

RESEARCH ARTICLE

GENOMIC INSIGHTS INTO SAUDI ARABIAN BIODIVERSITY: A SURVEY OF ANIMALS' WHOLE GENOME SEQUENCING STUDIES

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Abstract

Saudi Arabia has a rich and diverse array of fauna, which faces constant threats from human activities such as habitat destruction and overhunting. This study aimed to provide an overview of the animals in Saudi Arabia that have undergone whole genome sequencing, contributing to their conservation and management efforts. The literature was searched in two databases, Web of Science and Google Scholar, using various combinations of keywords. A total of 14 articles published between 2017 and 2023 were retrieved. These studies covered 13 animal taxa, with mitochondrial genome sequencing being the predominant focus in 78% of the articles, largely facilitated by Illumina technology. Notably, the surveyed literature highlighted a significant gap in genomic coverage, particularly concerning endangered and endemic species. Despite the strides made in understanding species evolution and population genetics, the limited genomic data underscore the urgent need for expanded research efforts, including the incorporation of more local samples. Such endeavors hold immense potential in bolstering conservation and management strategies tailored to Saudi Arabia's unique biodiversity.

Keywords: Animal, Biodiversity, Illumina, Mitochondrial genome, Nuclear genome, NGS, Saudi Arabia.

1. Introduction

Saudi Arabia's remarkable biodiversity, encompassing a diverse array of flora and fauna, is a testament to its unique natural heritage. This heritage, characterized by the combination of traits from African and Eurasian continents, necessitates special consideration and conservation [1]. The Kingdom of Saudi Arabia harbors a diverse fauna, including 79 mammal species, 432 bird species, 862 Saltwater fish species, 103 reptile species, and 7 amphibian species [1]. However, this valuable biodiversity is confronted with numerous challenges, including habitat destruction, over-grazing, overhunting, alterations in intensive modern agricultural practices, pollution, recreational activities, urban expansion, and the introduction of exotic and invasive species [1]. The cumulative impact of these challenges disrupts the delicate balance of Saudi Arabia's ecosystems and puts its unique flora and fauna at risk of extinction [1].

Genomic technologies have emerged as a promising tool for characterizing biodiversity [2]. These technologies,

in conjunction with traditional conservation efforts, can aid in the prioritization of conservation strategies [2]. As a result, several national and international initiatives have been initiated to enhance the availability of genetic resources for conservation purposes. These include the Global Invertebrate Genomics Alliance [3], the Vertebrate Genomes Project [4] the Bat1K Project [5], and the Earth BioGenome Project (EBP) [6], which seeks to catalog the genome sequence variation of all of Earth's eukaryotic species.

Whole genome sequencing (WGS) provides the most comprehensive data about a given organism's genome, which is the complete set of genetic material, comprising nuclear DNA and mitochondrial DNA [7]. Next-generation Sequencing (NGS) technologies, which emerged in 2005, have revolutionized biodiversity research by enabling the parallel sequencing of millions of short reads at a fraction of the cost and time of previous methods [8]. The NGS is a potent tool that is revolutionizing how we perceive and safeguard the variety of life on Earth.

Whole genome sequencing is a powerful tool for conservation biology. It can be used to identify and characterize endangered species that are difficult to study using traditional methods [9]. It can also be used to understand the genetic diversity of populations and how it affects their adaptation and resilience to environmental changes [10]. A third application is to track the movement of individuals and populations across landscapes and borders, which can help monitor their distribution and migration patterns [2]. These applications have many benefits to develop effective conservation strategies, such as captive breeding programs, assisted reproduction techniques, and anti-poaching measures [2]. Whole genome sequencing gives conservationists new insights and solutions for biodiversity.

Aligning with the Vision 2030 objectives, the Kingdom of Saudi Arabia is committed to protecting the environment and conserving biodiversity [11]. This commitment has led to projects such as the Kingdom of Saudi Arabia Native Genome Project (KSA NGP), a scientific initiative that aims to sequence and analyze the genomes of all native plants and animals in Saudi Arabia [12]. This project will generate a comprehensive dataset of the country's biodiversity, which will be used to identify new species and subspecies and to develop novel conservation and management tools [12].

This review article sets out to provide an overview of animals in Saudi Arabia that have undergone complete genomic sequencing. The review aims to synthesize and evaluate the existing research, shedding light on the latest progress in this field and paving the way for future research opportunities involving a larger number of animals. Despite the limited amount of research available in this field, these studies encompass a range of species, from mammals such as the camels [13] and Arabian horses [14] to reptiles [15], bony fish [16], coral reefs [17], and insects [18].

2. Methods

This review primarily focuses on examining the current state of knowledge regarding whole-genome sequencing-based studies on Saudi Arabian animals. The literature survey was conducted using the Google Scholar and Web of Science ISI databases in October 2023. The search utilized the following combinations of keywords: 'Arabia + chromosome-scale'; 'Arabia + whole-genome + Animal'; 'Red Sea + Arabia + Mitogenome'; 'Red Sea + Arabia + Mitochondrial genome'; 'Arabia + Mitochondrial genome + Animal'.

The keywords were searched in the title, abstract, and keywords fields of the articles. Only peer-reviewed articles reporting original research on whole-genome sequencing-based studies conducted on animal samples collected from Saudi Arabia were included. Articles focusing on other genomic studies, such as transcriptomics, were excluded. A total of 14 articles meeting the inclusion criteria were selected for full-text analysis.

Data from each article was extracted and organized in an Excel spreadsheet (available in supplementary material). The following information was recorded for each article: publication year, first author name, country, affiliation, DOI, species name, classification, locality, current species status, genome type and size, sequencing platform, study approach, study aim, key results, conclusions, and implications.

Descriptive statistics were utilized to report the frequency and distribution of the articles by publication year, first author affiliation, and genome type. Graphs were created using Excel to illustrate trends and patterns in the data.

3. Results

The search yielded 14 articles published between 2017 and 2023 (Figure 1), with eight originating from Saudi organizations and six from international entities (Figure 2). These publications encompassed the complete genome sequencing of 13 animal taxa spanning diverse classes and families, including Actinopterygii (2), Mammalia (4), Reptilia (2), Anthozoa (2), Arachnida (1), and Insecta (2), with several species flagged as endangered, native, or endemic (Table 1). Notably, 78% of the articles focused on mitochondrial genome sequencing, primarily employing Illumina technology (Table 1). Since 2018, four articles have delved into nuclear genome studies, with one 2023 publication associated with whole genome data (Figure 1). Genome assembly reports emerged as the predominant topic across these articles, with a notable emphasis on species evolution through various studies probing population genetics, genome characterization, and phylogenomics.

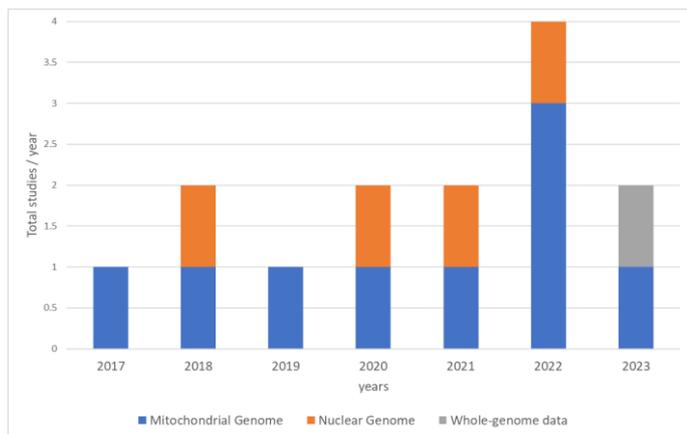


Fig. 1: The number of whole-genome sequencing studies in animals of Saudi Arabia by the year of publication

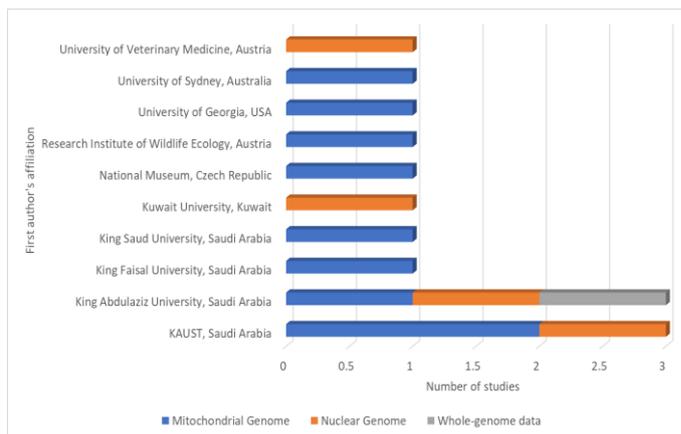


Fig. 2: The number of whole-genome studies in animals of Saudi Arabia by the first author's affiliation.

Table 1: Animal genomes sequenced in Saudi Arabia

Animal	Status	Genome type	Genome size (bp)	Sequencing technology	Reference
Vertebrates					
Actinopterygii					
<i>Chaetodon austriacus</i> Rüppell	Red Sea endemic	Nuclear Genome	712,378,618	Illumina HiSeq 2000	[19]
<i>Oreochromis spilurus</i> Günther subsp. <i>saudii</i>	Cultured marine tilapia	Nuclear Genome	6,144,000,000	Illumina Hi-Seq	[16]
Mammalia					
<i>Camelus bactrianus</i> L.	Multipurpose livestock species	Nuclear Genome	NA	Illumina HiSeq	[20], [21]
<i>Camelus dromedarius</i> L.		Nuclear Genome	NA	Illumina Hiseq 2000	[21]
<i>Camelus dromedarius</i> L.		Mitochondrial Genome	16,379	Illumina Hiseq 2000	[22]
<i>Panthera pardus</i> L. subsp. <i>nimr</i> Hemprich & Ehrenberg	Critically Endangered	Whole-genome data	NA	Illumina HiSeq 4000	[23]
<i>Equus caballus</i> L. (Kehilan)	The Arabian horse breed is are pure breed used to improve other horses worldwid	Mitochondrial Genome	16,649	Sanger Sequencing	[24]
<i>Equus caballus</i> L. (Hamdani)		Mitochondrial Genome	16,655	Sanger Sequencing	[24]
<i>Equus caballus</i> L. (Seglawi)		Mitochondrial Genome	16,656	Sanger Sequencing	[14]
<i>Equus caballus</i> L. (Hadban)		Mitochondrial Genome	16,655	Sanger Sequencing	[14]
Reptilia					
<i>Hemidactylus farasani</i> Šmid et al.	Endemic	Mitochondrial Genome	16,815	Illumina NovaSeq 6000	[15]
<i>Hemidactylus almakhwah</i> Šmid et al.	Endemic	Mitochondrial Genome	16,932	Illumina NovaSeq 6000	[15]
Invertebrates					
Anthozoa					
<i>Dendrophyllia minuscula</i> Bourne	Main framework builder in the Red Sea lower mesophotic and deep waters	Mitochondrial Genome	19,054	ezRAD, NovaSeq 6000	[25]
<i>Porites harrisoni</i> Veron	Common corals	Mitochondrial Genome	18,630	ezRAD, Illumina HiSeq 4000	[26]
Arachnida					
<i>Rhipicephalus camicasi</i> Morel, Mouchet & Rodhain	Pest for domestic animals	Mitochondrial Genome	14,725	Illumina HiSeq 2500	[27]
Insecta					
<i>Apis mellifera</i> L. subsp. <i>jemenitica</i> Ruttner	Native subspecies of Arabian Peninsula	Mitochondrial Genome	16,352 to 16,445	Illumina Hi-Seq	[18]
<i>Jebusaea hammerschmidtii</i> Reiche	Pest of the date palm	Mitochondrial Genome	15,619	Illumina NextSeq 500	[28]

4. Discussion

The fauna of Saudi Arabia encompasses a rich diversity of species facing numerous conservation challenges and requires special consideration and conservation [29]. In this context, genomic technologies are emerging as a promising tool that can complement traditional conservation efforts and help in prioritizing conservation strategies [2]. This review aims to provide an overview of the latest progress in whole genome sequencing-based studies on Saudi Arabian animals and their implications for conservation.

This survey revealed a limited number of genomic-scale studies (14) focusing on Saudi Arabian fauna. However, there has been a noticeable uptick in the utilization of genome-wide markers over the past six years (Figure 1), signaling promising progress. This surge can be attributed to the increased accessibility and affordability of genome sequencing technologies, coupled with advancements in analytical techniques [30]. Notably, next-generation sequencing, particularly Illumina technology, was the main sequencing technology used in the surveyed studies (Table 1) as it made whole-genome sequencing more affordable and accessible for labs of all sizes [31].

Mitochondrial genome sequencing emerged as the predominant approach in the retrieved studies (78%) compared to nuclear genome sequencing (Figure 1, Table 1). This preference may stem from the relatively smaller size of mitochondrial genomes, coupled with lower bioinformatics and analysis requirements [32]. Additionally, mitochondrial genomes offer unique advantages, including maternal inheritance, rapid evolution, and high copy numbers [33], making them invaluable for exploring diverse aspects of animal biology.

Despite the progress, the genomic sequencing of Saudi Arabian fauna remains limited, encompassing only a small fraction (13 species and subspecies) of the total animal taxa documented in the region. However, it is essential to note that ongoing initiatives, such as the KSA native genome project, are expected to expand these numbers in the near future [34]. Nonetheless, even with the current limited scope, these studies have contributed significantly to our understanding of genetic variations among different species, thereby informing their effective protection and management in a sustainable manner.

5. Conclusion

The survey highlights progress in genome sequencing efforts for Saudi Arabian animals, revealing sequencing data for only 13 taxa across diverse classes and families. This limited coverage underscores a significant gap in our understanding of the country's biodiversity. Notably,

numerous endangered species, including the Nubian ibex, Arabian jird, and Sind bat, remain unsequenced, hindering targeted conservation efforts. Future research must prioritize sequencing these rare and threatened species to glean valuable insights essential for their effective conservation and management. Bridging this genomic knowledge gap is crucial for safeguarding Saudi Arabia's biodiversity and ensuring its preservation for future generations.

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رؤى جينومية للتنوع البيولوجي في المملكة العربية السعودية: دراسة مسحية لأدبيات تسلسل الجينوم الكامل للحيوانات

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المُلخَص

تمتلك المملكة العربية السعودية مجموعة غنية ومتنوعة من الحيوانات، التي تواجه تهديدات مستمرة من الأنشطة البشرية مثل تدمير الموائل والصيد الجائر. تهدف هذه الدراسة إلى تقديم لمحة عامة عن الحيوانات في المملكة العربية السعودية التي خضعت لتسلسل الجينوم الكامل، مما قد يساهم في جهود الحفاظ عليها وإدارتها. تم البحث في الأدبيات في قاعدتي بيانات، Google Scholar و Web of Science، باستخدام عدة توليفات من الكلمات المفتاحية. تم استرجاع إجمالي 14 مقالة منشورة بين عامي 2017 و 2023. غطت هذه الدراسات 13 نوع وتحت نوع حيواني، وكان تسلسل جينوم الميتوكوندريا هو السائد في 78% من المقالات، وقد تم تسهيل ذلك إلى حد كبير بواسطة تقنية Illumina. ومن الجدير بالذكر أن الأدبيات التي تم مسحها سلطت الضوء على فجوة كبيرة في التغطية الجينومية، لا سيما فيما يتعلق بالأنواع المهددة بالانقراض والمتوطنة. وعلى الرغم من الخطوات التي تم تحقيقها في فهم تطور الأنواع وعلم الوراثة السكانية من خلال هذه الدراسات، فإن البيانات الجينومية المحدودة تؤكد الحاجة الملحة لجهود بحثية موسعة، بما في ذلك دمج المزيد من العينات المحلية. تحمل مثل هذه المساعي إمكانات هائلة في تعزيز استراتيجيات الحفظ والإدارة المصممة خصيصاً للتنوع البيولوجي الفريد في المملكة العربية السعودية.

الكلمات المفتاحية: التنوع الحيواني، تسلسل الجينوم الكامل، تسلسل الجيل التالي، جينوم، جينوم الميتوكوندريا، المملكة العربية السعودية.

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