Molecular Identification of Captive African Grey Parrots and Screening for Their Host Pathogens in Kenya.

MIYUNGA, Antoinette Aluoch
JAP82/61241/2023

ABSTRACT

Background

African Grey Parrots are an endangered bird species whose numbers are rapidly declining in the wild due to habitat loss, but mostly due to unregulated trade. They are charismatic, intelligent birds that can mimic human speech, making them popular pets. Apart from the threat of extinction in the wild, there is public health concern as these birds being traded, illegally crossing borders and could be carrying pathogens that are transmissible to humans. These birds are only native in a few African countries but have spread all over the world through pet trade. This study aims to employ molecular techniques to determine the gene pool structure and host pathogens in captive African Grey Parrots in Kenya to inform their conservation.

Objectives

The study will determine taxonomy and estimate the genetic diversity of captive African Grey Parrots in Kenya. This will be done using primers targeting the dloop hypervariable region and a microsatellite panel for Grey Parrots. Taxonomy will be confirmed using mitochondrial cytochrome oxidase markers. Molecular markers will be designed from the CHD gene to determine the sex of captive parrots. Sex ratios and genetic diversity will be used to estimate the population viability. Zoonotic pathogens circulating in captive African Grey Parrots will be identified using next-generation sequencing metagenomics analyses.

Expected Outcomes

The genetic diversity will give insights into relatedness to local populations and establish species boundaries. This will help inform the Kenyan government on status of African Grey Parrots in the country. It will also help uncover parrot trafficking routes and identify whether birds are being captured locally or from other African range states. Sexing grey parrots is difficult because there are no easily distinguishable features between males and females physically. Understanding the sex ratio will provide an indicator of population viability. The current pandemic has highlighted the importance of a one health approach in preventing the spillover of diseases from wildlife to humans. The results of this study will be provided to local health authorities as well as the owners to inform them of any health risks in their homes.

UTILIZATION AND QUALITY OF PROSOPIS JULIFLORA PODS IN MERTI SUB COUNTY, ISIOLO COUNTY.

Musya, E.M and Gachuiri, C.K

Abstract

Livestock production is the main economic activity in arid and semi-arid land (ASAL) regions in Kenya supporting the livelihood of over 14 million people. Shortage of feed supply during dry seasons accounts for up to 80% of the leading causes of livestock loses in the ASALs. *Prosopis juliflora,* a leguminous tree that produces pods which was introduced in Kenya with the aim of restoring vegetation cover has since greatly spread and adapted in these ASAL areas. These pods have desirable nutritional properties that can be utilized by animals. However, adverse effects have been reported when fed alone to animals and therefore necessitating the need for mixing with other feed ingredients to minimize these effects. Research involving supplementation of diets using *P. juliflora* pods have been performed but testing the effect of incorporation of the pods with locally available feed resources and effect on diet quality has not been tested. The proposed study has been designed to achieve the following specific objectives: 1) To Assess the perceptions on and utilization of *P. Juliflora* in Merti sub county, Isiolo County. 2) To determine the quality of diets formulated using *P. juliflora* pods in Merti sub county, Isiolo county. A cross-sectional study will be used for collection of data from the residents of Merti sub county on *P. juliflora* by use of semi structured questionnaires and a sample size of 370 households. Samples of *P. juliflora* pods, Acacia pods and locally available grass species will be collected from Merti sub county and analyzed for nutrient content. Diets will then be formulated using the local feed ingredients, analyzed for their nutrient properties, keeping quality (of pelleted diets) and digestibility by *in vitro* dry matter disappearance technique and *in vivo* using nylon bag technique.

Key Words: *Prosopis juliflora,* ASAL, Livestock, Nutritional quality

ASSESSMENT OF GUT MICROBIOTA USING 16S rRNA METAGENOMICS IN BROILER CHICKEN FED ON GUAVA BY-PRODUCTS.

By Dennis Nyakundi Kamsingi J56/78969/2009

ABSTRACT:

Foods of animal origin contribute 25% and 18% of global human nutritional diet protein and calories requirements respectively (Kim *et al.,* 2019). Broiler chicken production is a crucial part of the global poultry sector and poultry meat is the most extensively consumed meat which accounts for 35% of the meat consumed in the world (Panyako *et al.,* 2024). However, expensive feeds which account for approximately 70% of the total production cost is a major limiting factor. This has led to research on alternative feed ingredients such as guava by-products in order to reduce the cost of production. Inclusion of up to 5% guava fruit processing by-products in the broiler chicken diet has been shown to result in similar phenotypic performance compared to broiler chicken fed on conventional mash diet (Ogega *et al,.* 2022). Nevertheless, the effect on the gut microbial ecosystem is unknown. Therefore, the objective of this study is to investigate the effect of inclusion of guava fruit processing by-products on the diversity and abundance of microbiota in different sections of the broiler chicken gut using 16S rRNA metagenomic analysis.

The research project will be conducted at the University of Nairobi. Preparation of guava by-product, experimental diets and feeding, experimental birds have been previously described by (Ogega *et al,.* 2022). The by-products were processed and incorporated during formulation of four experimental diets which had a 0%, 2.5%, 5%, and 7.5% guava by-product inclusion levels fed to the chicken in four replicates, each having 10 birds. At the end of the experiment,32 birds were randomly selected, humanely slaughtered, and samples collected from three different sections of the GIT, i.e. the crop, gizzard and caeca. The samples were and stored at stored at -20℃ awaiting DNA extraction and further processing. DNA extraction will be conducted at the University of Nairobi Animal Genetics Laboratory using QIAGEN's QIAamp DNA Stool Mini Kit, according to the manufacturer's instructions. The library preparation and sequencing will be conducted at Macrogen Europe Laboratory in France. Library preparation will be done using Nextera DNA Preparation Kit and the Nextera Index Kit (Illumina, San Diego, CA, USA), following the Illumina 16s Protocol to amplify the V3-V4 regions of the 16S rRNA gene. The normalized pooled libraries will be denatured and loaded into an Illumina MiSeq sequencer, and sequencing done using v3 reagents. The sequencing will target to have 250 bp paired-end reads.

Bioinformatics analysis of the sequenced data will then be conducted using QIIME 2 (Quantitative Insights into Microbial Ecology) to identify bacterial taxonomy and estimate the abundance of each taxon. Statistical analysis will be performed on PAST and R software. Relative abundance data obtained from taxonomic assignment, and the diversity indices will be compared between diets and various GIT sections using two-way permutational multivariate analyses of variance (two-way PERMANOVA). Spearman's rank correlation will be used to test the correlations between the abundances of genera and growth performance of chicken