Marine biotoxin depuration rates: management applications, research priorities, and predictions for unstudied species

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Abstract

Monitoring and managing the public health risk posed by marine biotoxins is a daunting challenge. With expansive coastlines, 1000s of seafood species, and dozens of biotoxins, monitoring cannot occur everywhere at once. Improving the cost-effectiveness of biotoxin monitoring is thus critical to expanding coverage to include more species, toxins, and locations. Notably, understanding the rate at which seafood species depurate biotoxins can be used to optimize the cadence of monitoring. We conducted a systematic review to collate marine biotoxin depuration rates and synthesize the factors that influence them; identify knowledge gaps, best practices, and research priorities; and generate predictions of depuration rates for unstudied species. We found that only 85 marine species have been studied for their biotoxin depuration rates. Depuration rates for non-bivalves and for toxins besides paralytic shellfish toxins (PSTs) are especially understudied. Depuration half-lives varied from 0.03 to 1269 days based on species, toxin, tissue, and environmental conditions. In general, depuration accelerates with increased temperature and food availability, with implications for aquaculture siting, depuration enhancement, and biotoxin monitoring. We identified unstudied bivalve and finfish species that are highly produced and vulnerable to HABs that are high priorities for future research. Finally, we used a Bayesian regression model to predict PST depuration rates for 102 unstudied bivalve species, the only clade-syndrome with sufficient training data. These predictions can guide efficient monitoring and management until lab- or field-based depuration rates become available. We recommend that future studies directly estimate depuration rates to ensure their comparability across studies and utility to managers.

Keywords: harmful algal blooms, phycotoxin, toxin, elimination, detoxification, excretion, toxicokinetics

36 # 1. Introduction

37   Harmful algal blooms (HABs) that produce biotoxins that accumulate in seafood species
38 represent a growing threat to public health and marine fisheries and aquaculture (Hallegraeff et
39 al., 2021). More than 200 taxa of marine algae produce biotoxins that threaten human health
40 (Lundholm et al., 2009), with risk present in nearly all coastal waters (OBIS, 2025). Collectively,
41 these toxins cause seven major poisoning syndromes in humans – paralytic, amnesic,
42 diarrhetic, neurotoxic, azaspiracid, cyanotoxin, and ciguatera poisoning – with new toxins and
43 syndromes discovered each decade (Nicolas et al., 2017). These syndromes cause symptoms
44 ranging from gastrointestinal issues to neurological issues to death (Grattan et al., 2016). As a
45 result, managers often close fisheries and aquaculture to protect public health, which can cause
46 significant socioeconomic impacts from lost commercial, recreational, and cultural activities
47 (Moore et al., 2020). HABs are expected to increase in frequency, duration, and intensity with
48 climate change (IPCC, 2019), making them critical to study to ensure that seafood can safely
49 remain a source of healthy, sustainable food for a growing human population.
50
51   To protect public health, many governments use biotoxin monitoring programs to track
52 seafood safety and manage fisheries and aquaculture operations that are vulnerable to biotoxin
53 risk (Andersen et al., 2004). In general, these programs monitor the toxicity of seafood species
54 and trigger management actions when toxicity rises above a threshold deemed unsafe for
55 human consumption, commonly referred to as the "action threshold" (Langlois and Morton,
56 2018). The management action, which could be a closure or an evisceration requirement (i.e.,
57 required removal of toxic body parts), is not ceased until toxicity falls below the action threshold,
58 often after several successive tests to ensure safety. Ideally, all vulnerable species would be
59 monitored to fully protect public health (Costa et al., 2017) and sampling would be highly
60 spatially and temporally resolved to protect public health while also avoiding unnecessary
61 management restrictions (Free et al., 2022). However, given limited resources to support
62 expensive lab testing, expansive taxonomic, spatial, and temporal coverage is rarely possible
63 (Langlois and Morton, 2018). Improving the cost-effectiveness of biotoxin monitoring is thus
64 necessary to monitor more species, in more places, at more times. This could be achieved by
65 either lowering the cost of each test (i.e., cheaper monitoring) or by lowering the number of tests
66 required to effectively manage risk (i.e., more efficient monitoring).
67

68   One pathway for improving the efficiency of biotoxin monitoring programs is to tailor the

69   frequency of sampling to the toxicokinetics of the monitored species (Blanco, 2009).

70   Toxicokinetics describe the processes and rates of accumulation (a.k.a., uptake, adsorption),

71   distribution, metabolism, and depuration (a.k.a., excretion, elimination, detoxification) of

72   biotoxins within a species (Landrum et al., 1992). The rate at which species accumulate toxins

73   determines how quickly monitoring should begin and proceed after a HAB is detected. For

74   example, monitoring could begin later and advance more slowly if accumulation is slow but

75   should begin sooner and advance more quickly if accumulation is fast. The distribution of toxin

76   burden among different tissues is important because it determines what tissue is the most

77   useful indicator of public health risk and whether a species could be safely consumed and

78   successfully marketed following the evisceration (removal) of the most toxic tissue. The

79   metabolism of the consumed toxin into new compounds, which can be either more or less toxic

80   than the original compound (Bricelj and Shumway, 1998), contributes to the duration of seafood

81   toxicity. Finally, the rate of depuration determines how frequently monitoring is needed after a

82   species becomes toxic to facilitate the timely end of management actions. It can also be used to

83   provide seafood harvesters, processors, and dealers forecasts of when management actions

84   are likely to cease.

85

86   The use of depuration rates to design more efficient biotoxin monitoring and

87   management is particularly promising because of the availability of good mathematical models

88   for describing depuration and forecasting the duration of high toxicity. In general, depuration

89   kinetics are theorized to follow either one- or two-compartment exponential decay (Blanco,

90   2009). In a one-compartment model, biotoxins are assumed to accumulate within a single

91   "compartment", which can represent a single tissue, a group of tissues, or even a whole

92   organism, and are assumed to be exponentially lost to the environment at a single rate. For

93   example, a toxin might accumulate in the digestive system following ingestion and then be

94   quickly eliminated through egestion. In a two-compartment model, biotoxins are assumed to

95   accumulate in an initial compartment (e.g., the digestive system) with some transference to a

96   second compartment (e.g., muscle) with a slower exponential depuration rate. Theoretically,

97   depuration rates could be described using even more compartments, though statistical support

98   for increasingly complex models to offer more parsimonious fits seems unlikely; to our

99   knowledge, the maximum number of compartments used in practice is three (Ye et al., 2021).

100   With knowledge of the exponential decay constants for any of these models, managers could

101   forecast depuration timelines (**Fig. 1**) and provide themselves, fishermen, and aquaculture

102   farmers with valuable predictions of when seafood is expected to be safe for consumption.

103

104   To illustrate how knowledge of depuration rates could improve the efficiency of biotoxin

105   monitoring, we consider a species that depurates a biotoxin at 0.03 day^{-1} (2.9% day^{-1}; 23.1 day

106   half-life) based on one-compartment depuration kinetics (**Fig. 1**). This is roughly equivalent to

107   the rate at which Atlantic surfclams (*Spisula solidissima*) depurate paralytic shellfish toxins

108   (PSTs) under warm conditions (Bricelj et al., 2014). After reaching peak toxicity, managers

109   could use this depuration rate to forecast when toxicity is expected to fall below the action

110   threshold and tailor the cadence of monitoring accordingly (**Fig. 1A**). Specifically, managers

111   could pause regular testing while toxicity is expected to remain well above the action threshold

112   and resume it when toxicity is expected to approach the threshold. In this example, optimized

113   testing eliminates the need for four tests, which accumulates when applied across many

114   management zones (e.g., 10 zones = 40 saved tests). This frees up resources to monitor new

115   management zones or new species at the same cost as the original monitoring program.

116   Importantly, knowledge of depuration rates can improve efficiency even before peak toxicity is

117   attained (**Fig. 1B**). If the first test conducted after a forecast is higher than expected (because

118   the species is still accumulating toxins from an ongoing bloom or from toxins in the food web),

119   the forecast can be repeated and the cadence of monitoring updated accordingly.

120

121   The widespread use of depuration rates to increase the efficiency of biotoxin monitoring

122   programs requires the consolidation of known depuration rates, identification of the factors that

123   affect biotoxin depuration, and prioritization of depuration rates still needing study. This is

124   partially supported by a small number of review papers. A review by Fernandez et al. (2003)

125   provided biotoxin "retention times", the time required for toxicity to fall below either the action

126   threshold or the limit of detection, for 34 species-toxin combinations representing 31 bivalve

127   species and five toxin syndromes (paralytic, diarrhetic, amnesic, neurotoxic, other). Although

128   these values provide credible evidence that depuration rates are species- and toxin-specific,

129   they are challenging to interpret and cannot be operationalized as rates. A review by Bricelj and

130   Shumway (1998) provides operational PST depuration rates (% per day) for 21 species of

131   bivalves. A handful of research papers provide non-systematically collated depuration rates to

132   place measured depuration rates within a broader context (Garcia-Corona et al., 2024; Martins

133   et al., 2020; Schultz et al., 2013). While valuable, these reviews collectively lack depuration

134 rates for non-bivalves, three notable biotoxin syndromes (ciguatera, cyanotoxin, azaspiracid),
135 and over two decades of research into marine biotoxin depuration processes.

136

137 Here, we seek to empower more efficient marine biotoxin monitoring and management
138 through a multi-pronged assessment of biotoxin depuration rates. First, we conducted a
139 systematic literature review to collate published depuration rates, synthesize information on the
140 factors that impact biotoxin depuration, and identify best practices for future depuration studies.
141 Second, we prioritized species for future depuration study by identifying highly produced
142 seafood species that are vulnerable and exposed to each biotoxin syndrome yet have no
143 published depuration rates. Finally, we used a Bayesian regression model trained on our
144 database of biotoxin depuration rates to predict rates for unstudied species, which can be used
145 to guide monitoring programs until depuration studies are completed. Overall, we demonstrate
146 how biotoxin depuration rates can forecast depuration timelines, which can be used to design
147 more efficient monitoring programs and to support informed management and business
148 decisions.

149 ## 2. Methods

150 ## 2.1 Literature review

151 ### 2.1.1 Database development

152 We conducted a systematic review of marine biotoxin depuration rates following the
153 PRISMA review protocol (**Fig. S1**) (Page et al., 2021). First, we identified 797 candidate papers
154 by using the following search query in Web of Science on July 30, 2025: ("depurat*" or "excret*"
155 or "eliminat*" or "detox*") AND ("toxin*" or "biotoxin*" or "phycotoxin" or "domoic" or "okadaic" or
156 "saxitoxin" or "brevetoxin" or "azaspiracid" or "cyanotoxin" or "ciguatoxin") AND ("marine" or
157 "ocean"). This query was designed to identify papers that study the depuration (a.k.a. excretion,
158 elimination, or detoxification; term 1) of marine phycotoxins (term 2) from marine species (term
159 3). We only considered papers that either quantified the depuration rates of biotoxins produced
160 by harmful algae from marine species or presented the data required for us to externally
161 quantify depuration rates. Thus, we excluded 643 papers that did not study a marine species,
162 did not study a biotoxin produced by a harmful algae species, or did not quantify a depuration
163 rate or present the data needed to externally derive a depuration rate (**Fig. S1**). We

164   supplemented this systematic review with a targeted search of the Chinese literature to identify

165   depuration rates not represented in the English literature; this non-systematic review added two

166   papers on paralytic shellfish toxin depuration rates in Manila clam (*Ruditapes philippinarum*).

167

168   We reviewed the resulting 156 papers (**Fig. S2**) and extracted the following attributes of

169   the study (**Table S1**): species studied (common and scientific name), biotoxin studied and its

170   causative agent, tissue studied (e.g., meat, viscera, hepatopancreas; **Table S2**), study type (lab

171   or field), feeding conditions during depuration (starved, fed a non-toxic diet, or foraged in the

172   wild), and other experimental conditions (e.g., varied temperature, salinity, diets, etc.). If the

173   depuration rate (exponential decay constant or half-life) was directly reported, we recorded the

174   rate and whether it was derived from a one- or two-compartment exponential decay model

175   (details below). These are also known as first- or second-order or one- or two-phase (biphasic)

176   decay models. We grouped the studied biotoxins into eight syndromes of shellfish poisoning

177   (Nicolas et al., 2017): amnesic, diarrhetic, paralytic, ciguatera, neurotoxic, azaspiracid,

178   cyanotoxin, and other shellfish poisoning (**Table 1**). Cyanotoxin poisoning describes toxins

179   formed by cyano-bacteria including microcystin, nodularin, and homoanatoxin. The other

180   category includes yessotoxins, pectenotoxins, tetrodotoxins, gymnodimines, and karlotoxins.

181   2.1.2 Deriving depuration rates

182   If the depuration rate was not directly reported as either an exponential decay constant

183   or half-life, we extracted the data needed to derive the depuration rate using WebPlotDigitizer

184   (Rohatgi, 2025). We estimated depuration rates using a one-compartment exponential decay

185   model fit to the depuration phase of the data. For field studies with long time series, depuration

186   rates were often estimated for discrete depuration events **(Fig. S3**). We calculated tissue-

187   specific depuration rates such that:

188

189     $$N_t = N_o e^{-kt}$$

190

191   where toxicity at time t (N_t) is a function of initial toxicity (N_0) and the decay constant k.

192

193   We calculated the half-life, the time required for toxicity to halve, associated with each

194   reported or derived one-compartment model depuration rate as:

195

196     $$t_{1/2} = ln(2)/k$$

197

198   If a paper reported a half-life but not the decay constant (k), we inverted this equation to

199   calculate the decay constant. We standardized all decay constants and half-lives to be in terms

200   of days (i.e., some fast depuration rates were reported or derived in terms of hours). Finally, we

201   calculated the percent daily loss of biotoxin burden as:

202

203   *% daily loss = 1 – exp(-k)*

204   2.2 Priority species for depuration study

205   We identified priority species for depuration study as vulnerable species that have high

206   commercial harvests from countries with HAB exposure but that lack published depuration

207   rates. First, we identified countries exposed to HAB species associated with each biotoxin

208   syndrome (**Table 1**) using data from the Ocean Biodiversity Information System (OBIS) (OBIS,

209   2025), which provides geotagged observations of HAB species (**Fig. S4**). We classified a

210   country's waters as exposed to biotoxin syndrome if an associated species (OBIS) has ever

211   been recorded within its Exclusive Economic Zone (EEZ) (Flanders Marine Institute, 2025). We

212   note that this likely underestimates countries exposed to HABs as many countries, especially in

213   Africa and the Middle East **(Fig. S4**), lack HAB monitoring programs (Andersen et al., 2004).

214

215   Second, we identified shellfish and finfish species that are vulnerable to HABs and

216   harvested in exposed countries using national fisheries and aquaculture production data from

217   the Food and Agriculture Organization (FAO) of the United Nations (FAO, 2024). We identified

218   vulnerable shellfish as filter-feeding molluscs (e.g., oysters, mussels, clams, scallops), as they

219   readily accumulate toxins by directly consuming HAB species, even within aquaculture facilities

220   where they generally feed directly from the surrounding environment. We excluded predatory

221   molluscs (e.g., cephalopods), grazing molluscs (e.g., gastropods), and non-mollusc shellfish

222   (e.g., crustaceans, echinoderms), which are challenging to prioritize because their indirect

223   biotoxin accumulation pathways make their vulnerability to biotoxins highly heterogeneous. The

224   shellfish prioritization excludes ciguatera, which is principally a finfish biotoxin syndrome.

225

226   We identified vulnerable finfish as those vulnerable to ciguatera, the primary biotoxin

227   syndrome affecting finfish. Ciguatera is most common in large, tropical, reef-associated,

228   predators (Lewis and Holmes, 1993; Randall, 1958). We thus used information on habitat

229   associations, maximum length, and trophic level from FishBase (Boettiger et al., 2012; Froese

230 and Pauly, 2025) to identify reef-associated predators larger than 25 cm that are harvested in
231 capture fisheries. A threshold of 25 cm was selected as the smallest fish with detectable
232 ciguatoxins in the review of (Li et al., 2023) was striated surgeonfish (*Ctenochaetus striatus*) at
233 26 cm maximum length. Because FishBase information on trophic level is relatively sparse, we
234 could only exclude known herbivores (i.e., we could not filter for known predators). FishBase
235 also identifies fish with known ciguatera observations; these species were considered in the
236 prioritization even if they did not meet the criteria above. We excluded aquaculture production
237 from the finfish prioritization analysis because predatory finfish are generally fed non-toxic food
238 and are thus less exposed to ciguatoxins through the food web.
239
240 Finally, we identified the 20 vulnerable species with the highest annual production
241 (bivalves: aquaculture+fisheries; finfish: fisheries only) from 2014-2023 in EEZs exposed to
242 each biotoxin syndrome and classified species without published depuration rates as priorities
243 for study. We highlighted unstudied species that would provide the first depuration estimate at
244 the order, family, or genus levels as particularly valuable. To illustrate the value of these
245 estimates, we quantified the (1) number of currently harvested species in the taxonomic group
246 using the FAO data and (2) total number of species in the group using FishBase and
247 SeaLifeBase (Palomares and Pauly, 2025), which captures potential future harvest diversity.
248
249 Although we did not prioritize non-bivalve invertebrates for depuration study, we
250 compared maximum biotoxin toxicities reported in non-bivalves by select review papers (Costa
251 et al., 2017; Deeds et al., 2008; Lefebvre and Robertson, 2010) relative to common international
252 action thresholds (Langlois and Morton, 2018) to assess the importance of conducting
253 depuration studies for non-bivalve vectors of seafood poisoning syndromes. These review
254 papers were opportunistically selected from the systematic literature search but do not
255 constitute a systematic review of all observed non-bivalve toxicities.

256 2.3 Predicting bivalve PST depuration rates

257 We compared the ability for one generalized linear model and three mixed effects
258 models to predict paralytic shellfish toxin (PST) depuration rates in marine bivalves. We focused
259 on PST depuration rates in bivalves based on the *a priori* expectation that this was the only
260 clade-syndrome combination with sufficient data (**Fig. 2**) to generate a model with good
261 predictive skill. All four models predict the log depuration rate to normalize the response variable
262 and to constrain predictions to positive depuration rates (i.e., exponential decay rather than

263 exponential growth). All four models include five fixed effects: (1) study type (lab vs. field), (2)

264 tissue type (e.g. muscle, hepatopancreas, etc.); (3) maximum length (cm), (4) von Bertalanffy

265 somatic growth rate (1/yr), which describes the rate at which an organism grows towards its

266 maximum size, and (5) preferred temperature (°C). These variables were selected based on

267 hypotheses that (a) depuration rates would be faster in the lab, where species are fed non-toxic

268 diets; (b) depuration rates would vary by tissue; and (c) depuration rates would be faster for

269 smaller, faster growing, warmer water species, which are expected to have faster metabolisms

270 (Robinson et al., 1983) and therefore faster egestion. We retrieved the maximum length, growth

271 rate, and preferred temperature from SeaLifeBase (Palomares and Pauly, 2025) using the

272 *rfishbase* R package (Boettiger et al., 2012). When values were missing for a species, we

273 preferentially used the genus-, family-, order-, or class-level median, depending on availability.

274

275   The first model includes only the five fixed effects variables (the "fixed effects only"

276 model) while the subsequent models use different approaches for incorporating taxonomic

277 random effects. The inclusion of taxonomic random effects evaluates the hypothesis that traits

278 besides those explicitly evaluated as fixed effects may also determine depuration rates. For

279 example, species-specific physiology and feeding ecology may play an important role in

280 depuration, but we lack the data to explicitly incorporate these traits as fixed effects. The

281 "phylogenetic random effects" model evaluates the hypothesis that depuration rates are

282 phylogenetically conserved and correlated to ancestry. This model includes species-specific

283 random effects that were modelled using a variance-covariance matrix derived from the bivalve

284 phylogenetic tree. We constructed a phylogenetic tree of all bivalve species using the Open

285 Tree of Life API (Hinchliff et al., 2015) via the *rotl* R package (Michonneau et al., 2016). We

286 estimated branch lengths using the Grafen method (Grafen, 1997), which scales internal nodes

287 to approximate evolutionary divergence when branch-length information is incomplete,

288 implemented through the *ape* R package (Paradis and Schliep, 2019). The "taxonomically

289 nested model" has hierarchically nested order, family, genus, and species random effects. This

290 model evaluates the hypothesis that depuration rates are similar within a clade but that

291 differences between clades are not related to ancestry (as in the phylogenetic model). Finally,

292 the "species random effects" model includes species-level random effects that are not

293 structured by phylogeny or taxonomy. This model evaluates the hypothesis that unobserved

294 species traits impact depuration rates but that these impacts are idiosyncratic and not related to

295 taxonomy.

296

297   We fit all four models using a Bayesian estimation approach implemented through the

298   *brms* R package (Bürkner, 2017). The models were compared using efficient approximate

299   leave-one-out cross-validation (LOO) using the *loo* R package (Vehtari et al., 2024), where the

300   best model was identified as the one with the largest expected log predictive density (ELPD),

301   which characterizes the ability of the model to predict the data withheld in the cross-validation.

302   The fit of all four models was also evaluated through the estimation of a Bayesian R^2 (Gelman et

303   al., 2019). We evaluated the coefficients and conditional effects of predictors in the best fitting

304   model to understand the impact of each variable on PST depuration rates. Finally, we used the

305   best fitting model to estimate PST depuration rates for all harvested marine bivalves, as

306   determined through the analysis of the FAO production data (FAO, 2024) described above. We

307   included all harvested bivalves, not just those harvested from EEZs with known PST occurrence

308   (**Fig. S4**), given that PST may be present but undetected in many of these EEZs and the

309   potential for the range of PST causative agents to expand in the future. The life history traits for

310   these species were also retrieved from SeaLifeBase using the *rfishbase* R package.

3. Results

3.1 Literature review

3.1.1 General characteristics

314   Biotoxin depuration rates have been studied in 85 marine species spanning 66 genera,

315   39 families, 26 orders, and 10 classes (**Fig. 2A; Table S3**). Marine invertebrates, especially

316   bivalves, have been much more studied than marine vertebrates: only 13 papers (8%) have

317   evaluated biotoxin depuration rates in finfish whereas 145 papers (93%) have assessed biotoxin

318   depuration rates in invertebrates (some papers studied both an invertebrate and a vertebrate

319   allowing this statistic to sum to >100%; this applies to other results as well). Most of the

320   evaluated papers studied bivalves (124 papers; 80%), with a particular focus on blue mussels

321   (31 papers; 20%), Mediterranean mussels (17 papers; 11%), Pacific oysters (13 papers; 8%),

322   eastern oysters (8 papers; 5%), and king scallops (6 papers; 4%). Notably, blue mussels are the

323   only species with depuration rates estimated for six of the eight biotoxin syndromes (**Fig. 2B**).

324

325   The depuration of PSTs from marine species has been studied more than the depuration

326   of any other biotoxin (66 papers; 42%) (**Fig. 2B**). Domoic acid (24 papers, 15%), diarrhetic

327   shellfish toxin (DST) (24 papers; 15%), and cyanotoxin (16 papers; 10%) depuration rates have

328   received similar levels of attention. Brevetoxin depuration has been evaluated in 9 papers (6%),

329   which evaluate four bivalve, two finfish, and one dolphin species. Ciguatoxin depuration has

330   only been studied in four finfish species (4 papers) and azaspiracid depuration has only been

331   measured in three bivalve species (3 papers). Eighteen papers (12%) have assessed the

332   depuration rates of "other" biotoxins (**Table 1**), which include yessotoxins, tetrodotoxins,

333   pectenotoxins, karlotoxins, and gymnodimines (**Fig. 2B**).

334

335   Biotoxin depuration has been studied in many tissue types (**Fig. S5**) with some papers

336   comparing depuration rates among many tissues (**Fig. 3B**). In general, the tissues most

337   evaluated are those that either harbor the greatest toxin burden or are consumed by people. For

338   bivalves, studies have largely focused on the soft tissue (eaten by people) and the

339   hepatopancreas (greatest toxin burden; Bricelj and Shumway, 1998). Similarly, crustacean

340   depuration rates have largely been evaluated in the hepatopancreas (greatest toxin burden;

341   Schultz et al., 2013) and the soft tissue (eaten by people). For finfish, the dominant tissues

342   studied are the liver and muscle (eaten by people). Most gastropod studies have measured

343   depuration in the foot (eaten by people) or the whole organism. All cephalopod studies have

344   focused exclusively on the viscera, and all phytoplankton, zooplankton, and sea squirt studies

345   have exclusively analysed the whole organism (**Fig. S6**).

346

347   Most depuration studies occur in the lab (71%; 110 papers), where depuration can be

348   measured under controlled diet and environmental conditions (**Fig. 3C**). 23% (36 papers) of

349   depuration studies occur in the field, where organisms are potentially exposed to toxic algae

350   while depurating (i.e., depuration may be offset by uptake), but where depuration is quantified in

351   a real-world setting. Four studies (3%) depurate organisms fed toxic algae in the lab at non-toxic

352   field sites to mimic depuration in a natural, but non-toxic, setting. Five studies (3%) directly

353   compared lab and field depuration rates. Houle et al. (2023) find that PST depuration in Purple-

354   hinged rock scallop (*Crassadoma gigantea*) is 3.1 times slower in the field. Slower depuration in

355   the field is also found for the depuration of domoic acid by Peruvian calico scallops (*Argopecten*

356   *purpuratus*) (Alvarez et al., 2020) and variegated scallops (*Mimachlamys varia*) (Le Moan et al.,

357   2025) and the depuration of PSTs from purple clams (*Hiatula rostrata*) (Chen and Chou, 2002)

358   and blue mussel (*Mytilus edulis*) (Scarratt et al., 1991). Our meta-analysis confirms this result

359   for most species with depuration rates estimated for common tissues in field and lab studies

360   (**Fig. S6**).

361   3.1.2 Experimental results

362   Many of the evaluated papers assessed depuration rates under different experimental

363   treatments (**Fig. 3G**). In particular, many lab studies considered the impacts of water

364   temperature, dietary factors, and biotoxin exposure characteristics on depuration rates. A few

365   lab studies also considered the impacts of size and/or age on depuration rates, the ability for

366   industrial additives to enhance depuration rates, and the sensitivity of depuration rate estimates

367   to measurement technique. Many field studies assessed depuration rates across different

368   locations and/or years and two field studies compared depuration rates at the seafloor and

369   surface. Five studies directly compared depuration rates in the lab, where organisms are fed a

370   controlled non-toxic diet, versus the field, where organisms experience a natural diet that may

371   not be completely toxin-free (**Fig. 3G**).

372   3.1.2.1 Impacts of exposure intensity

373   Because studies of biotoxin depuration rates are often conducted following studies of

374   biotoxin accumulation (e.g. Kwong et al., 2006; Lopes et al., 2014a; Lund et al., 1997), many of

375   the evaluated studies (n=22) included trials with different exposure intensities. However, the

376   primary purpose of these treatments is to quantify feeding clearance rates and associated

377   biotoxin uptake rates, which are density-dependent. Although these treatments impact the peak

378   toxicity (N_0) of a one-compartment depuration model, they would not be expected to affect the

379   depuration rate constant (k), which is, by definition, the same at any toxicity. As a result, most of

380   these papers do not explicitly compare depuration rates across treatments and we made no

381   attempt to make these comparisons ourselves. Most of these studies (n=16) manipulated

382   exposure intensity by varying the density (dosage) of the causative agent. The remaining

383   studies varied exposure intensity by varying the composition of causative agents in the diet

384   (n=3; Bricelj et al., 1991; Jauffrais et al., 2012; Lewis et al., 2022), the duration of exposure to

385   the causative agent (n=1; Lin et al., 2024), the nutrient conditions during exposure (n=1;

386   Strogyloudi et al., 2006), or the method of exposure (n=1; i.e., oral exposure vs. injection;

387   Kankaanpää et al., 2005).

388   3.1.2.2 Impacts of dietary factors

389   The eleven papers that evaluate the impact of dietary factors on biotoxin depuration

390   rates generally find that individuals depurate faster when fed than when starved and that they

391   depurate even faster when provided more food or when hungrier. This is generally believed to

392   occur because depuration largely occurs through egestion of feces or pseudofeces and

393   egestion is generally higher when eating (Bricelj and Shumway, 1998). Faster depuration has

394   been found for fed versus starved individuals for: (i) PSTs in Pacific oysters (*Crassostrea gigas*)

395   (Medhioub et al., 2012) and Jinjiang oysters (*Ostrea rivularis*) (Yang et al., 2021); (ii) okadaic

396   acid in blue mussels (Marcaillou et al., 2010); (iii) domoic acid in Dungeness crab (*Metacarcinus*

397   *magister*) (Lund et al., 1997); and (iv) gymnodimines in grooved carpet shells (*Ruditapes*

398   *decussatus*) (Medhioub et al., 2010). Blue mussels depurated okadaic acid faster when fed

399   more food (Marcaillou et al., 2010). Relatedly, field-collected brown crabs (*Cancer pagrus*) in

400   poor body condition (hungrier) depurated faster okadaic acid faster than lab-fed brown crabs in

401   better body condition (less hungry). The depuration rate of okadaic acid (Svensson, 2003) and

402   domoic acid (Wohlgeschaffen et al., 1992) from blue mussels and of domoic acid from three

403   *Calanus* copepod species (*C. finmarchicus, C. glacialis, C. finmarchicus*) (Hardardottir et al.,

404   2019; Leandro et al., 2010) were all so rapid that they were not affected by whether they were

405   starved or fed. Only northern quahog (*Mercenaria mercenaria*) and constricted tagelus

406   (*Sinonovacula constricta*) were found to depurate karlotoxins faster when starved than when fed

407   (Li et al., 2024). The authors hypothesize that this surprising finding may be because stomach

408   contents, including residual toxic algae, are evacuated more efficiently when starved.

409   3.1.2.3 Impacts of temperature

410   The nine papers that evaluated the impact of temperature on biotoxin rates generally

411   find that depuration is faster in warmer waters. Blue mussels (*Mytilus edulis*) depurated domoic

412   acid faster at 11°C than 6°C (Novaczek et al., 1992) and faster at 11°C than 6°C (Scarratt et al.,

413   1991). Similarly, wedge shells (*Donax trunculus*) depurated okadaic acid 71% faster at 20°C

414   than at 17°C (Botelho et al., 2018). Atlantic surfclams (*Spisula solidissima*) viscera, where

415   toxicity is highest, depurated okadaic acid faster under warmer conditions though temperature

416   did not impact depuration rates in other tissues (Bricelj et al., 2014). On the other hand,

417   Svensson and Förlin (2004) found that even though blue mussels (*Mytilus edulis*) eliminated

418   lipids faster in warmer waters, water temperature did not affect the depuration rate of okadaic

419   acid, a lipophilic phycotoxin. Farrell et al. (2015) found that Sydney rock oyster (*Saccostrea*

420   *glomerata*) and diploid Pacific oysters (*Crassostrea gigas*) depurated PST faster at 27°C than at

421   22°C, but that temperature did not affect depuration rates for triploid Pacific oysters. Tang et al.

422   (2021b) found that Korean hard-shelled mussel (*Mytilus coruscus*) depurated PSTs faster at

423   30°C than at 25°C. In the only study examining the impact of temperature on the biotoxin

424   depuration rate of a finfish, Barbosa et al. (2019) found that gilthead seabream (*Sparus aurata*)

425   depurated PST so quickly that an impact of temperature could not be measured. Finally, Braga

426 et al. (2018) is the only paper to find slower depuration under warming, where Mediterranean
427 mussels depurated PSTs faster at 19°C than at 24°C.

428 3.1.2.4 Impacts of body size and age

429   The five papers that considered the impact of size or age on biotoxin depuration rates
430 generally found that smaller/younger individuals depurate faster than larger/older individuals.
431 Bogan et al., (2007) found that smaller king scallops (*Pecten maximus*) depurated domoic acid
432 faster than larger scallops. Mafra et al. (2010) found that smaller Eastern oysters (*Crassostrea
433 virginica*) depurated domoic acid faster than larger oysters but that size did not affect the
434 domoic acid depuration rates of blue mussels (*Mytilus edulis*). Similarly, Duinker et al. (2007a)
435 found no difference in the okadaic acid depuration rates of 1- and 2-year-old blue mussels.
436 Finally, Min et al. (2018) show that cyanotoxin depuration began earlier for juvenile mysid
437 crustaceans (*Neomysis awatschensis*) and thus progressed faster.

438 3.1.2.5 Impacts of depuration enhancers

439   A few papers examined the ability for additives to enhance the depuration process. Xie
440 et al. (2013) found that supplementing Jinjiang oyster (*Ostrea rivularis*) diets with chitosan, a
441 natural polymer that adsorbs PST toxins and prevents their reuptake by depurating filter
442 feeders, significantly accelerated their PST depuration. Qiu et al. (2018) found that adding
443 activated carbon, which also adsorbs PST toxins and prevents their reuptake by depurating filter
444 feeders, to depuration tanks significantly accelerated PST depuration from both Mediterranean
445 mussels (*Mytilus galloprovincialis*) and Farrer's scallops (*Chlamys farreri*). Activated carbon is a
446 highly effective biotoxin adsorbent because of its high porosity, surface area, and cationic
447 charge. Similarly, Peña-Llopis et al. (2014) found that adding N-Acetylcysteine, which boosts
448 the production of compounds central to the detoxification process, resulted in a four-fold
449 increase in the depuration of domoic acid from king scallops (*Pecten maximus*), one of the
450 slowest depurating bivalve species (Blanco et al., 2002). On the other hand, Leal et al. (2023)
451 found that adding cation-exchange resins (CER), which adsorb positively charged toxic
452 compounds, did not significantly accelerate PST depuration in blue mussel (*Mytilus edulis*).

453 3.1.3 Depuration rates by species

454   Only 41% (n=64) of the evaluated studies reported biotoxin depuration rates in terms of
455 exponential decay constants or half-lives, which are quantitative values that can be directly
456 compared across studies, species, tissues, experimental conditions, biotoxins, etc. (**Fig. 3E**).

457   The remaining 59% of studies (n=92) described depuration rates in bespoke terms that are not

458   directly comparable across studies, such as "*after 14 days, the [domoic acid] concentration in*

459   *the fed crabs decreased by 73%*" (Lund et al., 1997) or "*[toxicity decreased] from 3.1 µg*

460   *[okadaic acid] g^{-1} …. at day 1 to 1.51 µg [okadaic acid] g^{-1} at day 32*" (Svensson, 2003). Among

461   the 66 studies that reported exponential decay constants or half-lives, 50 (76%) estimated these

462   values using one-compartment exponential decay models, 3 (5%) estimated these values using

463   two-compartment models (Choi et al., 2003; Schultz et al., 2008; Yu et al., 2005), 8 (12%)

464   compared the results of one- and two-compartment models (Alvarez et al., 2020; Blanco et al.,

465   1999; Jauffrais et al., 2012; Lopes et al., 2014; Mafra et al., 2010; Moroño et al., 2003; Nielsen

466   et al., 2016; Woofter et al., 2005), and one compared the results of one-, two-, and three-

467   compartment models (Kennedy et al., 1992). Only four of the studies comparing one- and multi-

468   compartment models found significantly more support for the multi-compartment model (Alvarez

469   et al., 2020; Jauffrais et al., 2012; Kennedy et al., 1992; Woofter et al., 2005). These

470   comparisons were made on a mixture of expert judgement and comparison of R^2 values, which

471   also involved extensive expert judgement (**Fig. 3F**). Note that many studies (n=39) compared

472   depuration rates among different tissues (**Fig. 3B**), which also provides information on multi-

473   compartment depuration rates.

474

475   Depuration rates varied from 22.3 day^{-1} (0.03 day half-life) for microcystin from whole

476   *Eurytemora affinis* copepods (Karjalainen et al., 2006) to 0.0005 day^{-1} (1269 day half-life) for

477   domoic acid from the gills of Dungeness crab (*Metacarcinus magister*) (Schultz et al., 2013)

478   (**Fig. 4**). Depuration rates appeared relatively similar among species of the same genus (**Fig. 4**),

479   motivating the taxonomic regression analysis described in *Section 2.3*.

480   ## 3.2 Priority species for depuration study

481   Thirteen of the top-20 most harvested marine filter-feeding mollusc species from

482   countries exposed to PSTs have had their PST depuration rates studied (**Fig. 5A**), the highest

483   of any of the biotoxin types (**Fig. 5**). However, three of the top-5 species have not had their PST

484   depuration rates examined: constricted tagelus (*Sinonovacula constricta*) and blood cockle

485   (*Tegillarca granosa*). PST depuration rates for 1 new order, 2 new families, and 4 new genera

486   could be gained through the evaluation of 7 of the 10 unstudied species (**Table S4**). In

487   particular, evaluation of blood cockle (*Tegillarca granosa*) would provide information for 8

488   harvested and 360 total species in the Arcoida order.

489

490   Only six of the top-20 most harvested marine filter-feeding mollusc species from

491   countries exposed to domoic acid have had their domoic acid depuration rates studied (**Fig.**

492   **5B**). Notably, none of the four most intensely harvested species have had their domoic acid

493   depuration rates examined: Manila clam, constricted tagelus, blood cockle (*Tegillarca granosa*),

494   or Chilean mussel (*Mytilus chilensis*). Domoic acid depuration rates for 1 new order, 4 new

495   families, and 2 new genera could be gained through the evaluation of 11 of the 14 unstudied

496   species (**Table S4**). In particular, evaluation of Manila clam (*Ruditapes philippinarum*), striped

497   venus (*Chamelea gallina*), or northern quahog (*Mercenaria mercenaria*) would provide

498   information for 22 harvested and 428 total species in the Veneridae family.

499

500   Only four of the top-20 most harvested marine filter-feeding mollusc species from

501   countries exposed to DSTs have had their DST depuration rates studied (**Fig. 5C**). Notably, six

502   of the seven most intensely harvested species have had their DST depuration rates examined:

503   constricted tagelus, Pacific oyster (*Magallana gigas*), Japanese scallop (*Mizuhopecten*

504   *yessoensis*), blood cockle, Chilean mussel, and Atlantic sea scallop (*Placopecten*

505   *magellanicus*). DST depuration rates for 2 new orders, 3 new families, and 7 new genera could

506   be gained through the evaluation of 14 of the 17 unstudied species (**Table S4**). In particular,

507   evaluation of blood cockle would provide information for 8 harvested and 360 total species in

508   the Arcoida order.

509

510   Only five of the top-20 most harvested marine filter-feeding mollusc species from

511   countries exposed to cyanotoxins have had their cyanotoxin depuration rates studied (**Fig. 5D**).

512   Notably, neither of the two most intensely harvested species have had their cyanotoxin

513   depuration rates examined: Chilean mussel or Atlantic sea scallop. Cyanotoxin depuration rates

514   for 4 new families, and 2 new genera could be gained through the evaluation of 14 of the 16

515   unstudied species (**Table S4**). In particular, evaluation of Atlantic sea scallop (*Placopecten*

516   *magellanicus*), Patagonian scallop (*Zygochlamys patagonica*), or king scallop (*Pecten maximus*)

517   would provide information for 20 harvested and 297 total species in the Pectinidae family.

518

519   Only two of the top-20 most harvested marine filter-feeding mollusc species from

520   countries exposed to brevetoxins have had their brevetoxin depuration rates studied (**Fig. 5E**).

521   Notably, none of the six most intensely harvested species have had their brevetoxin depuration

522   rates examined: Manila clam, constricted tagelus, Japanese scallop, blood cockle, Chilean

523   mussel, or Pacific oyster. Brevetoxin depuration rates for 2 new orders, 5 new families, and 5

524   new genera could be gained through the evaluation of 17 of the 18 unstudied species (**Table**

525   **S4**). In particular, evaluation of Japanese scallop (*Mizuhopecten yessoensis*), Atlantic sea

526   scallop, king scallop, or queen scallop (*Aequipecten opercularis*) would provide information for

527   20 harvested and 297 total species in the Pectinidae family.

528

529   Only one of the top-20 most harvested marine filter-feeding mollusc species from

530   countries exposed to azaspiracids have had their azaspiracid depuration rates studied (**Fig. 5F**).

531   Notably, none of the seven most intensely harvested species have had their azaspiracid

532   depuration rates examined: Manila clam, constricted tagelus, blood cockle, greenshell mussel

533   (*Perna canaliculus*), Mediterranean mussel (*Mytilus galloprovincialis*), Peruvian calico scallop

534   (*Argopecten purpuratus*), or Patagonian scallop (*Zygochlamys patagonica*). Azaspiracid

535   depuration rates for 4 new orders and 2 new genera could be gained through the evaluation of

536   17 of the 19 unstudied species (**Table S4**). In particular, evaluation of Manila clam, constricted

537   tagelus, striped venus, common cockle (*Cerastoderma edule*), grooved carpet shell (*Ruditapes*

538   *decussatus*), triangular tivela (*Tivela mactroides*), or smooth callista (*Callista chione*) would

539   provide information for 58 harvested and 2549 total species in the Veneroida order.

540

541   Striped mullet (*Mugil cephalus*) is the only finfish in the top-50 most harvested finfish

542   with known or hypothesized vulnerability to ciguatera from countries exposed to ciguatera to

543   have had its ciguatera depuration rates studied (Ledreux et al., 2014) (**Fig. S7**). Otherwise,

544   ciguatera depuration rates have only been quantified for minor fisheries species. Pinfish

545   (*Lagodon rhomboides*) (Bennett and Robertson, 2021), orange-spotted grouper (*Epinephelus*

546   *coioides*) (Li et al., 2020), and lionfish (*Pterois volitans*) (Leite et al., 2021) have had depuration

547   rates measured but are the 88th, 99th, and 114th most important large, predatory, reef-associated

548   fisheries species occurring in countries where ciguatera is known to occur.

549

550   Although only 34 non-bivalves species have had their depuration rates studied, many

551   non-bivalves have been observed within toxicities exceeding action thresholds (**Fig. S8**),

552   highlighting the importance of studying biotoxin depuration in more non-bivalve species. In

553   particular, a large number of harvested gastropods and crustaceans have been observed with

554   PST toxicities far above the PST action threshold.

3.3 Predicting bivalve PST depuration rates

555

556   All four models exhibited good convergence ($\hat{R} < 1.01$, no divergent transitions) and

557   passed posterior predictive checks (**Figure S9**). The models with taxonomic random effects

558   significantly outperformed the model with only life history, location, and tissue fixed effects

559   (ΔELPD > 26; ΔR2=0.18; **Table S5**). The models with taxonomic random effects exhibited

560   similar performance with the greatest statistical support for the taxonomically random effects

561   model (ELPD=-229.4, R^2=0.67) followed by the non-phylogenetic random effects model

562   (ΔELPD=0.3, ΔELPD-SE=0.3, ΔR^2=0.01) then the phylogenetic random effects model

563   (ΔELPD=1.3, ΔELPD-SE=0.0, ΔR^2=0.02). The taxonomic random effects model was therefore

564   selected as the best performing model.

565

566   The taxonomic random effects model estimated that depuration rates are significantly

567   slower (smaller) in the field relative to the lab (**Fig. 6A; Fig. S10A**). On average, field depuration

568   rates are 2.5 times slower than lab depuration rates. The model estimated non-significant

569   impacts of the three life history variables, which exhibited a mixture of non-significant positive

570   (growth rate) and negative (maximum length, preferred temperature) effects. The model

571   estimated significant differences in PST depuration rates among bivalve tissues with the

572   hepatopancreas and soft tissues exhibiting faster depuration rates than other tissues. The

573   conditional effects of the fixed effects variable, which estimate the depuration rate with all other

574   effects estimated at their average, are shown in **Fig. S10**. The greater statistical support for this

575   model over the "fixed effects only" model indicates a significant impact of taxonomy on

576   depuration rates with the relative impacts of taxonomy on depuration rates illustrated in **Fig. 6B**.

577   The greater support of this model over the phylogenetic model suggests that, based on the

578   current data, while depuration rates vary by clade, they do not vary based on the relatedness of

579   clades (**Table S5**).

580

581   The field-based PST depuration rates for species included in model fitting were

582   estimated to vary from 0.0009 day^{-1} for smooth clam (*Callista chione*) to 0.20 day^{-1} for noble

583   scallop (*Mimachlamys crassicostata*) (**Fig. 7; Table S6**). The field-based PST depuration rates

584   for all harvested bivalves were estimated to vary from 0.0009 day^{-1} for smooth clam to 1.94 day^{-1}

585   ^{1} for Pacific calico scallop (*Argopecten ventricosus*) (**Fig. 8; Table S7**), after excluding

586   exceptionally high and uncertain estimated depuration rates for giant clam (*Tridacna gigas*) and

587   mangrove cupped oyster (*Crassostrea rhizophorae*). Giant clam (91.5 day^{-1}) and mangrove

588   copper oyster (16.7 day^{-1}) exhibited high depuration rates because of their exceptionally large

589   maximum size (137 cm) and fast growth rate (2.8 yr^{-1}), respectively. Because no species in the

590   Arcida or Liminda order were available in the training dataset, predictions for species in this

591   order are not informed by taxonomic information. The lab- and field-based depuration rates

592   predicted for harvested marine bivalves are provided in **Table S7**.

593   # 4. Discussion

594   Ensuring the safety of marine seafood is a daunting task. An estimated ~200 taxa

595   produce biotoxins that accumulate in marine food webs and threaten public health (Lundholm et

596   al., 2009). These taxa produce a diverse range of toxins, which require independent chemical

597   assays to detect and monitor (Hallegraeff et al., 2004). With over 3,000 species of marine fish

598   and invertebrates harvested by commercial fisheries and aquaculture along hundreds of

599   thousands of kilometers of coastline (FAO, 2024), it is impossible for biotoxin monitoring to

600   cover all species, toxins, and locations. Thus, managers need every tool in the toolbox to design

601   cost-effective biotoxin monitoring programs that protect public health while also limiting closures

602   to commercially, recreationally, and culturally important coastal food systems.

603

604   Forecasting depuration timelines using depuration rates offers one such tool. With

605   knowledge of how quickly a species eliminates toxins, managers can predict when toxicity will

606   fall to levels deemed safe for human consumption. This information is valuable for several

607   reasons. First, it provides seafood businesses with predictions of how long production is likely to

608   be delayed, which can empower adaptive business decisions. For example, during long delays,

609   harvesters may decide to pivot to new species, fishing grounds, or even alternative livelihoods

610   (Moore et al., 2020). Second, such predictions could help managers decide whether to close

611   fisheries, which could be preferred during short depuration timelines, or let them operate under

612   an "evisceration order" that requires the removal of toxic viscera before sale, which can lower

613   product value (Hackett et al., 2003), but may be preferable to closures during long depuration

614   timelines. Finally, as described in the introduction, such predictions could be used to improve

615   the efficiency of biotoxin monitoring (Blanco, 2009). Eliminating unnecessary tests would free up

616   limited resources to allow monitoring of more sites or species, which has large economic and

617   public health benefits. Monitoring more sites increases the resolution of biotoxin management

618   and could lead to less restrictive fisheries closures (Free et al., 2022) while monitoring

619   previously unmonitored species could more fully protect public health (Costa et al., 2017).

620

621   Our results show that depuration is slower in the field than in the lab, which has

622   important implications for the application of lab-based depuration rates in natural settings. While

623   lab studies quantify depuration rates while organisms are either staved or fed a non-toxic diet,

624   field studies quantify depuration while organisms continue the uptake of biotoxins from

625   dwindling blooms (Rourke et al., 2021), residual biotoxins in the food web (Yang et al., 2016), or

626   dormant benthic cysts, which can be directly consumed by detritivores or planktivores if

627   resuspended (Persson et al., 2006). This means that depuration timelines projected using lab-

628   base depuration rates are likely to be optimistic (i.e., forecast faster declines in toxicity than

629   reality). Fortunately, this is a favorable bias as testing sooner than necessary protects public

630   health without unnecessarily delaying openings to fisheries or aquaculture operations (Free et

631   al., 2022). The opposite bias (slower declines than reality) would be less favorable as it could

632   delay testing until after toxicity has fallen below the action threshold, resulting in unnecessarily

633   long closures to fisheries and aquaculture operations. However, managers may want to assume

634   slower depuration rates than predicted by lab studies as more accurate forecasts will result in

635   higher cost savings while still protecting public health and avoiding unnecessary closures. For

636   example, managers could assume that depuration occurs 2.5 times more slowly in the field, the

637   average estimated by our best performing Bayesian regression model.

638

639   Managers may also adjust the expected depuration rate and associated cadence of

640   monitoring based on observations of temperature, food availability, body condition, or other

641   factors that impact depuration rates. For example, managers may expect faster than average

642   depuration rates if temperatures are warm (Bricelj et al., 2014), food availability and

643   consumption is high (Bricelj and Shumway, 1998), or body condition is poor (Castberg et al.,

644   2004). However, caution is necessary as these factors can have confounding impacts on bloom

645   toxicity and biotoxin uptake. If warm water stimulates HAB productivity and toxicity (McKibben et

646   al., 2017), elevated uptake may offset accelerated depuration. Similarly, if consumption is high

647   due to either high food availability or low body condition, then rapid toxin uptake may offset

648   accelerated depuration. Adjusting depuration rates based on these considerations may

649   therefore be most useful once there is evidence that the bloom has abated and there is

650   significantly less biotoxin available for uptake. Then, managers can use knowledge of recent

651   temperature, food availability, or body condition to adjust the expected depuration rate and

652   recalculate the optimized cadence of biotoxin monitoring.

653

654   Our review indicates that aquaculture farmers can take several actions to accelerate
655   biotoxin depuration. Because depuration rates increase with food ingestion and egestion (Bricelj
656   and Shumway, 1998), farms can enhance depuration by increasing food availability and/or
657   stimulating food consumption. In the case of fed aquaculture for finfish and crustaceans, this
658   could involve providing more food than usual. In the case of unfed bivalve aquaculture,
659   consumption could be stimulated by reducing stocking density to reduce competition for ambient
660   food (Cubillo et al., 2012). Another strategy could be to limit or inhibit feeding during a bloom to
661   avoid biotoxin accumulation but also to reduce body condition and increase hunger to stimulate
662   rapid consumption and depuration after the bloom abates (Castberg et al., 2004). Because
663   depuration rates increase with temperature, which increases metabolism, consumption, and
664   egestion (Bricelj et al., 2014; Novaczek et al., 1992), farmers could move racks, lines, rafts, or
665   nets into warmer areas after a HAB to accelerate depuration. Furthermore, if warm water does
666   not result in increased mortality, disease, HAB risk, or other detrimental effects, aquaculture
667   could be strategically sited in warm areas to enhance depuration when necessary. Relatedly,
668   aquaculture species with fast depuration rates (and slow uptake rates) may be good candidates
669   for areas with high HAB risk. Finally, there is evidence that a number of industrial additives can
670   be used to enhance depuration rates (Bian et al., 2024; Martinez-Albores et al., 2020), but these
671   are often cost prohibitive or not allowed by regulation (Leal and Cristiano, 2024).
672
673   Biotoxin depuration rates of marine seafood species are understudied, especially for
674   non-filter feeders. Higher trophic level species, including herbivorous gastropods, detritivorous
675   crustaceans, and carnivorous fish, are particularly understudied, despite observations of unsafe
676   levels of toxicity in these species (Costa et al., 2017; Deeds et al., 2008; Lefebvre and
677   Robertson, 2010). The quantification of depuration rates for vulnerable gastropods,
678   crustaceans, and finfish and their broader inclusion in biotoxin monitoring programs, where they
679   are often overlooked (Costa et al., 2017), is thus important for fully protecting public health. It is
680   frequently asserted that biotoxins in finfish pose minimum human health risk because the toxins
681   do not accumulate in muscle tissue (e.g., Deeds et al., 2008; Lefebvre et al., 2002); however,
682   the consumption of non-muscle tissue is common in many cultures and many preparation
683   techniques use the whole fish (Golden et al., 2021). Furthermore, the processing of
684   planktivorous forage fish into fish meal and fish oil uses the whole fish, presenting a potential
685   pathway for unmonitored toxins to enter aquaculture and livestock feed (Adeyemo-Eleyode et
686   al., 2025). Finally, the study of species that are not harvested by humans but represent
687   important nodes in marine food webs is critical to understanding the trophic transfer of biotoxins

688 (Holmes and Lewis, 2022; Lefebvre et al., 2002). Besides three unharvested copepod species

689 (*Calanus finmarchicus* are harvested in Norway; FAO, 2024), we found that only two

690 unharvested species (opossum shrimp, *Neomysis awatschensis* and Pacific mole crab, *Emerita*

691 *analoga*) have had their depuration rates studied.

692

693 Although bivalves have undergone the most study, depuration rates have still not been

694 quantified for most bivalve species harvested in commercial fisheries and aquaculture. For

695 example, PST depuration rates are unquantified for 104 species, 60 entire genera, 12 entire

696 families, and 2 entire orders of harvested marine bivalves. To our knowledge, we provide the

697 first evidence that PST depuration rates are structured by bivalve taxonomy, meaning that

698 closely related species exhibit similar depuration rates. Although we did not find evidence that

699 PST depuration rates are phylogenetically conserved, this may be due to low taxonomic

700 representation in current depuration studies, given that nested taxonomic identity was found to

701 be an important predictor of PST depuration rates. As a result, managers can use either our

702 predicted depuration rates or collated observed depuration rates from related species as proxies

703 for species without known depuration rates. This finding also highlights the immense value of

704 empirically quantifying PST depuration rates for a new order, family, or genus to provide

705 guidance on depuration rates for the greatest number of new species. The expanded

706 quantification of depuration rates would be useful to confirm whether depuration rates are

707 taxonomically structured, or even phylogenetically conserved, across other toxins and

708 taxonomic classes (i.e., not just a result for PSTs in bivalves). We suspect this is the case given

709 the similarity in physiology and feeding ecology among related organisms (Leahy et al., 2025).

710

711 Biotoxin monitoring programs present a direct and underutilized data source for

712 measuring depuration rates under natural conditions. Although marine biotoxin monitoring

713 programs are used by many wealthy coastal countries (Andersen et al., 2004), our literature

714 review found only 18 papers that directly reported depuration rates quantified from monitoring

715 programs. These programs document the rise and fall of biotoxins in diverse species across

716 many sites and years, representing a large and informative store of already collected data on

717 seafood toxicokinetics. The analysis of these data would yield depuration rates for new species

718 and toxins (e.g., Mcguire et al. (2025) provide the only source of DST depuration rates for

719 eastern oyster, *Crassostrea virginica*) and would quantify the variability in depuration rates

720 stemming from different environmental conditions (e.g., Blanco et al. (1997) show that impacts

721 of salinity, temperature, light availability, and primary productivity on PST depuration in

722   mussels), all without additional field or lab costs. As a start, we quantified depuration rates for

723   45 species-toxin combinations from 30 field studies that did not directly estimate depuration

724   rates but were discovered in our systematic review due to the inclusion of depuration-related

725   words in their abstract or keywords (e.g., Haya et al., 2003; Kvrgić et al., 2022; Rourke et al.,

726   2021). However, this still overlooks the likely large number of biotoxin monitoring programs that

727   are either not documented, are documented without these keywords, or are only documented in

728   the grey or non-English literature. The optimization of monitoring programs using depuration

729   rates derived from their own data would free up resources to expand monitoring to new species,

730   thereby funding the iterative derivation of depuration rates and optimization of monitoring.

731

732   The utility of new depuration studies would be maximized through the adoption of a few

733   best practices. In particular, surprisingly few of the evaluated studies (41% of papers) directly

734   quantified depuration rates using standard depuration models, which complicates comparisons

735   between studies and limits utility to managers. New studies should use standard depuration

736   models (see Blanco, 2009) to quantify depuration rates to ease interpretability and use. If

737   comparing one- and multi-compartment models, we recommend the use of Akaike information

738   criterion (AIC) to select the most parsimonious model, recognizing that multi-compartment

739   models have more parameters and should nearly always generate tighter, though not

740   necessarily more parsimonious, fits (Burnham and Anderson, 2004). All of the studies

741   comparing one- and multi-compartment models compared fits used either R^2 (e.g., Nielsen et

742   al., 2016), which is biased to favor more complex models, or subjective judgements of fit and

743   parsimony (e.g., Kennedy et al., 1992), which is not replicable. Next, given that depuration in

744   real-world fisheries and aquaculture settings is likely to occur while feeding, new studies should

745   always include a scenario in which the treated organism is fed during the depuration phase.

746   24% of the evaluated studies only considered depuration under starved conditions (e.g.,

747   Duinker et al., 2007b), limiting their relevance to real-world settings. Finally, depuration studies

748   should consider management-relevant tissues to maximize utility. For example, 10% of the

749   evaluated studies did not generate a depuration rate for tissues targeted for consumption by

750   people or with the greatest toxin burden (e.g., focused only on the hemolymph; Schultz et al.,

751   2008).

752

753   As the public health risk posed by HABs worsens under the combined effects of

754   eutrophication and climate change (IPCC, 2019), managers will need every tool in the toolbox to

755   improve the cost effectiveness of biotoxin monitoring. The use of depuration rates to adjust the

756   cadence of monitoring during the depuration phase of HAB events is only one such tool. For

757   example, the development of reliable early warning indicators of HAB risk could be used to

758   more efficiently time the onset of biotoxin monitoring, sparing the need for testing while risk is

759   low (Anderson et al., 2019). Similarly, knowledge of biotoxin uptake rates by seafood species

760   could be used to optimize the cadence of testing during the uptake phase of HAB events. These

761   advances will be critical to fully protecting public health while simultaneously avoiding

762   unnecessary fisheries and aquaculture closures in a rapidly changing ocean.

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Tables and Figures

Table 1. Marine biotoxin poisoning syndromes and their causative organisms.

Syndrome	Biotoxin	Causative organisms
Amnesic (ASP)	Domoic acid (DA)	Diatom: *Pseudo-nitzschia* spp.
Diarrhetic (DSP)	Diarrhetic shellfish toxins (DSTs)	Dinoflagellate: *Dinophysis* spp., *Prorocentrum* spp.
Paralytic (PSP)	Paralytic shellfish toxins (PSTs)[2]	Dinoflagellate: *Alexandrium* spp, *Pyrodinium bahamense*, *Gymnodinium catenatum*
Azaspiracid (AZP)	Azaspiracid (AZA)	Dinoflagellate: *Azadinium* spp., *Amphidoma spinosum*
Ciguatera (CFP)	Ciguatoxin (CTX)	Dinoflagellate: *Gambierdiscus* spp., *Fukuyoa* spp.
Neurotoxic (NSP)	Brevetoxin (PbTx)	Dinoflagellate: *Karenia* spp.
Cyanotoxin	Cyanotoxins[3]	Cyanobacteria
Other	Other phycotoxins[1]	Dinoflagellate: *Protoceratium reticulatum*, *Lingulodinium polyedra*, *Gonyaulax* spp.
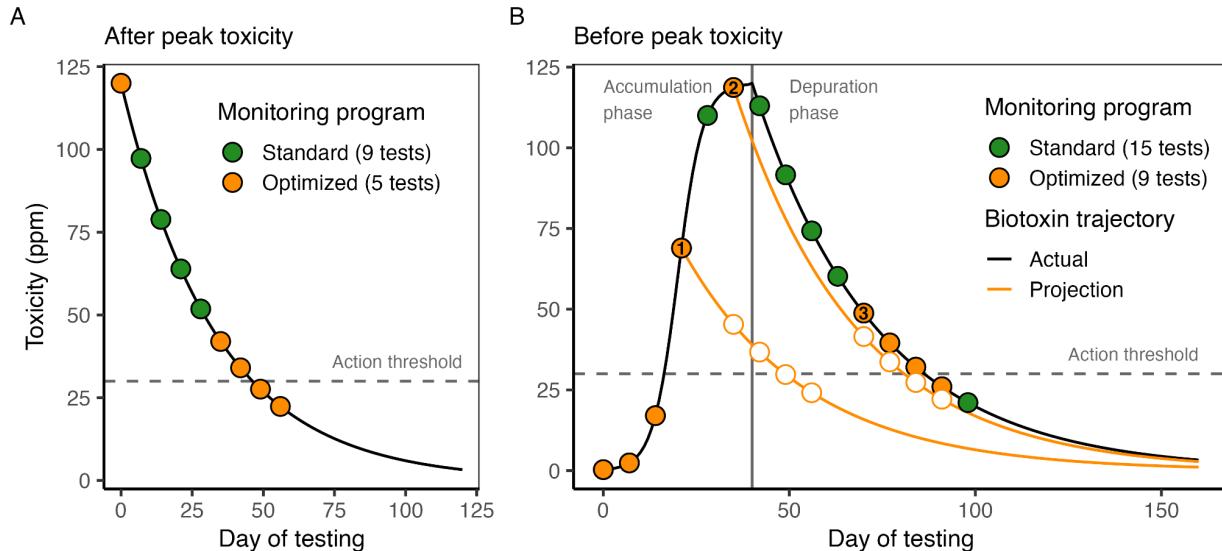
[1] Okadaic acid (OA), dinophysistoxin (DTX)
[2] Saxitoxin (STX), gonyautoxin (GTX)
[3] Microcystin, nodularin, homoanatoxin, cylindrospermopsin
[4] Yessotoxin (YTX), pectenotoxin (PTX, associated with DSTs but do not cause DSP), tetrodotoxin (TTX), gymnodimine (GYM), karlotoxin
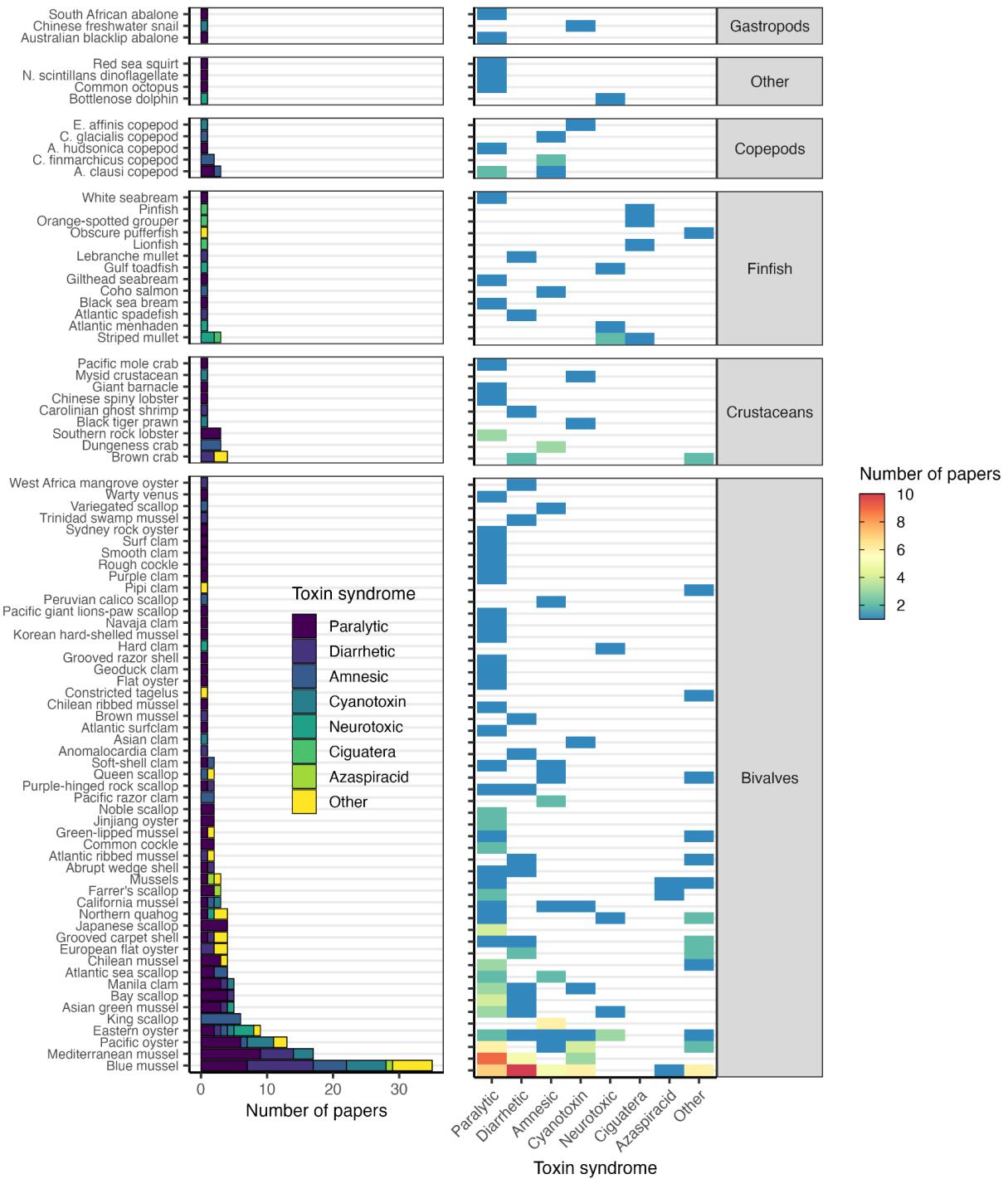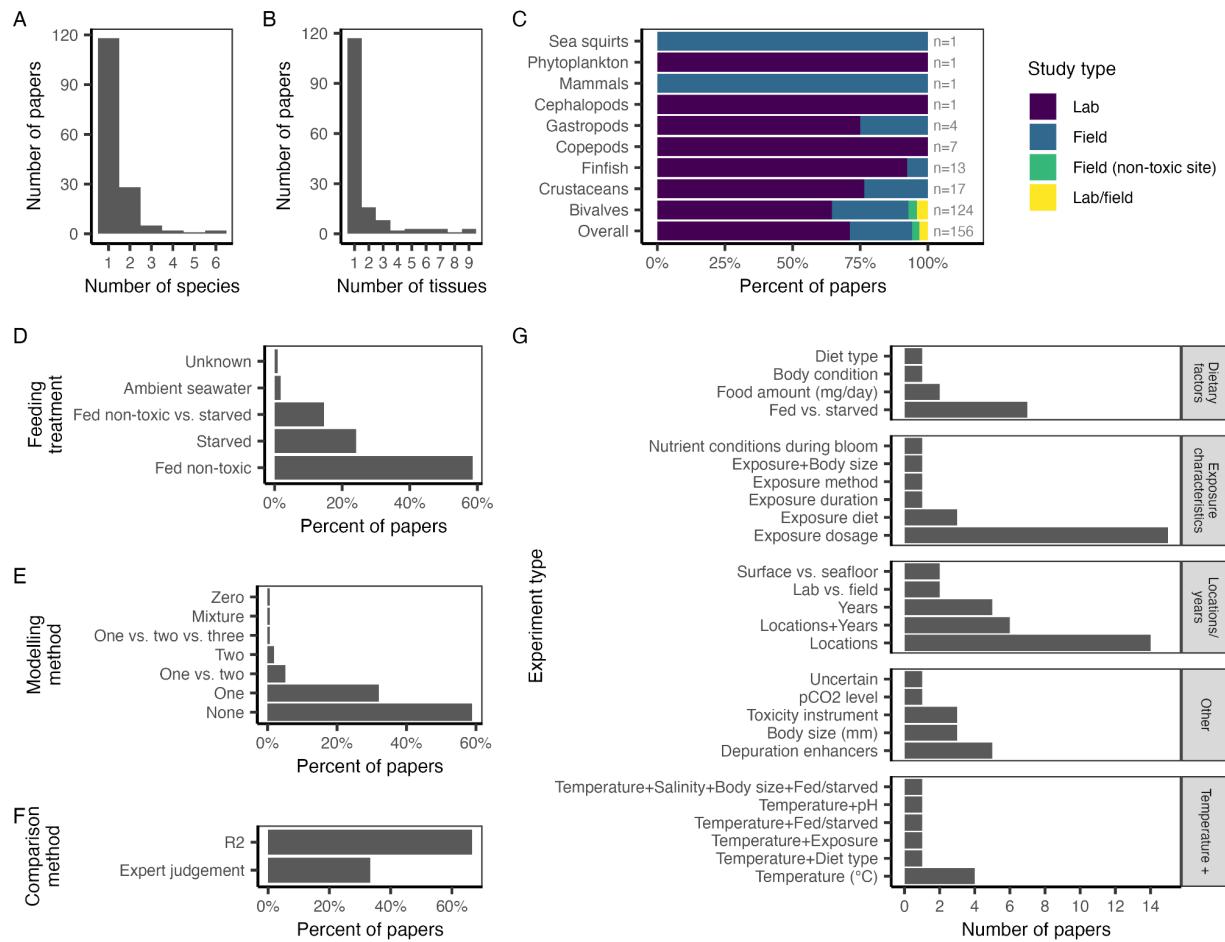
Figure 1. An illustration of the value of biotoxin depuration rates in efficiently monitoring and managing biotoxin risk both **(A)** after and **(B)** before peak toxicity is attained. In both panels, the black curve shows a hypothetical accumulation (B only) and depuration trajectory for a marine seafood species that depurates at 0.03 day^{-1}. The points indicate weekly sampling that ceases once toxicity falls below the management action threshold (horizontal dashed line) in two consecutive weeks, a common requirement for opening a fishery closed due to biotoxin risk. In **(A)**, standard weekly sampling would require nine tests (all points), but pausing testing until two weeks before toxicity is projected to fall below the action threshold would require only five tests (orange points only). In **(B)**, scheduling tests based on three projections (marked by numbers) eliminates the need for six tests. The white circles indicate the projected testing schedule that is updated when toxicity is found to be higher than expected.
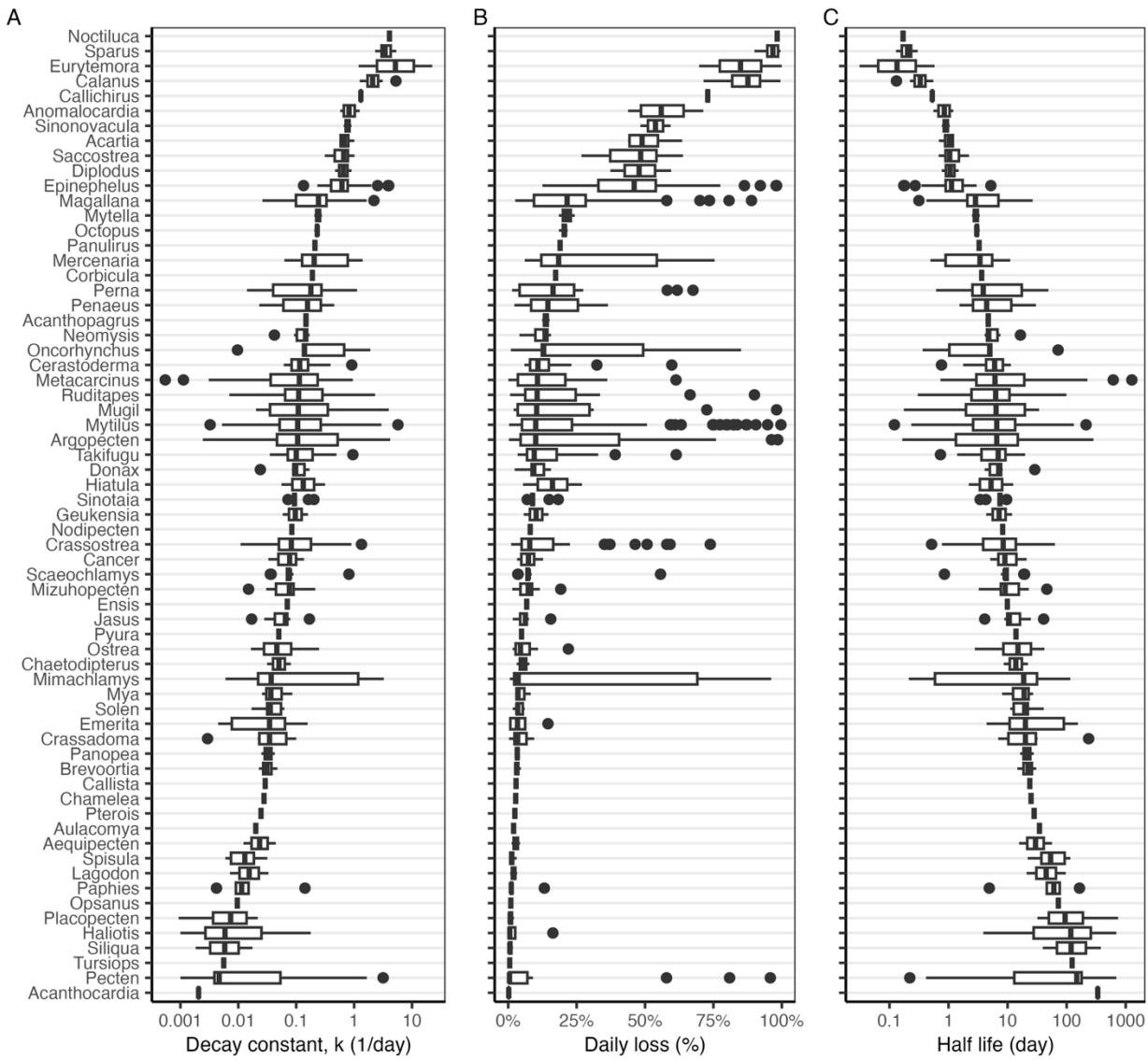
1167
1168 **Figure 2.** The number of papers measuring depuration rates by species and biotoxin. Species
1169 are grouped by taxonomic class and are ordered by increasing sample size (bottom to top).
1170 Biotoxins are also ordered by increasing sample size (left to right). See **Table S3** for the
1171 scientific names of all species shown here.

Figure 3. Characteristics of papers measuring biotoxin depuration in marine species. Panel **A** shows the number of species studied in a paper. Panel **B** shows the number of tissues evaluated in a paper. Panel **C** shows the percent of papers that conduct lab and/or field studies of depuration rates; a few studies conduct depuration studies at non-toxic field sites. Panel **D** shows the feeding treatment used during the depuration phase of each study; all field studies use wild diets. Panel **E** shows the modeling method used to quantify depuration rates (i.e., one- or two-compartment exponential decay models). Panel **F** shows the method used to compare models with different numbers of compartments in papers making such comparisons. Panel **G** shows the number of studies conducting experiments to measure depuration rates under different conditions. Experiment types are grouped into broader categories.
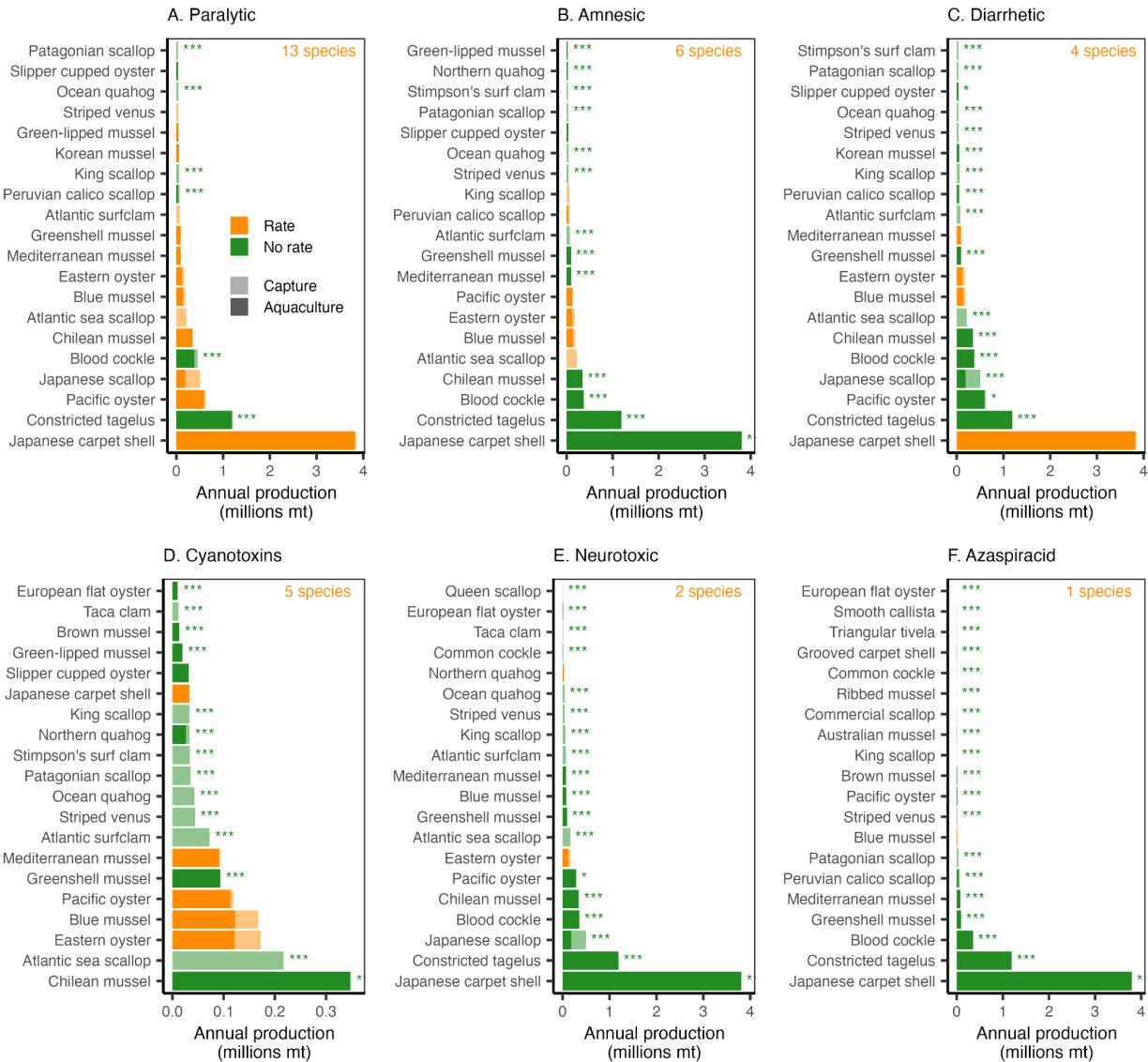
Figure 4. The **(A)** exponential decay constant (k, day^{-1}), **(B)** daily percent loss (%), and **(C)** half-life (days) of marine biotoxins by genus. In the boxplots, the solid line indicates the median, the box indicates the interquartile range (IQR; 25th to 75th percentiles), the whiskers indicate 1.5 times the IQR, and points indicate outliers.
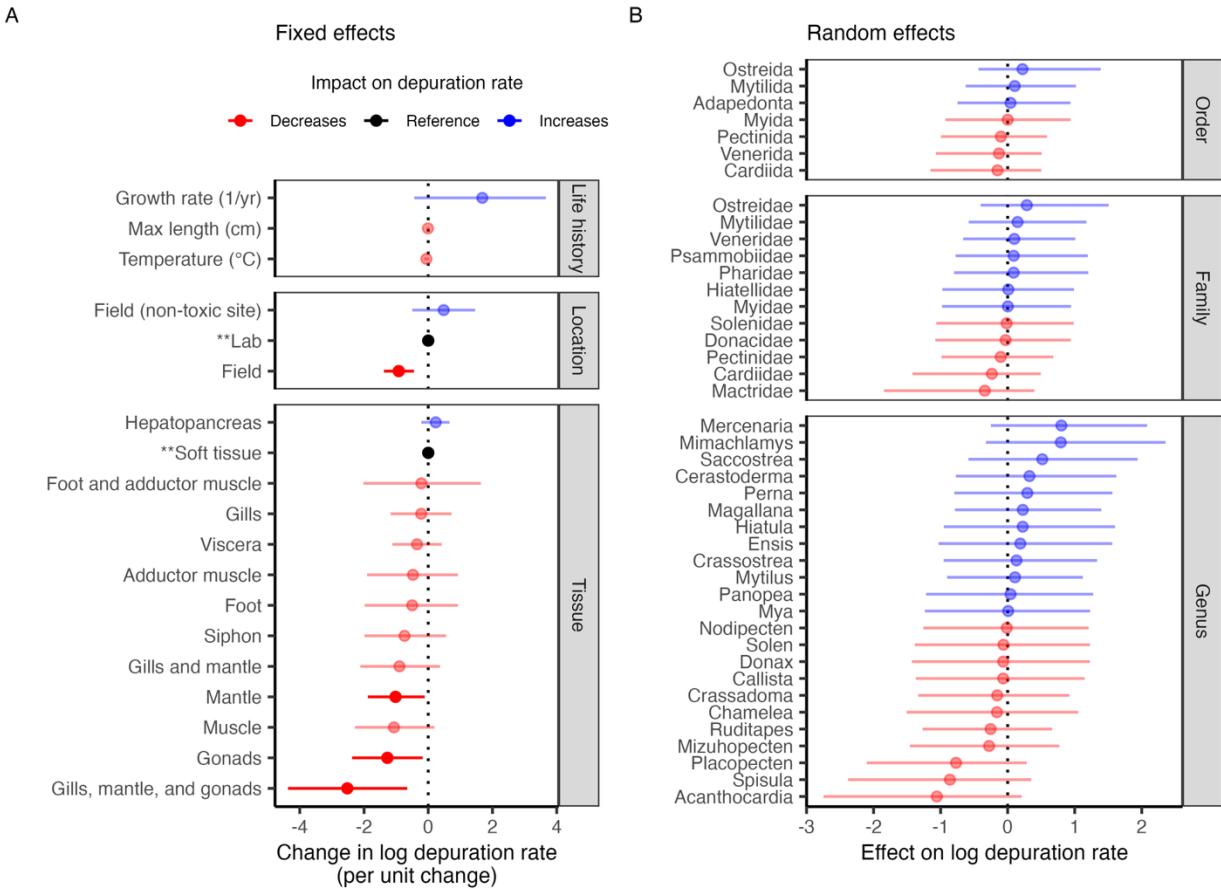
1189
1190 **Figure 5.** The twenty filter-feeding marine mollusc species with the greatest annual production
1191 (millions mt, 2014-2023) within Exclusive Economic Zones (**Fig. S5**) exposed to harmful algal
1192 blooms causing each of the evaluated biotoxin syndromes and an indication of whether (orange)
1193 or not (green) the depuration rate of the causative biotoxin has been studied. The species are
1194 sorted in order of decreasing annual production across both aquaculture (solid) and fisheries
1195 (transparent). The number of species whose depuration rates have been studied is printed in
1196 the top-right corner of each plot. The asterisks mark species whose depuration rate would
1197 contribute a new order (***), family (**), or genus (*) if studied. Ciguatera is evaluated separately
1198 because it is more strongly associated with large, predatory, tropical reef fish (**Fig. S7**).
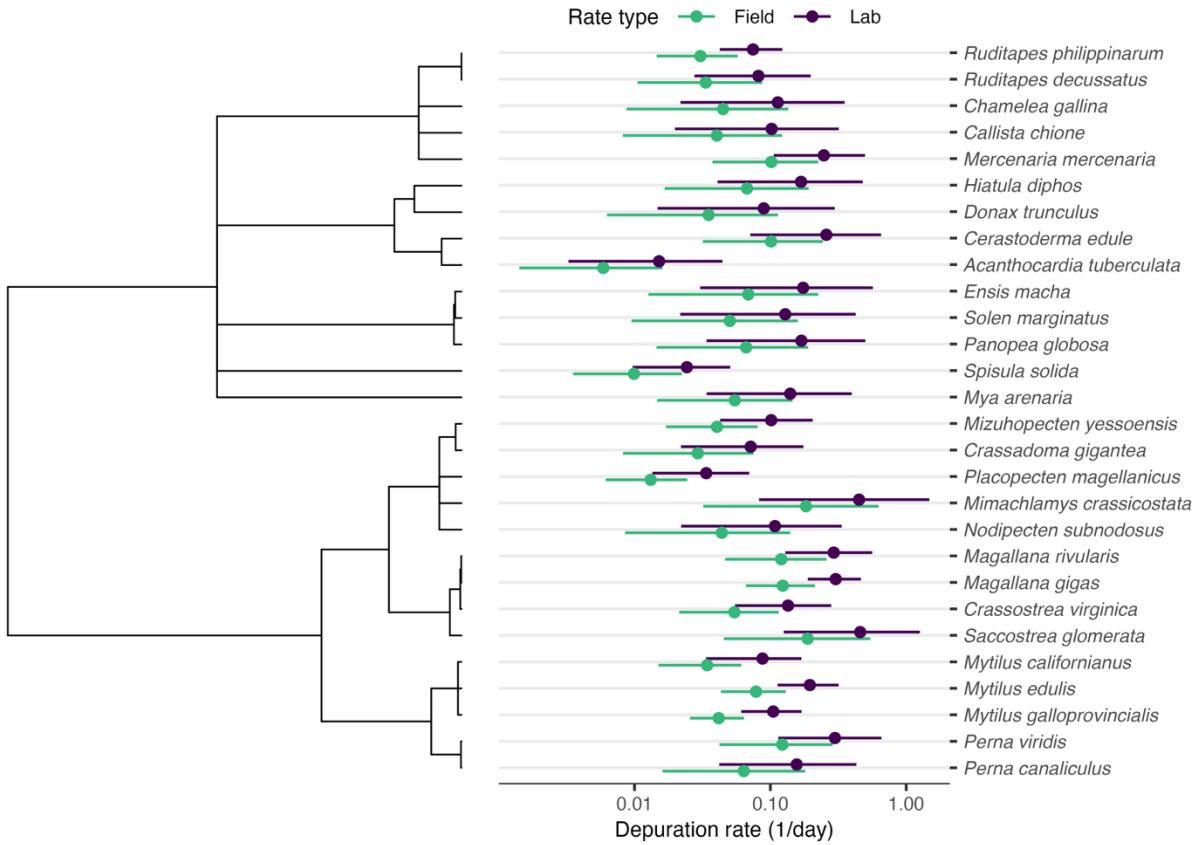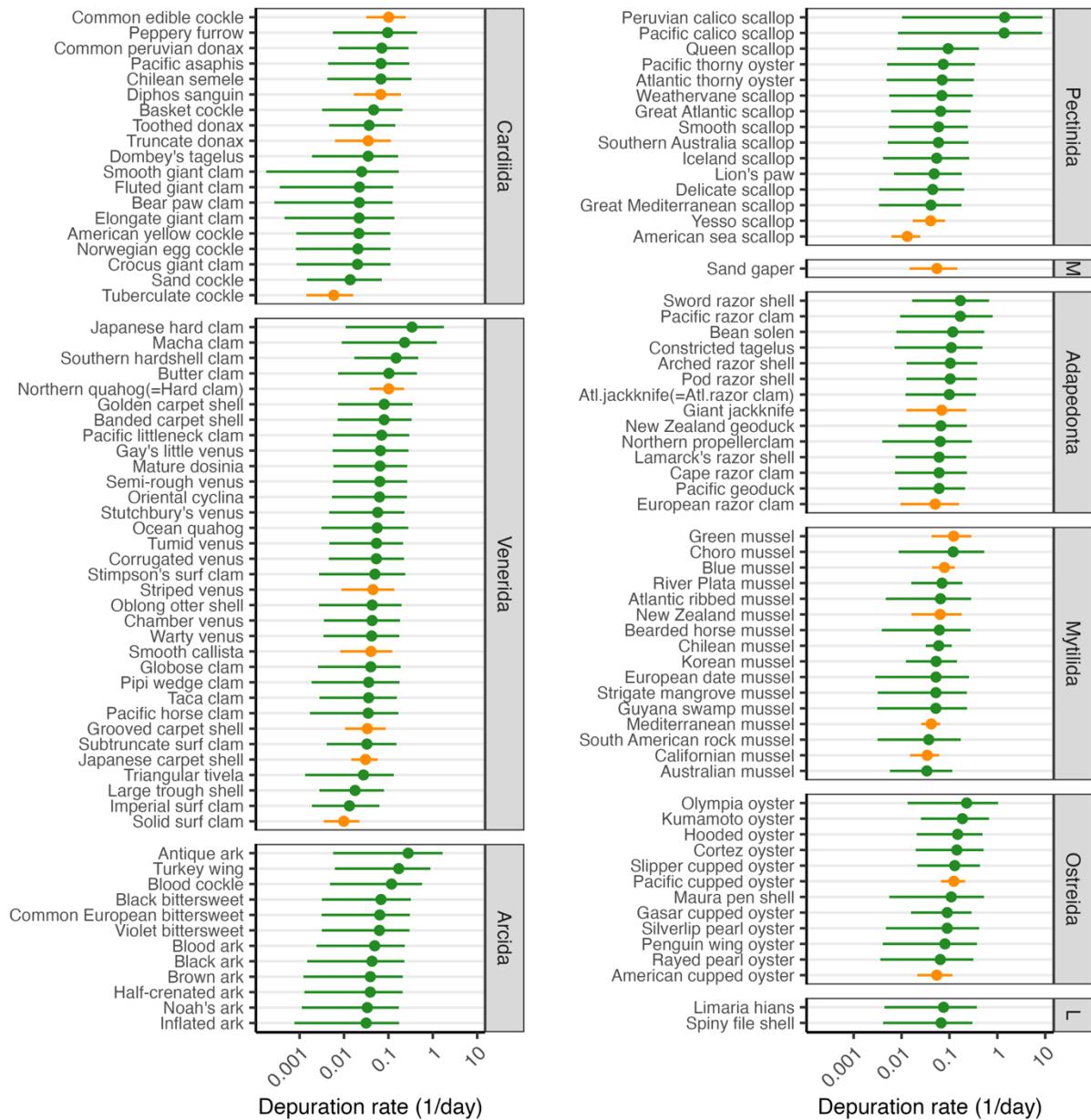
Figure 6. The **(A)** fixed effects and **(B)** random effects coefficients estimated by the final model. Points indicate the median estimate and lines indicate the 95% credible interval. Color indicates the impact of the point estimate of the effect on depuration rates. Transparency indicates whether the 95% credible intervals overlap with zero (solid=no overlap, transparent=overlap). The categorical fixed effects (location and tissue) are estimated relative to a reference level, which is marked with asterisks and is indicated in black. The conditional effects of the fixed effects variables are shown in **Fig. S10**.

Figure 7. Paralytic shellfish toxin (PST) depuration rate estimates for species with measured depuration rates from the final regression model. Species are organized by phylogeny. Points indicate the median estimate and lines indicate the 95% credible interval. See **Table S6** for details.

Figure 8. Paralytic shellfish toxin (PST) depuration rates for harvest marine bivalve species predicted by the final regression model. Species are organized by taxonomic order (M=Myida, L=Limida). Points indicate the median estimate and lines indicate the 95% credible interval. Species represented in the training data are marked in blue. Large predicted depuration rates for giant clam (*Tridacna gigas*) and mangrove cupped oyster (*Crassostrea rhizophorae*) are suppressed to ease visualization. See **Table S7** for details on the predicted depuration rates.