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RESEARCH ARTICLE

GENOMIC INSIGHTS INTO SAUDI ARABIAN PLANT BIODIVERSITY: PROGRESS AND FUTURE DIRECTIONS

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Abstract

Saudi Arabia, despite its arid environment, harbors a rich plant diversity with approximately 2,253 species. However, the conservation of this biodiversity faces significant challenges due to habitat loss, climate change, and limited genomic data. This study provides a comprehensive survey of the current state of plant genomic research in Saudi Arabia, highlighting progress made and identifying key gaps in the literature. A survey of scientific databases identified 46 relevant studies published between 2010 and 2024, reflecting growing interest in the genomic analysis of Saudi plants. These studies cover nuclear, chloroplast, and/or mitochondrial genomes of 51 plant species from 19 families, with a predominant focus on medicinal plants collected from the western and southwestern regions. Among these, the Apocynaceae family, known for its medicinal species, is the most frequently represented in genomic research. Chloroplast genome data is the most prevalent, accounting for 75.4% of the genomes analyzed, underscoring its utility in taxonomic and phylogenomic analyses. Nuclear genome data, though less frequent (16.3%), has increased, particularly through initiatives like the KSA Native Genome Project. Mitochondrial genome data remains sporadic (8.1%), contributing to the understanding of gene transfers and genetic variation. While genomic research on Saudi plants is still limited, existing data provide essential insights for conservation, understanding plant adaptation, and guiding future research. This review underscores the need for expanded genomic studies, particularly nuclear genome sequencing, and greater focus on rare, endemic, and endangered plants to support biodiversity conservation and agricultural innovation in Saudi Arabia.

Keywords: Chloroplast sequencing, Genomic research, Medicinal plants, Nuclear genome sequencing, Plant biodiversity conservation, Saudi Arabia.

1. Introduction

Saudi Arabia, the largest arid land in the Arabian Peninsula, covers an area of approximately 2,250,000 km^2, known for its diverse environmental factors such as topography, geomorphology, climate, and soil [1]. These variations contribute to the unique ecological habitats, vegetational zones, and abundant flora found within the country [2]. Saudi Arabia is blessed with a wide array of ecosystems and a diverse range of species [3]. There are around 2,250 species, including 27 fern species, which make up about 1.2% of the total flora, and 2,223 seed plants, accounting for approximately 98.8% [4]. These species are further categorized into 835 genera and 142 families. Therefore, Saudi Arabia is a rich and valuable source of biodiversity that deserves more attention and conservation efforts from both national and international stakeholders.

The global rise in endangered species is mirrored in the Kingdom of Saudi Arabia, where a significant portion of plant and animal species, approximately 33%, are officially recognized as being at risk of extinction. Moreover, there is a concerning possibility of a drastic decline, estimated at around 70%, in the population sizes of plants and animals [5]. Ecologists place significant emphasis on the fact that the main causes of biodiversity decline are habitat loss, which occurs when natural areas like forests, wetlands, and grasslands are converted for urban and agricultural purposes, as well as the introduction of invasive species. However, they acknowledge that as we move further into the 21st century, climate change has the potential to become a leading cause of biodiversity loss [6]. This emphasizes the importance of intensifying the endeavors to encourage the sustainable utilization of genetic resources and devise effective conservation strategies for them. While preserving and restoring habitats remain the main approaches for safeguarding biodiversity, genomic technologies provide a range of innovative methods for identifying biodiversity [7].

Genomics is the study of all the genes of a given cell, tissue, and organism [8]. It uses large-scale sequencing and bioinformatics to determine and analyze the entire DNA sequence of various organisms. One main goal of plant genomics is to reveal the adaptive mechanisms that enable plants to survive in harsh environments with extreme heat, drought, and salinity [9]. Plant cells contain three types of genomes—nuclear, mitochondrial, and chloroplast (plastome)—that each contribute uniquely to the overall genetic landscape [10]. By comparing genomic variations among species, researchers can discover genes for key traits such as drought tolerance and heat resistance [11]. This can help breed improved cultivars with higher resilience and productivity [8]. Additionally, plant genomics provides valuable insights into the evolutionary history of species [12]. It can reconstruct phylogenetic relationships, explain speciation patterns, and identify adaptation signatures. These findings enhance our knowledge of plant evolution and have implications for biodiversity conservation and priority areas [13].

Saudi Arabia's Vision 2030 emphasizes the protection of the environment and the preservation of biodiversity as key goals for sustainable development [14]. To achieve these goals, the country has launched the Native Genome Project (NGP), a collaboration between King Abdullah University of Science and Technology (KAUST) and the Ministry of Environment, Water and Agriculture (MEWA). The NGP aims to interrogate hundreds of terrestrial and aquatic ecosystems and understand how they adapt to extreme environments [15]. This project will not only enhance the scientific knowledge of Saudi Arabia’s biodiversity, but also provide valuable data for environmental protection, restoration, and management.

This review article aims to provide a comprehensive survey of genomic studies conducted on Saudi Arabian plants. This project would serve as an extensive record of the progress made in plant genomics field within Saudi Arabia. It would summarize the different plant species that have been studied, the methodologies employed, and the key findings and insights obtained from these studies. This documentation is essential for researchers and policymakers to understand the current state of plant genomics in the country.

2. Methods

This review focuses primarily on examine the current state of knowledge on genomic studies on Saudi Arabian Plants. The literature survey was carried out in the Google Scholar and Web of Science databases. The search was performed on July 2024 using the following combination of keywords: ‘Arabia+ plastome’; ‘Arabia + chloroplast genome’; ‘Arabia+ mitochondrial genome + plant’; ‘Arabia + Mitogenome + plant’; ‘Arabia + plastid genome’; Arabia + genome size + plant’; ‘Arabia + chromosome-scale + plant’.

These keywords were searched within the title, abstract, and keywords fields of the articles. Only peer-reviewed sources reporting original research on plant genomics, specifically involving plants collected from Saudi Arabia, were included. Additionally, one poster related to the KSA native genome project was also considered. Articles focusing on other types of genomic studies, such as transcriptomics, were excluded.

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

3. Results

The survey of scientific databases identified 46 materials related to the genomics of Saudi Arabian plant biodiversity, covering nuclear, chloroplast, and/or mitochondrial genomes. These materials include research articles, master’s theses, and a poster, with publication dates ranging from 2010 to 2024. As shown in Figure 1, there has been a notable rise in studies on plant genomics in Saudi Arabia, reaching a peak of 13 studies in 2022.

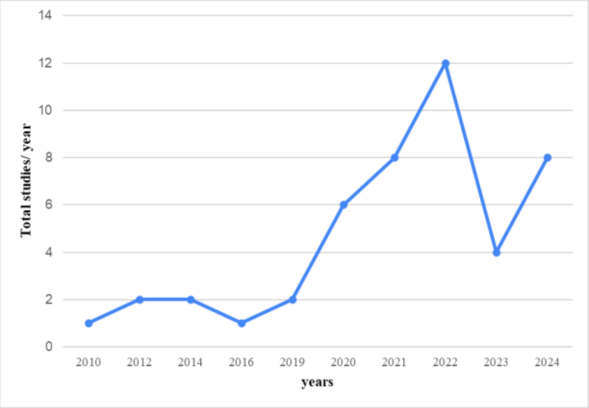

Fig. 1: Trends in the number of publications per year on plant genomics in Saudi Arabia, based on data retrieved from Google Scholar and Web of Science.

These studies investigated 51 plant species, primarily of medicinal value, from 19 families (Figure 2), with samples predominantly collected from the western and southwestern regions of Saudi Arabia. Among these, economically significant cultivars such as date palm and Hassawi rice were included (Table 1). The most represented family is Apocynaceae, accounting for 18% of the species studied, followed by Capparaceae (12%), Fabaceae (8%), and Boraginaceae (8%). Other notable families include Acanthaceae, Heliotropiaceae, and Zygophyllaceae, each contributing 6%. Lamiaceae and Poaceae each account for 4%, while the remaining families, including Cupressaceae, Moraceae, and Malvaceae, each represent 2% of the species studied (Figure 2).

Figure 3 and Table 1 present a breakdown of the number and types of genomic data generated each year. Chloroplast genome data are the most frequent (75.4%), with significant peaks in 2021 and 2022. Nuclear genome data show a smaller but noticeable increase (16.3%), particularly in 2022. Mitochondrial genome data, though less common (8.1%), have been generated sporadically, with notable contributions in 2012 and 2014.

The 3D bar graph in Figure 4 illustrates the distribution of sequencing technologies used across different genome types in the surveyed literature. Chloroplast genomes were sequenced using short-read technologies, predominantly with Illumina, followed by DNBseq. Nuclear genomes were sequenced primarily with long-read technologies, mainly Pacific Biosciences technology (PacBio). The sequencing of mitochondrial genomes relied on Roche GS FLX & SOLiD, with occasional use of Illumina and PacBio.

Chloroplast genomic research has primarily addressed taxonomic questions through comparative genomic and phylogenomic analyses. Nuclear genomic studies were mainly associated with the Native Genome Project (NGP), reporting the construction of the first large-scale reference sequence data, which serves as a foundation for future genetic research. Mitochondrial genomes have been sequenced for several species, including date palm cultivars (*Phoenix dactylifera*), with analyses focusing on single nucleotide polymorphisms (SNPs)[16], [17] and Hasawi rice (*Oryza sativa* L.) and its hybrid, which involved sequence variation analysis and breeding history[18]. Additionally, the mitochondrial genome of the medicinal species *Rhazya stricta* Decne. was sequenced to elucidate inter-compartmental genome transfers and evolutionary patterns [19]. Detailed information is provided in Table 1 and Supporting Information.

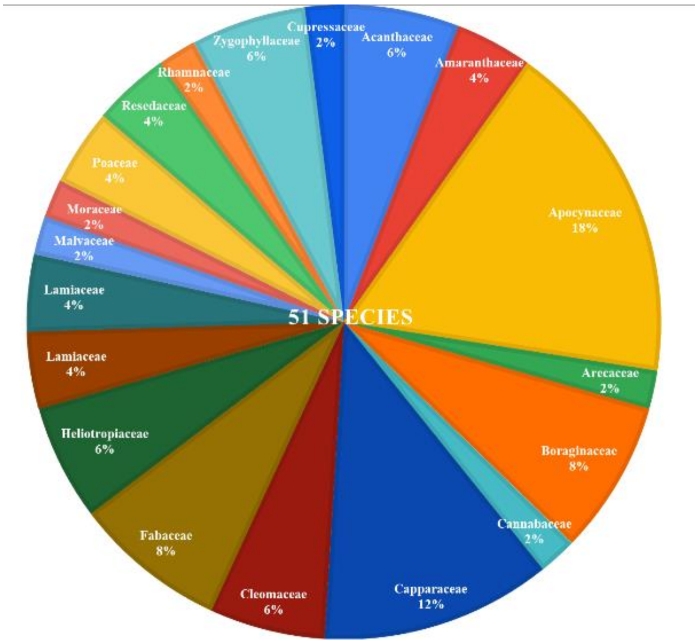

Fig. 2: Distribution of 51 plant species across 19 families, primarily of medicinal value, as identified in the surveyed studies.

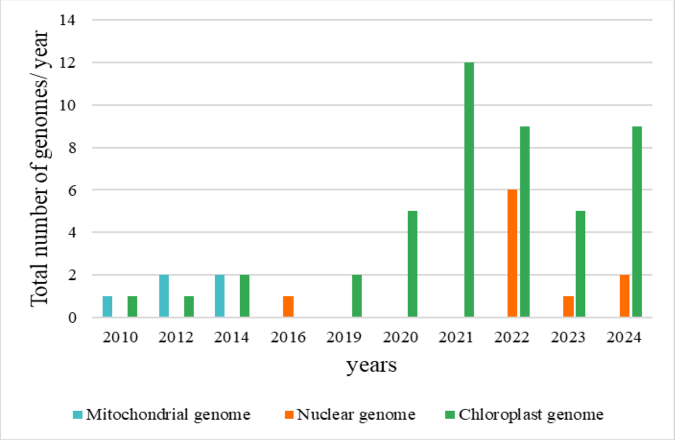

Fig. 3: Number and types of genomic data generated per year (mitochondrial, nuclear, chloroplast) for Saudi Arabian plants.

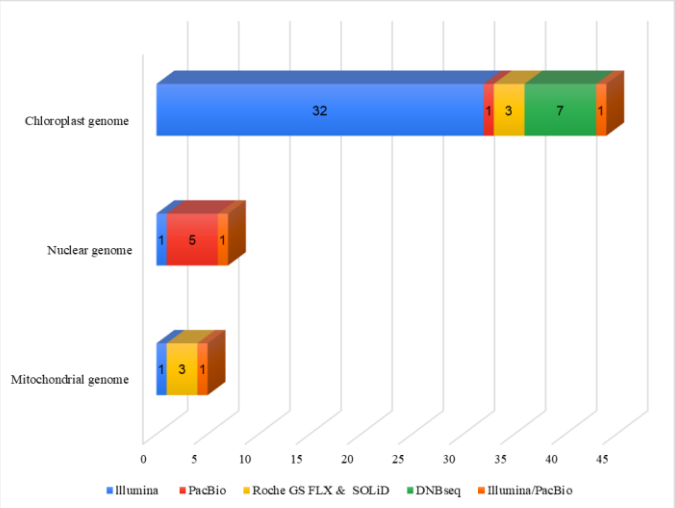

Fig. 4: Distribution of Sequencing Technologies for Different Genome Types in the surveyed Studies

Table 1: Plant genomic data generated in Saudi Arabia. All genome sizes are given in base pairs (bp), unless otherwise specified. NA: Not Available; PacBio: Pacific Biosciences

Plant	Status	Genome type	Genome size	Sequencing platform	Reference
Angiosperms					
Acanthaceae Juss.					
Barleria prionitis L.	endangered medicinal	plastome	152,217	Illumina Hiseq2500	[20]
Blepharis ciliaris (L.) B.L.Burtt	medicinal	plastome	149,717	Illumina Hiseq2500	[22] ,[21]
Justicia flava (Forssk.) Vahl	endangered medicinal	plastome	150.888	Illumina	[23]
Amaranthaceae Juss.					
Haloxylon persicum Bunge	common native species	nuclear genome	NA	PacBio Hifi	[24]
Suaeda monoica Forssk. ex J. F. Gmel*.*	medicinal	plastome	151,789	NA	[25]
Apocynaceae Juss.					
Adenium obesum (Forssk.) Roem. & Schult.	medicinal	plastome	154,437	Illumina	[26]
Calotropis procera (Aiton) W.T.Aiton	stress tolerant medicinal shrub	nuclear genome	221Mb	Illumina	[27]
Caralluma quadrangula (Forssk.) N.E.Br.	medicinal	plastome	161,456	Illumina	[28]
Desmidorchis penicillata (Deflers) Plowes	medicinal	plastome	161,776	Illumina NovaSeq PE150	[29]
Desmidorchis retrospiciens Ehrenb.	medicinal	plastome	162,277	Illumina NovaSeq PE150	[29]
Duvalia velutina Lavranos	medicinal	plastome	154, 478	Illumina Hisq 2500	[30]
Gomphocarpus sinaicus Boiss.	medicinal	plastome	162,570	Illumina Hisq 2500	[30]
Pergularia tomentosa L.	medicinal	plastome	164,213	Illumina Hiseq2500	[32] ,[31]
Rhazya stricta Decne.	medicinal	plastome	154,841	Illumina Hiseq2000/PacBio RS II	[19]
Rhazya stricta Decne.	medicinal	mitochondrial genome	548,608	Illumina Hiseq2000/PacBio RS II	[19]
Rhazya stricta Decne.	medicinal	nuclear genome	200 Mb	Illumina HiSeq 2500/ PacBio	[33]
Arecaceae Bercht. & J.Presl					
Phoenix dactylifera L. (Sukry, Dekhaini, Ajwa, Perny, Rabia, Shalaby, Moshwaq)	important crop	plastome	NA	Illumina HiSeq 2000	[17]
	important crop	mitochondrial genome	NA	Illumina HiSeq 2000	[17]
Phoenix dactylifera L. (Khalas, Fahal, and Sukry)	important crop	mitochondrial genome	715,001	Roche GS FLX & SOLiD	[16]
Phoenix dactylifera L. (Kalas)	important crop	plastome	158,462	Roche GS FLX system	[34]
Boraginaceae Juss.					
Cordia monoica Roxb. (Faifa mountains)	medicinal	plastome	148,711	Illumina Hiseq4000	[35]
Cordia monoica Roxb. (Al-Baha region)	medicinal	plastome	151,813	DNBseq	[36]
Cordia sinensis Lam.	NA	plastome	152,050	DNBseq	[36]
Ehretia cymosa Thonn.	NA	plastome	156,328	DNBseq	[37]
Ehretia obtusifolia Hochst. ex A.DC.	NA	plastome	155,961	DNBseq	[37]
Cannabaceae Martinov					
Trema orientalis L.	NA	plastome	157,134	NA	[38]
Capparaceae Juss.					
Cadaba farinosa Forssk.	medicinal	plastome	156,481	Illumina Hiseq2500	[39]
Cadaba glandulosa Forssk.	medicinal	plastome	156,560	Illumina Hiseq2500	[39]
Capparis decidua (Forssk.) Edgew.	medicinal	plastome	157,573	Illumina Hiseq2500	[41] ,[40]
Capparis spinosa L.	medicinal	plastome	157,728	Illumina Hiseq2500	[42] ,[41]
Maerua crassifolia Forssk.	medicinal	plastome	155,685	Illumina Hiseq2500	[39]
Maerua oblongifolia (Forssk.) A.Rich.	medicinal	plastome	155,436	Illumina Hiseq2500	[39]
Cleomaceae Airy Shaw					
Dipterygium glaucum Decne.	medicinal	plastome	158,576	Illumina Hiseq2500	[44] ,[43]

Cleome chrysantha Decne.	medicinal	plastome	158,111	lllumina Hiseq2500	[44]
Cleome paradoxa R.Br. ex DC.	medicinal	plastome	159,393	Illumina	[45]
Fabaceae Lindl.					
Acacia etbaica Schweinf.	near endemic	nuclear genome	1867.38–2162.38 Mbp	No sequences were determined. 2C DNA content measured using flow cytometry	[46]
Acacia johnwoodii Boulos	threatened	nuclear genome	2024.46–2142.42 Mbp		[46]
Acacia origena Hunde	near endemic	nuclear genome	2046.42–2396.10 Mbp		[46]
Tamarindus indica L.	threatened	nuclear genome	NA	CCS, Pac-Bio Sequel II	[47]
Heliotropiaceae Schrad.					
Euploca strigosa (Willd.) Diane & Hilger	medicinal	plastome	155,174	DNBseq	[48]
Heliotropium arbainense Fresen.	medicinal	plastome	154,709	DNBseq	[48]
Heliotropium longiflorum (A.DC.) Jaub. & Spach	medicinal	plastome	154,496	DNBseq	[48]
Lamiaceae Martinov					
Mentha x verticillate	medicinal plants, economic value	plastome	152,026	Illumina HiSeq2500	[49]
Mentha longifolia (L.) L.	medicinal plants, economic value	plastome	152,078	Illumina HiSeq2500	[49]
Loranthaceae Juss.					
Plicosepalus acacia (Zucc.) Wiens & Polhill	hemiparasitic, medicinal	plastome	120,181	Illumina	[50]
Plicosepalus curviflorus (Benth. ex Oliv.) Tiegh.	hemiparasitic, medicinal	plastome	121,086	Illumina	[50]
Malvaceae Juss.					
Abutilon fruticosum Guill. & Perr.	medicinal	plastome	160,357	Illumina	[51]
Moraceae Gaudich.					
Ficus populifolia Vahl	threatened	plastome	160,610	Illumina	[52]
Poaceae Barnhart					
Aeluropus littoralis (Gouan) Parl.	halophytic forage grass	plastome	135,532	PacBio Hifi	[53]
Oryza sativa L. (wild-type Hassawi-1)	cereal crop	plastome	134,448	455GS FLX and SOLiD 4.0	[18]
		mitochondrial genome	454,820	455GS FLX and SOLiD 4.0	[18]
Oryza sativa L. (dwarf hybrid Hassawi-2)	cereal crop	plastome	134,459	455GS FLX and SOLiD 4.0	[18]
		mitochondrial genome	454,894	455GS FLX and SOLiD 4.0	[18]
Oryza sativa L.	cereal crop	nuclear genome	391Mbp	PacBio Hifi	[54]
Resedaceae Martinov					
Caylusea hexagyna (Forssk.) M.L.Green	medicinal	plastome	154,390	Illumina HiSeq2500	[55]
Ochradenus baccatus Delile	medicinal	plastome	153,380	Illumina HiSeq2500	[55]
Rhamnaceae Juss.					
Ziziphus spina-christi (L.) Desf.	common native species	nuclear genome	NA	PacBio Hifi	[56]
Zygophyllaceae R.Br.					
Balanites aegyptiaca (L.) Delile	food and medicines	plastome	155,800	Illumina sequencing	[57]
Fagonia indica Burm.f.	medicinal	plastome	128,379	Illumina	[58] ,[11]
Tribulus Macropterus var. *Arabicus* (Hosni) Al-Hemaid & J. Thomas	medicinal	plastome	158,179	Illumina Novaseq 6000	[59]
Gymnosperms					
Cupressaceae Gray					
Juniperus procera Hochst. ex Endl.	common species	nuclear genome	10.5GB	PacBio Sequel II	[60]

4. Discussion

Saudi Arabia, despite its arid climate, hosts a remarkably diverse flora, with approximately 2,250 plant species [4]. Among these species, over 200 are important as bee forage [61], and more than 1,200 have potential therapeutic applications [62]. However, around 30% of Saudi plant species are rare or confined to specific locations, and approximately 18 species are considered to be locally extinct [63]. Given the biodiversity threats facing Saudi Arabia, this literature survey was conducted to highlight the progress made in applying genomic approaches to study plant species in the region, which can have implications for the conservation of plant diversity in Saudi Arabia.

Our survey highlighted a significant gap in genomic data on Saudi plants, particularly for rare, endangered, and ecologically or economically important species (Figure 2, Table 1). This situation parallels that of animal genomic studies in Saudi Arabia [64]. However, we noticed a growing interest in plant genomic studies in Saudi Arabia over the past decade, with a sharp increase observed in the last two years (Figure 1). This trend mirrors global advancements in genomic research, driven by technological progress that has made large-scale sequencing projects more feasible and cost-effective [65], [66], [67], [68]. These advancements have enabled researchers to explore a wide range of genomes, including those of non-model organisms and species from unique ecological niches [69], [70], resulting in an increase in publicly available genomic data [71]. The rise in plant genomic research can be attributed to the potential for genomic data to enhance our understanding of plant biology, support agricultural innovation and the urgent need for biodiversity conservation [72]. The peak in studies observed in 2022 may be linked to increased funding and strategic initiatives by Saudi research institutions, reflecting a national commitment to advancing scientific knowledge and supporting global biodiversity efforts [14].

The survey also revealed a clear preference for chloroplast genome sequencing in Saudi plants, accounting for 75.4% of all genomic data generated (Figure 3, Table 1). Chloroplast genomics is favored worldwide due to its manageable size, simpler structure, and high conservation across plant species, making it a cost-effective tool for studying plant evolution and phylogenetics [73], [74]. Chloroplast genomes have numerous applications, including in plant systematics to elucidate evolutionary relationships among species [75], [76] and in barcoding for species identification and biodiversity conservation [77]. Chloroplast genetic engineering has also been used to enhance crop traits, such as resistance to pests and diseases, and to produce biopharmaceuticals and industrial enzymes [73], [78], For instance, inserting commercially valuable traits such as herbicide and insect resistance into soybeans plastid genome led to high-level expression and excellent transgene containment [79], [80]. The complete chloroplast genomes of 43 Saudi plant species, primarily of medicinal value, could provide a foundation for developing improved medicinal plants with enhanced traits, contributing to the sustainable use and preservation of Saudi Arabia's plant biodiversity.

In contrast, mitochondrial genome sequencing is less common, representing only 8.1% of the genomes studied in the surveyed literature (Figure 3, Table 1). Mitochondrial genomes are more complex and variable, posing challenges in sequencing and analysis [81], [82]. Additionally, the low nucleotide substitution rates in mitochondrial DNA limit its usefulness for phylogenetic studies [74]. This complexity is reflected in the sporadic nature of mitochondrial genome research on Saudi plants. Despite these difficulties, ongoing advancements in sequencing technologies and bioinformatics tools hold promise for overcoming these hurdles in the future.

Nuclear genomic data, though less prevalent (16.3%), has seen a noticeable increase, particularly in 2022 (Figure 3, Table 1), driven by initiatives like the KSA Native Genome Project [15]. Nuclear genomes are more complex than organellar genomes, requiring advanced bioinformatics approaches and skilled personnel [83]. The advent of third-generation long-read sequencing technologies, such as those from Oxford Nanopore Technologies and Pacific Biosciences, has enabled the production of high-quality reference genomes [84]. These reference genomes are crucial for understanding plant genetics, including aspects related to development, adaptation, and resilience [85], [86]. For example, the generation of a high-quality reference genome for Hassawi red rice from Saudi Arabia has enabled the editing of key genes, resulting in modified rice with desirable traits that could promote large-scale cultivation and address malnutrition [54]. Generating 15 reference genomes of threatened, common, and rangeland species in Saudi Arabia, targeted by the KSA Native Genome Project [60], will support conservation efforts, ecological and evolutionary studies, agricultural improvements, medicinal discoveries, climate change adaptation, and the preservation of traditional knowledge.

Comparative genomic analysis is crucial for understanding evolutionary relationships, identifying genetic markers, elucidating gene functions, and assessing environmental adaptability [87], [88]. Although comparative genomic studies on Saudi Arabian plants are limited, they have provided significant insights into key plant families, particularly those with medicinal value. For instance, the Apocynaceae family, rich in medicinal plants, is notably well-represented in genomic studies, with nine species analyzed. These studies have identified chloroplast markers for barcoding and repetitive regions useful for population genetics in several plants widely used in folk medicine, such as *Pergularia tomentosa* [31], *Caralluma quadrangula* [28], *Desmidorchis penicillata*, and *Desmidorchis retrospiciens* [29]. Moreover, comparative analyses of the mitochondrial genome of *Rhazya stricta* with other asterids have revealed unique features of the *Rhazya* genome, particularly in the types of events that have shaped its mitochondrial evolution [19]. This data provides a valuable resource for biotechnological applications, particularly in utilizing this important medicinal plant. Additionally, comparative genomics uncovered a unique gene inversion in the *trnM-rbcL* region of the chloroplast genome in *Cordia monoica* and *Cordia sinensis* (Cordiaceae), collected from the Al-Baha region [36]. Such inversion events are rare, and gene relocations in chloroplast genomes are considered valuable for phylogenetic analysis [89], offering new avenues for further research.

Another interesting group of Saudi plants that has been investigated is the hemiparasitic plants of the Loranthaceae family. Comparative genomics of *Plicosepalus acaciae* and *Plicosepalus curviflorus* with other hemiparasitic and holoparasitic species in the Santalales order has shown a lesser degree of chloroplast genome reduction and gene loss in these two species than typically observed in the order [50]. This finding provides insights into the unique evolutionary adaptations of these species and could has practical implications for weed management and improving host plant resistance. The aforementioned examples underscore the importance of even the limited genomic studies conducted on Saudi Arabian plants. They reveal unique evolutionary events and genetic markers that are crucial for conservation efforts, understanding the evolutionary relationships among species, and identifying traits that enhance plant adaptation and resilience to environmental challenges. As genomic research expands, it will undoubtedly provide a deeper understanding of Saudi Arabia's rich and diverse plant biodiversity, guiding future conservation strategies and agricultural innovations.

5. Conclusion and Future Directions

This survey highlighted significant growth in publications related to genomic research on Saudi Arabian plants over the past decade. Despite this progress, our analysis revealed notable biases in taxonomic and geographic sampling, with certain regions and plant families remaining underrepresented. The current body of research has substantially advanced our understanding of Saudi plant biodiversity, particularly by sequencing organellar genomes. These studies have been instrumental in uncovering evolutionary histories and genetic diversity. However, to achieve a more comprehensive understanding of the genetic architecture and functional traits of Saudi plants, there is a crucial need to increase the sequencing of nuclear genomes. Given their complexity and size, nuclear genomes encompass the majority of genetic information related to adaptation, development, and environmental response. Expanding nuclear genome sequencing efforts will offer deeper insights that are essential for enhancing conservation strategies and supporting agricultural innovation. Additionally, strengthening mitochondrial genome research can provide valuable evolutionary patterns and gene transfer information. Integrating genomic data with conservation efforts will be pivotal for developing genetic barcodes and supporting biodiversity monitoring. Applying functional genomics to medicinal plants could drive advancements in agriculture and biotechnology. Encouraging collaboration among local and international researchers, along with the use of public genomic databases, will facilitate data sharing and accelerate discoveries. By addressing these future directions, researchers can better support the sustainable management and conservation of Saudi Arabia's unique plant biodiversity.

References

[1] A. G. Miller and T. A. Cope, Flora of the Arabian peninsula and Socotra volume 1, vol. 1. Edinburgh University Press in association with Royal Botanic GardeN, 1996.

[2] J. Thomas, "Plant Diversity in Saudi Arabia." [Online]. Available: http://www.plantdiversityofsaudiarabia.info/index.htm

[3] S. A. Al-Robai, H. A. Mohamed, S. M. Howladar, and A. A. Ahmed, "Vegetation structure and species diversity of Wadi Turbah Zahran, Albaha area, southwestern Saudi Arabia," Annals of Agricultural Sciences, vol. 62, no. 1, pp. 61–69, Jun. 2017, doi: 10.1016/J.AOAS.2017.04.001.

[4] S. Collenette, Wildflowers of Saudi Arabia, vol. 1370679501. Riyadh: National Commission for Wildlife Conservation and Development, 1999.

[5] C. Boland, "Developing a model to protect the biodiversity of Saudi Arabia. The highest conservation priority species in Saudi Arabia," Aramco. Accessed: Oct. 20, 2023. [Online]. Available: https://www.aramco.com/ar/magazine/elements/2021/developing-a-model-to-protect-the-biodiversity-of-saudi-arabia

[6] J. P. Rafferty, "Biodiversity loss," Encyclopedia Britannica.

[7] K. Ghildiyal et al., “Genomic insights into the conservation of wild and domestic animal diversity: A review,” Gene, vol. 886, p. 147719, 2023, doi: https://doi.org/10.1016/j.gene.2023.147719.

[8] X. Zhang, J. Tan, M. Yang, Y. Yin, I. S. Al-Mssallem, and J. Yu, “Palm Date Genome Project at the Kingdom of Saudi Arabia,” Date Palm Biotechnology, pp. 427–448, 2011, doi: 10.1007/978-94-007-1318-5_21.

[9] T. Usha et al., “Whole-Genome Sequencing of Plants: Past, Present, and Future,” Plant Genomics for Sustainable Agriculture, pp. 191–239, Jan. 2022, doi: 10.1007/978-981-16-6974-3_8/COVER.

[10] B. Alberts, A. Johnson, J. Lewis, M. Raff, K. Roberts, and P. Walter, Molecular Biology of the Cell, 4th ed. New York: Garland Science, 2002. Accessed: Aug. 08, 2024. [Online]. Available: https://www.ncbi.nlm.nih.gov/books/NBK21054/

[11] M. S. Elshikh et al., “Comparative analysis of cp genome of Fagonia indica growing in desert and its implications in pattern of similarity and variations,” Saudi J Biol Sci, vol. 27, no. 1, pp. 229–232, Jan. 2020, doi: 10.1016/j.sjbs.2019.08.016.

[12] M. Kulmanov et al., “A personal, reference quality, fully annotated genome from a Saudi individual,” bioRxiv, p. 2022.11.05.515129, Nov. 2022, doi: 10.1101/2022.11.05.515129.

[13] M. A. Supple and B. Shapiro, “Conservation of biodiversity in the genomics era,” Genome Biol, vol. 19, no. 1, pp. 1–12, Sep. 2018, doi: 10.1186/S13059-018-1520-3/FIGURES/3.

[14] Vision 2030, “Environment & Nature.” Accessed: Oct. 24, 2023. [Online]. Available: https://www.vision2030.gov.sa/en/progress/environment-nature/

[15] King Abdullah University of Science and Technology, “Native Genome.” Accessed: Oct. 24, 2023. [Online]. Available: https://cda.kaust.edu.sa/research/research-projects/native-genome-project

[16] Y. Fang et al., “A complete sequence and transcriptomic analyses of date palm (Phoenix dactylifera L.) mitochondrial genome,” PLoS One, vol. 7, no. 5, May 2012, doi: 10.1371/journal.pone.0037164.

[17] J. S. M. Sabir et al., “Whole Mitochondrial and Plastid Genome SNP Analysis of Nine Date Palm Cultivars Reveals Plastid Heteroplasmy and Close Phylogenetic Relationships among Cultivars,” PLoS One, vol. 9, no. 4, p. e94158, Apr. 2014, doi: 10.1371/JOURNAL.PONE.0094158.

[18] T. Zhang et al., “The Organelle Genomes of Hassawi Rice (Oryza sativa L.) and Its Hybrid in Saudi Arabia: Genome Variation, Rearrangement, and Origins,” PLoS One, vol. 7, no. 7, p. e42041, Jul. 2012, doi: 10.1371/JOURNAL.PONE.0042041.

[19] S. Park et al., “Complete sequences of organelle genomes from the medicinal plant Rhazya stricta (Apocynaceae) and contrasting patterns of mitochondrial genome evolution across asterids,” BMC Genomics, vol. 15, no. 1, May 2014, doi: 10.1186/1471-2164-15-405.

[20] D. A. Alzahrani, S. S. Yaradua, S. S. Yaradua, E. J. Albokhari, E. J. Albokhari, and A. Abba, “Complete chloroplast genome sequence of Barleria prionitis, comparative chloroplast genomics and phylogenetic relationships among Acanthoideae,” BMC Genomics, vol. 21, no. 1, pp. 1–19, Jun. 2020, doi: 10.1186/S12864-020-06798-2/TABLES/8.

[21] S. S. Yaradua, D. A. Alzahrani, A. Abba, E. J. Albokhari, and A. Bello, “The complete chloroplast genome of Blepharis ciliaris (Acanthaceae),” Mitochondrial DNA B Resour, vol. 4, no. 2, pp. 3729–3730, Jul. 2019, doi: 10.1080/23802359.2019.1681315.

[22] S. S. Yaradua, D. A. Alzahrani, A. Abba, and E. J. Albokhary, “Characterization of the Complete Chloroplast Genome of Blepharis ciliaris (Acanthoideae, Acanthaceae),” Jordan J Biol Sci, vol. 13, 2020.

[23] S. S. Yaradua, D. A. Alzahrani, E. J. Albokhari, A. Abba, and A. Bello, “Complete Chloroplast Genome Sequence of Justicia flava: Genome Comparative Analysis and Phylogenetic Relationships among Acanthaceae,” Biomed Res Int, vol. 2019, 2019, doi: 10.1155/2019/4370258.

[24] A. M. Bantan, “De novo assembly of the Haloxylon persicum genome as a part of the KSA Native Genome Project,” MSc, KAUST , 2023. doi: 10.25781/KAUST-5409I.

[25] R. M. Alshegaihi, “The complete chloroplast genome of the halophyte flowering plant Suaeda monoica from Jeddah, Saudi Arabia,” Mol Biol Rep, vol. 51, no. 1, pp. 1–11, Dec. 2024, doi: 10.1007/S11033-023-09069-X/METRICS.

[26] M. A. Ali, “Complete chloroplast genome of medicinally important poisonous shrub Adenium obesum (Forssk.) Roem. & Schult. (Apocynaceae),” Mitochondrial DNA Part B, vol. 5, no. 1, pp. 568–569, Jan. 2020, doi: 10.1080/23802359.2019.1710292.

[27] A. R. Z. Gaafar, F. Al-Qurainy, S. Khan, M. Nadeem, M. Tarroum, and A. Al-Hashimi, “First draft of the nuclear genome assembly and annotation of the multi-stress tolerant desert giant milkweed Calotropis procera,” South African Journal of Botany, vol. 166, pp. 442–454, Mar. 2024, doi: 10.1016/J.SAJB.2024.01.030.

[28] A. Abba, D. A. Alzahrani, S. S. Yaradua, and E. J. Albokhari, “Complete chloroplast genome sequencing of Caralluma quadrangula and comparative analysis of the Asclepiadoideae subfamily (Apocynaceae),” Journal of Applied Botany and Food Quality, vol. 94, pp. 148–161, Sep. 2021, doi: 10.5073/JABFQ.2021.094.018.

[29] S. Alharbi and E. Albokhari, “Complete Chloroplast Genomes of Desmidorchis penicillata (Deflers) Plowes and Desmidorchis retrospiciens Ehrenb.: Comparative and Phylogenetic Analyses among subtribe Stapeliinae (Ceropegieae, Asclepiadoideae, Apocynaceae),” Nord J Bot, 2024: e04526. https://doi.org/10.1111/njb.04526

[30] D. A. Alzahrani, A. Abba, S. S. Yaradua, and E. J. Albokhari, “An insight on the complete chloroplast genome of Gomphocarpus siniacus and Duvalia velutina, Asclepiadoideae (Apocynaceae),” Brazilian Journal of Biology, vol. 84, p. e257145, Aug. 2022, doi: 10.1590/1519-6984.257145.

[31] A. Abba, D. Alzahrani, S. Yaradua, and E. Albokhari, “Comparative Chloroplast Genome Analysis and Evolutionary Relationships in Some Species of Asclepiadeae, Apocynaceae,” LEGUME RESEARCH - AN INTERNATIONAL JOURNAL, no. Of, Jan. 2021, doi: 10.18805/LR-565.

[32] A. Abba, D. Alzahrani, S. Yaradua, and E. B. Albokhari, “Complete plastome genome of Pergularia tomentosa L. (Asclepiadoideae, Apocynaceae),” Mitochondrial DNA Part B, vol. 5, no. 1, pp. 566–567, Jan. 2020, doi: 10.1080/23802359.2019.1710291.

[33] J. S. M. Sabir et al., “The nuclear genome of Rhazya stricta and the evolution of alkaloid diversity in a medically relevant clade of Apocynaceae,” Scientific Reports 2016 6:1, vol. 6, no. 1, pp. 1–10, Sep. 2016, doi: 10.1038/srep33782.

[34] M. Yang et al., “The complete chloroplast genome sequence of date palm (phoenix dactylifera L.),” PLoS One, vol. 5, no. 9, pp. 1–14, 2010, doi: 10.1371/journal.pone.0012762.

[35] R. M. Alshegaihi, H. Mansour, S. A. Alrobaish, N. A. Al Shaye, and D. Abd El-Moneim, “The First Complete Chloroplast Genome of Cordia monoica: Structure and Comparative Analysis,” Genes (Basel), vol. 14, no. 5, p. 976, Apr. 2023, doi: 10.3390/genes14050976.

[36] M. S. Alawfi and E. J. Albokhari, “Comparative Chloroplast Genomics Reveals a Unique Gene Inversion in Two Cordia Trees (Cordiaceae),” Forests, vol. 14, no. 9, p. 1778, Aug. 2023, doi: 10.3390/F14091778.

[37] M. S. Alawfi, D. A. Alzahrani, and E. J. Albokhari, “Complete Chloroplast Genome Sequences of Two Ehretia Trees (Ehretia cymosa and Ehretia obtusifolia): Genome Structures and Phylogenetic Analysis,” Forests, vol. 14, no. 7, p. 1486, Jul. 2023, doi: 10.3390/F14071486/S1.

[38] A. A. Ibrahim et al., “Characterization and comparative genomic analyses of complete chloroplast genome on Trema orientalis L.,” Genet Resour Crop Evol, vol. 71, no. 3, pp. 1085–1099, Mar. 2024, doi: 10.1007/S10722-023-01678-6/METRICS.

[39] D. A. Alzahrani, E. J. Albokhari, S. S. Yaradua, and A. Abba, “Comparative Analysis of Chloroplast Genomes of Four Medicinal Capparaceae Species: Genome Structures, Phylogenetic Relationships and Adaptive Evolution,” Plants, vol. 10, no. 6, p. 1229, Jun. 2021, doi: 10.3390/plants10061229.

[40] D. Alzahrani and E. Albokhari, “Characterization of Plastid Genome of a Medicinal Plant Capparis decidua (Forsk) Edgew,” Appl Biol Res, vol. 24, no. 2, pp. 156–167, 2022, [Online]. Available: https://www.indianjournals.com/ijor.aspx?target=ijor:abr&volume=24&issue=2&article=005

[41] D. Alzahrani, E. Albokhari, S. Yaradua, and A. Abba, “The complete chloroplast genomes of two species from Capparaceae,” Mitochondrial DNA B Resour, vol. 6, no. 2, pp. 601–603, 2021, doi: 10.1080/23802359.2020.1852902.

[42] D. Alzahrani, E. Albokhari, S. Yaradua, and A. Abba, “The complete plastome sequence for the medicinal species Capparis spinosa L. (Capparaceae),” Gene Rep, vol. 23, p. 101059, Jun. 2021, doi: 10.1016/J.GENREP.2021.101059.

[43] D. Alzahrani, E. Albokhari, S. Yaradua, and A. Abba, “Complete plastome genome of Dipterygium glaucum, Dipterygieae, Cleomaceae,” Mitochondrial DNA Part B, vol. 5, no. 2, pp. 1872–1873, Apr. 2020, doi: 10.1080/23802359.2020.1750978.

[44] D. Alzahrani, E. Albokhari, S. Yaradua, and A. Abba, "Complete chloroplast genome sequences of Dipterygium glaucum and Cleome chrysantha and other Cleomaceae Species, comparative analysis and phylogenetic relationships," Saudi J Biol Sci, vol. 28, no. 4, pp. 2476–2490, Apr. 2021, doi: 10.1016/j.sjbs.2021.01.049.

[45] W. S. ALJuhani and A. Y. Aljohani, "Complete chloroplast genome of the medicinal plant Cleome paradoxa R.Br. Ex DC: Comparative analysis, and phylogenetic relationships among the members of Cleomaceae," Gene, vol. 845, p. 146851, Dec. 2022, doi: 10.1016/J.GENE.2022.146851.

[46] S. Khan et al., "Comparative Study on Genome Size and Phytochemical Profile of Three Potential Species of Acacia: Threatened and Endemic to Saudi Arabia," Horticulturae 2022, Vol. 8, Page 994, vol. 8, no. 11, p. 994, Oct. 2022, doi: 10.3390/HORTICULTURAE8110994.

[47] M. E. Navarrete Rodriguez, "De novo assembly of the Tamarindus indica genome as part of the Kingdom of Saudi Arabia Native Genome Project," MSc, KAUST, 2022. doi: 10.25781/KAUST-X9IF9.

[48] M. S. Alawfi, D. A. Alzahrani, and E. J. Albokhari, "Complete plastome genomes of three medicinal heliotropiaceae species: comparative analyses and phylogenetic relationships," BMC Plant Biol, vol. 24, no. 1, pp. 1–15, Dec. 2024, doi: 10.1186/S12870-024-05388-8/FIGURES/11.

[49] F. Zubair Filimban, S. S. Yarádua, A. Bello, and H. Choudhry, "Complete chloroplast genomes of two mint species (Lamiaceae) from Al-Madinah, Saudi Arabia: phylogenetic and genomic comparative analyses," Mitochondrial DNA B Resour, vol. 7, no. 10, pp. 1797–1799, 2022, doi: 10.1080/23802359.2022.2130713.

[50] W. AL-Juhani, N. T. Al Thagafi, and R. N. Al-Qthanin, "Gene Losses and Plastome Degradation in the Hemiparasitic Species Plicosepalus acaciae and Plicosepalus curviflorus: Comparative Analyses and Phylogenetic Relationships among Santalales Members," Plants, vol. 11, no. 14, Jul. 2022, doi: 10.3390/plants11141869.

[51] D. A. Alzahrani, "Complete chloroplast genome of abutilon fruticosum: Genome structure, comparative and phylogenetic analysis," Plants, vol. 10, no. 2, pp. 1–19, Feb. 2021, doi: 10.3390/plants10020270.

[52] S. A. Alharbi, W. S. AL-Juhani, and E. J. Albokhari, "Plastome Characterization, Phylogenetic Relationships, and Regional Conservation Status of Ficus populifolia Vahl. (Moraceae), a Peripherally Isolated Plant Population in the Arabian Peninsula," Forests, vol. 13, no. 12, p. 2063, Dec. 2022, doi: 10.3390/F13122063/S1.

[53] W. Ben Romdhane, A. Al-Doss, and A. Hassairi, "The newly assembled chloroplast genome of Aeluropus littoralis: molecular feature characterization and phylogenetic analysis with related species," Scientific Reports 2024 14:1, vol. 14, no. 1, pp. 1–13, Mar. 2024, doi: 10.1038/s41598-024-57141-8.

[54] K. Sedeek et al., "Multitrait engineering of Hassawi red rice for sustainable cultivation," Plant Science, vol. 341, p. 112018, Apr. 2024, doi: 10.1016/J.PLANTSCI.2024.112018.

[55] D. Alzahrani, E. Albokhari, A. Abba, and S. Yaradua, "The first complete chloroplast genome sequences in Resedaceae: Genome structure and comparative analysis," Sci Prog, vol. 104, no. 4, p. 003685042110599, Oct. 2021, doi: 10.1177/00368504211059973.

[56] R. H. Shuwaikan, "Draft Assembly and Baseline Annotation of the Ziziphus spina-christi Genome," KAUST, 2022. doi: 10.25781/KAUST-37BD2.

[57] W. S. AL-Juhani, S. A. Alharbi, N. M. Al Aboud, and A. Y. Aljohani, "Complete chloroplast genome of the desert date (Balanites aegyptiaca (L.) Del. comparative analysis, and phylogenetic relationships among the members of Zygophyllaceae," BMC Genomics, vol. 23, no. 1, Dec. 2022, doi: 10.1186/s12864-022-08850-9.

[58] M. S. Elshikh et al., "Insights into plastome of Fagonia indica Burm.f. (Zygophyllaceae): organization, annotation and phylogeny," Saudi J Biol Sci, vol. 29, no. 3, pp. 1313–1321, Mar. 2022, doi: 10.1016/j.sjbs.2021.11.011.

[59] A. S. Albediwi et al., "Unveiling the Complete Chloroplast Genome of Tribulus Macropterus Var. Arabicus (Hosni) Al-Hemaid & J. Thomas: Genome Structure, Comparative Analysis and Phylogeny," Bangladesh J Plant Taxon, vol. 31, no. 1, pp. 1–14, Jun. 2024, doi: 10.3329/BJPT.V31I1.74370.

[60] N. Mohammed, K. Abdullah Alabdulkader, A. Ali Alghamdi, and R. A. Wing, "The KSA Native Genome Project," in KAUST Workshop for Sustainable Food Security, 2022.

[61] Food and Agriculture Organization of the United Nations, "Beekeeping and honey production sector review and situation analysis in the Kingdom of Saudi Arabia," Riyadh , 2019.

[62] S. N. Alqahtani, S. O. Alkholy, and M. P. Ferreira, "Antidiabetic and Anticancer Potential of Native Medicinal Plants from Saudi Arabia," in Polyphenols in Human Health and Disease, R. R. Watson, V. R. Preedy, and S. Zibadi, Eds., San Diego: Academic Press, 2014, pp. 119–132. doi: https://doi.org/10.1016/B978-0-12-398456-2.00011-6.

[63] J. Thomas, "Current status of plant conservation in Saudi Arabia," Plant Diversity in Saudi Arabia.

[64] S. A. Alharbi, M. M. Alyoubi, A. I. Al-luhaybi, R. H. Fatani, A. E. Al-Subhi, and R. H. Mulawi, "Genomic Insights Into Saudi Arabian Biodiversity: A Survey of Animals' Whole Genome Sequencing Studies," Electronic Journal of University of Aden for Basic and Applied Sciences, vol. 5, no. 1, pp. 44–50, Mar. 2024, doi: 10.47372/ejua-ba.2024.1.326.

[65] R. A. Marks, S. Hotaling, P. B. Frandsen, and R. VanBuren, "Representation and participation across 20 years of plant genome sequencing," Nature Plants 2021 7:12, vol. 7, no. 12, pp. 1571–1578, Nov. 2021, doi: 10.1038/s41477-021-01031-8.

[66] E. L. van Dijk, Y. Jaszczyszyn, D. Naquin, and C. Thermes, "The Third Revolution in Sequencing Technology," Trends in Genetics, vol. 34, no. 9, pp. 666–681, Sep. 2018, doi: 10.1016/j.tig.2018.05.008.

[67] E. L. van Dijk, H. Auger, Y. Jaszczyszyn, and C. Thermes, "Ten years of next-generation sequencing technology.," Trends Genet, vol. 30, no. 9, pp. 418–26, Sep. 2014, doi: 10.1016/j.tig.2014.07.001.

[68] S. Goodwin, J. D. McPherson, and W. R. McCombie, "Coming of age: ten years of next-generation sequencing technologies," Nat Rev Genet, vol. 17, no. 6, pp. 333–351, Jun. 2016, doi: 10.1038/nrg.2016.49.

[69] H. Satam et al., "Next-Generation Sequencing Technology: Current Trends and Advancements," Biology (Basel), vol. 12, no. 7, Jul. 2023, doi: 10.3390/BIOLOGY12070997.

[70] M. K. Tello-Ruiz et al., "Gramene 2021: harnessing the power of comparative genomics and pathways for plant research," Nucleic Acids Res, vol. 49, no. D1, pp. D1452–D1463, Jan. 2021, doi: 10.1093/NAR/GKAA979.

[71] E. W. Sayers, M. Cavanaugh, K. Clark, J. Ostell, K. D. Pruitt, and I. Karsch-Mizrachi, "GenBank," Nucleic Acids Res, vol. 48, no. D1, pp. D84–D86, Jan. 2020, doi: 10.1093/NAR/GKZ956.

[72] I. Y. Abdurakhmonov, "Genomics Era for Plants and Crop Species – Advances Made and Needed Tasks Ahead," in Plant Genomics, InTech, 2016. doi: 10.5772/62083.

[73] H. Daniell, C. S. Lin, M. Yu, and W. J. Chang, "Chloroplast genomes: diversity, evolution, and applications in genetic engineering," Genome Biology 2016 17:1, vol. 17, no. 1, pp. 1–29, Jun. 2016, doi: 10.1186/S13059-016-1004-2.

[74] V. Ravi, J. P. Khurana, A. K. Tyagi, and P. Khurana, "An update on chloroplast genomes," Plant Systematics and Evolution 2007 271:1, vol. 271, no. 1, pp. 101–122, Nov. 2007, doi: 10.1007/S00606-007-0608-0.

[75] M. A. Gitzendanner, P. S. Soltis, G. K.-S. Wong, B. R. Ruhfel, and D. E. Soltis, "Plastid phylogenomic analysis of green plants: A billion years of evolutionary history," Am J Bot, vol. 105, no. 3, pp. 291–301, Mar. 2018, doi: https://doi.org/10.1002/ajb2.1048.

[76] S. Wicke, G. M. Schneeweiss, C. W. dePamphilis, K. F. Müller, and D. Quandt, "The evolution of the plastid chromosome in land plants: Gene content, gene order, gene function," Plant Mol Biol, vol. 76, no. 3–5, pp. 273–297, Jul. 2011, doi: 10.1007/S11103-011-9762-4/TABLES/1.

[77] P. M. Hollingsworth et al., "A DNA barcode for land plants," Proc Natl Acad Sci U S A, vol. 106, no. 31, pp. 12794–12797, Aug. 2009, doi: 10.1073/PNAS.0905845106/SUPPL_FILE/0905845106SI.PDF.

[78] C. De-la-Peña, P. León, and T. D. Sharkey, "Editorial: Chloroplast Biotechnology for Crop Improvement," Front Plant Sci, vol. 13, p. 848034, Feb. 2022, doi: 10.3389/FPLS.2022.848034.

[79] N. Dufourmantel, B. Pelissier, F. Garçon, G. Peltier, J. M. Ferullo, and G. Tissot, "Generation of fertile transplastomic soybean," Plant Mol Biol, vol. 55, no. 4, pp. 479–489, 2004, doi: 10.1007/S11103-004-0192-4/METRICS.

[80] N. Dufourmantel et al., "Generation and analysis of soybean plastid transformants expressing Bacillus thuringiensis Cry1Ab protoxin," Plant Mol Biol, vol. 58, no. 5, pp. 659–668, Jul. 2005, doi: 10.1007/S11103-005-7405-3/METRICS.

[81] J. Li, H. Tang, H. Luo, J. Tang, N. Zhong, and L. Xiao, "Complete mitochondrial genome assembly and comparison of Camellia sinensis var. Assamica cv. Duntsa," Front Plant Sci, vol. 14, p. 1117002, Jan. 2023, doi: 10.3389/FPLS.2023.1117002/BIBTEX.

[82] S. Singh, J. Naik, and A. Pandey, "Genetics of Plant Organelles: Plastid and Mitochondrial Genomes," Plant Genomics for Sustainable Agriculture, pp. 313–330, Jan. 2022, doi: 10.1007/978-981-16-6974-3_12/COVER.

[83] B. Alberts, Molecular biology of the cell. Garland science, 2017.

[84] B. Pucker, I. Irisarri, J. De Vries, and B. Xu, "Plant genome sequence assembly in the era of long reads: Progress, challenges and future directions," Quantitative Plant Biology, vol. 3, p. e5, Mar. 2022, doi: 10.1017/QPB.2021.18.

[85] P. C. Ronald, "Enhancing sustainable development through plant genetics," Nature Reviews Genetics 2023 24:10, vol. 24, no. 10, pp. 659–660, Aug. 2023, doi: 10.1038/s41576-023-00651-4.

[86] R. J. Henry, "Progress in Plant Genome Sequencing," Applied Biosciences 2022, Vol. 1, Pages 113-128, vol. 1, no. 2, pp. 113–128, Jul. 2022, doi: 10.3390/APPLBIOSCI1020008.

[87] J. Wang, Y. Chen, and Q. Zou, "Comparative Genomics and Functional Genomics Analysis in Plants," Int J Mol Sci, vol. 24, no. 7, p. 6539, Apr. 2023, doi: 10.3390/IJMS24076539.

[88] V. de Crécy-Lagard and A. Hanson, "Comparative Genomics," Brenner's Encyclopedia of Genetics: Second Edition, pp. 102–105, Jan. 2013, doi: 10.1016/B978-0-12-374984-0.00299-0.

[89] H. Liu et al., "Comparative analysis of complete chloroplast genomes of Anemoclema, Anemone, Pulsatilla, and hepatica revealing structural variations among genera in tribe anemoneae (Ranunculaceae)," Front Plant Sci, vol. 9, p. 347180, Jul. 2018, doi: 10.3389/FPLS.2018.01097/BIBTEX.

مقالة بحثية

رؤى جينومية للتنوع النباتي في المملكة العربية السعودية: التقدم والتوجهات المستقبلية

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المُلخّص

تتميز المملكة العربية السعودية بتنوع نباتي غني رغم بيئتها القاحلة، حيث تحتوي على حوالي 2,253 نوعًا نباتيًا. ومع ذلك، تواجه جهود الحفاظ على هذا التنوع تحديات كبيرة تشمل فقدان الموائل، وتغير المناخ، ونقص البيانات الجينومية. تستعرض هذه الدراسة حالة ابحاث الجينوم للنباتات في المملكة العربية السعودية، مسلطةً الضوء على التقدم المحرز والثغرات في الأدبيات العلمية. من خلال مسح قواعد البيانات العلمية، تم تحديد 46 دراسة منشورة بين عامي 2010 و2024، تعكس تزايد الاهتمام بتحليل جينومات النباتات السعودية. تغطي هذه الدراسات تحليلات للجينوم النووي وجينوم البلاستيدات الخضراء و/أو الميتوكوندريا لـ 51 نوعًا نباتيًا تنتمي الى 19 فصيلة، مع تركيز خاص على النباتات الطبية، لا سيما تلك من المناطق الغربية والجنوبية الغربية. برزت الفصيلة الدفلية (Apocynaceae) كالأكثر تمثيلًا في الأدبيات الجينومية نظرًا لأهميتها الطبية. تشكل بيانات جينوم البلاستيدات الخضراء النسبة الأكبر من البيانات المنتجة في الدراسات (75.4%)، مما يعزز دورها في حل المشكلات التصنيفية ودراسة النشوء والتطور. وعلى الرغم من قلة بيانات الجينوم النووي (16.3%)، إلا أنها شهدت زيادة ملحوظة بفضل مبادرات مثل مشروع الجينوم الأصلي السعودي. أما بيانات الجينوم الميتوكوندري، فقد كانت الأقل تمثيلًا (8.1%)، لكنها أسهمت في فهم انتقال الجينات بين النواة والبلاستيدات إلى الميتوكوندريا في الأنواع المدروسة. ورغم محدودية الأبحاث الجينومية على النباتات في المملكة، إلا أن البيانات المتاحة تقدم رؤى مهمة لحماية التنوع البيولوجي وفهم تكيف النباتات، مما يساعد في توجيه الأبحاث المستقبلية. وتؤكد هذه المراجعة ضرورة توسيع الدراسات الجينومية، خصوصًا تسلسل الجينوم النووي، وزيادة التركيز على النباتات النادرة والمتوطنة والمهددة بالانقراض لدعم جهود الحفاظ على التنوع البيولوجي وتعزيز الابتكار الزراعي في السعودية.

الكلمات المفتاحية: تسلسل جينوم البلاستيدات الخضراء، ابحاث الجينوم، النباتات الطبية، تسلسل الجينوم النووي، الحفاظ على التنوع النباتي، المملكة العربية السعودية.

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