Genetic Diversity of Giant African Land Snails (GALS)

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Abstract: A total of Nine (9) protein sequences of GALS were retrieved from National Center for Biotechnology Information (NCBI) GenBank. The GenBank accession numbers for Achatina achatina proteins sequence are AKQ76249, CDL67813 and AKQ76251, Achatina fulica are YP009049162, YP009049157 and YP009049167 and Archachatina marginata are AKQ76228, AKQ76224 and AGV55728. The sequence length variation in Achatina fulica ranged from 347 – 516bp, Achatina achatina ranged from 184 – 214bp, while Archachatina marginata ranged from 135 – 214bp. The genetic distances between the GALS were computed using the Poisson correction method. The results of the genetic distance between Achatina fulica and Achatina achatina was 0.919, Achatina fulica and Archachatina marginata was 0.933 while that of Achatina achatina and Archachatina marginata was 0.926. This implied that they are genetically far apart. The nucleotide diversity and Tajima test for selection results were estimated using MEGA7. The nucleotide diversity ranged from 0.926 – 0.929, implying that giant African Land snails (GALS) can adapt to varying environmental conditions. The Tajima’s (D) test for selection revealed high positive value ranging from 9.933 – 10.538. This could signify that multiple alleles are actively maintained in the gene pool of a population at frequencies larger than expected from genetic drift alone. Information from this study may therefore be exploited for conservation and studies of biodiversity.

Keywords: Genetic, Diversity, Nucleotide, Selection, Snails

INTRODUCTION
Information on sizes of populations and levels of genetic diversity of species of interest is important for the development of the appropriate natural resource management and conservation schemes for different groups of plants and animals (Odey et al., 2015). Habitat fragmentation and instability of human-disturbed environments may impose severe restrictions on gene flow and increase random genetic drift. Extinction and recolonization dynamics in local populations may also modify the distribution of genetic variability, leading to a decrease or an increase of variations among populations (Schluthuizen and Lombaerts, 1994; Ruckelshaus, 1998).

Genetic diversity plays an important role in the survival and adaptability of a species. When a population's habitat changes, the population may have to adapt to survive; the ability of the population to adapt to the changing environment will determine their ability to cope with an environmental challenge (Frankham, 2005). Variation in the population's gene pool allows natural selection to act upon traits that allow the population to adapt to changing environments. The more genetic diversity a population has, the more likelihood the population will be able to adapt (Pullin, 2002). Genetic diversity is essential for a species to evolve. With very little genetic diversity within the species, healthy reproduction becomes increasingly difficult, and offspring are more likely to have problems resulting from inbreeding (NBII, 2008). The genetic diversity of livestock species allows animal production to be practiced in a range of environments and with a range of different objectives. It provides the raw material for selective breeding programmes and allows livestock populations to adapt as environmental conditions change (FAO, 2015). To exploit animal genetic resources it is pertinent to have background knowledge of the amount of genetic variation that exists between and within the species.

Snails have the highest number of recorded extinction known in recent times; many more edible snail species are under threat of extinction (Odey et al., 2015). Generally, there is limited information on the genetic diversity of giant African land snails. This paper was designed to investigate sequence length variation, genetic distance, nucleotide diversity and test for selection using amino acid sequences of GALS.

MATERIALS AND METHODS
Nine (9) sequences of GALS, three sequences each of the three breeds (Archachatina marginata, Achatina achatina and Achatina fulica) were retrieved from GenBank (www.ncbi.nlm.nih.gov) of National Center for Biotechnology Information (NCBI). The GenBank accession numbers for Achatina achatina proteins sequence are AKQ76249, CDL67813 and AKQ76251, Achatina fulica are YP009049162, YP009049157 and YP009049167 and Archachatina marginata are AKQ76228, AKQ76224 and AGV55728. Sequences alignment and comparison were done with ClustalW as described by Larkin et al. (2007) using IUB substitution matrix, gap open penalty of 15 and gap extension penalty of 6.66. The genetic distances were computed using the Poisson correction method (Zuckerkandl and Pauling, 1965) and are in the units of the number of amino acids substitution per site. The analysis involved
9 amino acid sequences. There was a total of 172 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al., 2016). The Tajima test statistic (Tajima, 1989) was estimated using MEGA7. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). The abbreviations used are as follows: \( m = \) number of sites, \( S = \) Number of segregating sites, \( p_s = S/m, \Theta = p_s/a_i, \) and \( \pi = \) nucleotide diversity. \( D \) is the Tajima test statistic (Tajima, 1989).

**RESULTS AND DISCUSSION**

**Sequence Length Variation**

The sequence length variation between and within GALS results are presented in Table 1. The results showed that sequence length in *Achatina fulica* ranges from 347 – 516bp, *Achatina achatina* ranges from 184 – 214bp, while that of *Archachatina marginata* ranges from 135 – 214bp. The sequence length of GALS in this study showed variation between and within breeds. The variations in sequence length between and within GALS might be as a result of physical and chemical changes, mutation such as DNA duplication, DNA rearrangement, short tandem repeat (STR), insertions or deletion of sequences. This corroborated the views of Vincent et al. (2014) and Dauda et al. (2016a) who reported that variation between and within sequence could be due to mutation and evolution. The length variation observed within and across these breeds might also be due to differences in the genomic region where the sequences were obtained. All the sequences in this study revealed partial coding with base pair (bp) (<6000bp). This is in agreement with the report of Yakubu et al. (2014) who opined that variation in sequence length could be due to differences in breeds and location where the sequences are obtained. This variability may initiate unique structures between individual members, conferring different biological activities such as cell signaling, transport of membrane-impermeable molecules and cell–cell communication (Dauda et al., 2017). Besides, genetic distance which is the degree of genetic difference (genomic difference) between breeds/species or populations are measured by some numerical method. Thus, the average number of codon or nucleotide differences per gene is a measure of genetic distance. There are various molecular data that can be used for measuring genetic distance. When the two species to be compared are distantly related, data on amino acid or nucleotide sequences are used in the comparison of closely related breeds/species or populations (Nei and Kumar, 2000).

**Genetic Distance**

The results of estimates of genetic distance between GALS are presented in Table 2. The upper diagonal represents standard error estimate(s), while the lower diagonal is the average genetic distance between the GALS which is also known as the average nucleotide substitutions per site (Dxy). The Dxy is an index of divergence between and within breeds/species where Dxy=distance between sequence X and Y. The higher the value of Dxy the far apart the breeds/species are and the lower the value the closer the breeds/species (Dauda et al., 2016b). The genetic distance between *Achatina fulica* and *Achatina achatina* is 0.919 that between *Achatina fulica* and *Archachatina marginata* is 0.933, while that between *Achatina achatina* and *Archachatina marginata* is 0.926.

All the GALS breeds in this study showed high Dxy values which imply that they are genetically far apart or genetically not the same and therefore, crossbreeding may not be possible. Only inbreeding practice will be suitable for GALS improvement. The inbreeding should be between the same breeds but from different environments in order to increase adaptation to various environmental conditions. The results of this study agreed with the report of Okon et al. (2017) who opined that giant African land snail have different chromosome number and could not be crossbred. The authors also opined that they could be genetically far apart.

**Nucleotide Diversity**

The results of nucleotide diversity and Tajima Test for Selection are presented in Table 3. The results of this study revealed high nucleotide diversity among the GALS breeds evaluated. This implied that the breeds may adapt to various environmental conditions. The different genetic information between and within breeds emanating from this study could be useful in exploiting genetic diversity and selection for improvement. The Tajima’s (D) test for selection revealed high positive values which ranged from 9.933 – 10.538 for all the GALS breeds studied. Positive Tajima’s D test signifies balance selection (Fu and Li, 1993).

Balance selection refers to a number of selective processes by which multiple alleles are actively maintained in the gene pool of a population at frequencies larger than expected from genetic drift alone (King et al., 2006). These authors further stated that balance selection can happen by various mechanisms, in particular, when the heterozygote for the alleles under consideration have a higher fitness than the homozygotes, this means that genetic polymorphism is conserved.
Table 1: Sequence length variation between and within GALS

<table>
<thead>
<tr>
<th>Species</th>
<th>Number</th>
<th>Sequence Length Variation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Achatina fulica</td>
<td>3</td>
<td>347, 449 and 516bp</td>
</tr>
<tr>
<td>Achatina achatina</td>
<td>3</td>
<td>184, 204 and 214bp</td>
</tr>
<tr>
<td>Archachatina marginata</td>
<td>3</td>
<td>135, 213 and 214bp</td>
</tr>
</tbody>
</table>

Table 2: Estimates of genetic Distant between GALS

<table>
<thead>
<tr>
<th>Species</th>
<th>Achatina fulica</th>
<th>Achatina achatina</th>
<th>Archachatina marginata</th>
</tr>
</thead>
<tbody>
<tr>
<td>Achatina fulica</td>
<td>0.023</td>
<td>0.019</td>
<td>0.021</td>
</tr>
<tr>
<td>Achatina achatina</td>
<td>0.919</td>
<td>0.926</td>
<td>0.022</td>
</tr>
<tr>
<td>Archachatina marginata</td>
<td>0.933</td>
<td>0.926</td>
<td></td>
</tr>
</tbody>
</table>

Table 3: Nucleotide Diversity and Tajima Test for Selection

<table>
<thead>
<tr>
<th>Species</th>
<th>M</th>
<th>S</th>
<th>Ps</th>
<th>$\Theta$</th>
<th>$\pi$</th>
<th>$D$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Achatina fulica</td>
<td>3</td>
<td>371</td>
<td>0.992</td>
<td>0.661</td>
<td>0.929</td>
<td>10.249</td>
</tr>
<tr>
<td>Achatina achatina</td>
<td>3</td>
<td>181</td>
<td>0.984</td>
<td>0.656</td>
<td>0.928</td>
<td>10.538</td>
</tr>
<tr>
<td>Archachatina marginata</td>
<td>3</td>
<td>135</td>
<td>1.000</td>
<td>0.667</td>
<td>0.926</td>
<td>9.933</td>
</tr>
</tbody>
</table>

Abbreviations: M = number of sequences, n = total number of sites, S = Number of segregating sites, $p_s = S/n$, $\Theta = p/a_1$, $\pi$ = nucleotide diversity, and $D$ is the Tajima test for selection.

Nucleotide Diversity

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CONCLUSION

The study revealed variations in the length sequences between and within the breeds of GALS. All the GALS are genetically far apart from each other. The study also revealed high nucleotide diversity, a demonstration of genetic variation and heterozygosity. Besides, the Tajima’s test for selection showed balance selection, signifying the existence of multiple alleles, a situation which actively maintains the gene pool. Information from this study may be exploited for conservation and studies of biodiversity.

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REFERENCE


