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GENOMIC ADAPTATIONS AND EVOLUTIONARY RESILIENCE OF THE SIRENIAN LINEAGE: A SYSTEMATIC LITERATURE REVIEW

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ABSTRACT
This review evaluates the genomic mechanisms and physiological adjustments enabling the transition of sirenians from terrestrial to fully aquatic environments (Huang et al., 2024; Tian et al., 2023). By synthesising findings from recent chromosome-level genome assemblies, we identify molecular solutions to aquatic life, including recalibrated circadian clocks, modified iodide transport, and a convergent regression of integumentary system genes shared with cetaceans (Huang et al., 2024; Tian et al., 2023. Functional characterisation of resurrected recombinant proteins from the extinct Steller's sea cow reveals an extreme hemoglobin phenotype that facilitated sub-Arctic survival through reduced intrinsic temperature sensitivity and insensitivity to 2,3-DPG (Signore et al., 2023). Furthermore, we assess the metabolic requirements of wild dugongs using indirect calorimetry, finding resting rates significantly lower than predicted for terrestrial herbivores (Lanyon et al., 2025). Finally, population genomics reveals critical genetic breaks and declining heterozygosity, particularly in isolated populations, necessitating urgent in situ conservation strategies (Huang et al., 2024; Plön et al., 2019; Tian et al., 2023).

Keywords: *Sirenia, comparative genomics, thermal adaptation, paleophysiology, conservation genomics, metabolic rate, Steller's sea cow.*

1. INTRODUCTION
The Order Sirenia, encompassing the only extant herbivorous marine mammals, currently faces a precarious evolutionary threshold defined by rapid population decline and habitat fragmentation (Huang et al., 2024; Tian et al., 2023). Globally, sirenian populations have decreased significantly over the last century; notably, the dugong was declared functionally extinct in Chinese waters in 2022 (Huang et al., 2024). These demographic pressures are compounded by unique physiological vulnerabilities; for example, the African manatee maintains a remarkably low metabolic rate that can drop to 36% of the average for placental mammals during food scarcity (Huang et al., 2024). Recent genomic assessments reveal a dangerously narrow genetic base, with the African manatee possessing a genome-wide heterozygosity of only 4.97 \times $10^{(-4)}$ (Huang et al., 2024).

Current research has transitioned from morphological descriptions to targeted genetic and physiological studies. However, until recently, the lack of high-quality, chromosome-level genomic resources restricted a deeper understanding of the sirenian transition from land to water compared to other aquatic lineages (Huang et al., 2024; Tian et al., 2023). A profound lack of functional data regarding the paleophysiology of extinct members, such as the Steller's sea cow, has further prevented a comprehensive understanding of how the lineage negotiated extreme thermal environments (Huang et al., 2024; Signore et al., 2023).

1.1 AIMS AND OBJECTIVES
This review aims to provide a comprehensive, multi-omic synthesis of sirenian evolutionary resilience. The primary objectives are:

1. To decode the genetic basis of unique phenotypes, including extreme bone densification (osteopetrosis) and specialized thermal adaptations.
2. To evaluate the metabolic thresholds and nutritional requirements of wild sirenians to establish survival viability.
3. To investigate how convergent gene loss and genetic assimilation facilitated the transition from terrestrial African ancestors to fully aquatic and sub-Arctic specialists.

2. LITERATURE REVIEW

2.1 GENOMIC AND MOLECULAR ADAPTATIONS
(Huang et al. 2024) addressed the genetic mechanisms underlying unique sirenian phenotypes in the African manatee by producing a 3.19 Gb genome assembly with high continuity (Contig N50 of 118.90 Mb). Their study identified that genes associated with osteopetrosis (*CSF1R*, *LRRK1*) underwent positive selection, while

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thermosensation genes (*KCNK18*) were pseudogenised (Huang et al., 2024). These findings provide a robust map of sirenian evolution, though the researchers emphasised that *in vivo* functional experiments are still required to validate these genes (Huang et al., 2024).

(Signore et al. 2023) utilised a protein resurrection framework to interpret the paleophysiology of the extinct Steller's sea cow. Their work demonstrated that a unique amino acid replacement (β/δ82Asn) rendered the species' hemoglobin insensitive to 2,3-DPG and reduced its intrinsic thermal sensitivity. This extreme phenotype facilitated oxygen delivery to cool peripheral tissues, a trait unique among mammals (Signore et al., 2023).

2.2 COMPARATIVE INTEGUMENTARY AND PHYSIOLOGICAL EVOLUTION

Comparative genomics reveals that the dugong underwent convergent loss of filaggrin (*FLG*) and caspase-14 (*CASP14*) with cetaceans, while the manatee retained functional orthologs (Steinbinder et al., 2024). In terms of bioenergetics, (Lanyon et al. 2025) utilised indirect calorimetry to establish that wild adult dugongs possess metabolic rates approximately half that predicted for terrestrial mammals (0.719–0.988~W/kg). This study concluded that an individual requires 40–65 kg of fresh seagrass daily to maintain homeostasis (Lanyon et al., 2025).

3. RESEARCH METHODOLOGY

This review adopts an integrative, multimodal framework to evaluate sirenian resilience across multiple biological scales

1. **Genomic Integration:** We synthesise data from circular consensus long-read sequencing (HiFi) and Hi-C linked reads used to generate chromosome-level assemblies for *T. senegalensis* and *D. dugon* (Huang et al., 2024; Tian et al., 2023). These resources allow for a comparative analysis of chromosome fission and fusion events against other Afrotherians (Huang et al., 2024).

2. **Functional Paleophysiology:** We incorporate findings from the synthesis of recombinant hemoglobin proteins in *E. coli* expression vectors. These "resurrected" proteins were assessed via thin-film respirometry to determine O_2-equilibrium curves across varying temperatures (Signore et al., 2023).

3. **Eco-Physiological Modelling:** Field-based indirect calorimetry and telomere attrition models were used to establish metabolic thresholds and age relationships in wild populations (Cherdsukjai et al., 2020; Lanyon et al., 2025).

4. **Habitat Dynamics:** Suitability was predicted using Generalized Additive Models (GAMs) and MaxEnt modelling, overlaid with anthropogenic pressure layers to identify Critical Dugong Habitats (Seal et al., 2024).

4. RESULTS AND DISCUSSION

4.1 GENOMIC SOLUTIONS FOR BUOYANCY AND COLD SENSITIVITY

Positive selection in bone mineralization genes (*CSF1R*, *LRRK1*) explains the extreme bone density (osteopetrosis) required for buoyancy in shallow-water foragers (Huang et al., 2024). Simultaneously, the pseudogenisation of the *KCNK18* gene is linked to enhanced cold sensitivity, acting as a molecular "alarm system" that encourages migration to warm-water refugia to avoid cold stress syndrome (Huang et al., 2024; Tian et al., 2023).

4.2 PALEOPHYSIOLOGY OF THE STELLER'S SEA COW

The β/δ82Asn replacement permanently conferred the Steller's sea cow with reduced intrinsic thermal sensitivity (Signore et al., 2023). By uncoupling hemoglobin sensitivity from allosteric effector concentrations, this species achieved a form of genetic assimilation that supported a whale-sized herbivore in the North Pacific (Signore et al., 2023).

4.3 BIOENERGETICS AND HABITAT USE

1. Dugongs exhibit a resting metabolic rate approximately half that of predicted terrestrial herbivores, yet higher than manatees (Lanyon et al., 2025). This explains their slower growth and protracted reproductive cycles (Lanyon et al., 2025). Satellite tracking confirms that dugongs utilise oceanic fore-reef shelves during the cool season for behavioural thermoregulation, as these areas provide a 1.9 C^o temperature advantage over lagoons (Cleguer et al., 2024; Derville et al., 2022).

5. CONCLUSION

This review demonstrates that the sirenian lineage has navigated a 60-million-year journey from land to sea through a combination of convergent gene loss and genetic assimilation.

Key adaptations include the recalibration of the circadian clock for aquatic life, the positive selection of genes for osteopetrosis to facilitate buoyancy, and a unique 2,3-DPG-insensitive hemoglobin phenotype that permitted sub-Arctic survival.

However, the resilience of extant populations is severely compromised by low genetic heterozygosity and high metabolic sensitivity to habitat loss. The functional extinction of regional populations in China and Japan signals that current conservation efforts are insufficient. This investigation concludes that integrated *in situ* protection of seagrass biomass and fore-reef shelves is essential. Future research must prioritise the *in vivo* functional validation of candidate genes associated with bone density and cold sensitivity to fully understand the adaptive limits of this unique mammalian order.

6. FUTURE SCOPE

- Functional Validation: Prioritise in vivo and in vitro experiments to validate the efficacy of candidate genes associated with thermosensation (*KCNK18*) and bone density (*CSF1R*, *LRRK1*) (Huang, X., et al. 2024).
- Global Resequencing: Implement whole-genome resequencing for isolated populations (e.g., Red Sea, Andaman Sea, Okinawa) to manage inbreeding depression (Tian, R., et al. 2023).
- Carry-Capacity Modelling: Integrate indirect calorimetry data into spatial management to ensure protected areas meet the nutritional biomass requirements of wild herds (Lanyon, J. M., et al. 2025).
- Non-Invasive Monitoring: Expand the use of drone photogrammetry for body condition monitoring and epidermal steroid monitoring to track the health of elusive populations without capture (Cleguer, C., et al. 2021).

7. ETHICAL STATEMENT

The authors confirm that this review is an original work and has not been published elsewhere. All synthesized data involving animal subjects were originally collected under appropriate University Animal Ethics Permits following the Animals for Scientific Purposes Act (Cherdsukjai et al., 2020; Lanyon et al., 2025).

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