High genetic diversity and low differentiation reflect the ecological versatility of the African leopard

Penerová, Patrícia; Garcia-Erill, Genís; Liu, Xiaodong; Nursyifa, Casia; Waples, Ryan K.; Santander, Cindy G.; Quinn, Liam; Frandsen, Peter; Meisner, Jonas; Stæger, Frederik Filip; Rasmussen, Mafthe Sebro; Brüniche-Olsen, Anna; Jørgensen, Christian Hviid Friis; da Fonseca, Rute R.; Siegismund, Hans R.; Albrechtsen, Anders; Heller, Rasmus; Moltke, Ida; Hanghøj, Kristian

Published in:
Current Biology

DOI:
10.1016/j.cub.2021.01.064

Publication date:
2021

Document version
Publisher's PDF, also known as Version of record

Document license:
Other

Citation for published version (APA):

Download date: 04. jul., 2023
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Graphical Abstract

The leopard has the highest diversity and lowest differentiation of African large cats.

Highlights

- African and Amur leopards have markedly different demographic trajectories
- Among big cats, African leopards have the highest genetic diversity
- Gene flow on a continent-wide scale maintains low genetic differentiation
- Broad dietary and habitat niche likely explain the extraordinary genetic makeup

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In Brief

Pečnerová et al. analyze whole-genome data from 53 African leopards and identify genetic features that set the African leopard apart from the Amur leopards, as well as the other big cats. This includes long-term high effective population size and exceptionally high levels of genetic diversity and connectivity.
High genetic diversity and low differentiation reflect the ecological versatility of the African leopard

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https://doi.org/10.1016/j.cub.2021.01.064

SUMMARY

Large carnivores are generally sensitive to ecosystem changes because their specialized diet and position at the top of the trophic pyramid is associated with small population sizes. Accordingly, low genetic diversity at the whole-genome level has been reported for all big cat species, including the widely distributed leopard. However, all previous whole-genome analyses of leopards are based on the Far Eastern Amur leopards that live at the extremity of the species’ distribution and therefore are not necessarily representative of the whole species. We sequenced 53 whole genomes of African leopards. Strikingly, we found that the genomic diversity in the African leopard is 2- to 5-fold higher than in other big cats, including the Amur leopard, likely because of an exceptionally high effective population size maintained by the African leopard throughout the Pleistocene. Furthermore, we detected ongoing gene flow and very low population differentiation within African leopards compared with those of other big cats. We corroborated this by showing a complete absence of an otherwise ubiquitous equatorial forest barrier to gene flow. This sets the leopard apart from most other widely distributed large African mammals, including lions. These results revise our understanding of trophic sensitivity and highlight the remarkable resilience of the African leopard, likely because of its extraordinary habitat versatility and broad dietary niche.

INTRODUCTION

Apex predators are more sensitive to climate change and other ecological disturbances than species at lower trophic levels.1-3 This makes them more prone to demographic fluctuations and thus more susceptible to population crashes and even extinction.4 Given that genetic diversity is linked to demographic fluctuations, apex predators are expected to have on average lower genetic diversity than their herbivorous prey species. A rapidly accumulating body of evidence from whole-genome studies5,6 has confirmed this in, among others, all of the big cats, i.e., the species belonging to Panthera,7 a genus of typical apex predators.

Among the big cats, the leopard, Panthera pardus, stands out because of its extensive geographic distribution and its ability to persist under a wide range of ecological conditions, even close to human settlements, labeling it as a habitat and dietary generalist.8,9 Given that genetic diversity is related to ecological resilience, the leopard should have higher genetic diversity than other big cats, yet this was not found in previous genome-wide studies.5 However, the only published whole-genome data from the leopard5,10 originates from the Amur leopard (P. p. orientalis), which lives at the eastern extremity of the species’ geographic distribution (Figure S1). This population has a history of severe range and population contractions, making it the most critically endangered leopard subspecies with less than 60 individuals surviving in the wild.11

The leopard is thought to have originated in eastern Africa approximately 2–4 million years ago (mya).12,13 The divergence between African and Asian leopards has been dated to ~710 thousand years ago (kya) on the basis of a mitogenome phylogeny calibrated by using historical and ancient samples.12
Subsequently, the divergence between Asian and Pleistocene-era European leopards was dated to \(483 \text{ kya} \), and if we assume that this divergence reflects the out-of-Africa event, this sets the likely timing of leopards entering Eurasia to 710–483 kya. Because of this long period of separation, Asian and African leopards might differ markedly in their evolutionary trajectories, including effective population size and population connectivity. This, combined with the Amur leopard’s very limited census population size and the fact that population contractions reduce genetic diversity, suggests that the results of genomic analyses of Amur leopards might not represent the entire leopard species and in particular not the African leopards.

Although a few genetic studies have been performed on the African leopard, they have all been based on microsatellites and/or mitochondrial data. Based on these studies, which identified low population differentiation, all African leopards have been classified as a single subspecies \(P. p. pardus\). On the contrary, a recent fine-scale sampling of 182 African leopards by using 611 base pairs of mitochondrial DNA suggested substantial population structure and deep divergence within Africa. Therefore, our genetic understanding of leopards in their proposed continent of origin remains conflicted and scarce.

In this study, we investigated population structure, demographic history, and genetic diversity in African leopards by sequencing and analyzing 53 whole genomes, covering most of their current range in Africa. The aim was to learn more about the evolutionary dynamics of the leopard in its biogeographic cradle and to assess whether the generalist ecology of the leopard sets it apart from other big cats.

RESULTS

We generated whole-genome sequencing data for 53 African leopards from 10 locations in sub-Saharan Africa and a total of 5 countries: Ghana, Namibia, Tanzania, Uganda, and Zambia.
size and/or little differentiation between them. However, we note that an evaluation of the admixture model fit using evalAdmix indicates that the discrete clustering imposed by NGSadmix is not a good fit to the data, as shown by the presence of numerous non-zero residuals within clusters, consistent with the genetic continuity across geographic space suggested by the PCA (Figure 2A).

To get a better sense of how the samples are genetically clustered, we built a neighbor-joining (NJ) tree based on the 39 individuals from the PCA, as well as two previously published Amur leopards (IDs 3042211 and 3042212). We found that all African leopards form a cluster with a branching pattern consistent with the north-to-south cline observed in the PCA; however, it is evident from the NJ tree that there is very low differentiation between the different sampling locations with short internal branch lengths. Ghana was the most divergent group, whereas the other sampling locations formed a separate cluster with a substructure representing the sampling locations (with the exception of Zambia) in the following order of divergence: Uganda; Tanzania North, East, and West; Zambia; and Namibia (Figure 2C). One sample (ID 5180) stands out as being labeled Tanzania West and clustering with Tanzania North; however, this result is consistent with NGSadmix results, indicating that the sample is a mixture of the Tanzania West and North ancestral sources (Figures 2B and 2C).

Given that the estimated NJ tree largely supports our initial geography-based grouping of the samples, we decided to treat these groupings as populations and quantify the magnitude of genetic differentiation between them by using $F_{ST}$. However, before doing so, we first confirmed that this population grouping was justifiable by performing a population homogeneity test using $D$-statistics (ABBA-BABA) on the low-coverage samples that were not inferred to be admixed in the NGSadmix analysis. Because of low sample sizes, Tanzania East (n = 2) and Uganda (n = 1) were excluded. We tested for relative differences in genetic affinity between all pairs of individuals within a location (H1 and H2) and another sampling location (H3), while using the Amur leopard reference (Pan-Par1.0) as an outgroup (H4). We found strong signals of substructure in Zambia, where all $D$-statistics were significant (suggesting gene flow with the other sampling locations), in contrast to Ghana, Namibia, Tanzania North, and Tanzania West, where we found zero or one significant test ($|Z$-score|>3) (Figure 3). This result is consistent with the population structure analyses (Figure 2) and suggests that Ghana, Namibia, Tanzania North, and Tanzania West are meaningful population groupings. We therefore quantified the magnitude of genetic differentiation between populations by estimating pairwise $F_{ST}$. Overall, we find low levels of differentiation, and the highest values of $F_{ST}$ were 0.118–0.145 (Table 1, lower triangle) between Ghana and the remaining populations, again consistent with the population structure results (Figure 2). In addition, we estimated $F_{ST}$ between all pairs of individuals to factor out any downward bias from potential substructure within the populations. Note that we used the Reich $F_{ST}$ estimator because simulations show that it is robust to low sample size, even down to a single sample from each population (Figure S7B). Because this analysis was based on called genotypes, we restricted it to our five high-coverage samples.
The results show a similar range in $F_{ST}$ (0.12–0.17) between Ghana and the remaining populations as the population-based $F_{ST}$ analysis.

Migration within Africa

The migration patterns between the different sampling locations were further investigated by using Estimation of Effective Migration Surfaces (EEMS)\textsuperscript{29} (Figure 4). The results fit with an isolation-by-distance model in most parts of the range (Figure S3), suggesting that roughly distance-dependent gene flow is a major determinant of the observed genetic differences. In addition, we find that African leopards show only weak signatures of migration barriers across the latitudinal cline, in particular across the equatorial tropical rainforest. This is in sharp contrast to other African mammals with sub-Saharan distribution, including the lion (*Panthera leo*), for which the dense rainforest is a barrier (Figure 4).

Migration between Africa and Asia

We also tested for signals of post-divergence gene flow between the Amur and African leopards by using $D$-statistics with the domestic cat as an outgroup (H4). We found that all other populations (H2) contrasted against Ghana (H1) show a positive $D$-statistic (Figure 5), suggesting an excess of gene flow in the eastern and southern African lineages with a source represented by, but not necessarily equal to, the Amur leopard (H3). This is consistent with the West African samples being more genetically distant from the Amur leopard than leopards from East and Southern Africa.

Demographic history across the big cats

To investigate the demographic history of the African leopard, we inferred the effective population size through time by using pairwise sequentially Markovian coalescent (PSMC)\textsuperscript{30} (Figure 6A). Because PSMC requires called genotypes, we restricted the analysis to the five high-coverage African leopards. We scaled the population size assuming a mutation rate of $10^{-8}$ per base per year, which has previously been used in studies of big cat species,\textsuperscript{10} and a generation time of 7.5 years.\textsuperscript{11} For comparison, we applied the same procedure to genomes representing all the other big cats for which we could find publicly available data.\textsuperscript{5,10,31} We detected a clear signal of divergence between the African and Amur leopards (Figure 6A), given that their population size trajectories start to differ markedly around 300–400 kya, likely representing the out-of-Africa event. Our PSMC results further show that after the divergence, the African leopards maintained a high effective population size, in contrast to the Amur leopards that went through a bottleneck. Notably, the maintenance of high effective population sizes above 20,000 throughout the Pleistocene is unique for the African leopard in comparison with all other big cats, which all show decreasing effective population sizes in recent times.

Genetic diversity

Finally, we inferred the present-day genetic diversity of African leopards by estimating the genome-wide heterozygosity, i.e., the proportion of heterozygous sites per sample. We inferred on average ~2 heterozygous sites per 1,000 base pairs (bp), with little variation between the various populations of African leopards (Figure 6B). However, we note that the samples from Ghana were within the higher end of the error rate distribution, which could slightly upward-bias the estimates. To investigate the minor differences in heterozygosity between the different populations, we correlated the estimated heterozygosity levels against tracts of runs of homozygosity (ROH) for the five high-coverage samples. We found a negative linear correlation between the total length of ROH and heterozygosity (Figure S4B). This indicates that the majority of variability in genetic diversity among African leopard populations can be explained by differences in recent inbreeding rather than differences in demographic histories.

In line with the distinctive demographic trajectories inferred from PSMC (Figure 6A), the estimated heterozygosity levels for
the African leopards are 3-fold higher than those in the Amur leopards. They are also markedly higher than for any other big cat species, and most felid species in general (Figure 6A; Table S6), with the exception of two distantly related felids: the leopard cat (*Prionailurus bengalensis*) and to a lesser degree the puma (*Puma concolor*).

**DISCUSSION**

Our results provide new insights into the evolutionary history and molecular ecology of the leopard in its biogeographic cradle, the African continent. We found that the genetic diversity of the leopard was previously severely underestimated due to being characterized in Amur leopards, which have an unrepresentative population history for the species. We show that, in addition to suffering recent population declines, Amur leopards also carry a genetic legacy of the out-of-Africa event occurring in the middle Pleistocene (Figure 6A) and possibly a number of subsequent founder events. Lower genetic diversity is also frequently observed at the edge of species ranges because of somewhat extreme demographic histories.33

In contrast to the Amur leopards, African leopards retained large effective population sizes after the split. Furthermore, African leopards consistently maintained much higher population sizes than all other big cats throughout the Pleistocene (Figure 6A). Declining population sizes were also recently inferred in the puma34 and the cheetah (*Acinonyx jubatus*).35 Consistent with these differences in effective population size histories, the African leopards have by far the highest genetic diversity not only among big cats (Figure 6B) but among wild cats in general, matched only by the leopard cat, a small felid mesopredator species with a wide distribution in southern and eastern Asia.34,36

Interestingly, our results suggest that after the divergence, the African populations remained genetically connected with the Asian populations, given that we detected gene flow with a population represented by the Amur leopard lineage and the African leopards (Figure 5). The extent of Asian ancestry is not equal between African populations, suggesting either ancestral population structure before the split or a backflow into the ancestral branch of the eastern and southern African populations. Uphyrkina et al.14 found that the South Arabian leopard (*P. p. nimr*) could not be consistently placed with either African or Asian
leopards, which would be in accordance with genetic connectivity between a proto-eastern African leopard population and those of the Arabian Peninsula and the Middle East. Our results therefore suggest Pleistocene-era intercontinental genetic connectivity comparable to the level observed in another versatile carnivore, the spotted hyena.\textsuperscript{37}

The topology of our genome-wide NJ tree is consistent with a southward expansion of the eastern African lineage after divergence with Ghana (Figure 2C); however, the internal branch lengths are very short, suggesting that any such pattern is only tentative and obscured by pervasive gene flow. Overall, we found signatures of an isolation-by-distance model in most parts of the range, but this pattern is attenuated by extensive gene flow on a continent-wide scale within Africa (Figure S3). Concordantly, we found that African leopards show at best weak signatures of dispersal barriers across the latitudinal cline (Figure 4). Although the character of sampling and low density of samples from western and northern Africa prevent us from resolving genetic connectivity patterns on a finer scale, the continent-level pattern in leopards clearly stands out compared with that of other co-distributed African mammals by presence of gene flow across the equatorial rainforest. The equatorial tropical rainforest is one of the main drivers of diversification for many African mammals,\textsuperscript{38} but we found no evidence of it being a barrier for leopards, underlining their exceptional habitat tolerance. Accordingly, the leopard also stands out as having low levels of population structure compared with that of the majority of other species in the African large-mammal savanna guild that show strong regional structuring.\textsuperscript{38–41} The average pairwise $F_{ST}$ between populations was 0.10, which is considerably lower than corresponding values for other co-distributed African carnivores (cheetah: 0.29\textsuperscript{12} and lion: 0.25\textsuperscript{43}). Although genome-wide data can be expected to capture finer-scale structure, our results are consistent with early studies based on microsatellite data and partial mitochondrial sequences, which reported limited genetic structure within the African continent.\textsuperscript{14,15} However, a recent and densely sampled study contrastingly found strong structure in Africa.\textsuperscript{17} This discrepancy is possibly explained by the use of mitochondrial data,\textsuperscript{17} which only reflects the female lineage and fails to capture the male-biased dispersal in leopards.\textsuperscript{34}

As typical apex predators, the big cats of the genus \textit{Panthera} are specialized hypercarnivores depending on large prey species.\textsuperscript{35,46} Being at the top of the trophic pyramid,\textsuperscript{3,4} carnivores tend to have lower effective population sizes, and are thus more affected by environmental fluctuations and habitat fragmentation in periods when the climatic conditions are not favorable.\textsuperscript{47,48} As a consequence, carnivores are prone to increased genetic drift and low genetic diversity compared with herbivores,\textsuperscript{5,6,49} leading to an increased risk of extinction.\textsuperscript{4,50} with Holliday and Steppan\textsuperscript{45} labeling highly specialized carnivory as an evolutionary “dead end.” In stark contrast to its congeners, we find that the African leopard is an exceptionally adaptable apex predator. High mobility,\textsuperscript{51,52} habitat versatility,\textsuperscript{8,9} and dietary generalism\textsuperscript{13,53} have buffered the long-term high effective population sizes in the African leopards by making them less sensitive to habitat fragmentation and environmental fluctuations during the Pleistocene climatic cycles. In this light, our results are surprising, but they are in line with the biology of the leopard being defined by a broader dietary and habitat niche than any other big cat. We argue that the African leopard might constitute an evolutionary anomaly with a better chance of long-term survival than other \textit{Panthera} species. Future studies involving more extensive sampling throughout the leopard range will resolve how current genetic diversity is connected with
demographic history. We speculate that the Amur leopard will most likely not be representative of other Asian leopard subspecies because of its recent bottleneck and its position at the extremity of the leopard geographic range (Figure S1).

Despite their resilience, leopards have lost 48%–67% of their original distribution in Africa within the last ~300 years (Figure S1), and their range is contracting at a similar rate to some of the other big cats. Even though our results highlight that the...
leopards might be among the most adaptable of apex predators, and therefore relatively robust to environmental change and disturbance, anthropogenic activities can pose an unprecedented threat to their survival. Until recently, these have not had a major effect on leopard populations in Africa, but their potential effect is evident in the other leopard subspecies, particularly the critically endangered Amur leopard, which has been strongly affected by the lack of available prey, illegal hunting, and fragmentation of habitat. In addition, unlike species that went through periods of low population size, African leopards have had constantly high population sizes and have not endured bottlenecks, which would have purged strongly deleterious variation from the gene pool. African leopards might therefore harbor a larger number of strongly deleterious mutations at low population frequencies. These can increase in frequency as a result of population contractions, placing the African leopard at risk of inbreeding depression.

In conclusion, we correct the existing bias in the assessment of leopard genetic diversity and show that African leopards have exceptionally high genetic diversity for their trophic position, coupled with a continent-wide genetic connectivity in one of their biogeographic strongholds. Also, on the basis of our observations of low population differentiation and lack of migration barriers across Africa, we hypothesize that these unusual genetic features are caused by the resilience, adaptability, and high mobility of the leopard. This study represents a rare positive narrative in conservation genetics and, to our knowledge, one of the most convincing couplings of a species' generalist ecology with its correspondingly exceptional long-term evolutionary dynamics and genetic features.

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SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at https://doi.org/10.1016/j.cub.2021.01.064.

ACKNOWLEDGMENTS

The authors would like to thank Peter Arctander for providing access to his existing collection of leopard samples that were analyzed in this study. We also thank David Moyer for contributing samples to the collection. The wildlife management authorities of Ghana, Namibia, Tanzania, Uganda, and Zambia are thanked for collaborating with Peter Arctander in the sample collection. P.F. was supported by the Innovation Fund Denmark, Candys Foundation, and the Alfred Benzon Fund. R.H. was supported by a Villum Foundation Young investigator grant (VKR023447) and a Danish Research Council Sapere Aude grant (DFF8049-00098B). G.G.E., J.M., A.A., and K.H. were supported by a Lundbeck Foundation grant (R215-2015-4174). I.M. and X.L. were supported by a Villum Foundation Young Investigator grant (19114). R.R.d.F. thanks the Danish National Research Foundation for its funding of the Center for Macroecology, Evolution, and Climate (DNRF98).

AUTHOR CONTRIBUTIONS


DECLARATION OF INTERESTS

The authors declare no competing interests.

Received: September 8, 2020
Revised: November 13, 2020
Accepted: January 19, 2021
Published: February 25, 2021

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<td>Panthera pardus mitogenome</td>
<td>Wei et al.</td>
<td>GenBank: NC_010641.1</td>
</tr>
</tbody>
</table>

## RESOURCE AVAILABILITY

### Lead contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Kristian Hanghøj (kristian.hanghoej@gmail.com).

### Materials availability

This study did not generate new unique reagents

### Data and code availability

The accession number for the sequencing data reported in this paper is ENA: PRJEB41230. The code used for analyses in this project is available on the project’s github: https://github.com/KHanghoj/leopardpaper. Some pipelines were developed using snakemake.68

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*e1* Current Biology 31, 1862–1871.e1–e5, May 10, 2021
EXPERIMENTAL MODEL AND SUBJECT DETAILS

We analyzed fifty-three tissue samples of African leopards kindly provided from an existing collection of Peter Arctander. These samples were collected between 1993–1998 in Ghana, Namibia, Tanzania, Uganda, and Zambia (Table S1), with the assistance of the local wildlife management authorities and in compliance with the local and international legislation. Most samples were from skin tissue and were kept in a DMSO buffer in the field and stored at −20 °C as soon as possible. The samples were subsequently transferred to a −80 °C freezer for long-term storage.

METHOD DETAILS

DNA extraction

For DNA extraction, we used the QIAGEN DNeasy Blood & Tissue Kit (QIAGEN, Valencia, CA, USA), following the manufacturer’s protocol. 10μL RNase A was added to get RNA-free genomic DNA. DNA concentrations were measured with a Qubit 2.0 Fluorometer and with a Nanodrop. We subsequently used gel electrophoresis to ascertain genomic DNA quality.

Sequencing

After DNA extraction, 1 μg genomic DNA was randomly fragmented by Covaris (350 bp on average), followed by purification by Ax-yPrep Mag PCR clean up kit. The fragments were end repaired by End Repair Mix and purified afterward. The repaired DNAs were combined with A-Tailing Mix, then the Illumina adaptors were ligated to the DNA adenylate 3’ ends, followed by product purification. Size selection was performed targeting insert size of 350 base pairs. Several rounds of PCR amplification with PCR Primer Cocktail and PCR Master Mix were performed to enrich the Adaptor-ligated DNA fragments. After purification, the libraries were assessed by the Agilent Technologies 2100 Bioanalyzer and ABI StepOnePlus Realtime PCR System.

All samples were sequenced in paired-end 2x150 bp mode, 47 of these to approximately 2-5X depth of coverage on the Illumina NovaSeq platform, and six samples were sequenced to approximately 15-20X depth of coverage on the Illumina HiSeq2500 platform. In total, 7.2 billion raw reads were generated and analyzed (Table S2).

Mapping

Cleaned paired-end reads were collapsed when read termini overlapped by at least 11 base pairs (bp) using NGmerge (options: -b 11 -g -f). Collapsed reads and uncollapsed paired-end reads were mapped separately with BWA-MEM (v0.7.17; default settings) to: 1) a Panthera pardus reference genome (PanPar1.0; GenBank: GCF_001857705.1, representing a female zoo specimen of an Amur leopard), and 2) a reference genome from a female domestic cat (Felix_catus_9.0; GenBank: GCA_000181335.4). Read duplicates (markdup, default settings) were marked and removed (-F 3852) using Samtools (v1.9). We retained mapped collapsed reads, and properly paired and mapped paired-end reads. All reads with mapping quality below 30 were excluded from all downstream analysis. For mapping statistics, see Table S2.

QUANTIFICATION AND STATISTICAL ANALYSES

Reference Quality filtering: Mappability and RepeatMasker

We estimated the mappability of each site in the reference genomes using GENMAP (v1.2.0). Mappability scores were computed with 100 bp k-mers, allowing two mismatches (-K 100 -E 2), with remaining settings set to default. We excluded all sites with a mappability score less than one. We also excluded low complexity and repeat sequences as identified with RepeatMasker (v.4.0.8, sensitive mode, -engine wublast -s -no_is -cutoff 255 -frag 20000, http://www.repeatmasker.org/). Lastly, we removed all scaffolds smaller than 1 MB.

Reference Quality filtering: Global Sequencing Depth filter

We calculated the global depth (read count across all samples) for each site using ANGSD. Next, we calculated the lower and upper 1% percentile global depth threshold and excluded all sites outside this range. This analysis was done for all samples as well as separately for the low-coverage and high-coverage samples (Figure S5A).

Reference Quality filtering: Autosomal and sex-linked scaffold identification

To identify sex-linked scaffolds, we first calculated the average depth for each scaffold for each sample normalized by the average depth of the five largest scaffolds. Based on the normalized depths, we then performed a principal component analysis (PCA) and identified two main clusters of samples, likely representing males and females (Figure S5B). Finally, considering that in leopards females have two X chromosomes and males have a single X chromosome, we designated and excluded putative sex-linked scaffolds where the mean difference was greater than 0.4 between the two clusters. In addition, we excluded all scaffolds with an average normalized depth greater than 1.1 or lower than 0.9 across all samples (Figure S5C). This resulted in 23 scaffolds being identified as X chromosome-linked (Figure S5D) and excluded from further analyses.
**Reference Quality filtering: Excessive heterozygosity filter**

Several factors related to genomic repeats, like the presence of copy number variation between the reference genome and the analyzed samples, can lead to mis-mapping of reads originating from multiple genome locations to a single location. Any differences in these locations will result in inferred sites with an excess of heterozygosity that can be used to identify and mask these regions. We computed a preliminary genotype likelihoods file for common polymorphic sites (MAF \( \geq 0.05 \) and SNP p value \( < 10^{-6} \)) restricted to data with a base quality of at least 30.\(^7\) Using these genotype likelihoods as input to PCAngsd,\(^6\) we calculated per-site inbreeding coefficients (F), ranging from −1 where all samples are heterozygous to 1 where all samples are homozygous, and performed a Hardy-Weinberg equilibrium (HWE) likelihood ratio test accounting for population structure.\(^7\) To identify and exclude highly error-prone samples from the dataset, we estimated error rates in ANGSD\(^2\) using the “perfect-individual” approach as described in Orlando et al.\(^7\) Sample 3241 was selected as the “perfect-individual” sample for the analysis based on the overall mapping statistics. A consensus sequence was generated for this sample with the -doFasta 2 option in ANGSD,\(^2\) taking the most commonly observed base (-doAncError 2) as the consensus. Since the “perfect-individual” approach assumes equal genetic distances of the samples to the outgroup, we used the domestic cat reference genome as the ancestral (outgroup) sequence. Error rates were then measured as an excess/deficit of derived alleles from the outgroup compared to the “perfect-individual” sample. Both for generating the consensus sequence and for the error estimation, we restricted the data to a base quality of at least 30. Based on the estimated error rates, we removed four samples from the dataset (sample IDs 6350, 6352, 7465, 7466), which differed considerably from the “perfect-individual” approach (Figures S6A and S6B).

**Sample quality filtering: Error rates estimation**

To identify and exclude highly error-prone samples from the dataset, we estimated error rates in ANGSD\(^2\) using the “perfect-individual” approach as described in Orlando et al.\(^7\) Sample 3241 was selected as the “perfect-individual” sample for the analysis based on the overall mapping statistics. A consensus sequence was generated for this sample with the -doFasta 2 option in ANGSD,\(^2\) taking the most commonly observed base (-doAncError 2) as the consensus. Since the “perfect-individual” approach assumes equal genetic distances of the samples to the outgroup, we used the domestic cat reference genome as the ancestral (outgroup) sequence. Error rates were then measured as an excess/deficit of derived alleles from the outgroup compared to the “perfect-individual” sample. Both for generating the consensus sequence and for the error estimation, we restricted the data to a base quality of at least 30. Based on the estimated error rates, we removed four samples from the dataset (sample IDs 6350, 6352, 7465, 7466), which differed considerably from the “perfect-individual” estimate (Figures S6A and S6B).

**Sample quality filtering: BLAST analyses of mtDNA**

To ensure that all samples were leopard samples, we investigated the genetic similarity between the mitochondrial genome for each sample and the leopard mitogenome. Mitochondrial genomes for each sample were reconstructed by creating consensus sequences using BLAST analyses of mtDNA which differed considerably from the “perfect-individual” estimate (Figures S6A and S6B). All samples were inspected and summary statistics for the samples with extreme results are available in Table S4. Since these overlapped with the samples with high error rates this analysis did not lead to removal of any additional samples.

**Sample quality filtering: Identification of related and duplicated samples**

Using the methodology described in Waples et al.,\(^7\) we identified and removed closely related and potentially duplicated samples by first inferring two-dimensional site frequency spectrum (2d-SFS) for each pair of samples. Then we calculated three statistics directly from the 2d-SFS for each pair of samples: R\(^0\), R\(^1\), and KING-robust kinship\(^7\) that can be used to identify close familial relatives\(^7\) without estimates of population allele frequencies.

Using this approach, we identified 12 duplicated samples. All of these had KING-robust kinship values > 0.470, R\(^1\) values > 10, and R\(^0\) values < \(10^{-6}\). Within each set of duplicated samples, we removed the sample with the highest error rate, thus removing eight samples for further analyses (sample IDs 6342, 6344, 6348, 6349, 6353, 6556, 6357, 6359). All duplicated samples originated from Zambia (Table S2). We also identified pairs of related samples, down to second-degree relatives (expected kinship = 0.125), based on R\(^0\), R\(^1\), and KING-robust kinship following the criteria from Manichaikul et al.\(^7\) and Waples et al.\(^7\) In total, we found two pairs of first-degree relatives: one parent-offspring pair and one full-sibling pair, and seven second-degree pairs of relatives (Table S5). For some of the analyses we removed one of the pairs from each of the pairs of first-degree relatives (samples 8647 and 7943).

For a summary of the sample sizes used for each analysis, see Table S3.

**Genotype likelihoods, SNPs, and genotype calling**

We used ANGSD\(^2\) to estimate genotype likelihoods using the genotype likelihood (GL) model from GATK\(^6\) inferring major and minor from GL data (-doMajorMinor 1), estimating allele frequencies from the GL data (-doMaf 1), and applying the strictref filter (-sites). We restricted the analysis to bases with base quality of at least 30.

For SNP calling we used a likelihood ratio test (p value = \(10^{-6}\)) as implemented in ANGSD.\(^2\) We only included common alleles (MAF > 0.05).
For the five high-coverage samples, we called genotypes using bcftools (v.1.9). We called the genotypes per sample using the multiallelic caller methodology (-m). We disabled base alignment qualities (BAQ: -B) and restricted the analysis to base qualities of at least 30. In addition to the strictref filter (-T), we also excluded sites with a depth of coverage below 10 and heterozygous calls with less than 3 reads support for each allele using plugin setGT to reduce genotype calling errors. These additional genotype calling filters were validated based on heterozygous calls in runs of homozygosity (ROH) in these five samples (Figure S4A).

**PCA analyses**
We performed PCA (Figure 2A) on 39 individuals based on genotype likelihoods using PCAngsd, which accounts for missingness in low-coverage samples. We excluded the two first-degree relatives (sample IDs 8647 and 7943) from the analysis. We used three eigenvectors to model population structure in the iterative procedure of PCAngsd as anything higher would reflect genetic variation within populations (Figure S2A).

**NGSAdmixture**
We estimated admixture proportions for 38 individuals with NGSAdmixture (Figure 2B) based on genotype likelihoods. Besides removing the two first-degree relatives, we also removed the only individual sampled in Uganda (sample ID 8540), as unbalanced sample sizes prevent from accurately characterizing the genetic composition of its population of origin. We ran NGSAdmixture from K = 2 to K = 6. For each K, we performed several independent optimization runs either until convergence, defined as having the 3 top maximum likelihood results within 2 log-likelihoods unit of each other, or until a limit of 100 runs was reached without convergence. For the values of K where the results converged (Figure S2), we assessed the model fit of the resulting admixture proportion with evalAdmixture, which estimates the pairwise correlation of the residual between individuals. Individuals within a population with a bad model fit show a positive correlation of their residuals (Figure 2D).

**Runs of homozygosity (ROH) analysis**
We estimated ROH with the filtered genotypes of high coverage samples (see STAR Methods). We used the command ‘–homozyg’ in PLINK v1.9 with default settings, except using a minimum of 500 kilobases to detect a ROH (–homozyg-kb 500).

**D-statistics**
We used the D-Statistics (ABBA-BABA) method to test for population homogeneity and gene flow. We used ANGSD option -doAbbababa 1, which samples a random base at each position to estimate the counts of ABBA and BABA sites between each triplet of H1, H2 and H3 individuals in blocks of a predefined size of 5 MB. We calculated the Z-score based on jackknife procedure with 475 blocks for data mapped to domestic cat reference and 567 blocks for samples mapped to Amur leopard.

First, we explored the homogeneity of the designated groupings (Figure 3). For each sampling location group, we tested all low-depth individuals in a pairwise manner as (H1, H2) against the remaining African groups (H3). We excluded all individuals from Uganda and Tanzania East due to low sample size, and three individuals with distinct ancestry profiles in the NGSadmix analyses with K = 4 compared to the rest of samples in their group (marked with an asterisk in Figure 2). The Amur leopard reference (PanPar1.0) was used as an outgroup (H4). Second, we tested for relative differences in gene flow between the African groups (H1, H2) and the Asian leopard (H3; ID 3042211). As an outgroup, we used the cat reference genome (H4). We excluded one Zambian sample (sample ID 2523) due to low mapping quality, which the D-statistics is sensitive to when placed in H1 or H2, and the same three individuals with distinct ancestry profiles in the NGSadmix analyses that were also excluded from the D-statistics to test for population homogeneity.

**Site frequency spectrum**
We estimated the site frequency spectrum (SFS) with the realSFS program (v.0.931) within ANGSD, using default settings, based on saf files generated with ANGSD (-dosaf 1 -gl 2 -minQ 30). This procedure was used to estimate one-dimensional (1d) SFS per individual and per population and two-dimensional (2d) SFS for all pairs of individuals and populations.

**SFS-based analyses: FST estimation**
A genome-wide estimate of \( F_{ST} \) (Table 1) for each pair of populations was computed directly from the 2d-SFS, estimated with realSFS, using the Reich estimator. To estimate \( F_{ST} \) between a pair of high-coverage individuals, we used as input the 2d-SFS based on called genotypes.

**SFS-based analyses: Estimation of heterozygosity**
We estimated heterozygosity for each sample in ANGSD as the proportion of heterozygous loci in the obtained per-individual 1d-SFS. For the population and species comparison (Figure 6B), we only used the final dataset of 41 samples, minus two samples with slightly elevated error rates, which show a linear trend between heterozygosity and error rates (Figure S6C). For genetic diversity comparisons, we obtained whole-genome-based estimates from the literature (see Table S6 for details). To ensure that these were comparable to our estimates we also re-estimated those for the genomes that we re-analyzed for our PSMC analyses.
We used PSMC\textsuperscript{30} to estimate the population size trajectory back through time for our five high coverage African leopards. We followed the recommended procedure for generating a diploid sequence per individual using bcftools (v 1.9)\textsuperscript{67} and -c for calling genotypes. PSMC was applied with default settings. For scaling, we used a mutation rate of 10\textsuperscript{\(-8\)} and generation time of 5 and 7.5 years.\textsuperscript{5,10,11} Five years is the generation time most commonly used in similar studies, but the IUCN\textsuperscript{11} lists the leopard generation time at 7.42 years. Hence, we consider 7.5 more appropriate (Figure 6A), but we also performed the analysis with a generation time of 5 years (Figure S7A) for consistency with previous studies.

For PSMC comparisons, we re-analyzed whole genome data from published studies of other big cats, including Amur leopards,\textsuperscript{5} tiger,\textsuperscript{31} lion,\textsuperscript{31} jaguar,\textsuperscript{10} and snow leopard.\textsuperscript{31} Briefly, we mapped the sequencing data to the cat reference genome using the same pipeline as for the African leopard sequencing data. Unless otherwise noted, we also applied the strictref filter to all analyses.

Identity-by-state (IBS)

We estimated the pairwise genetic distance matrix (IBS) between all individuals by randomly sampling a single read from each position from each sample applying the strictref filter, using -dolIBS in ANGSD. This determines the allelic distance (0 or 1) in sites with information from both individuals and calculates the average identity-by-state (IBS) across all sites.

IBS-based analyses: Neighbor-joining (NJ) tree

We used the IBS matrix to construct a NJ tree (Figure 2C) using the R package ape\textsuperscript{22} (https://cran.r-project.org/package=ape). The NJ tree included samples with distinct ancestry profiles as inferred from NGSadmix, denoted with an asterisk.

IBS-based analyses: Estimation of Effective Migration Surfaces (EEMS)

We used the pairwise IBS matrix as input to EEMS\textsuperscript{29} to estimate the relative migration rates (Figure 5, Figure S3). For each sampling location we visually inferred the centroid of its geographical coordinates and used this as the coordinate input to EEMS. EEMS was run using the runeems_snps program and default settings for 5 million steps and a burn-in of 1 million steps, with 400 demes and the number of sites (n = 1,374,592,127) based on the IBS matrix. For comparison, we ran EEMS with the same settings for other African mammals with available SNP datasets - waterbuck,\textsuperscript{19} African buffalo (Nursyifa et al., in prep.), and common warthog (Jørgensen et al., in prep.). Furthermore, we included the savanna African elephant\textsuperscript{16} and African lion,\textsuperscript{77} for which microsatellite datasets with continent-wide sampling were available. For the microsatellite data, the runeems-sats was run using the genotypes and individual sample coordinates as input and the same settings as above. The elephant data by Wasser et al.\textsuperscript{76} has been previously used for the estimation of relative migration rates in the original EEMS publication.\textsuperscript{29} Unlike Petkova et al. we used the full savannah elephant dataset (n = 1001), including samples assumed to be hybrids; however, the results are very similar.

For all species, the same habitat outline was used and was selected to encompass the sampling localities of all included species. The outline was drawn manually using the tool available here: http://www.birdtheme.org/useful/v3tool.html. The results were visualized in RStudio v1.2.5033 using the make_eems_plots script (available here: https://github.com/dipetkov/reemsplots2) as the log10-transformed migration rates with posterior probabilities > 0.90. An outline of the equatorial rainforest was added based on the spatial distribution of African rainforests in Mayaux et al.\textsuperscript{18}