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Review of Grasscutter (*Thryonomys Swinderianus*) Genetics

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Abstract **– The objective of this study was to review articles on the genetics of grasscutter *Thryonomys swinderianus*, a micro livestock that has not been extensively studied. Access to a comprehensive information on Grasscutter genetics isn't readily available hence the need to put together the results of all the efforts made in researches about Grasscutter genetics. The study on heritability of grasscutter revealed that litter weights at birth (0.56) and weaning (0.66) are highly heritable with strong genetic correlation (r = 0.59). Maternal effect is important in grasscutter and should be accounted for in breeding value estimation. Grasscutter is also seen to tend to be restless and hence need to be selected to be more docile. 1,209 Single Nucleotide Polymorphisms (SNPs) has been discovered from a total of more than 21 000 candidate loci containing single SNPs. Also 33 novel microsatellite markers have been developed using next-generation sequencing technology and 26 different haplotypes with high haplotype diversity discovered among grasscutters in some agro ecological zones compared and this is attributed to the high mutation rate of the Mitochondria D-loop DNA.**

Keywords **– Thryonomys Swinderianus, SNPs, Microsatellite Markers, Genetics.**

I. INTRODUCTION

Globally, wildlife domestication has great potentials for meat production and serves as an important source of the highly desired animal protein to the people of Africa, both in urban areas and rural communities because of the preference for bush meat (Fonweban and Njwe, 1990). Grasscutters has been sourced from the wild over the years (Adu *et al*. 2005; Mensah and Okeyo 2006). Domestication and commercialization of the Grasscutter, *thryonomys swinderianus*, a large rodent, represents an important opportunity to secure sustainable animal protein for local communities in West Africa (Adenyo et al., 2016). Domestication of Grasscutter can prove to be very vital to increase protein supply in Nigeria where majority of the over 180 million population are still not able to meet FAO minimum daily protein requirement of 0.75g per kg per day. With meat that has great appeal across the economic levels, improving productivity and growth of these rodents can be of a huge economic importance. Domestication of Grasscutter has been slow due to husbandry challenges including high mortality and morbidity rate due to aggression. To accelerate and optimize the domestication process, DNA makers are needed for applications including population diversity assessment, pedigree analysis and marker-assisted selection (Adenyo et al. 2016). Annor et al (2014) identified growth rate, docility, litter size and pre-weaning survival as the traits of most economic importance that requires improvement. Improvement of these traits can be achieved faster through advanced genetic approach. There have been rapid recent changes in technology that have revolutionized the study of the inheritance of many traits of biological and commercial importance (Hocking 2005). The objective of this paper is to review the genetic approaches that have been used in the improvement of grasscutter genetics and production.

II. GENETIC MARKERS IN THE GRASSCUTTER

Genetic markers are specific genes that produce recognizable trait that can be used in population genetics studi-

-es. Anenyo et al (2016) in their work sequenced blood tissue samples of grasscutter using double digest restriction site-associated DNA (ddRAD) sequencing as described by Peterson *et al* (2012). The ddRAD library preparation protocol followed the methodology described in Palaiokostas *et al*. (2015), with some modifications. From a total of 46,412,480 raw reads, 117,932 putative RAD tag loci were discovered after filtering and this finally led to the generation of 1,209 Single Nucleotide Polymorphisms (SNPs) from a total of more than 21 000 candidate loci containing single SNPs. The ddRAD sequence data set represents the first genome-wide resource available to support ongoing efforts to domesticate and improve production of grasscutter (Adenyo et al. 2016).

III. MICROSATELLITE IN THE GRASSCUTTER

A microsatellite is a tract of tandemly repeated (i.e. adjacent) DNA motifs that range in length from two to five nucleotides, and are typically repeated 5-50 times. (Turnpenny and Ellard 2005). Microsatellites occur at thousands of locations within an organism's genome; additionally, they have a higher mutation rate than other areas of DNA (Brinkmann et al, 1998). This is one major cause of genetic diversity.

There is little or no work as regards microsatellite in grasscutter except Adenyo et al (2012) who reported 33 novel microsatellite markers developed using next-generation sequencing technology with the number of alleles ranging from 3 to 11 (mean 6.4) while the observed and expected heterozygosities ranged from 0.188 to 1.000 (mean 0.591) and 0.322–0.873 (mean 0.713), respectively.

IV. GENETICS OF DOCILITY IN THE GRASSCUTTER

Docility or temperament is the ability of an animal to accept human presence. Burrows (1997) defined docility as the animal’s behavioral response to handling by humans. Docility is an important trait because it is related to many production traits. For example, it has been reported that cattle with higher body weights are more docile than those with lower body weights, and grow faster during fattening than aggressive animals (Fordyce et al 1988).

Selection for grasscutters with more favorable docility scores will be more effective in producing animals with more acceptable temperaments. Annor et *al* (2011) in their work on genetics of docility in the grasscutter reported an average docility score of 2.6 on a scale of 1-4 for the population they studied. They reported that direct heritability for docility was high (0.58) while the maternal heritability was medium (0.41), and there were low genetic and phenotypic correlations between docility and all traits (body weight, growth rate, days of joining to conception, survival, feed intake and feed conversion ratio), except litter size and that litter size, sex, parity, year of birth, season of mating and season of birth, and their interactions did not influence ($p>0.05$) docility.

V. MITOCHONDRIAL D-LOOP DIVERSITY OF GRASSCUTTER

Mitochondrial DNA is known to be maternally inherited, and non-recombinant with a high mutation rate (Avise *et al*, 1987), and regulates transcription and replication (Larizza et al, 2002).

Adenyo et al (2013) found 26 different haplotypes with high haplotype diversity among the agro ecological zones he compared and attributed this to the high mutation rate of the Mitochondria D-loop in agreement to Larizza et al, (2002). Adenyo et al (2013) further adduced that the high haplotype diversity could be due to unrestricted gene flow among the populations studied and suggest their work as a baseline for further population genetics studies.

VI. Phenotypic and Genetic Parameters of Traits in the Grasscutter

The reasons for making comparisons of genetic variation for quantitative characters are to compare ability to respond to selection and secondly to make inferences about the forces that maintain genetic variability or diversity (Annor *et al*. 2012). Heritability is a very important parameter in quantitative genetics and animal breeding. It is useful in predicting genetic changes that may result from selection (Falconer and Mackay 1996; Ibe 1998). Heritability estimates also assist the breeder in drawing a breeding plan as regards the selection method to apply in an attempt to achieve his aim (Annor et al. 2012).

Henry *et al*. (2014) reported high heritability values for litter weights at birth (0.56) and weaning (0.66) with a strong genetic correlation (r = 0.59) between both traits.

Annor *et al*. (2012) in their work reported high additive genetic variation between body weight and growth rate and low additive genetic variation with reproductive and survival traits, and feed intake, and that body weight and growth rate had medium to high direct heritability (0.30-0.84). And that Maternal heritability for most traits were low to high Phenotypic and Genetic parameters of traits in the Grasscutter.

The reasons for making comparisons of genetic variation for quantitative characters are to compare ability to respond to selection and secondly to make inferences about the forces that maintain genetic variability or diversity (Annor et al. 2012). Heritability is a very important parameter in quantitative genetics and animal breeding. It is useful in predicting genetic changes that may result from selection (Falconer and Mackay 1996; Ibe 1998). Heritability estimates also assist the breeder in drawing a breeding plan as regards the selection method to apply in an attempt to achieve his aim (Annor et al. 2012). Henry et al. (2014) reported high heritability values for litter weights at birth (0.56) and weaning (0.66) with a strong genetic correlation (r = 0.59) between both traits. Annor et al. (2012) in their work reported high additive genetic variation between body weight and growth rate and low additive genetic variation with reproductive and survival traits, and feed intake, and that body weight and growth rate had medium to high direct heritability (0.30-0.84). And that Maternal heritability for most traits were low to high (0.13-0.99). Medium direct heritability was obtained for feed intake (0.30) and feed efficiency (0.38) while all reproductive traits, apart from those associated with weight, and survival traits had low direct heritability (0.02-0.06). They concluded that opportunity exists for fast genetic gains in the improvement of growth and body weight traits, whilst slow genetic progress may be made in reproductive and survival traits. And also that maternal effects are important in the grasscutter, and must be accounted for in breeding value estimations.

VII. Reproduction and Reproductive Management

Determining the sex in grasscutter is a bit difficult as farmers tends to rely on the shape and or the size of the head to distinguish between the sexes. The use of ano-genital distance is the second most popular and acceptable method of sex determination. The study by Adu and Yeboah (2002) has led to the promotion of the use of ano-genital distance as the gold standard of sex determination in the grasscutter. At birth, the ano-genital distance is 10 mm in the males and less than 5 mm in the females. In adults, it measures an average of 38 mm in males and 12 mm in females.

The paired testicles are situated abdominally in the male genital tract and there is no scrotum. Appertaining to the accessory sex glands are a pair of seminal vesicles, the prostate gland, composed of three lobes and a pair of compact pea-sized cowper’s glands. There is another pair of glands (glands coagulate) between the base of the se-

-minal vesticles and prostate glands (*Addo et al., 2003).*

The vaginal opening between the urinary papilla and the anus is sealed with a thin membrane in the female genital tract. This membrane has been observed in all hystricomophic rodents, except the Nutria (*Myocoaster coypus)*. (Addo *et al,* 2003).

The grasscuter is easy to house, though its handling requires skills. Among rural communities and even some urban people with adequate space, the animal has been bred and kept in boxes, empty drums, poly vinyl chloride (PVC) pipes and enclosures (Adu, 2002). However, the grasscutter can be properly managed under these three systems: enclosure, cage and floor.

VIII. CONCLUSION

Grasscutter is cherished by a vast majority of the populace of Africa as a good source of animal protein. There is great potential for improvement of grasscutter through application of molecular genetic principles for fast genetic gains.

Some advances has been made in the discovery of SNPs and microsatellite markers in grasscutter but the is need for studies to discover quantitative trait loci (QTLs) as this will pinpoint specific genes of economic importance which can be manipulated for fast genetic gains and improved docility in the grasscutter.

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