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CYTOGENETICS OF *ARTEMIA*: A COMPREHENSIVE REVIEW

The genus Artemia containing brine shrimps, is a landmark model organism in cytogenetics research due to its remarkable adaptability to hypersaline, anoxic and high-altitude environments, as well as its diverse reproductive modes, including bisexual reproduction and parthenogenesis. This exhaustive review reflects progress in Artemia cytogenetics, with a major focus on chromosome scale genome assemblies, karyotypic polymorphisms, sex chromosome evolution, molecular cytogenetic techniques e.g. fluorescence in situ hybridisation (FISH).

A significant taxonomic update is the recent description of Artemia amati by Asem et al. (2023), a bisexual species native to Kazakhstan (previously "Artemia sp. Kazakhstan"), which provides a new framework for studying Central Asian populations. One of the most important findings is the chromosome-scale genome assembly of the Qinghai-Tibet Plateau species A. tibetiana, which contains 21 pseudochromosomes and provides insights into adaptations to high-altitude stress.

Assemblies of the A. franciscana have defined ZW sex determination systems with differentiated evolutionary strata and possible meiotic silencing pathway. The population-genomic studies of Chinese Artemia define the four different clades, which, in turn, were affected by the geologic uplift, climatic variations, and anthropogenic effects, with high nucleotide diversity in Tibetan populations. Single-nucleus profiling shows that the Z chromosome was repressed in germline oogenesis indicating that the meiotic sex chromosomal inactivation had taken place.

The diapause termination networks controlled by the transcriptional factors include SVP, MYC, RXR, and SMAD6 that regulate cell adhesion, signal transduction, and redox homeostasis. These findings shed light on the evolutionary cytogenetics, stress-adaptation, and biotechnological perspectives of aquaculture and conservation of the species Artemia. Future research needs to capitalize on integrative multi-omics to solve the remaining problems, such as full W chromosome-level resolution and interspecies dynamic-hybridisation.

Keywords: Artemia cytogenetics, Artemia amati, genome assembly, karyotype variation, sex chromosomes, parthenogenesis, population genetics, diapause regulation

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Artemia цитогенетикасы: кешенді шолу

Желбезекаяқты шаянтәрізділерге жататын Artemia туысы гипертұзды, анаэробты және биік таулы орта жағдайларына ерекше бейімделу қабілетіне, сондай-ақ дара жыныстылық пен партеногенезді қамтитын көбею стратегияларының алуан түрлілігіне байланысты цитогенетикалық зерттеулердегі маңызды модельдік организмдер тобына жатады. Бұл шолу Artemia цитогенетика саласындағы заманауи жетістіктерді жинақтай отырып, хромосомалық деңгейдегі геномдық жинақтарға, кариотиптік полиморфизмге, жыныс хромосомаларының эволюциясына және in situ жағдайында флуоресцентті гибридизация (FISH) сияқты молекулалық-цитогенетикалық әдістерге ерекше назар аударады.

Маңызды таксономиялық жаңалықтардың біріне – жақында сипатталған Artemia amati Asem et al. (2023) түрі жатады. Бұл Қазақстанда эндемик болып табылатын дара жынысты түр (бұрын «Artemia sp. Kazakhstan» ретінде белгіленген) және Орталық Азия популяцияларын зерттеуге жаңа негіз қалыптастырды. Ең маңызды жетістіктердің бірі – Цинхай–Тибет үстіртінен шыққан биік таулы A. tibetiana түрінің 21 псевдохромосомадан тұратын хромосомалық деңгейдегі геномдық жинағының жасалуы. Бұл жинақ биік таулы орта стрессіне бейімделу механизмдері туралы жаңа мәліметтер береді.

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A. franciscana геномының жинақтары дифференциацияланған эволюциялық страталары және ықтимал мейоздық сайленсинг механизмі бар ZW типті жынысты анықтау жүйесін сипаттауға мүмкіндік берді. Қытайдағы Artemia популяцияларына жүргізілген популяциялық-геномдық зерттеулер төрт түрлі кладаның бар екенін көрсетті. Олардың қалыптасуына аумақтардың геологиялық өзгерістері, климаттық өзгерістер және антропогендік әсер ықпал еткен. Сонымен қатар, Тибет популяциялары нуклеотидтік әртүрліліктің жоғары деңгейімен сипатталады. Жеке ядроларды профильдеу нәтижелері ұрықтық линияның оогенезі барысында Z-хромосоманың репрессияға ұшырайтынын көрсетті, бұл жыныс хромосомаларында мейоздық инактивация механизмі бар екенін дәлелдейді.

Артеминяың диапауза сатысынан шығуды реттейтін жасушалық адгезияны, сигналдық трансдукцияны және редокс-гомеостазды реттеуге қатысатын SVP, MYC, RXR және SMAD6 транскрипциялық факторлар арқылы бақыланатыны анықталды. Алынған нәтижелер эволюциялық цитогенетика, стресс-төзімділік механизмдер және Artemia-ның аквакультура мен биоалуантүрлілікті сақтау салаларындағы биотехнологиялық ерекшеліктері туралы түсініктерді кеңейтеді. Болашақ зерттеулер W-хромосоманы толық карталау және тұраралық динамикалық гибридизацияны зерттеу сияқты өзекті мәселелерді шешу үшін интегративті мультиомдық тәсілдерге негізделуі тиіс.

Түйін сөздер: Artemia цитогенетикасы, Artemia amati, геномдық жинақ, кариотиптік өзгергіштік, жыныс хромосомалары, партеногенез, популяциялық генетика, диапаузаны реттеу.

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Цитогенетика *Artemia*: всесторонний обзор

Род Artemia, включающий жаброногих рачков, является важной модельной группой организмов в цитогенетических исследованиях благодаря своей исключительной способности адаптироваться к гиперсолёным, анаэробным и высокогорным условиям среды, а также разнообразию репродуктивных стратегий, включая двуполое размножение и партеногенез. Настоящий обзор обобщает современные достижения в области цитогенетики Artemia, уделяя особое внимание сборкам геномов хромосомного уровня, кариотипическому полиморфизму, эволюции половых хромосом и молекулярно-цитогенетическим методам, таким как флуоресцентная гибридизация in situ (FSH).

Существенным таксономическим обновлением стало недавнее описание Artemia amati Asem et al. (2023) – двуполого вида, эндемичного для Казахстана (ранее обозначавшегося как “Artemia sp. Kazakhstan”), что создало новую основу для изучения центральноазиатских популяций. Одним из наиболее значимых достижений является создание сборки генома хромосомного уровня для высокогорного вида A. tibetiana с Цинхай-Тибетского плато, включающей 21 псевдохромосому и предоставляющей новые данные о механизмах адаптации к высокогорному стрессу.

Сборки генома A. franciscana позволили охарактеризовать систему определения пола типа ZW с дифференцированными эволюционными стратами и возможным механизмом мейотического сайленсинга. Популяционно-геномные исследования китайских популяций Artemia выявили существование четырёх различных клад, формирование которых было обусловлено геологическим изменением территорий, климатическими изменениями и антропогенным воздействием; при этом тибетские популяции характеризуются высоким уровнем нуклеотидного разнообразия. Профилирование отдельных ядер показало репрессию Z-хромосомы в процессе оогенеза зародышевой линии, что свидетельствует о наличии механизма мейотической инактивации половых хромосом.

Установлено, что сети регуляции выхода из диапаузы контролируются транскрипционными факторами SVP, MYC, RXR и SMAD6, участвующими в регуляции клеточной адгезии, сигнальной трансдукции и поддержании редокс-гомеостаза. Полученные результаты расширяют представления об эволюционной цитогенетике, механизмах стрессоустойчивости и биотехнологическом потенциале Artemia в аквакультуре и сохранении биоразнообразия. Перспективные исследования должны основываться на интегративных мультиомных подходах для решения сохраняющихся проблем, включая полное картирование W-хромосомы и изучение межвидовой динамической гибридизации.

Ключевые слова: цитогенетика Artemia, Artemia amati, сборка генома, вариации кариотипа, половые хромосомы, партеногенез, популяционная генетика, регуляция диапаузы.

Introduction

The genus *Artemia* (Leach, 1819), belonging to the order *Anostraca* and the class *Branchiopoda*, lives in hyper-salty habitats all over the world such as coastal salt-water marshes in the Americas and inland lakes in Asia. Such crustaceans are physiologically resilient, as they can withstand salinities well above 300 g/L, long-term anoxia, desiccation, and low temperatures down to -18^{o}C and high temperatures up to 40^{o}C (De Vos et al., 2021). There are also cytogenetically interesting aspects of the organism, such as varying modes of reproduction: bisexual species have the standard diploid number of chromosomes (2n = 42), but the parthenogenetic populations can be polyploid or aneuploid, with a maximum of 84 chromosomes or more (Abetzopoulos et al., 2009; Bett et al., 2024). Early cytogenetic studies involved the use of traditional karyotyping and banding methods which showed metacentric and submetacentric chromosomes where heterochromatin was mainly concentrated in centromere areas (Parraguez et al., 2009).

The latest technological advances, such as *next-generation sequencing (NGS)*, long-read sequencing such as *Oxford Nanopore*, and *chromosome-conformation capture (Hi-C),* have brought cytogenetics of the *Artemia* to chromosome-resolutions. Conserved synteny, expansions in stress-response gene families and complex sex-determination systems have been revealed by genome assemblies of several species, such as *A. franciscana, A. tibetiana* and *A. sinica*. In aquaculture, the live feed provided by cysts of the *Artemia* species has generated huge revenues, and the diapause ability has provided useful models of cryptobiosis and biomedical applications (Gajardo, 2012). However, the native population is threatened by the processes of climate change, habitat deterioration, and invasive species, which also highlights the need to conserve these species with cytogenetic-based conservation (Sainz-Escudero et al., 2022).

The review is carefully incorporated with a combination of karyotype variations, genome assemblies, sex chromosomes, molecular cytogenetics, population dynamics, and diapause regulation as well as practical uses. The synthesis describes evolution pathways, including contagious parthenogenesis and *ZW* chromosome divergence, while identifying gaps, including molecular bases of polyploidy stability. This work will help develop improvements in the field of cytogenetics of the organism, *Artemia*.

Karyotype Analysis in *Artemia* Species

Classical Karyotyping and Chromosomal Morphology

Karyotypic investigations constitute the bedrock of *Artemia* cytogenetics. Bisexual species, such as *A. franciscana*, *A. sinica*, and *A. tibetiana*, predominantly possess 2n=42 chromosomes, organized into 21 pairs with primarily metacentric and submetacentric morphologies (Dhont & Sorgeloos, 2002; Chen et al., 2025). Crucially, the recent taxonomic revision by Asem et al. (2023) has officially described *Artemia amati* (n. sp.) from Kazakhstan. This species, which was long referred to as "*Artemia sp*. Kazakhstan" in genetic studies, represents a key bisexual taxon in Central Asia. There are inter- and intra-specific diversifications; one instance is that 2n= 44 of *A. persimilis* is a product of chromosomal duplication that sets it apart of *A. franciscana* (Rodriguez-Gil et al., 2009). Parthenogenetic lineages often exhibit a polyploidy, with tetraploid (4n=84) configurations being common in the Eurasian populations, possibly reflecting an increased resilience to environmental stresses (Bett et al., 2024).

Heterochromatin composition is quite variable, having an effect on genome size and stability. Heterochromatin in the genome of, and up to 26% in the *A. franciscana*, can contribute to greatly to the size of the absolute chromosomes compared to *A. persimilis* (Rodríquez Gil et al., 2009). Chromocentres are detected using *DAPI stain*, and Yucatlan populations have 1-8 chromocentres, which in some populations represent heteromorphic sex chromosomes (Lipko et al., 2004).

Evolutionary Dynamics of Karyotypic Polymorphisms

The process of karyotype evolution in the organism reflects the phylogenetic divergence of the organism, and this phenomenon is observed in the case of the organism, namely, in the case of the organism, *Artemia*. Synteny analysis of the genome of a species, namely *A. tibetiana*, reveals that it shares chromosome numbers with the genome of the species, Asian species, *A. sinica*, without significant rearrangements, which suggests that the Asian clades possess a similar structure (Chen et al., 2025). On the contrary, conservation species like the New World species, i.e. species of *A. franciscana* and *A. monica*, exhibit heterochromatin expansion related to speciation (Papeschi et al., 2000). Aneuploidy in

parthenogenetic forms are probably adoptive and result from meiotic anomalies and give a selective advantage in volatile habitats (Lima et al., 2021).

The changes in heterochromatin are associated with ionic content and size of the nucleus. Interphase heterochromatin of American populations is low in Yucatcan, and high in San Francisco Bay, which may be correlates of adaptation to environmental saline gradient (Torrentera 2004). The cytogenetic observations of the Iranian populations indicate that bisexual *A. urminae* share a consistent 2n=42 along with parthenogenetic ones experiencing ploidy ranging between 2n and 5n (Asem et al., 2025).

Table 1
Comparative Karyotype Features Across Major Artemia Species

Species	Diploid Number (2n)	Assembly Size (Gb)	Notable Variations
A. franciscana	42	1.27	*ZW* sex system, high heterochromatin blocks
A. amati	42		New species (Kazakhstan), previously "sp. Kazakhstan"
A. tibetiana	42	1.69	Adapted to high altitude
A. sinica	42	1.12	Asian lineage stability
A. persimilis	44		Smaller genome, low heterochromatin
A. urmiana	42		Altitude-related variations
Parthenogenetic spp.	42-84 (up to 105)		Tetraploidy in Eurasia, pentaploidy rare

This table encapsulates key cytogenetic attributes, highlighting evolutionary divergences (Data synthesized from Bett et al., 2024; Chen et al., 2025; Li et al., 2024c).

Genome Assemblies and Chromosomal Organization

Technological Advances in Sequencing and Assembly

Contemporary genome assemblies have elevated *Artemia* cytogenetics to unprecedented detail. The *A. tibetian* genome, which is derived in a high-altitude Tibetan lake (4 620 m), has 1.69 Gb of genome size, 21 pseudo-chromosomes, 79.7% of repetitive DNA, and 24,370 protein-coding genes (Chen et al., 2025). The findings of the Hi -C mapping supported the integrity of chromosomes, with a contig N50 of 81.9 Mb. Relatively, the female *A. franciscana* assembly has a 1.27 Gb scaffold N50 of 45.3 Mb and 26 923 genes, naming chromosome 1 as Z and finding fragments of putative W (Jo et al., 2024). An additional *A. franciscana* assembly from the Great Salt Lake is estimated to be 1Gb, crosslinked into 21 linkage groups (Bett et al., 2024).

The extremophile *Artemia* genome discloses expansions in ion transport, oxidative stress response, and DNA repair orthogroups, facilitating tolerance to hypersalinity (De Vos et al., 2021).

Synteny, Repeat Elements, and Functional Annotations

Comparative genomics between *A. franciscana* and *A. tibetiana* show little rearrangement of their genome structures, and repetitive material is dominated by transposable elements (TEs) like LINEs and LTRs, making up 67-80% of genomes (Chen et al., 2025; Jo et al., 2024). These repeats may drive karyotypic evolution by insertions/deletions. Functional annotations indicate enrichment in pathways such as protein processing in the endoplasmic reticulum, pointing to adaptive features.

Sex Chromosomes and Determination Systems

Structure and Differentiation of *ZW* Chromosomes

Artemia utilizes a *ZW* sex determination system, with females heterogametic (*ZW*) and males homogametic (*ZZ*) (Bowen, 1963). In *A. franciscana*, chromosome 1 functions as the Z chromosome that expands by nearly 100Mb with a 13Mb differentiated region comprising evolutionary strata (S0-S2) through recombination suppression (Bett et al., 2024). The W chromosome persists as fragmented, but candidates include five contigs that contain female-specific sequences (Jo et al., 2024).

Single-nucleus RNA-seq reveals Z-repression in the female germ line, similar to meiotic sex chromosome inactivation (MSCI), equivalent to the dynamics of the XY in mammals (Elkrewi & Vicoso, 2024). The dosage compensation balances the expression between Z and autosomes (Huylmans et al., 2019).

Contagious Parthenogenesis and Sex Chromosome Evolution

There are cases of contagious parthenogenesis in Eurasian taxa, including in examples of asexual reproduction (e.g. *Artemia sinica*), where rare males produced by asexual reproduction can mate with sexually reproducing females to transmit the asexual model of reproduction (Elkrewi et al., 2022). This is a paradoxical evolution, which is closely connected to the evolution of *ZW* sex chromosomes, since the parthenogenetic individuals do not have differentiated sex chromosomes in most cases. The similarity of the *ZW* regions between species is a strong implication of a deeper ancestral origin, and that parthenogenesis is, at least in some degree, controlled by genes present at the *Z* chromosome.

The result of sex-biased gene expression reveals no significant *Z*-autosome differences, which is a sign of strong dosage compensation (Huylmans et al., 2019). The *Z* has evolutionary strata, implying progressive cessation of recombination, dated millions of years ago.

Molecular Cytogenetics and Genomic Insights

The *ZW* Sex Determination System

Sex determination in the sexual species of *Artemia* takes the form of a female heterogametic *ZW* system, where females have sex chromosomes composed of *ZW*, maternal homogametic *ZZ* sex chromosomes. Such a system is typical of birds, part of the fish and some insects, but its discovery and characterization in *Artemia* has played a key role in understanding sex evolution in crustaceans (Asem et al., 2025).

The *Artemia ZW* system is comparatively young and dynamic, and that has made it difficult to identify the master sex-determining gene. Initial molecular methods made use of genetic linkage maps to localize sex-linked markers but the physical location of sex chromosomes was never identified until the discovery of high-quality genome sequencing (Jo et al., 2024).

Identification of Sex Chromosomes: A Genomic Breakthrough

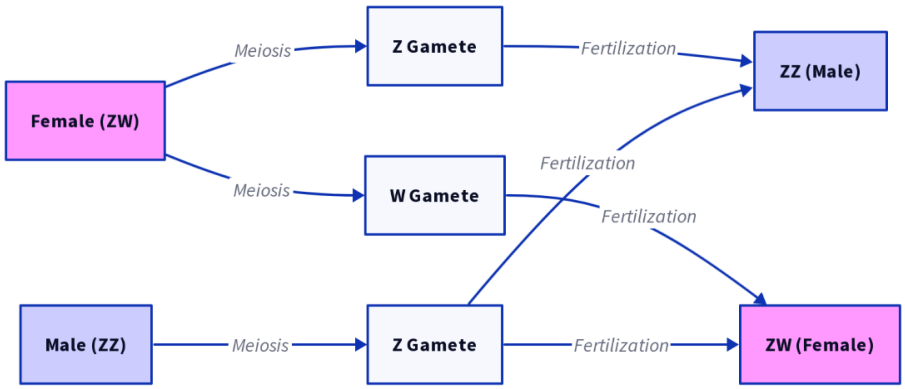
High-quality, chromosome-scale assemblies of genome have now been published as the most important recent development in *Artemia* cytogenetics. These assemblies have enabled the physical mapping and identification of the sex chromosomes and have brought the field out of the theoretical models and into real-world cytogenetic reality (Elkrewi et al., 2024).

In a recent study, Jo et al. (2024) reported a high-quality chromosome level genome assembly of female *A. franciscana*. This collection that led to the formation of 21 chromosomal scaffolds was the first conclusive information to the physical position of the sex chromosomes.

It was indicated that chromosome 1 was a sex chromosome Z, and five contigs of putative W chromosome fragments and the candidate sex-determining genes were proposed (Elkrewi et al., 2024).

This result is transformative as it ascertains that the Z chromosome of *A. franciscana* is one of largest chromosomes of the complement and which offers physical framework upon which sex-linked genes will be researched. Recovery of fragments of the very repetitive and gene-poor W chromosome is also an essential step since the W chromosome is usually hard to assemble owing to its heterochromatic nature. This recent work by Jo et al. (2024) serves as the most current and critical citation for the field of *Artemia* cytogenetics.

Figure 1
The ZW Sex Determination System in Artemia



This diagram schematically represents the female heterogametic *ZW* sex determination system, where females (*ZW*) produce Z and W gametes, and males (*ZZ*) produce only Z gametes. Fertilization results in a 1:1 ratio of *ZW* (female) and *ZZ* (male) offspring.

Genome Organization and Evolution

The new chromosome-level assemblies have provided unprecedented detail on the overall genome organization of *Artemia*. The *A. franciscana* genome is approximately 1.27 Gb in length, with a high proportion of repetitive sequences (Elkrewi et al., 2024).

Key Genomic Statistics

The comparison of genomic statistics across the newly assembled *Artemia* species highlights the rapid progress in the field:

Table 3
Key Genomic Statistics for Recent Chromosome-Level Artemia Assemblies

Species	Assembly Year	Genome Size (Gb)	Chromosome Scaffolds	Repetitive Sequence Content	Key Finding
A. franciscana	2024 (Jo et al., 2024)	1.27	21	67.26%	Z chromosome (Chr 1) identified
A. sinica	2023 (Jo, Lee, & Park, 2023)	~1.2	21	High	First chromosome-level assembly in the genus
A. tibetiana	2025 (Chen et al., 2025)	~1.1	21	High	High-altitude species assembly

A notable cytogenetic characteristic is the high proportion of repetitive sequences (more than 67 % in *A. franciscana*). These features such as transposable elements and the satellite DNA are significant contributors to the size of the genome and are commonly found in the areas of heterochromatin. Their prominence implies that they play an important role in the evolutionary dynamics and differentiation in karyotype in the genus.

Hox Gene Cluster Cytogenetics

The Hox genes are a set of associated genes that regulate the embryo body plan along the axis of anterior posteriors. The Hox cluster of their localization at the chromosome is highly conserved throughout the animal phyla. *Artemia* genome assemblies have explained the cytogenetic structure of this cluster. The ten canonical Hox genes were also found in *A. franciscana* and localized to Chromosome 14 (Elkrewi et al., 2024). The cluster is further divided into two sub clusters with a significant distance in between, a designation that is very conserved within Anostraca (Jo et al., 2024). The discovery gives an important cytogenetic predictor of comparative genomics, showing that although the *Artemia* karyotype is small overall and uniform, the synteny of major clusters of developmental genes is retained, which is indicative of a strong evolutionary limitation.

Population Cytogenetics and Phylogenetic Insights

Chinese *Artemia* populations segregate into four groups: Tibetan Plateau, Qinghai, Inner Mongolia/Xinjiang, and coastal, with high FST values denoting isolation (Li et al., 2024). Bird-mediated dispersal shapes gene flow in the *A. urmiana* complex (Li et al., 2024c).

Table 4
Genetic Diversity and Differentiation Indices for Chinese Artemia Populations

Population Group	Nucleotide Diversity (π)	FST (vs. Tibetan)	Gene Flow (Nm)	Effective Population Size (Ne)
Tibetan Plateau	0.015	-	-	High
Qinghai	0.012	0.25	0.75	Moderate
Inner Mongolia/Xinjiang	0.010	0.32	0.53	Low
Coastal	0.008	0.40	0.38	Low

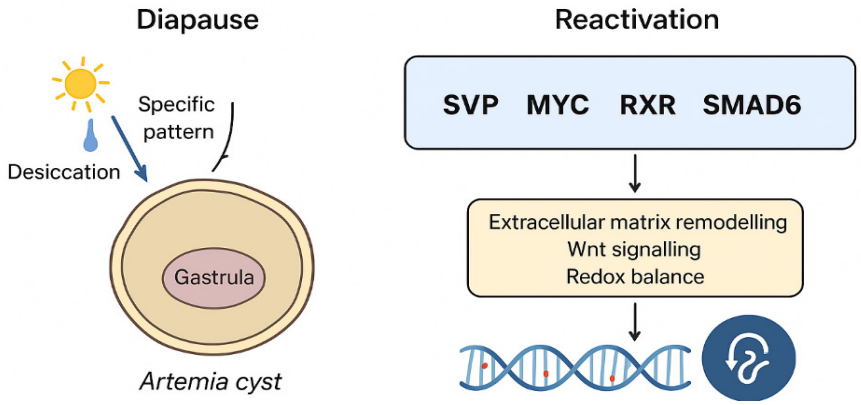
(Data from Li et al., 2024).

Transcriptional Regulation in Diapause

The cysts of *Artemia* are in the diapause state with a developmental arrest in the gastrula stage. This can be aborted when the environmental signal such as desiccation, a fall in temperature or even a specific pattern of light exposure. Complex regulatory networks, involving a group of fundamental transcription factors, such as SVP, MYC, RXR, and SMAD6, coordinate the reactivation of development, which in turn regulates the extracellular matrix remodelling, Wnt signalling pathways and the preservation of the redox balance during diapause exit (Wang et al., 2025). Recent integrative approaches to genomics studies using ATAC-seq and RNA-seq have further revealed that G-protein-coupled receptors appear to play key roles in the re-activation process, involving dynamic changes in chromatin accessibility and transcriptional activity that are responsible for the re-inception of embryogenesis (Li et al, 2024a).

Figure 3

Mechanism of Diapause and Developmental Reactivation in Artemia Cysts



Cytogenetic Adaptations to Salinity Stress

Parthenogenetic *Artemia* lineages exhibit diverse cytogenetic response to salinity in which ploidy level can determine reproductive and lifespan traits in adverse environments. Studies on diploid (2n, Ga Hai Lake, China), triploid (3n, Ankiembe Saltern, Madagascar), tetraploid (4n, Hoh Lake, China), and pentaploid (5n, Yinggehai Saltern, China) lineages show no direct relationship between ploidy and salinity tolerance in any way. Tetraploid lineages are more euryhinaline, reproduce best at 150 ppt but are inhibited at 50 ppt with pentaploids being stenohaline and short-lived. Verification of ploidy through C-banding karyotype analysis using microscope is critical in making rightful evaluation, and ploidy-specific reactions to low salinity as a stressor promoting oviparity (Asem et al., 2025).

Salinity (50, 100, 150 ppt) sets up heterogeneous reproductive patterns in diploid and tetraploid lineages, contrary to homogeneous ones in triploid and pentaploid. The analysis of group discrimination is so high that they discriminate groups based on multifactorial effect on cytogenetic stability under environmental pressure (Asem et al., 2025).

Applications in Aquaculture, Conservation, and Biotechnology

Aquaculture Applications

Selective breeding of stress-tolerant breeds in aquaculture is made possible by cytogenetic markers such as ploidy levels and polymorphisms of chromosomes, and allows the production of *Artemia* strains with improved salinity tolerance and reproductive performance (FAO, 2024). An example is the use of genome assemblies, which indicate the increase of ion transport and oxidative stress genes, to inform breeding to produce a maximum amount of cyst and a high-quality naupliar to feed fish and shrimp larvae on live feed (FAO, 2024). There are strain-specific characteristics, including the small cysts and high hatching rates in Vinh Chau *A. franciscana*, which are used to commercially produce eggs, and biofloc technology has increased fecundity rate by 30-50%, while recycling nutrients (FAO, 2024). Genetic information is used in order to prevent loss of biodiversity during introductions to support sustainable harvesting of solar salt ponds and integrated multi-trophic systems (Li et al., 2024). The applications promote aquaculture across the world by supplying

nutrient-rich feed with the consumption of about 1,700 tonnes of dry *Artemia* product every year in China highlighting the economic importance of the product (FAO, 2024).

Conservation Applications

The conservation initiative uses the data of single-nucleotide polymorphisms (SNP) and population genetic frameworks to conserve diversity in the endangered *Artemia* populations and offers clear clades susceptible to habitat deterioration and intrusions (Li et al., 2024). Research shows that there are four genetic clusters in China, the nucleotide diversity of Tibetans is high, directing the resistance against shrinking the habitats of climate changes (Li et al., 2024b). Resurrection ecology employs genetic archives of the extirpated species in the form of diapausing cysts of sediment cores, which can be used to revive the lost species and monitor evolutionary dynamics over time (Lenormand et al., 2018). Banks of cysts that are viable over decades and stored in laboratories are used to reintroduce cysts and monitor biodiversity in hypersaline wetlands (Lenormand et al., 2018). Risk assessment of anthropogenic effects, based on cytogenetics, including the ploidy change in parthenogenetic stocks, will help manage the situation sustainably during geological and climatic changes (Asem et al., 2025).

Biotechnology Applications

Artemia cytogenetics have biotechnological potential in cryptobiosis models to explore space, cyst tolerance models to space environments (UV, anoxia, desiccation) informs life-supports and pharmaceutical preservation (Lenormand et al., 2018). Transcription factors such as SVP and MYC regulate diapause mechanisms and are an insight into suspended animation to be used in medical practice such as organ storage (Wang et al., 2025). *Artemia* is used as a toxicity test model in ecotoxicology, and genetic markers are used to measure the effects of pollutants on growth and reproduction (FAO, 2024). Genome-guided bioencapsulation improves nutrient delivery, vectors probiotics and high-unsaturated fatty acids (HUFA) in aquaculture, and ancient DNA in cysts allows research on long-term adaptation, linking the fields of evolutionary biology and biotech innovations (De Vos et al., 2021).

Conclusion

This comprehensive review synthesizes the recent progress in the cytogenetics of *Artemia*, including variation of karyotype, genome assemblies, sex chromosome dynamics, molecular methods, population structures, and transcriptional networks during diapause. These shows the preserved chromosomal setup across species, the complexity of *ZW* sex determination, and the adaptive processes to survive in harsh environmental conditions. Multi-omics and comparative genomics approaches are likely to provoke answers to some unresolved questions such as the full characterisation of the W chromosome, the molecular basis of stability in polyploidy, and the evolutionary forces behind parthenogenesis. This field of study combines the classical cytogenetics with the use of the latest sequencing technology, which not only increases our knowledge on the evolutionary biology of *Artemia* but also improves its use in aquaculture, conservation, and biotechnology. The interdisciplinary collaborations should be given priority in the future in order to investigate cytogenetic response to new environmental challenges to sustainably manage this useful model organism.

Author Contributions

Conceptualization, S.N.; methodology, K.B., A.I.; software, A.I.; validation, A.I., K.B., and N.AGH; formal analysis, S.N.; investigation A.I., K.B.; resources, A.I.; data curation A.I., K.B., and N.AGH.; writing–original draft preparation, S.N., A.I., K.B. and N.AGH.; writing–review and editing, A.I. and K.B.; visualization, S.N.; supervision, S.N. and Naser .AGH.; project administration, S.N.; funding acquisition, K.B.

References

Asem, A., Li, Y., Yan, X., Zhang, Y., Zhu, Y., Kangarloei, B. A., & Yang, C. (2025). Effects of Salinity on the Reproductive and Lifespan Traits of *Artemia* Parthenogenetic Lineages with Different Ploidy Levels. Biology, 14(8), 1055. https://doi.org/10.3390/biology14081055

Asem, A., Yang, C., Eimanifar, A., Hontoria, F., Varó, I., Mahmoudi, F., Fu, C.-Z., Shen, C.-Y., Rastegar-Pouyani, N., Wang, P.-Z., Li, W., Yao, L., Meng, X., Dan, Y.-T., Rogers, D. C., & Gajardo, G. (2023). Phylogenetic analysis of problematic Asian species of *Artemia* Leach, 1819 (Crustacea, Anostraca), with the descriptions of two new species. *Journal of Crustacean Biology, 43*(1), ruad002. https://doi.org/10.1093/jcbiol/ruad002

Bett, V. K., Macon, A., Vicoso, B., & Elkrewi, M. (2024). Chromosome-level assembly of *Artemia franciscana* sheds light on sex chromosome differentiation. *Genome Biology and Evolution, 16*(1), evae006. https://doi.org/10.1093/gbe/evae006

Bowen S. T. (1965). The genetics of *Artemia* salina. V. Crossing over between the X and Y chromosomes. *Genetics*, *52*(3), 695–710. https://doi.org/10.1093/genetics/52.3.695

Chen, P., Zhong, Z., Jin, W. X., Sun, J., & Sun, S. C. (2025). Chromosome-scale assembly of *Artemia tibetiana* genome, first aquatic invertebrate genome from Tibet Plateau. *Scientific data*, *12*(1), 777. https://doi.org/10.1038/s41597-025-05136-z

De Vos, S., Rombauts, S., Coussement, L., Dermauw, W., Vuylsteke, M., Sorgeloos, P., Clegg, J. S., Nambu, Z., Van Nieuwerburgh, F., Norouzitallab, P., Van Leeuwen, T., De Meyer, T., Van Stappen, G., Van de Peer, Y., & Bossier, P. (2021). The genome of the extremophile *Artemia* provides insight into strategies to cope with extreme environments. BMC Genomics, 22(1), 635. https://doi.org/10.1186/s12864-021-07937-z

Dhont, J., & Sorgeloos, P. (2002). *Applications of Artemia*. In T. J. Abatzopoulos, J. A. Beardmore, J. S. Clegg, & P. Sorgeloos (Eds.), *Artemia: Basic and applied biology* (Vol. 1). Springer. https://doi.org/10.1007/978-94-017-0791-6_6

Elkrewi, M. N., & Vicoso, B. (2024). Single-nucleus atlas of the *Artemia* female reproductive system suggests germline repression of the Z chromosome. *PLOS Genetics, 20*(8), e1011376. https://doi.org/10.1371/journal.pgen.1011376

Elkrewi, M. N., Khauratovich, U., Toups, M. A., Bett, V. K., Mrnjavac, A., Macon, A., Fraisse, C., Sax, L., Huylmans, A. K., Hontoria, F., & Vicoso, B. (2022). *ZW* sex-chromosome evolution and contagious parthenogenesis in *Artemia* brine shrimp. *Genetics, 222*(2), iyac123. https://doi.org/10.1093/genetics/iyac123

FAO. (2024). Manual on *Artemia* production and use. FAO Fisheries and Aquaculture Technical Paper No. XXX. Rome. https://users.ugent.be/~psorgelo/A4BreportClosingMayJune2024/FAO%20*Artemia*%20Manual%202024.pdf

Gajardo, G. M., & Beardmore, J. A. (2012). The brine shrimp *Artemia*: Adapted to critical life conditions. *Frontiers in Physiology, 3*, 185. https://doi.org/10.3389/fphys.2012.00185

Huylmans, A. K., Toups, M. A., Macon, A., Gammerdinger, W. J., & Vicoso, B. (2019). Sex-biased gene expression and dosage compensation on the *Artemia franciscana* Z-chromosome. *Genome Biology and Evolution, 11*(4), 1033–1044. https://doi.org/10.1093/gbe/evz053

Jo, E., Cho, M., Choi, S., Lee, S. J., Choi, E., Kim, J., Kim, J. Y., Kwon, S., Lee, J. H., & Park, H. (2024). High-quality chromosome-level genome assembly of female *Artemia franciscana* reveals sex chromosome and Hox gene organization. *Heliyon, 10*(19), e38687. https://doi.org/10.1016/j.heliyon.2024.e38687

Lenormand, T., Nougué, O., Joven, N., Tran, F., Sureteau, L., Cheptou, P. O., & Pool, J. E. (2018). Resurrection ecology in *Artemia*. Evolutionary Applications, 11(1), 76–83. https://doi.org/10.1111/eva.12522

Li, A., Song, Z., Zhang, M., Duan, H., Sui, L., Wang, B., & Hao, T. (2024a). Integrating ATAC-Seq and RNA-Seq reveals the signal regulation involved in the *Artemia* embryonic reactivation process. *Genes, 15*(8), 1083. https://doi.org/10.3390/genes15081083

Li, K., Zhang, R., Sui, L.-Y., Zhang, C., & Han, X.-K. (2024b). Genetic structure of ten *Artemia* populations from China: Cumulative effects of ancient geological events, climatic changes, and human activities. *Frontiers in Marine Science, 11*, 1375641. https://doi.org/10.3389/fmars.2024.1375641

Li, W. J., Guo, Y., & Sun, S. C. (2024c). Population genetics of *Artemia* urmiana species complex (Crustacea, Anostraca): A group with asymmetrical dispersal and gene flow mediated by migratory waterfowl. *Gene*, *894*, 147957. https://doi.org/10.1016/j.gene.2023.147957

Lima, L. V., Sousa, S. M., Almeida, T. E., & Salino, A. (2021). State of the art in cytogenetics, insights into chromosome number evolution, and new C-value reports for the fern family Gleicheniaceae. *Anais da Academia Brasileira de Ciências, 93*(Suppl. 3), e20201881. https://repositorio.ufmg.br/server/api/core/bitstreams/c907df73-fd3b-4b2f-98b6-25cdc9b7af15/content

Lipko, P., Papeschi, A. G., & Cohen, R. G. (2004). Cytogenetic analysis of four Argentinean populations of *Artemia* (Crustacea, Branchiopoda: Anostraca). *Caryologia, 57*(3), 283–289. https://doi.org/10.1080/00087114.2004.10589406

Papeschi, A. G., Cohen, R. G., Pastorino, X. I., & Amat, F. (2000). Cytogenetic proof that the brine shrimp *Artemia franciscana* (Crustacea, Branchiopoda) is found in Argentina. *Hereditas, 133*(2), 159–166. https://doi.org/10.1111/j.1601-5223.2000.00159.x

Parraguez, M., Gajardo, G., & Beardmore, J. A. (2009). The New World *Artemia* species *A. franciscana* and *A. persimilis* are highly differentiated for chromosome size and heterochromatin content. *Hereditas, 146*(2), 93–103. https://doi.org/10.1111/j.1601-5223.2009.02109.x

Sainz-Escudero, L., López-Estrada, E. K., Rodríguez-Flores, P. C., & García-París, M. (2022). Brine shrimps adrift: Historical species turnover in Western Mediterranean *Artemia* (Anostraca). *Biological Invasions, 24*, 2477–2498. https://doi.org/10.1007/s10530-022-02779

Wang, B., He, Z., Zhang, M., Zhang, R., Song, Z., Li, A., & Hao, T. (2025). Transcriptional Regulatory Network of the Embryonic Diapause Termination Process in *Artemia*. *Genes*, *16*(2), 175. https://doi.org/10.3390/genes16020175

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