

A Spatial Analysis to Identify Viral Transmission Risk to Humans from *Papio anubis* and *Papio Hamadryas* utilizing Species Distribution Modeling and Multi-Criteria Analysis

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Introduction

There are many viruses around the world that have contributed to pandemics amongst humans. The most common viruses that have led to global pandemics were carried and transmitted from animals. This is a major theme of 2020, where communities across the globe have suffered due to a novel coronavirus pandemic that was most likely caused by a zoonotic shift. The global pandemic has generated more interest in viruses carried by animals. Non-human primates are one of the major taxonomic orders that are considered when studying viral transmission risk between animals and humans. Of the non-human primates, the *Papio* genus of baboons is of major interest among the biological community due to species hybridization. There are six major species of *Papio* baboons that span across the continent of Africa and Arabia. *Papio* baboons are most known for their ecological flexibility and large geographical ranges (Winder, 2014). Additionally, *Papio* baboons are of interest because of their capability to become infected and transmit deadly viruses. There are four of interest, cercopithecine herpesvirus 16 (HVP2), primate t-lymphotropic virus 1 (PTLV-1), yaba monkey tumor virus (YMTA), and yellow fever virus.

The primary objective of this analysis is to assess the range and suitability of two of the *Papio* baboon species, the hamadryas baboon and the olive baboon. In addition, this study will investigate the human population in Sub-Saharan-Africa that may be at risk for coming into contact with baboons. With an increased likelihood of human-baboon contact there is a greater chance of a zoonotic shift to occur.

The hamadryas baboon (*Papio hamadryas*, also called sacred or Arabian baboon) is found in the shrublands, grasslands, and rocky areas of northeastern Africa and the Arabian Peninsula. They are usually found at elevations greater than 1,500 meters and are dependent on water sources, which may limit their range in this typically arid region. The species is abundant and of least concern according to the IUCN Red List Category and Criteria. In fact, the species currently has an increasing population trend due to the loss of predators and small scale agriculture (Gippoliti). Although the species is currently abundant, its primary threats include local agricultural expansion and hunting and trapping for pelts.

The olive baboon (*Papio anubis*) is found in the forest, savanna, and grasslands of central Africa, ranging as far west as Guinea and Sierra Leone to as far east as Ethiopia and Somalia.

Apparent by their large range, the olive baboon habitat includes fragmented forest, rainforest, and even rocky hills. They are found in regions with elevation up to 2,500 meters (Wallis). This species is also abundant and of least concern to the IUCN Red List Category and Criteria. The population is currently stable, although threats include non-timber crops, livestock farming, and hunting and trapping (Wallis).

This study uses species distribution modeling and multi-criteria evaluation to analyze the risk of viral transmission from *Papio hamadryas* and *Papio anubis* to human populations. From this analysis we reveal regions at greatest risk of disease transmission, and provide a future scenario of risk in 2070. The results of this study reveal that the *Papio anubis* and *Papio hamadryas* will have an increase in habitat suitability over the next century, most notably in regions lying in Sub-Saharan Africa. The increased habitat suitability, when combined with the results of the MCE analysis, indicate that expansion of risk for viral transmission within the continent.

Literature Review

Species Distribution Modeling

Species distribution models (SDMs) are used across multiple disciplines as a way to incorporate spatial analysis. Baboons are a popular research subject because they are carriers of disease, are subject species hybridization, and are often in close contact with humans. SDMs have been used by both Almeida (2019) and Winder (2014) to analyze the movements of *Papio* baboons. de Almeida (2019) uses *Papio* presence data along with environmental suitability layers to map yellow fever risk. de Almeida (2019) also uses mosquito distribution data and applies the maxent algorithm to define risk. Hayes & Piaggio (2015) also applied SDM to model virus risk in the context of rabies and the common vampire bat in Texas. In their research, they applied current and future climate scenarios for a better assessment of potential impacts of climate change on the distribution of rabies.

Viral Transmission from non-human primates to humans

As humans change landscapes, humans and non-human primates are put into closer and more frequent contact. This increased proximity increases the risk of disease transmission. Chapman, Gissespie, & Goldberg (2005) explain that this risk increases as anthropogenic climate change occurs. Global climate warming and the subsequent effects on weather, affects the

infection of non-human primates by creating more suitable conditions for host-vector interactions (Chapman et al., 2005). *Papio anubis* and *Papio hamadryas* species are both carriers and/or susceptible to three main viruses. These viruses are cercopithecine herpesvirus 16 (HVP2), primate t-lymphotropic virus 1 (PTLV-1), and yaba monkey tumor virus (YMTA).

Cercopithecine herpesvirus 16 (HVP2)

HVP2 is common among wild and captive baboons and is associated with genital infections of adult baboons, increased stillbirths, and hydrocephalus (Black & Eberle, 1997). Spread is common through oral transmission from mother to child (Elmore & Eberle, 2008). HVP2 is very closely related to *Cercopithecine herpesvirus 1* (BV) in macaques (Brush et al., 2014; Elmore & Eberle, 2008). BV is fatal to humans and is transmitted through bites and scratches (Brush et al., 2014). Due to this similarity, most research on HVP2 is related to testing for BV (Black & Eberle, 1997; Elmore & Eberle, 2008; Brush et al., 2014). Currently, there are no reported transmissions to humans of the HVP2 virus (Elmore & Eberle 2008).

Primate t-lymphotrophic virus 1 (PTLV-1)

PTLV-1 is also referred to as Human T-cell Leukemia Virus-1 (HTLV-1) and Simian T-Lymphotropic Virus (STLV-1), depending on the infected species (Saksena et al., 2003). *Papio anubis* is one of four species that had a high seropositivity (having blood serum test positive for a given pathogen) to STLV-1 in Central and Western Africa. The virus is transmitted from non-human primates to humans through bite (Alais et al., 2018). The infected saliva of the primate then infects the blood of the recipient and causes leukemia and myelopathy (Goubao et al., 1994). The virus is non-pathogenic in humans.

Yaba Monkey Tumor Virus (YMTA)

YMTA is a species of yatapoxvirus genus and is closely related to the tanapox. This virus only affects primates, including humans. It can be transmitted by direct contact of the skin or by transmission from mosquitoes. In general, the only symptoms of the virus will be the formation of tumors. Natural infection with YMTA has been reported only once, in Yaba, Nigeria, in 1957. Other encounters with this tumor virus have primarily been related to experimental infection in monkeys and accidental or experimental infections in human beings. (Brunetti et al., 2003; Cho and Wenner, 1973). Infection with the virus is endemic in African and Malaysian monkeys, but does not occur or is very rare in Indian rhesus and New World monkeys (Downie, 1973).

Although there have not been many known cases of viral transmission between humans and the baboon species of this study, there is a plethora of research regarding the transmission of parasites between humans and the *Papio* species. The *Papio hamadryas* species is most studied in this subject. According to (Alqumber, 2014) and (Larbi et al. 2020), there have been an increasing number of cases of *Papio hamadryas* spreading gastrointestinal parasites amongst communities in Ghana and southern Saudi Arabia. The distribution of parasites is likely due to the increased contact between humans and the baboon species. The majority of fecal samples from humans that were tested for the parasites in (Alqumber, 2014) found that the city peripheries were most at risk in comparison to city centers. This risk is precisely why species observation reporting is important, with more observations of a species, they can be better modeled to reflect their current habits.

This analysis is novel because it combines Species Distribution Modeling and Multi-Criteria Evaluation (MCE) in order to determine which spatial regions presented the greatest risk of disease transmission to humans in present and future conditions. Humans and baboons in central and east Africa often live in the same territory, which increases the risk for humans to contract diseases carried by baboon colonies. Modeling the potential interactions to yield risk can provide local communities with a critical understanding of both species range and the impact olive and sacred baboons can have on the health of the region.

Data & Methods

Species Distribution Modeling

The species distribution models (SDM) for *Papio anubis* and *Papio hamadryas* were generated using R and were adapted from [this tutorial](#). Species observation data was gathered from the Global Biodiversity Information Facility (GBIF) for both *Papio anubis* and *Papio hamadryas*. Species points were clipped to the species range to remove extraneous observation points. Bioclimatic data was extracted from Worldclim and landcover and elevation datasets were downloaded from ASTER, using the species observation points as reference. Suitability maps were created using current bioclimatic variables and using RCP 8.5 variables. Bioclimatic variables include: annual mean temperature, max temperature of warmest month, minimum temperature of coldest month, temperature annual range, mean temperature - wettest quarter,

mean temperature - driest quarter, annual precipitation, precipitation - wettest quarter, precipitation - driest quarter, precipitation - warmest quarter, precipitation - coldest quarter. The other variables were also added, including the Digital Elevation Model (DEM), and EVI (Enhanced Vegetation Index). Variables were cropped to model extent and resampled to the model environment. Training data was created using 80% of the species observations, leaving the other 20% as testing data. The MaxEnt function is then applied as a predictive model to determine possible other suitable locations.

Risk

To determine risk of virus spread, an accessibility dataset and a population density dataset were used. The accessibility data was created by Nelson et al. 2019 in “A Suite of Global Accessibility Indicators”. To prepare the data for analysis in this project, the product was resampled to eliminate “no data” and clipped to the study area. The population density data was downloaded from the Center for International Earth Science Information Network. For this project, the 2020 1 km resolution data was used. This dataset was also clipped to the study area. Lastly, human impact data was included in the risk analysis, this is a crowdsourced dataset containing millions of point data indicating the degree to which the landscape modified by humans visible from satellite images (Liu, H et al. 2020; Fritz, S et al. 2016), which can be regarded as the degree of human impact on a certain landscape. The data was interpolated using the Inverse Distance Weighted interpolation method and clipped to our study area, the original data is expressed in percentage, ranging from 0 to 100, it was rescaled to a value range from 0 to 1, matching the value range of other risk factors. The data was created by Fritz et al. 2016 in “A Global Dataset of Crowdsourced Land Cover and Land Use Reference Data”.

The risk data layers, along with the SDM outputs for *Papio anubis* and *Papio hamadryas* were then utilized in a Multi-Criteria Evaluation (MCE) in order to determine which spatial regions presented the greatest risk of disease transmission to humans. The MCE analysis was conducted through TerrSet’s MCE module, utilizing both the Ordered Weighted Average (OWA) and Weighted Linear Combination (WLC) techniques. In preparation for this analysis, the three risk variables were processed through the FUZZY module to rescale the values from 1 - 0. Then, the rescaled images, along with the SDM outputs were assigned weights using the WEIGHT module. This involved creating a matrix of weights with values from 1/9 to 9 ,

comparing the relative importance of each variable to all other variables. The module then generated weights for each variable to be used when conducting the MCE.

When conducting the MCE using the WLC method, the five variables were included as weighted factors. We did not include any constraints because each variable layer was already clipped to the study area. This technique utilized the weights of each factor to determine how they tradeoff with each other, with higher weights having more influence on the result. The OWA method also included each variable as a weighted factor, however in this technique the ordered weights are also used. The ordered weights are the same values as the factor weights, however these values are assigned to the rank order position of factor values for a specific location (pixel), with the lowest factor weight having the first order weight.

Results

*Species Distribution Model: Predicted Habitat Suitability , *Papio anubis**

The species distribution of *Papio anubis* is primarily concentrated in both eastern and western Africa, featuring a distinct separation between these clusters (Figure 1a). Current and 2070 temperature variables demonstrate the climate of *Papio anubis* in which temperature varies from roughly 20 to 35 degrees Celsius (Figure 2a, 2b). Additional influences on *Papio anubis* suitability includes elevation and vegetation based on the DEM and EVI homogeneity variables (Figure 2c, 2d). The species is primarily located in elevation ranging from sea level to 2000 m. Additionally, EVI illustrates the presence of vegetation in these species observations. These factors, in addition to the other bioclimatic and environmental variables, project higher suitability for *Papio anubis* in 2070 compared to current suitability for the species (Figure 3). Future suitability shows higher suitability overall, primarily in western Africa, however there is a decrease in suitability in parts of eastern Africa.

The most influential variable in MaxEnt is annual precipitation contributing 47.1% to the model with 8.8 permutation importance (Figure 6). Additional variables influencing the model include precipitation of the coldest quarter, annual mean temperature, and maximum temperature of the warmest month with 13.1%, 7.3%, and 6.6% contribution and 3.2, 8.1, and 2.6 permutation importance respectively. The response of *Papio anubis* to the bioclimatic variables, elevation and EVI is also depicted alongside variable contribution to the model. The response of

Papio anubis to annual precipitation demonstrates the greatest response at lower values, meanwhile annual mean temperature has a strong response at higher values. The response of *Papio anubis* to other variables includes a concentration of the species at low elevation, meanwhile the EVI homogeneity variable shows a response just above 0.

The species distribution model for *Papio anubis* performed with an AUC score of 0.969. Suitability change for *Papio anubis* observations features increasing suitability by 53.79%. With 2,402 observations of the species in Africa, 1,292 *Papio anubis* observations are projected to experience greater suitability. In contrast, 1,097 species observations indicate a decrease in habitat suitability in the year 2070. The 13 remaining observations experience no change from present to 2070 suitability.

Species Distribution Model: Predicted Habitat Suitability , Papio hamadryas

The second species assessed in this analysis, *Papio hamadryas*, is most concentrated in central and eastern Africa. This species tends to live in the harshest environments of the *Papio* species, being situated around the horn of Africa and the southern tip of Arabia (Figure 1b). This region experiences higher elevations, lower annual rainfall, and lower amount of lush vegetation (Winder, 2014). Exploratory analysis with the observation data revealed that the suitability for *Papio hamadryas* was most dependent on a few of the bioclimatic variables. Precipitation of the driest quarter, elevation, and annual precipitation were the most notable bioclimatic variables with the highest contributions of 34%, 28%, and 9%, respectively. However, other bioclimatic variables such as precipitation of the warmest quarter, annual temperature range, min temperature of coldest month, and annual mean temperature were important factors in predicting the species suitability across central and eastern Africa.

The results hold true that the species prefers higher elevation, with an average observation elevation of 1,217.7 meters above sea level. Additionally, the average annual temperature and precipitation were calculated to be 22 degrees Celsius and 645 mm, respectively. The species observations revealed that the average EVI was lower, a value of 0.56, which correlates with areas with a lower density of lush vegetation. It is also evident from the data that the observations are most reliant on the warmest quarter vegetation, with an average value of 169 mm.

The predicted present suitability of *Papio hamadryas* (Figure 5a) was generated with an accuracy of 95%. The data of the model indicates that the areas most suitable for the species are along the horn of africa, southern arabia, and along the southeastern tip of africa. The predicted 2070 suitability of *Papio hamadryas* (Figure 5b) reveals the generous increase in suitable areas for the species. Only 7.69% of the observations had a negative change in suitability, in addition, the average suitability for each observation grew more than 10%. In a spatial context, the most notable change is the addition of the central belt and western portion Africa (Figure 5c). The amount of suitable area grew more than 50% of its previous extent. This may be evident that the central and eastern areas of Africa are subject to a large change in the climate and landscape as the *Papio hamadryas* species prefer cooler average temperatures and lower amounts of precipitation that are currently existent in the 2070 predicted areas.

Multi-Criteria Evaluation

The MCE analysis reveals which regions within the study areas are at high risk of disease transmission from the baboon species to humans. In the current scenario, the results indicate higher risk along the northern edge of the study area, where population density and accessibility are greater (Figure 7a, 7b). This region includes Algeria, Niger, Chad, and Sudan. Risk also increases along the eastern border of the study area, where baboon populations are concentrated (Figure 7a, 7b). The greatest risk value presented in the current scenario is 0.93 using the OWA method (Figure 7a). The spatial pattern of risk values in the future scenario, which makes predictions for the year 2070, displays a similar distribution in risk, with expansion of high risk values. The most notable increase in risk occurs along the eastern border where baboon populations are projected to increase. Furthermore, the OWA method displays a new region of high risk from Cote d'Ivoire through Nigeria. There is also an increase observed in southern Africa. While high risk patterns are predicted to expand in the future, the actual risk values do not increase substantially, as the highest value in 2070 is 0.95 presented in the OWA method (Figure 7c). The WLC method presents very little change between the 2020 and 2070 predictions, with the maximum risk values of 0.687 and 0.689 respectively.

We performed both the Ordered Weighted Average (OWA) method (presented in Figure 7a and 7c) and the Weighted Linear Combination (WLC) method (presented in Figure 7b and 7d) for running the MCE analysis. Generally speaking, the relative high and low values of risk

generated by the two methods are similar, with the Northwest and North part of Africa, Ethiopia, Central Africa and the south part of the Arabian Peninsula generally having higher risk values than the other parts of the study region in both the current and future scenarios. The biggest difference between OWA and WLC in terms of the relative risk factor values is in the Eastern part of Africa, across parts of Ethiopia and Kenya, where OWA shows a particularly high risk values in this region, which has one of the highest values in the entire study region along with areas like the Northeast part of the continent, the WLS result only shows a relatively medium high risk in this region, the Northeast Africa, the region with the highest risk values in the WLS method output, have a substantially higher value than this region. For the absolute risk values, the OWA method generally has a substantially larger value range than the WLC method, while the lowest risk values are both close to zero for the two methods, the highest risk values for OWA is 0.95, and for WLC is only 0.69.

Discussion

From the result of both of the species distribution models it is clear that the environment of central Africa will be experiencing some changes. Both species of *Papio* will have expanding range and will be in closer contact with humans and will likely be in close contact with each other as their ranges combine even further. Both species revealed a significant increase in suitability, but the *Papio hamadryas* species acquired more suitable areas than the *Papio anubis* species. This was an interesting finding because the *Papio hamadryas* species has one of the smallest ranges of the *Papio* species while the *Papio anubis* species has a much larger range across Africa. The results of the MCE Analysis are characterized by the expansion of high-risk transmission regions between a current scenario and the future scenario. This trend is attributed to the SDM projection results, as all other variables utilized were static between the 2020 and 2070 risk scenarios. Therefore, the expansion of the high-risk areas is the result of how environmental variables change, allowing for the spatial expansion of baboon range.

When analyzing the results of the MCE analysis, taking into account the dynamic environmental variables used in the SDM for each species, it is clear that temperature and precipitation change play a dominant role in the expansion of risk. Based on the SDM outputs, temperature is projected to increase by approximately 5°C within regions of the baboon population. Precipitation also increased by 500 mm per year within the study area. Increasing

temperature and precipitation allowed for the study area to become more suitable for the baboon species, contributing to the spatial expansion of baboon populations. Such expansion then interacts the risk variables incorporated in this analysis. As populations expand, they encroach upon regions of high accessibility and human population density. This then increases the risk of the disease transmission from baboon to human. However, owing to the expansion of suitable baboon habitat, the increased risk is not observed in the risk values themselves, but in the increased spatial extent of high-risk areas. Disease transmission from baboon to human it's a pertinent concern, as climate change causes warming in the study area into baboon populations continue to increase and expand.

Species Distribution Model: Predicted Habitat Suitability

Papio anubis

The variable contribution of the model identified, in the results, indicates that the suitability of *Papio anubis* is heavily determined by annual precipitation. Additionally the results show a large influence of annual temperature more so than elevation and EVI. The model demonstrated the overwhelming influence of bioclimatic variables on suitability with other highly important variables such as precipitation of the coldest quarter and maximum temperature of the warmest month. The response of *Papio anubis* to these variables demonstrates the climate that is most suitable to the species. Specifically the greatest response of the species to the climate is at low to moderate precipitation and moderate to high temperatures. Additionally, the species is accustomed to vegetated regions, or areas of $EVI > 0$. The response of *Papio anubis* also points to suitable habitats being at lower elevations. While increased suitability is projected for 2070, the expected output was decreased suitability similar to the results of recent studies. According to (Chala et al., 2019), the suitability of *Papio anubis* decreased as a result of their SDM by 13.3% with an AUC of 0.83-0.85. These differing results suggest the need for further studies.

Increasing suitability for *Papio anubis* suggests the potential for increased species population. An increase in the population of *Papio anubis* would likely result in greater likelihood of species-human interactions. With this potential increase in human interaction, the transmission of disease will more likely pose a risk to nearby civilizations in 2070 than present. Differing results between studies may result due to variations in data such as sources for species observation points and environmental variables. Further studies on the species and projected

suitability should be implemented to further determine the trend of either increasing or decreasing suitability for *Papio anubis*.

Papio hamadryas

The results of the species distribution model for the *Papio hamadryas* were unexpected. We hypothesized that the species would have an expanded range of suitability that would reach further south, rather than west and in southern Saudi Arabia. However, SDM did not include land cover or population density, which may have impacted the result of the range of suitable areas in the region. If land cover and population density were included it might have changed the suitability values in more populated areas. Additionally, we hypothesized that annual mean precipitation and annual mean temperature would be the important variables chosen due to the species habits of harsh environments defined by rough terrain.

When compared with other research like that of (Winder, 2014) the key results are similar, but the observation data varied, which produced some differing geospatial results. The results in this analysis could have been skewed due to mis-identification of the species that was recorded through GBIF. For a future study continuing this research it might also be beneficial to look at land cover, especially with the sahel region. Climate Changing is impacting all regions around the Sahara Desert, with some areas greening and some being impacted by increased desertification.

Multi Criteria Evaluation

While the results of this analysis predict the expansion of high-risk disease transmission areas, the reality of this scenario could be more severe. Research shows that urban populations in Africa are expected to triple by 2050 (Hajjar, 2020). Increasing human population combined with increasing baboon populations and habitat expansion presents the potential for further transmission risk. The role of human population change is not incorporated in our analysis, as population density is a static variable. However, rural populations in Africa have been migrating towards urban centers over recent years (Hajjar, 2020). This could potentially decrease the probability of human and baboon contact, decreasing risk. Although our analysis addresses the effect of baboon habitat expansion on disease transmission risk, more research is necessary in order to determine how human population trends would affect these outcomes.

Weighted Linear Combination vs Ordered Weighted Average

To determine the spatial regions with the greatest risk of disease transmission to humans, the MCE analysis was conducted through TerrSet's MCE module, utilizing both the Ordered Weighted Average (OWA) and Weighted Linear Combination (WLC) techniques. The difference in result between the WLC method and the OWA method is caused by the different methodology applied by the two methods. WLC technique multiplies each factor by its factor weight and then adds to the results. Factors weights are very important in this method because they determine how individual factors will tradeoff relative to each other. The higher the factor weight the more influence that factor has on the final suitability map. While the OWA method also takes factor weights into account, which directly controls the levels of tradeoff and risk, the method also considers order weights, which are a set of weights assigned not to factors but to the rank order position of factor values for a given position. Factors with the lowest suitability score are given the first order weight.

Along with the full trade off, the WLC method is characterized by an average level of risk, the factor with a higher weight compensates for low suitability in other factors that have low tradeoff weights, so there is no strong skew towards the highest level of risk. While in the OWA method, the level of tradeoff is further determined by the order weights assigned in the method.

As observed in the result section, the OWA method produced a higher risk value relatively compared with the WLS method in the Eastern region of Africa, and also the larger value range of OWA method (Figure 7). These differences are most probably due to the assignment of order weights in addition to the factor weights when applying the OWA method. The order weights we used were the same as the factor weights, with lower factor weights value given the higher order weights, since higher order weights represent lower suitability values, we are assigning higher weights to those factors with higher suitability values in each location. Therefore, for factors that have a high suitability value in a certain location, it will also be given a high order weight in the OWA method, which will further enlarge the risk values, making the value range of the risk values from the OWA method larger than that of the WLS method. For Eastern Africa, the human impact layer and the suitability map of the two baboon species generally have high values in the region, but the factors were assigned a relatively medium factor

weight, and other human risk layers, some with higher factor weights, generally have relatively low values in the region. Given the full trade off characteristic of the WLS method, this would result in a low to medium risk value, however in the OWA method, larger weights are assigned to those factors that have a higher suitability values, therefore the human impact factor and the baboon suitability factor were given a higher weight, resulting in a high risk value generated by the OWA method. If we use a different set of order weights in the OWA method, the result would probably be very different.

Challenges/Constraints

Land cover initially was intended to be included as a SDM variable, however due to time limitations and technical difficulties, it was ultimately not included in the final analysis. We had preferred to use the most recent land cover information, but this was creating too many obstacles and we eventually decided to move on without it.

For the result of the MCE analysis, the biggest limitation is the lack of reference data to validate the reliability of our outputs. We have utilized two methods for doing the MCE analysis, which produced different results. However, we are not able to determine which result is more reliable since we don't have any validation data. Some occurrence datasets of a relevant virus may help with the situation. Another uncertainty in the MCE analysis are the weights we utilized. They were assigned based on our understandings of the relevant importance of each factor, which is quite arbitrary. A different set of weights applied could alter the result substantially.

Conclusion

The habitat suitability for *Papio anubis* and *Papio hamadryas* will likely increase in the next 50 years, most notably in regions lying in Sub-Saharan Africa. The increased suitability, when combined with the results of the MCE analysis, indicate that there is an expansion in risk of viral transmission in this region. With the predicted tripling of Africa's urban population by 2050 (Hajjar, 2020), the risk of interaction and transmission between these baboon species and human populations is further heightened and on the horizon.

This study was a preliminary step in what could be a more substantial look into the interactions between *Papio anubis* and *Papio hamadryas* and the human populations of central

Africa. Including current and predicted land cover data would add another angle of analysis. Furthermore, including a more dynamic human population and density dataset could reveal interesting information and potential contact points for humans and baboons. Beyond additional variables, researching the hybridization of these two species and the subsequent crossing of their ranges could highlight another level of viral transmission risk.

As Climate Change becomes a more prevalent force, humans and non-human primates will be forced to adapt to their surroundings, which could bring the two species in closer contact. The new coronavirus pandemic has highlighted the risk of viral transmission from many species to humans, with continued research about species habitat suitability and predicted ranges research may prevail in preventing another global pandemic.

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Tables & Figures

Variable	Eigenvector Weight
Hamandryas SDM	0.0408
Anubis SDM	0.0408
Accessibility	0.2637
Population Density	0.5062
Human Impact	0.1486

Table 1. Factor Weights and Order Weights utilized in MCE Figures

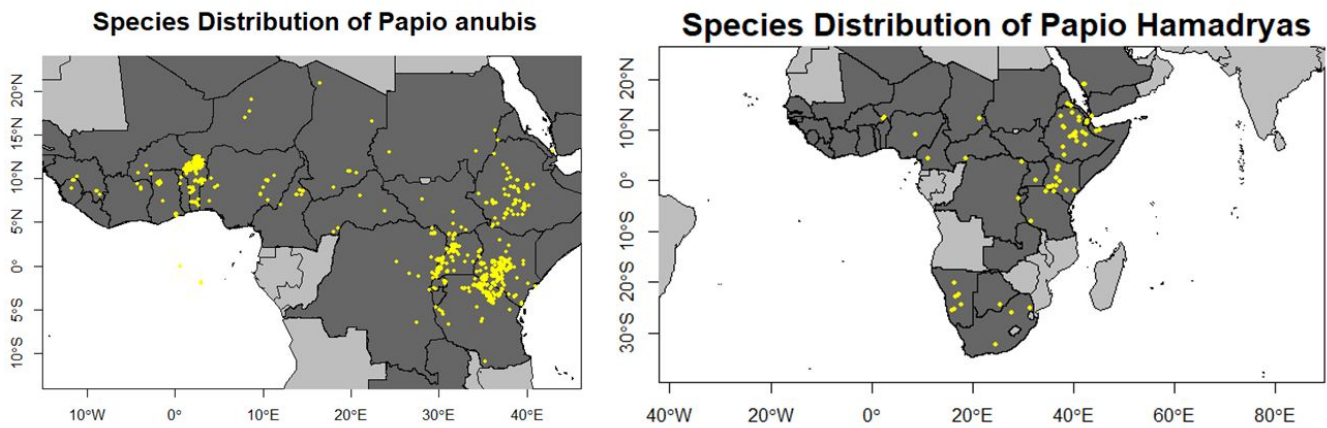


Figure 1. Species distribution of the *Papio anubis* and *Papio hamadryas*

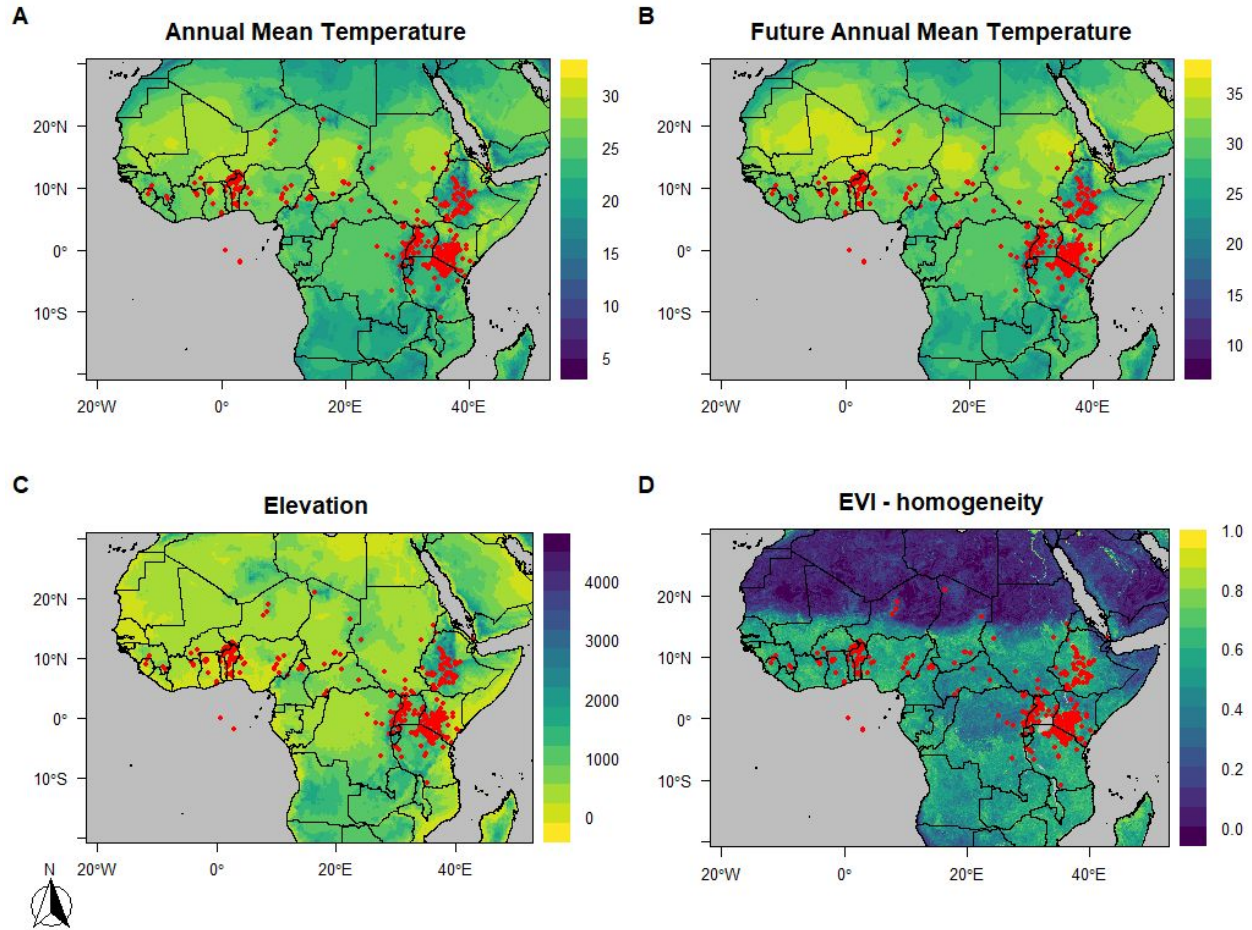


Figure 2. Variables used for the *Papio anubis* SDM model (a) annual mean temperature (b) future annual mean temperature, 2070 (c) elevation (d) enhanced vegetation index (EVI) homogeneity

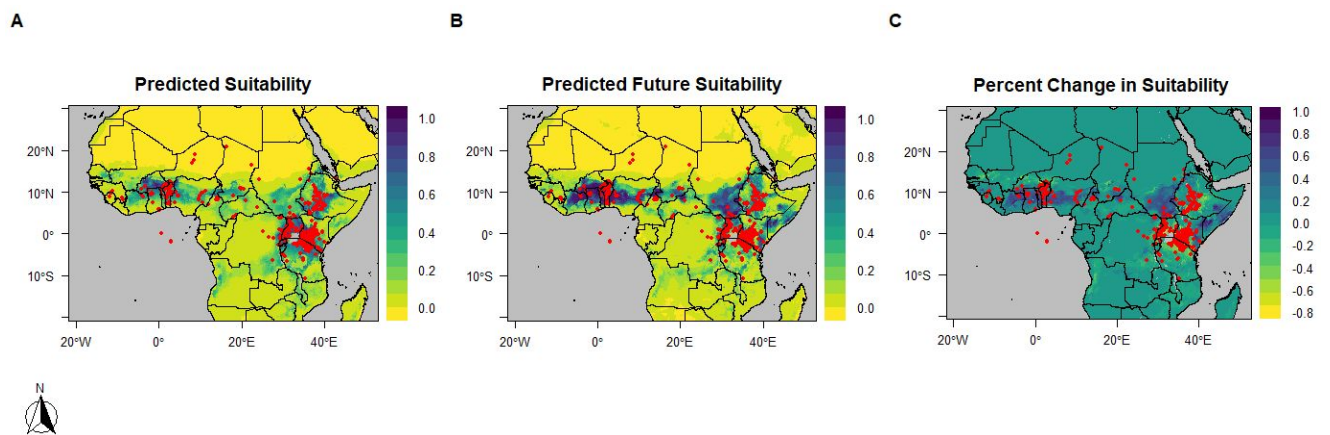


Figure 3. SDM outputs for *Papio anubis* (a) predicted suitability (b) predicted future suitability for 2070 (c) percent change in suitability from current to future (2070)

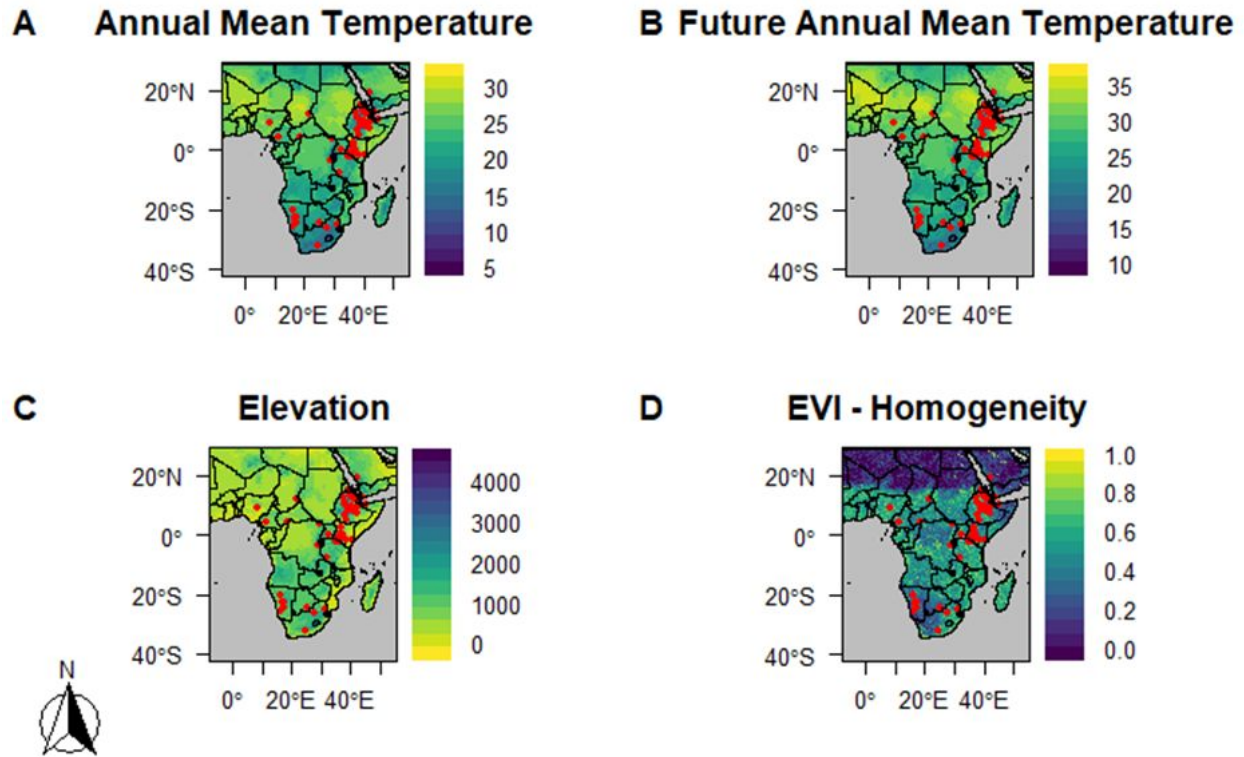


Figure 4. Variables used for the SDM model for *Papio hamadryas* (a) annual mean temperature (b) future annual mean temperature for 2070 (c) elevation (d) enhanced vegetation index (EVI) homogeneity

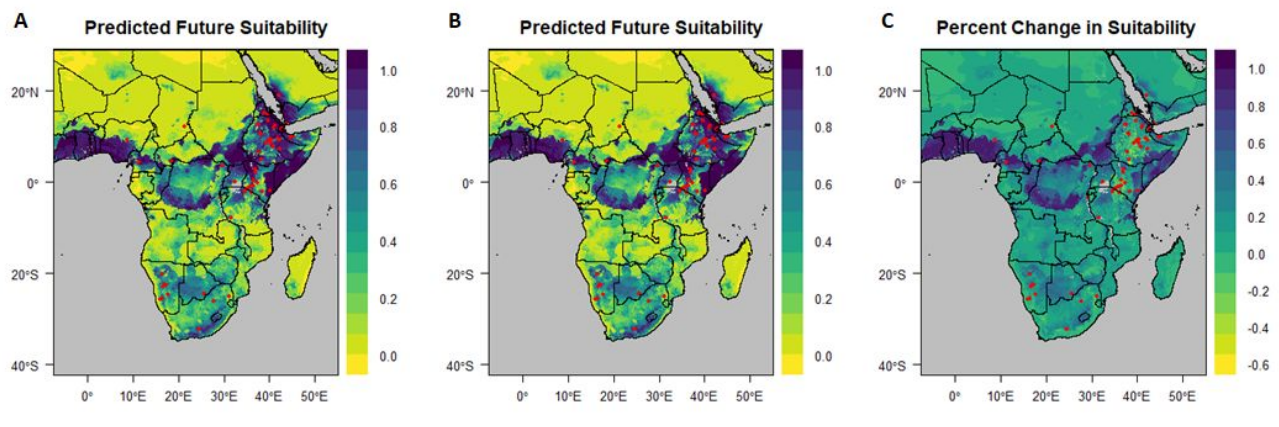


Figure 5. SDM outputs for *Papio hamadryas* (a) predicted suitability (b) predicted future suitability (c) percent change in suitability from current to future.

BIO1 = Annual Mean Temperature
 BIO5 = Max Temperature of Warmest Month
 BIO6 = Min Temperature of Coldest Month
 BIO7 = Temperature Annual Range (BIO5-BIO6)
 BIO8 = Mean Temperature of Wettest Quarter
 BIO9 = Mean Temperature of Driest Quarter

BIO12 = Annual Precipitation
 BIO16 = Precipitation of Wettest Quarter
 BIO17 = Precipitation of Driest Quarter
 BIO18 = Precipitation of Warmest Quarter
 BIO19 = Precipitation of Coldest Quarter

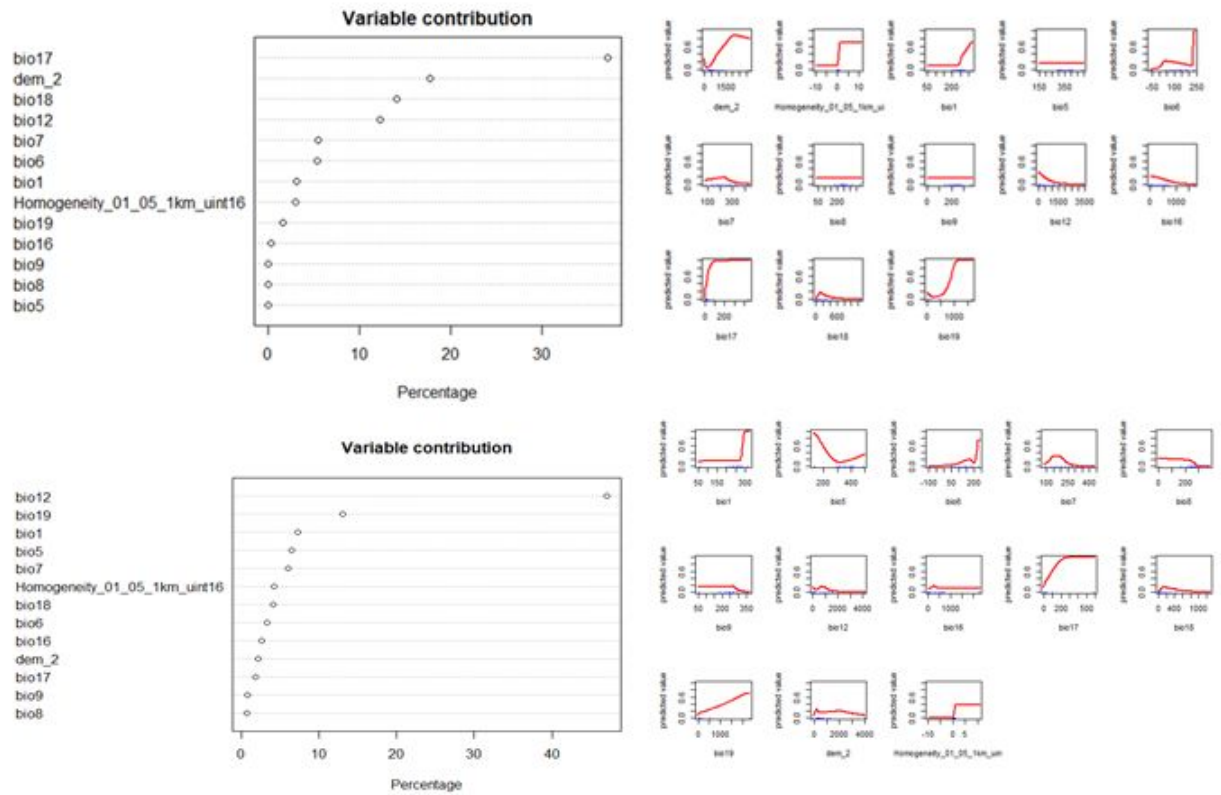


Figure 6. Percent of Variable Contribution and Variable Response Plots for Papio Anubis and Papio Hamadryas Species Distribution Model using MaxENT

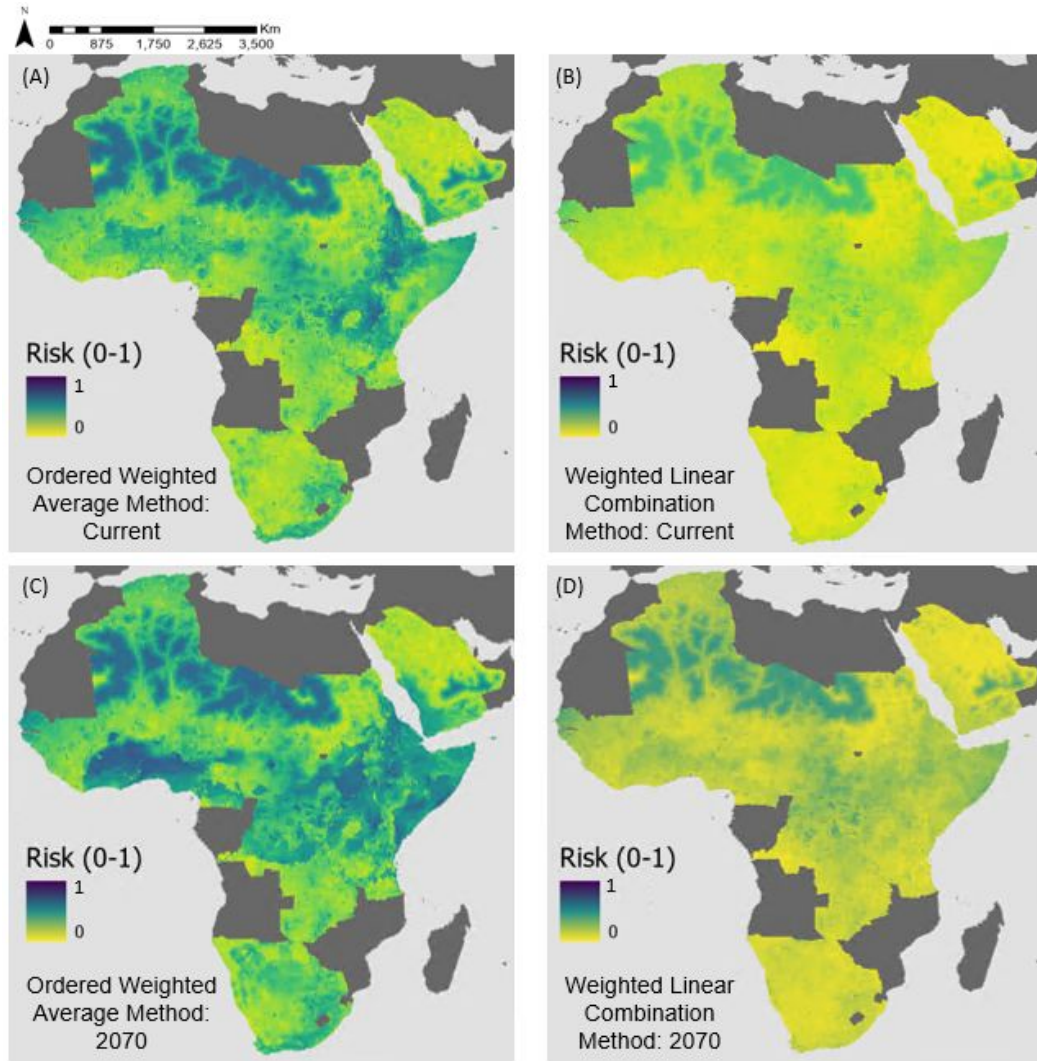


Figure 7. Results of the multi criteria evaluation (MCE), run with two different methods (a) ordered weight average (OWA) method for current year (b) weighted linear combination (WLC) method for current year (c) OWA for 2070 (d) WLC for 2070

Appendix

SDM Notes:

- SDM derived/ adapted from tutorial (url: <https://www.rpubs.com/kerkhoffa/SDMMaxent>)
- Added environmental variables (elevation and EVI) to model
- Incorporated these new variables by cropping them to the model extent, resampling them to the model environment, and added these raster images to the climatic variables' RasterStack in R
- What the script/ model does step by step...
 1. Import the following libraries/ packages in R (raster, rgdal, maps, mapdata, dismo, rJava, maptools, jsonlite, dplyr, sf, readr)
 2. Use GetData to get worldClim data (current and future - rcp8.5)
 3. Remove additional bioclimatic variables
 4. Climatic variables include:
 - a. Annual mean Temp
 - b. Max temp of warmest month
 - c. Min temp of coldest month
 - d. Temp annual range
 - e. Mean temp - wettest quarter
 - f. Mean temp - driest quarter
 - g. Annual precip
 - h. Precip - wettest quarter
 - i. Precip - driest quarter
 - j. Precip - warmest quarter
 - k. Precip- coldest quarter
 5. Obtain GBIF species data and remove duplicate locations
 6. Conserve SDM to native species range
 7. Add new variables/ read in (elevation, land cover, EVI) - previously download
 8. Create model extent and crop and resample variables to it
 9. Add variables into one rasterStack/ raster group
 10. Create training data (80%) and testing data (20%) of species observations
 11. Use maxent (input - species data and env variables)
 12. Predict habitat suitability