorial Matings,

also known as North Carolina mating design II, employs sets of matings involving sires and dams from different strains. This allows for the partitioning of variance components, with theoretical expectations for additive and nonadditive effects as follows (McKay *et al.*, 1986):

σ^2_A = variance due to additive genetic effects

σ^2_D = variance due to dominance

$\sigma^2_{AA}\sigma\ ^2_{AD},\sigma^2_{DD}$ = variance due to epistatic interactions of additive-additive, additive-dominance, and dominance-dominance types, respectively

σ^2_{Ec} = variance due to environmental effects between tanks

σ^2_{EG} = other environmental effects not due to tank effects

σ^2_M = variance due to maternal effects

(iv) Breeding Values employ best linear unbiased prediction (BLUP) of additive genetic effects for selecting potential parents in large datasets. Another commonly used method for estimating variance components in mixed linear models in animal breeding is the restricted maximum likelihood (REML) method (Hofer, 1998).

(v) Inbred Lines utilizes the variance between and within inbred lines to estimate genetic variance and heritability, as given by the formula:

$h^2_t = h^2_0 (1 - F_t)/(1 - F_t)$

Where (h^2_0)is the heritability in the base population, and (h^2_t and (F_t) are the heritability and inbreeding coefficients at time represented by generations \(t\).

(vi) Linear Heritability Estimates is based on the selection of potential parents, for which estimates of average genotypic and phenotypic values are obtained from a pedigree population (Abplanalp, 1961). This method involves estimating the regression of genotypic and phenotypic values from a straight line connecting the mean genotype and phenotype of selected parents on one axis and the population mean genotype and phenotype on the other.

(vii) Clonal Lines first produce mitotic gynogenetic diploids that are reared in a common environment. Then, the lines were identified using DNA fingerprinting and after that human twin models were employed to observe the separated genetic and environmental variances (Taniguchi *et al*. 1996).

(viii) Discrete Traits

In this method, heritability can be estimated from an underlying continuous scale using techniques, which provide a quantification of multiple gene effects (Robertson and Lerner 1949).

(ix) Animal Model

In this method, an animal model is used for heritability estimate by estimating its breeding value through the information of animal's records, its parents, and its progeny details. This method is based on the condition that provided pedigree information of the animal is accurate and complete.

The significance of heritability estimates in breeding programs cannot be overstated. Heritability estimates provide a measure of the potential for genetic improvement of a trait through selective breeding programs. Heritability estimates are also important in determining the appropriate breeding strategies to improve a particular trait. Traits with high heritability are best improved through selection, while traits with low heritability are best improved through manipulation of environmental conditions or other non-genetic approaches (Falconer and Mackay, 1996).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 STUDY LOCATION

The study was conducted at the Teaching and Research Farm of the University of Benin, situated in Edo state, Nigeria. The University of Benin is positioned at latitude 6.02° N and longitude 5.06° E, within the Humid Rain Forest Zone of Southern Nigeria. The area experiences an annual temperature range of 24.5 to 32.7°C, with an average of 28.6°C. The annual rainfall ranges from 1498 to 3574 mm, with a mean of 2430 mm. Relative humidity falls between 63.3% and 81.7%, while daily sunshine hours range from 5.85 to 7.5 hours, with means of 73.5% and 6.68 hours, respectively (NAA, 2013).

3.2 HOUSING

The rabbitry was oriented in an east-west direction and featured standard dwarf walls. Two types of hutches were utilized: the first being six-compartment iron hutches arranged in a three-tier configuration, and the second being four-compartment hutches constructed with a combination of wood and wire mesh. Prior to commencing the experiment and on a regular basis thereafter, the house, hutches, and equipment underwent thorough cleaning and disinfection. Each occupied hutch was equipped with hanging feeders and drinkers.

3.3 EXPERIMENTAL ANIMALS AND MANAGEMENT

A total of twenty rabbits, comprising five bucks and fifteen does of New Zealand, Chinchilla, Hyla, and Dutch breeds, were involved in the study. The experiment spanned from April 2023 to September 2023. The animals were intensively managed in individual hutches. They were provided with ad libitum access to pelleted grower's feed containing 15% crude protein and 2600 Kcal/kg metabolizable energy, along with forages (Panicum maximum). Does received a supplemental feeding of commercial growers feed prior to mating and were further supported with commercial grower feed before parturition. Any leftover feed and soiled water were discarded. The animals were periodically administered anticoccidiosis, antibacterial, and multivitamins. Additionally, they received subcutaneous injections of Ivomec to combat both endoparasites and ectoparasites. Routine management tasks included hutch cleaning, rabbit unit sweeping, feces tray washing, regular drinker and feeding trough cleaning. Animals were monitored daily for signs of illness, with treatment provided for sick individuals and prompt removal and burial of deceased animals. Cage identification was carried out.

Mating occurred once the rabbits reached at least 5 months of age and weighed 1.5 kg or more. Does were introduced to bucks for mating and cohabitated until successful mating was confirmed. Mating took place in the early morning, and pregnancy was assessed by palpation 14 days post-mating. Kindling boxes were introduced to the hutches of pregnant does four days before the anticipated kindling date. Following kindling, nests were checked daily for stillborn and deceased kits. Weaning was performed at four weeks of age.

3.4 DATA COLLECTION

The data collected encompassed: Weight of the buck at mating, Weight of the doe at mating, Number born alive ,Litter size at birth, Litter weight at birth, Litter size at 2 weeks, Litter weight at 2 weeks, Litter size at weaning, Litter weight at weaning, Individual litter weight at weaning

CHAPTER FOUR

4.0 RESULTS

4.1 ESTIMATE OF HERITABILITY OF GROWTH RATE IN RABBIT

The table below (Table 2) presents estimates of heritability and variance components for productive traits in rabbit production showing growth rate. These estimates range from 0.2 to 0.7. A value of 0.2 below is considered low heritability, while a value of 0.5 as moderate and 0.6 above is classified as high heritability.

Table 2.Variance component (due to sire, error and phenotype) and Heritability of growth traits.

TRAITS	σe	σs	σp	h^2
LSB	1.58	0.27	1.88	0.64
LS2	1.80	0.36	2.16	0.74
LSW	3.03	0.5	3.53	0.57
ALWB	0.000046	0.000041	0.000087	0.37
ALW2	0.00037	0.000023	0.00039	0.24
ALWW	0.0013	0.0000067	0.0013	0.02

LSB = Litter size at birth, LS2 = Litter size at two weeks, LSW = Litter size at weaning ,ALWB = Average litter weight at birth, ALW2 = Average litter weight at two weeks, ALWW = Average litter weight at weaning.

CHAPTER FIVE

5.1 DISCUSSION

Over the years animal producers have adopted different ways to improve animal production to meet a significant portion of the global population which relies on animal-based protein, yet its production diminishes amid escalating human population demands (McIntire *et al*., 1992).

Growth rate which stands as an important trait influencing the overall productivity and profitability of rabbit farming enterprises can be improved by using heritability in breeding programmes.

Heritability aids in the identification of the genetic factors contributing to these traits, enabling the selection of individuals with those traits for breeding purposes (Collard *et al*., 2008

heritability is a central measure for quantifying the extent to which genetic differences contribute to the observed variability in a trait.

In the result in Table 2, a review of quantitative genetic components for variance components litter size and growth rate was carried out. For litter size at birth, the estimates of heritability shown in general have high values (0.64), litter size at two weeks estimate of heritability is high (0.74) which is significant and litter size at weaning is(0.57).

For weight gain, Litter weight at birth (0.37), Litter weight at two weeks (0.24) and Litter weight at weaning (0.02).The estimate of Heritability of weight gain is low. . (Ragab and Baselga, 2010).

The heritability estimates and their SE for the litter size as presented in table 2 shows a medium to high value for all the traits measured which ranged from 0.57 to 0.74 and that of litter weight 0.02 to 0.37which is low. The same moderate to high estimates in litter traits had been reported by several authors (Khalil *et al*, 1987; Iraqi *et al*, 2006; Akanno and Ibe, 2005). This implies that these traits could be improved by combining pedigree and individual selection as the results show that these traits were under the strong in-fluence of additive genes and that individual selection would successfully improve them. Also,(Njon and Nwakalor, 1998) obtained such high estimates in a mixed population of purebred and crossbred rabbits.

This research underscores the critical role of heritability in shaping growth traits in rabbits, offering actionable insights for the optimization of breeding programs. These findings contribute significantly to the body of knowledge in animal genetics and breeding, with far-reaching implications for the efficiency and sustainability of rabbit farming enterprises.

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATION

6.1 CONCLUSION

In conclusion, this study has shed light on the heritability of growth rate in rabbits, providing valuable insights into the genetic factors influencing this crucial trait. The findings indicate a significant contribution of genetics to the observed variation in growth rates within the population. This knowledge holds substantial implications for selective breeding programs, offering the potential to strategically enhance growth rates in rabbit populations. Furthermore, our study underscores the potential for targeted genetic interventions to drive improvements in rabbit growth rates. By estimating the heritability of this trait, we provide a solid foundation for future breeding programs aimed at optimizing growth performance. This research represents a significant stride towards the refinement of breeding strategies, with broader implications for livestock industries seeking to enhance efficiency and sustainability.

However, heritability estimates can be influenced by environmental and non-additive genetic factors, which can limit their accuracy and applicability.

Despite the limitations, heritability remains a valuable tool for genetic improvement in various fields, including animal and plant breeding, as well as human genetics.

6.2 RECOMMENDATION

1. Implement selective breeding programs that emphasize the selection of rabbits with superior growth rates will help in gradually improving the overall growth performance of the rabbit population.

3. Develop and utilize advanced genetic evaluation tools to accurately assess the genetic potential of individual rabbits for growth traits. This can aid in making informed breeding decisions.

4.Providing training and education to breeders and stakeholders involved in breeding programmes will enhance their understanding of genetic principles and breeding techniques.

5.Fostering collaboration with other breeders, researchers, and organizations in the field of rabbit genetics and breeding and Sharing knowledge and experiences can lead to collective advancements.

6. Further Studies should be carried out by adapting the new Methods of improving Genetic Traits in Animals to meet the needs of the Farmer and society.

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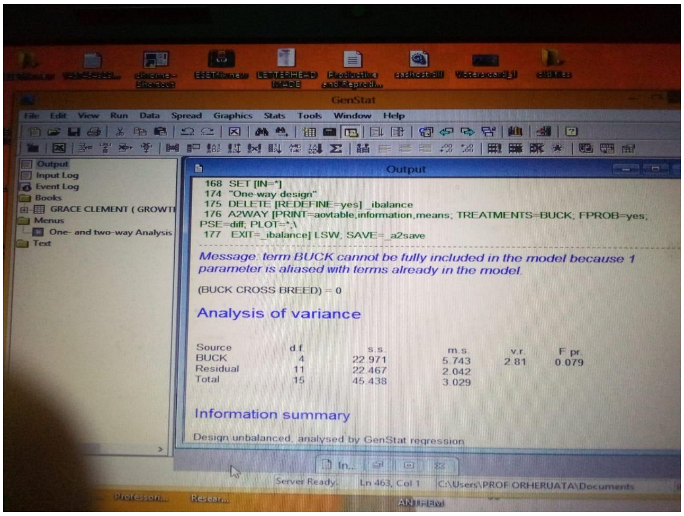
APPENDIX



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175  DELETE [REDEFINE=yes] _ibalance
176  A2WAY [PRINT=aovtable,information,means; TREATMENTS=BUCK; FPROB=yes;
PSE=diff; PLOT=*;\
177   EXIT=_ibalance] LSW; SAVE=_a2save

Message: term BUCK cannot be fully included in the model because 1
parameter is aliased with terms already in the model.

(BUCK CROSS BREED) = 0

Analysis of variance

Source        d.f.       s.s.       m.s.     v.r.    F pr.
BUCK            4      22.971      5.743     2.81    0.079
Residual       11      22.467      2.042
Total          15      45.438      3.029

Information summary

Design unbalanced, analysed by GenStat regression
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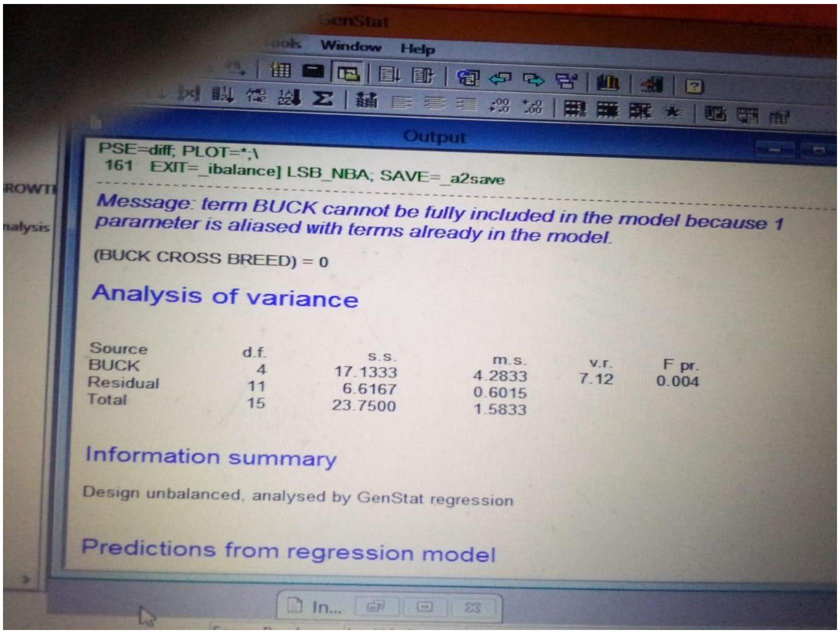
Litter size at weaning



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Message: term BUCK cannot be fully included in the model because 1
parameter is aliased with terms already in the model.

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Analysis of variance

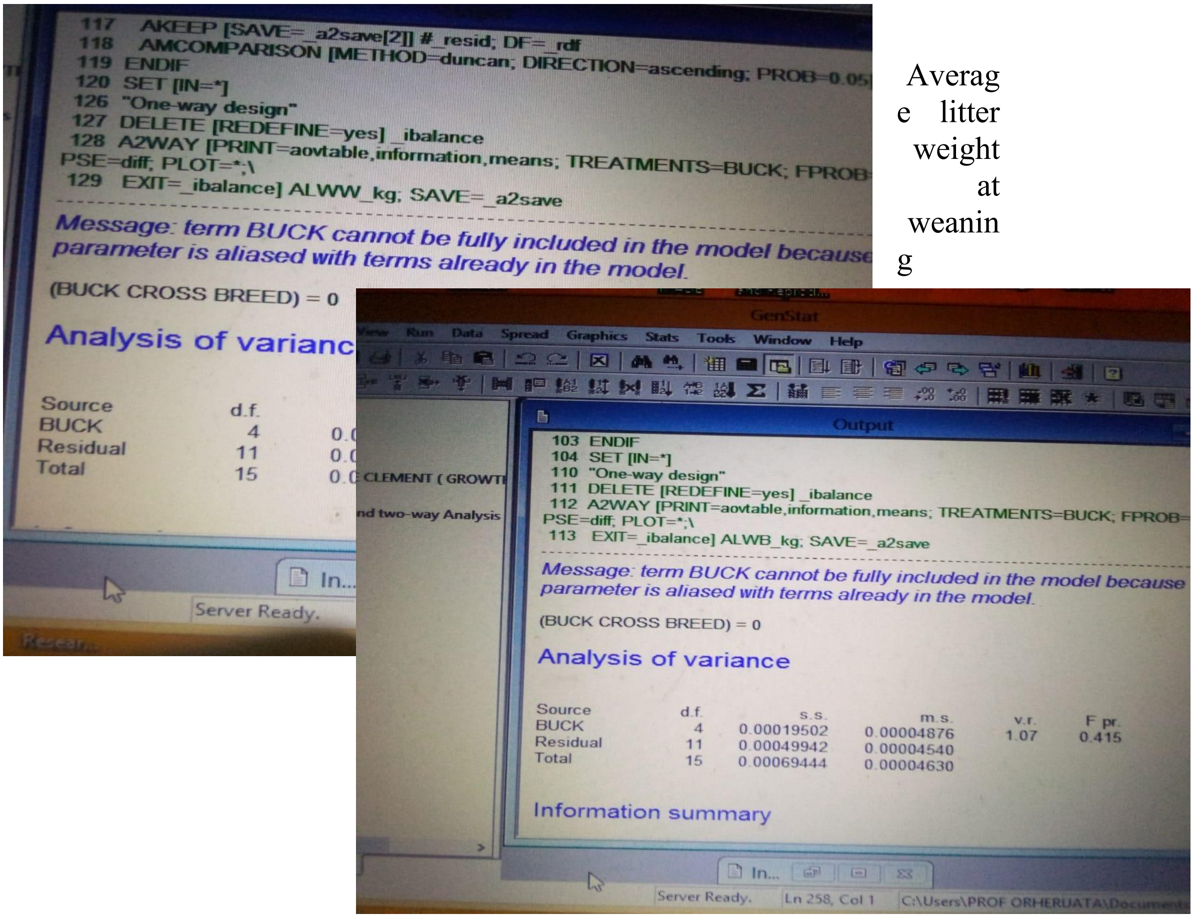
Source        d.f.        s.s.        m.s.     v.r.    F pr.
BUCK            4      17.1333      4.2833     7.12    0.004
Residual       11       6.6167      0.6015
Total          15      23.7500      1.5833

Information summary

Design unbalanced, analysed by GenStat regression

Predictions from regression model
```

Litter size at Birth



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127  DELETE [REDEFINE=yes] _ibalance
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------------------------------------------------------------------------

Message: term BUCK cannot be fully included in the model because
parameter is aliased with terms already in the model.

(BUCK CROSS BREED) = 0

Analysis of varianc

Source          d.f.
BUCK              4      0.0
Residual         11      0.0
Total            15      0.0
```

```
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104  SET [IN=*]
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111  DELETE [REDEFINE=yes] _ibalance
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PSE=diff; PLOT=*;\
113  EXIT=_ibalance] ALWB_kg; SAVE=_a2save
------------------------------------------------------------------------

Message: term BUCK cannot be fully included in the model because
parameter is aliased with terms already in the model.

(BUCK CROSS BREED) = 0

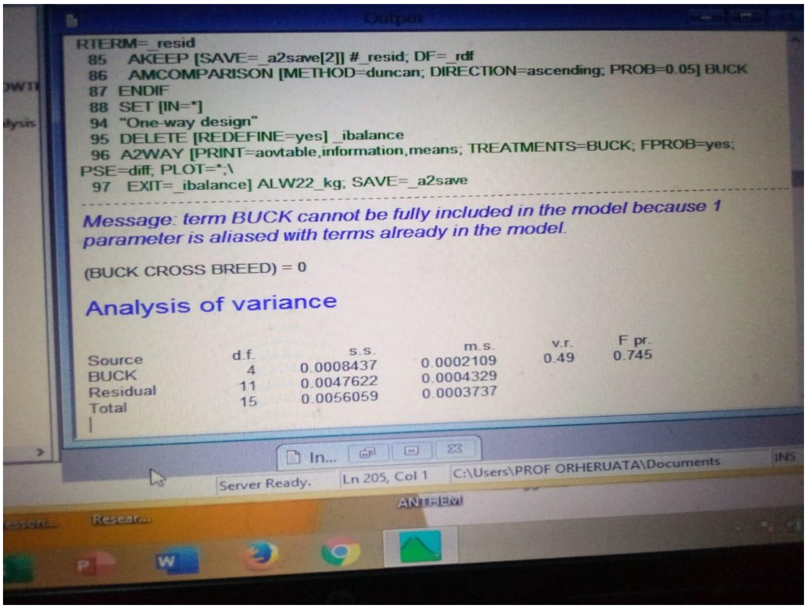
Analysis of variance

Source          d.f.          s.s.          m.s.      v.r.    F pr.
BUCK              4     0.00019502    0.00004876      1.07    0.415
Residual         11     0.00049942    0.00004540
Total            15     0.00069444    0.00004630

Information summary
```

Average litter weight at weaning

Average litter weight at Birth



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 ENDIF
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 DELETE [REDEFINE=yes] _ibalance
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PSE=diff; PLOT=*;\
  EXIT=_ibalance] ALW22_kg; SAVE=_a2save
--------------------------------------------------------------------------

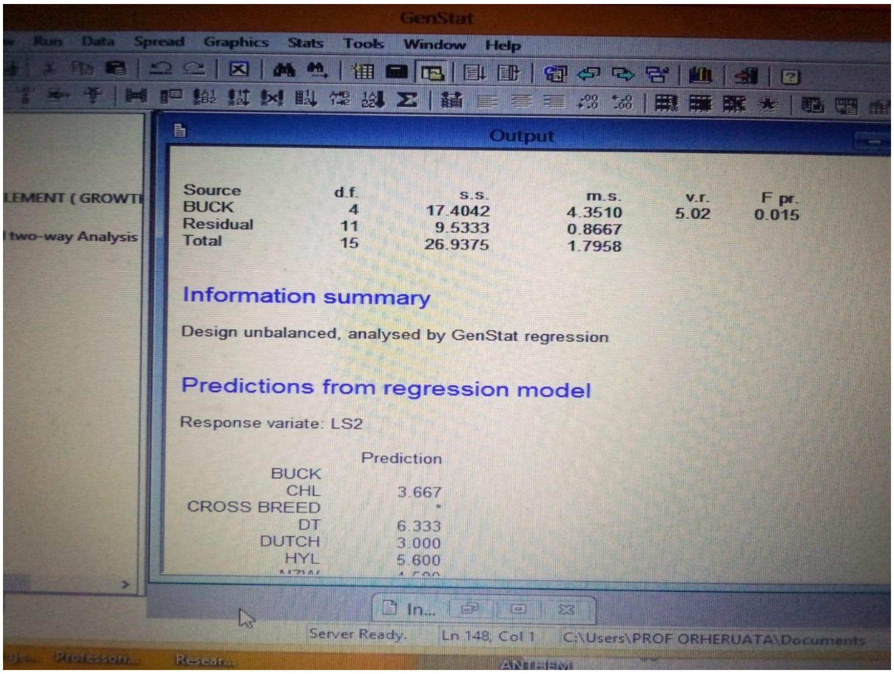
Message: term BUCK cannot be fully included in the model because 1
parameter is aliased with terms already in the model.

(BUCK CROSS BREED) = 0

Analysis of variance

Source          d.f.        s.s.         m.s.      v.r.    F pr.
BUCK               4   0.0008437    0.0002109      0.49    0.745
Residual          11   0.0047622    0.0004329
Total             15   0.0056059    0.0003737
```

Average litter weight at 2weeks



```
Source          d.f.        s.s.        m.s.     v.r.    F pr.
BUCK               4     17.4042      4.3510     5.02    0.015
Residual          11      9.5333      0.8667
Total             15     26.9375      1.7958

Information summary

Design unbalanced, analysed by GenStat regression

Predictions from regression model

Response variate: LS2

               Prediction
        BUCK
         CHL        3.667
 CROSS BREED            *
          DT        6.333
       DUTCH        3.000
         HYL        5.600
```

Litter size at 2weeks