EFFECTS OF FOREST FRAGMENTATION ON COMPOSITION, GENETIC DIVERSITY AND DISTRIBUTION OF GREENBUL BIRDS AND OTHER AVIFAUNA COMMUNITY WITHIN CHERANGANI ECOSYSTEM.

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DECLARATION

This is my original work and has not been presented for a degree in the University of Nairobi or other institution.

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DEDICATION

This piece of work is dedicated to Almighty GOD who has enabled me achieve it. My family who have been always there for me through all challenges and who have given me all support.

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Abstract

This study was conducted between the month of January and June 2015. The aim was to find out whether forest fragmentation was negatively affecting bird populations. Using species from two genera of greenbul (*Andropadus and Phyllastrephus* as key forest ecological indicators the effect of fragmentation on genetic diversity was assessed. Of which three species were sampled out of five target species. Other avifauna diversity similarity, distribution and threat level were documented, through the survey methods; point counts, mist-netting and opportunistic birding. Overall the survey recorded one hundred and sixty-four (164) bird species, from 50 families. Of which, 33 species were forest specialists (FF), 35 forest generalists (F), and 47 forest visitors (f). Sixteen species were migrants; 9 Palaearctic (PM), 2 Afrotropic (AM) and 5 partial migrants (am, pm, species with individuals that occur alongside resident birds).

Fourteen species were on the IUCN red list, 1 Critically Endangered (CR), 9 Endangered (E), and 2 Vulnerable (V). Regionally threatened species 2 out of 4 known to exist in Cherangani were recorded; Crowned Eagle (*Stephanoaetus coronatus*) and Thick-billed Seedeater (*Crithagra burtoni*) (*Birdlife International Data Zone, 2015*). Thirty-eight (38) species out of 49, known Afrotropical Highlands Biome, and 3 out of 5 IBA designator species (*S. coronatus, C. burtoni* and *Campephaga quiscalina*) were recorded.

Overall 124 samples –77 *A. latirostris*, 36 *P. cabanisi*, and 11 *A. nigriceps* – were analysed; 87 from Kapcherop and 37 from Kapsowar Genetic analysis was conducted on three of the five indicator study species, from two genera. The analysis showed that there was no significant genetic variation within the populations of different fragments. This suggests that the two genera formed one isolated population of Greenbul..

Threat impacts were evaluated at all sites, chronologically, the severe threat being grazing, logging, firewood collection and poaching. Based upon PCA analyses, threat levels and species composition on seasonality, (wet and dry) showed a significant difference in species' variety. These conditions limited the ecological interaction of species, hence giving rise to a negative impact, based on the threat level.

The study concluded that fragmendation was less than two dicades so less impact of genetics diversity.The ecosystem proved to be rich in biodiversity but under increasing threats.Theres urgent need to carry out long term intensive biodiversity survey enganging local community and groups, local government and central government on social economic , cultural and ecological impact of losing these potentential resource.

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ABBREVIATIONS

AM - Afrotropic migrant

AMOVA - Analysis of Molecular Varience

ArcGIS - Arc Global Information System

asl - Above sea level

bp - Base pair

CR - Critically endangered

d.f - degree of freedom

DNA - Deoxyribose Nucleic Acid

FIS - Fixation Index Sequencing

GIS - Geographic Information System

GPS - Global Positioning System

ha - Hectare

HWE - Hardy Weinberg Equilibrium

IBA - Important Bird Area

IUCN - International Union of Conservation for Nature

K -Total numbers individual that represent the population

NDVI - Normalize different Vegetation Index

NT - Nearly threatened

PC - Point count

PCA - Principal Component Analysis

PCR - Polymerase Chain Reaction

PM - Palearctic migrant

SSG - Site Support Group

CHAPTER ONE

1.0 INTRODUCTION

1.I Background

Cherangani ecosystems form part of the Eastern Afromontane Protected Areas in Kenya. This ecosystem is the second-largest water tower after Mau Forest, and they have rich flora and fauna. Cherengani as an ecosystem was designated an Important Bird Area (IBA) No. 43 in 1999 (*Bennun and Njoroge 1999*). It is located on the western edge of the Rift Valley, on a 17 hilly landscape, and the highest peak of this hills reaches an elevation of 3,365 m. above sea level (a.s.l),. The forest ecosystem consists of 13 administrative forest station blocks, totalling 95,600 ha of gazetted areas. Out of 95,600 ha, 60,500 ha have a closed-canopy forest, and 4,000 ha is moorland with an altitude of 3,000m (a.s.l), comprising bamboo, scrub, and rock, in both Kiptaberr and Kipkunurr Hills forest blocks. The mountain ecosystems lie in the Kerio River catchment that feeds both Lake Turkana and source the Nzoia River that feeds Lake Victoria (Fig.1: Kenya Water Tower Agency Strategic Ecosystem Management Plan 2016–2020) REF. Its wildlife includes endemic butterfly (*Bennun et-al 1999*) and unique bird taxa, including Kenya's last breeding population of Lammergeier (*Gypaetus barbatus*). Forty-nine out 67 Kenya's African highland biome species have been recorded in Cherangani forest ecosystems (*Bennun and Njoroge 1999*).

There is currently human encroachment and settlement in the ecosystem, which has led to degradation above 3,000m (a. s. l.), and deforestation. Like other Kenyan highland forests, Cherangani Hills now face serious threats, like over-grazing, logging, firewood collection, and a regular outbreak of fire from honey harvestor, regardless of the potential they hold, like water towers, a haven to important flora and fauna and unique scenic landscape. The overexploitation forest degradation has resulted to change of habitat structure which is very

noticeable (*Bennun and Njoroge, 1999; unpublished data*). Continuous loss of habitat is one of the most serious threats to species survival (*Birdlife International, 2014*). When habitat specialists within a forest are isolated by fragmentation, this generally leads to population decline (*Bennett, A. F. 1990*).

The study aimed to provide evidence for the different impact of recent Cherangani Hill forest fragmentation, on Greenbul birds species. Greenbul species are characterised by their different ecological affinities to the forest FF and F, so they act as a habitat indicator for they exist in gregarious.

This study documented overall bird diversity while focusing on key indicator study species from the two genera *Andropadus and Phyllastrephus* of Greenbul. The study aimed to establish the genetic diversity of one family Pycnonotidae, for they are forest specialist and they are a key indicator of forest status and assessing the anthropogenic activities that threaten both the habitat and biodiversity of the fragmented forest Cherangani. The survey investigated avifauna species diversity, distribution, and threats within fragments of the Cherangani forest ecosystem.

From the previous survey within this ecosystem five species from the two genera have been recorded. Three species of the genus *Andropadus*, -Mountain Greenbul (*A. nigriceps*), Little Greenbul (*A. virens*), and Yellow Whiskered Greenbul (*A. latirostris*). Two species of *Phyllastrephus* –Cabanis's Greenbul (*P. cabanisi*) and Terrestrial Brownbul (*P. terrestris*).

For the study hypothesis, we focused on threats as one of the influencing factors of species diversity, abundance, similarity and distribution. About species composition, we considered how threats influence the genetic distribution, diversity, and abundance of species. The vegetation assessment was based on the density of lower, mid and upper canopy cover, trying to link the state of the Afromontane forest with biodiversity found in it.

During the study, we captured two species of Andropadus (*A. latirostris and A. Nigriceps),* and one species of Phyllastrephus *(P. Cabanisi).* But we were not lucky to capture the other two species, *A. virens* and *P. Terrestris,* which had been recorded from the previous survey which is early milt signs of the impact of fragmentation on forest dependant species.

1.2 Problem statement.

Habitat, degradation, overexploitation, alteration, fragmentation and loss is the origin of species decline, threatened and extinction in the natural resource settings. In the condition of scarce resource-poor ecological condition, leads a natural population to lack reproduction, inbreeding bottle neck hence serious survival threat. Of recent, most conservation research work has focused on natural ecological events and anthropogenic activities as major threats to biodiversity, and its habitat being triggered by anthropic activities and climate change. Birdlife International's model, tool Kit has been the approach for a couple of years in conserving both biodiversity and sites under threats

Genetic studies remain underused in most conservation research, conservation policy formulation and management decision. Most of the genetic studies in the tropics have focused on medical and agricultural research on a large scale. It has been illustrated in improving food production, through activities like cloning, transgenesis and gene mapping, and genomic medicine. This is attributed to a lack of properly equipped laboratories, limitation of competent skills, and technical hitches within natural resource research institutions, especially in tropical regions. This study aimed at adding value to basic ecological and conservation findings on, species composition, distribution within the habitat, and changes in the genetic diversity, of habitat key indicators of *Andropadus* and *Phyllostrephus*.

1.3. Broad Objective .

Assess the effects of forest degradation and fragmentation on the genetic diversity of *Andropadus* and *Pyllostrephus*, and the composition of avifauna within Cherangani forest ecosystem Kenya.

1.4. Specific Objectives.

1. To examine similarity and kinship (genetic drift) of *Andropadus* and *Phyllastrephus*populations across the forest fragments.
2. Assess bird species diversity, richness and distribution within Cherangani Hills forest.
3. Assess the level of threats about the distribution and diversity of the avian community within Cherangani forest fragments.
4. To relate the genetic diversity within *Andropadus* and *Phyllastrephus* within different fragments of Cherangani forest.

1.5 . Study Hypothessis

The analyses of Molecular Variance (AMOVA), was applied to verify the two alternative study hypotheses:

i) Whether there no = H0: genetic structure among and within forest fragments or

ii) If there's-presence=H1: of a genetic structure among and within forest fragments (Kapcherop and Kapsowarr).

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Introduction

Habitat loss, over-exploitation of natural resources, the introduction of alien species, unbalanced prey/predator populations and global climate change, are some of the main factors that contribute to a decline in biodiversity. As populations size reduces, they face a greater risk of extinction, through demographic old age, failure in successful breeding and environmental variation like prolonged drought, the fire that can destroy breeding niche catastrophic events, for instance, outbreak or seasonal avian disease, genetic drift and inbreeding (*Hedrick et, al 1996; Harris, L. D., 1984; Johansson, M., et, al 2007*). The changes in the spatial pattern of suitable habitats, result in increasingly isolated populations (*Brown, et, al 2009; Luoy, D., et, al 2007*), and alter the movement of animals between patches, (*McDonough, et, al 2005; Porter, et, al 1999*), hence limiting genetic diversity. Following habitat disturbance and human settlement, subsequent population recovery is influenced by many factors including, the number and demographic parameters of the survivors (*Brooker, 1998; Sanz and Aquilar, et, al 2011*), resource availability (Murphy, 1998), post-disturbance succession pathways (*Whelan, 1995; Turner, et, al 2011*), species' dispersal ability (*Fauvelot, et, al 2006*), and the geographic scale and patchiness at which, the disturbance occurred on the population (*Whelan, et, al 1995; Banks, et, al 2011; Watson, 2012; Bush, K., et, al. 2005*). All the highlighted factors at least should be in place for a specific population within an ecosystem to recover.

But when an individual of certain populations has varying degrees of contact, from non-existent to frequent genetic interchange. Connectedness is generally measured by, examining the frequencies of different alleles or forms of a specific gene, at several different gene loci, which in such case illustrate the degree of variation **(***Taberlet, P., et al (1991*). If the

frequencies differ significantly between two populations, there is likely some restriction in gene flow between them. If it appears that there is no difference in frequencies from one area to another, it may be supposed to be that there is a strong inter-population connectedness (presumably through frequent mixing), that is good for maintaining overall genetic diversity. (*Fine, P. V. (2002*). Rare alleles are less likely to disappear in a large population. However, a disadvantage to strong inter-population connectedness is that deleterious alleles and diseases may more easily spread through a species whose populations is in frequent contact with each other. It is important to understand the threats to a species to properly interpret information on the inter-population structure.

In general, genetic diversity is considered to be a good thing, and the more the better. In terms of population structure, large populations of a species, which are in some way in contact with each other, provide a good situation for maintaining variation (*Reed, D. H. (2010*). However, in the case of endangered species, we are generally faced with the opposite situation a small number of populations, which are isolated from one another, each containing a small number of individuals. Applying population genetic theory to such situations may point the management strategies, which will maximize the maintenance of the existing variation. If sufficient genetic variation, and thus life strategy variation exists, the population can be assured of persistence, through the survival and reproduction of at least some of its members.

2.2 Description of greenbuls .

Greenbuls are groups of bird within the bulbul family Pycnonotidae. They are large drab olive-green above and paler below, with few distinguishing features within species **(***Moyle & Marks 2006)***.** Approximately Pycnonotidae, comprises 130 species globally, widely distributed across Africa and Asia, mainly in evergreen thickets and forest (*Zimmerman et, al.*

2015; Vann share et, al.1996). The African clade comprises approximately 50 species in three genera– *Andropadus Phyllastrephus* and *Chlorocichla* – which are widely distributed in Africa including East Africa and Kenya (*Zimmerman, et, al 2015Mech, S. G., et, al 2001.; Anon, 2012*).

***ANDROPADUS* (Figs. 5, 6).**

The genus Andropadus is represented by ten species in East Africa, of which three – *A. nigriceps*, *A. virens,* and *A. latirostris* – have been recorded in Cherangani forest.

***PHLLASTREPHUS* (Figs. 7).**

The *Phyllastrephus* are eight species in Africa, of which two have been also recorded in Cherangani – *P. cabanisi* and *P. terrestris* (*personal observations 2009 and 2011*)

IMAGES OF THE STUDIED BIRDS

GENUS *ANDROPADUS*

Figure 1. Mountain Greenbul (A. nigreceps)

Figure 2. Yellow Whiskered Greenbul (A. latirostris)

GENUS *PHLLASTREPHUS*

Figure 3. Cabanis's Greenbul (Phyllostrephus cabanis)

2.2.1 Morphology

There;s a lot of Correlation between fitness and genetic diversity in most species (*Reed, D. H., et, al 2003; Saunders, D.A.m., et, al 1991).* For *Andropadus* species are well known to be difficult to identify. They have mostly dull plumage, are slightly stocky, short, or medium birds, solitary or in pairs. The species occur in the mid-canopy of the forest unless they are feeding on a fruit tree (*Roy, M. S. (1997*)).

The Yellow Whiskered Greenbul (*A. latirostris*), is a songbird without sex dimorphism apart from body size and all are omnivores. The body size is approximately 120mm long with average measurements as follows:

wing	male = 87.1mm	female = 80.3mm
tail	male = 79.8mm	female = 74.5mm
bill	male = 16.2mm	female = 15.2mm
tarsus	male = 21.2mm	female = 20.7mm

The western Kenyan greenbul group, weight, ranges between 19–21g for males, and 22–29g for females birds. These biometrics are used to determine sex morphologically (*Paruk, J. D. (2018*).

The overall body plumage is dark brown and dull olive green, with a diagnostic yellow moustached stripe on the side of the throat, which is raised in display. The bird has brown flanks, pale yellow on the centre of the lower breast, belly, under tail coverts, are pale brown tipped with pale brownish-yellow. Both Primary and secondary feathers are, brown or web edged greenish olive. Upper wing-coverts dark olive-brown, the underside of flight feathers, have greyish cast inner web. The axillaries and under-wing coverts have a dull yellowish colour (*Clegg, S. M., and Owens, P. F. (2002*) .

The legs and toes have dull orange or yellowish. The dark bill often shows some orange-yellow, at cutting edges and gape. Juvenile Bird lack yellowish stripe and eyes are dark brownish or grey-brown.

The Immature birds are like the adult, but with more rufous wash under part, mainly dingy brown without olive tone. Their natural habitats are subtropical or tropical dry forests, moist lowland forests, moist montane forests, and moist shrubland .

The Mountain Greenbul (*A. nigriceps*), comprises two subspecies, sometimes considered to be full species; *A. n. chlorigula* (Yellow-throated Greenbul), and *A. n. kikuyuensis* (Olive-

breasted Greenbul). During the survey, we only caught *A. n. kikuyensis*. This is endemic to the Albertine Rift, and Central Kenya. It has brighter greenish-yellow underparts and a more obvious pale broken eye-ring (*Smart, N., and Andrews, J. (1985*). Mantle to rump, upper tail coverts and upper wing coverts brighter greenish. The tail feathers, olive with bright green edges. The Chin, throat, and upper breast are, grey and the rest of the underparts are, bright olive-yellowish, belly purely yellow. The primaries and secondary's dark brown. Bill-black, eye-brown, hazel red-brown or dark brown. The sexes are alike, but males are larger. The individual sexes are defined by average male and female body biometrics, including:

Wing length	male = 88.5mm	female = 85.5mm
Tail length	male = 83.7mm	female = 80.8mm
Bill length	male = 17.6mm	female = 16.8mm
Tarsus length	male = 23.3mm	female = 23.0mm
(knee joint to dorsal joint)		

Although weight is an imprecise measure,for the purpose of sexing, the average weight of *A. n. kikuyensis* is considered to be 33.1g for males, and 30.3g for females..

Phyllastrephus species are also difficult to identify from their body plumage. Their behaviour and vocalization provide the best clues for identification. Most species are insectivores and depend on the mid- and lower forest canopy as forest specialists (FF). We captured only one species, the Cabanis's Greenbul (*P. cabanisi*).

Cabanis's Greenbul has a fairly long, slender tail with brownish olive on upper part of the rump towards the scapular and the head. The upper tail coverts are rufous, slightly greenish on the outer edges, with shaft red brown above straw below. The lore is greyish brown slightly paler than the forehead eye ring white and cheeks ear coverts brown with fine paler streaks. The chin towards throat varies between whitish to creamy it is not pure yellow as in other races (*Del Hoyo, J., et al. (1992*).

The primary and secondary feathers are dark brown on outer webs; on the upper wing coverts they appear olive-brown. The axillaries and underwing coverts are creamy white on the underside of the inner webs. The bill is horny brown with a yellowish grey lower mandible. Eye is dark brown to grey-brown dull yellow to brown to ochre (*Brown, M., & Sandwith, M. (2007)*) . Legs are scaly grey or slaty blue. Soles olive yellow or dull orange. Claws are pale red brown.

Immature individuals have tawny feathers which appear dark brown red on the upper coverts. The wing and upper tail coverts are creamy white like the adult. The sexual dimorphism is determined by body biometrics which relies on average measurements for both sexes. They include:

Wing length	male = 85.0mm	female = 78.6mm
Tail length	male = 82.1mm	female = 76.5mm.
(tip of cloak to tip of longest tail feather)		
Bill length	male = 19.0mm	female = 18.6mm
Tarsus length	male = 22.8mm	female = 22.8mm

Average weight is 27.5g for males, and 23.5g for females **(***Smart, N., & Andrews, J. (1985). Brown, M., & Sandwith, M. (2007).*

CHAPTER THREE

3.0 MATERIAL AND METHODS

3.1 Study Area

The study was conducted in Cherangani Hills forest, Trans-Nzoia county in part of North-western Kenya. Cherangani hill is one of the remnants of Afromontane highland forests (Fig. 4). The hills were formed as a result of faulting of non-volcanic rocks from an undulating upland plateau. They are located at 01 16 S; 35 52; E. between 2,000–3,365 m a. s. l.on the western edge of the Rift Valley, but towards the Northwest, the altitude lowers.

Cherangani Hills forest landscape cut across six counties which are used as the administrative office headquarter for the forest blocks. Most of the forest fragments/blocks lie within Elgeyo Marakwet County on the east, which drops to the floor of the Kerio Valley. It extends to, Tranz-Nzoia and West Pokot Counties on the west. The northern part of the forest is in West Pokot County and

Trans-Nzoia County to the west at Kapcherop. The Southwest forest blocks extend to Uasin Gishu and part of Baringo County NK (*Management plan 2015*).

The study was conducted in two forest blocks called Kapcherop and Kapsowarr, approximately 52km apart. The two blocks were selected on the basis that initially the forest was one ecosystem, but over time, with human intrusion, fragmentation started slowly resulting into two isolated blocks below (Fig. 5 and 6).

Kapcherop block had three fragments, separated by human settlement, grazing fields, exotic forest plantations, community cultivated fields and the government Nyayo Tea Zone. Every fragment was given two replicates transects, A and B, 1-3 km apart,(Fig.5). At the Kapsowarr block, all sites were within one large connected forest patch, covering the Kipkunurr Hills, (Fig.3). The site selection was influenced by the forest canopy cover, where chances of

catching target species were increased. Each site was as wide as possible to increase the chances of assessing the degree of genetic variation.

THE STUDY AREA MAPS FOR KAPCHEROP AND KAPSOWARR BLOCKS

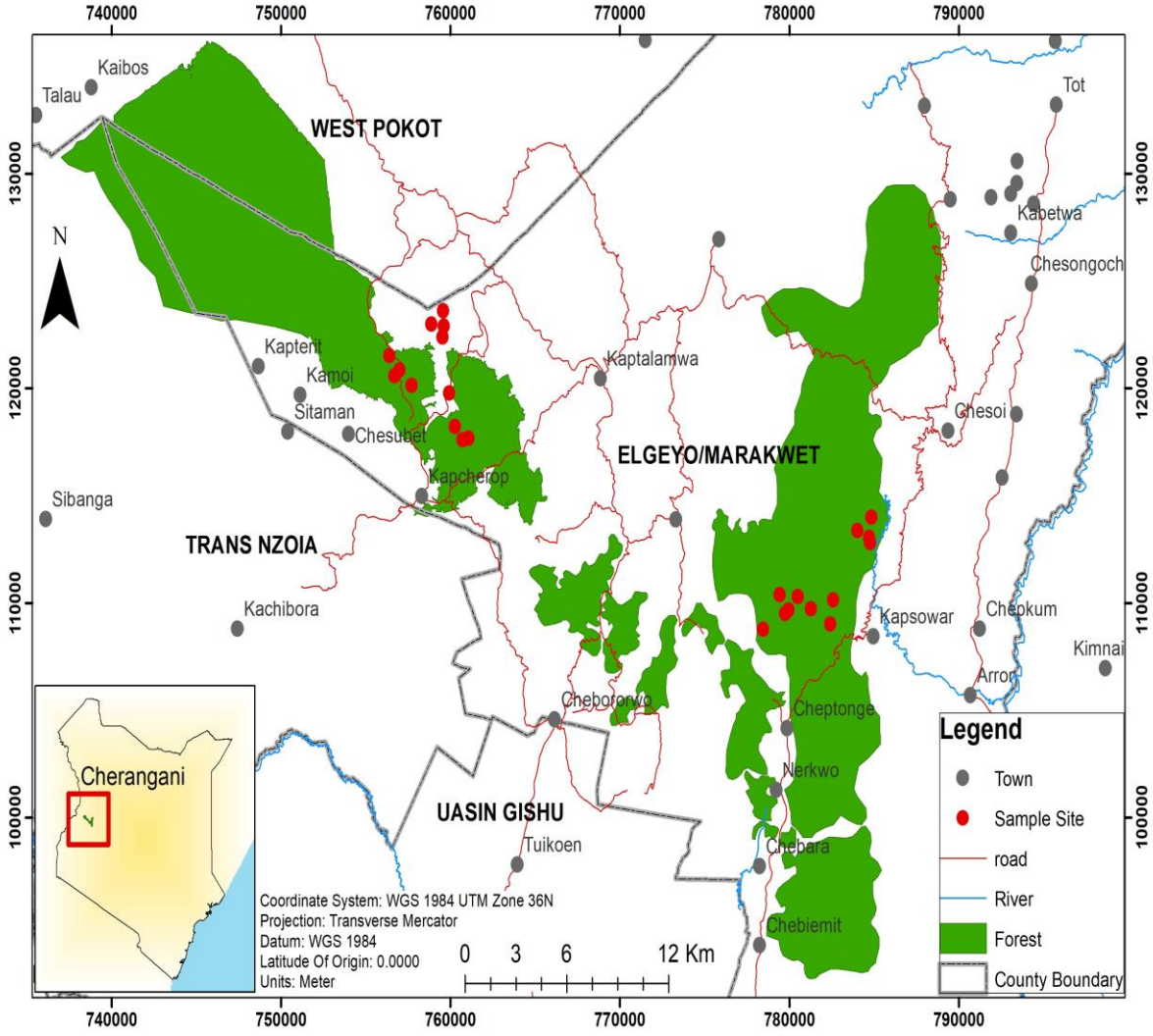

Figure 4. Study areas Map for Kapcherop and Kapsowarr samping points in Cherangani.

The studied fragments within Kapcherop block were; Kiptaberr, Kiplegetet, and Embayat. Transects were marked using a highly sensitive G.P.S. (Appendix).

Red dots in the map indicates surveyed sites; major forest fragments are shown in green.

Kapcherop forest fragments were 4–14 km apart separated by; cabbage, carrot and potato crops, and grazing fields.

KAPCHEROP FRAGMENTS TRANSECT AND SAMPLING POINTS MAP.

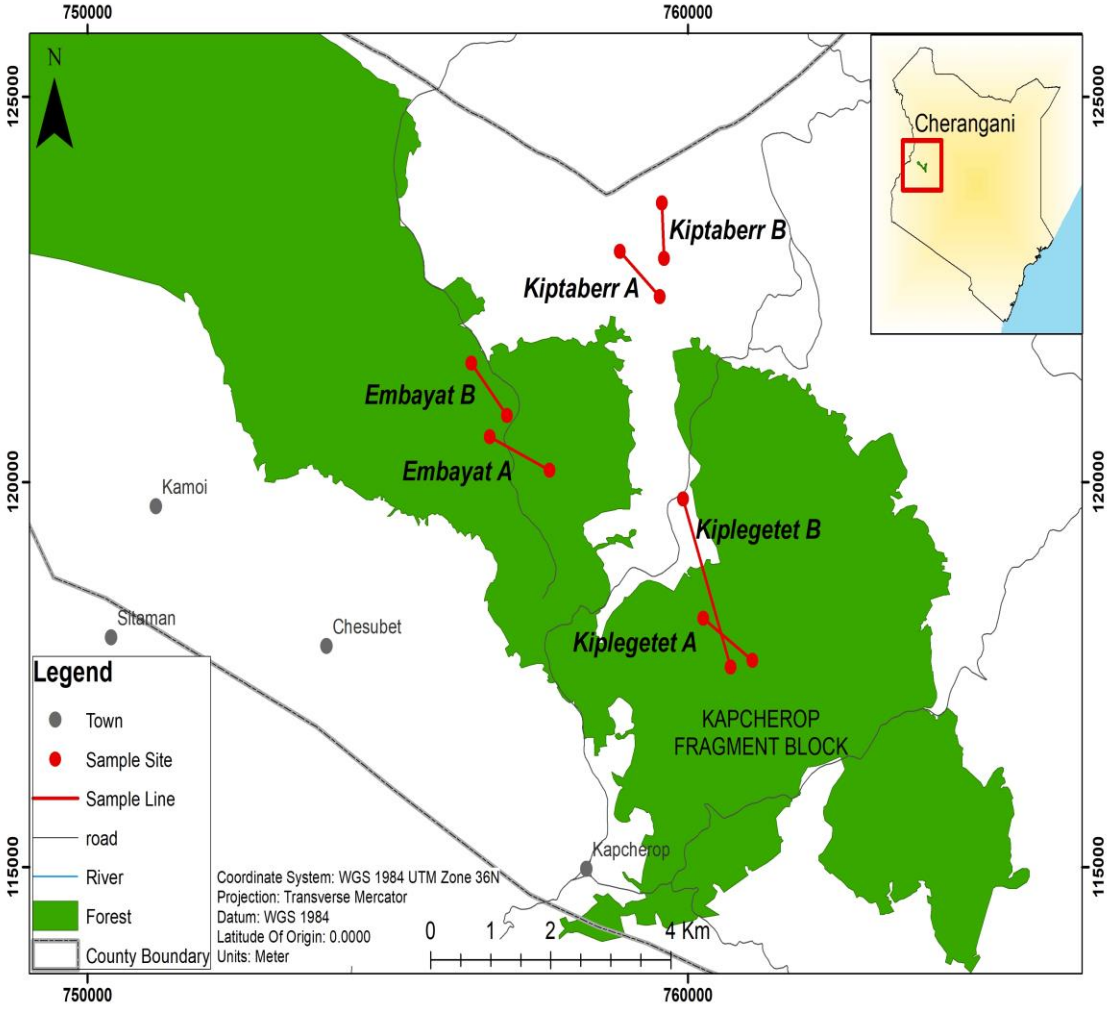

Figure 5. Map for Kapcherop fragments transect and sampling points at high magnification

Study sites in the Kapsowarr block were; Kipkunurr West (4.8km from Chelesi Primary school), Kipkunurr peak ridge (300m below Kipkunurr Hill peak, at 3,000m a. s. l.) and Hossein **(**4.3 km from Hossein Primary School). The closest sites were Kipkunurr West and Kipkunurr Ridge which were 4 km apart. The rest of the fragments were between 4-15km apart. Most of the Kipkunurr fragments were separated by grazing fields and abandoned cultivated fields. Transects were marked using a highly sensitive GPS (Fig. 6).

KAPSOWARR FRAGMENTS TRANSECT AND SAMPLING POINTS MAP

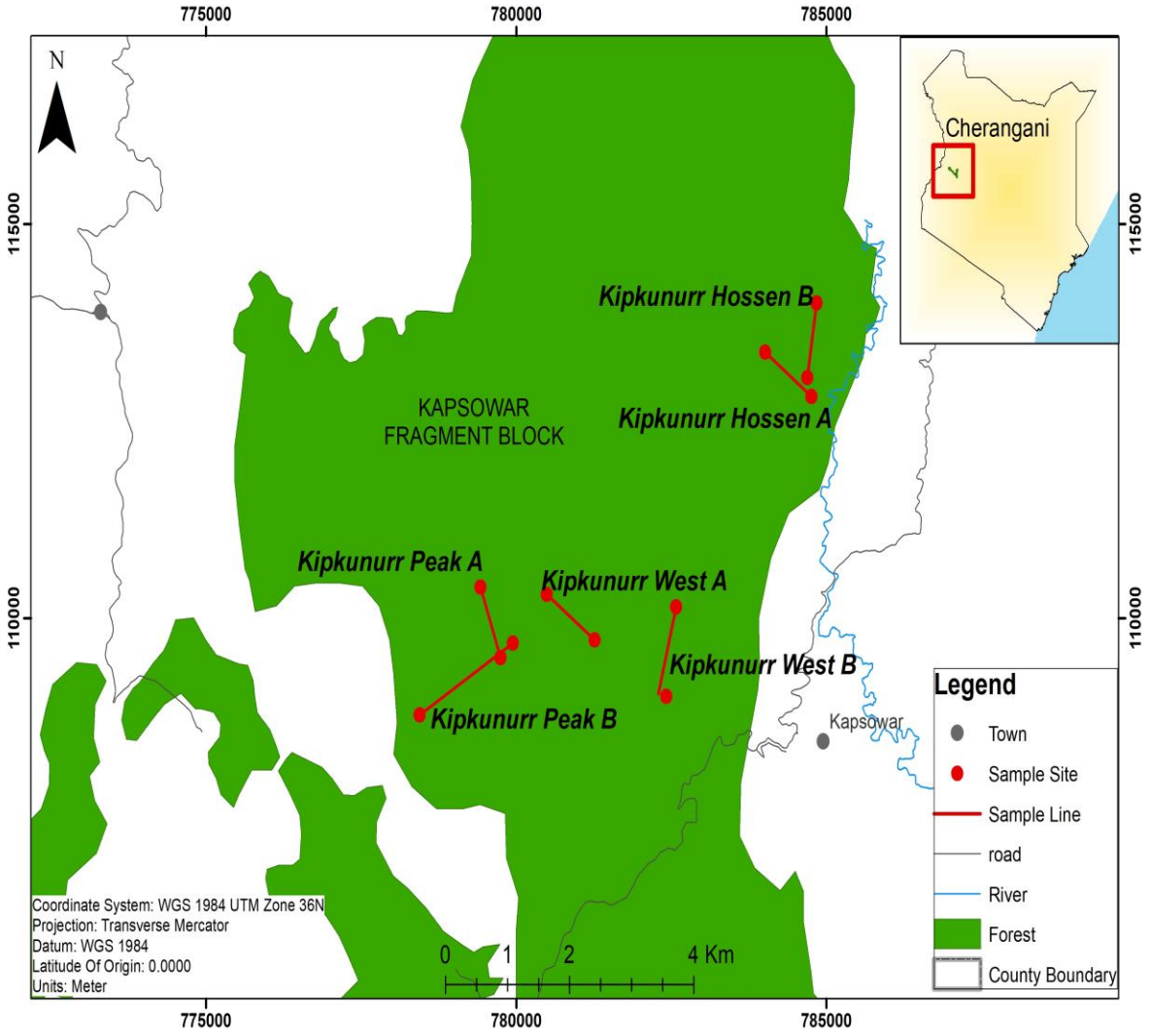

Figure 6. Map for Kapsowarr fragments transects and sampling points at high magnification

3.2 Materials and equipment

The survey was conducted using binoculars, camera, notebook, and a pencil or pen. A portable Global Positioning System (GPS) was used to mark coordinates at every surveyed point and site (*Whitman A. A. et, al (1997*). Detailed studies were made using mist nets erected on bamboo poles to capture birds. Ringing data and bird biometrics were recorded in a notebook. Birds caught were identified, measured using a ruler scaled in millimetres (mm)

and weighing scale in grams (g) and ring. A special ringing ruler was used to measure wing length, and callipers were used to measure the head from the nape to the tip of the bill, and the tarsus. An appropriately scaled spring balance was used to measure the weight of each caught bird before release. Blood sampling kits containing vials, gloves, syringe, cotton wool, 96% absolute alcohol, and EDTA, were used to collect and preserve DNA samples collected in the field. Feather samples were taken and kept in self-seal envelopes.

A checkerboard, datasheet, pen or pencil, and a camera were used to assess vegetation and threats **(***Birdlife international tool kit 2016*).

3.3 Birds species diversity survey methods

Point counts and mist-netting were used together with scientific birding or general observation to collect the bird diversity data. (*Bibby, Colin J (2000)*

3.3.1 Point Count (PC) is a tally of birds detected by a single observer from one station, within a fixed radius of 50m. Two transects per fragment were surveyed, over 1km from 06:00–10:00 Hr, under the same weather conditions (*Hamel et, al 1996*). Each transect had six points of 50m radius 200m apart. At every point, below 2 minutes was allowed for birds to settle after arrival on the Transect and 10 minutes were spent watching, listening and recording all individuals seen and heard. Variations in observer ability and environmental conditions can influence the probability of detecting birds in point counts, but statistical and methodological developments have begun to provide practical ways of overcoming some of these problems (*Sutherland, W. J. et, al (2004).*

3.3.2 Mist netting is an effective means of recording forest, under-storey (below 3m), quite, and "skulking" bird species. Some of which may not be recorded easily using other birding

techniques (*Bibby et, al 1998; Bennun et, al 2002*). A total of nine mist nets comprising (3 x 18m nets; 5 x 12m nets; 1 x 9m net and 1 x 6m net) covering 129m length were set on each transect (*Bibby et al 1998, Laurence et, al 2004).* The nets were opened through a process called unfurling, early mornings from 06:00 Hr –12:00 Hr the time when birds are most active (*Bibby et, al 1998).* The nets are closed and left in a role state, to avoid capturing bats and nocturnal birds. Opening the role (fulled nets) is opening the nets referred to as unfurling. Every fragment had two transects, whereby two days were spent ringing birds on one transect, totalling four days in every fragment.

3.3.3 Scientific birding is where daily all species are recorded where ever and whenever they are seen or heard .

3.4 Assessment of threats.

Threats and vegetation were assessed through descriptive recording. Threat categories focused on human activities, like fuelwood collection with axes, and power saws, where the collector focuses on a commercial market, grazing, logging, poaching using traps and snares, and even community hunting with dogs, spears, and arrows were among other threats recognized through observation and witnessing across all surveyed fragments.

For data collection, keen observation, on threats Scope, severity and intensity were guiding aspect for the score. Collected data were standardized under birdlife international tool Kit, being subjective to score of 0 = non-existent, 1 = low impact, 2 = medium, 3 = bad, and 4 = critical (*Birdlife international Toolkit 2015*). The data set per fragment considered season dry and Wet. Invasive species, fire, encroachment into the forest, grazing, were part of the frequently recorded threats in the study.

Vegetation surveys were carried out on a radius of 25m quadrants, in all directions. The number of trees over 60cm diameter at breast height (DBH); between 30–60cm DBH; and

seedlings were recorded within a quadrant of 20cm^2.(*Banks, J. E., et, al (2017*).The checkerboard was used to assess vegetation coverage of mid-canopy and forest density. Where one person on the far corner of the quadrant held the Checkerboard to try and see how many full square can be seen. In an area of 2m^{2,} the canopy cover under store's was assessed according to several seedlings, dead wood, either naturally fallen or through logging, leaves and detritus and biodegradable litters mixed **(***Rouget, M. et, al (2003*).

3.5 Data analyses.

3.5.1 Species accumulation curve.

Cumulative data collected through point counts, bird ringing/(MN), and opportunistic birding. The recorded daily checklist was used to plot species accumulation curves. This assessed completeness of bird species list within the ecosystem. It was fitted on the asymptotic linear dependence model as described by (*Soberón and Llorente, 1993, Gaidetm, et, al 2005)* to species accumulation curve. This is for relatively less diverse assemblages of well-known groups such as mammals and birds (*Moreno and Halffter, 2000;).* In this model, predicted number of species S (p), added to the list decreases linearly as the number of days sampled (p) increases S(p) = a/b [1-exp (-b*p)].

The parameter represents the increase rate at the beginning of the sampling period, and a/b is the asymptote (*Chao, A., et, al 2013, Soberón and Llorente 1993*). Two values were based on first, the mean increase in the rate of species, over the initial 18 days including the 1st day (i.e.,days 1 to 18), and second rate of increase over the initial 18 days, (i.e., days 2 to 18), these two models approach was used to create an accumulative curve on Fig.11 and 12 Pg 35 (*Gaidetm, et, al 2005*).

Diversity Index was tested through exponential of H, dividing it with Hmax which is equivalent to (1), minus the sum of species which is exponential of HMX greater than (1). (equitability Ex=H/H max =H/1nS,) (*Lähde, E., et al (1999*).

For similarity Primer 5.0 was used to develop a similarity dendrogram and diversity indices, to assess species diversity within sampled forests fragment (*Campbell, B. M., (1978*).

Principal Component Analysis (PCA), was used to explain the biological variation, to analyze species variation, associations within the sites, and similarity in terms of composition, in different sites. It is after organizing the species along the surveyed transect within specific blocks and fragments in a special matrix. The analyses extracts, components of variation(Principal Component), used to pool species according to commonness and similarity of species in fragment.

Threats assessment was done along with the bird survey methods. The data was converted into a matrix, to be run against threats level score per transect. The Redundancy Analysis (RDA) was used for each transect, each threat had been summarized by applying a weighted sum.

3.6 Blood sampling.

Two blood samples were extracted from the brachial vein, through a puncture with a 0.6 mm needle to avoid rupture/injuries of the tiny vain it is recommended one to use the smallest needle for small birds. Depending on individual bird and weather, 10-20 micro-litre of blood was collected in a 50 micro-L capillary tube and preserved in a vial with 96% ethanol (*Dawson et, al 1998; Segelbacher, G. 2002*). On the same individual, one pair of the feather was plucked from both sides of the flank which was kept immediately in a sealed enveloped safely. After the process of sample collection, an individual was released back to nature. In total, 124 blood and feather sample**.**

Molecular analysis was carried out on samples from 124 individuals collected in Cherangani Forest belonging to forest specialist species (FF) and forest generalists (F).

- *Andropadus latirostris* (F)
- *Phyllastrephus cabanisi (FF)*

- *Andropadus nigriceps (FF)*

In summary Table 1 illustrate species of Greenbul sampled, forest block, habitat category of each species, and sample number, per individuals, per site.

Table 1. Totals of collected samples from blocks Per Species in Cherangani Ecosystem.

SPECIES	HABITAT	N	KAPCHEROP	KAPSOWARR
A. latirostris	F	77	56	21
P. cabanisi	FF	36	29	7
A. nigriceps	FF	11	2	9
Total		124	87	37

3.7 Genetic Analyses

3.7.1 DNA extraction

DNA extraction was done from 200µl of liquid blood, dry filter paper blood spot and feathers using DNeasy Blood and Tissue Kit - QIAGEN, according to (MAV producer instructions). After successful extractions of DNA, the extract DNA samples were isolated and tested using the electrophoresis method *(Bimboim, H. C., and Doly, J. (1979)*. About 5 µL of each extracted DNA was put on an Agarose gel, at 1% in SBA, (Sodium-boric-acid, electrophoresis buffer). For the electrophoretic run, the gel was exposed to a UV-light, for view of the amount of DNA extracted through comparison with a marker (1 Kb DNA ladder, Sib enzyme). These markers, composed of DNA fragments, of known dimension and thus they permit the operator to determine the amount of DNA, that is present in the lane (Fig. 7)

Markers of a gel under UV-light of Agarose gel some DNA samples are charge

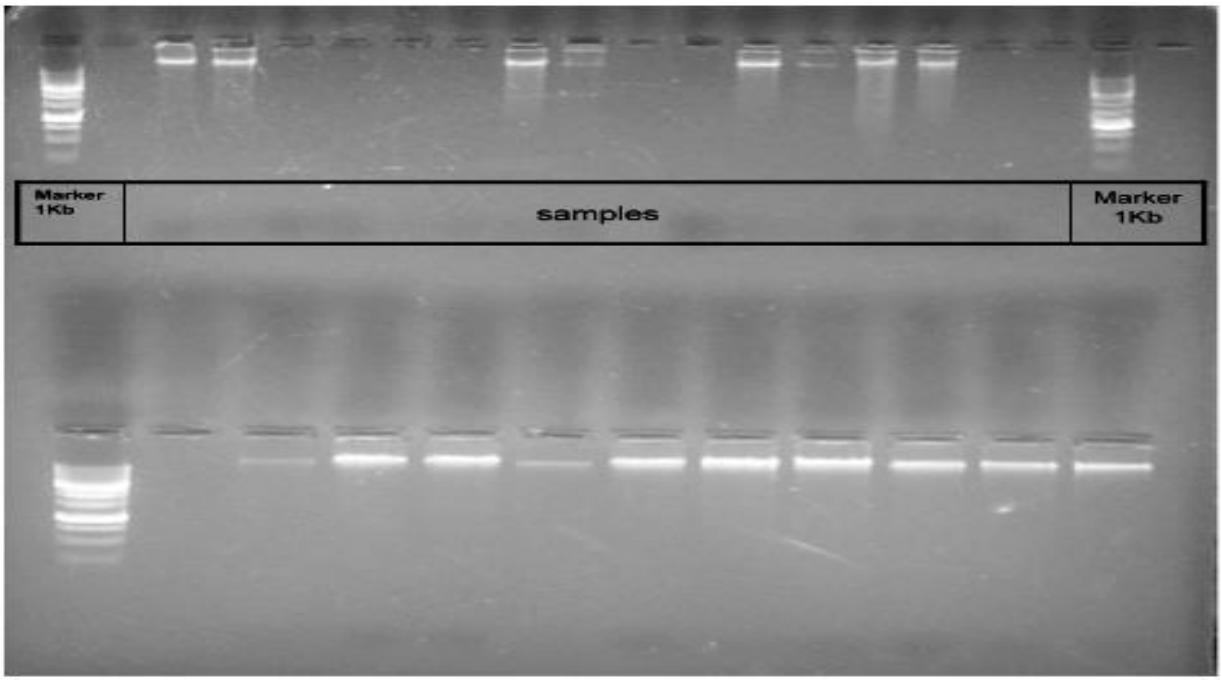

Figure 7. Cherengani Greenbuls DNA extracted in 1 % agarose gel under UV light.

3.7.2. Genotyping and sequencing of the extracted DNA.

All samples were genotyped at 8 different microsatellite loci, chosen from literature by selecting common sequence pairs (Table 2). Two multiplex-PCR reactions were designed to improve genotyping throughout, as well as cost-effectiveness. One of these two different reaction mixes were run at the annealing temperature of 57°C and one at 59°C. For each mix, four primer pairs of sequencing were us

Table 2. PCR(sequencing) of successful extracted Greenbul DNA from Cherangani Ecosystem.

LOCUS		Primer Sequence	Product size	Repetition type	Source	Accession N°
Pca3	F	GGTGTTTGTGAGCCGGGG	200-230 bp	(GT)6CT(GT)3CT(GT)5CT(GT)3CT(GT)13	Callens et al., 2011	AJ279805
	R	TGTTACAACCAAAGCGGTCATTTG				
AAGG-9m	F	TGTCCTTAGGGCTTGTCTCC	100-190 bp	(CCTT)3(CCTC)2	Bardeleben, 2004	AY644960
	R	AGGTTTGGGTGAATGACTCAG				
Dpμ16	F	ACAGCAAGGTCAGAATTAAA	200-210 bp	(AC)12(GC)4ACGCAC(GC)2	Callens et al., 2011	
	R	AACTGTTGTGTCTGAGCCT				
Pfl51	F	GCAGCGTCTAACCAATAACTCCTG	250-290 bp	(TATC)13	Lokugalapatti et al., 2007	EU048242
	R	CTGATTAATACAGTGACTTGGCTTTCACC				
AAGG-123	F	CATTCTGGGATTTGGATTCCTG	190-200 bp	(AAGGG)8	Bardeleben, 2004	AY644959
	R	ATTCCTGAACCACAGAAACC				
Pdoμ1	F	TCTGGGCTGTTGCTATCAGAAGGA	160-170 bp		Callens et al., 2011	X93503
	R	GCAGGGCTGTCCTTTCAACAAACT				
AAGG-26	F	GGCAATAAAACAGGACTGATGG	120-150 bp	(CCTT)5	Bardeleben, 2004	AY644954
	R	CACCAGTCGAACCTTTTAAG				
Pfl77	F	GGTGTGCAGAATTTGGCTGC	200-300 bp	(TAGA)12	Lokugalapatti et al., 2007	EU048246
	R	CTGCTGATCTTCCAGCCCTTC				

This was marked forwards by four different fluorochromes, one for each locus. The subsequent table (Table 3) reports the primers pair combination for each mix and respective size range attended for *Andropadus latirostris* and *Phyllastrephus cabanisi*. These ranges were estimated from an Agarose gel (1.5% SBA) on which 10 μL of PCR product was charged with same concept through which extraction success was evaluated using another marker (100 bp DNA ladder, Sibenzyme).

Table 3 below shows the two different mixes used for PCR. Each mix contains four primer pairs, each one marked with different fluorochromes (ROX, FAM, HEX, and TAMRA). The

table also reports the estimated range for each amplified locus for *A. latirostris* and *P. cabanisi*.

Table 3. Two Different Mixes Used For PCR For Greenbul Extracted DNA

MIX 1			
TD-57°C		*Andropadus latirostris*	*Phyllastrephus cabanisi*
Pca3	ROX	220-230 bp	200-220 bp
AAGG-9m	FAM	180-190 bp	100-120 bp
Dpμ16	HEX	200-210 bp	200 bp
Pfl51	TAMRA	250-260 bp	280-290 bp
MIX 2			
TD-59°C		*Andropadus latirostris*	*Phyllastrephus cabanisi*
AAGG-123	ROX	190-200 bp	190-200 bp
Pdo μ1	FAM	160-170 bp	300 bp
AAGG-26	HEX	120-150 bp	120-150 bp
Pfl77	TAMRA	250-300 bp	200-250 bp

The PCR reactions were carried out in a volume of 10 µl made up from 1 µl of the isolated DNA, 5 µl of QIAGEN Master Mix, 0.25 µM of each primer and QIAGEN H2O to reach the final reaction volume of 10U. PCR was performed with a Touch-Down (TD) method (Don et, al. 1991). This method consists of decreasing annealing temperature by -0.5°C per cycle, starting above the expected annealing temperature to avoid the formation of specific bands (Table 4). Thereafter, amplicons were sent to Macrogen Inc for genotyping. The resulting raw data were analysed by PeakScanner software v1 to obtain length information for each sample at each locus. The resulting allele matrix was tested for the presence and frequency of null alleles at each locus using MicroChecker (*van Oosterhout et, al 2004*) and corrected according to software suggestions.

Table 4. Sequencing at various temperature using Two different mixes used for PCR in this work:

Step	***Time***	***Temperature °C***	***N° of cycles***
Initial heat activation	15:00	95°C	
Denaturation	00:30	95°C	
Annealing	01:00	TD-62°C	11 cycles -0.5°C (cycle)
extension	01:30	72°C	
Denaturation	00:30	95°	
Annealing	01:00	TD-57°C or 59°C	21 cycles
extension	01:30	72°C	
Denaturation	00:30	95°C	
Annealing	01:00	TD-55°C	8 cycles
extension	01:30	72°C	
Final extension	30 min	60°C	
	∞	10°C	

Genetic diversity and genetic differentiation indexes (Ho, He, FIS and FST) were estimated using GenAlEx 6.0 (Peakall et, al 2006) and Genetix software (Belkhir et, al. 1996-2004 GENETIX 4.05). Deviation from Hardy-Weinberg equilibrium (HWE) was calculated by using the exact test (Guo and Thompson, 1992) with significance estimated by a Markov chain method after 1,000 randomizations.

The population structure was evaluated for each species using the Bayesian model-based clustering approach implemented in STRUCTURE v. 2.3.4 (Pritchard et, al 2000). Twenty

independent runs were made for K comprised between 1 and 6, with each run consisting of a burn-in of 100000 Markov-Chain Monte Carlo steps, followed by 500000 steps. Selection of the most likely number of genetic clusters (K) was based on the second-order rate of change in probability between successive Genetic cluster (K) values as described in (Evanno et, al. (2005) and implemented in structure harvester (Earl and von Holdt, 2012).

For analysis, every sample loci were isolated and specific annealing done at constant temperatures (Kapil 2005), amplified with dependence on the allelic length (in bp) of each locus.

The genetic structure, diversity and deviations from Hardy-Weinberg Equilibrium (HWE) principle were tested by microsatellite analysis, for all the loci on the identified populations by determining the departure of FIS from zero according to taste inbreeding co-efficient (Guo et, al 1992). Genetic differentiation was evaluated by computing FST according to (Weir et, al 1984). The FST analogue for microsatellites, RST (Slatkin et, al 1995), evaluated size differences between the alleles to further assess differentiation between populations. The genetic diversity of each population was characterized by calculating the allele frequencies per locus and observed and expected heterozygosis using GENALEX 6.0 (Peakall et, al 2006). During the genetic analysis, only one sample was used; the second sample was kept as reference/backup samples.

3.7.3 Statistical analyses

Two alternative hypotheses were evaluated by Analysis of Molecular Variance (AMOVA), as implemented in Arlequin software (Excoffier, and Lischer 2010; Arlequin suite ver 3.5) to test two alternative hypotheses: H0: no genetic diversity H1: the presence of genetic diversity among and within forest fragments.

3.8 GIS Analyses Methods.

3.8.1 Extrapolation of species abundance and distribution.

The Least Squares Method was used to model the distribution of bird species richness over the wider landscape by fitting point values using a regression equation ($y = ax + b$), where y is bird species richness, which is assumed to be dependent on x, which is the Normalized Difference Vegetation Index (NDVI) (Luoto, M., et, al (2004) Davies, R. G., et, al (2007). The coinciding values of richness and NDVI models were used. The models were then used in an ArcGIS raster calculator to generate extrapolate local spatial model for visualization of predicted bird species richness distribution over the NDVI for the wider landscapes (Lowe, M. (2014) .

CHAPTER FOUR

4.0 RESULTS

These study findings are illustrated first in; genetic analysis of two genera of Greenbul, *Andropadus* and *Phyllastrephus*. Second, species diversity, abundance and similarity. Third, the effects of habitat change to the spatial distribution of species, and fourth, the impact of threats on species genetics, distribution, and abundance. All the analysis were based on collected data in both dry and wet seasons.

4.1 Sampling and Genetic Analyses

Through the evaluation of the genetic signature, we wanted to understand the genetic interaction of *Andropadus* and *Phyllastrephus* due to fragmentation. The result showed that the two forest-dependent models characterised with two different ecological specializations reported similar genetic patterns within fragments.

Molecular analysis was carried out from 124 individuals where genetic diversity was organised at three levels: (i) at the molecular level (nuclear loci); (ii) at the species level (heterozygosity) at Cherangani Hills forest; (iii) at geographic level testing the effects of fragmentation at the species level partially.

4.2. Molecular level (nuclear loci).

After isolating 8 microsatellites loci that hosted 105 distinct alleles. The total number of alleles per locus varied from 4 (locus Pdoμ1) to 27 (locus Pfl51) (Table 5).

Table 5. Range of variability expressed in PCR Lucus base-pair (bp) for Greenbuls.

LOCUS	**Observed range (bp)**	**Allele n°**	**He**	**Ho**	**F_{IS}**
Pca3	150-200 bp	15	0.738	0.445	0.400
AAGG-9m	82-98 bp	5	0.532	0.059	0.890
Dpμ16	148-168 bp	11	0.793	0.598	0.249
Pfl51	194-398 bp	27	0.881	0.726	0.180
AAGG-123	93-168 bp	15	0.762	0.527	0.313
Pdoμ1	158-166 bp	4	0.588	0.000	1.000
AAGG-26	86-102 bp	5	0.520	0.148	0.718
Pfl77	198-294 bp	23	0.862	0.784	0.094

Key

Allele n° = Number of allele per locus **Ho=** observed heterozygosity

He = expected heterozigosity **$F_{IS=}$** fixation index,

4.2.1 Species heterozigosity at Cherangani Hills Forest :

The three species display medium-high values of expected heterozygosity (He = 0.4÷0.7) congruent with bird populations from Taita Hills (Callens et, al, 2011). All diversity indices are reported in the table (Table 6).

Table 6: Diversity indices of bird forest specialist species in Cherangani hill Forest.

N = number of individuals, He = expected heterozigosity, Ho = observed heterozigosity, <Na> = medium number of alleles, FIS = fixation index, HW = Hardy-Weinberg equilibrium.

Table 6. Genetic Diversity Indices for Greenbuls in Cherengani Ecosystem.

SPECIES	Ecology	N	He	Ho	<Na>	F_{IS}	HW
A. latirostris	F	77	0.468	0.408	8.5	**0.136**	no
P. cabanisi	FF	36	0.610	0.436	9.0	**0.299**	no
A. nigriceps	FF	11	0.401	0.357	3.9	**0.161**	no

4.2.2 Geographic level

The effects on the genetic signature of forest fragmentation were evaluated on the most represented species: *A. latirostris* (N= 77), and *P. cabanisi* (N= 37). Within Kapcherop fragment three populations were identified.

Table 7. *Andropadus latirostris* diversity indices

N=number of individuals, He= expected heterozigosity, Ho= observed heterozygosity, <Na>= medium number of alleles, FIS=fixation index, HW= Hardy-Weinberg equilibrium.

Table 7. Yellow Whiskered (Andropadus latirotris) genetic diversity indices within two blocks.

Yellow Whiskered Greenbul (*Andropadus latirostris*)							
FOREST BLOCK	**FRAGMENT**	**N**	**He**	**Ho**	**<Na>**	**F_{IS}**	**HW**
	EMBAYAT	12	0.383	0.421	3.9	**-0.046**	no
KAPCHEROP	KIPLEKATET	34	0.441	0.416	6.0	**0.074**	no
	KIPTABERR	10	0.422	0.433	4.4	**0.029**	no
KAPSOWARR	KAPSOWARR	21	0.482	0.387	5.6	**0.220**	no

Table 8. Cabanis's Greenbul (Phyllostrephus cabanis) diversity indices within two blocks.

Cabanis's Greenbul (*Phyllastrephus cabanisi*)							
FOREST BLOCK	**FRAGMENT**	**N**	**He**	**Ho**	**<Na>**	**F_{IS}**	**HW**
	EMBAYAT	7	0.494	0.470	4.0	**0.136**	no
KAPCHEROP	KIPLEKATET	18	0.529	0.392	7.4	**0.363**	no
	KIPTABERR	4	0.481	0.563	3.8	**-0.029**	no
KAPSOWARR	KAPSOWARR	7	0.643	0.446	5.1	**0.374**	no

significant values ($p<0.05$) in bold.

All the populations for each species showed significant deviations from the Hardy-Weinberg equilibrium, medium of the expected value **He** and observed **Ho**.

4.2.3 Population genetics structure:

The genetic signature of the population structure may be inferred at different temporal scales: (i) The origin of genetic pools from which derived the actual populations; (ii) the more recent pairwise genetic differentiation between populations; (iii) testing the actual role of fragmentation between two Forest fragments and within the same fragment.

4.2.4. The unique metapopulation of Phyllostrephus cabanis and Andropadus latirostris.

That outcome suggested that the Cherengani meta population did not have time to split genetically in more than one population. This result indicates that bird populations from Cherangani should be considered as a unique metapopulation.

The genetic Cluster of Meta population for the analysed Species within Cherengani.

In figure 8, structure plots for K=1 for *A. latirostris* (n=77), and for *P. cabanisi* (n=37) ordered by population. Each column represented a single individual.

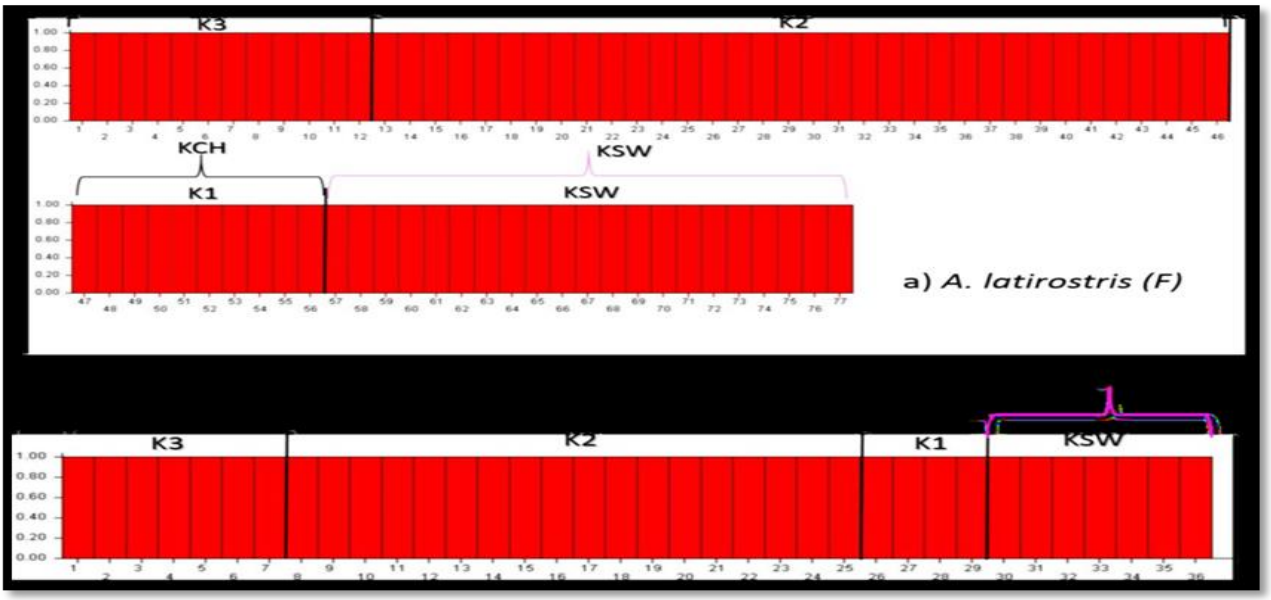

Figure 8. The cluster analysis of various population from the six fragments which forms the Metapopulatiom of Greenbul within Cherangan ecosystem.

4.2.5 Pair wise genetic differentiation

The genetic divergence between Cherangani fragments populations was inferred, using the pairwise statistic program (*FST)* 1000 permutation and its significance was tested. From the result, No significant values were observed neither in *A. nigriceps*, (*FST*=0.01, *p>0.05*), nor in *P. cabanisi*, (*FST* =0.03, p>0.05). Among the populations in the two main blocks, there were no significant values were found for the sub-population of *P. cabanisi among* Kapcherop's fragments and Kapsowar. There were very low Significant values found,

in *A. latirostris*, both between the two main fragments (*FST*=0.05, p<0.05) and among Kapcherop's subfragments and Kapsowarr (Table 9).

For *A. latirostris* very low values, 0.00553, 0.0064 and 0.21852 of genetic differentiation between populations were observed, whereas no significant values were recorded for *P. cabanisi* (Table 9).

Table 9. Pair wise genetic differentiation index FST in Andropadus latirostris among the three Kapcherop's populations (Embayat, Kiplekatet, Kiptaberr) and Kapsowar.

A.latirostris :				
	EMBAYAT	**KIPLEGATET**	**KIPTABERR**	**KAPSOWAR**
EMBAYAT	0	**0.044**	**0.088**	**0.064**
KIPLEGATET		0	**0.016**	**0.055**
KIPTABERR			0	**0.040**
KAPSOWAR				0

3. **Forest fragmentation**

AMOVA for both species indicated that variation is mainly within populations, according to previous results from structure and FST analyses, suggesting accepting the H_0.

A. latirostris

Representation of the main variance component in Cherangani Forest TransNzoia county Kenya:

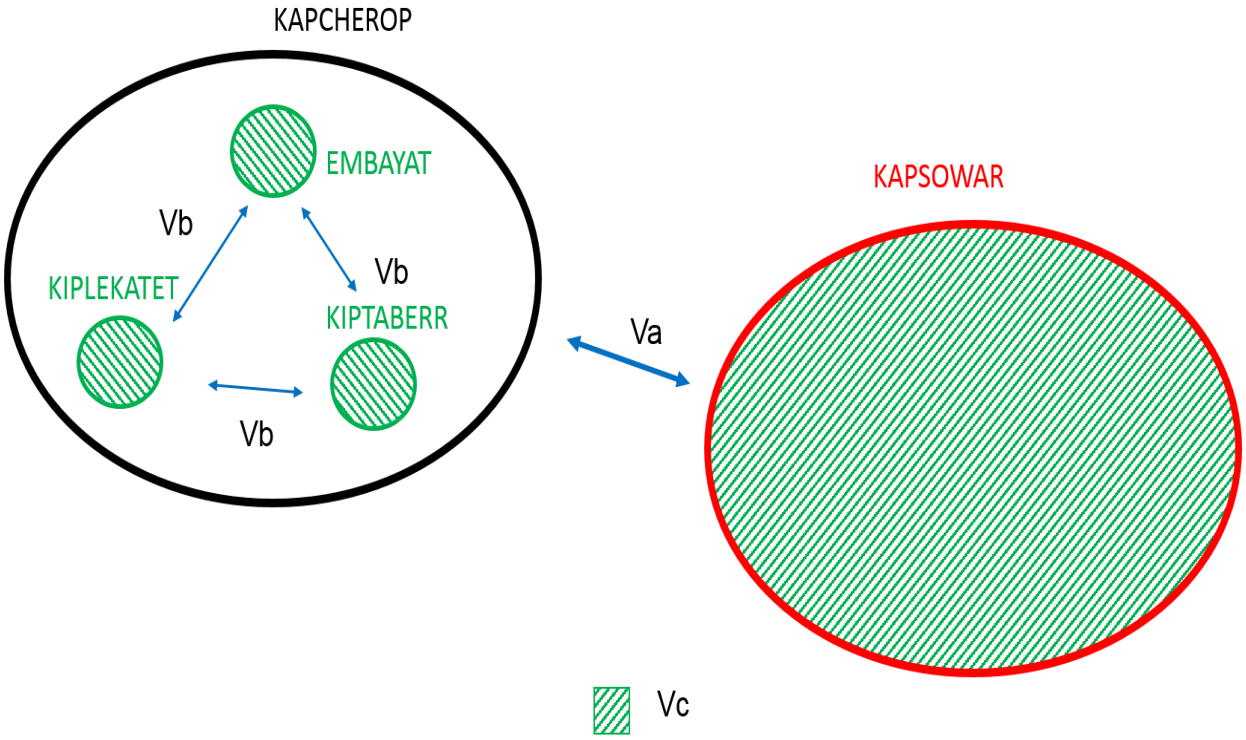

Figure 9. Hierarchical organisation of genetic variability distribution in Cherangani.

Va = among the main Cherangani blocks; Vb = among the population of the main blocks;

Vc = among individuals within each population.,

The results of the analysis, reported in the following tables (Table 5 and 6), indicated that the main genetic diversity is represented, in both species (*A. latirostris*, Table 7 and *P. cabanisi*, Table 8) among individuals within each population (Vc).

Table 10. Summary of Amova for Analysis A. latirostris Within

Source of variation	**d.f.**	**Sum of squares**	**Variance components**		**Percentage of variation**
Among groups	1	0.163	-0.00553	Va	-2.52
Among populations within groups	2	0.831	0.0064	Vb	2.92
Within populations	148	32.342	0.21852	Vc	99.6
	151	**33.336**	**0.2194**		

Table 11. Summary of Amova Analysis for P. cabanisi Within Cherangani ecosystem

Source of variation	**d.f.**	**Sum of squares**	**Variance components**		**Percentage of variation**
Among groups	1	4.452	0.08889	Va	3.70
Among populations within groups	2	4.878	0.00867	Vb	0.36
Within populations	68	156.657	2.30378	Vc	95.94
	71	**165.986**	**2.40133**		

The outcomes revealed that the forest specialist and forest generalist bird populations from Cherangani Hills forest do not suffer the effect of habitat fragmentation on genetic structure.

4.3 SPECIES DIVERSITY, ABUNDANCE, SIMILARITY, AND DISTRIBUTION

4.3.1 Introduction

Overall, 164 bird species were recorded from, mist-netting, point counts and scientific birding methods. Mist netting caught 622 birds, of 54 species, 53 individuals being recaptured in dry and wet seasons. Six-point counts were made along each transect, recorded 103 species from 12 transects, in six fragments of the two blocks, Kapcherop and Kipsowarr. Shannon Wiener index illustrated that the ecosystem is rich in terms of avifauna, with a 95% confidence interval. Between fragments, there was no significant difference, in species diversity with a diverse range of less than $H<1.00$. Out of six fragments, five had almost equal equitability, of species distribution. The exception was Kipkunurr Hossen, which had the lowest of 11 %, as compared to the other fragments which had over 15%, although less than 19% of the equitability.

For species distribution map, most species were strongly influenced by vegetation indices, due to human activities that have altered the habitat structure. Some species found having a favourable habitat outside sampling point, according to NDVI. The effect of anthropogenic activities on species diversity and abundance were tested in different fragments and found to be constant, in almost the entire ecosystem. So, species diversity abundance is not affected by this threat, but their distribution is related to the adaptation of some species on on-going human activity, which does affect habitat structure hence change in species distribution and can be reflected in the maps.

SPECIES LINEAR ACCUMULATION CURVE FOR KAPCHEROP AND KIPKUNURR FRAGMENTS.

The two accumulation curve, (Fig. 10 and 11) show species prediction based on 12 transects for three sampling methods PC, MN and opportunistic birding observation daily. The curves express temporal new species richness in birding based on seasonality phase (Wet and Dry) within the survey site. While species list illustrates that all bird's species recorded in both seasons did not reach the maximum horizontal plateau when plotted S (p) =a/b*(1-exp (-b*p) (*Gaidet et, al. 2005; Soberón & Llorente 1993*). But within the two seasons, there was a split of one month, which does not allow continuous accumulative curve for the entire survey period that ought to total (164) species, for the entire survey.

DRY SEASON SPECIES LINEAR ACCUMULATION CURVE FOR KAPCHEROP AND KAPSOWARR FRAGMENTS :

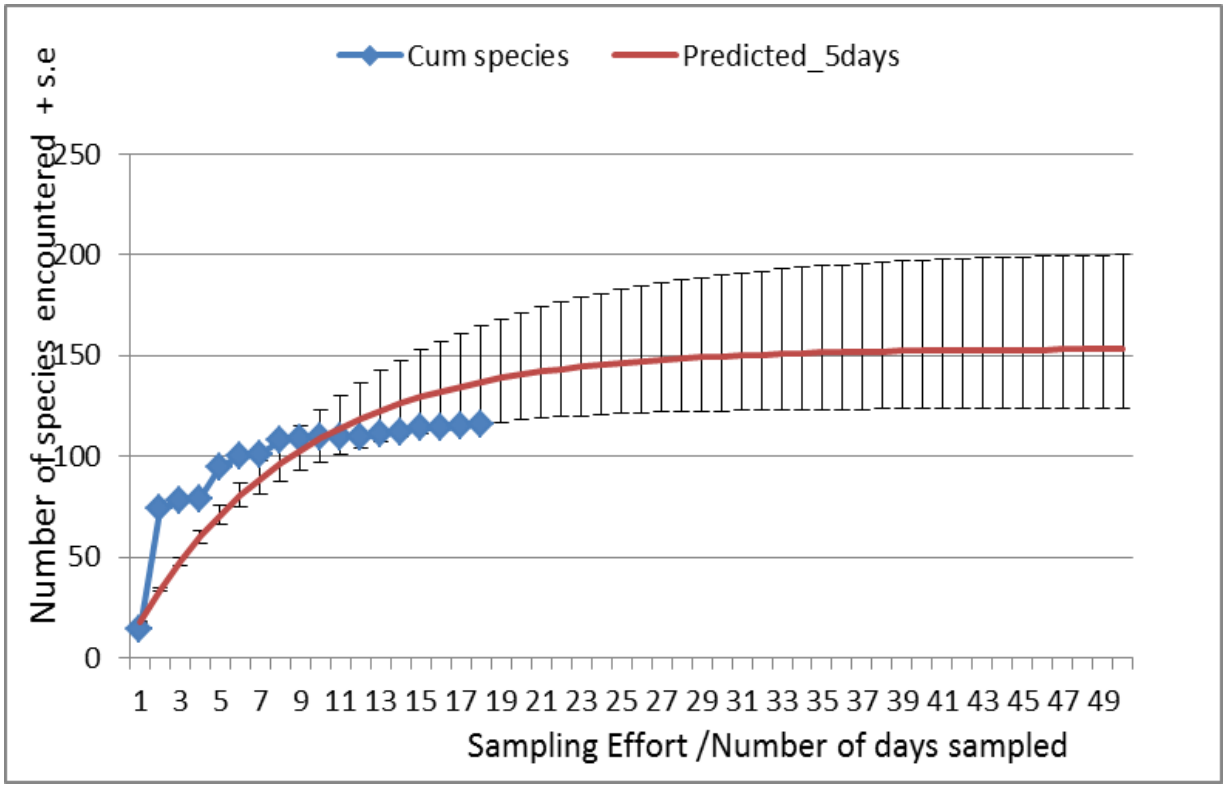

Figure 10. Species accumulative curve in dry season for Cherangan

The accumulative curve illustrates the number of new species recorded daily for 18 days. The blue line curve indicates accumulatively recorded species. The red line is the predictive curve, and horizontal black bars are minimum and maximum error marks/bars. The blue line, species curve indicates that in the first ten days, a high number of new species was recorded daily, almost over maximum error bars. That is normal there was a maximum effort, initial sampling in the area, and being first days all species were new on the record. The last eight days indicates low numbers of new species, which could be attributed to concentration on one survey method, focus within the specific fragment, and slow development of fatigue. Though predictive curve did not rich horizontal plateau, the red line still expressed the need for three more days, on the same efforts to rich Horizontal Plateau.

WET SEASON SPECIES LINEAR ACCUMULATION CURVE FOR KAPCHEROP AND KAPSOWARR FRAGMENTS:

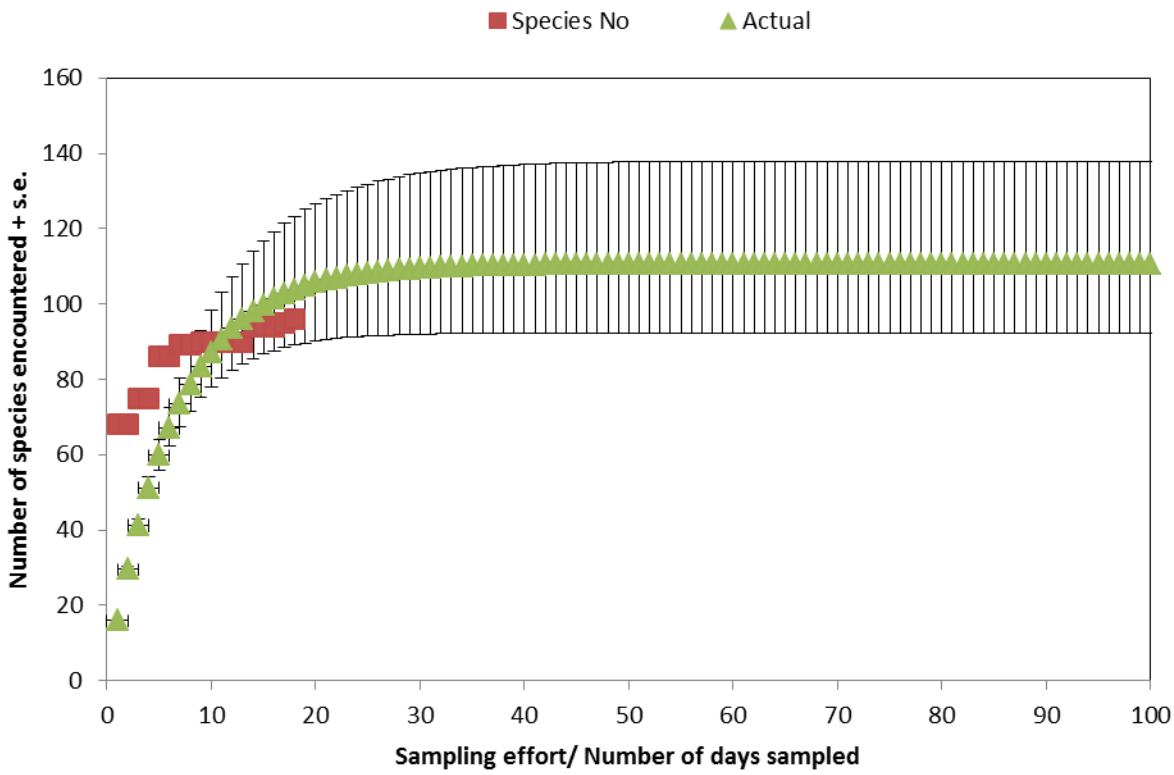

Figure 11. Species accumulative curve in wet season

In the wet season, more than 5 days with the same effort (Fig.11) could have enabled the curve to reach the horizontal plateau. At the same time, maximum error bars give more room as compared to the minimum error bar about the green predictive curve.

4.3.2 Avifauna diversity, similarity abundance and location within Kapcherop and Kapsowarr blocks .

There was a minimum difference in species richness between fragments but wide variation in species abundance as expressed by ringing data (Table 12).

Table 12. Ringing data and diversity indices for Cherangan Forest fragments

FOREST FRAGMENT	**DRY**		**WET**	
	No individuals	**No Species**	**No individuals**	**No Species**
Kiptaberr	56	19	29	13
Kiplaketet	96	19	84	17
Embayat	74	20	54	20
Kipkunurr West	52	17	66	18
Kipkunurr Peak /Ridge	40	13	34	14
Kipkunurr Hossen	30	9	23	11

IMPACT OF FRAGMENTATION ON FOREST BIRD SPECIES (FF, F, f) IN TWO BLOCKS KAPCHEROP AND KAPSOWAR FOR DRY AND WET SEASON:

Ringing data expressed on forest dependant bird species alone in the two forest blocks in dry season.The graphs illustrate species diversity and the abundance.

Kapcherop Block

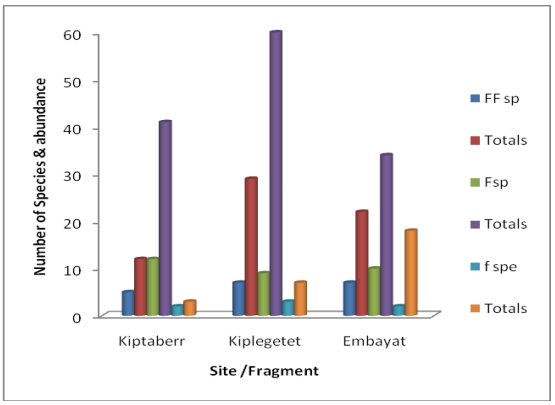

Figure 13. Kapcherop fragments

Kapsowarr Block

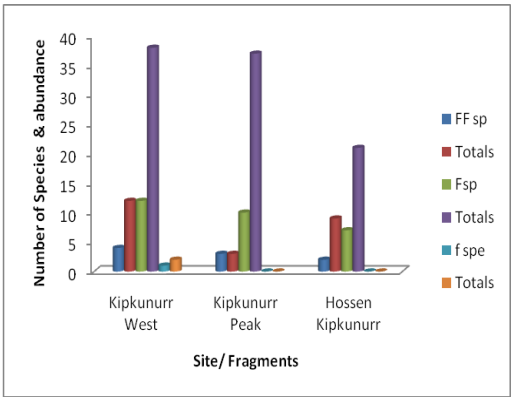

Figure 12. Kapsowarr fragments

The forest dependant species expressed in species diversity and abundance in the two forest blocks during wet season.

Kapcherop Block

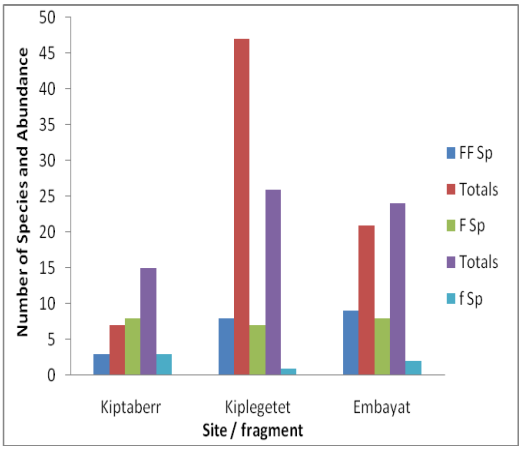

Figure 15. Kapcherop fragments

Kipsowarr Block

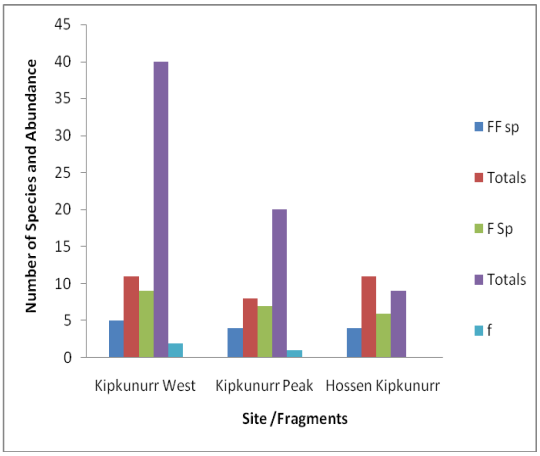

Figure 14. Kapsowar fragments

Forest dependent birds, combined with vegetation survey and canopy cover recording, can be used to assess forest status. Forest diversity category species, (FF, F, f) within each fragment in the two blocks remained trivial across all sites, during the two-season. Forest generalist (F) species, were slightly higher in the dry season than the wet season. On forest visitors (f) species were rare in both blocks, with zero being recorded in Kapsowarr block an indication that there's still existing forest.

Significant variation in abundance, both FF and F species, for the dry season in both block, F species were caught in largest number compared to FF. It illustrated that when herbs and shrubs dry's up, the forest becomes open hence less movement of (FF). They are forced crowd within a specific niche, for they are adopted within the closed canopy, hence the difference between (FF) and (F). In wet season variant in numbers between F and FF across the fragments was very minimal. It is a result of free movement of (FF) because of the dense vegetation the herbs and shrubs are connecting with mid-canopy. That creates a thick hideout and foraging site, which makes them feed easily. In both season Kiplegatet fragment stands unique, considering species abundance FF, and F, across other fragments, which directly attributed to the level and density of threat in the fragment and habitat status be it lower, mid and upper canopy. On the contrary, Kipknurr Hossein recorded the lowest relative abundance in both seasons, in all forest categories FF, F, f, also that attributed to threat and disturbance level.

4.3.3 Diversity index and chi-square test

The ringing data wet and dry season was combined to assess the species diversity and similarity in the entire ecosystem and within studied fragments. From the raw data, there was minimal difference in several species within fragments.

Table 13. Simpson index, Shannon, Evenness, and Equitability analyses on Ringing data in both dry and wet season for studied fragments in Cherangan ecosystem .

	Kiptaberr.	Kipleketet.	Embayat.	Kipkunurr West.	Kipkunurr Peak.	Kipkunurr Hossen.
Taxa_S	24	26	29	29	20	16
Individuals	84	180	128	118	74	53
Dominance_D	0.066	0.095	0.076	0.087	0.092	0.119
Simpson_1-D	0.934	0.905	0.924	0.913	0.908	0.881
Shannon_H	2.934	2.732	2.915	2.845	2.657	2.406
Evenness_e^H/S	0.784	0.591	0.636	0.593	0.713	0.693
Equitability_J	0.923	0.839	0.866	0.845	0.887	0.868
Chao-1	25.43	28	47.33	32.27	23	23
95 % confidence						

Diversity within the entire ecosystem was higher than means H<1,but almost the same in all six fragments. The species diversity range had a minimal variation, the highest being H< 2.934 at Kiplegatet, and H < 2.406 lowest at Kipkunurr Hossein. Diversity indices range indicated that the fragmentation effect on species was still insignificant . That expressed that the ecosystem was one and fragmentation is of recently less than 5 decades.

Table 14. Chi-square table testing diversity of studied fragments in Cherangani forest.

2 X 1= ∑(O-E)^2/E							
	Embayat	Kiplegetet	Kiptaberr	Kipkunurr West	Kipkunurr Hossen	Kipkunurr Peak	
Observed (O)	2.883	2.662	2.898	2.766	2.393	2.610	16.212
Expected (E)	2.702	2.702	2.702	2.702	2.702	2.702	
O - E	0.181	-0.040	0.196	0.064	-0.309	-0.092	
(O-E)^2	0.033	0.002	0.038	0.004	0.095	0.009	
(O-E)^2/E	0.012	0.001	0.014	0.002	0.035	0.003	
X2						0.067	
A						0.05	
df						5	
Critical value 2						11.07	
X < Critical value			Null Hypothesis				
There is no difference in species diversity across the six transects (X2 = 0.07, df = 5, p > 0.05)							

Chi-Square test was conducted to verify diversity indices. From this analysis, there was no significant difference in species diversity in the two surveyed blocks of the six fragments as it reflects in diversity indices. Where, the degree of freedom (df) was = 5 and P > 0.05 in all fragments, with the critical value being = 0

4.3.4. Mean abundance of ringed individuals with the two blocks in the two seasons

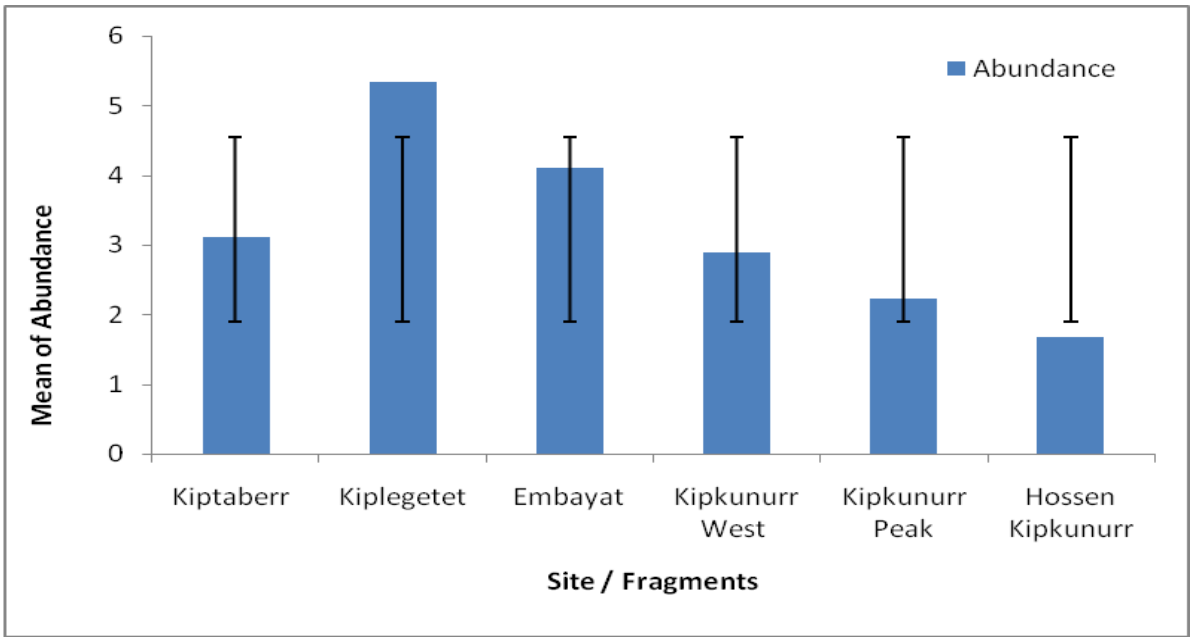

Figure 16. Mean abundance from the ringing data for all fragments in Cherangan.

There was very minimal significant in species diversity (Table 15) as illustrated in two blocks of six fragments. We had a wide variation of abundance from the species caught(Fig.16). The mean range indicated some difference within fragments. One fragment was above the mean range Kiplegetet, and Hossein in Kipkunurr was below. Other fragments, had significant difference although still within the mean range. The bar graph illustrates that the impact of fragmentation is of recent, but it is slowly taking shape.

4.3.5 Species equitability test from Shannon Index

Ex = H/H max =H/1nS

Table 15. Species equitability table across all fragments within studied fragments of Cherangan ecosystem;

	Spp Count	**Equitability**
Embayat	26	0.885
Kiplegetet	23	0.849
Kiptaberr	22	0.937
Kipkunurr West	27	0.839
Kipkunurr Hossen	15	0.884
Kipkunurr Peak	19	0.886

After Verifying species diversity and diversity index within fragments. We went further ahead to find out how species diversity was less the same in all fragments. Through exponential of (diversity) H, divided it with the number of species (Hmax), to test for equitability. The result in all fragments was very close to 1, which mean, it was equivalent to equitability. It indicated that the entire ecosystem was rich in species diversity. Presence of species occurred in all fragments, although some individuals were very few in numbers/abundance, as indicated in the mean abundance graph (Fig.16) and Shannon wiener table. That could be attributed to ecological, anthropogenic, and climatic factors, that allow the presence and absence of species in certain fragments, and how some species are adopting with the type of threats in the ecosystem.

4.3.6 Similarity and location

The similarity between fragments, based upon the presence or absence of species, was tested. Two sites from the two different blocks exhibited that there was a similarity between Kiplegetet in the Kapcherop block and Hossein in Kapsowarr block. The entire surveyed fragments showed some connection from one fragment to another (Fig.16)

Dendrogram illustrating species similarity in studied fragments in the two seasons

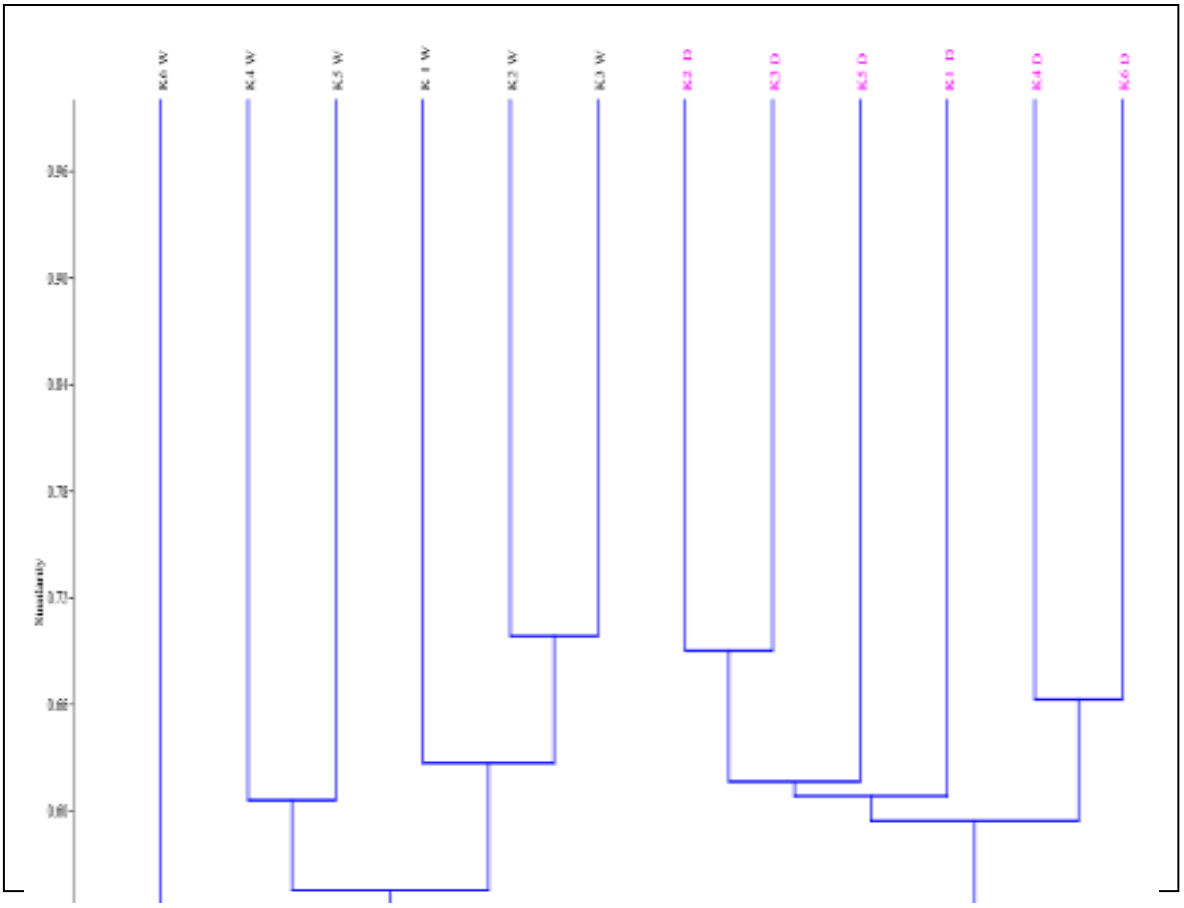

Figure 17. Similarity of presence and absence of species from different transects

F

K
K

K3 = Embayat

K4 = Kipkunurr West

K5 = Kipkunurr Peak/Ridge

K6 = Kipkunurr Hossen

W = wet season

D = dry season

In the wet season, Kipkunurr Hossein K6W and Kiptaberr K1W were more isolated from other fragments within Kapsowarr block. They joined the entire ecosystem at a distance, tracing the species composition year backs to be same. The two blocks Kapcherop and Kapsowarr showed some separation, but still connected as one ecosystem.

In the dry season, species were similar in the entire ecosystem. Kipkunurr Hossein K6D showed close similarity to Kapcherop fragments (K2D, and K3D), and K1of Kapcherop showed close similarity to Kipkunurr fragment (K5D, and K4D). From the dendrogram above, it is a clear indication that the ecosystem is still connected.

4.3.7 Spatial species distribution modelling

Fig 9, species distribution map shows that most sampling points were not within the selected avifaunal high diversity areas calculated from the NDVI, although some were close to the sampling transect.

Kapsowarr block (Kipkunurr West, Kipkunurr ridge/peak, and Kipkunurr Hossein) were relatively close. Kapcherop block (Kiptaberr Kiplegetet, and Embayat) some were displaced. The model illustrates that in

Kipkunurr block sampling point, approximately 80% of the sites were within selected, hot spot areas points and the remaining 20% sites, were slightly outside selected sites. In the Kapcherop block, approximately 50% of the site was outside hot spot areas, apart from Kiptaberr and Kiplegetet which were close to the sampling point, but not exactly within our sampling point, Embayat was almost outside the entire sampling points.

Species Richness distribution map within the entire ecosystem

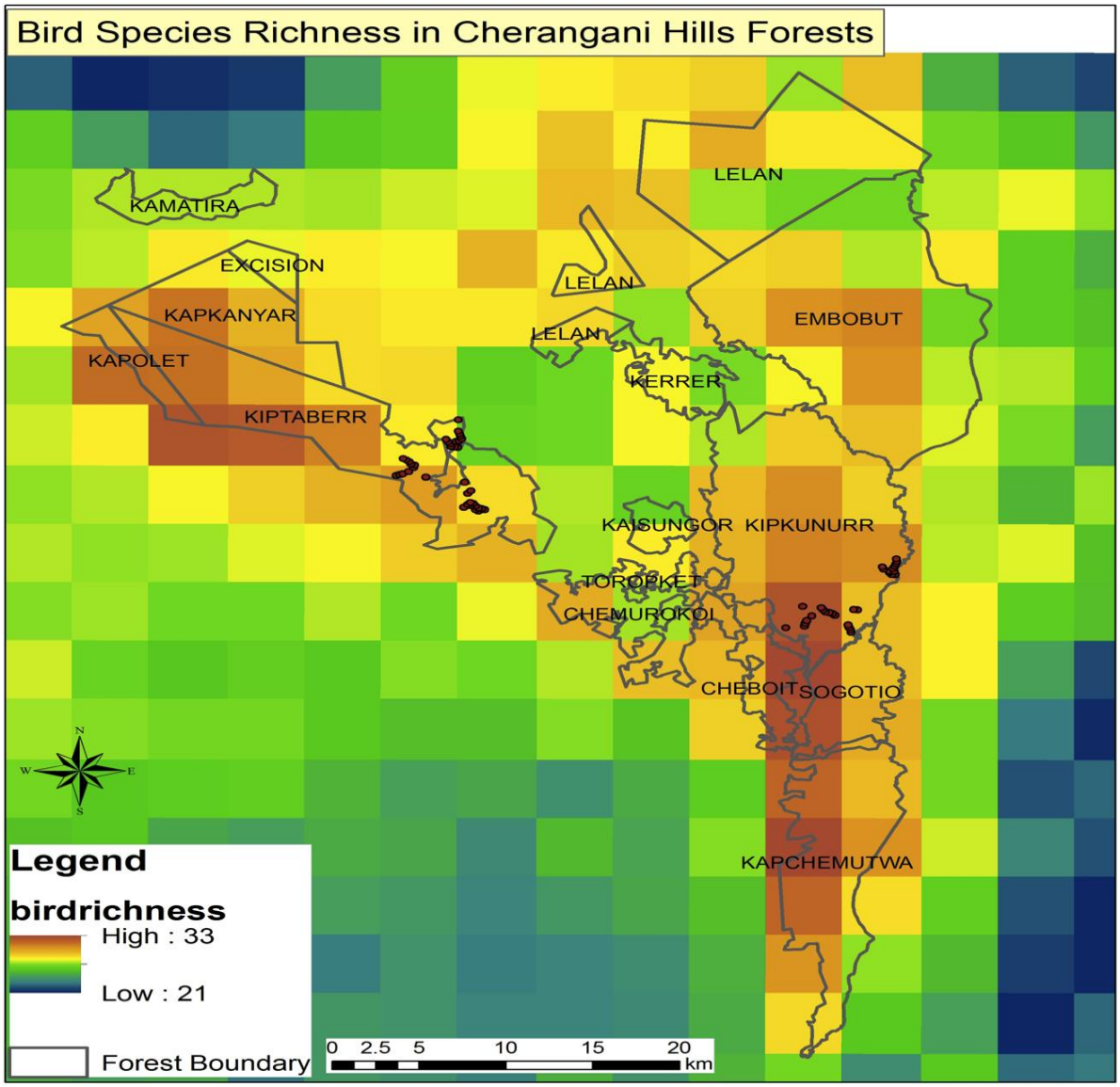

Figure 18. Species distribution Map within Cherangani forest fragments,Trans-nzoia county

The map above indicates avifauna richness and how they were distributed in the entire ecosystem in relation to the location of our study site.

4.4 Distribution maps for most abundant and Common species in wet and dry seasons from mist netting and point count data.

Through expert, modelling maps were developed, on how species were distributed within the forest ecosystem using collected data. By use of species frequency occurrence on the transect, from both mist-netting and point count methods. The least-square recreation was used to extrapolate dominant species after arranging the data in 2x2 matrix. Six species were found, of which included; Montane Oriole (*Oriolus percivali*), Abyssinian Crimsonwing (*Cryptospiza salvadorii*), Cinnamon Bracken Warbler (*Bradypterus cinnamomeus*), Black-collared Apalis (*Apalis pulchra*), Mountain Yellow Warbler (*Chloropeta similis*) and Yellow Whiskered Greenbul (*Andropardus latirostris*).

Through Arch GIS raster calculator and NDVI model (Fig. 20), their abundance was plotted against NDVI (Fig. 21, 22, 23, and 24), that showed how distribution correlated with vegetation cover within the ecosystem. All transect were within the forest ecosystem, irrespective of the habitat status.

Using NDVI with raster image, calculation indicated that there was variation in habitat structure, which directly related to species distribution. The maps created indicate that not all species identified were within sampling points and transect, but some species were outside the sampling points and transect. Certain vegetation types, dominated with specific birds, which separated species occurrence within the sampled points.

LEAST SQUEARE REGRESSION GRAPH FOR MOST DOMINAND SPECIES

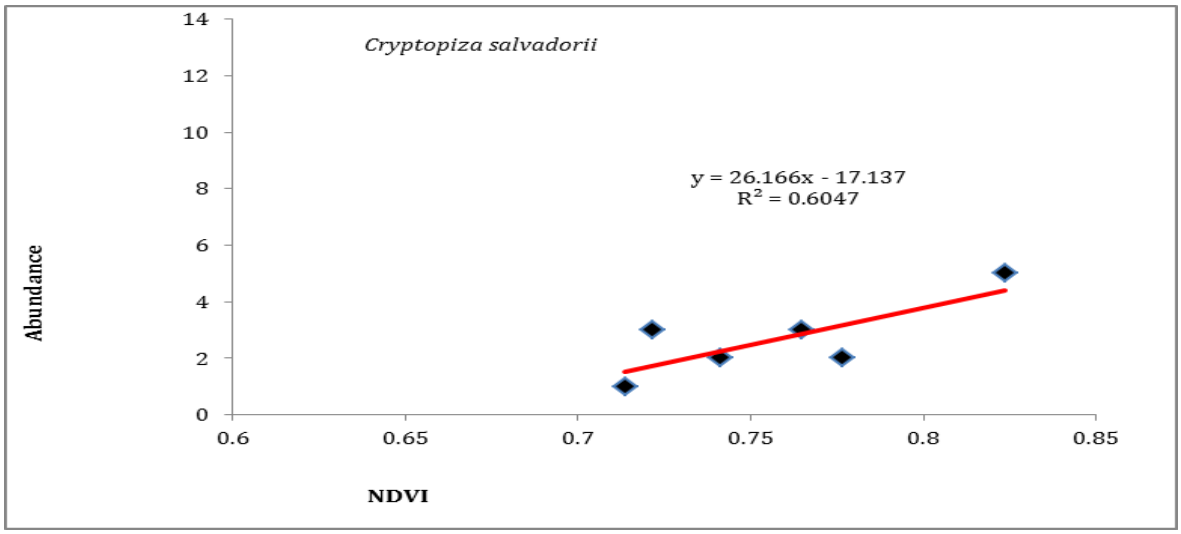

Figure 19. Least square regression for most common species Within Cherangani Ecosystem

Cinnamon Bracken Warbler (*Bradypterus. Cinnamomeus*), abundance was mostly placed within sampling site, especially in the Kapsowarr block (Fig 20 and 21). The highest density of Black Collared Apalis (*Apalis pulchra*), was outside the sampling points, transect, the fragments and blocks, meaning it utilizes forest as a functional niche.

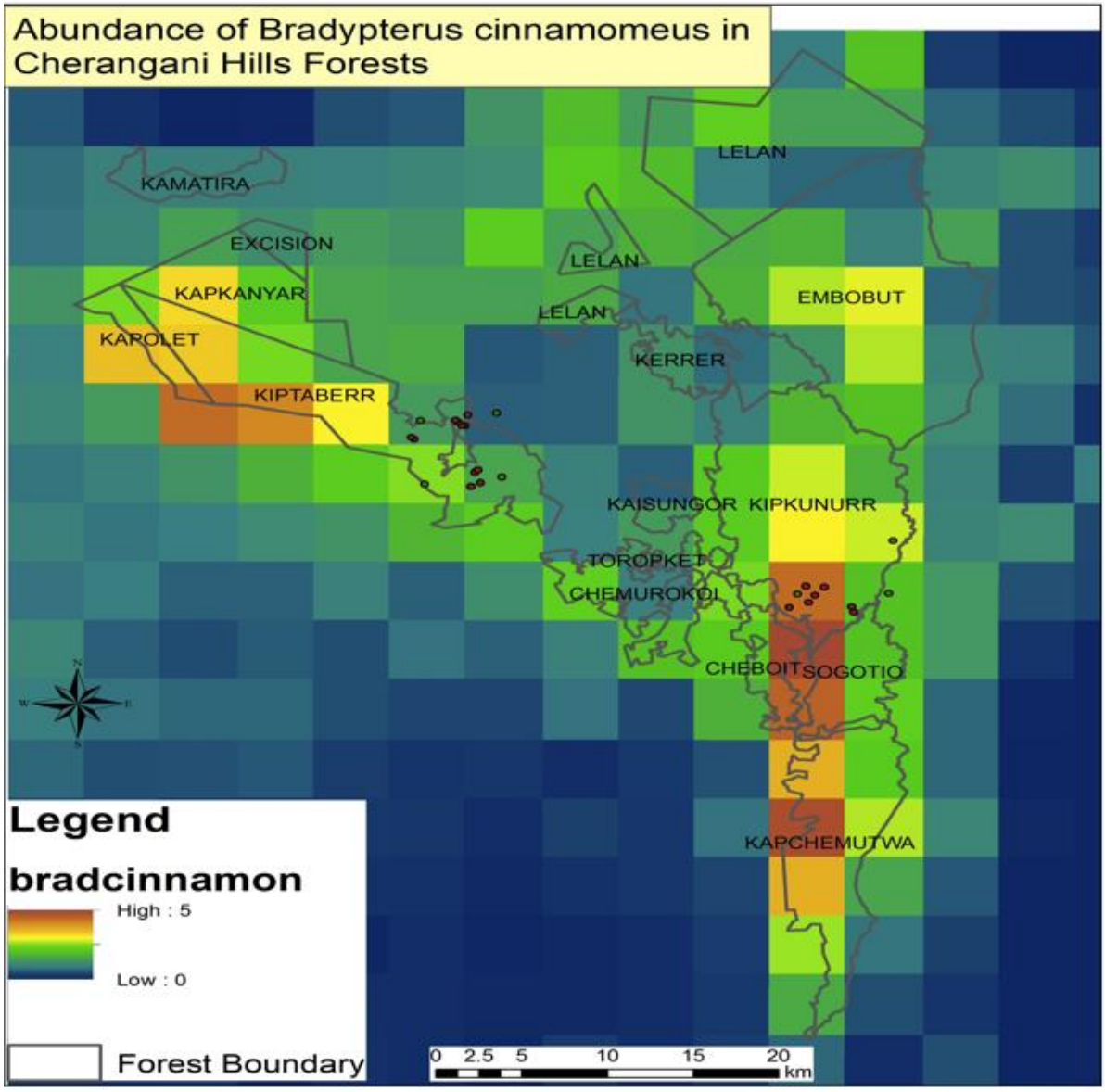

Figure 20. Distribution map for Cinnamon Bracken Warbler Bradypterus cinnamomeus Within Cherangan Ecosystem

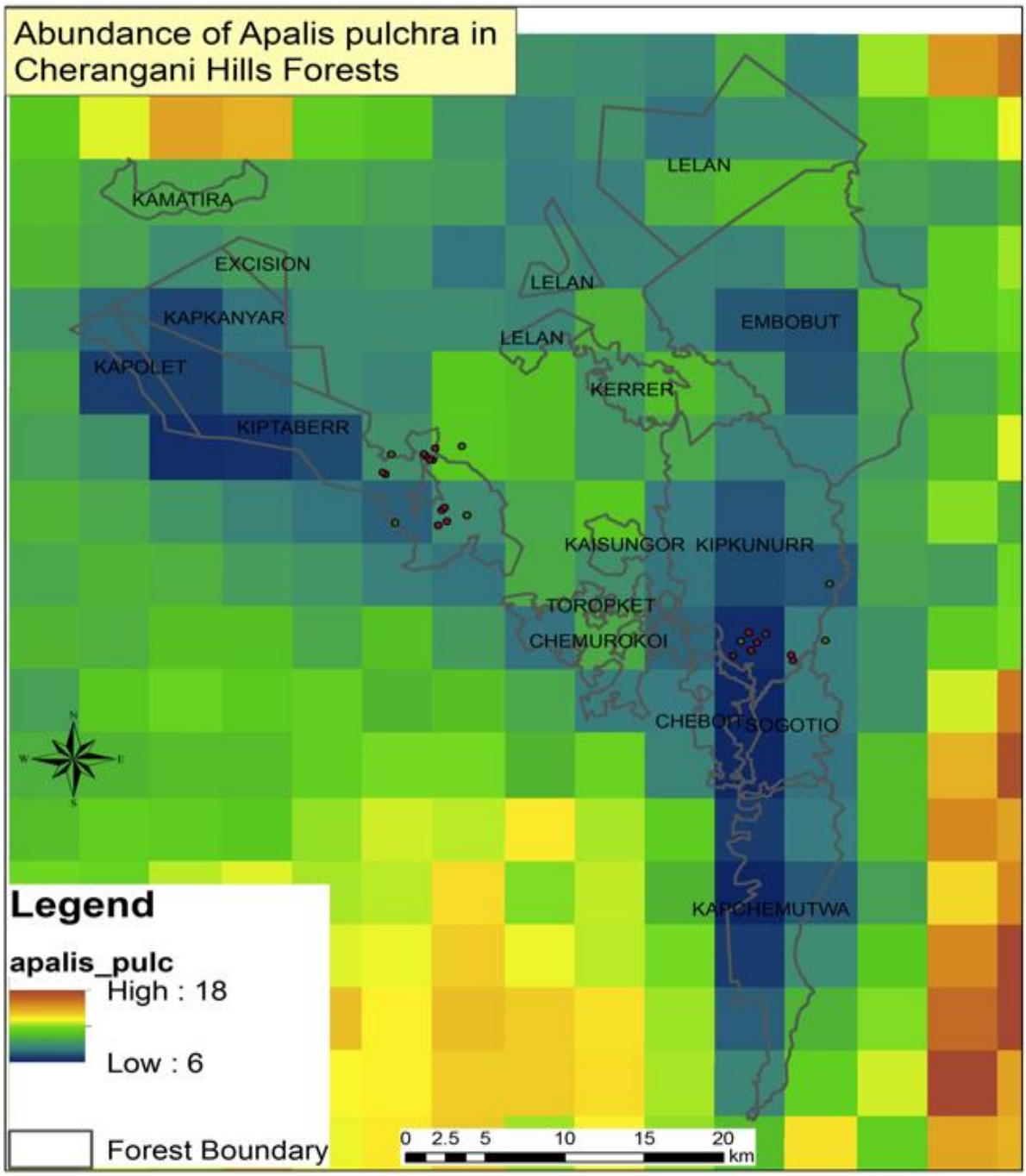

Figure 21. Distribution map for Black-collared Apalis Apalis pulchra Within Cherangan Ecosystem

Montane Oriole (*Oriolus percivali*) and Abyssinian Crimson wing (*Cryptospiza salvadorii*) (Fig. 23 and 24), have a very similar distribution pattern. Both species within Kapsowarr fragments show a high density within our sampling points. However, in the Kapcherop fragments, our sampling point was slightly outside the highest abundance of the model.

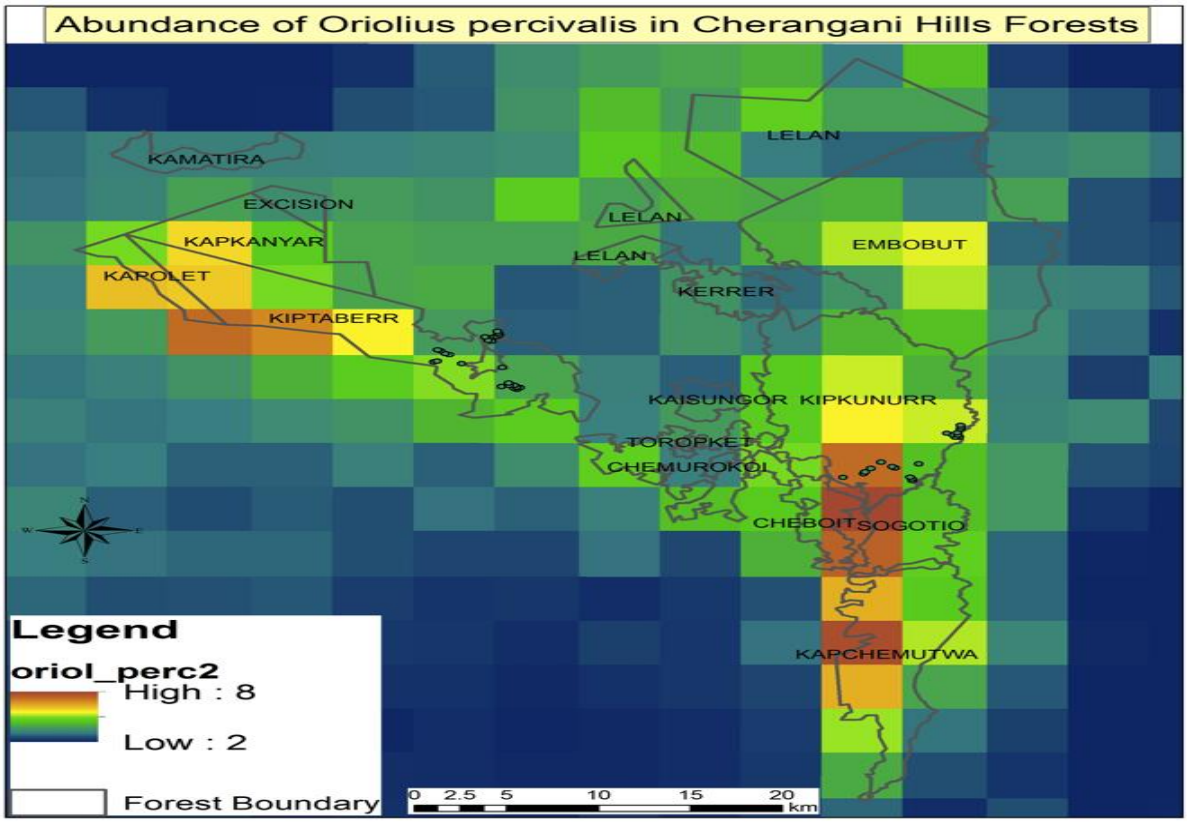

Figure 22. Distribution map for Montane Oriole (Oriolus percivali Within Cherangan Ecosystem

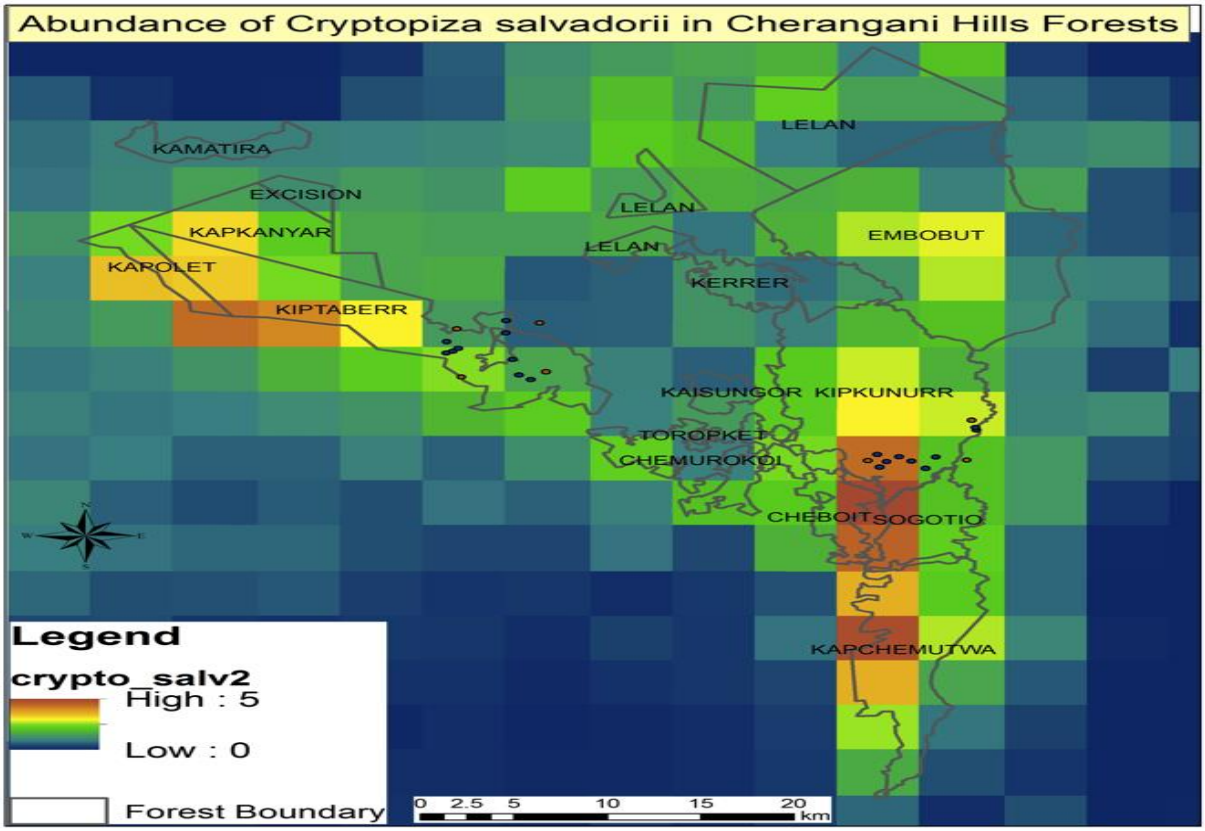

Figure 23. Distribution map for Abyssinian Crimsonwing (Cryptospiza salvadorii) Within Cherangan Ecosystem

Yellow Whiskered Greenbul (*Adropardus latirotris*) and Montane Yellow warbler

(*Chloropeta similis*), are both forest-dependent species (F). But the model (Fig. 25), gave different distribution patterns. Yellow Whiskered Greenbul at Kapsowarr, high density was inside sampling points and transect, although at Kapcherop block, slightly they extended outside the transects. That illustrated that part of the fragment at Kapcherop areas being referred to as outside the forest it was part of the forest, so still, it allows species survival. Montane Yellow warbler distribution patterns were completely outside the sampling site in either block, Kipkunurr or Kapchrop.

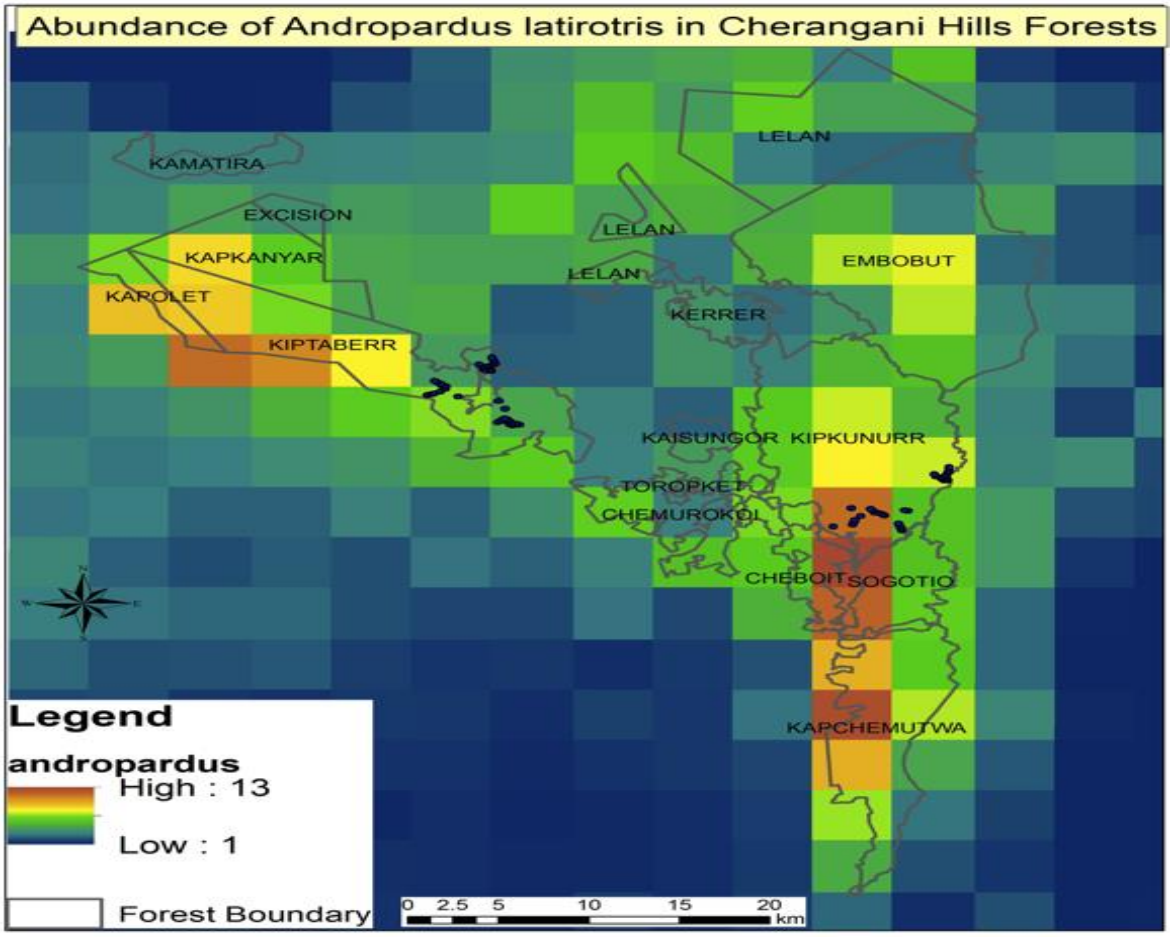

Figure 24. Distribution map for Yellow Whiskered Greenbul Andropardus latirostris Within Cherangan Ecosystem

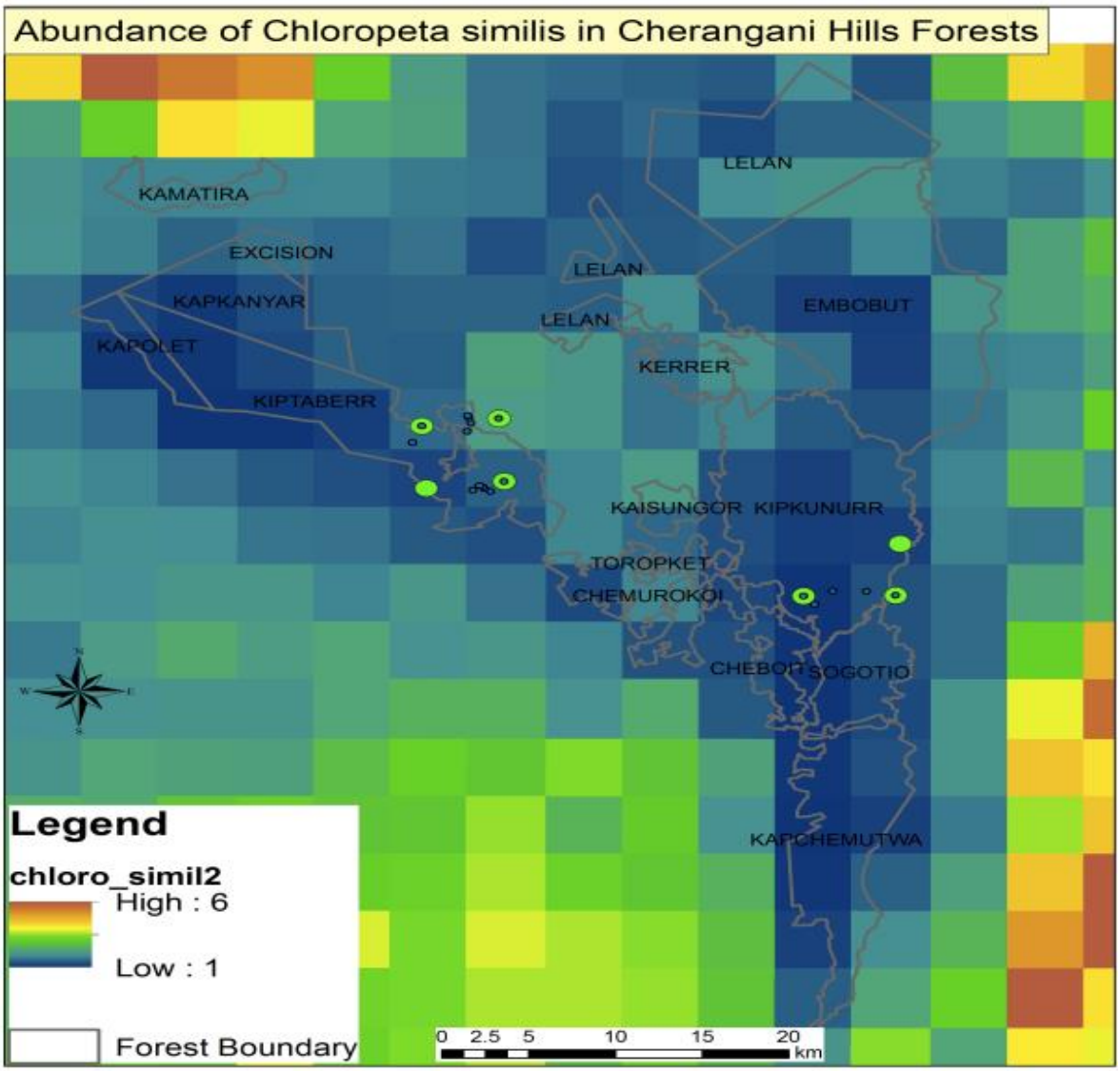

Figure 25. Distribution map for Mountain Yellow Warbler Chloropeta similis Within Cherangan Ecosystem

4.5 IMPACT OF SEASONALITY

DRY SEASON SPECIES LINEAR ACCUMULATION CURVE FOR KAPCHEROP AND KAPSOWARR FRAGMENTS

Seasonality was merged with migration season. The dry season is experienced in January to March, is when the migrants are within the country. Towards the end of the dry season, they go back to Europe. From the data that we collected Cherangani happens to be on their migratory route North. The wet season is from May to August we only have local species. It is from September to April when we have a lot of Palearctic Migrants. In dry and wet season we captured 54 species in ringing, recorded 103 species from point counts and 52 species from opportunistic birding. We matched all record to produce a species survey checklist (Table15 Appendix1). Basing on the point count record, we came up with a species accumulation curve trend for the two seasons. The predictive accumulation curve was created based on 12 transect results of daily point count observations. By use of statistics S(p) =a/b*(1-exp(-b*p), we tried to assess from fragment to another accumulatively recording new species. The curve illustrates that the first point count transect did record a lot of new species. The rest added very few new species hence gentle slope curve can be seen (Fig.26 and 27).

Table 16. Number of species recorded in every method used before creating bird list

METHOD USED	**WET**	**DRY**
	Species	Species
Ringing	39	35
Point count	53	75
Opportunistic birding	46	24

SPECIES ACCUMILATIVE CURVES GENERATED FROM POINT COUNT DATA TO COMPARE TWO BLOCKS SEASONALLY .

The Point count species a cumulative frequency in both graphs, indicates the ecosystem to be avifauna hot spot area, first two days had over 30 species. After, the recording maintains 5-10 new species per day. The interchange of species richness within the blocks also is evidence of the ecosystem being one despite ongoing fragmentation.

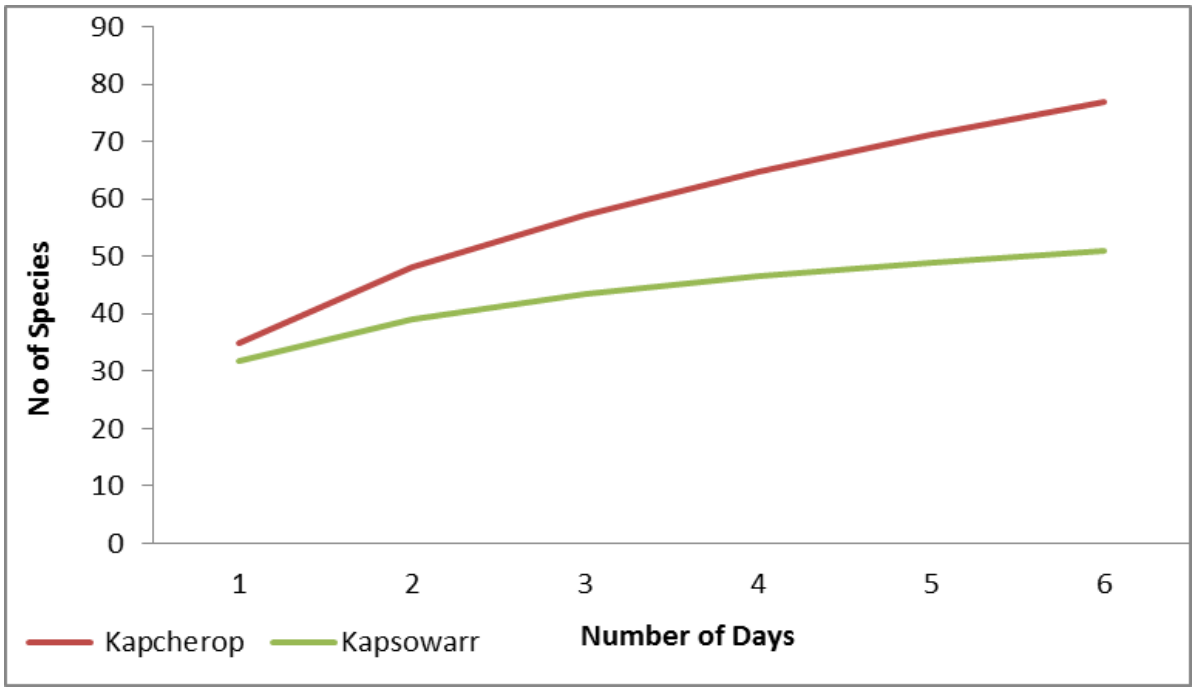

Figure 26. Point count species accumulative curve for Kapcherop and Kapsowarr fragments in the dry season

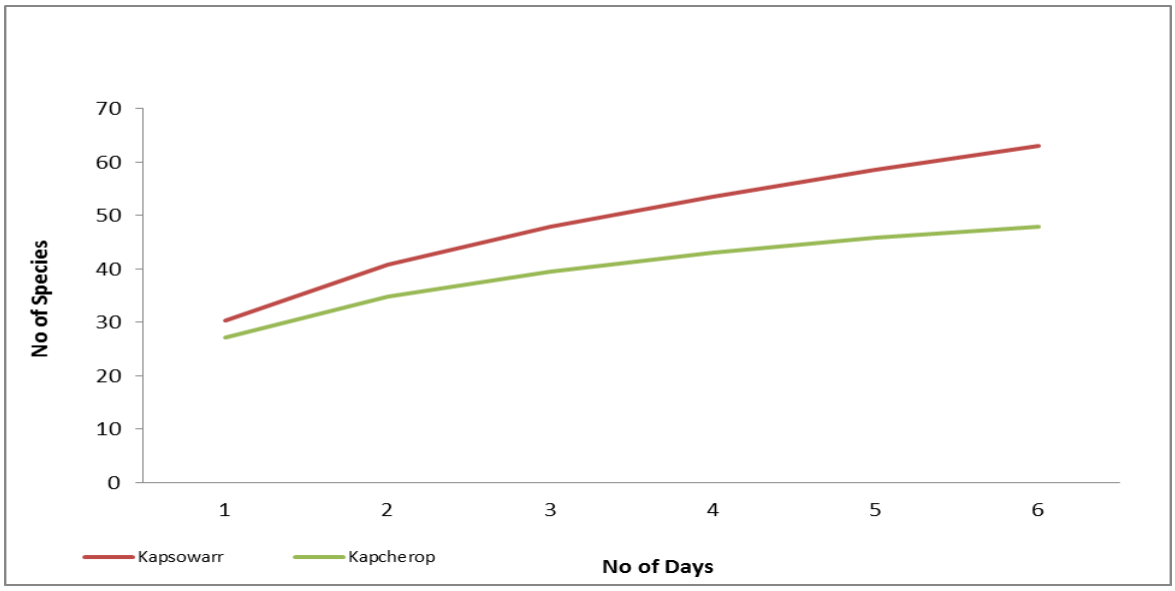

Figure 27. Point count species accumulative curve for Kapcherop and Kapsowarr fragments in wet season.

The two-season had an alternation of species richness (Fig. 26 and 27). In the dry season, Kapcherop block had more species than Kapsowarr block, while wet, Kapsowarr block had more than Kapcherop. That can be attributed to migration, where Kiptaberr hill forest fragment rocks, was used for roosting by migrants. For Wet season Kapsowarr fragments were within one continuous block, that played advantageous for species interaction, over Kapcherop where they were isolated fragments.

PRINCIPAL COMPONENT ANALYSIS (PCA).

The fact that this region is a migratory route, especially Kiptaberr Hills, species assemblage of both block can take such trend of regrouping together. But ecologically, during the wet season, the sites present biological variations due to anthropogenic activities, which can tilt species assemblage, about feeding and breeding behaviours. Hence 23.3% variation in species assemblage on seasonality. For some local species, we have a functional niche within the continuous large block, either for breeding, foraging and roosting that contribute to the assemblage of both block within one side. The binary number of presence or absence of

species was tested to illustrate how they cluster in terms of abundance and occurrence per site. Species clustering at the two sites from the two different blocks proved that there was a similarity between Kipleketet fragments at Kapcherop block and Hossein fragment at Kapsowarr Block.

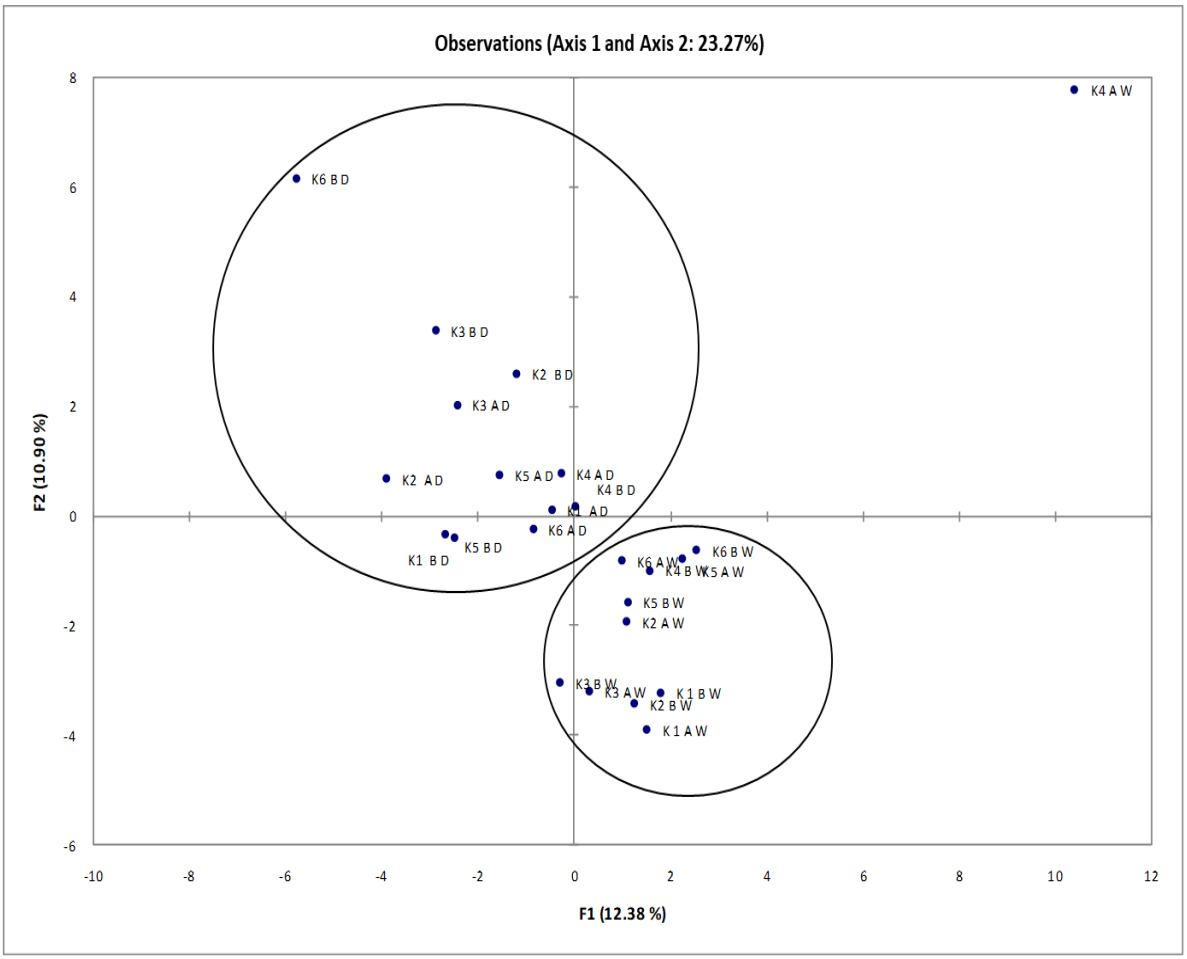

Figure 28. PCA species in respective fragments within Wet and Dry seasons within the six studied fragments Within Cherangan Ecosystem.

The sites were ordered about by species abundance and composition Fig. 29 Axis 1 accounts for 23.3% of the total species variation. The graph shows that there are differences in species assemblages between the dry and wet seasons; species utilize different fragments at different times.

Figure 29. Assemblage of Species according to forest specialization from species list data

KEY:

K1AB D&W; K2AB D&W; K3 AB D&W; K4 AB D&W; K5AB D&W;

K6AB D&W.

F = Forest generalist, top right **FF** = Forest specialist and top right **f** = Forest visitor

The above Fig. 28 shows the biological variations of (species assemblages) that account for the sites shown in Fig. 29. It was noted that in Fig. 29 (upper left quadrant) was a cluster of species representative for the dry season. The (bottom right quadrant) was a cluster of species representative for the wet season. In the three assemblages, the species indicated how some species utilized the forest, in terms of forest categories. The clusters being; (F) Forest

generalist, top right, (FF) forest specialist, bottom right, larger cluster (f) forest visitors, were scattered in the entire graph.

4.6 THREATS

The most consistent threats were grazing, logging, cultivation, firewood collection, and poaching. Others threats existed within fragments studied, but with a relatively minimal impact. Some happened due to the immediate human needs, such as the debarking of Podo due to finding enough beehive cover which was very also intensive (Appendix 3). The cultural practice of sharpening youth (moran) skill, for fighting through shooting the wildlife by bows, arrows and spears, which leads to unselective poaching. Despite it happening once a month, treated like training of community warriors, where community don't treat it like a threat to biodiversity, but it remains cultural practice. A threat like gold mining was long Aror River close to Kipkunurr Hossein, which was seasonal but created gulley along the river bank and heavy silt in the channel flaw.

i) CCA: two groups, impacted differently by environmental threats (38%)

ii) Dry group: T1, T8, T9 and T10

iii) Wet group: T2, T6, T11

Table 17. Type of more common threats Within the surveyed six Fragments.

Threat code	**Type of Threats**
T1	Illegal logging
T2	Firewood collection
T6	Poaching
T8	Selective logging
T9	Fire
T10	Invassive species
T11	Residential development

THE CATACIAN PLANE INDICATING THE LEVEL OF THREATS IN DIFFERENT FRAGMENTS

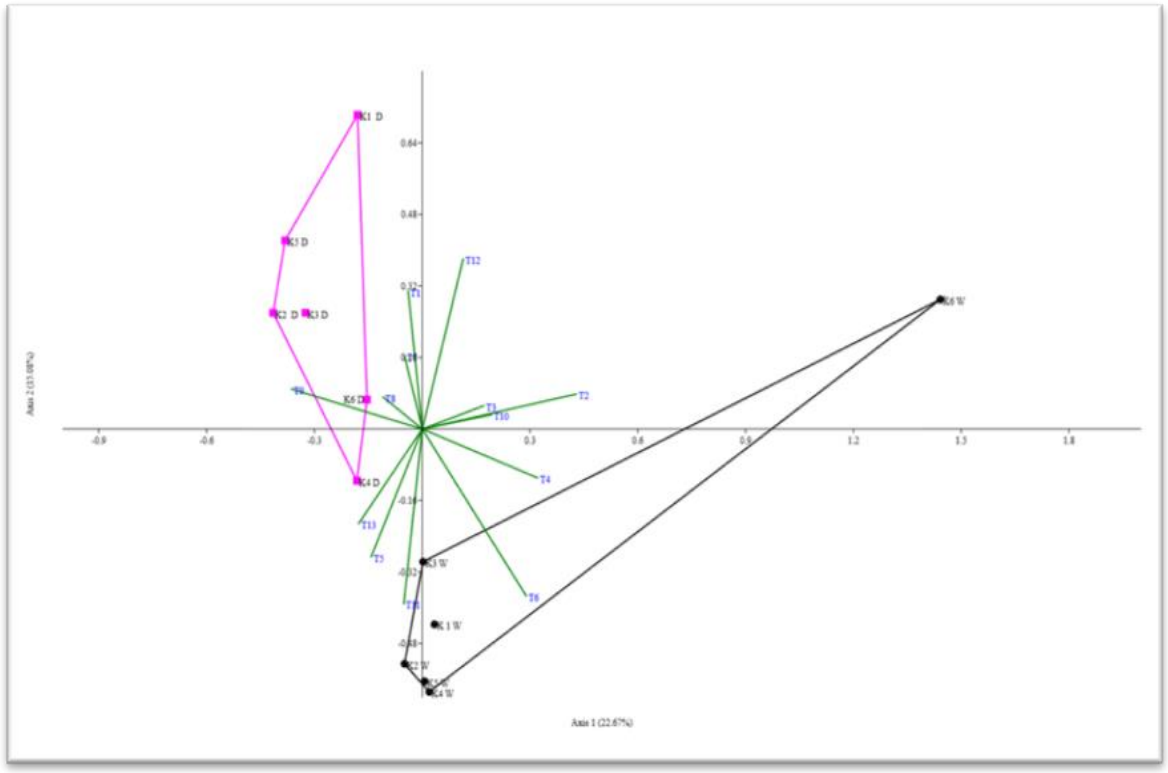

Figure 30. Permutation of species assemblage against threats Within six studied fragments in Cherangan Ecosystem. David Harper

Permutation test illustrated a non-significant relationship between species assemblage, variation and threat levels. Considering PCA results, it revealed that the main structured variation of species assemblages (23%) was associated with climate changes. My argument was that the potential effects of measured threats were not strong enough, to superimpose the anthropogenic pressures to natural ones. In both seasons, the threats were constant as well as species diversity, within the ecosystem.

4.7 VEGETATION SURVEYS

Some species, such as Red Stinkwood *Prunus africanus,* African Pencil Cedar *Juniperus procera*, African Olive *Olea africana*, Flat-crown Albizia *Albizia gummifera*, Water/red berry *Syzygium cordatum*, Forest Dombeya *Dombeya gotzenii*, Croton *Croton megalocarpus*, and Real yellowwood *Podocarpus latifolia* were all mixed scattered in most parts of our study transect, apart from Ndombeya which occupied some specific areas of the forest fragments, forming mono habitat. Towards the peak of the hills, there was some overgrazed bamboo with scattered *Euphobia*.

Overall species facing most threats, from illegal logging are *Podocarpus*, *Afrocrania volkensii*, African Olive *Olea Africana* and African pencil cedar *Juniperus procera* Appendix 3.

On average, upper canopy scored from min 0- Max40 %, mid-canopy Min 20 -Max 60 and under store basing on trees min 0%-max 30% in all fragments. The understorey was open or covered by herbs, shrubs, and woody vegetation. In cases where seedlings were recorded, it was dominated by a common species of seedlings, like *Croton* and *Dombeya*. That was an indication of successful natural regeneration within some section of the fragment. But the diversity of seedling was less than 40%. Due to heavy logging, invasive species were making their way into the forest-changing ecosystem.

CHAPTER FIVE

5.0 DISCUSSION CONCLUSSION AND RECOMENDATION

5.1 Genetic diversity

The study focused on two genera of Greenbul, *Androbadus* (*A. latirostris*, and *A. nigreceps*) and *Phyllostrephus* (*P. cabanis*). To use genetics study as a tool on the two genera to document the effects of forest habitat fragmentation and degradation on habitat restricted species (*Turner, T. L. et, al 2005*). From 124 samples collected in the two genera of five species, only two species, *A. latirostris and P. cabanis*, had enough samples for quantitative analysis in all studied fragments. The Mountain greenbul *A. nigreceps* had a small number of samples that could not generate enough genetic information for the assessment. From the analysis, on two molecular levels heterozygosity and geographical level testing within each fragment and among fragments.

The only difference that was found between the two main studied species (*A. latirostris* and *P. cabanisi*) related to their historical demography (Kakamega, Mt Elgon and Central Kenya population) (*Cibois, A. et al 2001; Frankham, R. 1996; Galbusera, P., et, al 2004; Hanski, I. 1999*). Both species were consistent as one population expansion, but they showed very minimal differences in the distribution of pairwise. In (*A. latirostris*) forest generalists, the demographic curve had a unimodal distribution, supported by high haplotype diversity and a small nucleotide diversity that suggested a recent expansion (Fauvelot, C. et, al 2006). However, the specialists (*P. cabanisi*) showed a bimodal distribution consistent with high levels of haplotype diversity and nucleotide diversity, which suggested a secondary contact between two different lineages. The result, however, was not supported by microsatellite outcomes. Both the two species appeared to be one nuclear population for Cabanis's Greenbul and Yellow Whiskered Greenbul, that has been isolated within the Cherangani ecosystem.

The Bayesian cluster analysis conducted on both species identified that the populations are not genetically different, contrary to my hypothesis that due to forest fragmentation and anthropogenic activities there was the impact of genetic diversity within forest fragment, block and the entire ecosystem. The evidencing was on one major group of greenbul according to the species (K = 1; Fig. 1a and 1b) Fig. 9. This outcome suggested a common origin for all the populations in each species, derived from unique populations that are different with others from, Mt Elgon, Kakamega, Arbardare, and even Coast forest groupTaita Hill forest, Arabuko forest and Shimba hills.

The genetic diversity, was not clear because the fragmentation of Cherangani is relatively recent, and genetic changes develop over time. But through FsT teste and statistical, there are family pools within studied fragment in *A. latirostris* which are related from fragment to fragment.

5.1.1 Biodiversity richness and abundance

Cherangani Hills forest is part of the threatened Eastern Afromontane biodiversity hot spot, and a protected area in Kenya (*Nature Kenya Technical report 2012*). From the study hypothesis, the ecosystem proved to be rich in flora and avifauna, being positioned on a migratory corridor for raptors moving north. Its rich diversity reflected in the ringing, point count and opportunistic birding, in the data collected (Fig.11 and 12) and species checklist (appendix 1). The study also illustrated that, despite bird communities in the ecosystem, the species had a varying response to habitat fragmentation in different landscapes (*James, E.M.W. et, al 2005; Cushman, S. 2006; Ezard, T. H. G. et, al 2006)*

The predictive curve illustrated that, with more time, on a wider scope, same effort, there are new more species to be recorded to obtain horizontal plateau. The 18 days in each surveyed block could still allow the recording of new species. That supported the need to have a more

expansive and intensive Avifauna survey, to explore the ecosystem and document the species fully (Bird list Appendix 1).

Changes in spatial habitat patterns resulted in the isolation of species and populations (*Brown et, al. 2009; Mech, S. G., et al 2001*). It also altered movement between patches (*Mc Donough and Loughry 2005; Porter et, al 1999)*. The study supported the theory that Cherangani Hills forest existed as one continuous ecosystem. Although the shift of species assemblage in dry season-high diversity at Kapcherop block, compared to Kapsowarr block. In the wet season, it was reverse, an indication that there's still the movement of species for functional niches (Fig. 26 and 27). Habitat disturbance in between fragment, the subsequent population within, could be influenced by many factors, number and demographic parameters of survivors (*Brooker, 1998; Sanz and Aquilar, et, al. 2011*), resource availability (*Murphy, 1998; Fahrig, L. 2003*), post-disturbance, succession pathways and species dispersal ability (*Whelan, 1995; Turne, et, al 2011; Fauvelot, et, al 2006*) geographic scale and patchiness, at which the disturbance occurred (*Whelan, R.J. et, al 1995; Banks, S.C. et, al 2011; Watson, 2012)*. High rates of dominance, in some species within fragments (Fig. 17) were, due to state of the habitat, dominancy of specific vegetation (mono micro-habitat) within the fragment and habitat selection, based on individual species. Totting up, the fragmentation of once extensive forests, into smaller isolated patches has hurt many bird species in the forest (*Lynch and Whitcomp, 1978; Robbins, 1979, Whitcomb, et, al. 1981).*

The Shannon Wiener index illustrated that the ecosystem is rich in terms of avifauna. It also illustrated that, between fragments, there were no significant differences in species diversity. It expressed a very minimal range of ($H<1.00$) in all fragments, which was close to 1. That indicated that the entire ecosystem was similar, also indicated by the Chi2 test (Table14 and 15). A comparison of a total number of ringed species and the sum of individuals based on FF, F, f per fragment, found no huge difference in species fragment to fragment (Fig.

13,14,16 and 16), in both ringed and forest categories species. But ecologically being forest category birds, when compared they could indicate the state of the forest. It only illustrated that in the wet season, the variation of both FF and F domination occurred per fragment reflecting the occupation of functional niches and micro-habitats. Out of which FF in Kiptaberr fragment showed the highest, the rest fragment insignificant difference. Kapsowarr block, Kipkunurr West F records the highest number as the rest FF, and F tends to be almost equal even in the dry season.

The species composition within the ecosystem revealed the connection of species assemblage, from one fragment to another dendrogram (Fig 18). Fragmentation as a product of forest over-exploitation is an ongoing process that leads to degradation. The threats stand tall, in the entire ecosystem (Fig. 28, 30 and Appendix 4). Fragmentation being evidence within the ecosystem, but as it increases, species abundance reduces within various fragments (Fig. 12, 13, 14 and 15) which slowly leads to bottle species bottleneck (*Williams, B.L., et al 2003; Young, A., et, al 1996).*

Effects of anthropogenic activities on the habitat is a serious concern, in the fight to preserve biodiversity (*Bates, J.M. et, al 2002; Fauvelot, C. et, al 2006).* The threats manifested in all sites, common being grazing, followed by logging, encroachment, firewood collection, and poaching. The conditions made it clear that there were limited ecological interactions between species. Hence, the negative impacts of sampling based on seasonality. The wet and dry season had minimal effects on the results (Fig. 26, 27, and 28). But at the same time, one could argue that seasonality could be merged with migration season, whereby, dry season (January - March), is when the migrants were within the country, and towards the end of the dry season they tend to go back to the breeding region, northern hemisphere. In wet season May to August, only the local species were recorded. Throughout the study, there was evidence of other taxes, which need also intensive and wider survey.

5.1.2 Avifauna spatial distribution

The Arc-GIS (NDVI) model illustrated that the entire ecosystem of Cherangani hill forest was one, despite current forest habitat fragmentation. However, our sampling site selection majorly focused on habitat state based on, underground growth cover, mid and upper canopy cover. The NDVI selection displaced some sampling points outside our predicted hot spot areas. That justified the fact that there's a need to exhaustively survey within Cherangani forest, based on the scope with equal effort to identify hot spot areas correctly. Alternatively, the model use, lower plant, herbs, shrubs and grass, that indicated cover from satellite imageries. That gave a reason for benefit of doubt if the model is correct about the dominance of species. If the species are not understory, then the hot spot areas placed them outside where we sampled, makes site correct.

For example, ecologically dominant species were both forest visitor and generalists, which uses the forest, but much of the time stay outside of closed-canopy or thicket forest. So that poses questions about habitat structure within the Kipsowarr as well compared to Kapcherop, blocks fragments. It is not known what other ecological factors play, in species distribution apart from NDVI.

The Montane Oriole is a forest specialist while Abyssinian Crimsonwing a forest-dependent species; both species in one way or another occupy mid or upper canopy cover forest habitat, which was expected to be reflected in NDVI (Fig. 22 and 23). The two species being (F), the distribution pattern was expected to be similar. The differences expressed that, other ecological factors played a role in the pattern, so the NDVI selection considered species habitat selection, as per the coordinates, which proved species distribution within microhabitat.

5.1.3 Habitat and biodiversity threats and impact on biodiversity:

On abundance, mist-netting data indicated significant differences, but a minimal variation on species diversity from fragment to another (Fig.4), which could be attributed to niche functionality and ecological state of the habitat.

The Principal Component Analysis (PCA) indicated up to 23% of species variation, from one fragment to another (Fig. 29-31). However, the seasonality aspect becomes clear, as it is common in animals, for weather patterns change triggers changes in physiological body function of birds, and other taxa at large. Hence change in character and behaviour, like in birds, it triggers breeding in most species of birds. That has direct implications for species caught in the wet and dry seasons.

On threats, important sites like Kapsowar block requires immediate attention. Kipkunurr forms part of the only remaining breeding site for Lammergeier (*Gypaetus barbatus*) in Kenya and fragmentation is a direct threat to the conservation of the species, as raptor specialist Thomsett, S. (unpublished) point out. Although we did not record the species, and the last record dates 2009. The local community reported that they believe the species still have an irregular visit in parts of the region.

Species distribution through ARC GIS was within the sampling points, others outside of sampling transect, but still within the same fragments. About the functionality of the model, satellite images were connected to specific vegetation, which reflected the utilization of species within certain habitat structure. Basing on the forest ecosystem, NDVI gave an impression that microhabitats were forming over time, it might lead to a change of habitat structure, leading to glades, woodland, and shrubland within Cherangani forest ecosystem (Fig 21-25).

The PCA indicated that threats and their level of intensity did not affect species diversity or distribution, which could be supported by species cumulative and bar graphs (Fig. 11-17). The current human population growth rate gives a very loud alarm to the sustainable utilization of this forest resources, to the local human community, as well as biodiversity. The level of destruction in Cherangan has taken the Mau Narok ecosystem trend. But this study could not verify this statistically, due to the area covered and time taken apart from images of heavy forest destruction (Appendix 4). If nothing is going to be done to save Cherangani Hills forest, the normal trend of evicting community from forest land and claim of the ownership may start.

5.2 CONCLUSION AND RECOMMENDATIONS

5.2.1 Conclusion;

Although forest fragmentation is less than two decades old, the impact of anthropogenic activities on wildlife was significant, for the type of threats remained constant within the ecosystem. The two genera of greenbuls (*Androbadus and Phyllostrephus) did* not express any genetic diversity or variation within fragment and among blocks. The metapopulation remains one unique pool. But it is well known that the birds (greenbul) do not fly long distances in discontinued habitat, so that means it is recent an ongoing fragmentation.

The Cherangani forests have rich biodiversity, with species similarity/connection, in the entire ecosystem and within fragments. But threatened flora and avifauna has not been fully explored, and their conservation status not documented fully by conservationists. Anthropogenic activities, population pressures, land-use change and economic development, are rapidly changing, the natural habitat, placing unknown biodiversity at risk of disappearance and changing the dominance of species.

There is a need to come up with mitigation measures to the constant threats within the region, to improve the forest status. From observation on avifauna, cluster community was seen in the PCA analysis, which means over time, the impact of fragmentation will be evident on wildlife behaviour, diversity, abundance and distribution within the ecosystem. It is well known that habitat loss, fragmentation or isolation is lethal and leads to species bottleneck, hence extinction. It is high time conservation communities addressed the situation before the habitat deteriorates to a level where species are consigned to vagaries of extinction or extirpation.

5.3 Recommendations

5.3.1. Impact of the survey

There is a need for more and intensive long term surveys to arrive at a better understanding of the existing flora and fauna. To set base information on conservation status, the impact of anthropogenic activities, climate change, and other natural events in the entire Cherangani Hills forest ecosystem that will improve its conservation status. Other forest fragments were pure farming field to date. Those forest fragment with indigenous hardwood trees were experiencing heavy logging. The encroachment and grazing were being practised in all fragments. From all anthropogenic activities experienced during the study, it becomes a challenge to equate this survey study as a sample study to represent the entire ecosystem. For this reason, I recommend a survey-based on an entire ecosystem-on a wider scope and a long spell, in almost every type of habitat.

5.3.2. Education and training

Environmental education and awareness should be emphasized within this region with an approach of incorporating indigenous knowledge. The environmental education and awareness program should cut across, age, gender, and economic status, institutions, and religion. It should also try to harmonize the direct benefit of the resources with population growth, with link to sustainable utilization approach of the resource considering the present state of the forest and level of degradation. That can be achieved through an emphasis on monitoring activities with intensive training to site support groups-forest scouts, community-based groups, youth environmental groups, and forest working associations – from all corners of the ecosystem.

5.3.3 Administrative law implementation

Through partnerships between conservation organizations and government, the number of recruits to Kenya Forest Service (KFS) rangers and scouts should be increased. The region should also promote the formation of more environmental interest groups. The groups' rangers and scouts should participate in joint conservation training about conservation matters and the ecosystem services of the forest. Define the roles of every group and have guidelines on how they can work in harmony without conflict of interest to implement the policy law and rules of protecting and conserving the forest.

5.3.4 Political interest

Through advocacy, those policy laws or rules that allow the politician to issue natural resource land to community members to win their political interest "votes" it is the time such rule should be considered to be changed or focus on how such law can impress conservation to save the resources that are under depletion in the interest of few individuals.

5.3.5 Address community benefit

Engage community members in eco-tourism activities like training local tour guides on the biodiversity within the ecosystem and encouraging them to take the lead in tour guiding.

Through conservation organisations on the ground try to arrange an exchange program for local groups, as an incentive to interested monitoring groups and site support groups (SSG). Try to create revenue-generating activities for the community and environmental groups like community campsites and pandas where they can generate their revenue to improve their livelihood.

5.3.6 Land management policy

Land management plans and farming methods should be drafted for the community around the forest. The land management plan should mitigate the community's interest in farming activities, cash crops, and promote the best domestic approach. Recommended farming methods should aim to maximise production through alternatives to destructive farming activities.

5.3.7 Social economic project.

A lot of microfinance and environment associated organization should be impressed upon on the ground. To give financial support to those groups who want to engage themselves in small businesses as a source of income, instead of the entire community focusing on the forest as a source of livelihood. Other conservation-friendly activities such as bee farming should be fully supported, from providing the correct beehives and harvesting gear, to helping to bring the honey to market after harvesting. Bee-farming groups, community-based organizations (CBOs), and associations could be formed to help improve the marketing and branding of their honey for local, regional, and international markets.

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Appendices

Appendix 1: Birds list

The bird list has been arranged according to checklist of the Birds of Kenya 4th Ed, EANHS 2009.

Location is within Kiptaberr near Kapcherop and Kipkunurr near Kapsowar forest fragment;

MIGRANTS CATEGORY; (AM = Afro tropic migrant, **PM =** Palaearctic migrant, **am, pm=**occurs alongside resident birds**)**
I.U. C.N ATEGORY (NT= nearly threatened**, V=**Vulnerable = Endangered**);**
FOREST ATEGORY; FF= Forest Specialist **F =** Forest generalist, **f =** forest visitors**;**
BIOME SPECIES; Afromontane highland biome species =**AHB; (**Bennun, L. A et, al. 1999; Bennun, L., et, al 1996**;** Bird Committee of Nature Kenya, 2009; **).**

	FAMILIES						
COMMON NAME	**SCIENTIFC NAME**	**Family**	**PM/ AM/ am/ pm**	**I.U .C. N**	**FO RES T**	**HIG HLA ND SP**	**FEEDI NG GUILD**
Crested Guineafowl	*Guttera pucherani*	**Numididae**					Ground mixed
Scaly Francolin	*Francolinus squamatus*	**Phasianida e**			F		Ground mixed
White Stork	*Ciconia ciconia*	**Ciconiidae**					Carnivor ous
Woolly-necked Stork	*Ciconia episcopus*	**Ciconiidae**		V			Carnivor ous
Hadada Ibis	*Bostrychia hagedash*	**Threskior nithidae**					Carnivor ous
Lanner Falcon	*Falco biarmicus*	**Falconidae**					Carnivor ous
Lesser Kestrel	*Falco naumanni*	**Falconidae**					Carnivor ous
Peregrine Falcon	*Falco peregrinus*	**Falconidae**					Carnivor ous
African Hobby	*Falco cuvieri*	**Falconidae**			F		Carnivor ous
Crowned Eagle	*Stephanoaetu s coronatus*	**Accipitrid ae**	am pm.		FF		Carnivor ous
Black Kite	*Milvus migrans*	**Accipitrid ae**					Carnivor ous
African Goshawk	*Accipiter tachiro*	**Accipitrid ae**					Carnivor ous
African Harrier Hawk	*Polyboroides typus*	**Accipitrid ae**			f		Carnivor ous

Augur Buzzard	*Buteo augur*	**Accipitridae**					Carnivorous
Great Sparrowhawk	*Accipiter melanoleucus*	**Accipitridae**			F		Carnivorous
Hooded Vulture	*Necrosyrtes monachus*	**Accipitridae**		CR	f		Scavenger
Little Sparrowhawk	*Accipiter minullus*	**Accipitridae**	PM		FF		Carnivorous
Long-crested Eagle	*Lophaetus occipitalis*	**Accipitridae**	PM		f		Carnivorous
Mountain Buzzard	*Buteo oreophilus*	**Accipitridae**			FF	AHB	Carnivorous
Common Buzzard	*Buteo buteo*	**Accipitridae**					Carnivorous
Steppe Eagle	*Aquila nepalensis*	**Accipitridae**	PM;	V			Carnivorous
Ayres's Hawk Eagle	*Aquila ayresii*	**Accipitridae**	pm				Carnivorous
Grey Crowned Crane	*Balearica regulorum*	**Gruidae**		E			Omnivores
Hamerkop	*Scopus umbretta*	**Scopidae**					omnivores,
Tambourine Dove	*Turtur tympanistria*	**Columbidae**			F		Granivorous
African Green Pigeon	*Treron calvus*	**Columbidae**			F		Frugivore
Blue-spotted Wood Dove	*Turtur afer*	**Columbidae**					Granivorous
Eastern Bronze-naped Pigeon	*Columba delegorguei*	**Columbidae**			FF		Grunivore
Dusky Turtle Dove	*Streptopelia lugens*	**Columbidae**			f		Granivorous
Lemon Dove	*Aplopelia larvata*	**Columbidae**			FF		Granivorous
African Olive Pigeon	*Columba arquatrix*	**Columbidae**			FF		Frugivore
Red-eyed Dove	*Streptopelia semitorquata*	**Columbidae**			f		Granivorous
Ring-necked Dove	*Streptopelia capicola*	**Columbidae**			f		Granivorous
Speckled Pigeon	*Columba guinea*	**Columbidae**	PM,				Frugivore
Red-fronted Parrot	*Poicephalus gulielmi*	**Psittacidae**	PM		FF		Granivorous/frugivores
Hartlaub's Turaco	*Tauraco hartlaubi*	**Musophagidae**			FF	AHB	Frugivores
Common Cuckoo	*Cuculus*	**Cuculidae**	am				Insectiv

	canorus						ores
Klaas's Cuckoo	*Chrysococcyx klaas*	**Cuculidae**			f		Insectivores
Red-chested Cuckoo	*Cuculus solitarius*	**Cuculidae**			F		Insectivores
African Emerald Cuckoo	*Chrysococcyx cupreus*	**Cuculidae**			F		Insectivores
African Wood Owl	*Strix woodfordii*	**Strigidae**					Insectivores
Verreaux's Eagle Owl	*Bubo lacteus*	**Strigidae**					Insectivores
Mountain Illadopsis	*Illadopsis pyrrhoptera*	**Timaliidae**			FF	AHB	Cleaner
African Hill Babbler	*Pseudoalcippe abyssinica*	**Timaliidae**			FF	AHB	Cleaner
Montane Nightjar	*Caprimulgus poliocephalus*	**Caprimulgidae**	am, mm		F	AHB	Insectivores
White-rumped Swift	*Apus caffer*	**Apodidae**					Flycatcher
Little Swift	*Apus affinis*	**Apodidae**					Flycatcher
Alpine Swift	*Tachymarptis melba*	**Apodidae**					Flycatcher
Mottled Swift	*Tachymarptis aequatorialis*	**Apodidae**					Flycatcher
Sabine's Spinetail	*Rhaphidura sabini*	**Apodidae**			FF		Frugivores
Speckled Mousebird	*Colius striatus*	**Coliidae**					Fruigivores
Narina Trogon	*Apaloderma narina*	**Trogonidae**			F		Fruigivores
Broad-billed Roller	*Eurystomus glaucurus*	**Coraciidae**					Flycatcher
Woodland Kingfisher	*Halcyon senegalensis*	**Alcedinidae**					Flycatcher
Cinnamon-chested Bee-eater	*Merops oreobates*	**Meropidae**			F	AHB	Flycatcher
Eurasian Bee-eater	*Merops apiaster*	**Meropidae**	PM		f		Flycatcher
Little Bee-eater	*Merops pusillus*	**Meropidae**					Flycatcher
White-headed Wood-hoopoe	*Pheoniculus bollei*	**Phoeniculidae**			FF		Mixed
Black-and-white Casqued Hornbill	*Bycanistes subcylindricus*	**Bucerotidae**					Mixed
Crowned Hornbill	*Tockus*	**Bucerotida**			f		Mixed

	alboterminatus	**e**					
Yellow-billed Barbet	*Trachylaemus purpuratus*	**Capitonidae**			F		Frugivores
Yellow-rumped Tinkerbird	*Pogoniulus bilineatus*	**Capitonidae**			F		Mixed
Grey-throated Barbet	*Gymnobucco bonapartei*	**Capitonidae**			F		Frugivores
Moustached Tinkerbird	*Pogoniulus leucomystax*	**Capitonidae**			FF	AHB	Mixed
Double-toothed Barbet	*Lybius bidentatus*	**Capitonidae**			f		Mixed
Least Honeyguide	*Indicator exilis*	**Indicatoridae**			FF		Insectivore
Lesser Honeyguide	*Indicator minor*	**Indicatoridae**			f		Insectivore
Scaly-throated Honeyguide	*Indicator variegatus*	**Indicatoridae**			f		Insectivores
African Grey Woodpecker	*Dendropicos goertae*	**Picidae**			f		Cleaner
Bearded Woodpecker	*Dendropicos namaquus*	**Picidae**			f		Cleaner
Cardinal Woodpecker	*Dendropicos fuscescens*	**Picidae**			f		Cleaner
Fine-banded Woodpecker	*Campethera tullbergi*	**Picidae**			FF	AHB	Cleaner
Red-throated Wryneck	*Jynx ruficollis*	**Picidae**			f		Cleaner
Black-throated Wattle-eye	*Platysteira peltata*	**Platysteiridae**			F		Cleaner
Chin-spot Batis	*Batis molitor*	**Platysteiridae**					Cleaner
Black-fronted Bushshrike	*Chlorophoneus nigrifrons*	**Malaconotidae**			FF		Cleaner
Brown-crowned Tchagra	*Tchagra australis*	**Malaconotidae**					Cleaner
Doherty's Bushshrike	*Chlorophoneus dohertyi*	**Malaconotidae**				AHB	Cleaner
Lühder's Bushshrike	*Laniarius luehderi*	**Malaconotidae**			F		Cleaner
Northern Puffback	*Dryoscopus gambensis*	**Malaconotidae**			F		Cleaner
Sulphur-breasted Bushshrike	*Chlorophoneus sulfureopectus*	**Malaconotidae**			f		Cleaner
Tropical Boubou	*Laniarius aethopicus*	**Malaconotidae**			f		Cleaner
Grey Cuckooshrike	*Coracina*	**Campepha**			FF	AHB	Cleaner

	caesia	**gidae**					
Petit's Cuckooshrike	*Campephaga petiti*	**Campephagidae**			FF		Cleaner
Purple-throated Cuckooshrike	*Campephaga quiscalina*	**Campephagidae**			FF		Cleaner
Common Fiscal	*Lanius collaris*	**Laniidae**					Flycatcher
Montane Oriole	*Oriolus percivali*	**Oriolidae**			FF	AHB	Mixed
White-tailed Crested Flycatcher	*Eliminia albonotata*	**Monarchidae**			FF	AHB	Flycatcher
African Paradise Flycatcher	*Terpsiphone viridis*	**Monarchidae**			f		Flycatcher
African Blue Flycatcher	*Elminia longicauda*	**Monarchidae**			f		Flycatcher
Fan-tailed Raven	*Corvus rhipidurus*	**Corvidae**	am				Carnivorous
Pied Crow	*Corvus albus*	**Corvidae**					Carnivorous
White-bellied Tit	*Parus albiventris*	**Paridae**			f		Flycatcher
Black Saw-wing	*Psalidoprocne pristoptera*	**Hirundinidae**			f		Flycatcher
Mosque Swallow	*Cecropis senegalensis*	**Hirundinidae**					Flycacher
Red-rumped Swallow	*Cecropis daurica*	**Hirundinidae**					Flycatcher
Rock Martin	*Ptyonoprogne fuligula*	**Hirundinidae**					Flycatcher
Wire-tailed Swallow	*Hirundo smithii*	**Hirundinidae**					Flycatcher
White-headed Saw-wing	*Psalidoprocne albiceps*	**Hirundinidae**			f		Flycatcher
Angola Swallow	*Hirundo angolensis*	**Hirundinidae**					Flycatcher
Black-collared Apalis	*Apalis pulchra*	**Cisticolidae**			F	AHB	Cleaner
Grey Apalis	*Apalis cinerea*	**Cisticolidae**			FF		Cleaner
Chestnut-throated Apalis	*Apalis porphyrolaema*	**Cisticolidae**			F	AHB	Cleaner
Grey-backed Camaroptera	*Camaroptera brachyura*	**Cisticolidae**					Cleaner
Tawny-flanked Prinia	*Prinia subflava*	**Cisticolidae**			f		Cleaner
Grey-capped Warbler	*Eminia lepida*	**Cisticolidae**			f		Cleaner
Chubb's Cisticola	*Cisticola*	**Cisticolida**			F	AHB	Cleaner

	chubbi	**e**					
Yellow Whiskered Greenbul	*Andropadus latirostris*	**Pycnonotidae**					Mixed
Cabanis's Greenbul	*Phyllastrephus cabanisi*	**Pycnonotidae**			FF		Mixed
Common Bulbul	*Pycnonotus barbatus*	**Pycnonotidae**			f		Mixed
Mountain Greenbul	*Andropadus nigriceps*	**Pycnonotidae**			FF	AHB	Mixed
Slender-billed Greenbul	*Andropadus gracilirostris*	**Pycnonotidae**			FF		Mixed
Cinnamon Bracken Warbler	*Bradypterus cinnamomeus*	**Sylviidae**			F	AHB	Cleaner
Brown Woodland Warbler	*Phylloscopus umbrovirens*	**Sylviidae**	PM		F	AHB	Cleaner
Mountain Yellow Warbler	*Chloropeta similis*	**Sylviidae**			F	AHB	Cleaner
Evergreen Forest Warbler	*Bradypterus lopezi*	**Sylviidae**	PM		FF		Cleaner
Blackcap	*Sylvia atricapilla*	**Sylviidae**			F		Cleaner
Dark-capped Yellow Warbler	*Chloropeta natalensis*	**Sylviidae**					Cleaner
Willow Warbler	*Phylloscopus trochilus*	**Sylviidae**	am		f		Cleaner
Yellow-bellied Eremomela	*Eremomela icteropygialis*	**Sylviidae**					Cleaner
White-browed Crombec	*Sylvietta leucophrys*	**Sylviidae**			FF	AHB	Cleaner
African Reed Warbler	*Acrocephalus baeticatus*	**Sylviidae**					Cleaner
Brown Parisoma	*Parisoma lugens*	**Sylviidae**				AHB	Cleaner
Mountain Illadopsis	*Illadopsis pyrrhoptera*	**Timaliidae**			FF	AHB	Cleaner
African Hill Babbler	*Pseudoalcippe abyssinica*	**Timaliidae**			FF	AHB	Cleaner
African Yellow White-eye	*Zosterops senegalensis*	**Zosteropidae**			f		Cleaner
Greater Blue-eared Starling	*Lamprotornis chalybaeus*	**Sturnidae**	AM				Cleaner
Red-winged Starling	*Onychognathus morio*	**Sturnidae**			f		Cleaner
Sharpe's Starling	*Pholia sharpii*	**Sturnidae**			FF	AHB	Cleaner
Violet-backed Starling	*Cynniricinclus*	**Sturnidae**			f		Cleaner

	leucogaster						
Stuhlmann's Starling	*Poeoptera stuhlmanni*	**Sturnidae**			FF	AHB	Cleaner
Lesser Blue-eared Starling	*Lamprotornis chloropterus*	**Sturnidae**					Cleaner
Waller's Starling	*Onychognathus walleri*	**Sturnidae**		V	FF	AHB	Cleaner
Olive Thrush	*Turdus olivaceus*	**Turdidae**			F		Ground
African Thrush	*Turdus pelios*	**Turdidae**			f		Ground
White-starred Robin	*Pogonocichla stellata*	**Muscicapidae**				AHB	Ground
African Dusky Flycatcher	*Muscicapa adusta*	**Muscicapidae**			F		Flycatcher
White-eyed Slaty Flycatcher	*Melaenornis fischeri*	**Muscicapidae**			F	AHB	Flycatcher
Northern Black Flycatcher	*Melaenornis edolioides*	**Muscicapidae**					Flycatcher
Cape Robin Chat	*Cossypha caffra*	**Muscicapidae**			f		Ground
Common Stonechat	*Saxicola torquatus*	**Muscicapidae**					Ground
Northern Anteater Chat	*Myrmecocichla aethiops*	***Muscicapidae***			f		Ground
White-browed Robin Chat	*Cossypha heuglini*	**Muscicapidae**					Ground
African Grey Flycatcher	*Bradornis microrhynchus*	**Muscicapidae**					Flycatcher
Northern Double-collared Sunbird	*Cinnyris reichenowi*	**Nectariniidae**					Cleaner
Green-headed Sunbird	*Cyanomitra verticalis*	**Nectariniidae**			F		Cleaner
Olive Sunbird	*Cyanomitra olivacea*	**Nectariniidae**			FF		Cleaner
Bronze Sunbird	*Nectarinia kilimensis*	**Nectariniidae**			f	AHB	Cleaner
Collared Sunbird	*Hedydipna collaris*	**Nectariniidae**			F		Cleaner
Eastern Double-collared Sunbird	*Cinnyris mediocris*	**Nectariniidae**			F	AHB	Cleaner
Marico Sunbird	*Cinnyris mariquensis*	**Nectariniidae**					Cleaner
Northern Double-collared Sunbird	*Cinnyris reichenowi*	**Nectariniidae**			F	AHB	Cleaner
Orange-tufted Sunbird	*Cinnyris bouvieri*	**Nectariniidae**			F		Cleaner
Tacazze Sunbird	*Nectarinia*	**Nectariniidae**			f	AHB	Cleaner

	tacazze	**dae**					
Variable Sunbird	*Cinnyris venustus*	**Nectariniidae**			f		Cleaner
Western Violet-backed Sunbird	*Anthreptes longuemarei*	**Nectariniidae**			f		Cleaner
Grey-headed Sparrow	*Passer griseus*	**Passeridae**					Cleaner
House Sparrow	*Passer domesticus*	**Passeridae**					Cleaner
Kenya Rufous Sparrow	*Passer rufocinctus*	**Passeridae**					Cleaner
Black-billed Weaver	*Ploceus melanogaster*	**Ploceidae**			FF	AHB	Mixed
Baglafecht Weaver	*Ploceus baglafecht*	**Ploceidae**			f	AHB	Mixed
Brown-capped Weaver	*Ploceus insignis*	**Ploceidae**			FF	AHB	Mixed
Grosbeak Weaver	*Amblyospiza albifrons*	**Ploceidae**			f		Mixed
Holub's Golden Weaver	*Ploceus xanthops*	**Ploceidae**					Mixed
Yellow Bishop	*Euplectes capensis*	**Ploceidae**					Mixed
Black-crowned Waxbill	*Estrilda nonnula*	**Estrildidae**			f		Mixed
Black-and-white Mannikin.	*Spermestes bicolor*	**Estrildidae**			f		Mixed
Abyssinian Crimsonwing	*Cryptospiza salvadorii*	**Estrildidae**			F	AHB	Mixed
Common Waxbill	*Estrilda astrild*	**Estrildidae**					Mixed
Grey-headed Negrofinch	*Nigrita canicapillus*	**Estrildidae**			F		Mixed
Red-cheeked Cordon-bleu	*Uraeginthus bengalus*	**Estrildidae**					Mixed
Red-headed Bluebill	*Spermophaga ruficapilla*	**Estrildidae**			F		Cleaner
Yellow-bellied Waxbill	*Coccopygia quartinia*	**Estrildidae**			f		Mixed
African Firefinch	*Lagonosticta rubricata*	**Estrildidae**					Mixed
Pin-tailed Whydah	*Vidua macroura*	**Viduidae**					Flycatcher
African Pied Wagtail	*Motacilla aguimp*	**Motacillidae**	PM				Mixed
Grassland Pipit	*Anthus cinnamomeus*	**Motacillidae**					Seedeater
Mountain Wagtail	*Motacilla*	**Motacillid**			F		Mixed

	clara	**ae**					
Tree Pipit	*Anthus trivialis*	**Motacillidae**			f		Seedeater
Long-billed Pipit	*Anthus similis*	**Motacillidae**					Seedeater
Oriole Finch	*Linurgus olivaceus*	**Fringillidae**			F	AHB	Mixed
Thick-billed Seedeater	*Crithagra burtoni*	**Fringillidae**				AHB	Mixed
African Citril	*Crithagra citrinelloides*	**Fringillidae**			f	AHB	Mixed
Streaky Seedeater	*Crithagra striolata*	**Fringillidae**			f	AHB	Mixed
Yellow-crowned Canary	*Serinus flavivertex*	**Fringillidae**			f		Seed-eater

Appendix 2: Matrix of species ringed in each fragments

SITE	TOTAL NUMBER OF SPECIES COUGHT PER TRANSECT					
	T1	**T2**	**T3**	**T4**	**T5**	**T6**
K1 A D	12					
K1 B D	16					
K 1 A W	8					
K 1 B W	11					
K2 A D		15				
K2 B D		13				
K2 A W		10				
K2 B W		12				
K3 A D			17			
K3 B D			11			
K3 A W			8			
K3 B W			14			
K4 A D				9		
K4 B D				11		
K4 A W				13		
K4 B W				11		
K5 A D					7	
K5 B D					11	
K5 A W					9	
K5 B W					8	
K6 A D						5
K6 B D						8
K6 A W						9
K6 B W						5

KEYS

K1	Kiptaberr Transect 1 A&B (W= Wet; D= Dry)
K2	Kiplegatet Transect 2 A&B (W= Wet; D= Dry)
K3	Embayat Transect 3A &B (W= Wet; D= Dry)
K4	Kipkunurr West Transect 4 A&B (W= Wet; D= Dry)
K5	Kipkunurr Peak/Ridge Transect A &B (W= Wet; D= Dry)
K6	Kipkunurr Hossen Transect 6A&B (W= Wet;D= Dry)

Appendix 3: Matrix of species recorded in point count ;

The Total Number of species observed during the point in transect A and Band in both season Dry and Wet

SITE	TOTAL NUMBER OF SPECIES RECORDED PER TRANSECT					
SPECIES	**T1**	**T2**	**T3**	**T4**	**T5**	**T6**
K1 A D	34					
K1 B D	38					
K 1 A W	23					
K 1 B W	28					
K2 A D		33				
K2 B D		30				
K2 A W		28				
K2 B W		26				
K3 A D			32			
K3 B D			36			
K3 A W			28			
K3 B W			19			
K4 A D				31		
K4 B D				26		
K4 A W				34		
K4 B W				34		
K5 A D					33	
K5 B D					34	
K5 A W					25	
K5 B W					31	
K6 A D						27
K6 B D						30
K6 A W						28
K6 B W						18

KEYS

K1	Kiptaberr Transect 1 A&B (W= Wet; D= Dry)
K2	Kiplegatet Transect 2 A&B (W= Wet; D= Dry)
K3	Embayat Transect 3A &B (W= Wet; D= Dry)
K4	Kipkunurr West Transect 4 A&B (W= Wet; D= Dry)
K5	Kipkunurr Peak/Ridge Transect A &B (W= Wet; D= Dry)
K6	Kipkunurr Hossen Transect 6A&B (W= Wet;D= Dry)

Appendix 4: Images of threats to the forest.

Podocarpus debacking for covering beehives

Grazing of livestock that stays in the forest

African Pencil Cedar for Fencing Post

Encroachment that is not under KFS program

Settlement In the forest (Kiptaberr)

Logging for wood and Timber

Appendix 5: Pictures of some rare birds within cherangani forest

Crowned Hornbill *Tockus alboterminatus*

Black-and-white Casqued Hornbill *Bycanistes subcylindricus*

Hartlaub's Turaco *Tauraco hartlaubi*

Green-headed Sunbird *Cyanomitra verticalis*

Ludha’s Bushshrike

Black Throated Wattle eye

Appendix 6: GPS coordinates of the sampled sites

Each block had three fragments and each fragment two transects. Below are co-ordinates of the surveyed Transects (Table 1).The cordinates are source of the maps and transect for the study site(fig. 4, 5, 6)

SITE NAME:		**G.P.S CO-ORDINATES**	
KAPCHEROP FRAGMENTS BLOCK		**POINT START**	**POINT END**
KIPTABERR	**A**	N 01 06.392	N 01 06.712
		E 035 19.928	E 035 19.568
	B	N 01 07.051	N 01 06.660
		E 035 19.945	E 035 19.966
KIPLEGETET	**A**	N 01 04.126	N 01 03.831
		E 035 20.316	E 035 20.756
	B	N 01 04.967	N 01 03.783
		E 03520.134	E 03520.561
EMBAYAT	**A**	N 01 05.406	N 01 05.169
		E 035 18.400	E 035 18.937
	B	N 01 05.555	N 01 05.923
		E 035 18.554	E 035 18.236
KAPSOWARR FRAGMENTS BLOCK			
KIPKUNURR WEST	**A**	N 00° 59.118	N 00 59.732
		E 035 32.054	E 035 32.341
	B	N 00 59.506	N 00 59. 818
		E035 31.632	E035 31.218
KIPKUNURR PEAKRIDGE / PEAK	**A**	N 00 59.870	N 00 59.383
		E 035 30.642	E 035 30.815
	B	N 00 59. 483	N 00 58.990
		E 035 30.922[8]	E 035 30.111
KIPKUNURR HOSSEN	**A**	N 01 01.178	N 01 01.483
		E 035 33.517	E 035 33.116
	B	N 01 01 308	N 01 01.819
		E 035 33.481	E 035 33.560

Appendix 7: DRAINAGE MAP OF CHERANGANI HILLS FOREST:

The map shows how Cherangani serves as a water tower for the Turkana region and Lake Victoria (Nature Kenya report, 2015).