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EDTA preserves high molecular weight DNA across tissues of diverse species stored at room temperature for more than five years

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Abstract

Cryopreservation is considered the gold standard for preserving high molecular weight (HMW) DNA in tissue but is often impractical in the field. Room-temperature storage in EDTA is an established short-term alternative for DNA preservation in tissue, yet its long-term performance remains poorly characterized. Here, we compared the percentages of DNA fragments > 10 kb (%HMW) in DNA extracts from fresh tissues with those from tissues stored at room temperature for 5.7–6.4 years in either EDTA (0.25 M, pH 10) or 95% ethanol (EtOH). Tissues came from specimens of five species spanning four phyla: *Alitta virens* (Annelida), *Faxonius virilis* and *Homarus americanus* (Arthropoda), *Scomberomorus maculatus* (Chordata), and *Mercenaria mercenaria* (Mollusca). After storage, EDTA-preserved tissues from all five species yielded significantly higher average %HMW values than those stored in EtOH. EDTA-preserved tissues also yielded significantly higher average %HMW values than fresh tissue extracts in four of the five species. Additionally, we recovered HMW DNA from the EDTA preservative supernatants, and in four species, the average %HMW from supernatants was greater than or equal to that extracted from tissue samples. However, EDTA was less effective than EtOH at maintaining tissue integrity. After storage, 30% of EDTA-preserved samples were partially or completely dissolved, whereas all EtOH-preserved samples remained intact. These findings indicate that EDTA can provide effective long-term, room-temperature preservation of HMW DNA and that EDTA supernatants may be an additional source of recoverable DNA for genomic analyses. Alternatively, EtOH may be preferable when tissue integrity—rather than DNA quality—is the priority.

Introduction

Increasingly, the preservation of high molecular weight (HMW) DNA—here defined as DNA fragments greater than 10 kb—is essential for research across biological disciplines. HMW DNA is required for many applications, including long-read DNA sequencing and genome assembly, as well as the preparation of large-insert libraries (Blom, 2021; Dahn et al., 2022; Minich et al., 2023; Oosting et al., 2020; Van Cise et al., 2024). Additionally, because many forms of damage render DNA more susceptible to strand breakage, molecular weight serves as a useful proxy for overall DNA quality (Lindahl, 1993).

Although DNA can be easily preserved and stored for downstream molecular applications once it has been purified, preserving and storing DNA in tissue samples is often more challenging. In tissue, DNA can begin to degrade rapidly upon cell death, largely due to the accelerated activity of nucleases and other biological reactions associated with necrosis (Tozzo et al., 2020). To prevent DNA and/or tissue degradation, many tissue preservation methods are designed to inhibit these processes (Nagy, 2010).

Flash freezing and subsequent storage at ultracold temperatures (typically − 80 to -196°C) is often considered the gold standard for preserving DNA in biological samples (Blom, 2021; Card et al., 2021; Jackson et al., 2011; Minich et al., 2023; Phillips et al., 2019; Van Cise et al., 2024; Zimkus & Ford, 2014). However, this form of preservation is logistically challenging, especially in field settings, and typically requires expensive equipment and hazardous materials, such as liquid nitrogen and dry ice. Liquid

preservatives, such as ethanol (EtOH) and ethylenediaminetetraacetic acid (EDTA), offer alternatives to cryopreservation, allowing for room-temperature preservation of HMW DNA (Nagy, 2010; Sharpe et al., 2020).

Among liquid preservatives that are compatible with DNA preservation, EtOH (70–95%) is the most widely used (Nagy, 2010). EtOH acts by dehydrating, denaturing, and aggregating proteins, effectively inhibiting the enzymatic reactions that degrade DNA (Dessauer et al., 1996; Flournoy et al., 1996). EtOH is inexpensive, readily available in many places, and effective for short-term DNA preservation, but is unreliable for long-term preservation of DNA in tissue samples, particularly when stored at room temperature (Dawson et al., 1998; Kilpatrick, 2002; Precioso et al., 2022).

EDTA is a preservative widely used for food (Natrajan & Sheldon, 2000; Tu & Mustapha, 2002) and cosmetics (Lundov et al., 2009; Maurício et al., 2017) and is a common component of buffers used to preserve purified DNA (Lahiri & Schnabel, 1993; Murakami, 2013; Yun-Tae et al., 2012). EDTA reduces DNA degradation by chelating divalent cations that activate deoxyribonucleases (DNases) (Gueroult et al., 2010; Kolarevic et al., 2014; Yang, 2011). It has long been used to preserve DNA in tissues as a component of the preservative solution DESS (Seutin et al., 1991). Indeed, DESS has been shown to be more effective than EtOH at preserving DNA in the tissues of a wide variety of taxa (Kilpatrick, 2002; Ogiso-Tanaka et al., 2025; Oosting et al., 2020; Robertson et al., 2013; Yoder et al., 2006). However, recent studies have demonstrated that EDTA is the primary active ingredient in DESS (Sharpe et al., 2020) and that EDTA alone performs as well as or better than DESS or 95% EtOH as a preservative of HMW DNA in tissue (DeSanctis et al., 2023; Sharpe et al., 2020). An additional study has shown that the effectiveness of EDTA as a preservative of DNA in tissue increases as the pH increases from 8 to 10, consistent with the observation that EDTA's ability to chelate divalent cations increases over this range (DeSanctis et al., 2023). However, the ability of EDTA to preserve DNA in tissue for storage periods greater than one year remains poorly characterized.

In this study, we evaluate the effectiveness of EDTA as a long-term, room-temperature preservative for DNA in tissue. We examine tissue samples from five aquatic species stored in EDTA (0.25 M, pH 10) or 95% EtOH at room temperature for more than five years and compare these stored samples to paired fresh tissues. Specifically, we evaluate the effect of treatment on the average percentage of DNA fragments > 10 kb (%HMW) in DNA extracts from samples and assess differences in tissue integrity among treatments.

Materials and methods

In this investigation, we evaluate samples stored in two preservative solutions at room temperature for more than five years. This work extends a previous study in which subsamples of the same tissues were evaluated after one year of storage in the same preservative solutions (DeSanctis et al., 2023). In that study, tissues from specimens of five aquatic species, *Alitta virens* (clam worm; *N* = 10), *Faxonius virilis* (virile crayfish; *N* = 10), *Homarus americanus* (American lobster; *N* = 10), *Scomberomorus maculatus*

(Spanish mackerel; *N* = 10), and *Mercenaria mercenaria* (quahog; *N* = 10), were sampled from body wall, tail, abdominal, or pectoral muscle, or mantle tissue, respectively (Fig. 1).

Approximately 100 mg (avg. 95.40 ± 9.16 mg) of tissue was collected from each specimen and added to a 1.8 mL cryotube containing 1 mL of EDTA (0.25 M, pH 10). In parallel, approximately 100 mg (avg. 96.80 ± 13.04 mg) of tissue was collected from each specimen and added to a 1.8 mL cryotube containing 1 mL of 95% EtOH. For comparison, approximately 25 mg (avg. 26.91 ± 9.70 mg) of each specimen was sampled for immediate DNA extraction without preservative treatment, hereafter referred to as fresh tissue. Treated samples were stored at room temperature in the dark for one year in their respective preservatives, after which, approximately 25 mg (avg. 25.46 ± 4.45 mg) of each tissue was subsampled for DNA extraction. The remaining tissue from each sample was then returned to its preservative solution and stored at room temperature for an additional 4.7–5.4 years before being resampled and reevaluated in this study.

DNA extraction and quantification

To evaluate the percentage of HMW DNA (%HMW) in DNA extracts from each preserved sample after 5.7–6.4 years of storage, approximately 25 mg (avg. 23.98 ± 5.51 mg) of each tissue was subsampled for DNA extraction. DNA was purified using the Qiagen DNeasy Blood and Tissue Kit (Hilden, Germany) according to the manufacturer's recommended protocol with the following modifications: all samples were treated with 4 µL of RNase A (100 mg/mL; Qiagen; Hilden, Germany) after digestion; DNA was eluted by adding two sequential 50 µL volumes of Buffer AE at room temperature for a total elution volume of 100 µL. DNA was also extracted from the preservative supernatant for all EDTA-preserved samples. For preservative supernatants, particulates were removed by centrifugation for 10 minutes at 6,000 rpm (RCF 2,000 g) using a Galaxy Mini Microcentrifuge (VWR; Radnor, PA), and 20–200 µL (avg. 183.24 ± 44.73 µL) of each supernatant was collected for DNA extraction, as above.

Extracted DNA was sized and visualized using agarose gel electrophoresis. 3 µL of each DNA extract (avg. 0.096 ± 0.119 µg DNA) was loaded into a 16 cm horizontal slab gel (0.8% agarose, 1x TAE buffer containing 1% GelRed nucleic acid gel stain (Biotium; Fremont, CA)). The first lanes of each gel were loaded with 1 µL of Quick-Load Purple 1 kb Plus DNA Ladder (100 µg/mL; New England Biolabs; Ipswich, MA). Electrophoresis was performed at 8.2 V/cm for 30 minutes. DNA in gels was visualized using a BioRad Gel Doc XR+ Molecular Imager (Hercules, CA).

Quantitative analyses of DNA extracts were performed using the Agilent Technologies TapeStation 2200 DNA Analyzer with the Agilent DNA Analyzer Genomic DNA ScreenTapes and TapeStation Analysis Software version A.02.02 (SR1; Santa Clara, CA). 1 µL of each DNA extract (avg. 0.035 ± 0.040 µg DNA) was analyzed to determine the percentage of HMW DNA (%HMW).

Statistical analysis

In this investigation, DNA fragments greater than 10 kb are considered HMW and fragments from 150 bp to 10 kb are considered low molecular weight (LMW) (DeSanctis et al., 2023; Messner, Becker, DeSanctis, Soranno, Pianka, Pierce, Johnson, Falco Poulin, et al., 2025; Mulcahy et al., 2016). The percentage of LMW DNA (%LMW) was determined by the Agilent DNA Analyzer and subsequently subtracted from 100 to estimate %HMW. This method avoids the exclusion of DNA fragments larger than the 60 kb resolution limit of the DNA Analyzer (DeSanctis et al., 2023; Messner, Becker, DeSanctis, Soranno, Pianka, Pierce, Johnson, Falco Poulin, et al., 2025).

$$\%HMW = (100 - \%LMW) = 100 - \left(\frac{LMW\ DNA\ concentration\ \left(\frac{ng}{\mu\ L}\right)}{total\ DNA\ concentration\ \left(\frac{ng}{\mu\ L}\right)} * 100 \right)$$

Data for each species were analyzed separately in RStudio using R version 4.5.2 (R Core Team, 2025) to examine the effect of treatment on %HMW. Some EDTA-preserved tissues were not recoverable due to dissolution. In these instances, data from preservative supernatant extracts were substituted for tissue extract data in our analyses. A Shapiro-Wilk normality test was used to determine if the data were normally distributed. Non-normally distributed data were analyzed with a non-parametric Friedman χ^2 followed by a Bonferroni-corrected Friedman Conover post-hoc test using the “PMCMRplus” package version 1.9.12 (Pohlert, 2024), the “multcompView” package version 0.1–11 (Graves et al., 2026), and the “rcompanion” package version 2.5.2 (Mangiafico, 2026). Normally distributed data were analyzed with a one-way repeated measures ANOVA using the “emmeans” package version 2.0.3 (Lenth & Piaskowski, 2026) followed by a Bonferroni-corrected Tukey post-hoc test using the “nlme” package version 3.1–168 (Pinheiro et al., 2025).

To evaluate the effect of DNA source (i.e., tissue versus preservative supernatant) on %HMW for EDTA samples, data for each species were similarly analyzed in RStudio. Specimens lacking either tissue or preservative supernatant samples were excluded from these quantitative analyses. A Shapiro-Wilk normality test was used to determine if the data were normally distributed. Non-normally distributed data were analyzed with a Wilcoxon signed ranks test, while normally distributed data were analyzed with a Welch’s paired *t*-test.

PCR and DNA barcoding

PCR amplification was performed to evaluate the suitability of DNA extracts for typical downstream applications, as in (DeSanctis et al., 2023; Messner, Becker, DeSanctis, Soranno, Pianka, Pierce, Johnson, Falco Poulin, et al., 2025). The mitochondrial cytochrome c oxidase I (COI) barcoding region was amplified by PCR from DNA extracts of *A. virens*, *F. virilis*, *H. americanus*, and *M. mercenaria* using the primers LCO1490_t1 (5’–TGTAAAACGACGGCCAGTGGTCAACAAATCATAAAGATATTGG–3’) and HCO2198_t2 (5’-CAGGAAACAGCTATGACTAAACTTCAGGGTGACCAAAAAATCA–3’) (Foottit et al., 2009). For *S. maculatus* FISHCOILBC_ts (5’-CACGACGTTGTAAAACGACTCAACYAATCAYAAAGATATYGGCAC–3’)

and FISHCOIHBC_ts (5'–GGATAACAATTTCACACAGGACTTCYGGGTGRCCRAARAATCA–3') (Handy et al., 2011) were used. Each reaction contained 1 µL DNA template, 12.5 µL OneTaq 2X Master Mix (New England Biolabs; Ipswich, MA), 10 µM of forward primer, 10 µM of reverse primer, and was brought to 25 µL total volume with ultrapure water. Reactions were initialized at 94°C for 30 seconds, followed by 34 or 30 cycles of denaturation at 94°C for 30 seconds, annealing at 45°C for 50 seconds or 52°C for 40 seconds, and extension at 68°C for 60 seconds, with a final extension at 68°C for 5 minutes for invertebrate species or *S. maculatus*, respectively, using a PTC-200 Thermocycler with a heated lid (MJ Research; Waltham, MA). PCR amplification success was determined by the presence of an appropriately sized band on a 0.8% agarose gel, as described above.

Additionally, we sequenced the COI gene from each of three randomly selected specimens of each species. Specifically, PCR products amplified from fresh tissues, tissues stored in EDTA or EtOH, and EDTA preservative supernatants were bidirectionally Sanger sequenced at Psomagen (Rockville, MD) using an ABI 3730XL Analyzer (Applied Biosystems; Foster City, CA). Resulting sequences were edited and analyzed using Geneious 2026.0.2 (Auckland, New Zealand), automatically trimming ends to remove regions with > 1% error probability. Sequences $\geq$ 500 bp in length and with a Q20 score $\geq$ 98% were considered successful.

Specimen and sample availability statement

Samples and associated data for all organisms used in this study have been deposited in the Ocean Genome Legacy Center Genomic Resource Collection (Falco et al., 2022) and are available via the Arctos database (https://arctos.database.museum/) (Cicero et al., 2024) under the catalog numbers listed in S1 Table.

Ethics statement

This study was carried out in accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health and Northeastern University's Institutional Animal Care and Use Committee policies. Although no live vertebrate animals were used in this study, the general principles of humane animal care were applied to the live invertebrate animals used.

Results and Discussion

After long-term room-temperature storage, we observed preservative-specific differences in both the preservation of HMW DNA and the integrity of tissue across all species.

Effect of preservative treatments on %HMW

DNA was extracted from 35 of the 50 tissue samples stored in EDTA, excluding 15 samples that disintegrated or dissolved and so could not be subsampled. For these 15 samples, %HMW values from the preservative supernatant extracts were used in the analysis. Across all species and treatments, %HMW values ranged from 2.6–87.9% (avg. 42.0 ± 25.3%) after 5.7–6.4 years of room-temperature storage.

For all species, treatment had a significant effect on %HMW (all *p*-values < 0.0074; Table 1). EDTA-preserved samples yielded significantly higher %HMW values than did those preserved in EtOH (Fig. 2). These results are consistent with the qualitative observations by gel electrophoresis (Fig. 3). This indicates that EDTA may be preferable to EtOH for field preservation of samples for applications in conservation genomics where long-term room-temperature storage of HMW DNA in tissues is desirable.

Table 1

Effect of treatment on the percentage of high molecular weight DNA in DNA extracts. Average percentage of high molecular weight DNA (%HMW) was determined for extracts from tissue or preservative supernatant samples of 10 specimens each of *Alitta virens*, *Faxonius virilis*, *Homarus americanus*, *Scomberomorus maculatus*, and *Mercenaria mercenaria*. DNA was either extracted immediately from fresh tissue or stored for 5.7–6.4 years at room temperature in EDTA (0.25 M, pH 10) or 95% ethanol. Degrees of freedom, df; sample size, *N*; asterisks (*) denote a significant treatment effect ($p < 0.05$).

%HMW	Species	*N*	Statistical test	Test statistic	df	*p*-value
	Alitta virens	10	Friedman χ^2	$\chi^2 = 20.0$	2	< 0.0001*
	Faxonius virilis	10	Repeated Measures ANOVA	$F = 19.2$	2	< 0.0001*
	Homarus americanus	10	Friedman χ^2	$\chi^2 = 12.2$	2	0.0022*
	Scomberomorus maculatus	10	Friedman χ^2	$\chi^2 = 20.0$	2	< 0.0001*
	Mercenaria mercenaria	10	Friedman χ^2	$\chi^2 = 9.8$	2	0.0074*

Interestingly, EDTA-preserved samples yielded significantly higher %HMW values than did fresh tissue samples in four of the five cases examined. While this may seem counterintuitive, DNA degradation can occur during DNA extraction from fresh untreated tissue (Lahiri & Schnabel, 1993) and previous studies have shown that this type of degradation can be prevented by treating and storing tissues in EDTA before DNA extraction (DeSanctis et al., 2023; Messner, Becker, DeSanctis, Soranno, Pianka, Pierce, Johnson, Poulin, et al., 2025). Similarly, in a previous study, treatment of frozen samples with EDTA before DNA extraction significantly increased %HMW compared with direct extraction from frozen untreated tissues (Messner, Becker, DeSanctis, Soranno, Pianka, Pierce, Johnson, Poulin, et al., 2025).

Effect of DNA source (tissue versus preservative supernatant) on %HMW

For all EDTA supernatants (*N* = 49; 1 of 50 samples was excluded because the preservative supernatant evaporated), %HMW ranged from 7.8–87.4% (avg. 55.3 ± 19.0%). Where both tissues and preservative supernatants were available (*N* = 34), we compared the %HMW values of DNA samples extracted from the EDTA-preserved tissue to those of DNA samples extracted from the corresponding EDTA supernatant. The average %HMW values from preservative supernatant extracts were the same as or greater than those from tissue extracts for four of the five species (Table 2, Fig. 4). The exception was *S. maculatus*, in which a small but significant decrease in average %HMW was observed (Fig. 4d). Thus, both the EDTA-preserved tissues and the EDTA supernatants may be viable sources of HMW DNA for downstream applications.

Table 2

The effect of DNA source (tissue versus preservative supernatant) on the percentage of high molecular weight DNA in DNA extracts from EDTA-preserved samples. For each species, the percentage of high molecular weight DNA (%HMW) in extracts from the preserved tissue was compared with that from the corresponding EDTA preservative supernatant. Degrees of freedom, df; not applicable, NA; number of paired samples are reported per species, *N*; asterisks (*) denote a significant difference between sources ($p < 0.05$).

%HMW	Species	*N*	Statistical test	Test statistic	df	*p*-value
	Alitta virens	3	Welch's paired *t*-test	*t* = -8.0	2	0.0152*
	Faxonius virilis	6	Welch's paired *t*-test	*t* = -0.5	5	0.6112
	Homarus americanus	7	Welch's paired *t*-test	*t* = 0.1	6	0.9151
	Scomberomorus maculatus	9	Welch's paired *t*-test	*t* = 3.1	8	0.0148*
	Mercenaria mercenaria	9	Wilcoxon signed-rank test	*V* = 38.0	NA	0.0742

PCR amplification and sequencing

We performed PCR amplification on the COI gene from all DNA extracts. We observed PCR products of the expected size from all EDTA-preserved tissues (*N* = 35), all EDTA preservative supernatant samples (*N* = 49), and all fresh tissue samples (*N* = 50). In comparison, only 36 of the 50 EtOH-preserved tissue samples produced COI amplicons (S1 Table). To evaluate amplicon quality, we selected three specimens per species and sequenced PCR amplicons from each of the four treatments for a total of 60 amplicons. 53 amplicons yielded bidirectional sequences meeting a threshold of $\geq$ 500 bp with a Q20 score $\geq$ 98%, five yielded unidirectional sequences meeting this threshold, and two sequences—both from *A. virens* EtOH-preserved tissue samples—failed to meet this threshold. In all cases, sequences obtained from the same individual were identical, regardless of treatment or DNA source (tissue versus

preservative supernatant; S2 Table). These results indicate that while preservative treatment had no discernable impact on sequence quality, PCR amplification success rates were greater for EDTA-preserved samples.

Effect of treatments on tissue integrity

After long-term storage in EtOH, preserved tissues were generally firmer than the fresh tissues and remained sufficiently intact for tissue subsampling. While in most cases these samples remained intact, samples of *S. maculatus* fragmented when handled, but could still be subsampled.

Conversely, EDTA-preserved tissues were generally softer than fresh tissues, with the extent of change in tissue integrity varying by tissue type and species. For example, most EDTA-preserved samples of *M. mercenaria* were soft, but sufficiently intact to be picked up with forceps and subsampled. In contrast, most samples of *A. virens* became mucilaginous or dissolved to such an extent that they could not be recovered or subsampled as intact tissue (Fig. 3). Tissues of the remaining species fell between these two extremes (see S3 Table).

The observed degradation of tissue integrity during storage in EDTA may be driven by the ability of EDTA to chelate divalent cations—the same property that makes EDTA an effective DNA preservative. This is because divalent cations are not only required for DNase activation (Gueroult et al., 2010; Kolarevic et al., 2014; Yang, 2011), but also contribute to cellular adhesion (Ogiso-Tanaka et al., 2025; Takeichi, 1977). Additionally, EDTA chelates calcium ions, which can cause the dissolution of calcium-rich internal structures that stabilize tissue (Li et al., 2024; Ogiso-Tanaka et al., 2025; Yap et al., 2025). Thus, these effects may be inextricably linked.

Conclusions

These findings indicate that EDTA can provide effective long-term, room-temperature preservation of HMW DNA and that EDTA supernatants may be an additional source of recoverable DNA for genomic analyses. Alternatively, EtOH may remain preferable when tissue integrity—rather than DNA quality—is the priority.

Declarations

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Competing interests

The authors have no relevant financial or non-financial interests to disclose.

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Data availability statement

All data supporting the findings of this study are available within the paper and its Supplementary Information. Samples and associated data for all organisms used in this study have been deposited in the Ocean Genome Legacy Center Genomic Resource Collection and are available via the Arctos database (https://arctos.database.museum/) under the catalog numbers listed in S1 Table.

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Figures

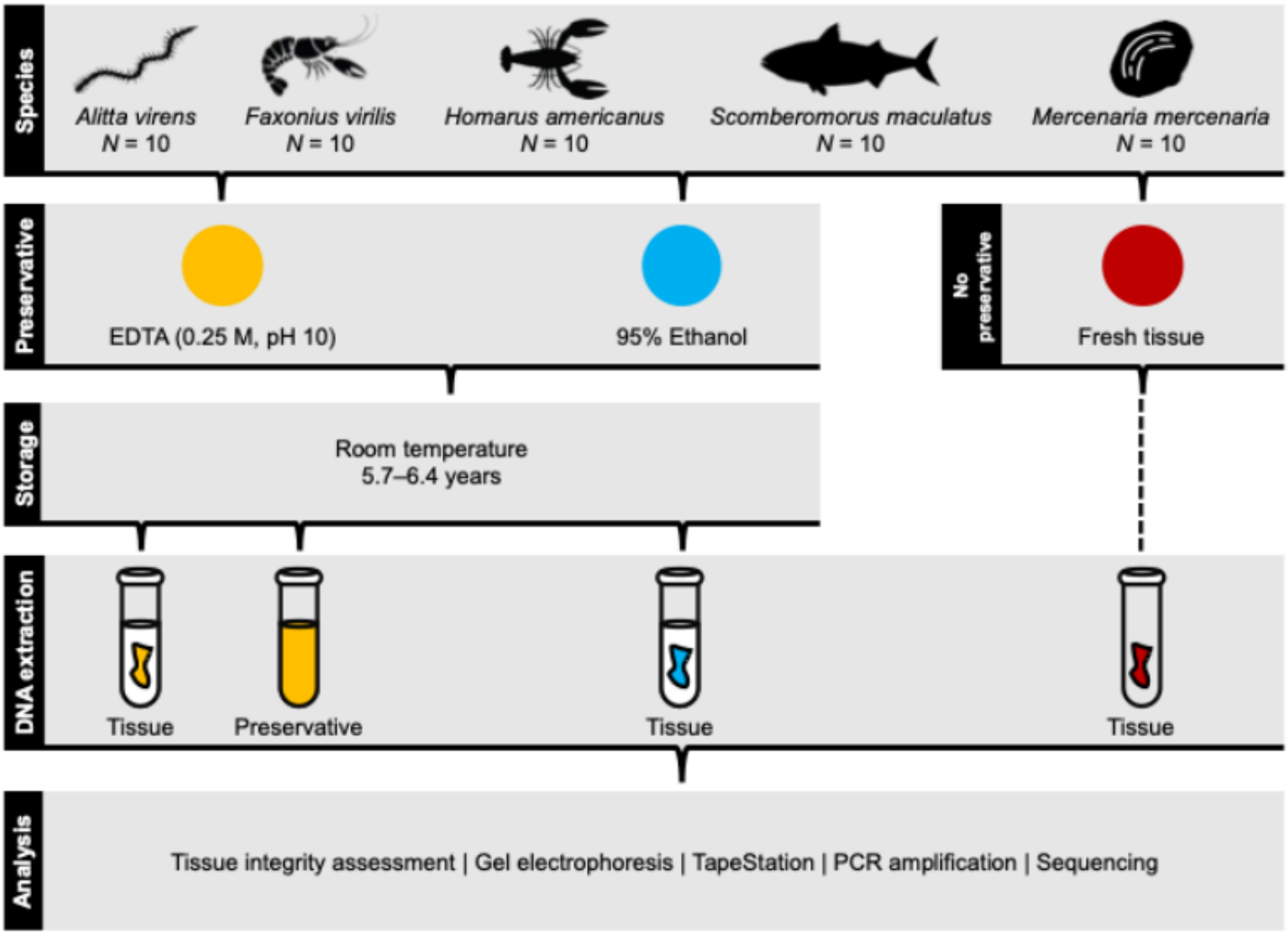


Figure 1

Experimental design. Tissue samples from five aquatic species were stored at room temperature for more than five years in EDTA (0.25 M, pH 10) or 95% ethanol, after which DNA was extracted from the tissues and/or preservative supernatants, analyzed, and compared to DNA extracted from fresh tissues.

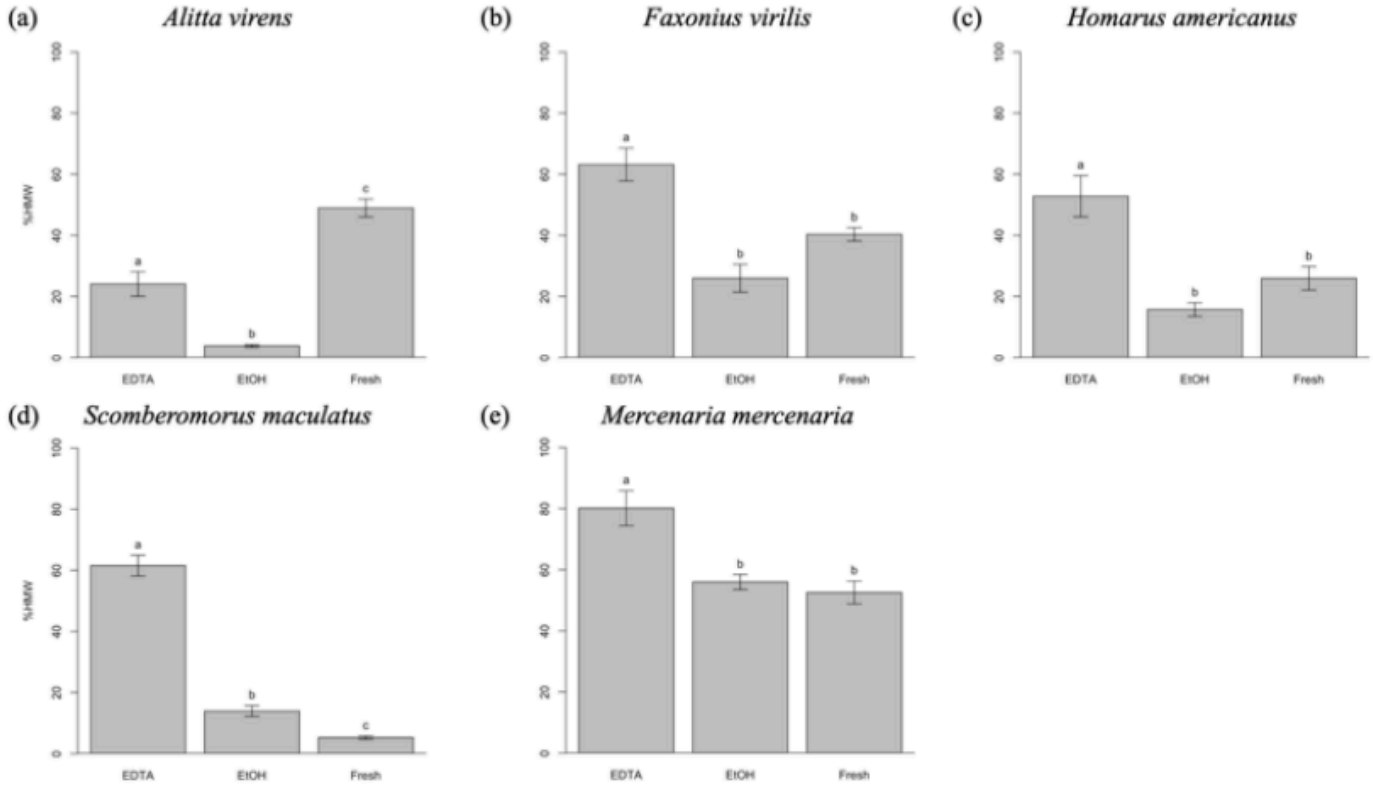


Figure 2

Average percentage of high molecular weight DNA in DNA extracts. Average percentage of high molecular weight DNA (%HMW) was determined for extracts from tissue or preservative supernatant samples of 10 specimens each of (a) *Alitta virens*, (b) *Faxonius virilis*, (c) *Homarus americanus*, (d) *Scomberomorus maculatus*, and (e) *Mercenaria mercenaria*. DNA was either extracted immediately from fresh tissue (Fresh) or stored for 5.7–6.4 years at room temperature in EDTA (0.25 M, pH 10; EDTA) or 95% ethanol (EtOH). Error bars represent standard error. Within each chart, treatments bearing different letters are significantly different at the Bonferroni-adjusted $p < 0.017$; matching letters indicate statistically indistinguishable treatments.

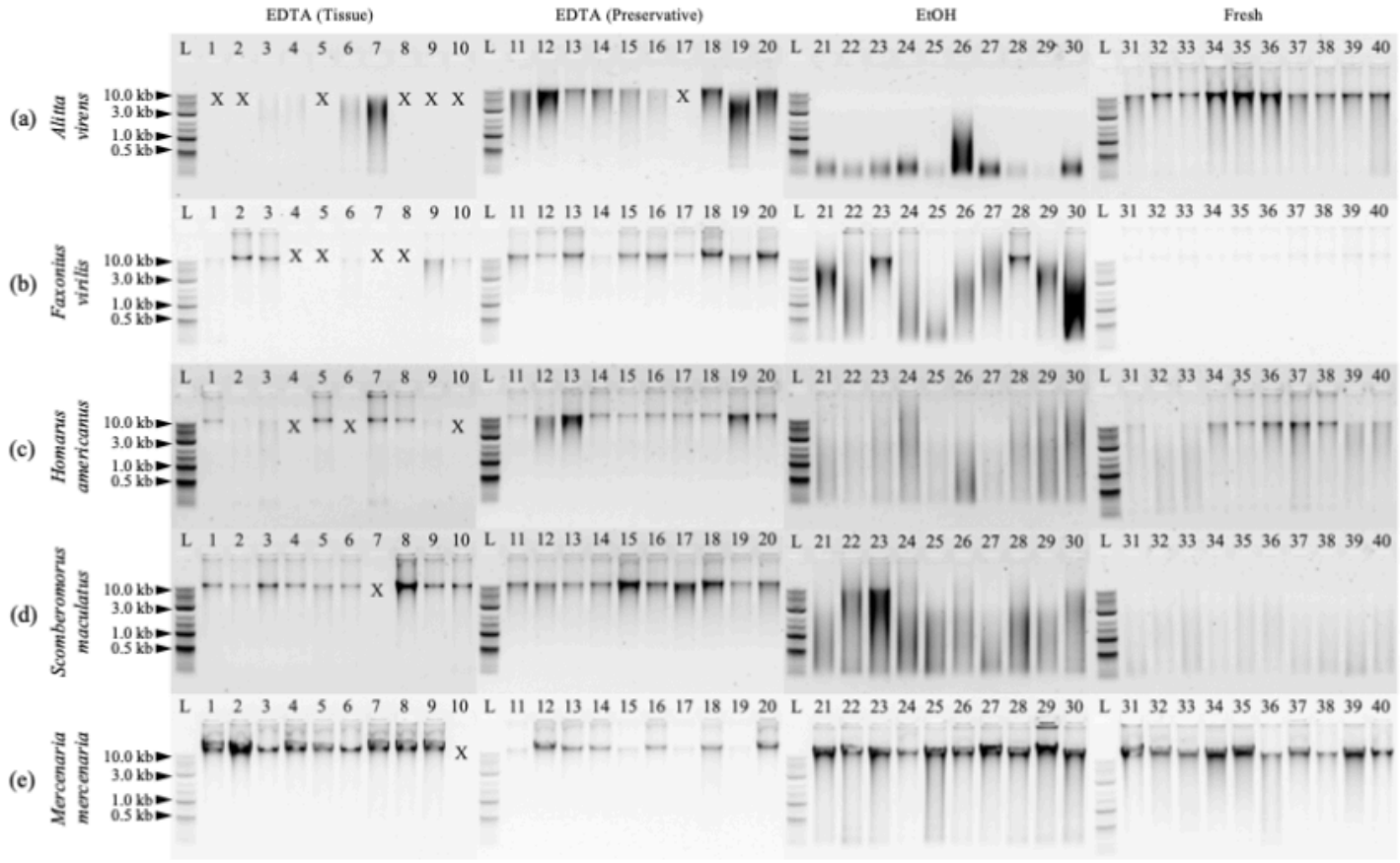


Figure 3

DNA extracted from stored and fresh samples of five aquatic species visualized by gel electrophoresis.DNA was extracted from (a) *Alitta virens*, (b) *Faxonius virilis*, (c) *Homarus americanus,* (d) *Scomberomorus maculatus*, and (e) *Mercenaria mercenaria* samples after storage at room temperature for 5.7–6.4 years in EDTA (0.25 M, pH 10; tissue extracts: lanes 1–10, preservative supernatant extracts: lanes 11–20) and 95% ethanol (lanes 21–30). DNA extracts from fresh tissue are shown in lanes 31–40. Lanes marked with an L contain 1 µL of Quick-Load Purple 1 kb Plus DNA Ladder (100 µg/mL; New England Biolabs; Ipswich, MA). Lanes marked with an X indicate samples that were not recoverable. Specimens are presented in the same order across all treatments.

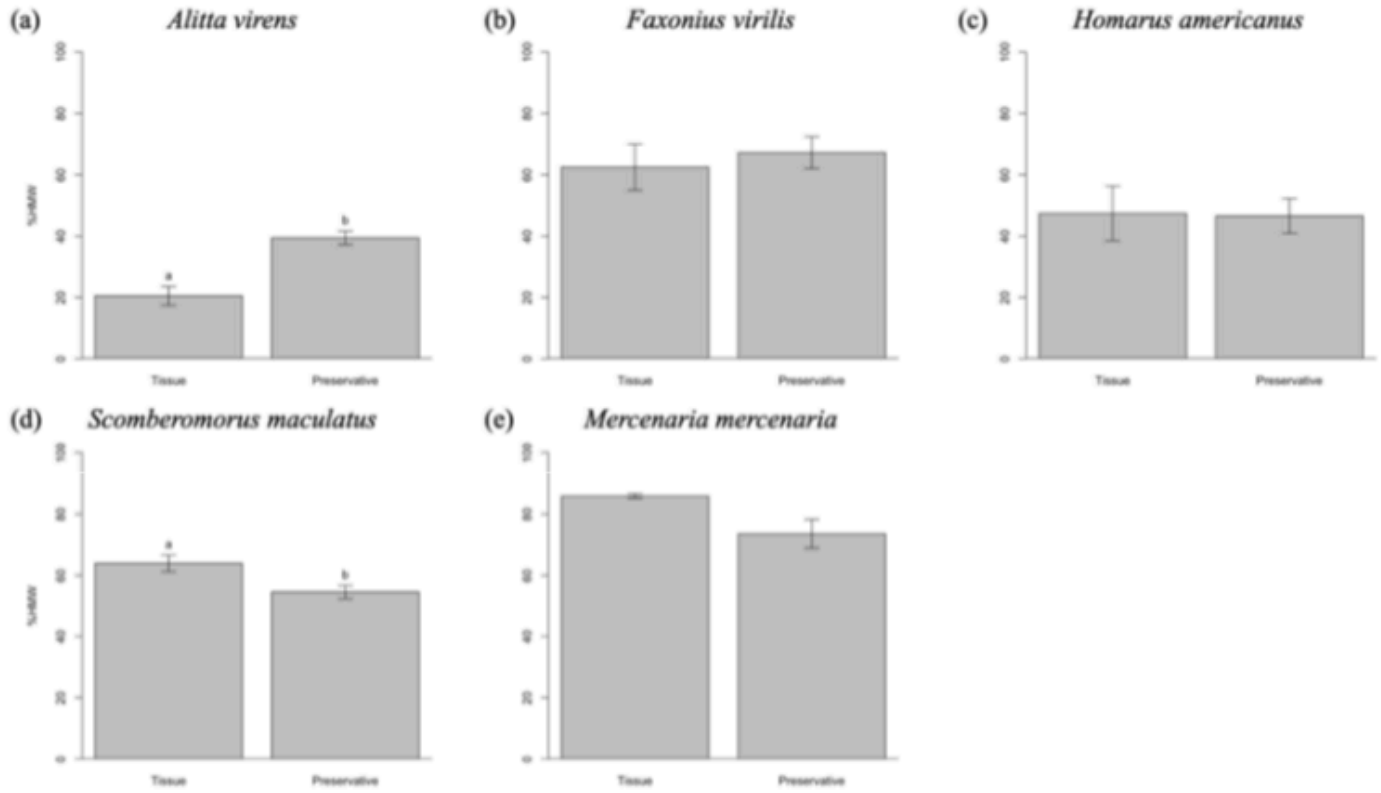


Figure 4

The effect of DNA source (tissue versus preservative supernatant) on the percentage of high molecular weight DNA in DNA extracts from EDTA-preserved samples. The average percentage of high molecular weight DNA (%HMW) was determined for (a) *Alitta virens* (*N*= 3), (b) *Faxonius virilis* (*N* = 6), (c) *Homarus americanus* (*N*= 7), (d) *Scomberomorus maculatus* (*N* = 9), and (e) *Mercenaria mercenaria* (*N* = 9). DNA was extracted from tissues stored in EDTA (0.25 M, pH 10; Tissue) or the preservative supernatant (Preservative). Error bars represent standard error. Within each chart, treatments bearing different letters differ significantly at $p < 0.05$; matching letters indicate statistically indistinguishable treatments; an absence of letters indicates no significant differences between treatments in a given model.

Supplementary Files

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