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UNDERSTANDING SINGLE-SPECIES AND MODEL ECOSYSTEM SENSITIVITY: DATA-BASED COMPARISON

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Abstract—Risk assessments for compounds released to the environment typically rely on single-species toxicity studies to predict concentrations at which effects may be observed. These single-species toxicity studies are usually conducted with a few species, cultured under optimum conditions (diet, temperature, light, etc.) and tested in clean water with constant exposure to the compound of interest. Chronic toxicity data are then extrapolated to the ecosystem during risk assessments to predict concentrations that will not adversely impact the environment. Several approaches have been developed that apply statistical methods to estimate toxicant concentrations adversely affecting a small percentage of single species (e.g., 5%). There are several rarely stated, and infrequently tested, biological and statistical assumptions required to make this extrapolation. One test of the ability to use single-species toxicity data to protect ecosystems is to compare effects on single species with effects on experimental and natural ecosystems (e.g., microcosms, model ecosystems, field). Towards this end, we summarized the chronic single-species and experimental ecosystem data on a variety of substances (n = 11), including heavy metals, pesticides, surfactants, and general organic and inorganic compounds. Single-species data were summarized as genus-specific geometric means using the NOEC or EC20 concentration. Genus mean values spanned a range of values with genera being affected at concentrations above and below those causing effects on model ecosystems. Geometric mean model ecosystem no effect concentrations corresponded to concentrations expected to exceed the NOEC of 10 to 52% of genera. This analysis suggests that laboratory-generated single-species chronic studies can be used to establish concentrations protective of model ecosystem, and likely whole ecosystem, effects. Further, the use of the 5% of genera affected level is conservative relative to mean model ecosystem data but is a fairly good predictor of the lower 95% confidence interval on the mean model ecosystem NOEC.

Keywords—Risk assessment Single species Model ecosystem Toxicity

INTRODUCTION

A basic tenet in applying laboratory-generated single-species toxicity test data within an ecological risk assessment is that these tests provide appropriate and useful information in establishing the effect concentration in the environment. Typically, the measurement endpoints are survival, growth, and reproduction of species tested singly in the laboratory, while the assessment endpoints include community and ecosystem structural and functional attributes in the field. An extrapolation procedure is used to link the measurement and assessment endpoints. Inherent in this extrapolation is the assumption that laboratory data can be used to protect populations of single species and that use of an appropriate level of single-species protection confers protection on populations, communities, and the ecosystem even though many of the species that will be exposed have not been tested. Two commonly used extrapolation procedures are the use of assessment factors [1–3] and the use of species sensitivity distributions [4–9]. Typically, the assessment factor approach is applied to data sets containing quantitative structure-activity relationships (QSAR) estimates, acute data, or a limited set of chronic data (i.e., one to seven chronic values), while the species sensitivity distribution approach is applied to larger data sets [10]. Assessment factors attempt to account for uncertainty in extrapolating among species and between tiers of data (i.e., QSAR, acute, chronic, model ecosystem) and typically range from approximately one for model ecosystem data to 1,000 or above for QSAR data [2,3,11]. The fact that there are unquantifiable uncertainties in extrapolating among species and among tiers of data leads to ongoing debate and discussion of the most appropriate set of assessment factors. Most assessment schemes agree that assessment factors for well-conducted model ecosystem studies, which assess species diversity, richness, population, and abundance, are low, as they are generally believed to be good surrogates for ecosystem-level effects. The ability of model ecosystems to act as surrogates for natural systems has been established [11–13].

In the species sensitivity distribution approach, the concentration protective of most single species (usually 5%, i.e., 95% of the species NOECs are greater) is calculated. A number of assumptions are imbedded in this approach, including (1) the species sensitivity distribution is well modeled by the selected distribution; (2) the sensitivity of species in the laboratory approximates the sensitivity of species in the field; (3) the sample of species is a random, or at least representative, sample; (4) protection of the prescribed percent of species confers an appropriate level of protection on ecosystem structure and function. The species sensitivity distribution approach has been criticized for these assumptions [14,15] and its lack of validation [2,10]. Cairns [16,17] discussed the last assumption as it applies to risk assessment in general, concluding that single-species tests cannot reliably account for ecosystem-

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level processes and thus should be poor predictors of ecosystem-level responses.

These criticisms concerning extrapolation of single-species toxicity data to the ecosystem level merit attention and form the central focus of this study. While these criticisms will always have technical merit and better approaches to establishing limited risk concentrations in the environment should be developed, we assessed whether these criticisms were sufficiently important to introduce a high level of uncertainty into the use of single-species data and the species sensitivity distribution approach in establishing low risk concentrations for environmental risk assessments. Hence, we compare single-species chronic toxicity data obtained from the open literature and our laboratory with published, high quality, chronic model ecosystem data. If single-species data are useful for extrapolating to the ecosystem, there should be substantial overlap in the distribution of single-species and model ecosystem data, while limited or no overlap in the distributions are to be expected if single-species data are of limited use for extrapolating to the ecosystem. This study also seeks to provide perspective on the selection of the 5% species affected level, the HC_5 of Aldenberg and Slob [8]. This is recognized as a risk management decision providing a level of protection to the ecosystem [18,19]. To date, the level of conservatism has not been investigated. In this paper, we focus on chronic effects. A similar study comparing acute effects with results from short-term model ecosystem studies or studies on compounds that rapidly degrade or dissipate in the environment could also be conducted.

METHODS

The selection of substances investigated in this study was based on the presence of high quality model ecosystem data and chronic toxicity data on a minimum of five genera. We use the genera as the lowest taxonomic classification to avoid taxonomic issues for any one species (e.g., *Ceriodaphnia*). This also prevents one genus (e.g., *Daphnia*) from controlling the effects data. The test substances spanned a wide range of physical properties and modes of toxic action and included heavy metals (cadmium, copper, zinc), pesticides (atrazine, lindane), surfactants [dodecyl linear alkylbenzene sulfonate (C_{12}LAS), dodecyl trimethyl ammonium chloride (C_{12}TMAC)], and general organic [3,4 dichloroaniline (3,4 DCA), phenol] and inorganic (ammonia, chlorine) substances.

Chronic single-species aquatic toxicity data and model ecosystem data from studies conducted in freshwater were obtained primarily from the literature using data compilations such as the U.S. Environmental Protection Agency (U.S. EPA) water quality criteria when available. To remove variability caused by use of different water hardnesses for metals, metal toxicity data were corrected to a hardness of 50 mg/L as $CaCO_3$ for all vertebrate and invertebrate species using the methods specified in the appropriate U.S. EPA water quality criteria [4]. Algal toxicity data for heavy metals were not corrected due to the lack of reported hardness or algal media information. For LAS, toxicity data from different alkyl chain lengths were normalized to a dodecyl chain length using the approach of Fendinger et al. [20]. No observed effects concentrations (NOECs) were used whenever available from the literature. When a NOEC was not available, the EC*x* value (where x = 10–20), MATC (maximum acceptable toxicant concentration), or LOEC (lowest observed effect concentration) was used and noted. If needed and sufficient data were provided in the primary reference, endpoints were estimated by the authors. When multiple studies were available for one genera, genus geometric mean NOEC values were calculated. In compiling distributions of laboratory-generated chronic toxicity data, a rule on taxa (i.e., algal, invertebrate, fish, and bacteria) inclusion was established. Chronic toxicity data for all taxa were used unless NOEC, MATC, LOEC or EC20 values could not be found or calculated from single-species toxicity tests (chlorine, zinc). Further, a taxa was excluded from the analysis if the mean for a given taxa was significantly different from the mean of the other taxa (lindane, ammonia) (*t* test; Excel® 7.0a, Microsoft, Redmond, WA, USA). The impact of taxa inclusion on the distributions was tested by changing the taxa inclusion rules for ammonia, cadmium, and copper and reanalyzing the plots. For ammonia, the plant and invertebrate taxa were included with fish even though their taxa means were significantly greater than the fish taxa mean ($p < 0.05$, *t* test). For cadmium and copper, plants were removed, leaving fish and invertebrates for analysis even though the plant taxa mean NOEC was not significantly different from the fish and invertebrate taxa mean ($p > 0.05$, *t* test). These revised distributions were not used to compare model ecosystem and single-species data.

Authoritative reviews and searches for model ecosystem data have recently been conducted or summarized by Hill et al. [21], Belanger [13], and the European Centre for Ecotoxicology and Toxicology of Chemicals (ECETOC) [22] and formed the basis for the model ecosystem results presented in this paper. In addition, selected searches were conducted to ensure that the most recent and available information was included beyond that found in the reviews. Only high-quality studies were used for comparisons with single-species toxicity data. Crossland et al. [23], in a workshop summary involving leading experts in the field of model ecosystem ecotoxicology, discussed the rationale as to why there is no single best model ecosystem. The primary reason offered was that the choice of test system and endpoint is made to address a particular question. Belanger [13] and ECETOC [22] point out that many factors will contribute to identifying how a test unit or approach is useful to address particular research questions. Attributes of model ecosystems that come into play include the test unit's size, physical habitat complexity, the biological complexity contained therein, the duration of the study, the robustness of the experimental design, and the measurement endpoints used to establish responses. High-quality studies are identified through meeting criteria germane to addressing the question posed in the experiment. Studies were included in this review that were not conducted specifically for the purpose of risk assessment. If the study was scientifically sound following objective review regardless of the NOEC conclusions, it was included in the analysis. It is beyond the scope of this paper to delineate how individual test systems addressed scientific criteria or needs.

All model ecosystem studies are unique. The factors discussed above, plus system-specific species assemblages, methods of dosing, replication, and quality of the water used, will also define the ultimate utility in risk assessment extrapolations by influencing the final conclusions of model ecosystem NOEC or EC*x* values. Belanger [13] showed that complexity of the biological assemblage used in most studies is relatively unrelated to test system dimensions (i.e., physical complexity). Therefore, depending on the research need being addressed, small or large test systems may be useful tools. The biological

complexity and suitability of the studies included in the research summarized in this paper were determined to contain adequately complex species assemblages to be considered as ecosystem surrogates. The studies were of high quality, typically used genus- to species-level taxonomic resolution, confirmed continuous exposure concentrations, used multiple ecological endpoints, and were statistically analyzed to determine NOEC and LOEC concentrations.

Plots of laboratory single-species and model ecosystem data are used to compare responses of each test type. Log-logistic, log-normal, exponential, extreme value, and uniform distributions were fit to single-species NOEC data for each chemical, with parameters estimated by maximum likelihood [24]. The goodness-of-fit for each distribution was evaluated by the one-sample Cramér-von Mises statistical test [25], which was also used as a means to compare the relative goodness-of-fit with the various distributions. Lower 95% confidence limits on the fitted NOEC distribution function were calculated analogous to the methods of Aldenberg and Slob [8], with the exception that here the maximum likelihood estimators were used as opposed to moment estimators. The maximum likelihood estimators are generally less biased and have better precision than moment estimators [26]. For a given percentile and its associated true (but unknown) NOEC value, there is 95% probability that this lower confidence limit is smaller than the true NOEC.

Model ecosystem data are presented graphically as geometric mean ± 95% confidence interval when three or more model ecosystem NOECs are available. The mean and range of ecosystem data are used when two values are available. To compare laboratory-generated chronic toxicity data on single-species and model ecosystem data, the intersection of the ecosystem geometric mean and 95% confidence intervals (or range as appropriate) around the NOEC are compared with the cumulative percent genera affected (i.e., cumulative probability) distribution (estimated distribution function and lower 95% confidence interval). This approach is used to evaluate whether single-species toxicity data are or are not generally useful in extrapolating to ecosystem-level effects. For any given set of conditions (i.e., compound or community), it may be appropriate to consider other specific factors in the assessment.

RESULTS

Single-species data

Single-species chronic toxicity data were obtained from the literature and summarized into genus geometric mean values (Appendices 1 through 3). A total of 14 distributions were generated from the data on the 11 compounds. One distribution for each compound was used for comparison with model ecosystem data. These distributions were developed using the taxa inclusion approach specified in the Methods section. The taxa used to generate distributions for ammonia, cadmium, and copper were modified to examine the impact of taxa inclusion on the distribution function.

The data used to estimate distribution functions for genera ranged from six data points for chlorine to 25 data points for copper. Both graphical displays (Figs. 1 and 2, only log-logistic models are shown) and Cramér-von Mises statistics (Table 1) suggest the log-logistic distribution is best among those considered for the distribution of genera-specific NOECs, though the comparison of p values is not a rigorous means of judging distributions. There was no one transformation that always provided the best fit to the data. All distributions were rejected at least once ($p < 0.05$) by the Cramér-von Mises test. The log-logistic and extreme-value distributions were rejected once and twice, respectively. All other distributions were rejected more often. If we raise the significance level to $p < 0.10$, then the log-logistic is rejected twice and all others at least three times. Based on this observation, we considered the log-logistic model to be best among those considered. We also noted that, on a chemical-by-chemical basis, the data on cadmium (with plants) was rejected for all distributions tested while cadmium without plants was rejected for all distributions except log-logistic and extreme value. The data on copper (with plants) was rejected for all distributions except the log-logistic. For consistency across substances, genera chronic NOEC values were plotted as cumulative percent versus log NOEC values with the best-fitting log-logistic distribution and its lower 95% confidence limits superimposed (Figs. 1 and 2).

The taxa comprising the ammonia, cadmium, and copper data sets were modified to investigate the effect of taxa (i.e., plants, invertebrates, fish) inclusion on the distribution functions. Plants were removed from the cadmium and copper data sets despite the t test statistic suggesting the data come from the same distribution as the other taxa. Invertebrates and plants were included in the ammonia distribution even though the chronic toxicity values are clearly in different distributions than fish data. Removal of plants from the cadmium and copper data sets increased the slope of the distribution function considerably (less spread in the data) and increased the fit of the data to the log-logistic distribution (Table 1 and Fig. 3). Despite the overall increase in the fit of the data, the chronic NOEC for *Daphnia*, which was on the lower 95% confidence interval for the original cadmium distribution, is well below the lower 95% confidence interval in the cadmium without plants distribution (Figs. 2 and 3). For ammonia, the plant and invertebrate data affected the slope of the distribution function and greatly improved the fit of the data to the log-logistic distribution as well as other distributions (Fig. 3).

Model ecosystem data

A total of 39 model ecosystem NOECs for 11 substances were included in this review. Most substances were tested in more than one model ecosystem (Appendices 4 through 6). The most frequently tested chemicals were atrazine (herbicide, $n = 6$), C_{12}TMAC (surfactant, $n = 5$), LAS (surfactant, $n = 6$), and copper (metal, $n = 7$). This represents a broad array of toxicities and modes of action. The final NOECs from the model ecosystem studies were a combination of both direct (e.g., mortality of dominant species) and indirect (e.g., alterations of feeding relationships or changes in community function) responses, recognizing that either are legitimate indicators of adverse effects. The emphasis was on studies with several trophic levels (producer to predator) and communities (autotrophic and heterotrophic periphyton, invertebrates, and fish). Measurement endpoints that drove NOEC conclusions were of a wide variety, suggesting some selective bias by researchers, test system-dependent sensitivities, and/or lack of a priori understanding for the importance of various measurements. However, most studies included assessments of multiple community functional and structural features (ranging from as few as eight to as many as several dozen), leading to robust conclusions. Of the 39 NOECs, 29 conclusions were based on evidence from multiple trophic levels and combinations of population- and community-level measurements. An example of the complexities of including all studies on a particular

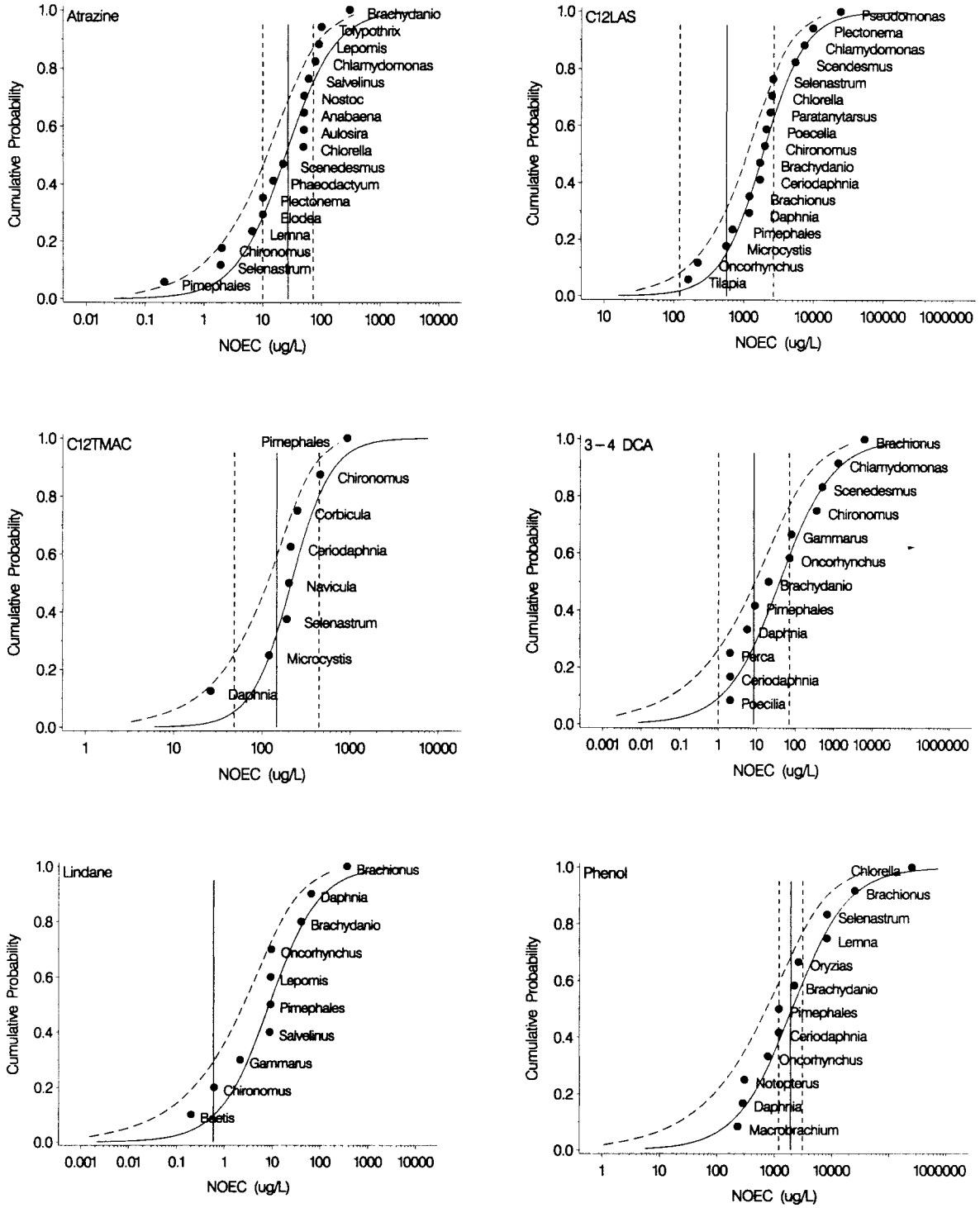

Fig. 1. Comparison of chronic toxicity and model ecosystem data for the organic compounds atrazine, dodecyl linear alkylbenzene sulfonate (C_{12}LAS), dodecyl trimethyl ammonium chloride (C_{12}TMAC), dichloroaniline (3,4 DCA), lindane, and phenol. Single-species data presented as cumulative probability versus chronic NOEC (symbols) with fitted log-logistic distribution (solid). The lower 95% confidence limits of the distribution percentiles are shown (dashed). Model ecosystem data presented as geometric mean (solid vertical line) and 95% confidence interval (dashed vertical lines) except for 3,4 DCA and phenol (mean and range of data, $n = 2$) and lindane ($n = 1$).

chemical in such an analysis is given here for copper. Studies were found that focused solely on periphyton in the absence of invertebrates [27], focused on invertebrates that made no attempt to assess periphyton (although periphyton was present) [12], or were truly ecosystem-based approaches that included all available biological components [28–31]. All are weighted equally in our analysis.

Comparison of single species and model ecosystem data

For the 11 cases presented (Table 2), the mean model ecosystem NOEC occurs, on average, at a concentration where 26% of genera NOECs would be exceeded (Figs. 1 and 2). The percent of genera affected at the mean model ecosystem NOEC ranges from a minimum of 9.6% of genera (lindane)

to a maximum of 52% (atrazine). When the lower limit of model ecosystem NOEC is considered (Figs. 1 and 2), the percent of genera affected ranges from 1 (zinc) to 40% (phenol), with most values being 10% or less. There was no relationship between the number of genera or model ecosystem values and the percent of genera affected at the mean model ecosystem NOEC.

DISCUSSION

Of the distributions fit to the single-species data (uniform, log-logistic, log-normal, extreme value, and exponential), the log-logistic provided the best overall fit to the data (Table 1). Use of the uniform distribution implies a threshold effect concentration below which no NOEC values would be expected. All other models used here imply no threshold and assume no upper or lower limits to the NOECs in a large population of species. The selection of a distribution for the single species data is a critical decision since the distributions have their greatest differences in the tails and it is currently the practice of toxicologists to extrapolate to the extremes of the distributions (i.e., 5%) [4–8]. Based on the better overall fit of the log-logistic model and the increased conservatism of this approach, we selected this approach to model all substances for this study. However, in a risk assessment, it may be more appropriate to assess each substance individually and select the distribution that best fits the available data. Additional research is needed to address questions concerning thresholds, the selection of distributions, and potential distribution-free methods for predicting low levels of effects.

Another important consideration is the inclusion of taxa in the analysis. In our study, insertion or deletion of a taxa from the analysis had a moderate effect on the distribution function. These effects can impact the extremes of the distribution where data is lacking but decisions about acceptable environmental concentrations are likely to be made. If sufficient data were available, each taxa could be assessed separately. Since this is not typically the case, the practice is to include all species [6,8,9,32] or to ensure selected taxa representative of diverse phyla are included [4]. We have included taxa when the assumption that all taxa come from the same species sensitivity distribution appears to be met as this is inherent in the selection and use of a unimodal distribution. Decisions on taxa inclusion were based on *t* test results; however, this approach is not without its own problems. For copper, plants were included with invertebrates and fish in the analysis. However, removal of the one single low plant toxicity value for *Selenastrum* (Appendix 1) from the data set would have resulted in the entire taxa being excluded from the distribution. In a risk assessment scenario, additional studies on this species could help clarify which taxa were most appropriate for inclusion in the sensitivity distribution. The impact that taxa inclusion had on the distributions in this study suggests care should be taken in selecting and including taxa in a distribution. Sound biological and statistical arguments should be used to include or exclude taxa from a distribution.

Single-species toxicity tests appear to be good predictors of effects at the community and ecosystem levels of organization. In a comparison of single-species and ecosystem levels responses to toxicants, Sloof et al. [33] observed a statistically significant relationship between community or ecosystem-level NOEC values and single-species chronic NOECs. For the 51 substances in the data set, on average, the mean single-species NOEC was less than the mean ecosystem NOEC. The ECETOC [22] evaluated single-species-model ecosystem relationships in the traditional risk assessment paradigm using quotients (assessment factors). Lowest single-species chronic NOECs from a battery of algal, invertebrate, and fish tests were compared to the lowest observed NOEC for any measured model ecosystem endpoint for marine, flowing freshwater, and standing freshwater systems. For 34 substances and 258 studies, the median model ecosystem NOEC:chronic single-species NOEC ratio was 0.69, suggesting that the model ecosystem response was at a slightly lower level than the single-species response. However, the comparative approach taken in the ECETOC review [22] was biased toward developing a conservative assessment factor or model ecosystem:single-species ratio. Any endpoint measured in a model ecosystem study was included, regardless of relevance, to derive the NOEC. If an approach would have been adopted that included the use of best professional ecological judgment, conclusions would have been different.

When using the single-species statistical approach, 5% of species affected has been established as a de facto standard by regulatory agencies worldwide and has been supported by the literature. Okkerman et al. [19] compared the 5% species effect level (i.e., 95% of laboratory single-species NOECs greater) with the lowest single-species NOEC obtained from microcosm, model ecosystem, and other multiple-species tests. When either log-normal or log-logistic distributions were selected for the single-species data, the ratio of the multiple-species NOEC to the 5% species level (at 50% confidence) ranged from less than 0.01 to greater than 100 across the seven substances. For five of the substances, ratios were between 1 and 10, but for six of the seven comparisons, the 5% species-effect level was less than the multiple-species NOEC. Based on these limited data, the authors concluded that the use of the 5% species-effect level from the species sensitivity distribution approach was a good starting point for establishing ''safe'' concentrations in the environment [19]. Using a similar approach, Emans et al. [18] compared NOECs for the most sensitive species from a multiple-species test with the 5% species level. They reported a multispecies NOEC to 5% single-species effect level ratio in the range of 0.2 to 5.0 for a variety of heavy metals and organic substances. Overall, 5% single-species effect concentrations produced effects levels that were lower than the corresponding multispecies NOECs. Our study is in agreement with those of Emans et al. [18] and Okkerman et al. [19], the 5% species-effect concentration is lower than the mean model ecosystem NOEC and thus should be protective of these systems on average. However, when using single-species data to protect the extremes of the model ecosystem data (lower 95th percentile), the 5% species-effect concentration does not provide a level of conservatism. In fact, the 5% species affected concentration may be a good a priori estimate of the concentration needed to protect 95% of model ecosystems. This raises the question of model ecosystem variability, that is, is the mean model ecosystem the best measure of ecosystem-level response or does the variability in model ecosystems reflect variability in the ecosystem such that protection of a lower confidence interval is appropriate? Resolution of this issue is central to decisions to apply the 5% species-effect concentration in a risk assessment.

It should be expected that different model ecosystems will have different sensitivities to different chemicals or even the same chemical. Only now is sufficient evidence available to begin to address this area (e.g., [34]); however, classical eco-

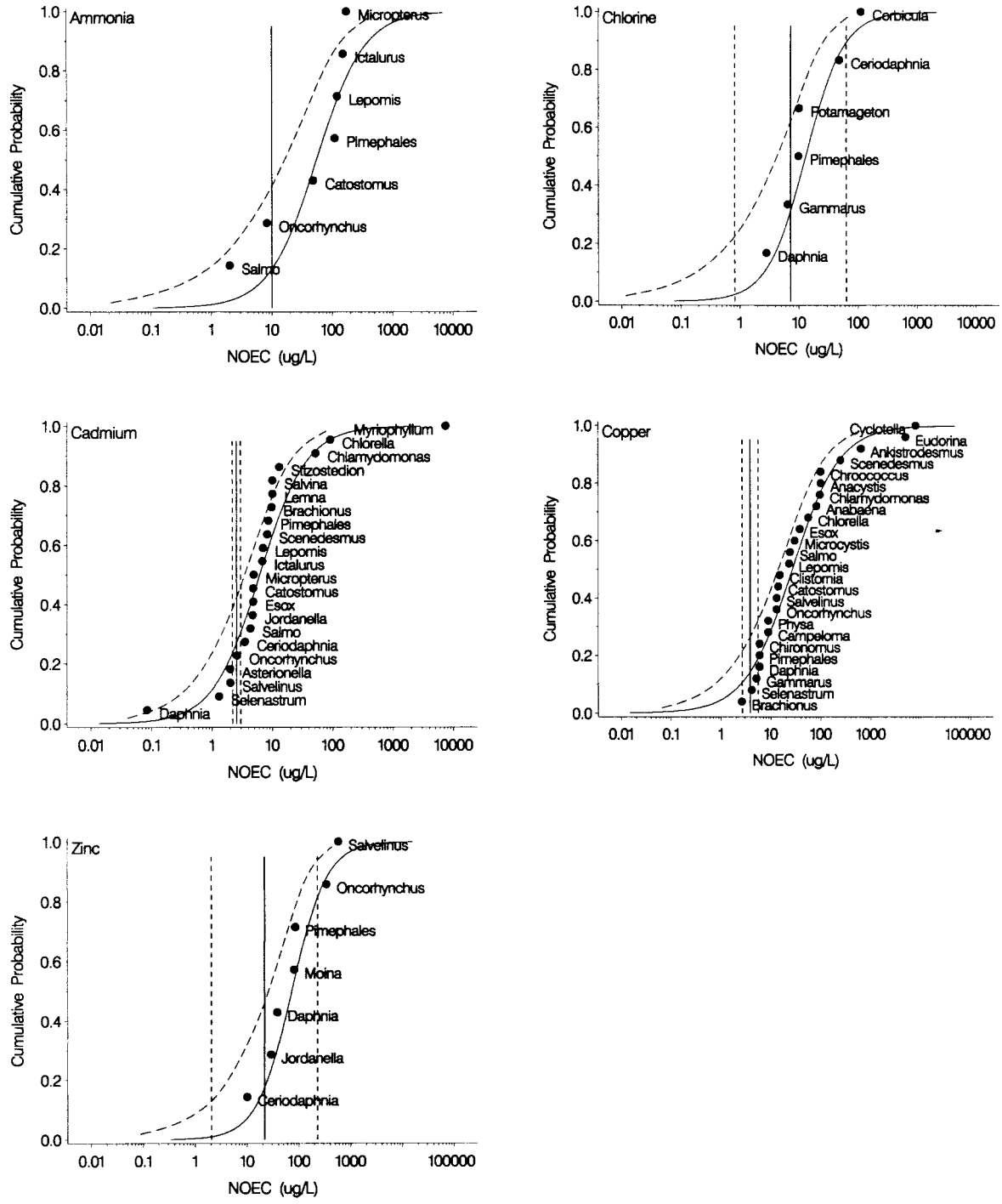

Fig. 2. Comparison of laboratory chronic toxicity and model ecosystem data for the inorganic compounds ammonia and chlorine and the heavy metals cadmium, copper, and zinc. Single-species data presented as cumulative probability versus chronic NOEC (symbols) with fitted log-logistic distribution (solid). The lower 95% confidence limits of the distribution percentiles are shown (dashed). Model ecosystem data presented as geometric mean (solid vertical line) and 95% confidence interval (dashed vertical lines) except for cadmium, where mean and range of data shown ($n = 2$) and ammonia ($n = 1$).

logical thinking should provide an appropriate perspective. It is well known that mayflies, stoneflies, and caddisflies represent the sensitive end of the insect community spectrum with respect to contaminant exposure and water quality parameters [35,36]. Systems that possess adequate representation of these orders should be more likely to respond to perturbation than those in which they are absent. Again, in this review, all model ecosystem results were treated as equal in importance. In reality, some probably deserve greater weight based on the sensitivity of the biota tested and the robustness of the experimental design.

The observation that protection of the majority of single species provides protection at higher levels of organization is not consistent with the concept of communities and ecosystems having emergent properties of increased sensitivity relative to single species. In fact, for some substances (e.g., atrazine and phenol), model ecosystem responses were not observed until concentrations were approximately equal to the NOEC for 50%

Table 1. *p* values from the Cramér–von Mises test for distribution goodness-of-fit versus chronic toxicity values for five distributions; the higher the *p* value the better the fit of the distribution to the data

Compounds	Uniform	Normal	Logistic	Extreme value	Exponential
Organic compounds					
Atrazine	0.038	0.088	0.11	0.42	0.26
C_{12}LAS	0.44	0.45	0.48	0.14	0.11
C_{12}TMAC	0.10	0.064	0.20	0.29	0.46
3,4Dichloroaniline	0.23	0.42	0.36	0.35	<0.001
Lindane	0.79	0.36	0.28	0.32	<0.001
Phenol	0.058	0.48	0.68	0.091	<0.001
Inorganic compounds and heavy metals					
Ammonia	0.019	0.050	0.095	0.19	0.25
Ammonia[a] (all taxa)	0.53	0.54	0.58	0.48	<0.001
Cadmium	<0.001	<0.001	0.010	<0.001	<0.001
Cadmium[a] (no plants)	<0.001	0.002	0.12	0.31	0.033
Chlorine	0.72	0.28	0.30	0.21	0.16
Copper	<0.001	0.030	0.20	<0.001	<0.001
Copper[a] (no plants)	0.77	0.64	0.47	0.45	0.15
Zinc	0.95	0.69	0.71	0.42	0.23
Number significant					
($p < 0.05$)	5	4	1	2	7
($p < 0.10$)	7	6	2	3	7

[a] Alternate taxa included to investigate the impact of taxa inclusion or exclusion; these data sets not compared with model ecosystem data.

of the genera. The increased sensitivity of single-species data relative to model ecosystems studies in these cases may be due, in part, to the methods used in single-species toxicity tests. One of the assumptions inherent in applying single-species effects distributions as models of all species is that the species tested are randomly selected from the distribution we are attempting to model (i.e., the single-species sensitivity distribution). If they are not, the species selected could lead to biased estimation of the distribution(s). In fact, the species selection choice for chronic effects tests is limited such that data sets almost always include *Daphnia, Pimephales, Oncorhynchus,* and *Selenastrum.* While it is generally accepted that there is no one species or group of species that is always most sensitive [37,38], it is also recognized that *Daphnia, Pimephales,* and *Oncorhynchus* are typically among the most sensitive species tested [37,39]. When these genera are tested, the most sensitive life stages or all life stages are tested. The lack of random species selection coupled with development of chronic test methods on species that tend to be more sensitive to toxicants, on average, may contribute to the conservative nature of single-species tests when compared with model ecosystem data. Unlike model ecosystems, laboratory toxicity test systems lack refugia where organisms can avoid or reduce exposure to test compounds. Finally, laboratory toxicity tests use waters low in organic carbon and solids. These constituents may reduce the bioavailability of test materials providing a degree of conservatism in laboratory single-species test data as compared to model ecosystem studies that are typically conducted with surface waters [40,41]. While the metals data were corrected for hardness and the LAS data normalized to a dodecyl chain length, we did not attempt to predict the bioavailable fraction in single-species and model ecosystem tests.

The possible lack of sensitivity of model ecosystems relative to single-species effects data can come from several sources, including (1) variability in data collected in these test systems, (2) level of understanding of how these systems operate and the most appropriate structural and functional attributes to measure (and the timing of these measurements), (3) experimental design considerations, and (4) density-dependent phenomena. Depending on the test system, variability in measured endpoints of model ecosystems were more or less equivalent to that of single-species tests. Pratt and Bowers [42] and Belanger et al. [27] determined coefficients of variation (CV) for numerous endpoints used in model ecosystems and found CVs ranged from approximately 5 to 30%. Some of the most ecologically meaningful measures, such as taxonomic richness, were the least variable. A more likely contributor to insensitivity for some selected studies is the choice of endpoints or inclusion of all relevant portions of the biological community in effects analyses. Research over time should identify which endpoints should be assessed and how often. These are usually test system-dependent properties. Small systems, for example, are most amenable to microbial studies, whereas large systems may include free-ranging fish. A key to the long-term utility of model ecosystems will be identification of what analyses work best for which research needs. Others state this as ''knowing what the question is'' [23].

Density-dependent phenomena at the community level could provide a level of protection to populations within communities relative to individual species [43]. These phenomena would compensate for toxic effects and appear as an apparent reduced sensitivity to toxic effects of the community relative to the population.

Differences in sensitivity can sometimes be tied to experimental design differences between single-species and model ecosystem tests, although there are no broadly applicable generalities. In an analysis of the ECETOC [22] and Belanger [13] model ecosystem data bases, it was determined that the average dilution ratio (i.e., factor between adjacent test concentrations) for all reviewed studies was 4.2; however, more recent studies (1990–1995) have an average dilution factor of 3.1 (Belanger, unpublished data). This compares to a dilution ratio ranging from 1.5 to 2.0 commonly employed in single-

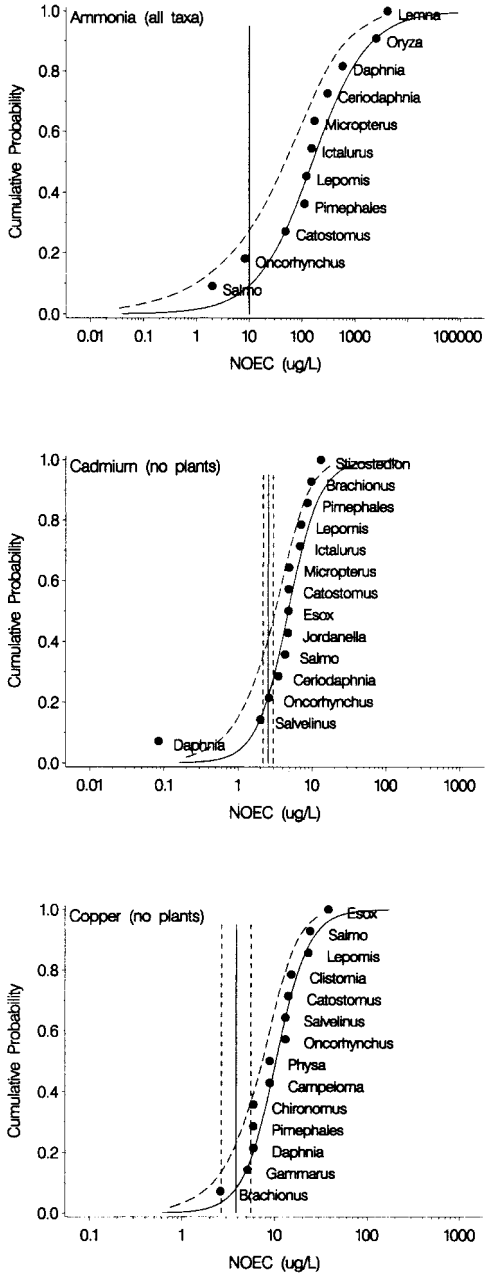

Fig. 3. Effect of taxa inclusion or exclusion on the distribution functions for ammonia (all taxa), cadmium (plant data omitted), and copper (plant data omitted). See Figure 2 for graph details.

species tests. This difference in NOEC precision may lead to over- or underestimates of between-system sensitivity depending on the data set. The trend in model ecosystem studies in the past decade has been to rely heavily on single treatments as opposed to replicated systems. In most cases, it appears the effort of highly replicated studies is unwarranted [13,44,45] relative to the great cost of conducting a comprehensive ecosystem-level assessment. Still, depending on the level of internal replication used to assess the condition of individual treatments, lower sensitivity can result if inadequate sampling is conducted.

Significant room for increasing our understanding of the relationship between single-species and model ecosystem tests exists. These include roles for benthic biota in the battery of available single-species assays, integrating bioavailability into the prediction process, identifying the best mechanisms to draw conclusions from ecological tests that integrate both direct and indirect effects to allow comparison to direct toxicity measures from single-species tests, and developing statistical tools that lead logically from making measurements to concluding overall ecosystem responses. Finally, there exists the need to better understand and quantifying the relationship between model ecosystems data and the response of natural systems. This brief list is by no means exhaustive but indicates that research needs are still large. Reasons for performing model ecosystem tests today remain as they were described by Crossland et al. [23,46] and are (1) to gain knowledge about ecosystem structure and function and thus to help develop better ecosystem models, (2) to develop and validate predictive models for chemical fate and/or effects, (3) to evaluate environmental quality standards derived from laboratory toxicity data, (4) to study resilience of ecosystems in terms of time required for restoration after disturbance, and (5) to obtain data required for regulatory purposes if assessing fate and/or effects in natural ecosystems.

Table 2. Relationship between single-species toxicity data and model ecosystem data

Compounds	Genera (*n*)	Model ecosystem (*n*)	% Genera affected at mean model ecosystem NOEC[a]
Organic compounds			
Atrazine	17	6	52 (29–76)
C_{12}LAS	17	6	15 (2–62)
C_{12}TMAC	8	5	2 (4–80)
3,4,Dichloroaniline	12	2	28 (9–58)
Lindane	10	1	9.6
Phenol	12	2	49 (40–58)
Inorganic compounds and heavy metals			
Ammonia	7	1	13
Cadmium	22	2	27 (24–30)
Chlorine	6	4	31 (2–88)
Copper	25	7	14 (10–18)
Zinc	7	3	17 (1–81)

[a] Values in parentheses refer to percent genera affected at lower and upper 95% confidence interval of model ecosystem data except for 3,4 DCA, phenol, and cadmium, where the range of data is used ($n = 2$).

Ecological risk assessments are used for a wide variety of purposes. Risks as diverse as chemical contamination, a rise in ocean temperatures, and removal of riparian zones are assessed for effects on individuals, populations, and entire communities. Ecological risk assessments can include a complete assessment of effects on functional and structural attributes within one well-defined ecosystem. Risk assessments are also used to derive limits of exposure and effects of chemicals for specific environmental compartments with the same limit applied across a large geographical area [1–4]. Due to the large number of compounds requiring assessments, single-species toxicity studies are typically used to derive these safe or low risk concentrations. One assumption in this approach is that single-species data provide information useful for understanding effects on complex ecological structures and processes. To assess the appropriateness of this assumption, we have compared chronic single-species toxicity data with model ecosystem NOECs. The single-species and model ecosystem data were assessed independently, much as a risk assessor would

in establishing a data base for an assessment. Data manipulations and reanalysis have been kept to a minimum in an attempt to apply the data as the original authors intended. Most authors assess their model ecosystems based on ecological significance; we have followed a similar approach in this paper. Resulting conclusions should be considered realistic estimates of ecologically relevant direct and indirect effects.

CONCLUSIONS

We have compared single-species chronic toxicity test results, typically NOEC values, with model ecosystem NOECs. Single-species data were presented as cumulative genera affected versus NOEC plots to facilitate a direct comparison between laboratory-generated toxicity data and model ecosystem results. Genera toxicity data spanned a range of values with NOECs occurring at concentrations above and below those causing effects at the model ecosystem level. Geometric mean model ecosystem NOECs corresponded to concentrations expected to exceed the chronic NOEC of 9 to 52% of genera. This analysis suggests that a sufficiently large set of laboratory-generated chronic test data (>5 species) can be used to set concentrations protective of model ecosystems and likely whole ecosystems. Further, the use of the 5% of genera affected level is conservative relative to mean model ecosystem data but is a fairly good predictor of the lower 95% confidence interval on the mean model ecosystem NOEC. Taxa inclusion impacted the genera distribution function, suggesting thought be given to the inclusion of taxa in effects assessments based on species distributions.

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APPENDIX 1

Chronic toxicity data by genera for ammonia (unionized), atrazine, chlorine, dodecyl trimethyl ammonium chloride (C_{12}TMAC), 3,4 dichlororaniline (3,4 DCA), lindane, and phenol; NOEC values shown unless specified; geometric mean genera values shown

Compound	Genera	NOEC (μg/L)	Genera mean (μg/L)	Reference
Ammonia	*Salmo*	2.0	2.0	[47]
	Oncorhynchus	2.4	8.2	[47]
		1.2		[47]
		10		[47]
		22		[47]
		60		[47]
	Catostomus	48	48	[47]
	Pimephales	88	110	[47]
		92		[47]
		150		[47]
	Lepomis	220	120	[47]
		63		[47]
	Ictalurus	73	150	[47]
		250		[47]
		200		[47]
		130		[47]
	Ceriodaphnia	200	300	[47]
		460[a]		[48]
	Micropterus	34	170	[47]
		120		[47]
		470		[47]
		430		[47]
	Daphnia	380	580	[47]
		530		[47]
		960		[47]
	Lemna	1,900	4,100	[49]
		8,800		[49]
	Oryza	1,200	2,500	[49]
		5,300		[49]
Atrazine	*Selenastrum*	16	1.9	[50]
		0.50		[50]
		10[b]		[51]
		0.17[c]		[52]
	Lemna	10	6.6	[50]
		8.3		[50]
		3.4		[50]
	Elodea	10	10	[50]
	Phaeodactyum	15	15	[50]
	Chlorella	500	49	[50]
		500		[50]
		10		[50]
		55		[50]
		100		[50]
		10[b]		[51]

APPENDIX 1

Continued

Compound	Genera	NOEC (μg/L)	Genera mean (μg/L)	Reference
	Chlamydomonas	500	78	[50]
		3.7		[53]
		120		[53]
		170		[54]
	Plectonema	10	10	[50]
	Scenedesmus	22	22	[53]
	Aulosira	50	50	[55]
	Tolypothrix	100	100	[55]
	Anabaena	50[d]	50	[55]
	Nostoc	50[d]	50	[55]
	Brachydanio	300	300	[56]
	Pimephales	0.21	0.21	[57]
	Lepomis	90[e]	90	[57]
	Salvelinus	60[e]	60	[57]
	Chironomus	2.0	2.0	[58]
Chlorine	*Daphnia*	4.0	2.8	[59]
		2.0		[59]
	Gammarus	12	6.4	[59]
		3.4		[59]
	Potamageton	10	10	[59]
	Pimephales	16	9.8	[59]
	Corbicula	6.0		[59]
	Ceriodaphnia	110	110	[59]
		48	48	[48]
3,4 DCA	*Brachionus*	5,000	6,300	[60]
		20,000		[60]
		2,500		[61]
	Poecilia	2.0[f]	2.0	[62]
	Brachydanio	20	20	[63]
	Ceriodaphnia	2.0	2.0	[64]
	Daphnia	10	5.6	[65]
		5.0		[66]
		5.0		[64]
		5.6		[64]
		12		[64]
		6.0		[67]
		2.5		[68]
		5.0		[68]
		4.9		[64]
		5.0		[69]
	Perca	2.0	2.0	[70]
	Pimephales	5.1	8.8	[71]
		15		[71]
	Chironomus	170	360	[58]
		760		[72]
	Chlamydomonas	2,500	1,300	[53]
		700		[53]
	Scenedesmus	500	500	[53]
	Oncorhynchus	71	71	[73]
	Gammarus	80	80	[72]
C_{12}TMAC	*Ceriodaphnia*	120	210	[44]
		250		[44]
		500		[44]
		120		[74]
		250		[74]
	Daphnia	10	26	[44]

APPENDIX 1

Continued

Compound	Genera	NOEC (μg/L)	Genera mean (μg/L)	Reference
		69		[44]
	Chironomus	450	450	[44]
	Pimephales	1,200	920	[44]
		700		[44]
	Corbicula	250	250	[44]
		250		[44]
		250		[44]
	Selenastrum	190	190	[75]
	Microcystis	120	120	[75]
	Navicula	200	200	[75]
Lindane	*Baetis*	0.20	0.20	[76]
	Brachionus	12	360	[77]
		55		[77]
		2,500[f]		[60]
		10,000		[61]
	Chironomus	1.1	0.60	[78]
		0.090		[58]
		2.2		[11]
	Daphnia	150	64	[79]
		11		[11]
		160		[80]
	Gammarus	0.80	2.1	[76]
		4.3		[11]
		2.7		[81]
	Salvelinus	8.8	8.8	[11]
	Pimephales	9.1	9.1	[11]
	Lepomis	9.1	9.1	[11]
	Oncorhynchus	9.5	9.5	[82]
	Brachydanio	40	40	[56]
		40		[83]
Phenol	*Brachionus*	25,000	25,000	[84]
	Ceriodaphnia	840	1,200	[85]
		1,800		[74]
	Notopterus	300	300	[86]
	Daphnia	160	280	[79]
		500		[85]
	Oncorhynchus	200[f]	770	[87]
		800		[88]
		2,800		[88]
	Oryzias	2,600	2,600	[89]
	Lemna	5,000	8,100	[90]
		14,000		
		7,500		[91]
	Selenastrum	70,000[d]	8,200	[92]
		970[c]		[52]
	Chlorella	250,000[d]	250,000	[92]
	Pimephales	1,800	1,200	[11]
		750		
	Macrobracnium	230[f]	230	[93]
	Brachydanio	2,200	2,200	[94]

[a] NOEC estimated for unionized ammonia.
[b] NOEC estimated from data provided.
[c] EC10 value.
[d] EC20 estimated from data provided.
[e] MATC.
[f] LOEC.

APPENDIX 2

Chronic toxicity data for linear alkylbenzene sulfonate (LAS) adjusted to dodecyl chain length using the procedure of Fendinger et al. [20]; NOEC values shown unless specified; geometric mean genera values shown

Genera	Alkyl chain length	NOEC (μg/L)	NOEC, adjusted (μg/L)	Genera mean (μg/L)	Reference
Pseudomonas	11.8	30,000	24,000	24,000	[95]
Chlamydomonas	11.2	15,000	7,300	7,300	[95]
Plectonema	11.2	20,000	9,700	9,700	[95]
Scenedesmus	11.6	7,700	5,400	5,400	[95]
Selenastrum	11.6	3,800	2,600	2,600	[95]
Microcystis	11.6	800	560	560	[95]
Chlorella	11.8	3,000	2,500	2,500	[95]
Paratanytarsus	11.6	3,400	2,400	2,400	[95]
Chironomus	11.8	2,400	2,000	2,000	[95]
Ceriodaphnia	11.7	3,000	2,300	1,700	[95]
	12.0	1,200	1,200		[95]
Daphnia	11.6	300	210	1,200	[95]
	11.8	300	250		[95]
	11.8	1,200	990		[95]
	11.8	1,200	1,000		[95]
	11.8	1,200	1,000		[95]
	12.0	4,900	4,900		[95]
	12.6	900	1,500		[95]
	13.0	800	2,000		[95]
	13.3	600	1,900		[95]
	12.0	4,200	4,200		[95]
Brachydanio	11.8	2,000	1,700	1,700	[95]
Pimephales	11.0	7,200	2,500	690	[95]
	11.2	5,100	2,200		[95]
	11.7	280	200		[95]
	11.7	480	350		[95]
	11.7	1,000	740		[95]
	12.0	1,100	1,100		[95]
	13.0	130	400		[95]
	13.3	110	400		[95]
Tilapia	11.6	250	160	160	[95]
Oncorhynchus	11.6	340	220	220	[95]
Poecelia	11.6	3,200	2,100	2,100	[95]
Brachionus	12.0	810[a]	810	1,200	[D.J. Versteeg, unpublished]
	12.3	1,400[a]	1,800		[96]

[a] EC20 value.

APPENDIX 3

Mean chronic toxicity data by genera for the heavy metals cadmium, copper, and zinc adjusted to a hardness of 50 mg/L $CaCO_3$; NOEC values shown unless specified; geometric mean genera values shown

Compound	Genera	Hardness (mg/L $CaCO_3$)	NOEC (μg/L)	NOEC, corrected (μg/L)	Genera mean (μg/L)	Reference
Cadmium	*Daphnia*	45	0.17	0.19	0.084	[97]
		53	0.08	0.08		[97]
		100	0.16	0.07		[97]
		210	0.21	0.05		[97]
	Oncorhynchus	44	1.3	1.5	2.6	[97]
		44	4.1	4.7		[97]
	Salvelinus	44	1.1	1.3	2.0	[97]
		44	1.7	1.9		[97]
		36	1.0	1.4		[97]
		190	7.0	1.8		[97]
		44	4.4	5.0		[97]
	Salmo	44	3.8	4.3	4.3	[97]
	Esox	44	4.2	4.8	4.8	[97]
	Pimephales	200	37	8.6	8.6	[97]
	Catostomus	44	4.2	4.8	4.8	[97]
	Ictalurus	37	11	15	6.8	[97]
		180	12	3.0		[97]
	Jordanella	44	4.1	4.7	4.7	[97]
	Micropterus	44	4.3	4.9	4.9	[97]
	Lepomis	210	31	7.0	7.0	[97]
	Stizostedion	35	9	13	13	[97]
	Asterionella	50	2		2.0	[97]
	Scenedesmus	50	6.1		8.2	[97]
		50	11			[53]
	Chlorella	50	250		91	[97]
		50	50			[97]
		50	60			[97]
	Selenastrum	50	50		1.3	[97]
		50	0.033[a]			[52]
	Myriophyllum	50	7,400		7,400	[97]
	Lemna	50	10		10	[97]
	Salvina	50	10		10	[97]
	Ceriodaphnia	170	8	2.2	3.5	[74]
		170	20	5.6		[74]
	Brachionus	90	18	9.7	9.7	[98]
	Chlamydomonas	50	38		52	[53]
		50	70			[53]
Copper	*Gammarus*	45	4.6	5.1	5.1	[99]
	Daphnia	51	11	11	5.9	[99]
		100	20	10		[99]
		210	7.2	1.9		[99]
	Pimephales	190	4.3	1.2	5.9	[99]
		200	14	4.0		[99]
		30	11	17		[99]
		200	24	6.5		[99]
		45	13	14		[99]
	Campeloma	45	8.0	8.8	8.8	[99]
	Physa	45	8.0	8.8	8.8	[99]
	Brachionus	90	2.5	1.4	2.6	[61]
		90	5.0	2.9		[60]
		150	12	4.2		[96]
	Oncorhynchus	23	7.4	15	13	[99]
		45	11	12		[99]
	Catostomus	45	13	14	14	[99]
	Clistornia	26	8.3	15	15	[99]
	Salvelinus	45	9.5	10	13	[99]
		45	22	24		[99]
		38	3.5	4.6		[99]
		45	22	24		[99]
	Lepomis	*45*	*21*	*23*	*23*	*[99]*
	Salmo	*45*	*22*	*24*	*24*	*[99]*
	Microcystis			*30*	*30*	*[99]*
	Esox	*45*	*35*	*38*	*38*	*[99]*

APPENDIX 3

Continued

Compound	Genera	Hardness (mg/L $CaCO_3$)	NOEC (μg/L)	NOEC, corrected (μg/L)	Genera mean (μg/L)	Reference
	Selenastrum		0.33[a]		4.1	[52]
			50		56	[99]
	Chlorella		56		82	[99]
	Anabaena		82		100	[99]
	Anacystis		100		100	[99]
	Chroococcus		100		640	[99]
	Ankistrodesmus		640		250	[99]
	Scenedesmus		1,100			[99]
			56		5,000	[53]
	Eudorina		5,000		96	[99]
	Chlamydomonas		8,000			[99]
			5.0			[53]
			22			[53]
	Cyclotella		8,000		8,000	[99]
	Chironomus	150	17	5.9	5.9	[58]
Zinc	*Daphnia*	45	70	76	38	[100]
		52	97	94		[100]
		100	43	23		[100]
		210	42	13		[100]
	Oncorhynchus	25	270	480	340	[100]
		26	140	240		[100]
	Salvelinus	45	530	580	580	[100]
	Pimephales	46	78	84	84	[100]
	Jordanella	44	26	29	29	[100]
	Ceriodaphnia	170	20	7.3	10	[74]
		170	40	15		[74]
	Moina	5.0	12	81	81	[101]

[a] EC10 value.

APPENDIX 4

Model ecosystem data for ammonia (unionized), atrazine, chlorine, dodecyl trimethyl ammonium chloride (C_{12}TMAC), 3,4-dichloroaniline, lindane, and phenol; all data presented as model ecosystem NOECs

Compound	NOEC (μg/L)	Test system	Location	Communities evaluated	Affected parameters	Reference
Ammonia	10	500-m-long stream	Monticello Ecological Research Station, Minnesota, USA	Benthos, phytoplankton, fish	Fish growth, invertebrate abundance	[102–104]
Atrazine	68	15-m^2 pond	Bavaria, Germany	Benthic and planktonic microbial and invertebrate communities	Community function, nutrient cycling	[105,106]
	10	7.5-L flow-through system	Blacksburg, Virginia, USA	Benthic algal and metazoan communities	Community function, nutrient cycling	[107]
	100	1.5-m-long flow-through system	College Station, Texas, USA	Periphytic algal community	Primary productivity, algal biomass	[108]
	11	5.7-m flow-through stream	Sittingbourne, UK	Benthic microbial and invertebrate communities, caged fish	Primary productivity, algal biomass	[31]
	25	6.0-m-long stream	Lansing, Michigan, USA	Benthic microbial and invertebrate communities	Primary productivity, algal biomass	[109,110]
	20	2-L flask, static	Duluth, Minnesota, USA	Planktonic community	Primary productivity	[111]
Chlorine	6.3	7.5-L volume, flow-through system	Blacksburg, Virginia, USA	Benthic algal and metazoan communities	Protozoan richness	[112]
	21	7.5-L volume, flow-through system	Blacksburg, Virginia, USA	Benthic algal and metazoan communities	Alkyl phosphatase activity	[113]
	52	500-m-long stream	Monticello Ecological Research Station, Minnesota, USA	Benthic invertebrate and phytoplankton communities, fish	Invertebrate drift and abundance	[114–116]
	4.1	21-L redosed static system	Douglas Lake, Michigan, USA	Phytoplankton and zooplankton communities	Zooplankton density	[113]
C_{12}TMAC	180	20-m-long flow-through stream	Cincinnati, Ohio, USA	Benthic microbial and invertebrate community, caged zooplankton	*Daphnia* reproduction	[117]
	230	12-m-long stream	Milford, Ohio, USA	Benthic microbial and invertebrate community	Algal and invertebrate abundance	[45,118,119]
	250	4.7-km-long dosed stream	Howesville, Indiana, USA	Benthic microbial and invertebrate community	Periphyton diversity and richness, invertebrate abundance	[117,120]
	300	20-L volume, static system	Acton Lake, Ohio, USA	Phytoplankton and zooplankton community	Phytoplankton community similarity	[120]
	210	1.5-m-long in-stream flume	Little Miami River, Ohio, USA	Benthic algal community	Periphyton community productivity, community similarity	[120]
3,4-Dichloroaniline	1.0	15-m^2 pond	Bavaria, Germany	Benthic and planktonic microbial and invertebrate communities	Periphytic productivity, invertebrate community structure	[121,122]
	70	15-m^2 pond	Bavaria, Germany	Benthic and planktonic microbial and invertebrate communities	Periphytic productivity, invertebrate community structure	[31]
Lindane	0.59	5.7-m-long stream	Sittingbourne, UK	Benthic microbial and invertebrate communities, caged fish	Invertebrate abundance, invertebrate drift, primary productivity	[31,44,76,123]
Phenol	3,100	7.5-L volume, flow-through system	Blacksburg, Virginia, USA	Benthic microbial and metazoan community	Species richness, chlorophyll biomass	[124]
	1,200	7.5-L volume, flow-through system	Murray Lake, Kentucky, USA	Benthic microbial and metazoan community	Dissolved oxygen evolution, chlorophyll biomass	[124]

APPENDIX 5

Summary of model ecosystem NOECs for linear alkylbenzene sulfonate (LAS) adjusted to dodecyl chain length using the procedure of Fendinger et al. [20]

Alkyl chain length	NOEC (μg/L)	NOEC, corrected (μg/L)	Test system	Location	Communities evaluated	Affected parameters	Reference
11.9	1,100	1,000	1.5-m-long in-stream flume	Little Miami River, Ohio, USA	Benthic algal community	Algal richness, primary productivity	[125]
12.3	360	470	45-m-long stream	Columbia, Missouri, USA	Benthic microbial and invertebrate communities	Invertebrate community structure	[126]
11.6	1,000	700	20-L volume, flow-through laboratory system	Cincinnati, Ohio, USA	Benthic microbial and invertebrate communities, restricted fish	Bluegill biomass	[127]
11.6	300	210	5.7-m-long stream	Sittingbourne, UK	Benthic microbial and invertebrate communities	Invertebrate abundance	[128]
13.3	1,900	6,100	20-L volume static enclosure	Acton Lake, Ohio, USA	Phytoplankton and zooplankton communities	Primary productivity	[75]
11.5	120	80	5.7-m-long stream	Sittingbourne, UK	Benthic microbial and invertebrate communities, caged fish	Rainbow trout growth, invertebrate abundance	[129]

APPENDIX 6

Model ecosystem NOEC values for the heavy metals cadmium, copper, and zinc adjusted to a hardness of 50 mg/L $CaCO_3$

Compound	Hardness (μg/L)	NOEC (μg/L)	NOEC, corrected (μg/L)	Test system	Location	Communities evaluated	Affected parameters	Reference
Cadmium	9.1	0.5	3.0	91.5-m-long stream	SREL, South Carolina, USA	Benthic and planktonic microbial and invertebrate communities, free-ranging fish	Periphyton community structure, invertebrate community structure	[130]
	57	2.5	2.2	20-L volume, 1.5-m-long stream	Glen Lyn, Virginia, USA	Benthic microbial and invertebrate communities		[131]
Copper	74	5.5	3.8	20-L volume, 1.5-m-long stream	Glen Lyn, Virginia, USA	Benthic algal and invertebrate communities	Invertebrate community	[132]
	250	9.5	2.1	1.5-L volume, flow-through lab system	Cincinnati, Ohio, USA	Benthic algal community	Taxa richness	[27]
	120	11	4.6	15-m^2 pond	Bavaria, Germany	Benthic and planktonic microbial and invertebrate communities	Invertebrate community structure, periphytic productivity	[160,121]
	220	10	2.5	5.7-m-long stream	Sittingbourne, UK	Benthic microbial and invertebrate communities	Periphyton and invertebrate community productivity	[31,133]
	30	2.5	4.0	800-m-long enclosed stream channel	Sierra Nevada range, California, USA	Benthic algal and invertebrate communities, free-ranging fish	Periphyton and invertebrate productivity	[3,13,29,30]
	55	6.6	6.3	7.5-L volume, flow-through system	Blacksburg, Virginia, USA	Benthic microbial and metazoan community	Protozoan taxa richness	[134]
	150	15	5.3	56-L volume, 2.5-m-long flow-through stream	Clinch River, Virginia, USA	Benthic invertebrate community	Invertebrate richness	[12,135]
Zinc	64	20	16	20-L volume, 1.5-m-long stream	Glen Lyn, Virginia, USA	Benthic microbial and invertebrate communities	Invertebrate growth and survival	[136–139]
	60	73	63	7.5-L volume, flow-through system	Blacksburg, Virginia, USA	Benthic microbial and metazoan community	Algal community structure	[140]
	54	10	10	7.5-L volume, flow-through system	Blacksburg, Virginia, USA	Benthic microbial and metazoan community	Algal community structure, protozoan colonization	[141]