

Genetic Diversity of *Puma concolor*, *Leopardus pardalis*, *Panthera onca*, and
Panthera leo

Elle Baker

Evolution (BIO461): West Virginia University Institute of Technology

Dr. Jonathan Mitchell

28 April 2023

Abstract

Big cats, like pumas, ocelots, jaguars, and lions, face catastrophic consequences from the increasing rate of deforestation due to their high space and prey requirements. Data was acquired from various populations of pumas, ocelots, jaguars, and lions; and a linear regression was conducted to evaluate the relationship between the F statistic and allelic richness for each individual population of big cat. It is hypothesized that as allelic richness increased, the population of heterozygotes would increase (the F statistic would decrease into the negatives). It was determined that there is a slight, positive correlation of increasing inbredness and allelic richness, which was quantified using a Pearson's correlation, equaling 0.1369. Allelic richness, being a good indicator of genetic diversity, was the lowest in lions, with pumas close behind. Lions also exhibited the largest difference in inbreeding and outbreeding among the four species tested. In these populations of big cats, there is an overall increasing rate of inbredness, causing shifts from heterozygosity excess to heterozygosity deficiency in some populations. Ocelots were the only big cats tested to exhibit a positive relationship between heterozygote excess and allelic richness. Effective population size and different legislations protecting these big cats could be indicative of the results that were acquired.

Introduction

The term species will be used to describe a population of individuals with the ability to produce viable and fertile offspring with other members of the population. Big cats, known for their ferocity and apex predatorial behavior, are fascinating walks of life and have been studied by humans for centuries. Out of the 41 known species of Felidae, all have exceptional predatory skills that include an extraordinary sense of sight, hearing, and smell (Janecka et al., 2014). Though they inhabit most notably around the equator, species of big cats occur in subsects independent of climate. These cats, with the exception of lions, predominantly live in isolation and require up to 400 square kilometers of roaming territory (Smitz et al., 2018). The incidence of inbreeding negatively impacts the animal, as fitness is greatly reduced.

As a result of the exponential growth of the population of humans, protected areas in Africa, Asia, South America, and the United States are decreasing due to deforestation at alarming rates (Miotto et al., 2011). This has drastically decreased roaming area for big cats and as a result, is hypothesized to increase inbreeding and decrease allelic richness within these populations.

Research on the genetic diversity of big cats, including pumas (*Puma concolor*), ocelots (*Leopardus pardalis*), leopards (*Panthera onca*), and lions (*Panthera leo*) is an extremely prevalent and visited topic, however those animals are not often compared to one another in terms of allelic richness. This paper is an in-depth analysis of the relationship between inbredness and allelic richness of four populations of pumas, three populations of ocelots, four populations of leopards, and four populations of lions. It is hypothesized that as allelic richness increases, the population of heterozygotes would also increase.

Methods

Data was downloaded from fifteen various papers. The datasets used were then programmed into R (RStudio2022.12.0+353), where certain analyses could take place. The data downloaded from papers ranged from genomic sequences taken from various samples of big cats to the expected (H_e) and observed (H_o) heterozygosity and allelic richness, which was calculated in the author's data. The F statistic, or inbreeding coefficient, was determined for each population of big cat by the formula $F_{stat} = (H_e - H_o)/H_e$. A simple linear regression was then plotted to express a relationship between allelic richness and the inbreeding coefficient. A Pearson's correlation test was then applied to quantify the level of correlation between allelic richness and the F statistic.

Results

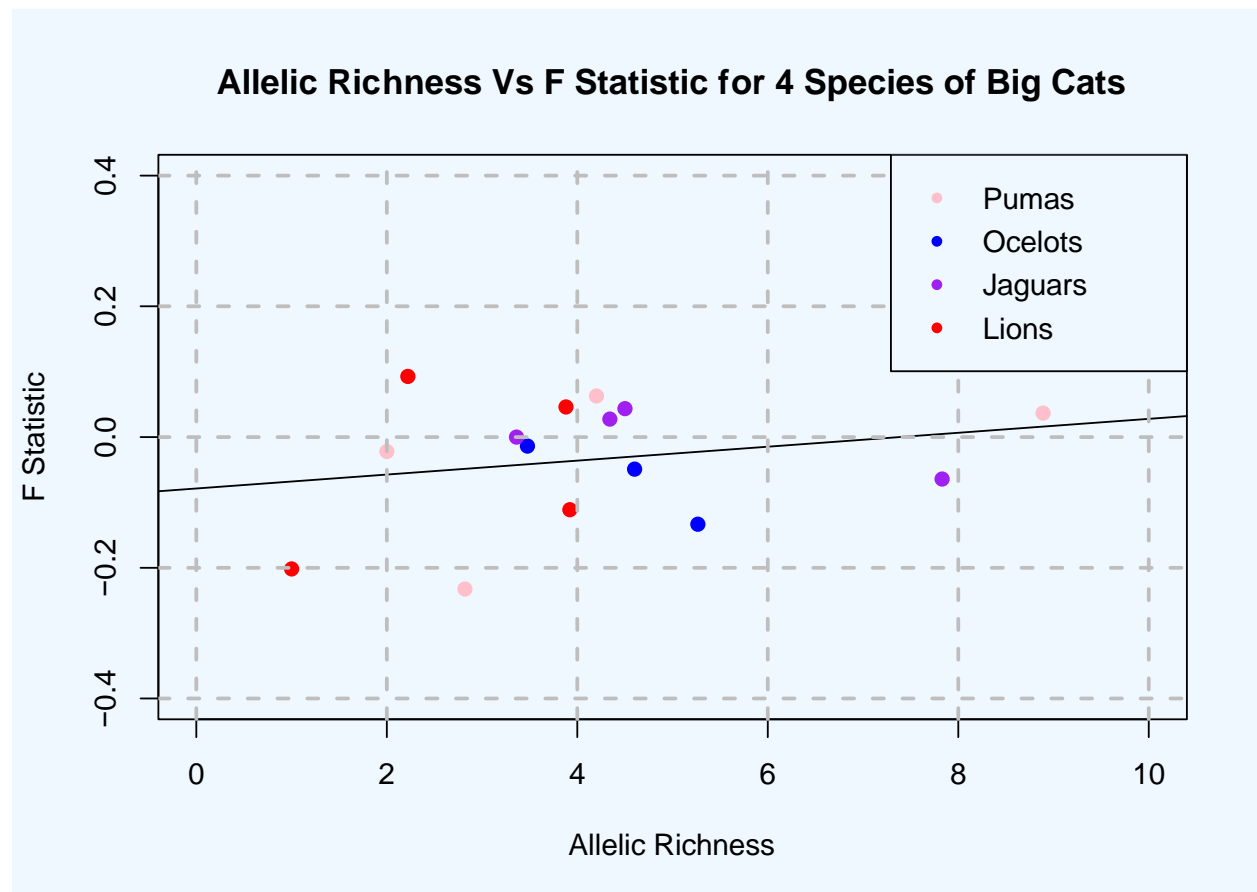


Figure 1: F statistic, calculated by $H_e - H_o / H_e$ in relation to Allelic Richness (Genetic Diversity). Negative values on the Y-axis indicate heterozygote excess (outbreeding), while positive values indicate heterozygosity deficiency (inbreeding)

Pearson's Correlation

t= 0.49829 df=13 p-value= 0.6266

at 95% Confidence Interval:

Correlation: 0.1369008

Figure 2: Pearson's correlation numerically defining the relationship between Allelic Richness and F Statistic

Based on the data, the graph suggests a very slight positive relationship between allelic richness and increasing inbredness in fifteen populations of big cats, which was corroborated by the Pearson's correlation ($=0.1369$) used to test if two variables have a linear relationship. This is representative of a weak correlation and is insignificant in supporting with certainty that allelic richness and the F statistic are correlated with one another. This is also depicted by the largeness of the p-value, which indicates a lack of evidence for a correlation. Jaguars appear to have the most inbred population, while ocelots have an excess of heterozygotes. Lions have the most drastic inbreeding/outbreeding margin.

Discussion

Allelic richness was used as an indicator of genetic diversity and took into account the effective population size. It is observed that lions exhibit the most drastic changes in F statistic, which could be due to a low number of allelic richness or effective population size. It also appears that there is a much less drastic change among the F statistic as allelic richness increases.

If allelic richness and the F statistic were linearly related, some discussion would take place regarding the differences in each population and species and why it might have occurred. In jaguars, they have a relatively steady relationship between the F statistic and allelic richness. This decrease in F statistic variation could be indicative of a larger effective population. The high fluctuation of gene flow in lions could be caused by a low effective population, and the fluctuations being caused by drift increasing in their populations. Selection, also, creates variation as exhibited by the lion's behavior of the graph.

Their reduced effective population indicated by reduced allelic richness could be explained by their social behavior and intense male competition for females. Females often do not leave the pride and only mate with one male for her reproductive life, unless another male claims the pride. These males oversee and mate with the same multiple females, so it makes sense that their allelic richness is much lower than the other solitary individuals that were tested.

Ocelots are the only big cat tested to exhibit a decrease in inbredness as allelic richness increased. This increase in heterozygosity suggests that they are hybridizing their genome at a faster rate than the other big cats. Ocelots are found in the wild in the United States, and the US has the most enforced legislation for protecting forests. These ocelots in the US have more space to inhabit, thus increasing gene flow and decreasing the impact of selection. High heterozygosity is likely not due to mutations because most mutations will drift to extinction regardless of selection.

US forest protection legislation has an inconclusive affect on pumas, however. Though commonly found in the US, they also exhibited very large fluctuations in the F statistic and allelic richness. This could be related to something that decreases the uniformity of mating, like sex ratio differences, that could be increasing drift and therefore cause a larger variation of the F statistic, though this is not researched in this paper. The mating disuniformity argument could be countered, however, as drift decreases genetic diversity. The outlier of allelic richness in pumas would indicate a larger effective population and reduce the variation of the F statistic, which does not happen.

Conclusion

Big cats all over the world are facing consequences from deforestation, such as lower rates of heterozygosity in the tested populations. This could be disastrous, as certain alleles drift closer and closer to fixation. The rate of mutation is negligible in this case, as they usually almost immediately go to extinction due to drift. Effective population size and differences in legislation could be factors in these differences between populations and additional research is warranted. Studying the changes in the F statistic between species suggests that deforestation is causing such change over time while allele frequency between species can help map the lasting impact of deforestation in their habitats.

References

- Benson, John F., Peter J. Mahoney, Jeff A. Sikich, Laurel E. K. Serieys, John P. Pollinger, Holly B. Ernest, and Seth P. D. Riley. "Interactions between Demography, Genetics, and Landscape Connectivity Increase Extinction Probability for a Small Population of Large Carnivores in a Major Metropolitan Area." *Proceedings of the Royal Society B: Biological Sciences* 283, no. 1837 (August 31, 2016): 20160957. <https://doi.org/10.1098/rspb.2016.0957>.
- Ernest, Holly B., T. Winston Vickers, Scott A. Morrison, Michael R. Buchalski, and Walter M. Boyce. "Fractured Genetic Connectivity Threatens a Southern California Puma (Puma Concolor) Population." *PLOS ONE* 9, no. 10 (October 8, 2014): e107985. <https://doi.org/10.1371/journal.pone.0107985>.
- Gustafson, Kyle D., T. Winston Vickers, Walter M. Boyce, and Holly B. Ernest. "A Single Migrant Enhances the Genetic Diversity of an Inbred Puma Population." *Royal Society Open Science* 4, no. 5 (May 24, 2017): 170115. <https://doi.org/10.1098/rsos.170115>.
- Janecka, Jan E., Michael E. Tewes, Linda Laack, Arturo Caso, Lon I. Grassman, and Rodney L. Honeycutt. "Loss of Genetic Diversity among Ocelots in the United States during the 20th Century Linked to Human Induced Population Reductions." *PLOS ONE* 9, no. 2 (February 26, 2014): e89384. <https://doi.org/10.1371/journal.pone.0089384>.
- Life at OSU. "Protected Areas See Continued Deforestation but at a Reduced Rate, OSU Research Shows," February 11, 2021. <https://today.oregonstate.edu/news/protected-areas-see-continued-deforestation-reduced-rate-osu-research-shows>.
- Miller, Susan M., Dave J. Druce, Desiré L. Dalton, Cindy K. Harper, Antoinette Kotze, Craig Packer, Rob Slotow, and Paulette Bloomer. "Genetic Rescue of an Isolated African Lion Population." *Conservation Genetics* 21, no. 1 (February 1, 2020): 41–53. <https://doi.org/10.1007/s10592-019-01231-y>.
- Miller, Susan M., Cindy K. Harper, Paulette Bloomer, Jennifer Hofmeyr, and Paul J. Funston. "Fenced and Fragmented: Conservation Value of Managed Metapopulations." *PLOS ONE* 10, no. 12 (December 23, 2015): e0144605. <https://doi.org/10.1371/journal.pone.0144605>.
- Miotto, R. A., M. Cervini, M. G. Figueiredo, R. A. Begotti, and P. M. Galetti. "Genetic Diversity and Population Structure of Pumas (Puma Concolor) in Southeastern Brazil: Implications for Conservation in a Human-Dominated Landscape." *Conservation Genetics* 12, no. 6 (December 1, 2011): 1447–55. <https://doi.org/10.1007/s10592-011-0243-8>.
- Salom-Pérez, Roberto, Claudia Wultsch, Jennifer R Adams, Sofía Soto-Fournier, Gustavo A Gutiérrez-Espeleta, and Lisette P Waits. "Genetic Diversity and Population Structure for Ocelots (Leopardus Pardalis) in Costa Rica." *Journal of Mammalogy* 103, no. 1 (February 1, 2022): 68–81. <https://doi.org/10.1093/jmammal/gyab146>.
- Smits, Nathalie, Olivia Jouvenet, Fredrick Ambwene Ligata, William-George Crosmay, Dennis Ikanda, Philippe Chardonnet, Alessandro Fusari, et al. "A Genome-Wide Data Assessment of the African Lion (Panthera Leo) Population Genetic Structure and Diversity in Tanzania." *PLOS ONE* 13, no. 11 (November 7, 2018): e0205395. <https://doi.org/10.1371/journal.pone.0205395>.
- Valdez, Fernanda Pedone, Taiana Haag, Fernando C. C. Azevedo, Leandro Silveira, Sandra M. C. Cavalcanti, Francisco M. Salzano, and Eduardo Eizirik. "Population Genetics of Jaguars (Panthera Onca) in the Brazilian Pantanal: Molecular Evidence for Demographic Connectivity on a Regional

Scale." *Journal of Heredity* 106, no. S1 (January 1, 2015): 503–11.

<https://doi.org/10.1093/jhered/esv046>.

Wulsch, Claudia, Lisette P. Waits, and Marcella J. Kelly. "A Comparative Analysis of Genetic Diversity and Structure in Jaguars (*Panthera Onca*), Pumas (*Puma Concolor*), and Ocelots (*Leopardus Pardalis*) in Fragmented Landscapes of a Critical Mesoamerican Linkage Zone." *PLOS ONE* 11, no. 3 (March 14, 2016): e0151043. <https://doi.org/10.1371/journal.pone.0151043>.