NTNU

Norwegian University of
Science and Technology

Dietary composition, overlap and competition between impala and domestic goat as revealed by DNA metabarcoding

Ingrid Aase Lingaas
Fossum

Biotechnology (5 year)
Submission date: May 2017
Supervisor: Eivin Røskaft, IBI
Co-supervisor: Frode Fossøy, IBI
Berit Johansen, IBI

Norwegian University of Science and Technology
Department of Biology

Abstract

In a world with a rapidly growing human population and limited resources, it is important to understand how we interact with wildlife to ensure their conservation. In Tanzania, the human population has more than tripled over the last 50 years. Many people live in rural areas, where they are directly dependent on the surrounding natural resources for food, water, grazing land for livestock, materials, firewood, and income. Simultaneously, Tanzania is home to Serengeti National Park, which is famous for its species diversity and for the annual large-scale migration of ungulates. With the growing human population, the number of domestic livestock also increases. Wild impala (*Aepyceros melampus*) outside the national park coexist with the domestic goat (*Capra hircus*) and could thus experience dietary competition from goats when they turn to browsing in the dry season. In this study, I investigated the dietary composition and overlap between impala and goat using DNA metabarcoding of faecal samples. I sampled impala inside Serengeti National Park, and west and east of the park, where I also sampled adjacent goats. Firstly, impala had a higher diversity of diet items, which could be an advantage for them in a potential competition with goats. Secondly, impala and goats share many of their most abundant species, especially shrubs and trees. One or more species of the *Fabaceae* family had the highest abundance and occurrence for both study species, and for impala, the diet was also dominated by one or more grasses of the PACMAD clade. It was also shown that the degree of dietary overlap between the species is higher than would be expected if they had used the resources independently of one another. Lastly, it was shown that habitat has a greater effect on the diet than the study species, implying that there is a great variance in habitat within the study area and that both goats and impala eat what is available in the different habitats. The dietary overlap indicates that there is potential for competition, especially in the dry season, when impala forage more on shrubs and trees, and when the human and livestock population continues to increase. However, to conclude on the degree of competition, more data is needed on the local plant abundance, and the genetic reference library should simultaneously be expanded with local plant species to know more about the diet on the plant species level. Meanwhile, management should consider the potential threat of domestic goats in the future studies on impala.

Innholdsfortegnelse

1. Introduction

1.1 Background

In a dramatically changing world, humans pose an increasing threat to our natural resources. Most species on the IUCN Redlist are threatened by habitat loss and degradation: in developing countries mostly due to different kinds of human use, while in developed countries, tourism, recreational use, and inappropriate management are some of the most significant threats to natural resources (Juffe-Bignoli et al., 2014). This has led to a rapid increase in the establishment of protected areas, and in 2014, 15.4% of the worlds terrestrial and inland water areas and 3.4% of the global ocean areas were classified as protected areas (Juffe-Bignoli et al., 2014). A large number of these protected areas are located in developing countries, where many people are also directly dependent on the natural resources, e.g. for grazing land and water. Establishing protected areas can exacerbate hostile attitudes among local communities, as they has often lead to the displacement of people from their homes, partial or total prohibition from exploiting natural resources, and of loss of life, property, or crops when wildlife emigrates from the protected area (Chape et al., 2005). Research on the many aspects of human-wildlife conflicts is therefore crucial, as it directly affects the welfare of the surrounding communities.

One of the threats to wildlife from human population growth is the inevitable increase of livestock. In 2011, the estimated number of ruminant livestock on Earth was 3.6 billion, and for the last 50 years, 25 million have been added to the planet every year (approximately 2 million per month) (Ripple et al., 2014). Several studies have shown that domestic livestock compete with wild herbivores (Prins, 2000, Odadi et al., 2011, Riginos et al., 2012). For competition to occur, the individuals have to forage on the same species in a shared habitat, the shared resources need to be limited, and the competition has to have a negative effect on one or both species (Wiens, 1989).

1.2 History of livestock and wild herbivores in East-Africa

In East-Africa, domestic goats, sheep (*Ovis Aries*) and cattle (*Bos taurus*) were introduced approximately 4000 years ago, which is short compared to the existence of native wild herbivores on an evolutionary time frame (Prins, 2000). Domestic livestock are thus non-indigenous species that invaded an assemblage of locally adapted species, and there therefore is a wide-spread concern that domestic livestock and wild ungulates compete for the same resources (Prins, 2000). The East-African savannah is rich in herbivore species, with the number of grazing species (>2 kg) reaching more than 31 (Prins and Olff, 1998). Using the traditional frameworks, large mammalian herbivores are characterized as predominantly grazers, non-grass-eating browsers, or as mixed feeders, which graze when grass is available but change to browsing when grass is unavailable in the dry season or winter (du Toit and Olff, 2014). However, to achieve such a diversity and abundance of herbivore species on a limited range of resource types, these species have to specialize and use food resources differently, on a finer level than simply consisting as grazers or browsers. The differential use of resources such as food and space by different organisms is often referred to as *resource partitioning* and can enable coexistence of species despite extensive overlap in ecological requirements (Schoener, 1974).

1.3 Population growth and human-wildlife conflict in Tanzania

Already in 2004, IUCN predicted that Tanzania was going to face severe human-wildlife conflicts, as it was one of the countries with both high human population growth rate and a high number of threatened species (Baillie et al., 2004). The country's population in 2012 (almost 45 million) was more than tripled since 1967, and if this growth rate is maintained, the population of the Tanzanian mainland is estimated to double by the year 2038 (Agwanda and Amani, 2014). Certain districts close to the western border of Serengeti National Park have grown rapidly since 1957, and villages close (<10 km) to the park border were shown to have substantially higher population growth rates than the national average of 2,9% between 1978 and 1988 (Hofer et al., 1996). The increase of Maasai, the largest ethnic group living in the Serengeti Ecosystem, in both Kenya and Tanzania east of the Serengeti National Park and Maasai Mara National Reserve has been shown to be as large as 3.9 % per year (Homewood et al., 2001).

Prior to colonization, the traditional societies of the Serengeti Ecosystem imposed little pressure on the natural resources. However, during post-colonial time, the pressure on wildlife has increased on a large scale, partly due to low governmental support, poverty, human population growth and illegal hunting (Hofer et al., 1996, Loibooki et al., 2002, Kaltenborn et al., 2003, Baillie et al., 2004). Due to human settlements and extensive livestock grazing, parts of the African savannah have suffered widespread degradation and loss of floristic and faunal diversity (Du Toit and Cumming, 1999).

1.4 Diet, competition and niche segregation

The effect of livestock husbandry on biodiversity both in Africa and worldwide has been a subject to much discussion, but relatively little controlled experimental research has been done (Voeten and Prins, 1999, Prins, 2000, Riginos et al., 2012, Kartzinel et al., 2015). From 1995 to 2011, a controlled, long-time experimental study was conducted in Laikipia in Kenya, studying the interactions between livestock, wild ungulate herbivores and the land they share. This study showed that cattle supress many wild herbivore species, mainly through dietary competition (Riginos et al., 2012). It was also shown that wild herbivores compete with cattle in the dry season, but facilitate them during the wet season (Odadi et al., 2011).

A study from the Mpala Research Centre in Kenya used DNA metabarcoding (see below) of faeces to assess diet breadth, composition, and overlap for six wild herbivore species and for cattle, in order to study resource partitioning on the species level in a semiarid savannah (Kartzinel et al., 2015). This study found that the diet composition was similar within species, but highly divergent between species. Even pairs of grazers that matched in size, digestive physiology, and location ate similar total amounts of grass, but different suites of grass species. Thus, herbivore species within the same guild partition their diet on a finer level than just grazing or browsing. Based on Bray-Curtis dissimilarity, the study also showed that the diets of different large mammalian herbivores clearly differed from each other, except for a small overlap between species with similar feeding strategies. Impala, together with buffalo *(Syncerus Caffer)*, was shown to have the greatest diet breadth of the species in the study (Kartzinel et al., 2015).

1.5 Assessing herbivore diets using DNA meta-barcoding

Information about food webs and their dynamics are important for understanding community ecology and ecosystem functions as well as for conservation biology. Besides that, there is a growing demand from consumers wanting to know the origin of food products (Pegard et al., 2009). It has therefore been important to develop accurate methods of determining components and ranges of animal diets. Previously, diets were mainly determined by direct observations of feeding animals or by microscopic examination of plant particles from gut contents or faeces. Although it provided some useful information, visual observation of feeding is limited or impossible in some situations. The microscopic examination requires time and expertise, and is highly dependent on the skills of the scientist (Pompanon et al., 2012, Kartzinel et al., 2015, Aziz et al., 2017).

A recently developed genetic methodology identifies DNA fragments from plant residues remaining in the faeces. To enable the amplification of a given DNA fragment for a large set of plant species in a single PCR, universal plant primer pairs are used. A common DNA sequence for such studies is the P6 loop of the chloroplast *trn*L (UAA) intron. This fragment is very suitable because its primers are highly conserved in plants, it has a short size (10-143 base pairs without priming sites) and is one of the most variable systems in size and sequence known to date (Pegard et al., 2009, Kartzinel et al., 2015). To determine the plant species ingested by the animal, the *trn*L sequence can be amplified by PCR and sequenced using next-gen methodology. The samples can then be compared to those of a reference database to identify the species and subsequently compute the relative distribution of each species (Pegard et al., 2009, Kartzinel et al., 2015).

In the mentioned study by Kartzinel et al. (2015) in Kenya, 70% of the dietary sequences were determined to species level and the remaining 30 % were identified to family level or better, using two different genetic reference databases. One of the libraries was a local library, constructed from plant species that had been sampled in the same area and thereafter sequenced, to complement the global NCBI Genbank library. In a dietary study in Ethiopia of goat and Walia Ibex, 40.7 % of the sequences were determined to species level and the remaining sequences to higher taxonomic levels (Gebremedhin et al., 2016).

1.6 Goals of the study

Most of the studies of diet overlap and competition between livestock and wild herbivores have used cattle as a study species, but fewer studies have investigated whether goats posed a similar threat to wild herbivores. In a recent study conducted in Simen Mountains National Park in Ethiopia, DNA metabarcoding was used to address dietary overlap between domestic goat and the endemic wild herbivore Walia Ibex (*Capra walie*). The study showed that there was a considerable overlap in dietary preferences between the species, which indicates a potential for competition, and could be a threat to the already endangered Walia Ibex (Gebremedhin et al., 2016). In this study, I wanted to investigate if impala have a dietary overlap with goats in the Serengeti Ecosystem, which could indicate a potential for competition between the two species.

Impala are mixed feeders using varying proportions of grass and browse. In the wet season they prefer grass, but change to browse during the dry season (Sinclair and Jarman, 1979). Inside Serengeti National Park, little to no livestock grazing occurs, but outside the western and eastern border of the park, people are allowed to graze their livestock. Impala who are resident outside the national park thus interact with people and domestic livestock, mainly cattle, sheep, and goats. Goats are browsers, and could be competing with impala for forage, especially in the dry season when impala change to a larger proportion of shrubs and trees in their diet. My hypothesis is that the diets of impala and goat overlap to a large extent, and that dietary competition occurs between the species.

In this study, I investigated the diet of impala both inside and outside Serengeti National Park, and goats outside the park foraging in close proximity to impala. My focus was to find out if impala and goats forage on the same plants, and if impala outside the park change their diet, particularly if they forage less on the species that are abundant in impala inside the park, due to competition with goats. To study the diet, I collected faecal samples from impala and goat, and DNA metabarcoding was used to sequence plant DNA to identify the plants foraged by the two study species.

2. Methods

2.1 Study area

The study was conducted in Serengeti national park and the neighbouring partially protected areas - Ikona Wildlife Management Area west of the park, and Loliondo Game Controlled Area east of the park (Figure 1). Serengeti National Park (14,763 km^2) is a part of the Serengeti-Mara ecosystem on the border between Tanzania and Kenya (Figure 1), which is famous for its spectacular biodiversity and of one of the last large-scale herbivore migrations in the world. The park was established in 1951, and was one of the first areas in the world to be proposed by UNESCO as a World Heritage site in 1972 (Sinclair, 1995, Kaltenborn et al., 2006).

Inside the park, no human settlement or extraction of natural resources is allowed. In Ikona Wildlife Management Area, settlements, cattle grazing, beekeeping, some cultivation, firewood collection, and game cropping are allowed. In the hunting season certain licensed tourist and resident hunting is permitted (Setsaas et al., 2007). In Loliondo Game Controlled Area, tourism, settlements, livestock, cultivation and hunting is allowed (Thirgood et al., 2004). Yearly, the park attracts approximately 350 000 tourists (336 177 in 2012/2013) (TANAPA, 2013), however, the number of tourists in SNP increases annually by about 10% (Fyumagwa et al., 2013). West and north of the national park, people belong to a great diversity of ethnic groups and tribes, where the majority are agropastoralists that are directly dependent on the natural resources (Kaltenborn et al., 2003, Kideghesho et al., 2007). East of the park, the majority of people are Maasai, who are traditionally pastoralists (Kaltenborn et al., 2003).

In this study, I categorized my samples into five different main areas: Ikona Wildlife Management Area (impala and goat), Western SNP (impala), Central SNP (impala), North-Eastern SNP (impala) and Loliondo Wildlife Management Area (impala and goat, figure 1), in total representing seven study groups.

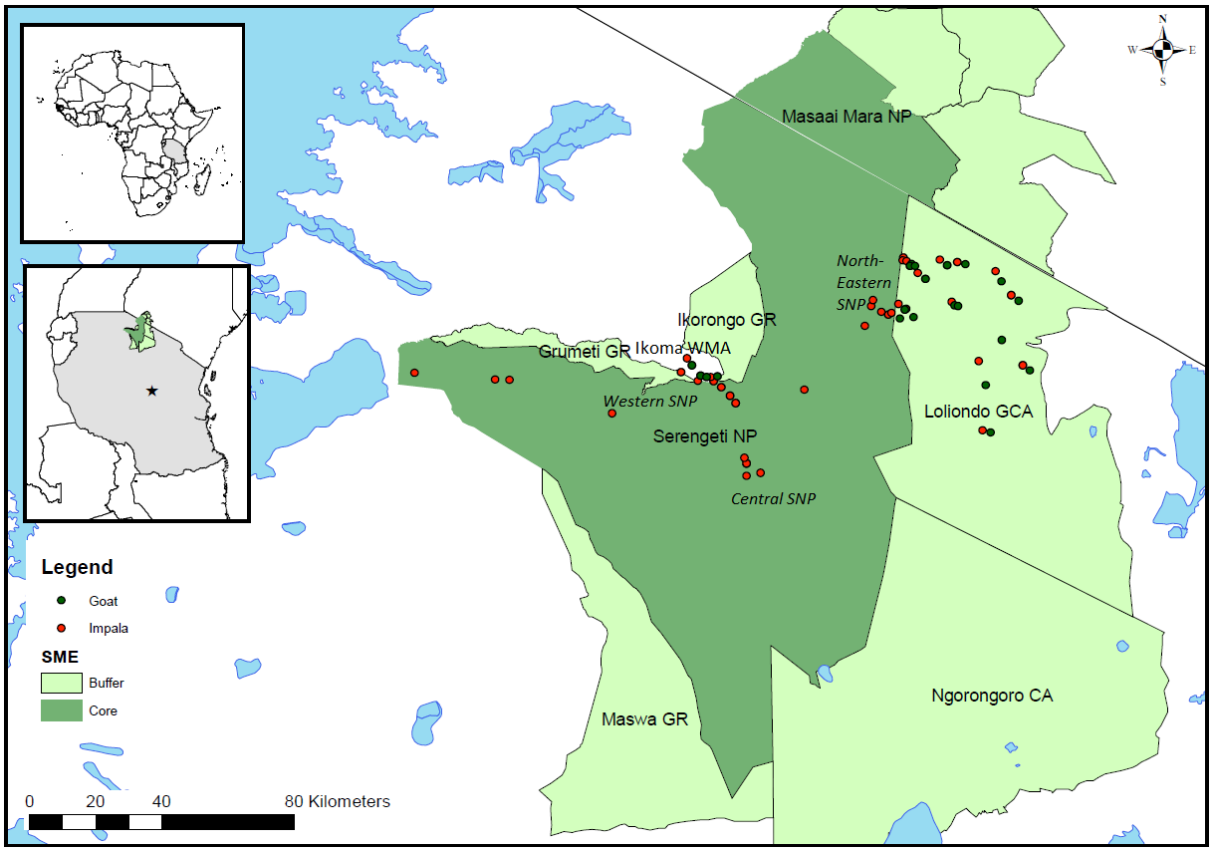

Figure 1: Map of Serengeti National Park in Northern Tanzania, with the adjacent Ikona Wildlife Management Area and Loliondo Game Controlled Area. The collection sites of the individual impala (red dots) and goat (green dots) samples are marked. The three sampling areas within Serengeti National Park (Western SNP, Central SNP and North-Eastern SNP) are also marked.

2.2 Study species

The investigated species were domestic goat and impala. They are both ruminants and belong to the family Bovidae (Van Soest, 1994). Goats are, in addition to cattle, sheep and donkey, the most common livestock in east Africa and often occur in large numbers across the African savannah (Du Toit and Cumming, 1999, Prins, 2000). In 2010, the total number of shoats (sheep and goats) in the Serengeti Ecosystem was estimated to 87612 (SE=19509) individuals, only outside the National Park (TAWIRI, 2010). Impala are medium-sized antelopes (40-55 kg) widely distributed throughout the woodlands of Africa south of the Saharan desert. In Serengeti, they are especially numerous in the middle and north of the park (Sinclair and Jarman, 1979). In 2010, the estimated abundance of impala in the Greater Serengeti Ecosystem was estimated to 75 000 (SE=9000) , with 6387 individuals (SE=2851) occurring in Loliondo Game Controlled Area (TAWIRI, 2010). Impala graze in large herds, where groups of females and their young are dominated by a dominant male. Other males form bachelor herds nearby

(Jarman and Jarman, 1973). The densities of impala has been shown to be significantly lower outside Serengeti National Park than inside, and the impalas outside the park have also been shown to be more vigilant, most likely due to illegal hunting (Setsaas et al., 2007).

Impala are known to be mixed feeders, that prefer to graze in the wet season, but that gradually change to browsing as the dry season progresses (Jarman, 1974, Sinclair and Jarman, 1979, Wronski, 2002). In Central SNP, impala was shown to prefer *Acacia Senegal* and *Acacia clavigera* woodlands in the wet season, while they preferred *Acacia drepanolobium* and *Acacia tortilis* woodland in the dry season. Of the grasses, *Digitaria macroblephora* and *Panicum maximum* were preferred. When offered both grass and browse, they ate predominantly grass species (Sinclair and Jarman, 1979). It has been shown that there is significant intersexual variations in impala, with the males consistently preferring grazing in larger degree than females in both the dry and wet season (Wronski, 2002).

2.3 Sample collection

The collection of impala faecal samples was done in the west, central and east of Serengeti national park, as shown on the map (Figure 1). Outside the park, in Ikona Wildlife Management Area and Loliondo Game Controlled Area, faecal samples from impala and goats in close proximity were always collected in pairs (mostly from ~500m to ~2km distance, except for the samples west of the park with ~2-5km distance). The time of sampling was from early June until end of July 2016. The sampling was non-invasive, as I observed the groups until they dropped and waited to collect feces until they had moved away. Only adult females were sampled, from 1-3 individuals per group. The faecal pellets were placed directly inside a tea bag in tubes with 96% ethanol for at least 72 hours to ensure absence of infectious disease and to prevent degradation of DNA. Thereafter the faecal pellets were transferred to tubes of silica crystals in order to dry, and exported from Tanzania to Norway on these tubes. The samples were declared free of infectious disease by Zoosanitary Inspectorate Services in Arusha (PERMIT NO: VIC/AR/ZIS/5806), and also declared for temporary storage in Norway by The Norwegian Food Safety Authority (Mattilsynet).

2.4 Genetic analysis

The extraction of DNA, and amplification and sequencing of trnl-P6 sequences was performed by the company SPYGEN in France. First, total DNA was extracted from about 10mg of faecal sample using the DNeasy Mini Stool Kit (Qiagen GmbH) following the manufacturer's instructions. The DNA extracts were recovered in a total volume of 200µL. Mock extractions without samples were systematically performed to monitor possible contaminations. Second, DNA amplifications were carried out using the universal plant primers gh (trnL gene; Taberlet *et al*. 2007). For each sample the DNA amplification was repeated twice. After amplification, all samples were purified using the MinElute PCR purification kit (Qiagen GmbH) and pooled for the pyrosequencing run (Illumine Hiseq). Each sample was recognized by a specific six base long tag for assignation of sequences to samples during bioinformatic segregation of sequences. Filtering of the sequences and inference of molecular operational taxonomic units (MOTUs, see (Floyd et al., 2002), will also be addressed as diet items) were performed using the *obitools* programs (Boyer et al., 2016). Taxonomic annotation was carried out with *obitools*, using a reference library based on all trnL-P6 sequences from the global European Molecular Biology Laboratory database (EMBL). This library includes trnL-P6 sequences from over 291 plant species collected in semiarid savanna at Mpala Research Centre in Kenya by Kartzinel et al in 2015 (Kartzinel et al., 2015).

No cross contaminations were detected. To eliminate errors due to PCR and/or sequencer, a bioinformatic filtering was performed and only sequences with 98% identity present in EMBL were kept in the analysis. Sequences present less than 10 times in each sample were discarded.

2.5 Statistical analysis

All analysis was conducted in RStudio version 1.0.143. The number of sequences detected for each MOTU was converted to relative abundance within samples using the function *decostand* in the *vegan* package (Oksanen et al., 2017). These relative abundances were the basis for all the data analysis. *ggplot2* (Wickham, 2009) was used to present the histogram of most common species across the three groups. To see if the number of faecal samples analyzed from goat and impala were enough to complete their dietary information, rarefaction analysis was conducted with the package *BiodiversityR* (Kindt and Coe, 2005) for all the samples. *BiodiversityR* was also used to calculate rank abundance plots, species richness and Shannon diversity index for

impala and goat. *Sciplot* (Morales and Murdoch, 2012) was used to present the mean species richness and Shannon diversity index for the different groups. A one-way ANOVA between the species richness and Shannon diversity of the study groups was performed, as well as a TukeyHSD posthoc test.

For the further study of diet overlap and potential competition, I focused my analysis on impala samples from North-Eastern SNP, and on impala and goat samples from Loliondo, as I had few samples from Central/Western SNP and Ikona Wildlife Management Area, and the habitat in these areas differ largely from the habitat in east. To compare the species composition between the groups of impala and goats in the Eastern Serengeti Ecosystem, Bray-Curtis dissimilarity was calculated using the package *vegan (Oksanen et al., 2017)*. This statistic compares the number of shared specimens between the samples with the total number of specimens counted at both sites, with resulting values between 0 and 1, where 0 represents an identical diet composition and 1 represents a completely different diet composition (Greenacre and Primicerio, 2013). The Bray-Curtis dissimilarity between the samples was visualized using Non-Metric Multidimensional Scaling (NMDS), with the function *metaMDS* in *vegan*. The algorithm of NMDS ranks the degree of dissimilarity between the samples, and the samples were mapped according to these distance ranks (Faith et al., 1987, Minchin, 1987, Ramette, 2007). NMDS was also used to visualize the overlap between all the impala groups in the study.

To explain the variance in diet composition between the coupled samples of goats and impala in Loliondo, I used Adonis analyses in *vegan*. Further, the average abundance of each MOTU was calculated for impala and goats in Loliondo, and used to calculate the Czekanowski niche overlap index, which is identical to 1-Bray-Curtis dissimilarity, using the R package *EcosimR* (Gotelli et al., 2015). This function simulates a random utilization matrix, and then compares the observed average overlap matrix with the simulated matrix, to suggest if the observed overlap is larger than what would be expected if the groups used resource categories independently of one another. The randomization algorithm RA3 was used, which simulates the random matrix by reshuffling all the plant abundance values to a random order, including the zeroes (Gotelli and Ellison, 2013). The number of replications of the simulated matrix was set to 5000.

3. Results

3.1 Dietary richness and diversity

82 faecal samples were collected (impala n=51, goats n=31). After filtering, a total of 2,112,628 sequences were kept. The number of sequences considered per sample ranged from 1619 to 71911 with an average of 30 156 (SD= 15 967). The number of MOTUs (Molecular Taxonomic Units) increased with number of sequences per sample, as seen in Figure S1. Due to this, I excluded three samples that contained less than 5000 sequences from the analysis. One sample was further excluded for the pairwise analysis of diet overlap in Loliondo, because the nearby impala had already been removed due to few sequences. Removing the plant species occurring in only one sample (N = 1 plant species) from the data did not change the main results, so I did not exclude these from the analysis. In total, 260 unique plant MOTUs were identified and assigned to species (102), genus (74), subfamily (52) and family (32) level. The number of MOTUs per sample ranged from 3 to 70, with an average of 31.23 (+-12.36) MOTUs per sample. The rarefaction curves show that the number of MOTUs have not reached a plateau, but are still increasing (Figure 2). Hence, more samples would likely find more species.

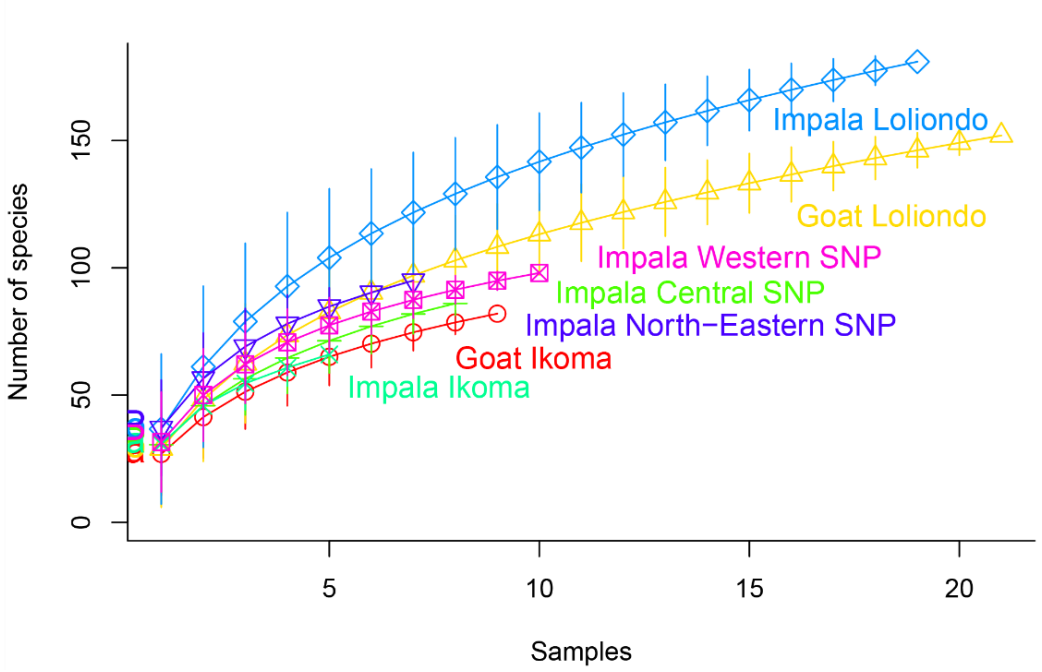

Figure 2: Sample-based rarefaction curves for all the seven sampled groups: Impala and goats in Loliondo Game Controlled Area, impala in western, eastern and central Serengeti and impala and goats in Ikona Wildlife Management Area.

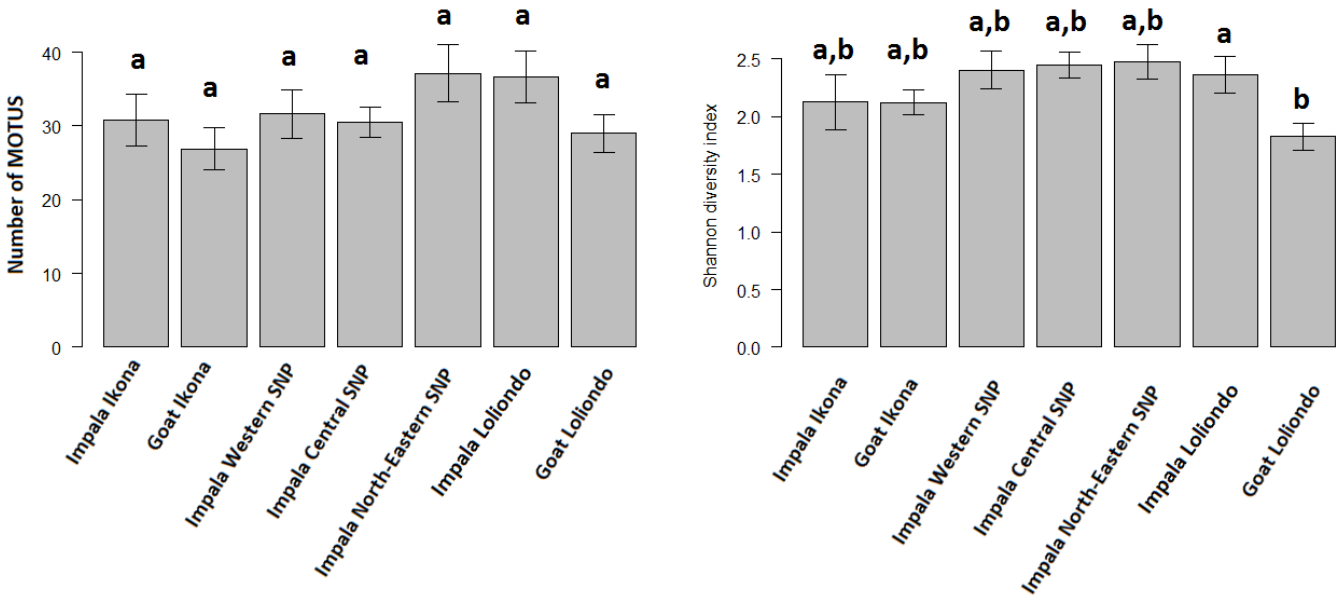

Figure 3: Average number of plant MOTUS (species) and Shannon diversity index for the seven groups of impala and goat in Serengeti National Park, Ikona Wildlife Management Area and Loliondo Game Controlled Area. The TukeyHSD posthoc results are assigned to the bars, showing that there is no significant difference in richness between the groups, but that there is a significant difference in Shannon diversity index of impala and goats in Loliondo.

An ANOVA-analysises showed that there was no significant difference in mean species richness between any of the groups (F=1.31, P=0.26), although there was a non-significant trend when comparing the paired samples of goats and impala in Loliondo using a paired t-test (t = -1.95, df = 16, P = 0.069). For the Shannon diversity, an ANOVA-analysis indicated significant difference between two or more groups (F=2.89, P=0.014). The TukeyHSD *posthoc* test showed a significant difference in Shannon diversity between goats and impala in Loliondo (P=0.036, figure 2), and non-significant trends between goats in Loliondo and the three impala groups inside Serengeti National Park (P = 0.087-0.092). The sample size, total species richness, mean species richness and the Shannon diversity index for the seven groups of impala are presented in Table 1, and the richness and Shannon diversity of the groups is visualized in figure 3.

Further, I looked closer at the impala in North-Eastern SNP and impala and goats in Loliondo. They shared 116 MOTUS in total, which constitutes 76 % of the goat's MOTUs and 64 % of impala's MOTUs. 36 MOTUs were private for goats and 65 for impala. The total plant richness

for Loliondo including MOTUs from both species was 217, which constitutes 84 % of the MOTUs found in the total analysis. The rank abundance plot shows that the abundance of species in impala is more evenly distributed than for goat, which has a few very dominant diet items (Figure S2).

Table 1: Sample size, species richness and Shannon diversity index of the seven groups of impala and goats sampled inside and outside of Serengeti National Park.

Group	Sample size	Total richness	Mean richness (SD)	Shannon diversity index (SD)
Impala Ikona	5	66	30.8 (7.9)	2.13 (0.54)
Goat Ikona	9	82	26.9 (8.9)	2.12 (0.32)
Impala Western SNP	10	98	31.6 (10.4)	2.4 (0.52)
Impala Central SNP	8	86	30.5 (6)	2.45 (0.31)
Impala North-Eastern SNP	7	95	37.1 (10.2)	2.48 (0.39)
Impala Loliondo	19	181	36.7 (15.2)	2.36 (0.7)
Goat Loliondo	21	152	29 (11.9)	1.82 (0.53)

3.2 Dietary composition and dominating dietary plant species

In the analysis of dietary composition, I used only the data from impala in North-Eastern SNP and from goat and impala in Loliondo GCA, due to the larger sample size in east and in order to minimize the effect of spatial habitat differences. The 10 diet items with the averagely highest relative abundance within diets represented a total of 25 MOTUs for all the three groups. For goat, the species *Cussonia holstii* had the highest abundance, but it occurred in only one individual, and in none of the impala groups. Otherwise, the diet item Fabaceae was most abundant for all the three groups (figure 3). This MOTU was one of in total 32 MOTUs identified to the Fabaceae family in Loliondo (table S2), from which most are identified to species or genus level, or to subfamilies of the large family. The MOTU of second highest abundance for all the three groups was identified to the genus *Vachellia*.

For impala, a MOTU in the PACMAD clade from the grass family *Poaceae* had the third highest abundance, while this was less abundant in the goats. This MOTU is one of in total 26 MOTUs identified to the *Poaceae* family. For goats, the three MOTUs *Fabaceae*, *Vachellia* and *Croton* averagely constituted close to two thirds of their diet, while the abundance of plant species was slightly more evenly distributed in impala. Apart from these most dominating diet

items, all of the studied impala and goats ate both grasses, herbs, shrubs and trees. However, from figure 3, it looks like impala in Serengeti National Park eat slightly more grasses and herbs than impala in Loliondo, who eat more of shrubs and trees, while goats in Loliondo eat more of other shrubs and trees than impala in the same area.

The ten diet items that occurred in the highest number of individuals in impala and goat in Loliondo and impala in North-Eastern SNP represented a total of 22 MOTUs, which occurrences are presented in figure 4. Two diet items, Asteraceae and Poaceae, had similar relative occurrence in the three groups. 6 diet items had higher occurrence inside Serengeti National Park: *Burseraceae*, *Dischrostachys spicata, Ingeae, Mimosoideae,* and the *PACMAD clade*, but lower occurrence in both goats and impala in Loliondo. Most of the species that have higher occurrence inside SNP had more than 85% occurrence versus less than 40% occurrence in Loliondo. Two diet items, *Celastraceae* and *Solanum*, had higher occurrence for goat and impala in Loliondo than in Serengeti.

Five diet items were higher for goats than for either of the impala groups: *Cordia, Croton, Fabaceae, Jasminum*, and *Vachellia*. These diet items are mostly characterized trees or shrubs, except for Fabaceae, which is unknown. Seven diet items dominate in both impala groups, but occur in less degree in goats: *Commelina, Dychoriste radicans, Eragrostidinae, Lamiaceae, Monsonia, Paniceae and Themeda,* which are all grasses or herbs. The diet item *Lantaneae*, a shrub, stands out. It was consumed by close to 75 % of impala in North-Eastern SNP and similar for goats in Loliondo, but only by around 35 % of impala in Loliondo. The classification of diet items to trees, shrubs, grasses and herbs used in this study are presented in table S2.

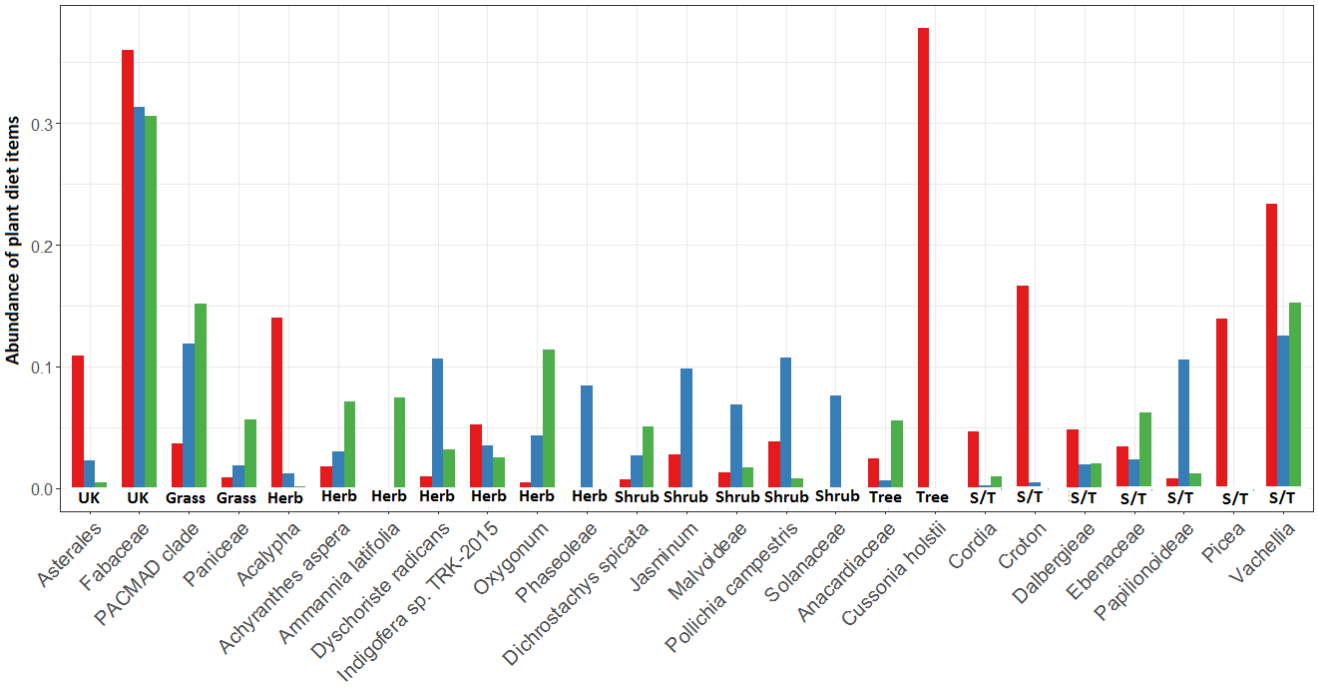

Figure 3: The 25 MOTUS that represented the 10 diet items with the averagely highest dietary abundance of impala in North-Eastern SNP (green bars), and in impala (blue bars) and goats (red bars) in Loliondo Game Controlled and Wildlife Management area. The classification of diet items is assigned underneath their abundances, where UK (unknown) indicates that the diet item could represent more than one growth form, while S/T (Shrub/Tree) indicates that the diet item could represent either a shrub or a tree.

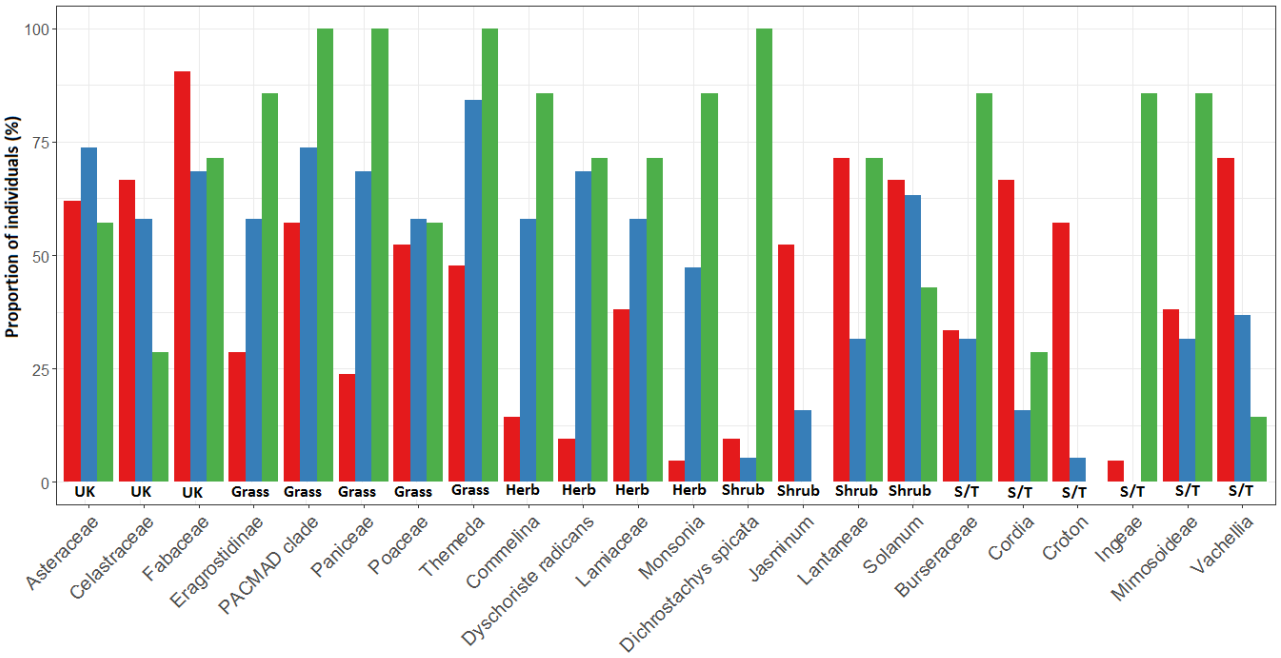

Figure 4: The 22 MOTUs that represented the ten most preferred diet items of impala in North-Eastern SNP (green bars), impala in Loliondo (blue bars) and goat in Loliondo (red bars), represented as percent of individuals of each group that consumed each diet item. The classification of diet items is assigned underneath their abundances, where UK (unknown) indicates that the diet item could represent more than one growth form, while S/T (Shrub/Tree) indicates that the diet item could represent either a shrub or a tree.

3.3 Dietary overlap and competition

The dietary dissimilarity within and among species was calculated using Bray-Curtis-Dissimilarity and Non-Metric Multidimensional Scaling. The impala in Loliondo overlapped with both goats and with impala in North-Eastern SNP. The samples of impala in North-Eastern SNP seem to be similar to a subset of the Loliondo impala samples, while another subset of the Loliondo samples overlap with a subset of the goat samples. However, there is close to no overlap between the diets of impala in the park and goats in Loliondo (Figure 5A). NMDS for all the impala groups, from Ikona across Serengeti National Park to Loliondo, is presented in figure 5B. There is some overlap between the impala in Western SNP and Ikona, and also between impala in North-Eastern SNP and Loliondo, while diet of impala in central SNP is grouped between eastern and western samples. The NMDS also shows that both latitude and longitude had independent effects on the dietary variation for the impala and goat samples in the Eastern Serengeti Ecosystem, while for the impala groups across the park, they don't show an independent effect.

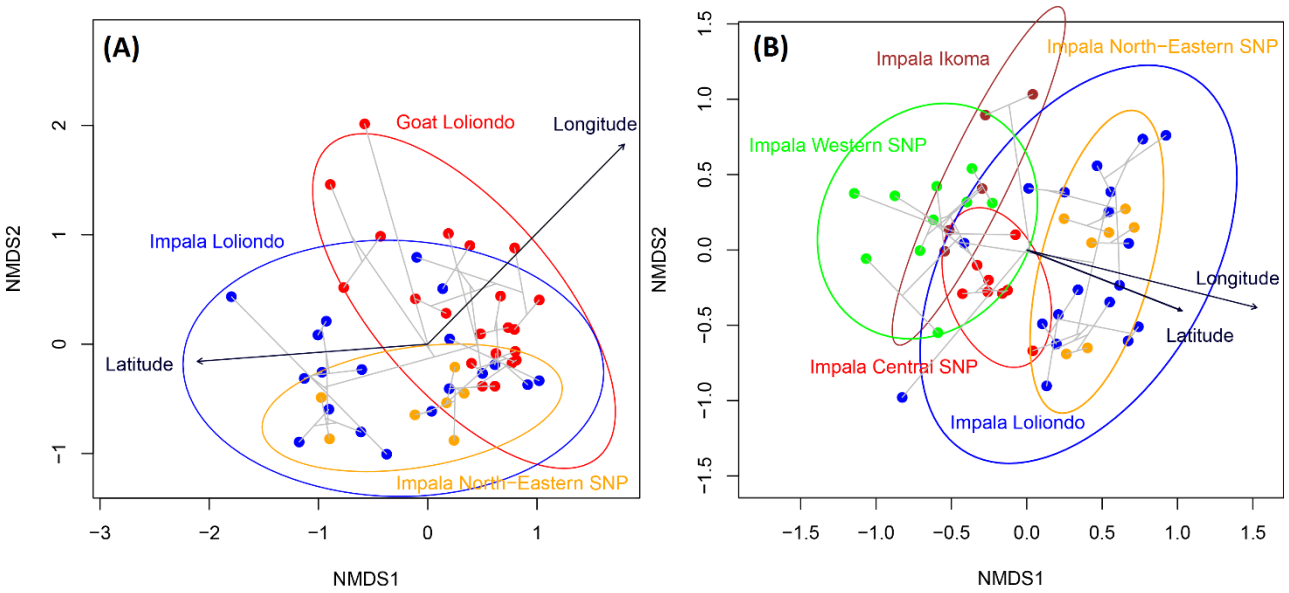

Figure 5: Niche partitioning between groups of impala and goat. NMDS of ranked Bray-Curtis Dissimilarity of samples from (A) Goat and impala in Loliondo and impala in North-Eastern SNP and (B) all impala groups from SNP, Ikona Wildlife Management Area and Loliondo Game Controlled Area. The circles show 95% confidence limits for each of the groups, the gray lines connects the samples with lower Bray-Curtis dissimilarity (higher similarity), and Longitude and Latitude shows the effect of the specific sample locations on the overlap.

The results of the Adonis test from the impala and goat samples in Loliondo show that there is a significant effect of species (impala or goat) on plant species composition, with species explaining 10% of the variance in diet. However, the location of the sample explained as much as 38% of the variance. The number of sequences also showed a significant effect on the dietary dissimilarity, but adding this variable did not affect the significance of species as a explanation variable for diet variation (Table 2). The observed czekanowski niche overlap index was calculated to 0.456, which was significantly higher than the simulated index, which had an average of 0.166 (SD=0.027) (figure 6).

Table 2: Results from the adonis (permutational multivariate analysis of variance) test, with species (goat or impala), location and number of sequences as explanatory factors. All three factors have a significant effect on diet composition.

	Df	**SS**	**MS**	**F**	**R^2**	**P**
Species	1	1.16	1.16	5.85	**0.10**	<0.001
Location	8	4.41	0.55	2.79	**0.38**	<0.001
Nr. of sequences	1	0.39	0.39	1.98	**0.03**	0.048
Residuals	28	5.54	0.2		**0.48**	
Total	38	11.5			1	

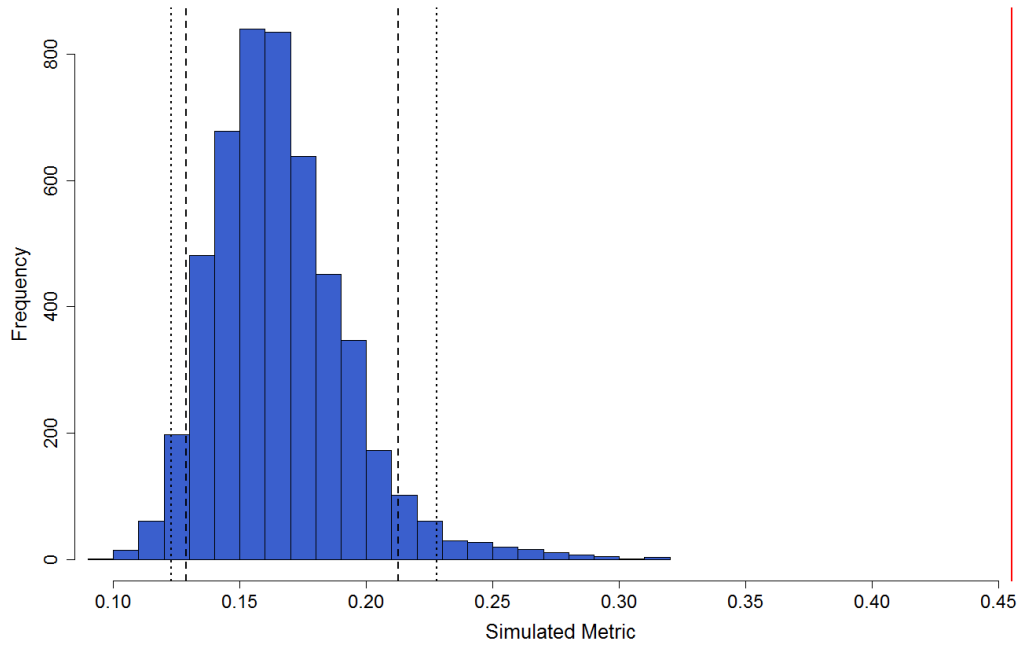

Figure 6: Observed Czekanowski niche overlap index (red line) between the diets of goat and impala in Loliondo Wildlife Management and Game Controlled Area, versus the simulated index (blue bars), with the upper and lower 95%-quantiles (1-tail shown with lines and 2-tail with smaller dots).

4. Discussion

In this study, I analyzed the diet of impala inside and outside of Serengeti National Park and its degree of dietary overlap with domestic goats. The results showed that there is a significant difference between the diets of impala and goats, even when controlled for the effects of habitat and the number of DNA sequences per sample. However, the results also showed that impala and goats share many of their most abundant and most occuring diet items, and that there is a larger overlap between the species than expected than if they chose species independently of one another. This indicates a potential for competition. It was also shown that impala in Loliondo Game Controlled area had higher diversity of diet items than goats on the same location, which could be an advantage for impala in a potential competition with goats.

4.1 Dietary richness and diversity

Firstly, a clear relationship was shown between the number of DNA-sequences per sample and number of MOTUs within a sample. This means that in most cases, samples with few sequences in total also have fewer unique sequences (MOTUs). A very low number of MOTUs could therefore be due to partial degradation of DNA in that sample or that some sequences failed to amplify during the PCR. A larger sampe size would thus be useful to get a more precise estimation of plant species richness and diversity. The species richness between the seven study groups was not significantly different. However, the paired t-test showed an almost significant difference between the paired samples of goats and impala in Loliondo. The rank abundance plot showed that goats have a higher abundance of their most abundant diet items than impala, and that the species items consumed by goats are thus less evenly distributed than those of impala. The Shannon diversity index is a combined measure of both plant species richness and evenness, and the lower plant species diversity of goats therefore suggests that combination of dietary plant richness and evenness of goats together contribute to a less diverse diet than impala, from the formal definition of diversity (Magurran, 1988, Kindt and Coe, 2005).

Since the goat samples in Loliondo were always collected in pairs with adjacent impala, the same plant species should be available for both species. This means that either goats eat proportionally to the occurrence of each plant species with no preference and impala selectively prefer a broader diet, or that goats prefer specific plant species and impala eats proportionally

to the occurrence of each plant species. However, from several studies conducted in different areas, it is clear that impala are flexible in their feeding behavior and have a species-rich diet (Jarman, 1974, Sinclair and Jarman, 1979, Wronski, 2002, Kartzinel et al., 2015). I therefore find it most likely that the difference in dietary diversity is due to a higher preference of goats to certain diet items. The higher diet diversity suggests that impala exploit more of their surrounding resources, which could be an advantage for them in a potential competition with goats. The higher dietary plant diversity of impala in Loliondo could also be a result of competition with goats, that more selective foraging of goats force impala to select a broader diet. However, the Shannon diversity index of the three impala groups inside the park were close to significantly different from the Shannon diversity of goats in Loliondo, which could indicate that they have a broad diet even without the presence of goats.

The average plant species richness for impala of approximately 37 diet items is lower than what Kartzinel et al. (2015) found in their study in Kenya (species richness of ~60). However, a higher species richness in their study is expected since they kept all sequences with a ≥95% match to their reference library, while I used only sequences with a ≥98% identity to EMBL. I chose to use 98% identity as limit since matches between 95 and 98 % to the reference library are less likely to represent the actual species of the match, and because it's less likely that more than one species is matched to the same refece DNA sequence. With a 98 % limit, it's a larger probability to separate between different plants than with 95 %, but it always hasto be considered that some newly evolved species could have a smaller difference in the trnl_P6 sequence than 2 %.

The total species richness of impala in North-Eastern SNP equals 95 plant spercies, almost half of that of Impala in Loliondo. I assume this to be due to the sampling of a small area compared to the area sampled in Loliondo.

4.2 Dietary composition and dominating dietary plant species

I only have data on diet items occurring in the faecal samples, and local plant abundance data would be necessary to conclude on whether some plant species are preferred or simply show a higher number of relative reads due to higher occurrence of this plant in the study area. However, some suggestions can be made from former studies of impala and goat diet. Most importantly, it's interesting that the two study species share many of their most abundant and most occurring diet items. This indicates that there is a potential for competition between impala and goat.

What does the MOTU Fabaceae, the most abundant and the most occurring diet item in all of the three study groups, represent? *Fabaceae* is the third largest plant family in the world, with more than 20 000 species of both herbs, shrubs, vines and trees (Wojciechowski et al., 2006). As mentioned, 32 MOTUs from goat and impala were characterized to the *Fabaceae* family, including the MOTU with name Fabaceae (see table S2). That this dietary sequence could only be identified to family level, means that it matched more than one sequence in the library and could therefore not be identified to species level. It might be that this MOTU represents more than one single species, if these species have more than 98% similarity in their trnl-P6 sequence. From the known dietary preferances of impala, this MOTU could represent one or more *Acacia* species, as the *Acacia* genus belongs to the *Fabaceae* family. Furthermore, no sequences in the analysis were identified to specific species the *Acacia* genus (except for Vachellia, as discussed below). Sinclair and Jarman (1979) found four different preferred Acacia species in a convential diet study. Two of these, *Acacia drepanolobium* and *Acacia tortilis,* were the most preferred species during the dry season. In his master's study, Valeri Mlingi also observed a strong preference for impala of *A. tortilis* compared to other plant species, which contributed to 20% of impalas' diet in the wet season, and as much as 44.7% in the dry season (Mlingi, 2015). Kartzinel et al. (2015) also identified several MOTUs with more than 70% occurrence that were identified to the Fabaceae family, including one MOTU suggested to be *A. tortillis* with 71 % occurrence in impala (Kartzinel et al., 2015). As Acacia belongs to the *Fabaceae* family, it is therefore possible that that the "Fabaceae" MOTU represents *Acacia tortilis*.

For goats, the MOTU Fabaceae also had the highest abundance. This could also represent *A. tortilis,* and/or another *Acacia* species preferred by goats if the sequence has more than 98% identity to the same reference sequences. Fabaceae was followed by a MOTU with name

Vachellia, which is the genus name for all the African *Acacia* species, but still widely known as *Acacia* (Kyalangalilwa et al., 2013). This MOTU had both higher abundance and occurrence in goats than in impala, and for impala in North-Eastern SNP, it was only detected for one of seven individuals. I therefore assume that this MOTU represents one (or more than one closely related) *Acacia* species more preferred by goats than impala. Skarpe et al. (2007) found that the most preferred *Acacia* species for goats are *Acacia mellifera, Acacia luederizii* and *Acacia Hebeclada*. The sequences that were identified as "Vachellia" could thus possibly include one or more of these *Acacia* species. However, if Fabaceae represents the same species in both of the study species, the higher preference of goats to this species and further growth in goat numbers could potentially lead to decreasing availability of the plant in the long term and force impala to forage more other species. That only two of 25 species on the list of most abundant plants in the diet, are grasses, is probably because the study was conducted in the dry season. With the mentioned intersexual differences in impala diet, there is also a possibility that the proportion of grass in the diet would be larger if male impala were sampled instead of females.

When it comes to plant *occurrence*, the mentioned diet items that had relatively high occurrence in impala inside the park and much lower for both goat and impala outside the park, and vice versa, are hypothesized to be a result of habitat differences inside and outside the park. One of these diet items is the PACMAD clade, which includes the C4 grasses (Kartzinel et al., 2015). All of the impala in North-Eastern SNP consume this diet item, while it's found in fewer of the impala and goat in Loliondo (~74 %and ~57 %, respectively). This might be due to difference in occurrence of the plant, and/or because the study area in North-Eastern SNP is smaller. Sinclair and Jarman (1979) showed that the grass species *Digitaria macroblephora* and *Panicum maximum* were preferred by impala. Both of these species belong to the PACMAD clade, and impalas known preference for these grasses, it's possible that this MOTU represents one or both of these two species.

The diet items that have higher occurrence for both impala groups than for goats, are interesting for explaining potential differences in plant preferences between the species. Since these diet items are found in both of the impala groups, they occur both inside and outside the park, but they are chosen by a larger proportion of the impala than the goats in the same area. This could be due to preference of these species by impala, and less preference of these species by goats. A similar assumption could be made for the species items with higher occurrence in goats than

in impala. What is interesting is that all the diet items that are higher in impala are grasses and herbs, while all the diet items with higher preference from goats are shrubs or trees. This confirms that goats are mostly browsers, while impala are mixed feeders who change from mostly grazing to mostly browsing from the dry season to the wet season, as shown in many studies (Dunham, 1980, Vanrooyen, 1992, Skarpe et al., 2007). However, I would expect to see more trees and shrubs in the diet of impala if I had sampled at the end of the dry season instead of in its beginning, as impala probably browse even more when grass becomes more scarce.

An interesting species in these results is *Lantaneae*: Since it has a high occurrence both for impala inside the park and for goats outside the park, we know that the species occurs in both areas, but that a smaller proportion of impala adjacent to the goats forage on this species. This result could imply that the impalas are prevented from eating this species due to competition with goats, and was what I had expected to see for more of the more of the diet items if competition occurs. That only one out of these 22 most common diet items is showing this tendency, could imply that the goats don't have a large negative effect on impala today even though they share many of the same species.

4.3 Dietary overlap and competition

The NMDS plot shows that there is indeed a certain degree of dietary overlap between goat and impala in Loliondo. That means that for overlapping samples, impala and goats eat more of the same (shared) diet items and less of other diet items. A dietary overlap could either be due to mutual preference of the same plant species, or that the local diversity of plants is less in these areas than others, so that they are forced to forage on the same plants. Since impala are shown to have a high diversity of plant species even in the presence of goats, I would assume that this could be due to lower plant diversity in the areas where the overlapping samples were collected. Nontheless, the overlap between goat and impala shows a potential for competition, and a further population increase of goats and/or decreasing availability of preferred plants can strengthen this competition. The NMDS also confirms that the impala in North-Eastern SNP eat similarly with many of the Loliondo impala. Almost all of the overlapping samples from Loliondo are from the western part, close to the SNP border. This could imply that the habitat in western Loliondo is more similar to the SNP than further east in Loliondo. That the North-Eastern SNP samples don't overlap with the goat samples could indicate that in western Loliondo, impala and goats in lesser degree tend to eat the same plant species. All in all, data

on the plant abundances would be needed to explain differences in the degree of overlap.

Some of the goat samples do not overlap with impala. This might be because the local variation in certain habitats are larger than others, so that impala and goat forage on different plant species in these areas and that their diets are therefore less similar. It could also be due to competition, if there's a limitation of certain plant species in these areas that force one of the species to eat differently. From the NMDS of the five impala groups, it looks as if their diet changes gradually from the samples in the north-east (Loliondo) to the samples in west (Ikona) of the sampling area, with almost no overlap between these two edges. The NMDS also indicated that latitude and longitude had different effects on the North-Eastern SNP/Loliondo samples, but not for the impala samples. For the impala samples, these were collected across a very large distance from east to west, but not from north to south, which can explain that most of the variation was explained by longitude. For the samples in Eastern Serengeti Ecosystem, however, the samples were spread more evenly from east to west and from north to south, and latitude therefore showed an independent effect. The two plots imply that there are large local differences in habitat across the Serengeti Ecosystem.

The Czekanowski niche overlap index, which compares the observed overlap with a simulated overlap index, was higher than what would be expected if the values of plant abundance were reshuffled to a random order. This implies that the mean abundance values of the two species did follow each other, and thus that goat and impala to some degree shared their more abundant and less abundant diet items. In the Adonis test, where an analysis of the variance in diet dissimilarities between samples was performed, the null hypothesis is that all diets are similar. Its result therefore indicates that whether the foraging animal is a goat or impala, has a significant effect on the diet composition. Interestingly, the location of the animals explains much more of the variance in diet than the species. This means that the location that the animal was foraging was more important for diet composition than if the animal foraging on that location was an impala or a goat. That indicates that there is large variation in local plant abundances within Loliondo Game Controlled Area. The test also showed a significant effect of number of sequences on the diet variation, but lower than both species and habitat. Importantly, controlling for this variable did not change the effect size of study species or of habitat.

4.4 Advantages and disadvantages of DNA metabarcoding

DNA metabarcoding has shown itself useful for describing occurrence and relative abundance of dietary plants, and to be more accurate and effective than traditional methods (Pompanon et al., 2012, Kartzinel et al., 2015, Aziz et al., 2017). For example, Sinclair and Jarman (1979) found that impala in the SNP east at least seventy plant species, which is less than a third of what I found in my study. Nonetheless, this method for describing diet is still new, and there are several aspects to consider in the analysis of its results. Firstly, since some plants are more digestible than others, it might be that the proportions of remaining plants in the faeces are different than the actual composition in their diet. This could especially effect the plants that are very easily digested or that makes a small percentage of the diet, if no DNA remains in the faeces. Also, during the PCR, some sequences can be amplified in less degree than others, e.g. because of their length or because of primer mismatches. That can again lead to wrong proportions of sequences within samples and even that some sequences will not be amplified at all.

The most obvious drawback of this method is that high-resolution results is dependent on an extensive local reference library. In my study, only 102 out of 260 sequences could be identified to species level, and many of the most common dietary plants could only be identified to family or genus level. This means that it's not possible to get any more than broad descriptions of the diets. In this study, we used 98% as a lower limit. I therefore assume that every MOTU is indeed a single species, but some species could have recently evolved and still have more than 98% similarity to other species, meaning that the two species will be characterized as one in the results. As mentioned, in the study of Kartzinel et al. (2015), they used a 95% match as a lower limit. This will result in a perceived higher dietary richness, but with less certainty that a dietary sequence actually represents the same species as the matching reference DNA.

Nevertheless, the problem of resolution using this method can be solved by collecting more plants to be sequenced and added to the reference library. Of course, this sampling will be time-consuming and will recquire people with knowledge of local plants, plus researchers to perform the lab work. However, such a library with extensive information on local plants could be useful to many areas of research.

5. Conclusion and future management directions

In this study, we have managed to get more information on the composition and richness of impala and goat diet in a semiarid savannah, in addition to information on their dietary overlap and potential competition. Firstly, impala have a higher dietary diversity then goats, which could imply that they have a better chance of adjusting than goats in a potential competition between the species. Secondly, impala and goats share many species in their diet, and some of the shared plant species have high occurrence and/or abundance in both of the study species. We also saw a certain degree of overlap when the occurrence and abundance of plant species was compared between samples using the NMDS. It's important to remember that overlap does not mean that competition occurs. For competition to occur, there has to be overlap in the diet, and the individuals/groups have to share the same habitat; but there also has to be a limitation in the shared resources, and lastly, the common resource use has to exert a negative effect on one or both of the species (Wiens, 1989). More studies have to be done on the two latter criteria to conclude further on the current and future competition. However, the results show that there is a strong potential for competition, which is likely to increase with increasing livestock number and habitat degradation.

As mentioned above, plant abundance data should be collected inside and outside Serengeti National Park to complete the information about competition between impala and goats. Further completing the genetic library of plant species occurring in the area could of great value, both on deciding the occurrence of plant species and on future diet studies. More diet studies should also be conducted on sheep, as the goats were very rarely observed without the company of sheep. Studies on dietary competition is very important, especially in developing countries like Tanzania as the increasing livestock populations are dependent on their surrounding resources and could be detrimental to the wild herbivores.

6. Acknowledgements

I acknowledge the European Union's Horizon 2020 research and innovation program under grant agreement No. 641918 (AfricanBioServices), for the support I received during my Masters study. I also acknowledge Tanzanian Wildlife Research Institute (TAWIRI) for their support and knowledge during my fieldwork in and outside Serengeti National Park. Further, I acknowledge my main supervisor professor Eivin Røskaft, for giving me the possibility to take part in AfricanBioServices, for enabling my fieldwork in Tanzania and for the help in my writeup. I also thank Frode Fossøy and Berit Johansen, for their tremendeous support and help in planning my fieldwork and in the analysis of my field data. I also want to thank Tuva Setsaas and Damari Samwel for their help during my fieldwork, and Louis for his help both with the fieldwork and valuable help with my results. I also acknowledge the Norwegian University of Science and Technology (NTNU) for hosting me as a student, and SPYGEN for their help with the extraction and sequencing of DNA from my samples. Last, but not least, I want to thank my family and friends for their endless support.

7. References

AGWANDA, A. & AMANI, H. 2014. Population Growth, Structure and Momentum in Tanzania. Dar Es Salaam, Tanzania: The Economic and Social Research Foundation (ESRF).

AZIZ, S. A., CLEMENTS, G. R., PENG, L. Y., CAMPOS-ARCEIZ, A., MCCONKEY, K. R., FORGET, P. M. & GAN, H. M. 2017. Elucidating the diet of the island flying fox (Pteropus hypomelanus) in Peninsular Malaysia through Illumina Next-Generation Sequencing. *PeerJ,* 5**,** e3176.

BAILLIE, J. E. M., HILTON-TAYLOR, C. & STUART, S. N. 2004. 2004 IUCN Red List of Threatened Species. A Global Species Assessment. *In:* BAILLIE, J. E. M., HILTON-TAYLOR, C. & STUART, S. N. (eds.). Gland, Switzerland and Cambridge, UK.

BOYER, F., MERCIER, C., BONIN, A., LE BRAS, Y., TABERLET, P. & COISSAC, E. 2016. obitools: a unix-inspired software package for DNA metabarcoding. *Molecular Ecology Resources,* 16**,** 176-82.

CHAPE, S., HARRISON, J., SPALDING, M. & LYSENKO, I. 2005. Measuring the extent and effectiveness of protected areas as an indicator for meeting global biodiversity targets. *Philosophical Transactions of the Royal Society of London B: Biological Sciences,* 360**,** 443-455.

DU TOIT, J. T. & CUMMING, D. H. M. 1999. Functional significance of ungulate diversity in African savannas and the ecological implications of the spread of pastoralism. *Biodiversity and Conservation,* 8**,** 1643–1661.

DU TOIT, J. T. & OLFF, H. 2014. Generalities in grazing and browsing ecology: using across-guild comparisons to control contingencies. *Oecologia,* 174**,** 1075-83.

DUNHAM, K. M. 1980. The Diet of Impala (Aepyceros-Melampus) in the Sengwa Wildlife Research Area, Rhodesia. *Journal of Zoology,* 192**,** 41-57.

FAITH, D. P., MINCHIN, P. R. & BELBIN, L. 1987. Compositional dissimilarity as a robust measure of ecological distance. *Vegetatio,* 69**,** 57-68.

FLOYD, R., ABEBE, E., PAPERT, A. & BLAXTER, M. 2002. Molecular barcodes for soil nematode identification. *Molecular Ecology,* 11**,** 839-50.

FYUMAGWA, R., GERETA, E., HASSAN, S., KIDEGHESHO, J. R., KOHI, E. M., KEYYU, J., MAGIGE, F., MFUNDA, I. M., MWAKATOBE, A., NTALWILA, J., NYAHONGO, J. W., RUNYORO, V. & RØSKAFT, E. 2013. Roads as a Threat to the Serengeti Ecosystem. *Conservation Biology,* 27**,** 1122-1125.

GEBREMEDHIN, B., FLAGSTAD, O., BEKELE, A., CHALA, D., BAKKESTUEN, V., BOESSENKOOL, S., POPP, M., GUSSAROVA, G., SCHRODER-NIELSEN, A., NEMOMISSA, S., BROCHMANN, C., STENSETH, N. C. & EPP, L. S. 2016. DNA Metabarcoding Reveals Diet Overlap between the Endangered Walia Ibex and Domestic Goats - Implications for Conservation. *PLoS One,* 11**,** e0159133.

GOTELLI, N. J. & ELLISON, A. M. 2013. *EcoSimR Niche Overlap Tutorial* [Online]. Available: https://www.uvm.edu/~ngotelli/EcoSim/Niche%20Overlap%20Tutorial.html [Accessed].

GOTELLI, N. J., HART, E. M. & ELLISON, A. M. 2015. EcoSimR: Null model analysis for ecological data.

GREENACRE, M. & PRIMICERIO, P. 2013. Multivariate Analysis of Ecological Data. *In:* GREENACRE, M. & PRIMICERIO, P. (eds.) *Multivariate Analysis of Ecological Data.* Bilbao, Spain: Fundacion BBVA.

HOFER, H., CAMPBELL, K. L. I., EAST, M. L. & HUISH, S. A. 1996. The impact of game meat hunting on target and non-target species in the Serengeti. . *In:* TAYLOR, J. & DUNSTONE, N. (eds.) *The exploitation of mammal populations.* London, UK: Chapman and Hall.

HOMEWOOD, K., LAMBIN, E. F., COAST, E., KARIUKI, A., KIKULA, I., KIVELIA, J., SAID, M., SERNEELS, S. & THOMPSON, M. 2001. Long-term changes in Serengeti-Mara wildebeest and land cover: pastoralism, population, or policies? *Proceedings of the National Academy of Sciences of the United States of America (PNAS),* 98**,** 12544-9.

JARMAN, M. V. & JARMAN, P. J. 1973. Daily activity of impala. *African Journal of Ecology,* 11**,** 75-92.

JARMAN, P. J. 1974. The Social Organisation of Antelope in Relation to Their Ecology. *Behaviour,* 48**,** 215-267.

JUFFE-BIGNOLI, D., BURGESS, N. D., BINGHAM, H., BELLE, E. M. S., DE LIMA, M. G., DEGUIGNET, M., BERTZKY, B., MILAM, A. N., MARTINEZ-LOPEZ, J. L., LEWIS, E., EASSOM, A., WICANDER, S., GELDMANN, J., VAN SOESBERGEN, A., ARNELL, A. P., O'CONNOR, B., PARK, S., SHI, Y. N., DANKS, F. S., MACSHARRY, B. & KINGSTON, N. 2014. Protected Planet Report 2014. *Tracking progress towards global targets for protected areas.* Cambridge, UK: The United Nations Environment Programme World Conservation Monitoring Centre (UNEP-WCMC).

KALTENBORN, B. P., BJERKE, T., NYAHONGO, W. & WILLIAMS, D. R. 2006. Animal preferences and acceptability of wildlife management actions around Serengeti National Park, Tanzania. *Biodiversity and Conservation,* 15**,** 4633–4649.

KALTENBORN, B. P., NYAHONGO, J. W. & MAYENGO, M. 2003. People and Wildlife Interactions around Serengeti National Park, Tanzania. *In:* KALTENBORN, B. P. (ed.) *NINA Project Report 22.* Lillehammer, Norway: Norwegian Institute for Nature Research (NINA).

KARTZINEL, T. R., CHEN, P. A., COVERDALE, T. C., ERICKSON, D. L., KRESS, W. J., KUZMINA, M. L., RUBENSTEIN, D. I., WANG, W. & PRINGLE, R. M. 2015. DNA metabarcoding illuminates dietary niche partitioning by African large herbivores. *Proceedings of the National Academy of Sciences of the United States of America (PNAS),* 112**,** 8019-24.

KIDEGHESHO, J. R., RØSKAFT, E. & KALTENBORN, B. P. 2007. Factors influencing conservation attitudes of local people in Western Serengeti, Tanzania. *Biodiversity and Conservation,* 16**,** 2213-2230.

KINDT, R. & COE, R. 2005. *Tree diversity analysis. A manual and software for common statistical methods for ecological and biodiversity studies,* Nairobi (Kenya), World Agroforestry Centre (ICRAF).

KYALANGALILWA, B., BOATWRIGHT, J. S., DARU, B. H., MAURIN, O. & VAN DER BANK, M. 2013. Phylogenetic position and revised classification of Acacia s.l. (Fabaceae: Mimosoideae) in Africa, including new combinations in Vachellia and Senegalia. *Botanical Journal of the Linnean Society,* 172**,** 500-523.

LOIBOOKI, M., HOFER, H., CAMPBELL, K. L. I. & EAST, M. L. 2002. Bushmeat hunting by communities adjacent to the Serengeti National Park, Tanzania: the importance of livestock ownership and alternative sources of protein and income. *Environmental Conservation,* 29**,** 391-398.

MAGURRAN, A. E. 1988. *Ecological Diversity and Its Measurement*, Springer Netherlands.

MINCHIN, P. R. 1987. An evaluation of the relative robustness of techniques for ecological ordination. *In:* PRENTICE, I. C. & VAN DER MAAREL, E. (eds.) *Theory and models in vegetation science: Proceedings of Symposium, Uppsala, July 8–13, 1985.* Dordrecht: Springer Netherlands.

MLINGI, V. 2015. *Foraging by elephant, giraffe and impala during wet and dry season in rich and poor savanna, Tanzania.* Master in Applied Ecology, Hedmark University College.

MORALES, M. & MURDOCH, D. 2012. sciplot: Scientific Graphing Functions for Factorial Designs. R package version 1.1-0 ed.: R Development Core Team.

ODADI, W. O., KARACHI, M. K., ABDULRAZAK, S. A. & YOUNG, T. P. 2011. African wild ungulates compete with or facilitate cattle depending on season. *Science,* 333**,** 1753-5.

OKSANEN, J., BLANCHET, F. G., FRIENDLY, M., KINDT, R., LEGENDRE, P., MCGLINN, D., MINCHIN, P. R., O'HARA, R. B., SIMPSON, G. L., SOLYMOS, P., STEVENS, M. H., SZOECS, E. & WAGNER, H. 2017. vegan: Community Ecology Package.

PEGARD, A., MIQUEL, C., VALENTINI, A., COISSAC, E., BOUVIER, F., FRANCOIS, D., TABERLET, P., ENGEL, E. & POMPANON, F. 2009. Universal DNA-based methods for assessing the diet of grazing livestock and wildlife from feces. *Journal of Agricultural and Food Chemistry,* 57**,** 5700-5706.

POMPANON, F., DEAGLE, B. E., SYMONDSON, W. O. C., BROWN, D. S., JARMAN, S. N. & TABERLET, P. 2012. Who is eating what: diet assessment using next generation sequencing. *Molecular Ecology,* 21**,** 1931–1950.

PRINS, H. H. T. 2000. Competition Between Wildlife and Livestock in Africa. *In:* PRINS, H. H. T., GROOTENHUIS, J. G. & DOLAN, T. T. (eds.) *Wildlife Conservation by Sustainable Use.* Dordrecht, Netherlands: Springer Netherlands.

PRINS, H. H. T. & OLFF, H. 1998. Species-richness of African grazer assemblages: towards a functional explanation. *In:* NEWBERY, D. M., PRINS, H. H. T. & BROWN, N. D. (eds.) *Dynamics of tropical communities: the 37th symposium of the British Ecological Society.* Cambridge University.
RAMETTE, A. 2007. Multivariate analyses in microbial ecology. *Fems Microbiology Ecology,* 62**,** 142-160.
RIGINOS, C., PORENSKY, L. M., VEBLEN, K. E., ODADI, W. O., SENSENIG, R. L., KIMUYU, D., KEESING, F., WILKERSON, M. L. & YOUNG, T. P. 2012. Lessons on the relationship between livestock husbandry and biodiversity from the Kenya Long-term Exclosure Experiment (KLEE). *Pastorialism: Research, Policy and Practice,* 2**,** 1-22.
RIPPLE, W. J., SMITH, P., HABERL, H., MONTZKA, S. A., MCALPINE, C. & BOUCHER, D. H. 2014. Ruminants, climate change and climate policy. *Nature Climate Change,* 4**,** 2-5.
SCHOENER, T. W. 1974. Competition and the form of habitat shift. *Theoretical Population Biology,* 6**,** 265-307.
SETSAAS, T. H., HOLMERN, T., MWAKALEBE, G., STOKKE, S. & RØSKAFT, E. 2007. How does human exploitation affect impala populations in protected and partially protected areas? A case study from the Serengeti Ecosystem, Tanzania. *Biological Conservation,* 136**,** 563-570.
SINCLAIR, A. R. E. 1995. Serengeti Past and Present. *In:* SINCLAIR, A. R. E. & ARCESE, P. (eds.) *Serengeti II: Dynamics, Management, and Conservation of an Ecosystem.* Chicago and London: The University of Chicago Press.
SINCLAIR, A. R. E. & JARMAN, P. J. 1979. Feeding Strategy and the Pattern of Resource Partitioning in Ungulates. *In:* SINCLAIR, A. R. E. & JARMAN, P. J. (eds.) *Serengeti: Dynamics of an Ecosystem.* Chicago and London: The University of Chicago Press.
SKARPE, C., JANSSON, I., SELJELI, L., BERGSTRÖM, R. & RØSKAFT, E. 2007. Browsing by goats on three spatial scales in a semi-arid savanna. *Journal of Arid Environments,* 68**,** 480-491.
TANAPA. 2013. *Tourism performance* [Online]. The official New Website for Tanzania National Parks: Tanzania National Parks (TANAPA). Available: http://www.tanzaniaparks.go.tz/index.php?option=com_content&view=article&id=14&Itemid=173 [Accessed].
TAWIRI 2010. Aerial Census in the Serengeti Ecosystem, Wet Season 2010. *SRF Report SE46.*
THIRGOOD, S., MOSSER, A., THAM, S., HOPCRAFT, G., MWANGOMO, E., MLENGEYA, T., KILEWO, M., FRYXELL, J., SINCLAIR, A. R. E. & BORNER, M. 2004. Can parks protect migratory ungulates? The case of the Serengeti wildebeest. *Animal Conservation,* 7**,** 113-120.
VAN SOEST, P. J. 1994. Nutritional Ecology of the Ruminant. *In:* VAN SOEST, P. J. (ed.). Ithaca, New York: Cornell University Press.
VANROOYEN, A. F. 1992. Diets of Impala and Nyala in 2 Game Reserves in Natal, South-Africa. *South African Journal of Wildlife Research,* 22**,** 98-101.
VOETEN, M. M. & PRINS, H. H. T. 1999. Resource partitioning between sympatric wild and domestic herbivores in the Tarangire region of Tanzania. *Oecologia,* 120**,** 287-294.
WICKHAM, H. 2009. ggplot2: Elegant Graphics for Data Analysis. New York: Springer-Verlag.
WIENS, J. A. 1989. Niche theory and guilds. *In:* BARNES, R. S. K. & BIRKS, H. J. B. C., E. F.

PAINE, R. T. (eds.) *The Ecology of Bird Communities.* Cambridge, United Kingdom: Cambridge University Press.
WOJCIECHOWSKI, M. F., MAHN, J. & JONES, B. 2006. *Fabaceae. legumes* [Online]. The Tree of Life Web Project. Available: http://tolweb.org/Fabaceae/21093/2006.06.14 [Accessed].
WRONSKI, T. 2002. Feeding ecology and foraging behaviour of impala Aepyceros melampus in Lake Mburo National Park, Uganda. *African Journal of Ecology,* 40**,** 205-211.

Appendix 1

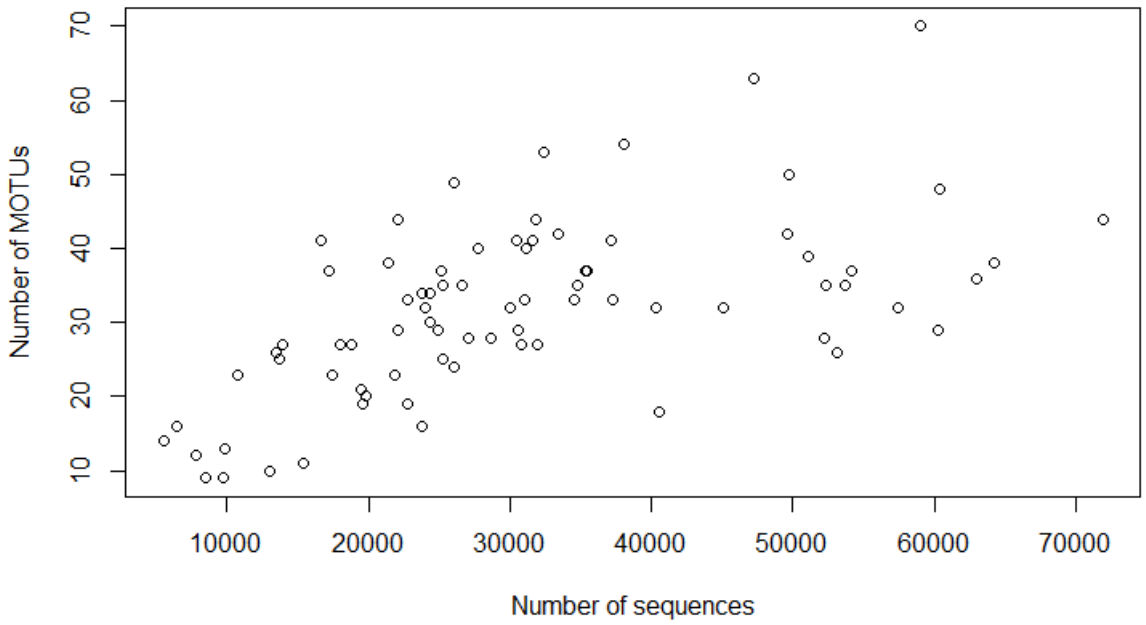

Figure S1: Number of sequences per sample and the associated number of MOTUs, showing that the number of MOTUs increases with number of sequences per sample.

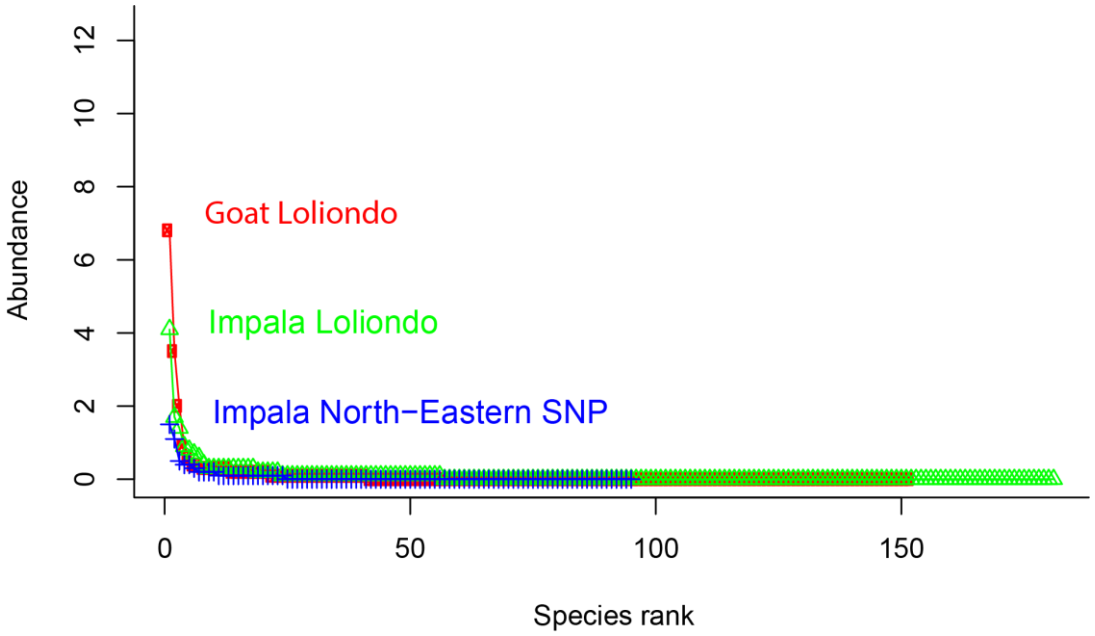

Figure S2: Rank abundance plots for impala (green) and goats (blue) in Loliondo and for Impala in North-Eastern Serengeti National Park (red). Diet items with highest average abundance within each group is ranked number one, second highest number two, etc. Goats in Loliondo have a higher relative abundance of their most abundant diet item than impala.

Appendix 2

Table S1: The trnl-P6 dietary sequences that matched to the GenBank® library, and their (1) average relative abundance per sample and (2) frequency of occurrence in the three main study groups: Impala in North-Eastern Serengeti National Park (n=7), and impala (n=19) and goat (n=21) in Loliondo Game Controlled Area. The sequences were identified to family or better, and had a 98% or larger match to the GenBank® library.

Family	Taxon/MOTU	Impala N/E SNP	Impala Lol.	Goat Lol.	Impala N/E SNP	Impala Lol.	Goat Lol.
Araliaceae	Cussonia holstii	0	0	0.3784	0	0	0.0476
Asparagaceae	Agavoideae	0	0.0028	0	0	0.0526	0
Amaryllidaceae	Allium sativum	0	0.0003	0	0	0.0526	0
Xanthorrhoeaceae	Aloe	0	0.0019	0.0002	0	0.0526	0.0476
Xanthorrhoeaceae	Aloe cameronii	0	0.0037	0	0	0.0526	0
Asparagaceae	Asparagus	0	0.0019	0.0025	0	0.1053	0.2381
Hypoxidaceae	Hypoxis	0.0006	0.0010	0	0.1429	0.0526	0
Asteraceae	Acanthospermum australe	0	0.0012	0	0	0.0526	0
Asteraceae	Asteraceae	0.0188	0.0306	0.0191	0.5714	0.7368	0.6190
NA	Asterales	0.0044	0.0228	0.1087	0.1429	0.5263	0.3810
Asteraceae	Asteroideae	0	0.0041	0	0	0.1053	0
Asteraceae	Cichorieae	0	0.0050	0.0124	0	0.1053	0.0476
Asteraceae	Emilia discifolia	0	0.0046	0.0005	0	0.2105	0.0476
Asteraceae	Heliantheae alliance	0	0.0012	0	0	0.0526	0
Asteraceae	Helichrysum glumaceum	0	0.0031	0	0	0.0526	0
Asteraceae	Helichrysum sp. TRK-2015	0.0026	0	0	0.1429	0	0
Asteraceae	Tagetes	0	0.0053	0.0220	0	0.0526	0.2857
Asteraceae	Tripteris vaillantii	0	0.0177	0	0	0.0526	0
Cordiaceae	Cordia	0.0098	0.0025	0.0461	0.2857	0.1579	0.6667
Boraginaceae	Cystostemon hispidus	0	0	0.0011	0	0	0.0476
Ehretiaceae	Ehretiaceae	0	0.0091	0	0	0.0526	0
Heliotropiaceae	Heliotropiaceae	0	0.0109	0.0083	0	0.0526	0.0476
Capparaceae	Boscia madagascariensis	0.0038	0.0042	0.0017	0.1429	0.1579	0.3333
Brassicaceae	Brassicaceae	0	0.0018	0.0004	0	0.0526	0.0952
Capparaceae	Cadaba	0	0.0397	0.0038	0	0.4211	0.1429
Capparaceae	Capparaceae	0	0.0024	0.0016	0	0.1053	0.1429
Capparaceae	Capparis tomentosa	0	0.0051	0.0029	0	0.1579	0.0952
Brassicaceae	Lepidieae	0	0.0016	0.0011	0	0.0526	0.0476
Brassicaceae	Lepidium	0	0	0.0014	0	0	0.0476
Capparaceae	Maerua angolensis	0	0	0	0	0	0

Capparaceae	Maerua triphylla	0	0.0029	0.0008	0	0.1053	0.0476
Salvadoraceae	Salvadora	0	0	0	0	0	0
Amaranthaceae	Achyranthes aspera	0.0708	0.0301	0.0181	0.4286	0.4737	0.4762
Amaranthaceae	Achyropsis avicularis	0.0026	0.0030	0.0020	0.4286	0.4211	0.3333
Amaranthaceae	Aerva lanata	0.0021	0.0010	0.0002	0.2857	0.3158	0.0476
Amaranthaceae	Alternanthera pungens	0	0.0004	0	0	0.0526	0
Amaranthaceae	Amaranthaceae	0.0150	0.0107	0.0082	0.5714	0.4737	0.4286
Amaranthaceae	Amaranthus	0	0.0265	0.0046	0	0.2105	0.1429
Amaranthaceae	Bassia scoparia	0	0.0022	0	0	0.0526	0
Amaranthaceae	Centrostachys aquatica	0	0	0	0	0	0
Amaranthaceae	Chenopodiastrum murale	0	0	0.0019	0	0	0.0952
Amaranthaceae	Chenopodioideae	0	0.0008	0.0007	0	0.0526	0.0476
Nyctaginaceae	Commicarpus pedunculosus	0	0	0	0	0	0
Amaranthaceae	Gomphrena	0	0.0038	0	0	0.0526	0
Amaranthaceae	Guilleminea	0	0.0003	0	0	0.0526	0
Polygonaceae	Oxygonum	0.1138	0.0429	0.0044	0.5714	0.3158	0.0952
Plumbaginaceae	Plumbago	0.0166	0.0223	0.0102	0.2857	0.3158	0.1905
Caryophyllaceae	Pollichia campestris	0.0079	0.1072	0.0381	0.1429	0.3684	0.3810
Polygonaceae	Polygonoideae	0	0.0632	0.0271	0	0.0526	0.1905
Amaranthaceae	Psilotrichum elliotii	0.0008	0.0086	0.0037	0.1429	0.0526	0.0952
Polygonaceae	Rumex	0	0.0006	0	0	0.0526	0
Aizoaceae	Zaleya	0	0.0077	0.0247	0	0.1579	0.0476
Celastraceae	Celastraceae	0.0108	0.0119	0.0094	0.2857	0.5789	0.6667
Celastraceae	Simicratea sp. Luke & Luke 4747	0	0.0029	0	0	0.0526	0
Commelinaceae	Commelina	0.0177	0.0283	0.0159	0.8571	0.5789	0.1429
Commelinaceae	Commelina benghalensis	0	0.0016	0	0	0.1053	0
Commelinaceae	Commelina erecta	0.0042	0.0100	0.0028	0.1429	0.3684	0.1905
NA	Cornales	0	0	0.0002	0	0	0.0476
Grubbiaceae	Grubbia rosmarinifolia	0	0	0.0009	0	0	0.0952
Cucurbitaceae	Cucurbitaceae	0.0030	0.0423	0.0112	0.1429	0.4211	0.2381
Cucurbitaceae	Momordica	0	0	0.0011	0	0	0.0476
Cucurbitaceae	Sicyos	0	0.0006	0	0	0.0526	0
Cupressaceae	Chamaecyparis lawsoniana	0	0	0	0	0	0
Cupressaceae	Cupressaceae	0	0	0.0141	0	0	0.0476
Caprifoliaceae	Lonicera	0	0	0.0016	0	0	0.0476
Primulaceae	Anagallis	0	0.0007	0	0	0.0526	0
Ebenaceae	Ebenaceae	0.0622	0.0231	0.0337	0.2857	0.1579	0.4762
Fabaceae	Acacieae	0.0299	0.0153	0.0138	0.1429	0.2105	0.3810
Fabaceae	Albizia brevifolia	0.0006	0	0	0.1429	0	0

Fabaceae	Caesalpinieae	0	0	0	0	0	0
Fabaceae	Crotalaria	0.0030	0.0004	0.0023	0.2857	0.0526	0.1429
Fabaceae	Cyamopsis tetragonoloba	0.0011	0.0010	0	0.1429	0.1053	0
Fabaceae	Dalbergia	0	0	0	0	0	0
Fabaceae	Dalbergieae	0.0204	0.0195	0.0477	0.2857	0.0526	0.0952
Fabaceae	Desmodieae	0.0010	0.0074	0	0.1429	0.1053	0
Fabaceae	Dichrostachys	0.0013	0	0.0003	0.4286	0	0.0476
Fabaceae	Dichrostachys cinerea	0	0	0.0003	0	0	0.0476
Fabaceae	Dichrostachys cinerea subsp. africana	0.0019	0	0.0007	0.4286	0	0.0476
Fabaceae	Dichrostachys spicata	0.0509	0.0266	0.0070	1.0000	0.0526	0.0952
Fabaceae	Eriosema	0.0048	0.0014	0.0014	0.1429	0.1053	0.0476
Fabaceae	Fabaceae	0.3063	0.3136	0.3599	0.7143	0.6842	0.9048
NA	Fabales	0	0	0.0005	0	0	0.0476
Fabaceae	Glycyrrhiza	0	0	0	0	0	0
Fabaceae	Indigofera hilaris	0.0103	0.0088	0.0107	0.2857	0.1579	0.0952
Fabaceae	Indigofera sp. TRK-2015	0.0253	0.0348	0.0525	0.4286	0.1579	0.2381
Fabaceae	Indigofereae	0	0.0219	0.0150	0	0.2632	0.1905
Fabaceae	Ingeae	0.0110	0	0.0060	0.8571	0	0.0476
Fabaceae	Leucaena	0	0	0	0	0	0
Fabaceae	Macrotyloma uniflorum	0	0.0067	0	0	0.0526	0
Fabaceae	Medicago	0	0.0032	0.0012	0	0.1053	0.0476
Fabaceae	Microcharis galpinii	0	0	0	0	0	0
Fabaceae	Mimosoideae	0.0042	0.0394	0.0087	0.8571	0.3158	0.3810
Fabaceae	Neonotonia wightii	0.0018	0.0174	0.0058	0.2857	0.4211	0.1905
Fabaceae	Papilionoideae	0.0123	0.1058	0.0080	0.1429	0.3684	0.0952
Fabaceae	Phaseoleae	0	0.0839	0	0	0.1579	0
Fabaceae	Phaseolus	0	0.0028	0.0005	0	0.1579	0.0476
Fabaceae	Philenoptera cyanescens	0	0	0	0	0	0
Fabaceae	Pithecellobium sp. DS14533_JM1598	0.0154	0	0	0.4286	0	0
Polygalaceae	Polygala	0	0.0027	0.0007	0	0.3684	0.0952
Fabaceae	Senegalia	0	0.0010	0	0	0.0526	0
Fabaceae	Senegalia modesta	0.0055	0	0	0.4286	0	0
Fabaceae	Senna gardneri	0.0070	0	0	0.5714	0	0
Fabaceae	Soja	0	0	0	0	0	0
Fabaceae	Vachellia	0.1525	0.1251	0.2339	0.1429	0.3684	0.7143
Fabaceae	Vigna	0.0007	0	0	0.1429	0	0
Fabaceae	Vigna marina	0	0	0.0013	0	0	0.0476
Fabaceae	Vigna vexillata	0.0074	0.0069	0	0.7143	0.2105	0
Fabaceae	Zornia	0.0025	0.0022	0.0008	0.1429	0.2632	0.0476

Fagaceae	Fagaceae	0.0045	0.0014	0.0009	0.1429	0.0526	0.0476
Apocynaceae	Apocynaceae	0.0015	0.0029	0.0052	0.1429	0.1579	0.1429
Apocynaceae	Asclepiadoideae	0	0	0.0010	0	0	0.0952
Apocynaceae	Carisseae	0	0.0229	0.0428	0	0.0526	0.2381
Gentianaceae	Enicostema verticillatum	0.0014	0.0008	0	0.1429	0.0526	0
Rubiaceae	Knoxieae	0.0007	0	0	0.1429	0	0
Rubiaceae	Oldenlandia corymbosa	0	0.0100	0	0	0.1053	0
Rubiaceae	Pentanisia	0.0102	0.0170	0.0064	0.5714	0.3158	0.0476
Apocynaceae	Rauvolfioideae	0	0.0011	0.0267	0	0.0526	0.0476
Rubiaceae	Rubiaceae	0.0013	0.0063	0.0048	0.1429	0.3158	0.2381
Rubiaceae	Rubioideae	0.0022	0.0139	0	0.5714	0.1579	0
Apocynaceae	Secamone filiformis	0	0	0.0078	0	0	0.0952
Rubiaceae	Thecorchus wauensis	0	0.0005	0	0	0.0526	0
Geraniaceae	Monsonia	0.0093	0.0114	0.0048	0.8571	0.4737	0.0476
Geraniaceae	Pelargonium	0	0	0.0010	0	0	0.0476
Acanthaceae	Acanthaceae	0	0	0	0	0	0
Acanthaceae	Acanthoideae	0.0019	0.0041	0.0056	0.4286	0.2632	0.0476
Lamiaceae	Ajuga	0	0.0053	0	0	0.0526	0
Acanthaceae	Blepharis integrifolia	0	0.0019	0	0	0.1053	0
Acanthaceae	Blepharis maderaspatensis	0	0.0167	0.0012	0	0.2632	0.0476
Acanthaceae	Crossandra	0.0049	0.0073	0	0.1429	0.1579	0
Orobanchaceae	Cycnium racemosum	0	0.0005	0	0	0.0526	0
Acanthaceae	Dicliptera magaliesbergensis	0	0.0169	0.0037	0	0.2105	0.3810
Acanthaceae	Dyschoriste radicans	0.0313	0.1062	0.0092	0.7143	0.6842	0.0952
Acanthaceae	Eranthemum tetragonum	0	0.0004	0	0	0.0526	0
Acanthaceae	Hypoestes	0.0116	0.0041	0.0038	0.1429	0.3158	0.4286
Oleaceae	Jasminum	0	0.0978	0.0272	0	0.1579	0.5238
Acanthaceae	Justicia	0	0	0.0007	0	0	0.0476
Acanthaceae	Justicia betonica	0.0160	0.0069	0.0023	0.2857	0.5263	0.3333
Acanthaceae	Justicia debilis	0	0.0023	0	0	0.2105	0
Acanthaceae	Justiciinae	0.0027	0.0067	0.0077	0.2857	0.5263	0.2857
Lamiaceae	Lamiaceae	0.0250	0.0261	0.0148	0.7143	0.5789	0.3810
Verbenaceae	Lantaneae	0.0131	0.0217	0.0104	0.7143	0.3158	0.7143
Lamiaceae	Leucadeae	0	0.0005	0	0	0.1579	0
Linderniaceae	Linderniaceae	0	0	0.0007	0	0	0.0476
Lamiaceae	Nepetoideae	0.0156	0.0085	0.0034	0.4286	0.2632	0.1905
Lamiaceae	Ocimeae	0	0.0074	0.0073	0	0.2105	0.2381
Lamiaceae	Ocimum	0	0	0.0004	0	0	0.0476
Orobanchaceae	Orobanchaceae	0	0.0029	0	0	0.0526	0

Pedaliaceae	Pedaliaceae	0.0038	0.0156	0	0.4286	0.0526	0
Lamiaceae	Plectranthus petiolaris	0	0.0037	0	0	0.1579	0
Lamiaceae	Plectranthus prostratus	0	0.0023	0.0003	0	0.0526	0.0476
Verbenaceae	Priva curtisiae	0.0025	0.0026	0	0.4286	0.2632	0
Acanthaceae	Ruellieae	0.0036	0.0430	0.0026	0.1429	0.3684	0.2381
Acanthaceae	Ruelliinae	0.0032	0.0195	0.0069	0.4286	0.3158	0.0476
Oleaceae	Schrebera	0	0	0.0070	0	0	0.0476
Acanthaceae	Strobilanthes	0	0.0005	0	0	0.1579	0
Acanthaceae	Thunbergia alata	0	0.0058	0.0078	0	0.1053	0.0952
Euphorbiaceae	Acalypha	0.0010	0.0122	0.1397	0.1429	0.2105	0.0952
Euphorbiaceae	Acalypheae	0	0	0	0	0	0
Euphorbiaceae	Acalyphoideae	0	0	0	0	0	0
Euphorbiaceae	Croton	0	0.0046	0.1667	0	0.0526	0.5714
Salicaceae	Dovyalis	0	0	0	0	0	0
Euphorbiaceae	Esula	0	0	0.0033	0	0	0.0476
Euphorbiaceae	Euphorbia	0	0.0071	0.0095	0	0.0526	0.0476
Euphorbiaceae	Euphorbia inaequilatera	0.0027	0.0117	0.0029	0.5714	0.5263	0.1905
Phyllanthaceae	Phyllanthus	0.0114	0.0129	0.0088	0.5714	0.3684	0.4286
Phyllanthaceae	Phyllanthus talbotii	0	0	0	0	0	0
Salicaceae	Salicaceae	0	0.0010	0.0421	0	0.0526	0.1429
Euphorbiaceae	Tragia urens	0	0	0	0	0	0
Malvaceae	Abutilon mauritianum	0.0240	0.0120	0.0085	0.1429	0.4211	0.2381
Malvaceae	Corchorus	0	0.0253	0	0	0.1053	0
Malvaceae	Grewia	0	0.0274	0.0239	0	0.5263	0.3333
Malvaceae	Grewia sp. Mada141	0.0144	0.0072	0.0220	0.2857	0.1579	0.4762
Malvaceae	Hermannia uhligii	0	0	0	0	0	0
Malvaceae	Hibiscus	0.0331	0.0146	0.0151	0.4286	0.4737	0.3333
Malvaceae	Kosteletzkya	0	0	0.0009	0	0	0.0476
Malvaceae	Malvaceae	0	0.0047	0	0	0.0526	0
Malvaceae	Malvoideae	0.0172	0.0684	0.0124	0.2857	0.4737	0.2857
Malvaceae	Melhania ovata	0	0.0302	0	0	0.1053	0
Malvaceae	Pachira quinata	0	0.0043	0	0	0.0526	0
Malvaceae	Pterospermum heterophyllum	0	0.0070	0.0157	0	0.2105	0.1905
Malvaceae	Sida sp. TRK-2015	0.0015	0.0046	0.0017	0.4286	0.4211	0.1905
Malvaceae	Sida tenuicarpa	0	0.0076	0.0051	0	0.2105	0.5238
Malvaceae	Waltheria indica	0	0.0032	0.0018	0	0.0526	0.0476
Lythraceae	Ammannia latifolia	0.0740	0	0	0.5714	0	0
Combretaceae	Terminalia	0	0	0	0	0	0
NA	fabids	0	0.0034	0.0010	0	0.1579	0.0476
Pinaceae	Cedrus	0	0.0018	0	0	0.0526	0
Pinaceae	Picea	0	0	0.1393	0	0	0.0476
Poaceae	Andropogoneae	0	0.0044	0.0025	0	0.0526	0.0476

Poaceae	Aristida	0.0009	0.0022	0.0009	0.4286	0.3684	0.2381
Poaceae	Aristideae	0	0	0	0	0	0
Poaceae	Arthraxon	0.0023	0	0	0.1429	0	0
Poaceae	BOP clade	0	0.0007	0	0	0.0526	0
Poaceae	Cenchrinae	0	0	0.0021	0	0	0.0952
Poaceae	Cenchrus	0.0121	0.0315	0.0028	0.5714	0.3158	0.1905
Poaceae	Chloris nutans	0	0.0028	0	0	0.0526	0
Cyperaceae	Cyperoideae	0	0.0008	0	0	0.0526	0
Cyperaceae	Cyperus clandestinus	0	0.0004	0	0	0.0526	0
Cyperaceae	Cyperus compressus	0.0010	0	0	0.1429	0	0
Cyperaceae	Cyperus cyperoides	0	0.0014	0	0	0.1053	0
Poaceae	Digitaria ischaemum	0	0.0053	0.0006	0	0.0526	0.0476
Poaceae	Ehrharta	0	0	0.0006	0	0	0.0476
Poaceae	Eleusininae	0	0.0005	0	0	0.0526	0
Poaceae	Enneapogon	0	0.0063	0.0011	0	0.0526	0.0476
Poaceae	Eragrostideae	0.0006	0	0	0.1429	0	0
Poaceae	Eragrostidinae	0.0186	0.0042	0.0022	0.8571	0.5789	0.2857
Poaceae	Eragrostis	0.0075	0	0	0.2857	0	0
Poaceae	Eriochloa	0	0.0025	0	0	0.1053	0
Poaceae	Garnotia acutigluma	0	0	0.0007	0	0	0.0476
Poaceae	Garnotia tenella	0	0	0	0	0	0
Poaceae	Heteropogon contortus	0.0051	0.0042	0.0017	0.7143	0.2632	0.1429
Poaceae	Hyperthelia dissoluta	0.0071	0.0023	0.0029	0.4286	0.1053	0.1905
Poaceae	PACMAD clade	0.1513	0.1187	0.0367	1.0000	0.7368	0.5714
Poaceae	Paniceae	0.0559	0.0183	0.0087	1.0000	0.6842	0.2381
Poaceae	Panicoideae	0.0012	0.0016	0.0073	0.4286	0.1053	0.0952
Poaceae	Poaceae	0.0177	0.0128	0.0041	0.5714	0.5789	0.5238
Poaceae	Poeae Chloroplast Group 1 (Aveneae type)	0	0	0.0016	0	0	0.0476
Poaceae	Sorghum	0	0	0	0	0	0
Poaceae	Sporobolus pyramidatus	0	0	0.0027	0	0	0.0476
Poaceae	Themeda	0.0143	0.0081	0.0033	1.0000	0.8421	0.4762
Poaceae	Urochloa	0.0016	0	0	0.1429	0	0
Pteridaceae	Pellaea	0	0.0005	0	0	0.0526	0
Jubulaceae	Nipponolejeunea pilifera	0	0	0	0	0	0
Menispermaceae	Menispermoideae	0	0.0055	0	0	0.0526	0
Rhamnaceae	Ampelozizyphus amazonicus	0	0	0	0	0	0
Ulmaceae	Chaetachme	0	0.0006	0	0	0.0526	0

Moraceae	Moraceae	0	0.0177	0.0069	0	0.1053	0.0476
Rhamnaceae	Rhamnus	0	0	0.0027	0	0	0.2381
Rosaceae	Rubus	0	0	0.0007	0	0	0.0476
Rhamnaceae	Scutia myrtina	0	0.0033	0.0255	0	0.0526	0.5238
Loranthaceae	Loranthaceae	0	0.0007	0.0003	0	0.1579	0.0476
Loranthaceae	Lysiana	0	0	0	0	0	0
Thesiaceae	Osyridicarpos schimperianus	0	0	0.0009	0	0	0.0476
Loranthaceae	Scurrula ferruginea	0	0.0474	0.0182	0	0.1579	0.1429
Rutaceae	Amyridoideae	0	0	0.0029	0	0	0.0952
Anacardiaceae	Anacardiaceae	0.0553	0.0062	0.0241	0.2857	0.1579	0.4286
Meliaceae	Azadirachta indica	0	0	0	0	0	0
Burseraceae	Burseraceae	0.0326	0.0273	0.0189	0.8571	0.3158	0.3333
Rutaceae	Harrisonia abyssinica	0	0	0	0	0	0
Rutaceae	Rutaceae	0	0	0.0004	0	0	0.0476
Sapindaceae	Sapindaceae	0.0316	0.0285	0.0084	0.1429	0.0526	0.1905
Meliaceae	Turraea mombassana	0	0	0.0039	0	0	0.0476
Crassulaceae	Crassula sieberiana	0	0.0024	0	0	0.2632	0
Crassulaceae	Crassula volkensii	0	0.0039	0	0	0.0526	0
Crassulaceae	Crassulaceae	0	0.0067	0	0	0.1053	0
Convolvulaceae	Convolvulaceae	0.0025	0.0025	0	0.2857	0.2105	0
Convolvulaceae	Convolvulus sabatius subsp. mauritanicus	0	0.0015	0	0	0.0526	0
Convolvulaceae	Cresseae	0	0.0026	0	0	0.1053	0
Convolvulaceae	Dichondreae	0	0.0015	0.0034	0	0.0526	0.0476
Convolvulaceae	Ipomoea cairica	0	0	0	0	0	0
Convolvulaceae	Ipomoeeae	0.0038	0.0126	0.0029	0.4286	0.5263	0.2857
Solanaceae	Solanaceae	0	0.0758	0	0	0.0526	0
Solanaceae	Solanoideae	0	0.0145	0.0047	0	0.4211	0.3333
Solanaceae	Solanum	0.0093	0.0116	0.0111	0.4286	0.6316	0.6667
Solanaceae	Solanum parcistrigosum	0	0.0021	0.0007	0	0.0526	0.0476
Vitaceae	Cissus	0	0.0007	0	0	0.0526	0
Vitaceae	Cissus oliveri	0	0	0	0	0	0
Vitaceae	Cyphostemma	0.0005	0.0008	0.0349	0.1429	0.1053	0.0952
Vitaceae	Vitaceae	0	0.0267	0.0101	0	0.1053	0.1905
Zygophyllaceae	Tribulus terrestris	0	0.0016	0	0	0.1053	0.0

Table S2: Characterization of all plant MOTUs by Richard Iyamuya (TAWIRI) in to grass, herbs, shrubs or trees. Diet items that can be more in more than one class, or have more than one growth form are mentioned in the comment section.

Order	Family	Genus	Taxon/ MOTU	Classification	Alt. class.
Apiales	Araliaceae	Cussonia	Cussonia holstii	Tree	
Asparagales	Amaryllidaceae	Allium	Allium sativum	Herb	
Asparagales	Asparagaceae	Asparagus	Asparagus	Herb	
Asparagales	Asparagaceae	NA	Agavoideae	Herb	Shruby herb
Asparagales	Hypoxidaceae	Hypoxis	Hypoxis	Herb	
Asparagales	Xanthorrhoeaceae	Aloe	Aloe	Shrub	
Asparagales	Xanthorrhoeaceae	Aloe	Aloe cameronii	Shrub	
Asterales	Asteraceae	Acanthospermum	Acanthospermum australe	Herb	
Asterales	Asteraceae	Emilia	Emilia discifolia	Herb	
Asterales	Asteraceae	Helichrysum	Helichrysum glumaceum	Herb	
Asterales	Asteraceae	Helichrysum	Helichrysum sp. TRK-2015	Herb	
Asterales	Asteraceae	NA	Asteraceae	Herb\ Shrubs	Tree
Asterales	Asteraceae	NA	Asteroideae	Herb	Shruby herb
Asterales	Asteraceae	NA	Cichorieae	Herb	
Asterales	Asteraceae	NA	Heliantheae alliance	Herb	Shruby herb
Asterales	Asteraceae	Tagetes	Tagetes	Herb	
Asterales	Asteraceae	Tripteris	Tripteris vaillantii	Herb	
Asterales	NA	NA	Asterales	Herb\ Shrubs	Tree
Boraginales	Boraginaceae	Cystostemon	Cystostemon hispidus	Herb	
Boraginales	Cordiaceae	Cordia	Cordia	Shrub	Tree
Boraginales	Ehretiaceae	NA	Ehretiaceae	Tree	
Boraginales	Heliotropiaceae	NA	Heliotropiaceae	Shrub	Tree
Brassicales	Brassicaceae	Lepidium	Lepidium	Herb	
Brassicales	Brassicaceae	NA	Brassicaceae	Herb	
Brassicales	Brassicaceae	NA	Lepidieae	Herb	Shruby herb
Brassicales	Capparaceae	Boscia	Boscia madagascariensis	Shrub	Tree
Brassicales	Capparaceae	Cadaba	Cadaba	Shrub	
Brassicales	Capparaceae	Capparis	Capparis tomentosa	Shrub	
Brassicales	Capparaceae	Maerua	Maerua angolensis	Shrub	
Brassicales	Capparaceae	Maerua	Maerua triphylla	Shrub	
Brassicales	Capparaceae	NA	Capparaceae	Shrub	
Brassicales	Salvadoraceae	Salvadora	Salvadora	Shrub	

Caryophyllales	Aizoaceae	Zaleya	Zaleya	Herb	
Caryophyllales	Amaranthaceae	Achyranthes	Achyranthes aspera	Herb	Shruby herb
Caryophyllales	Amaranthaceae	Achyropsis	Achyropsis avicularis	Shrub	
Caryophyllales	Amaranthaceae	Aerva	Aerva lanata	Herb	
Caryophyllales	Amaranthaceae	Alternanthera	Alternanthera pungens	Herb	
Caryophyllales	Amaranthaceae	Amaranthus	Amaranthus	Herb	
Caryophyllales	Amaranthaceae	Bassia	Bassia scoparia	Herb	Shruby herb
Caryophyllales	Amaranthaceae	Centrostachys	Centrostachys aquatica	Herb	Shruby herb
Caryophyllales	Amaranthaceae	Chenopodiastrum	Chenopodiastrum murale	Herb	Shruby herb
Caryophyllales	Amaranthaceae	Gomphrena	Gomphrena	Herb	Shruby herb
Caryophyllales	Amaranthaceae	Guilleminea	Guilleminea	Herb	
Caryophyllales	Amaranthaceae	NA	Amaranthaceae	Herb	
Caryophyllales	Amaranthaceae	NA	Chenopodioideae	Herb	Shruby herb
Caryophyllales	Amaranthaceae	Psilotrichum	Psilotrichum elliotii	Herb	Shruby herb
Caryophyllales	Caryophyllaceae	Pollichia	Pollichia campestris	Shrub	
Caryophyllales	Nyctaginaceae	Commicarpus	Commicarpus pedunculosus	Herb	
Caryophyllales	Plumbaginaceae	Plumbago	Plumbago	Herb	
Caryophyllales	Polygonaceae	NA	Polygonoideae	Herb	
Caryophyllales	Polygonaceae	Oxygonum	Oxygonum	Herb	
Caryophyllales	Polygonaceae	Rumex	Rumex	Herb	
Celastrales	Celastraceae	NA	Celastraceae	Herb	Shruby herb\ Tree
Celastrales	Celastraceae	Simicratea	Simicratea sp. Luke & Luke 4747	Shrub	
Commelinales	Commelinaceae	Commelina	Commelina	Herb	
Commelinales	Commelinaceae	Commelina	Commelina benghalensis	Herb	
Commelinales	Commelinaceae	Commelina	Commelina erecta	Herb	
Cornales	Grubbiaceae	Grubbia	Grubbia rosmarinifolia	Shrub	
Cornales	NA	NA	Cornales	Tree	shrub
Cucurbitales	Cucurbitaceae	Momordica	Momordica	Herb	Climber herb
Cucurbitales	Cucurbitaceae	NA	Cucurbitaceae	Herb	
Cucurbitales	Cucurbitaceae	Sicyos	Sicyos	Herb	Climber herb
Cupressales	Cupressaceae	Chamaecyparis	Chamaecyparis lawsoniana	Tree	
Cupressales	Cupressaceae	NA	Cupressaceae	Tree	
Dipsacales	Caprifoliaceae	Lonicera	Lonicera	Shrub	Climber herb

Ericales	Ebenaceae	NA	Ebenaceae	Tree	shrub
Ericales	Primulaceae	Anagallis	Anagallis	Herb	
Fabales	Fabaceae	Albizia	Albizia brevifolia	Tree	
Fabales	Fabaceae	Crotalaria	Crotalaria	Shrub	
Fabales	Fabaceae	Cyamopsis	Cyamopsis tetragonoloba	Herb	
Fabales	Fabaceae	Dalbergia	Dalbergia	Tree	
Fabales	Fabaceae	Dichrostachys	Dichrostachys	Shrub	
Fabales	Fabaceae	Dichrostachys	Dichrostachys cinerea	Shrub	
Fabales	Fabaceae	Dichrostachys	Dichrostachys cinerea subsp. africana	Shrub	
Fabales	Fabaceae	Dichrostachys	Dichrostachys spicata	Shrub	
Fabales	Fabaceae	Eriosema	Eriosema	Herb	
Fabales	Fabaceae	Glycine	Soja	Shrub	
Fabales	Fabaceae	Glycyrrhiza	Glycyrrhiza	Herb	
Fabales	Fabaceae	Indigofera	Indigofera hilaris	Herb	Shruby herb
Fabales	Fabaceae	Indigofera	Indigofera sp. TRK-2015	Herb	Shruby herb
Fabales	Fabaceae	Leucaena	Leucaena	Shrub	Tree
Fabales	Fabaceae	Macrotyloma	Macrotyloma uniflorum	herb	Climber herb
Fabales	Fabaceae	Medicago	Medicago	herb	
Fabales	Fabaceae	Microcharis	Microcharis galpinii	herb	
Fabales	Fabaceae	NA	Acacieae	Tree	Shrubs
Fabales	Fabaceae	NA	Caesalpinieae	Tree	
Fabales	Fabaceae	NA	Dalbergieae	Tree	Shrubs
Fabales	Fabaceae	NA	Desmodieae	herb	Shrubs
Fabales	Fabaceae	NA	Fabaceae	Tree/ Shrubs	Herbs
Fabales	Fabaceae	NA	Indigofereae	herb	Shrubs
Fabales	Fabaceae	NA	Ingeae	Tree	Shrubs
Fabales	Fabaceae	NA	Mimosoideae	Tree	Shrubs
Fabales	Fabaceae	NA	Papilionoideae	Tree	Shrubs
Fabales	Fabaceae	NA	Phaseoleae	Herb	Climber herb
Fabales	Fabaceae	Neonotonia	Neonotonia wightii	Herb	Climber herb
Fabales	Fabaceae	Phaseolus	Phaseolus	Herb	Climber herb
Fabales	Fabaceae	Philenoptera	Philenoptera cyanescens	Tree	Shrubs
Fabales	Fabaceae	Pithecellobium	Pithecellobium sp. DS14533_JM1598	Tree	Shrubs
Fabales	Fabaceae	Senegalia	Senegalia	Tree	Shrubs
Fabales	Fabaceae	Senegalia	Senegalia modesta	Tree	Shrubs
Fabales	Fabaceae	Senna	Senna gardneri	Tree	Shrubs

Fabales	Fabaceae	Vachellia	Vachellia	Tree	Shrubs
Fabales	Fabaceae	Vigna	Vigna	Herb	Climber herb
Fabales	Fabaceae	Vigna	Vigna marina	Herb	Climber herb
Fabales	Fabaceae	Vigna	Vigna vexillata	Herb	Climber herb
Fabales	Fabaceae	Zornia	Zornia	Herb	Shruby herb
Fabales	NA	NA	Fabales	Herb	Shrubs, trees
Fabales	Polygalaceae	Polygala	Polygala	Shrub	Shruby herb
Fagales	Fagaceae	NA	Fagaceae	Herb	Shrubs
Gentianales	Apocynaceae	NA	Apocynaceae	Shrub	Shruby herb
Gentianales	Apocynaceae	NA	Asclepiadoideae	Herb	Shruby herb
Gentianales	Apocynaceae	NA	Carisseae	Shrub	Tree
Gentianales	Apocynaceae	NA	Rauvolfioideae	Herb	Shrubs
Gentianales	Apocynaceae	Secamone	Secamone filiformis	Shrub	Shruby herb
Gentianales	Gentianaceae	Enicostema	Enicostema verticillatum	Herb	Shruby herb
Gentianales	Rubiaceae	NA	Knoxieae	Shrub	Shruby herb
Gentianales	Rubiaceae	NA	Rubiaceae	Herb	Shruby herb
Gentianales	Rubiaceae	NA	Rubioideae	Shrub	Shruby herb
Gentianales	Rubiaceae	Oldenlandia	Oldenlandia corymbosa	Herb	Shruby herb
Gentianales	Rubiaceae	Pentanisia	Pentanisia	Herb	Shruby herb
Gentianales	Rubiaceae	Thecorchus	Thecorchus wauensis	Herb	Shruby herb
Geraniales	Geraniaceae	Monsonia	Monsonia	Herb	Shruby herb
Geraniales	Geraniaceae	Pelargonium	Pelargonium	Herb	Shruby herb
Lamiales	Acanthaceae	Blepharis	Blepharis integrifolia	Herb	Shruby herb
Lamiales	Acanthaceae	Blepharis	Blepharis maderaspatensis	Herb	Shruby herb
Lamiales	Acanthaceae	Crossandra	Crossandra	Herb	Shruby herb
Lamiales	Acanthaceae	Dicliptera	Dicliptera magaliesbergensis	Herb	Shruby herb
Lamiales	Acanthaceae	Dyschoriste	Dyschoriste radicans	Herb	Shruby herb
Lamiales	Acanthaceae	Eranthemum	Eranthemum tetragonum	Herb	Shruby herb
Lamiales	Acanthaceae	Hypoestes	Hypoestes	Herb	Shruby herb

Lamiales	Acanthaceae	Justicia	Justicia	Herb	Shruby herb
Lamiales	Acanthaceae	Justicia	Justicia betonica	Herb	Shruby herb
Lamiales	Acanthaceae	Justicia	Justicia debilis	Herb	Shruby herb
Lamiales	Acanthaceae	NA	Acanthaceae	Herb	Shruby herb
Lamiales	Acanthaceae	NA	Acanthoideae	Herb	Shruby herb
Lamiales	Acanthaceae	NA	Justiciinae	Herb	Shruby herb
Lamiales	Acanthaceae	NA	Ruellieae	Herb	Shruby herb
Lamiales	Acanthaceae	NA	Ruelliinae	Herb	Shruby herb
Lamiales	Acanthaceae	Strobilanthes	Strobilanthes	Shrub	Shruby herb
Lamiales	Acanthaceae	Thunbergia	Thunbergia alata	Herb	Shruby herb
Lamiales	Lamiaceae	Ajuga	Ajuga	Herb	Shruby herb
Lamiales	Lamiaceae	NA	Lamiaceae	Herb	Shruby herb
Lamiales	Lamiaceae	NA	Leucadeae	Shrub	Shruby herb
Lamiales	Lamiaceae	NA	Nepetoideae	Herb	Shruby herb
Lamiales	Lamiaceae	NA	Ocimeae	Herb	Shruby herb
Lamiales	Lamiaceae	Ocimum	Ocimum	Herb	Shruby herb
Lamiales	Lamiaceae	Plectranthus	Plectranthus petiolaris	Shrub	Shruby herb
Lamiales	Lamiaceae	Plectranthus	Plectranthus prostratus	Shrub	Shruby herb
Lamiales	Linderniaceae	NA	Linderniaceae	Herb	Climber herb
Lamiales	Oleaceae	Jasminum	Jasminum	Shrub	Shruby herb
Lamiales	Oleaceae	Schrebera	Schrebera	Tree	Shrubs
Lamiales	Orobanchaceae	Cycnium	Cycnium racemosum	Herb	Shruby herb
Lamiales	Orobanchaceae	NA	Orobanchaceae	Herb	Shruby herb
Lamiales	Pedaliaceae	NA	Pedaliaceae	Herb	Shruby herb
Lamiales	Verbenaceae	NA	Lantaneae	Shrub	
Lamiales	Verbenaceae	Priva	Priva curtisiae	Shrub	
Malpighiales	Euphorbiaceae	Acalypha	Acalypha	Herb	Shruby herb
Malpighiales	Euphorbiaceae	Croton	Croton	Shrub	Tree
Malpighiales	Euphorbiaceae	Euphorbia	Esula	Herb	Shruby herb
Malpighiales	Euphorbiaceae	Euphorbia	Euphorbia	Shrub	

Malpighiales	Euphorbiaceae	Euphorbia	Euphorbia inaequilatera	Herb	Shruby herb
Malpighiales	Euphorbiaceae	NA	Acalypheae	Herb	Shruby herb
Malpighiales	Euphorbiaceae	NA	Acalyphoideae	Herb	Shrubs, trees
Malpighiales	Euphorbiaceae	Tragia	Tragia urens	Herb	Shrubs, trees
Malpighiales	Phyllanthaceae	Phyllanthus	Phyllanthus	Herb	Shruby herb
Malpighiales	Phyllanthaceae	Phyllanthus	Phyllanthus talbotii	Herb	Shruby herb
Malpighiales	Salicaceae	Dovyalis	Dovyalis	Tree	
Malpighiales	Salicaceae	NA	Salicaceae	Tree	Shrubs
Malvales	Malvaceae	Abutilon	Abutilon mauritianum	Shrub	
Malvales	Malvaceae	Corchorus	Corchorus	Herb	Shruby herb
Malvales	Malvaceae	Grewia	Grewia	Shrub	
Malvales	Malvaceae	Grewia	Grewia sp. Mada141	Shrub	
Malvales	Malvaceae	Hermannia	Hermannia uhligii	Herb	
Malvales	Malvaceae	Hibiscus	Hibiscus	Shrub	
Malvales	Malvaceae	Kosteletzkya	Kosteletzkya	Herb	Shruby herb
Malvales	Malvaceae	Melhania	Melhania ovata	Shrub	
Malvales	Malvaceae	NA	Malvaceae	Shrub	
Malvales	Malvaceae	NA	Malvoideae	Shrub	
Malvales	Malvaceae	Pachira	Pachira quinata	Tree	
Malvales	Malvaceae	Pterospermum	Pterospermum heterophyllum	Tree	
Malvales	Malvaceae	Sida	Sida sp. TRK-2015	Shrub	
Malvales	Malvaceae	Sida	Sida tenuicarpa	Shrub	
Malvales	Malvaceae	Waltheria	Waltheria indica	Shrub	
Myrtales	Combretaceae	Terminalia	Terminalia	Tree	Shrubs
Myrtales	Lythraceae	Ammannia	Ammannia latifolia	Herb	Shruby herb
NA	NA	NA	fabids	Shrub	
Pinales	Pinaceae	Cedrus	Cedrus	Tree	Shrubs
Pinales	Pinaceae	Picea	Picea	Tree	Shrubs
Poales	Cyperaceae	Cyperus	Cyperus clandestinus	Herb	Shruby herb
Poales	Cyperaceae	Cyperus	Cyperus compressus	Herb	Shruby herb
Poales	Cyperaceae	Cyperus	Cyperus cyperoides	Herb	Shruby herb
Poales	Cyperaceae	NA	Cyperoideae	Herb	Shruby herb
Poales	Poaceae	Aristida	Aristida	Grass	
Poales	Poaceae	Arthraxon	Arthraxon	Grass	
Poales	Poaceae	Cenchrus	Cenchrus	Grass	
Poales	Poaceae	Chloris	Chloris nutans	Grass	

Poales	Poaceae	Digitaria	Digitaria ischaemum	Grass	
Poales	Poaceae	Ehrharta	Ehrharta	Grass	
Poales	Poaceae	Enneapogon	Enneapogon	Grass	
Poales	Poaceae	Eragrostis	Eragrostis	Grass	
Poales	Poaceae	Eriochloa	Eriochloa	Grass	
Poales	Poaceae	Garnotia	Garnotia acutigluma	Grass	
Poales	Poaceae	Garnotia	Garnotia tenella	Grass	
Poales	Poaceae	Heteropogon	Heteropogon contortus	Grass	
Poales	Poaceae	Hyperthelia	Hyperthelia dissoluta	Grass	
Poales	Poaceae	NA	Andropogoneae	Grass	
Poales	Poaceae	NA	Aristideae	Grass	
Poales	Poaceae	NA	BOP clade	Grass	
Poales	Poaceae	NA	Cenchrinae	Grass	
Poales	Poaceae	NA	Eleusininae	Grass	
Poales	Poaceae	NA	Eragrostideae	Grass	
Poales	Poaceae	NA	Eragrostidinae	Grass	
Poales	Poaceae	NA	PACMAD clade	Grass	
Poales	Poaceae	NA	Paniceae	Grass	
Poales	Poaceae	NA	Panicoideae	Grass	
Poales	Poaceae	NA	Poaceae	Grass	
Poales	Poaceae	NA	Poeae Chloroplast Group 1 (Aveneae type)	Grass	
Poales	Poaceae	Sorghum	Sorghum	Grass	
Poales	Poaceae	Sporobolus	Sporobolus pyramidatus	Grass	
Poales	Poaceae	Themeda	Themeda	Grass	
Poales	Poaceae	Urochloa	Urochloa	Grass	
Polypodiales	Pteridaceae	Pellaea	Pellaea	Herb	
Porellales	Jubulaceae	Nipponolejeunea	Nipponolejeunea pilifera	Herb	
Ranunculales	Menispermaceae	NA	Menispermoideae	Shrub	Tree
Rosales	Moraceae	NA	Moraceae	trees	Shrubs
Rosales	Rhamnaceae	Ampelozizyphus	Ampelozizyphus amazonicus	Shrub	Tree
Rosales	Rhamnaceae	Rhamnus	Rhamnus	Shrub	Tree
Rosales	Rhamnaceae	Scutia	Scutia myrtina	Shrub	Tree
Rosales	Rosaceae	Rubus	Rubus	Shrub	
Rosales	Ulmaceae	Chaetachme	Chaetachme	tree	Shrubs
Santalales	Loranthaceae	Lysiana	Lysiana	Shrub	
Santalales	Loranthaceae	NA	Loranthaceae	Tree	Shrubs
Santalales	Loranthaceae	Scurrula	Scurrula ferruginea	Tree	Shrubs
Santalales	Thesiaceae	Osyridicarpos	Osyridicarpos schimperianus	Shrub	Tree
Sapindales	Anacardiaceae	NA	Anacardiaceae	Tree	
Sapindales	Burseraceae	NA	Burseraceae	Tree	Shrubs

Sapindales	Meliaceae	Azadirachta	Azadirachta indica	Tree	
Sapindales	Meliaceae	Turraea	Turraea mombassana	Tree	
Sapindales	Rutaceae	Harrisonia	Harrisonia abyssinica	Shrub	
Sapindales	Rutaceae	NA	Amyridoideae	Shrub	Tree
Sapindales	Rutaceae	NA	Rutaceae	Shrub	
Sapindales	Sapindaceae	NA	Sapindaceae	Tree	
Saxifragales	Crassulaceae	Crassula	Crassula sieberiana	Herb	Shruby herb
Saxifragales	Crassulaceae	Crassula	Crassula volkensii	Herb	Shruby herb
Saxifragales	Crassulaceae	NA	Crassulaceae	Herb	Shruby herb
Solanales	Convolvulaceae	Convolvulus	Convolvulus sabatius subsp. mauritanicus	Herb	
Solanales	Convolvulaceae	Ipomoea	Ipomoea cairica	Herb	Climber herb
Solanales	Convolvulaceae	NA	Convolvulaceae	Herb	Shruby herb
Solanales	Convolvulaceae	NA	Cresseae	Shrub	
Solanales	Convolvulaceae	NA	Dichondreae	Herb	Shruby herb
Solanales	Convolvulaceae	NA	Ipomoeeae	Shrub	
Solanales	Solanaceae	NA	Solanaceae	Shrub	
Solanales	Solanaceae	NA	Solanoideae	Shrub	
Solanales	Solanaceae	Solanum	Solanum	Shrub	
Solanales	Solanaceae	Solanum	Solanum parcistrigosum	Herb	
Vitales	Vitaceae	Cissus	Cissus	Herb	
Vitales	Vitaceae	Cissus	Cissus oliveri	Herb	
Vitales	Vitaceae	Cyphostemma	Cyphostemma	Herb	
Vitales	Vitaceae	NA	Vitaceae	Shrub	
Zygophyllales	Zygophyllaceae	Tribulus	Tribulus terrestris	Herb	