

Supplementary Material: Comparative Analysis of Toxicity Sensitivity and Life-History Traits in Fish

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Introduction

The document provides more detailed descriptive statistics and main results from a comparative analysis of toxicity sensitivity and life-history traits in fish species. The analysis is based on a dataset that includes toxicity data for various fish species and chemicals. The predictors under interest include:

- **Order:** the taxonomic order of the species
- **airBreathing:** whether the species is air-breathing or not
- **Main_habitat:** the main habitat of the species (freshwater, marine, brackish)
- **marineFreshMix:** whether the species is marine, freshwater or mixed
- **geogTemp:** whether the species is tropical, temperate, subtropical, boreal or polar living
- **waterColumn:** whether the species is benthic, pelagic, demersal or a mix
- **maxAge:** the maximum recorded lifespan of the species
- **maxLength:** the maximum length of the species
- **Feeding:** the feeding type of the fish like herbivore, carnivore, omnivore, planktivore, piscivore
- **Migration:** the migratory type of the fish like anadromous, catadromous, amphidromous, potamodromous oceanodromous, non-migratory

The file is ordered as follows:

- An overview of basic descriptive statistics, including sample sizes.
- Identification of fish and chemical groups that comprised the largest portion of the dataset.
- Ranking of the most sensitive and least sensitive species.
- Highlighting variability within species groups
- Comparing sensitivity to toxic substances across phylogenetic groups.
- Comparing toxic sensitivity between different life-history traits.

It must be noted that the file uses the **brms** package for the phylogenetic regressions hence to fully reproduce the results the package must be installed together with STAN.

Import and Prepare Data

There are essentially three data sources imported in the previous file: **S00_PrepareDataset.Rmd** that are merged into a single data frame.

The non-filtered dataset contains 4564 observations including 201 species (from 63 families, belonging to 30 orders)

The filtered dataset contains 3908 observations including 175 species (from 49 families, belonging to 18 orders)

Variable standardization

In order to compare sensitivity to different substances we can also standardize the toxicity values. We are going to compute z-scores for each substance.

Add the phylogeny

The branch lengths that are used in the phylogenetic adjustment are retrieved from (timetree.org)[<http://www.timetree.org/>]. See the `000_prepareData.R` script for details.

Decsriptive Results

The preliminary dataset contains 4564 observations including 201 species (from 30 orders) and 29 chemicals (from 7 chemical classes).

As there is a lot of data that comes from single studies or single species or single chemicals. To get a more robust results we have filtered out the Orders with less than 3 species and the chemical classes with less than 3 chemicals in the dataset.

The filtering lost us 658 observations. The filtered dataset includes 173 species (from 18 orders) and 25 chemicals (from 4 chemical classes).

Table 1: Table S1. The mean and median LC50 values for the substances in the dataset.

Substance	Class	Mean LC50	Median LC50	Nr Obs
Pentachlorophenol	organochlorine compound	0.27	0.2	562
4-nonylphenol	benzene derivative	0.34	0.3	281
Pb and its compounds	metal	183	32	164
Endosulfan	organochlorine compound	0.17	0.003	456
(6,7,8,9,10,10-Hexachloro-1,5...	organochlorine compound	85	0.15	474
Hexachlorocyclohexane	organochlorine compound	35	2.8	849
Cd and its compounds	metal	1.2	0.4	190
Hg and its compounds	metal	85	47	70
Ni and its compounds	PAH	0.96	0.098	47
Fluoranthene	organochlorine compound	2.5	2.1	24
Trichlorobenzene	organochlorine compound	16	7.6	25
Hexachlorobenzene	organochlorine compound	48	29	130
Trichloromethane	organochlorine compound	4	0.13	123
Trifluralin	benzene derivative	30	7.8	29
(2,6-Dinitro-N,N-dipropyl-4...	PAH	13	7.1	144
Naphthalene	organochlorine compound	4.2	4	38
Diuron	organochlorine compound			
(3-(3,4-dichlorophenyl)-1,1-dimet...	organochlorine compound			
Alachlor	organochlorine compound			
(2-Chloro-N-(2,6-diethylphenyl)...	organochlorine compound			

Substance	Class	Mean LC50	Median LC50	Nr Obs
Atrazine	organochlorine	31	20	89
(6-Chloro-N2-ethyl-N4-(propan-2-... Simazine	compound organochlorine	148	52	70
(6-Chloro-N,N'-diethyl-1,3,5-tr... Di(2-ethylhexyl)phthalate	compound benzene derivative	77	0.32	45
Hexachlorobutadiene	organochlorine	12	0.39	41
1,2-Dichloroethane	compound organochlorine	221	183	24
4-(1,1',3,3'-tetramethylbutyl)-phenol	benzene derivative	0.91	0.41	4
Dichloromethane	organochlorine	260	260	14
Anthracene and its compounds	compound PAH	4.6	0.2	4
Pentachlorobenzene	organochlorine	0.35	0.3	9
	compound			

Table 2: Table S2. The species in the dataset ordered by mean standardized toxicity LC50 z-scores (ie sensitivity to toxicants). The smaller the number the more sensitive is the species

Species	Order	Min	Mean	Median	Max	N
Tinca tinca	Cypriniformes	0.593	0.593	0.593	0.593	1
Alosa sapidissima	Clupeiformes	0.243	0.659	0.659	1.07	2
Acipenser oxyrinchus	Acipenseriformes	0.243	0.741	0.409	1.57	5
Etheostoma fonticola	Perciformes	0.458	0.832	0.783	1.3	4
Acipenser brevirostrum	Acipenseriformes	0.409	0.889	0.978	1.47	5
Erimonax monachus	Cypriniformes	0.409	0.947	0.789	1.8	4
Barbodes carnaticus	Cypriniformes	0.984	1.06	1.06	1.16	4
Rutilus rutilus	Cypriniformes	1.07	1.07	1.07	1.07	1
Coregonus muksun	Salmoniformes	1.01	1.08	1.08	1.16	3
Notropis mekistocholas	Cypriniformes	0.739	1.13	1.1	1.57	4
Etheostoma lepidum	Perciformes	0.954	1.13	1.02	1.54	4
Alburnus alburnus	Cypriniformes	1.16	1.18	1.18	1.2	2
Phoxinus phoxinus	Cypriniformes	0.984	1.23	1.09	1.79	5
Oncorhynchus clarkii ssp. stomias	Salmoniformes	0.794	1.25	0.975	3	30
Craterocephalus marjoriae	Atheriniformes	1.35	1.35	1.35	1.35	1
Amniataba percoides	Centrarchiformes	1.35	1.35	1.35	1.35	1
Leiopotherapon unicolor	Centrarchiformes	1.35	1.35	1.35	1.35	1
Notropis atherinoides	Cypriniformes	1.32	1.36	1.36	1.39	2
Chelon labrosus	Mugiliformes	1.36	1.36	1.36	1.36	4
Polyodon spathula	Acipenseriformes	1.37	1.38	1.38	1.39	2
Leucaspius delineatus	Cypriniformes	0.587	1.4	1.79	1.83	3
Jordanella floridae	Cyprinodontiformes	1.41	1.41	1.41	1.41	6
Poeciliopsis occidentalis	Cyprinodontiformes	1.13	1.43	1.27	2.06	4
Menidia beryllina	Atheriniformes	1.31	1.46	1.37	1.85	11
Lepomis gibbosus	Perciformes	1.09	1.47	1.59	1.71	9
Morone americana	Eupercaria	1.14	1.48	1.58	1.73	9
Salmo salar	Salmoniformes	0.684	1.49	1.7	2.59	11
Thymallus arcticus	Salmoniformes	1.44	1.5	1.44	1.7	5

Species	Order	Min	Mean	Median	Max	N
Trichopodus trichopterus	Anabantiformes	1.5	1.5	1.5	1.5	1
Xiphophorus hellerii	Cyprinodontiformes	1.51	1.51	1.51	1.51	1
Salvelinus namaycush	Salmoniformes	1.37	1.52	1.45	2.13	29
Oncorhynchus apache	Salmoniformes	0.849	1.54	1.37	3.66	48
Anguilla rostrata	Anguilliformes	1.14	1.54	1.63	1.79	12
Morone saxatilis	Eupercaria	1.07	1.55	1.67	2.68	23
Oncorhynchus clarkii	Salmoniformes	0.975	1.58	1.48	2.54	37
Pagrus major	Eupercaria	1.58	1.58	1.58	1.58	3
Parapristipoma trilineatum	Eupercaria	1.58	1.58	1.58	1.58	1
Acanthopagrus schlegelii	Eupercaria	1.58	1.58	1.58	1.58	1
Oncorhynchus clarkii ssp. henshawi	Salmoniformes	0.739	1.58	1.54	3.05	48
Fundulus diaphanus	Cyprinodontiformes	1.46	1.59	1.56	1.7	9
Sander vitreus	Perciformes	1.59	1.59	1.59	1.59	1
Mesopotamichthys sharpeyi	Cypriniformes	1.6	1.6	1.6	1.6	1
Misgurnus anguillicaudatus	Cypriniformes	1.41	1.61	1.6	1.79	5
Ameiurus melas	Siluriformes	1.17	1.62	1.68	2	8
Limanda limanda	Pleuronectiformes	1.37	1.63	1.68	1.84	3
Cyprinodon variegatus	Cyprinodontiformes	0.631	1.63	1.67	3.82	58
Terapon jarbua	Centrarchiformes	1.57	1.63	1.63	1.7	4
Lagodon rhomboides	Eupercaria	1.26	1.64	1.67	1.79	6
Mugil cephalus	Mugiliformes	1.31	1.64	1.69	1.84	15
Cirrhinus mrigala	Cypriniformes	1.54	1.65	1.67	1.67	5
Catostomus commersonii	Cypriniformes	1.22	1.66	1.68	1.96	22
Planiliza parsia	Mugiliformes	1.52	1.66	1.64	1.93	10
Lepomis macrochirus	Perciformes	0.701	1.67	1.66	4.74	318
Clupea pallasii	Clupeiformes	1.58	1.67	1.67	1.76	2
Leiostomus xanthurus	Eupercaria	1.67	1.67	1.67	1.67	2
Nematalosa erebi	Clupeiformes	1.67	1.67	1.67	1.67	1
Macquaria ambigua	Centrarchiformes	1.67	1.67	1.67	1.67	2
Oncorhynchus mykiss	Salmoniformes	0.331	1.67	1.7	8.08	680
Jenynsia multidentata	Cyprinodontiformes	1.67	1.67	1.67	1.67	2
Mystus cavasius	Siluriformes	1.67	1.67	1.67	1.67	1
Gymnocorymbus ternetzi	Characiformes	1.67	1.67	1.67	1.67	2
Bidyanus bidyanus	Centrarchiformes	1.67	1.67	1.67	1.67	2
Hyphessobrycon bifasciatus	Characiformes	1.67	1.67	1.67	1.67	1
Melanotaenia duboulayi	Atheriniformes	1.67	1.67	1.67	1.67	4
Pseudotroplus maculatus	Cichliformes	1.63	1.67	1.67	1.72	2
Esomus danrica	Cypriniformes	1.35	1.67	1.71	1.78	21
Scardinius erythrophthalmus	Cypriniformes	1.67	1.67	1.67	1.68	2
Schilbe mystus	Siluriformes	1.67	1.67	1.67	1.67	1
Cyprinodon bovinus	Cyprinodontiformes	0.695	1.68	1.24	3.01	9
Tilapia sparrmanii	Cichliformes	1.68	1.68	1.68	1.68	1
Anguilla japonica	Anguilliformes	1.68	1.69	1.69	1.7	2
Pseudopleuronectes americanus	Pleuronectiformes	1.31	1.69	1.42	2.34	3
Puntius sophore	Cypriniformes	1.67	1.69	1.67	1.79	12
Cyprinus carpio	Cypriniformes	0.591	1.7	1.7	3.88	105
Salvelinus confluentus	Salmoniformes	1.7	1.7	1.7	1.7	6
Periophthalmus waltoni	Gobiiformes	1.7	1.7	1.7	1.7	1
Rasbora sumatrana	Cypriniformes	1.7	1.7	1.7	1.7	1
Australoheros facetus	Cichliformes	1.7	1.7	1.7	1.7	4

Species	Order	Min	Mean	Median	Max	N
Menidia peninsulæ	Atheriniformes	1.7	1.7	1.7	1.7	2
Etroplus suratensis	Cichliformes	1.7	1.7	1.7	1.7	1
Pseudaspius hakonensis	Cypriniformes	1.7	1.7	1.7	1.7	2
Oreochromis aureus	Cichliformes	1.67	1.71	1.67	2.17	15
Chrysiptera cyanea	Ovalentaria	1.56	1.71	1.66	2	12
Parambassis ranga	Ovalentaria	1.71	1.71	1.71	1.71	1
Cymatogaster aggregata	Ovalentaria	1.67	1.71	1.71	1.75	4
Oncorhynchus nerka	Salmoniformes	1.7	1.71	1.71	1.72	3
Poecilia latipinna	Cyprinodontiformes	1.69	1.71	1.7	1.75	7
Pethia conchonius	Cypriniformes	1.69	1.71	1.71	1.73	2
Pethia ticto	Cypriniformes	1.25	1.71	1.8	1.87	18
Oncorhynchus gorbuscha	Salmoniformes	1.71	1.71	1.71	1.72	2
Salmo trutta	Salmoniformes	1.53	1.72	1.72	1.79	17
Ctenopharyngodon idella	Cypriniformes	1.7	1.72	1.71	1.73	4
Tanichthys albonubes	Cypriniformes	1.39	1.72	1.72	2.1	21
Barbatula barbatula	Cypriniformes	1.72	1.72	1.72	1.72	1
Oreochromis mossambicus	Cichliformes	1.25	1.72	1.74	2.03	40
Garra mullya	Cypriniformes	1.72	1.72	1.72	1.72	1
Cyprinella lutrensis	Cypriniformes	1.73	1.73	1.73	1.73	1
Gobiocypris rarus	Cypriniformes	1.72	1.73	1.73	1.73	4
Channa orientalis	Anabantiformes	1.67	1.73	1.68	2.39	25
Menidia menidia	Atheriniformes	1.7	1.73	1.71	1.79	14
Clarias gariepinus	Siluriformes	1.69	1.73	1.73	1.77	4
Barilius bendelisis	Cypriniformes	1.68	1.73	1.69	1.83	3
Zacco platypus	Cypriniformes	1.7	1.75	1.75	1.79	2
Labeo rohita	Cypriniformes	1.64	1.75	1.7	2.39	28
Mystus vittatus	Siluriformes	1.58	1.75	1.67	3.5	34
Planiliza macrolepis	Mugiliformes	1.58	1.75	1.79	1.79	7
Anguilla anguilla	Anguilliformes	1.69	1.75	1.79	1.79	48
Notemigonus crysoleucas	Cypriniformes	1.71	1.75	1.75	1.79	4
Salvelinus fontinalis	Salmoniformes	1.09	1.75	1.7	3.25	38
Mugil curema	Mugiliformes	1.72	1.76	1.77	1.8	4
Kryptolebias marmoratus	Cyprinodontiformes	1.71	1.77	1.77	1.83	10
Cyprinodon dearborni	Cyprinodontiformes	1.74	1.77	1.77	1.81	4
Lepidocephalichthys thermalis	Cypriniformes	1.7	1.77	1.79	1.79	25
Encrasicholina purpurea	Clupeiformes	1.79	1.79	1.79	1.79	1
Thalassoma bifasciatum	Eupercaria	1.79	1.79	1.79	1.79	3
Kuhlia sandvicensis	Centrarchiformes	1.79	1.79	1.79	1.79	3
Perca flavescens	Perciformes	1.79	1.79	1.79	1.79	2
Gobio gobio	Cypriniformes	1.79	1.79	1.79	1.79	2
Lepomis microlophus	Perciformes	1.79	1.79	1.79	1.79	1
Notropis stramineus	Cypriniformes	1.79	1.79	1.79	1.79	1
Trichogaster lalius	Anabantiformes	1.79	1.79	1.79	1.79	8
Sarotherodon galilaeus	Cichliformes	1.79	1.79	1.79	1.79	1
Paracheirodon axelrodi	Characiformes	1.79	1.79	1.79	1.79	8
Gambusia holbrooki	Cyprinodontiformes	1.79	1.79	1.79	1.79	1
Garra gotyla	Cypriniformes	1.79	1.79	1.79	1.79	1
Puntius dorsalis	Cypriniformes	1.79	1.8	1.8	1.8	3
Clarias batrachus	Siluriformes	1.67	1.8	1.68	3.05	26
Paralichthys olivaceus	Pleuronectiformes	1.56	1.8	1.82	2.12	9
Barbonymus gonionotus	Cypriniformes	1.8	1.8	1.8	1.8	3
Tautoglabrus adspersus	Eupercaria	1.8	1.8	1.8	1.8	1

Species	Order	Min	Mean	Median	Max	N
Chaenogobius annularis	Gobiiformes	1.59	1.81	1.82	1.93	25
Girella punctata	Centrarchiformes	1.59	1.81	1.81	1.9	19
Anabas testudineus	Anabantiformes	1.46	1.81	1.79	2.88	19
Poecilia vivipara	Cyprinodontiformes	1.78	1.82	1.8	1.9	4
Oncorhynchus kisutch	Salmoniformes	1.07	1.82	1.79	3.02	38
Lepomis cyanellus	Perciformes	1.71	1.83	1.79	2.05	12
Micropterus salmoides	Centrarchiformes	1.3	1.85	1.9	2.04	48
Carassius auratus	Cypriniformes	1.02	1.87	1.68	10.8	110
Fundulus majalis	Cyprinodontiformes	1.78	1.88	1.79	2.19	6
Ptychocheilus lucius	Cypriniformes	1.01	1.88	1.51	4.38	48
Oreochromis urolepis	Cichliformes	1.89	1.89	1.89	1.89	2
Oplegnathus fasciatus	Centrarchiformes	1.9	1.9	1.9	1.9	1
Pimephales promelas	Cypriniformes	0.269	1.91	1.71	30	448
Boleophthalmus dussumieri	Gobiiformes	1.73	1.93	1.96	2.09	3
Trichogaster fasciata	Anabantiformes	1.67	1.94	1.79	2.82	20
Devario malabaricus	Cypriniformes	1.8	1.94	1.94	2.09	2
Fundulus similis	Cyprinodontiformes	1.95	1.95	1.95	1.95	1
Oreochromis niloticus	Cichliformes	0.699	2	1.79	8.28	41
Heteropneustes fossilis	Siluriformes	0.0228	2.01	1.69	23.6	110
Xyrauchen texanus	Cypriniformes	0.849	2.03	1.85	5.48	48
Solea solea	Pleuronectiformes	1.59	2.03	2.08	2.43	3
Rasbora daniconius	Cypriniformes	1.43	2.04	2.03	2.6	6
Gambusia affinis	Cyprinodontiformes	1.49	2.08	1.79	5.26	65
Fundulus heteroclitus	Cyprinodontiformes	1.27	2.1	1.99	4.53	125
Labeo catla	Cypriniformes	1.72	2.12	2.03	2.97	10
Oncorhynchus tshawytscha	Salmoniformes	1.04	2.13	1.7	5.99	29
Danio rerio	Cypriniformes	1.02	2.16	1.79	8.37	87
Ictalurus punctatus	Siluriformes	1.12	2.17	1.68	11.9	69
Coptodon zillii	Cichliformes	1.4	2.23	2.23	3.07	2
Channa striata	Anabantiformes	1.45	2.24	1.78	5.69	20
Dawkinsia arulius	Cypriniformes	1.86	2.25	1.91	3.25	6
Poecilia reticulata	Cyprinodontiformes	0.762	2.38	1.79	7.89	135
Gila elegans	Cypriniformes	1.06	2.41	2.06	5.48	48
Platichthys flesus	Pleuronectiformes	1.73	2.41	2.4	3.48	7
Pomatoschistus minutus	Gobiiformes	2.43	2.43	2.43	2.43	2
Channa punctata	Anabantiformes	1.42	2.57	1.79	13	74
Leuciscus idus	Cypriniformes	0.073	2.78	2.05	8.09	26
Acanthocobitis botia	Cypriniformes	2.82	2.97	2.99	3.09	4
Carassius carassius	Cypriniformes	0.632	3.32	3.8	6.52	12
Trigonostigma heteromorpha	Cypriniformes	0.963	3.37	1.63	9.46	8

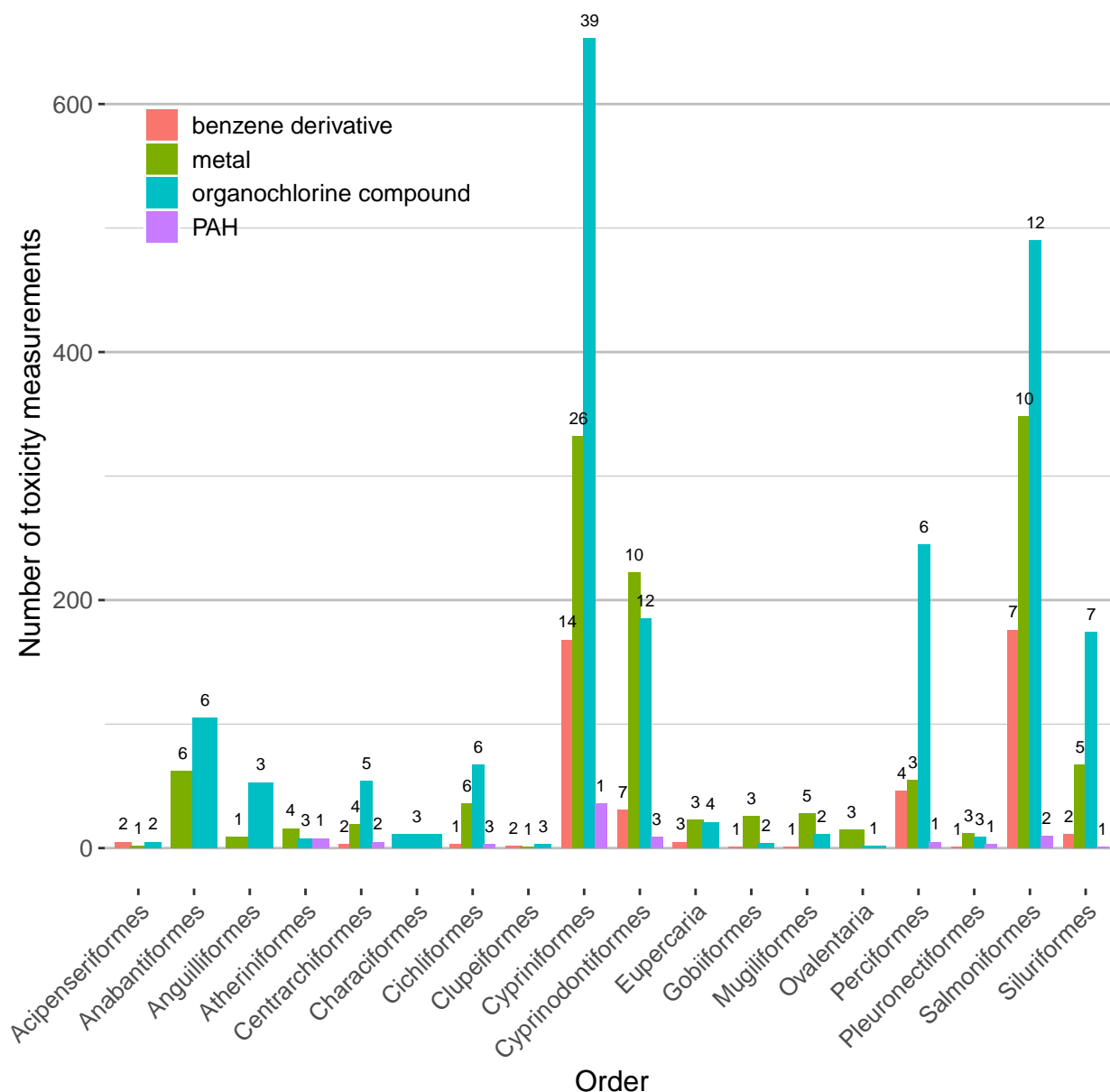


Figure 1. The number of observations for each order and chemical class combination. The numbers on the plot indicate the number of species for the respective chemical group and order.

Most of the measurements are from the orders *Cypriniformes* and *Salmoniformes*. The most common chemical classes are metals and organic compounds.

Over half of the measured data comes from a single chemical_class organochlorine compound (53.8%) .

The species composition is similarly disproportional as over half of the data is from Orders *Cypriniformes* (30.4%) and *Salmoniformes* (26.2%) (Figure 1).

Variance within orders

Table 3: Table S3. Fold difference in mean adjusted toxicity sensitivity between species within orders. The total number of data points (N), proportion of the data falling to an order (Prop %) and the mean adjusted toxicity for an order (Mean adj.tox) is also shown.

Order	Fold Diff.	N	Mean adj. tox	Prop. (%)
Cypriniformes	5.7	1189	1.9	30
Clupeiformes	2.7	6	1.4	0.15
Perciformes	2.2	351	1.7	9
Salmoniformes	2	1024	1.7	26
Acipenseriformes	1.9	12	0.91	0.31
Anabantiformes	1.7	167	2.2	4.3
Cyprinodontiformes	1.7	447	2.1	11
Pleuronectiformes	1.5	25	2	0.64
Gobiiformes	1.4	31	1.9	0.79
Centrarchiformes	1.4	81	1.8	2.1
Siluriformes	1.3	253	2	6.5
Cichliformes	1.3	109	1.8	2.8
Mugiliformes	1.3	40	1.7	1
Atheriniformes	1.3	32	1.6	0.82
Eupercaria	1.2	49	1.6	1.3
Anguilliformes	1.1	62	1.7	1.6
Characiformes	1.1	11	1.8	0.28
Ovalentaria	1	17	1.7	0.44

Around 65.8 % of the data comes from orders where the mean adjusted toxicity sensitivity between species within the order is at least 2-fold different (Table S 3) Among Cypriniformes the the difference is 5.7 fold.

At the same time the maximum difference between the means of orders is only 2.4 fold.

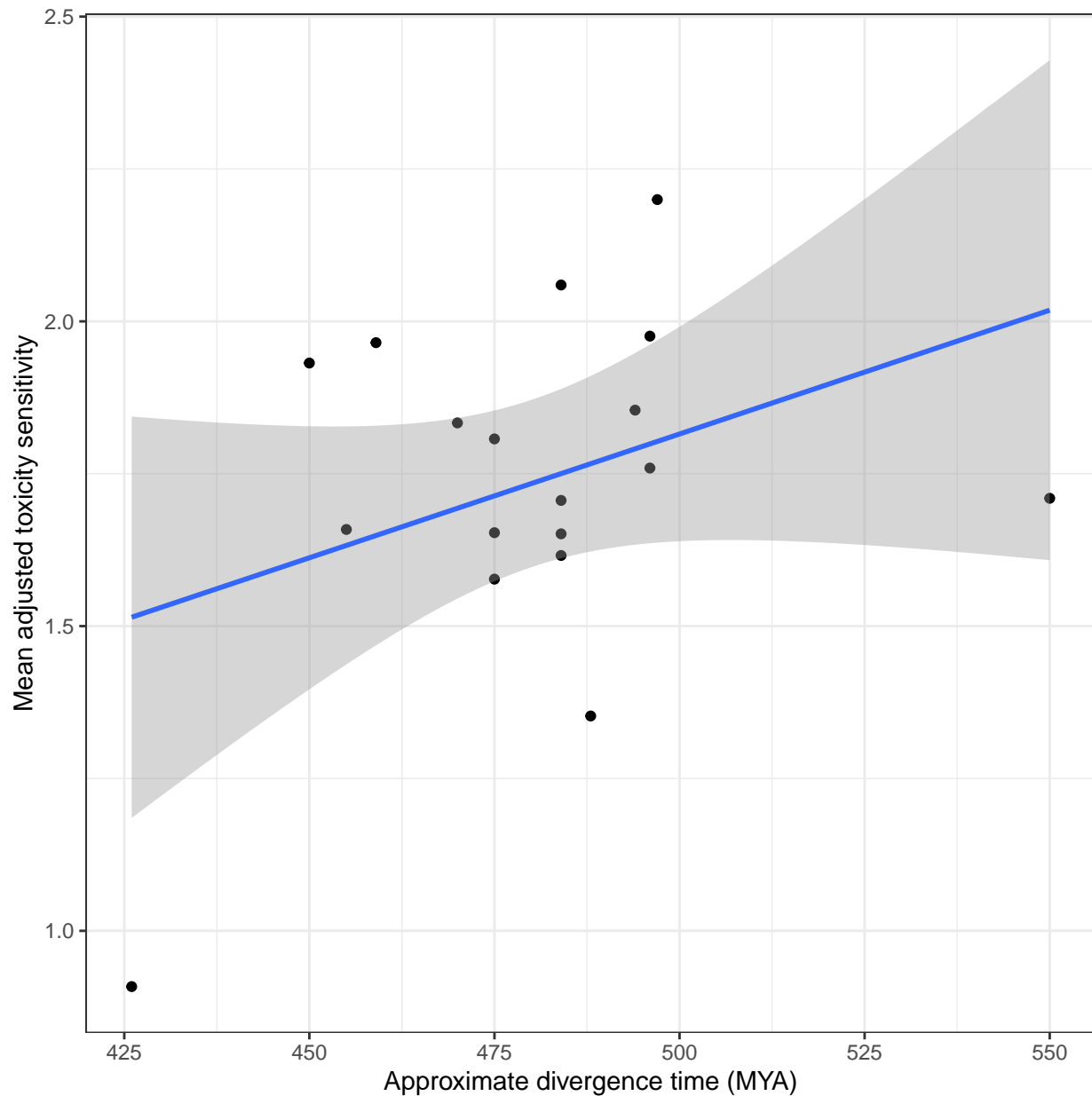
Orders Senistivity and Divergence Time

The divergence times are approximate and based on the cumulative branch lengths from the root to the most recent common ancestor (MRCA) of the species within each order, as inferred from the tree.

Methodology:

The tree was parsed to identify the nodes representing the MRCA of the species within each order. The divergence time for each order was calculated by summing the branch lengths from the root to the MRCA node of that order's species.

For some orders like *Beloniformes*, *Carangiformes*, *Synbranchiformes*, and *Tetraodontiformes*, the provided tree did include enough species to accurately determine the divergence times. The exact divergence times can vary depending on the phylogenetic methods and calibrations used in constructing the tree so we can consider this as a rough estimate.



Statistical Analysis

We are going to fit a Bayesian regression model with a log-normal family to the z-scores of LC50 concentration (`tox_conc_z`) response variable with the `brms` package. There going to be different predictor variables but each model has random effects for study (`ref_number`), species name with phylogenetic distances between species (`gr(sp, cov = A)`) and the log transformed maximum length. Both with and without phylogeny adjustment models are presented. The figures include 95% credible interval (CI), which means that given the observed data and the prior information, there is a 95% probability that the parameter lies within this interval. When comparing groups using credible intervals.

Non-overlapping intervals: If the credible intervals of two groups do not overlap, it suggests that the groups are likely different. The non-overlapping part can be interpreted as the range of values where the groups differ.

Overlapping intervals: If the credible intervals of two groups overlap, it means there is considerable

uncertainty about whether the groups are different or not. The overlapping part represents the range of values where the groups might be similar. However, it does not necessarily mean that the groups are the same. Even with some overlap, the groups could still be different. The degree of overlap and the width of the intervals should be considered when interpreting the results.

Remember, the interpretation of credible intervals is more intuitive than that of confidence intervals. While a confidence interval is a range that would contain the true parameter value in a certain percentage of repeated samples, a **credible interval is a range that contains the true parameter value with a certain probability** given the observed data.

Species Size Affecting Sensitivity

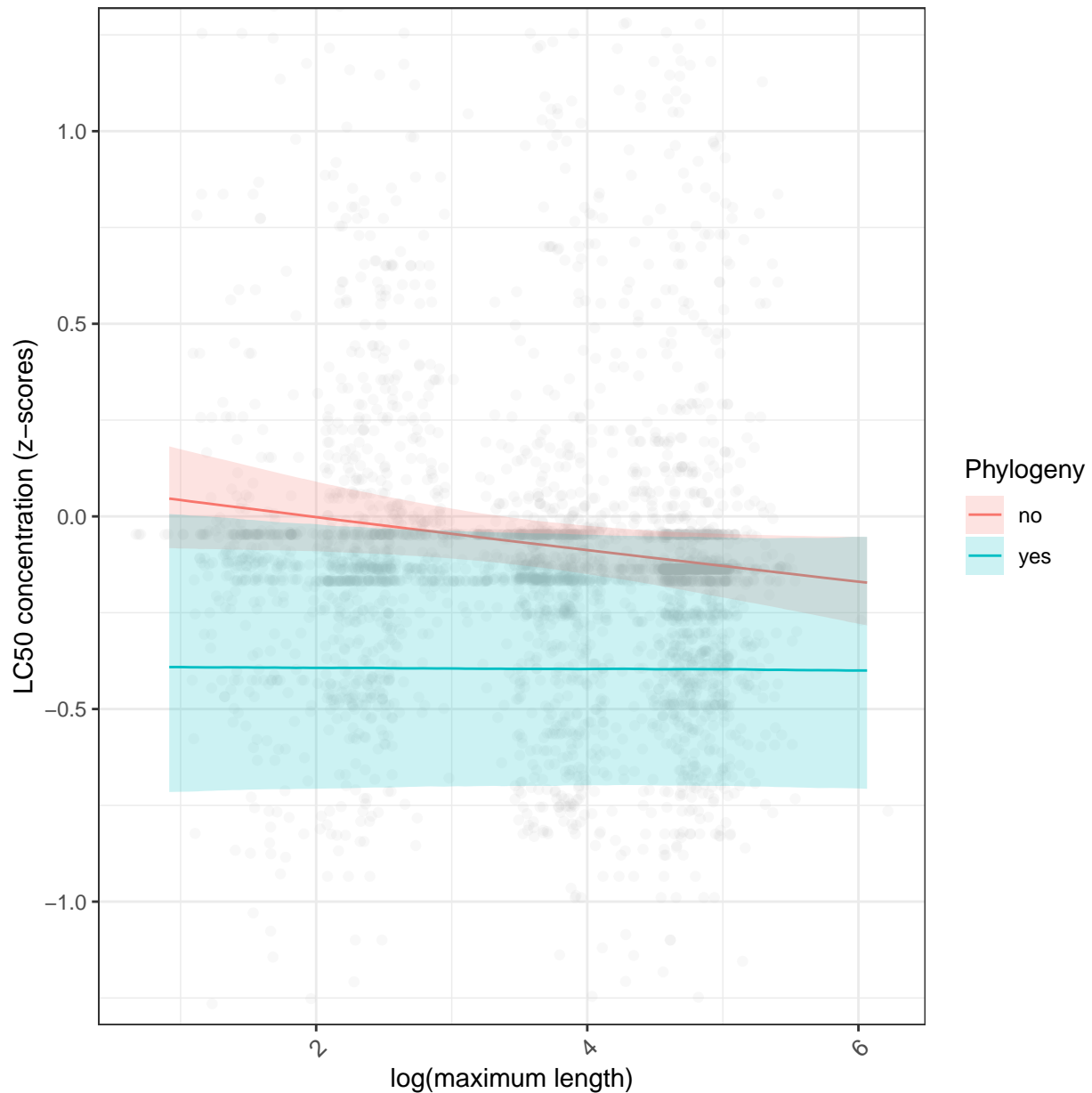


Figure S1. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is `log(maximum length)`, and random effects are included for study

(ref_number). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The shaded areas denote 95% credibility intervals (CI). The blue/red lines are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 4: Table S4 Model estimates with 95% credibitly intervals of the Bayesian regression model fitted to the data for the effect of log(maximum length). The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum lenght of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	Covariate	Estimate	Est.Error	l-95% CI	u-95% CI	Notable
yes	log_maxLength	Intercept	0.34	0.13	0.08	0.60	*
yes	log_maxLength	log_maxLength	0.00	0.01	-0.03	0.03	
no	log_maxLength	Intercept	0.63	0.05	0.54	0.72	*
no	log_maxLength	log_maxLength	-0.02	0.01	-0.05	0.00	*

With no phylogeny adjustment, the model suggests that the sensitivity to toxic substances increases with the maximum length of the species. The phylogeny adjusted model does not indicate any relationship between the maximum length and sensitivity to toxic substances (Figure S1, Table S4).

Orders Differing in Sensitivity

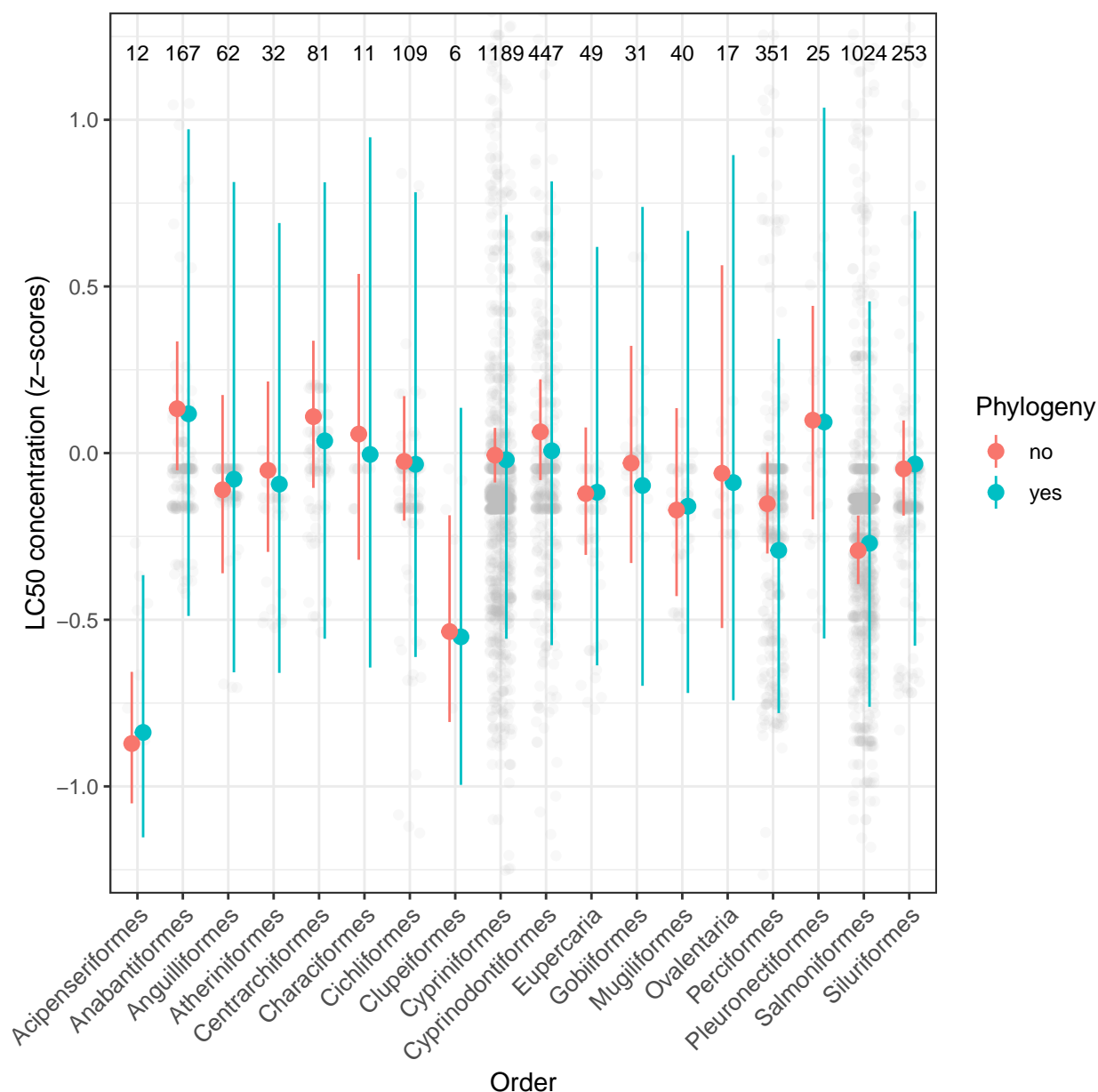


Figure S2. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is Order, and random effects are included for study (`ref_number`). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 5: Table S5 Pairwise comparisons from of the Bayesian regression models fitted to the data for the effect of Order. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum length of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	Order	Acipenseriformes	Anabantiformes	-0.673	-1.2	-0.131	*
yes	Order	Acipenseriformes	Anguilliformes	-0.562	-1.12	-0.00983	*
yes	Order	Acipenseriformes	Atheriniformes	-0.556	-1.1	-0.0104	*
yes	Order	Acipenseriformes	Centrarchiformes	-0.629	-1.13	-0.0785	*
yes	Order	Acipenseriformes	Characiformes	-0.603	-1.2	-0.0132	*
yes	Order	Acipenseriformes	Cichliformes	-0.59	-1.11	-0.0376	*
yes	Order	Acipenseriformes	Clupeiformes	-0.252	-0.797	0.307	
yes	Order	Acipenseriformes	Cypriniformes	-0.594	-1.1	-0.0706	*
yes	Order	Acipenseriformes	Cyprinodontiformes	-0.612	-1.14	-0.0553	*
yes	Order	Acipenseriformes	Eupercaria	-0.543	-1.06	-0.0187	*
yes	Order	Acipenseriformes	Gobiiformes	-0.555	-1.1	0.0242	
yes	Order	Acipenseriformes	Mugiliformes	-0.52	-1.06	0.0412	
yes	Order	Acipenseriformes	Ovalentaria	-0.56	-1.12	0.0878	
yes	Order	Acipenseriformes	Perciformes	-0.436	-0.954	0.102	
yes	Order	Acipenseriformes	Pleuronectiformes	-0.658	-1.19	-0.0805	*
yes	Order	Acipenseriformes	Salmoniformes	-0.449	-0.988	0.0895	
yes	Order	Acipenseriformes	Siluriformes	-0.589	-1.1	-0.0506	*
yes	Order	Anabantiformes	Anguilliformes	0.106	-0.372	0.539	
yes	Order	Anabantiformes	Atheriniformes	0.114	-0.157	0.384	
yes	Order	Anabantiformes	Centrarchiformes	0.0424	-0.204	0.305	
yes	Order	Anabantiformes	Characiformes	0.0625	-0.386	0.52	
yes	Order	Anabantiformes	Cichliformes	0.0808	-0.176	0.342	
yes	Order	Anabantiformes	Clupeiformes	0.42	-0.033	0.874	
yes	Order	Anabantiformes	Cypriniformes	0.0722	-0.3	0.452	
yes	Order	Anabantiformes	Cyprinodontiformes	0.0586	-0.185	0.304	
yes	Order	Anabantiformes	Eupercaria	0.129	-0.121	0.374	
yes	Order	Anabantiformes	Gobiiformes	0.116	-0.181	0.438	
yes	Order	Anabantiformes	Mugiliformes	0.152	-0.149	0.44	
yes	Order	Anabantiformes	Ovalentaria	0.111	-0.26	0.475	
yes	Order	Anabantiformes	Perciformes	0.236	-0.00174	0.493	
yes	Order	Anabantiformes	Pleuronectiformes	0.0131	-0.26	0.299	
yes	Order	Anabantiformes	Salmoniformes	0.22	-0.187	0.616	
yes	Order	Anabantiformes	Siluriformes	0.0812	-0.297	0.479	
yes	Order	Anguilliformes	Atheriniformes	0.0106	-0.469	0.491	
yes	Order	Anguilliformes	Centrarchiformes	-0.0632	-0.499	0.417	
yes	Order	Anguilliformes	Characiformes	-0.043	-0.557	0.483	
yes	Order	Anguilliformes	Cichliformes	-0.0243	-0.487	0.448	
yes	Order	Anguilliformes	Clupeiformes	0.313	-0.182	0.802	
yes	Order	Anguilliformes	Cypriniformes	-0.0336	-0.485	0.42	
yes	Order	Anguilliformes	Cyprinodontiformes	-0.0452	-0.528	0.4	

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	Order	Anguilliformes	Eupercaria	0.0224	-0.439	0.463	
yes	Order	Anguilliformes	Gobiiformes	0.0115	-0.468	0.516	
yes	Order	Anguilliformes	Mugiliformes	0.0491	-0.438	0.535	
yes	Order	Anguilliformes	Ovalentaria	0.00787	-0.532	0.549	
yes	Order	Anguilliformes	Perciformes	0.13	-0.304	0.608	
yes	Order	Anguilliformes	Pleuronectiformes	-0.0919	-0.587	0.378	
yes	Order	Anguilliformes	Salmoniformes	0.118	-0.361	0.587	
yes	Order	Anguilliformes	Siluriformes	-0.025	-0.49	0.438	
yes	Order	Atheriniformes	Centrarchiformes	-0.0714	-0.333	0.215	
yes	Order	Atheriniformes	Characiformes	-0.0519	-0.512	0.412	
yes	Order	Atheriniformes	Cichliformes	-0.0322	-0.312	0.227	
yes	Order	Atheriniformes	Clupeiformes	0.304	-0.175	0.753	
yes	Order	Atheriniformes	Cypriniformes	-0.0389	-0.444	0.351	
yes	Order	Atheriniformes	Cyprinodontiformes	-0.0548	-0.284	0.181	
yes	Order	Atheriniformes	Eupercaria	0.0145	-0.265	0.281	
yes	Order	Atheriniformes	Gobiiformes	0.00205	-0.326	0.323	
yes	Order	Atheriniformes	Mugiliformes	0.0375	-0.265	0.341	
yes	Order	Atheriniformes	Ovalentaria	-0.00335	-0.379	0.37	
yes	Order	Atheriniformes	Perciformes	0.122	-0.148	0.394	
yes	Order	Atheriniformes	Pleuronectiformes	-0.101	-0.416	0.218	
yes	Order	Atheriniformes	Salmoniformes	0.106	-0.292	0.522	
yes	Order	Atheriniformes	Siluriformes	-0.0346	-0.421	0.388	
yes	Order	Centrarchiformes	Characiformes	0.019	-0.423	0.476	
yes	Order	Centrarchiformes	Cichliformes	0.0396	-0.231	0.3	
yes	Order	Centrarchiformes	Clupeiformes	0.374	-0.0615	0.835	
yes	Order	Centrarchiformes	Cypriniformes	0.0309	-0.364	0.393	
yes	Order	Centrarchiformes	Cyprinodontiformes	0.0148	-0.253	0.257	
yes	Order	Centrarchiformes	Eupercaria	0.085	-0.127	0.293	
yes	Order	Centrarchiformes	Gobiiformes	0.0728	-0.193	0.371	
yes	Order	Centrarchiformes	Mugiliformes	0.108	-0.201	0.4	
yes	Order	Centrarchiformes	Ovalentaria	0.0668	-0.317	0.431	
yes	Order	Centrarchiformes	Perciformes	0.193	0.0438	0.333	*
yes	Order	Centrarchiformes	Pleuronectiformes	-0.0298	-0.349	0.255	
yes	Order	Centrarchiformes	Salmoniformes	0.177	-0.219	0.561	
yes	Order	Centrarchiformes	Siluriformes	0.0384	-0.355	0.41	
yes	Order	Characiformes	Cichliformes	0.0191	-0.446	0.481	
yes	Order	Characiformes	Clupeiformes	0.354	-0.114	0.855	
yes	Order	Characiformes	Cypriniformes	0.00901	-0.345	0.352	
yes	Order	Characiformes	Cyprinodontiformes	-0.00382	-0.456	0.443	
yes	Order	Characiformes	Eupercaria	0.0656	-0.375	0.513	
yes	Order	Characiformes	Gobiiformes	0.0518	-0.404	0.551	
yes	Order	Characiformes	Mugiliformes	0.0889	-0.393	0.579	
yes	Order	Characiformes	Ovalentaria	0.0496	-0.474	0.576	
yes	Order	Characiformes	Perciformes	0.174	-0.255	0.634	
yes	Order	Characiformes	Pleuronectiformes	-0.0495	-0.535	0.439	
yes	Order	Characiformes	Salmoniformes	0.158	-0.33	0.608	
yes	Order	Characiformes	Siluriformes	0.0171	-0.31	0.353	
yes	Order	Cichliformes	Clupeiformes	0.337	-0.135	0.779	
yes	Order	Cichliformes	Cypriniformes	-0.00799	-0.411	0.385	
yes	Order	Cichliformes	Cyprinodontiformes	-0.0221	-0.262	0.218	
yes	Order	Cichliformes	Eupercaria	0.0471	-0.225	0.303	

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	Order	Cichliformes	Gobiiformes	0.0348	-0.281	0.359	
yes	Order	Cichliformes	Mugiliformes	0.072	-0.211	0.362	
yes	Order	Cichliformes	Ovalentaria	0.0303	-0.322	0.394	
yes	Order	Cichliformes	Perciformes	0.155	-0.111	0.417	
yes	Order	Cichliformes	Pleuronectiformes	-0.0694	-0.383	0.231	
yes	Order	Cichliformes	Salmoniformes	0.136	-0.275	0.526	
yes	Order	Cichliformes	Siluriformes	-0.00416	-0.373	0.414	
yes	Order	Clupeiformes	Cypriniformes	-0.346	-0.757	0.0751	
yes	Order	Clupeiformes	Cyprinodontiformes	-0.361	-0.815	0.0881	
yes	Order	Clupeiformes	Eupercaria	-0.29	-0.72	0.158	
yes	Order	Clupeiformes	Gobiiformes	-0.306	-0.758	0.193	
yes	Order	Clupeiformes	Mugiliformes	-0.267	-0.748	0.193	
yes	Order	Clupeiformes	Ovalentaria	-0.31	-0.821	0.228	
yes	Order	Clupeiformes	Perciformes	-0.18	-0.634	0.27	
yes	Order	Clupeiformes	Pleuronectiformes	-0.404	-0.908	0.0385	
yes	Order	Clupeiformes	Salmoniformes	-0.197	-0.668	0.267	
yes	Order	Clupeiformes	Siluriformes	-0.337	-0.787	0.078	
yes	Order	Cypriniformes	Cyprinodontiformes	-0.0136	-0.4	0.364	
yes	Order	Cypriniformes	Eupercaria	0.0569	-0.319	0.429	
yes	Order	Cypriniformes	Gobiiformes	0.0411	-0.373	0.459	
yes	Order	Cypriniformes	Mugiliformes	0.0796	-0.33	0.498	
yes	Order	Cypriniformes	Ovalentaria	0.0374	-0.436	0.503	
yes	Order	Cypriniformes	Perciformes	0.163	-0.195	0.562	
yes	Order	Cypriniformes	Pleuronectiformes	-0.0576	-0.487	0.346	
yes	Order	Cypriniformes	Salmoniformes	0.148	-0.245	0.534	
yes	Order	Cypriniformes	Siluriformes	0.0052	-0.257	0.267	
yes	Order	Cyprinodontiformes	Eupercaria	0.0679	-0.181	0.317	
yes	Order	Cyprinodontiformes	Gobiiformes	0.0564	-0.241	0.366	
yes	Order	Cyprinodontiformes	Mugiliformes	0.094	-0.177	0.38	
yes	Order	Cyprinodontiformes	Ovalentaria	0.0515	-0.286	0.417	
yes	Order	Cyprinodontiformes	Perciformes	0.178	-0.0708	0.417	
yes	Order	Cyprinodontiformes	Pleuronectiformes	-0.0466	-0.343	0.246	
yes	Order	Cyprinodontiformes	Salmoniformes	0.162	-0.24	0.555	
yes	Order	Cyprinodontiformes	Siluriformes	0.0221	-0.381	0.412	
yes	Order	Eupercaria	Gobiiformes	-0.0126	-0.303	0.298	
yes	Order	Eupercaria	Mugiliformes	0.0238	-0.263	0.313	
yes	Order	Eupercaria	Ovalentaria	-0.0172	-0.391	0.349	
yes	Order	Eupercaria	Perciformes	0.109	-0.0983	0.315	
yes	Order	Eupercaria	Pleuronectiformes	-0.114	-0.404	0.18	
yes	Order	Eupercaria	Salmoniformes	0.0923	-0.304	0.463	
yes	Order	Eupercaria	Siluriformes	-0.049	-0.424	0.329	
yes	Order	Gobiiformes	Mugiliformes	0.0355	-0.329	0.374	
yes	Order	Gobiiformes	Ovalentaria	-0.006	-0.427	0.39	
yes	Order	Gobiiformes	Perciformes	0.121	-0.172	0.41	
yes	Order	Gobiiformes	Pleuronectiformes	-0.103	-0.456	0.25	
yes	Order	Gobiiformes	Salmoniformes	0.108	-0.329	0.53	
yes	Order	Gobiiformes	Siluriformes	-0.0334	-0.482	0.373	
yes	Order	Mugiliformes	Ovalentaria	-0.0408	-0.443	0.333	
yes	Order	Mugiliformes	Perciformes	0.0842	-0.208	0.387	
yes	Order	Mugiliformes	Pleuronectiformes	-0.139	-0.452	0.181	
yes	Order	Mugiliformes	Salmoniformes	0.0659	-0.367	0.478	

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	Order	Mugiliformes	Siluriformes	-0.0719	-0.485	0.356	
yes	Order	Ovalentaria	Perciformes	0.127	-0.246	0.493	
yes	Order	Ovalentaria	Pleuronectiformes	-0.0967	-0.499	0.298	
yes	Order	Ovalentaria	Salmoniformes	0.11	-0.374	0.591	
yes	Order	Ovalentaria	Siluriformes	-0.031	-0.491	0.456	
yes	Order	Perciformes	Pleuronectiformes	-0.224	-0.537	0.0626	
yes	Order	Perciformes	Salmoniformes	-0.0137	-0.415	0.366	
yes	Order	Perciformes	Siluriformes	-0.157	-0.546	0.224	
yes	Order	Pleuronectiformes	Salmoniformes	0.204	-0.239	0.607	
yes	Order	Pleuronectiformes	Siluriformes	0.0679	-0.354	0.488	
yes	Order	Salmoniformes	Siluriformes	-0.141	-0.533	0.279	
no	Order	Acipenseriformes	Anabantiformes	-0.713	-0.943	-0.492	*
no	Order	Acipenseriformes	Anguilliformes	-0.58	-0.832	-0.344	*
no	Order	Acipenseriformes	Atheriniformes	-0.611	-0.866	-0.364	*
no	Order	Acipenseriformes	Centrarchiformes	-0.7	-0.922	-0.475	*
no	Order	Acipenseriformes	Characiformes	-0.673	-0.982	-0.372	*
no	Order	Acipenseriformes	Cichliformes	-0.63	-0.863	-0.411	*
no	Order	Acipenseriformes	Clupeiformes	-0.301	-0.575	-0.0122	*
no	Order	Acipenseriformes	Cypriniformes	-0.639	-0.85	-0.443	*
no	Order	Acipenseriformes	Cyprinodontiformes	-0.677	-0.904	-0.46	*
no	Order	Acipenseriformes	Eupercaria	-0.575	-0.795	-0.35	*
no	Order	Acipenseriformes	Gobiiformes	-0.625	-0.893	-0.348	*
no	Order	Acipenseriformes	Mugiliformes	-0.544	-0.81	-0.298	*
no	Order	Acipenseriformes	Ovalentaria	-0.612	-0.981	-0.236	*
no	Order	Acipenseriformes	Perciformes	-0.555	-0.775	-0.348	*
no	Order	Acipenseriformes	Pleuronectiformes	-0.695	-0.947	-0.44	*
no	Order	Acipenseriformes	Salmoniformes	-0.47	-0.672	-0.263	*
no	Order	Acipenseriformes	Siluriformes	-0.616	-0.838	-0.406	*
no	Order	Anabantiformes	Anguilliformes	0.132	-0.0512	0.31	
no	Order	Anabantiformes	Atheriniformes	0.0976	-0.0653	0.273	
no	Order	Anabantiformes	Centrarchiformes	0.0115	-0.134	0.164	
no	Order	Anabantiformes	Characiformes	0.039	-0.212	0.267	
no	Order	Anabantiformes	Cichliformes	0.0846	-0.0573	0.227	
no	Order	Anabantiformes	Clupeiformes	0.415	0.171	0.681	*
no	Order	Anabantiformes	Cypriniformes	0.0731	-0.0286	0.176	
no	Order	Anabantiformes	Cyprinodontiformes	0.0359	-0.0847	0.153	
no	Order	Anabantiformes	Eupercaria	0.138	-0.0118	0.281	
no	Order	Anabantiformes	Gobiiformes	0.0856	-0.119	0.285	
no	Order	Anabantiformes	Mugiliformes	0.168	-0.028	0.361	
no	Order	Anabantiformes	Ovalentaria	0.103	-0.213	0.422	
no	Order	Anabantiformes	Perciformes	0.156	0.0323	0.291	*
no	Order	Anabantiformes	Pleuronectiformes	0.0181	-0.169	0.215	
no	Order	Anabantiformes	Salmoniformes	0.243	0.124	0.36	*
no	Order	Anabantiformes	Siluriformes	0.0955	-0.0246	0.213	
no	Order	Anguilliformes	Atheriniformes	-0.0327	-0.235	0.181	
no	Order	Anguilliformes	Centrarchiformes	-0.12	-0.302	0.0662	
no	Order	Anguilliformes	Characiformes	-0.0924	-0.377	0.18	
no	Order	Anguilliformes	Cichliformes	-0.0489	-0.229	0.132	
no	Order	Anguilliformes	Clupeiformes	0.28	0.00286	0.556	*
no	Order	Anguilliformes	Cypriniformes	-0.0583	-0.216	0.101	
no	Order	Anguilliformes	Cyprinodontiformes	-0.0972	-0.276	0.0717	

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
no	Order	Anguilliformes	Eupercaria	0.0051	-0.165	0.181	
no	Order	Anguilliformes	Gobiiformes	-0.0458	-0.288	0.184	
no	Order	Anguilliformes	Mugiliformes	0.0359	-0.184	0.259	
no	Order	Anguilliformes	Ovalentaria	-0.0297	-0.366	0.32	
no	Order	Anguilliformes	Perciformes	0.0236	-0.149	0.197	
no	Order	Anguilliformes	Pleuronectiformes	-0.113	-0.338	0.104	
no	Order	Anguilliformes	Salmoniformes	0.112	-0.0552	0.264	
no	Order	Anguilliformes	Siluriformes	-0.0358	-0.211	0.129	
no	Order	Atheriniformes	Centrarchiformes	-0.0871	-0.256	0.0883	
no	Order	Atheriniformes	Characiformes	-0.0582	-0.313	0.198	
no	Order	Atheriniformes	Cichliformes	-0.0153	-0.193	0.158	
no	Order	Atheriniformes	Clupeiformes	0.314	0.0431	0.576	*
no	Order	Atheriniformes	Cypriniformes	-0.0255	-0.172	0.119	
no	Order	Atheriniformes	Cyprinodontiformes	-0.063	-0.214	0.0808	
no	Order	Atheriniformes	Eupercaria	0.0384	-0.132	0.216	
no	Order	Atheriniformes	Gobiiformes	-0.0132	-0.234	0.204	
no	Order	Atheriniformes	Mugiliformes	0.069	-0.15	0.284	
no	Order	Atheriniformes	Ovalentaria	0.000728	-0.318	0.358	
no	Order	Atheriniformes	Perciformes	0.0574	-0.104	0.22	
no	Order	Atheriniformes	Pleuronectiformes	-0.0816	-0.288	0.127	
no	Order	Atheriniformes	Salmoniformes	0.145	-0.0118	0.306	
no	Order	Atheriniformes	Siluriformes	-0.00268	-0.162	0.163	
no	Order	Centrarchiformes	Characiformes	0.0278	-0.241	0.265	
no	Order	Centrarchiformes	Cichliformes	0.0712	-0.0798	0.222	
no	Order	Centrarchiformes	Clupeiformes	0.4	0.143	0.648	*
no	Order	Centrarchiformes	Cypriniformes	0.0607	-0.0586	0.177	
no	Order	Centrarchiformes	Cyprinodontiformes	0.0242	-0.118	0.156	
no	Order	Centrarchiformes	Eupercaria	0.124	-0.0274	0.275	
no	Order	Centrarchiformes	Gobiiformes	0.0734	-0.104	0.257	
no	Order	Centrarchiformes	Mugiliformes	0.155	-0.0526	0.348	
no	Order	Centrarchiformes	Ovalentaria	0.0879	-0.243	0.414	
no	Order	Centrarchiformes	Perciformes	0.144	0.00499	0.279	*
no	Order	Centrarchiformes	Pleuronectiformes	0.00483	-0.192	0.197	
no	Order	Centrarchiformes	Salmoniformes	0.231	0.104	0.352	*
no	Order	Centrarchiformes	Siluriformes	0.0846	-0.0533	0.215	
no	Order	Characiformes	Cichliformes	0.0447	-0.203	0.288	
no	Order	Characiformes	Clupeiformes	0.373	0.0592	0.694	*
no	Order	Characiformes	Cypriniformes	0.0347	-0.189	0.256	
no	Order	Characiformes	Cyprinodontiformes	-0.0041	-0.222	0.217	
no	Order	Characiformes	Eupercaria	0.099	-0.146	0.358	
no	Order	Characiformes	Gobiiformes	0.0478	-0.228	0.334	
no	Order	Characiformes	Mugiliformes	0.129	-0.157	0.415	
no	Order	Characiformes	Ovalentaria	0.0651	-0.308	0.435	
no	Order	Characiformes	Perciformes	0.117	-0.112	0.357	
no	Order	Characiformes	Pleuronectiformes	-0.0223	-0.301	0.252	
no	Order	Characiformes	Salmoniformes	0.204	-0.0187	0.457	
no	Order	Characiformes	Siluriformes	0.0566	-0.169	0.308	
no	Order	Cichliformes	Clupeiformes	0.33	0.0824	0.589	*
no	Order	Cichliformes	Cypriniformes	-0.00937	-0.117	0.101	
no	Order	Cichliformes	Cyprinodontiformes	-0.0475	-0.174	0.0806	
no	Order	Cichliformes	Eupercaria	0.0551	-0.092	0.202	

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
no	Order	Cichliformes	Gobiiformes	0.00244	-0.206	0.202	
no	Order	Cichliformes	Mugiliformes	0.0838	-0.111	0.283	
no	Order	Cichliformes	Ovalentaria	0.018	-0.296	0.335	
no	Order	Cichliformes	Perciformes	0.0732	-0.0587	0.21	
no	Order	Cichliformes	Pleuronectiformes	-0.0653	-0.248	0.141	
no	Order	Cichliformes	Salmoniformes	0.16	0.0407	0.278	*
no	Order	Cichliformes	Siluriformes	0.0127	-0.113	0.14	
no	Order	Clupeiformes	Cypriniformes	-0.34	-0.584	-0.108	*
no	Order	Clupeiformes	Cyprinodontiformes	-0.378	-0.625	-0.133	*
no	Order	Clupeiformes	Eupercaria	-0.275	-0.529	-0.0178	*
no	Order	Clupeiformes	Gobiiformes	-0.328	-0.62	-0.0387	*
no	Order	Clupeiformes	Mugiliformes	-0.246	-0.53	0.0388	
no	Order	Clupeiformes	Ovalentaria	-0.311	-0.677	0.0835	
no	Order	Clupeiformes	Perciformes	-0.257	-0.502	-0.0103	*
no	Order	Clupeiformes	Pleuronectiformes	-0.395	-0.674	-0.106	*
no	Order	Clupeiformes	Salmoniformes	-0.172	-0.417	0.0656	
no	Order	Clupeiformes	Siluriformes	-0.318	-0.566	-0.0714	*
no	Order	Cypriniformes	Cyprinodontiformes	-0.0378	-0.117	0.0524	
no	Order	Cypriniformes	Eupercaria	0.0645	-0.049	0.182	
no	Order	Cypriniformes	Gobiiformes	0.0127	-0.168	0.194	
no	Order	Cypriniformes	Mugiliformes	0.0947	-0.0759	0.27	
no	Order	Cypriniformes	Ovalentaria	0.0294	-0.27	0.343	
no	Order	Cypriniformes	Perciformes	0.0827	-0.00907	0.179	
no	Order	Cypriniformes	Pleuronectiformes	-0.0557	-0.224	0.114	
no	Order	Cypriniformes	Salmoniformes	0.17	0.0966	0.24	*
no	Order	Cypriniformes	Siluriformes	0.0228	-0.0659	0.106	
no	Order	Cyprinodontiformes	Eupercaria	0.102	-0.0267	0.236	
no	Order	Cyprinodontiformes	Gobiiformes	0.0497	-0.135	0.242	
no	Order	Cyprinodontiformes	Mugiliformes	0.132	-0.06	0.317	
no	Order	Cyprinodontiformes	Ovalentaria	0.0659	-0.251	0.371	
no	Order	Cyprinodontiformes	Perciformes	0.121	0.0139	0.229	*
no	Order	Cyprinodontiformes	Pleuronectiformes	-0.0183	-0.203	0.167	
no	Order	Cyprinodontiformes	Salmoniformes	0.208	0.098	0.32	*
no	Order	Cyprinodontiformes	Siluriformes	0.0595	-0.0524	0.174	
no	Order	Eupercaria	Gobiiformes	-0.0523	-0.252	0.158	
no	Order	Eupercaria	Mugiliformes	0.0298	-0.17	0.209	
no	Order	Eupercaria	Ovalentaria	-0.034	-0.36	0.285	
no	Order	Eupercaria	Perciformes	0.0182	-0.114	0.157	
no	Order	Eupercaria	Pleuronectiformes	-0.121	-0.306	0.0708	
no	Order	Eupercaria	Salmoniformes	0.105	-0.0133	0.232	
no	Order	Eupercaria	Siluriformes	-0.042	-0.175	0.0847	
no	Order	Gobiiformes	Mugiliformes	0.0827	-0.163	0.332	
no	Order	Gobiiformes	Ovalentaria	0.0149	-0.329	0.367	
no	Order	Gobiiformes	Perciformes	0.0708	-0.125	0.266	
no	Order	Gobiiformes	Pleuronectiformes	-0.0685	-0.316	0.167	
no	Order	Gobiiformes	Salmoniformes	0.157	-0.0269	0.356	
no	Order	Gobiiformes	Siluriformes	0.0104	-0.189	0.201	
no	Order	Mugiliformes	Ovalentaria	-0.0655	-0.421	0.275	
no	Order	Mugiliformes	Perciformes	-0.0105	-0.211	0.174	
no	Order	Mugiliformes	Pleuronectiformes	-0.15	-0.365	0.0495	
no	Order	Mugiliformes	Salmoniformes	0.0749	-0.104	0.25	

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
no	Order	Mugiliformes	Siluriformes	-0.0716	-0.263	0.106	
no	Order	Ovalentaria	Perciformes	0.0548	-0.267	0.366	
no	Order	Ovalentaria	Pleuronectiformes	-0.0844	-0.414	0.271	
no	Order	Ovalentaria	Salmoniformes	0.14	-0.17	0.452	
no	Order	Ovalentaria	Siluriformes	-0.00567	-0.307	0.32	
no	Order	Perciformes	Pleuronectiformes	-0.139	-0.323	0.0474	
no	Order	Perciformes	Salmoniformes	0.0873	-0.0176	0.193	
no	Order	Perciformes	Siluriformes	-0.0602	-0.174	0.054	
no	Order	Pleuronectiformes	Salmoniformes	0.226	0.0461	0.395	*
no	Order	Pleuronectiformes	Siluriformes	0.0801	-0.109	0.251	
no	Order	Salmoniformes	Siluriformes	-0.147	-0.243	-0.0507	*

The more stringent phylogeny adjusted model does not indicate clear differences between the orders as the CIs overlap considerably. The model without phylogeny adjustment suggests that *Acipenseriformes* are more sensitive to toxic substances than most other orders (Figure S2, Table S5).

Air-Breathing and Non-Air-Breathing Species Differing in Sensitivity

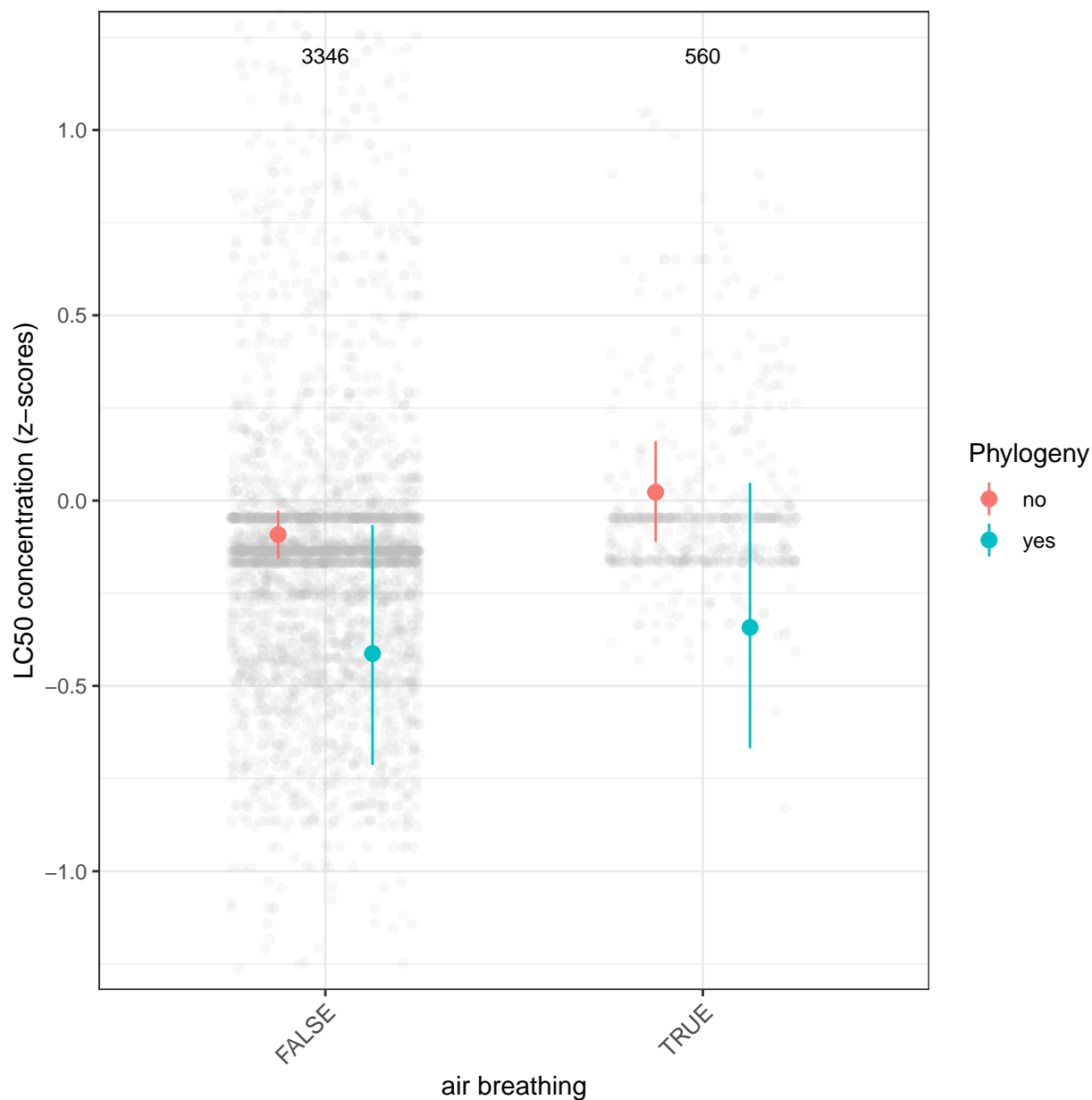


Figure S3. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is air breathing, and random effects are included for study (`ref_number`). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 6: Table S6 Pairwise comparisons from of the Bayesian regression models fitted to the data for the effect of air breathing. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum length of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	airBreathing	FALSE	TRUE	-0.0495	-0.139	0.0491	
no	airBreathing	FALSE	TRUE	-0.063	-0.14	0.0158	

Air breathing species appear not to be more sensitive to toxic substances than non-airbreathing species (Figure S3, Table S6).

Habitats Differing in Sensitivity

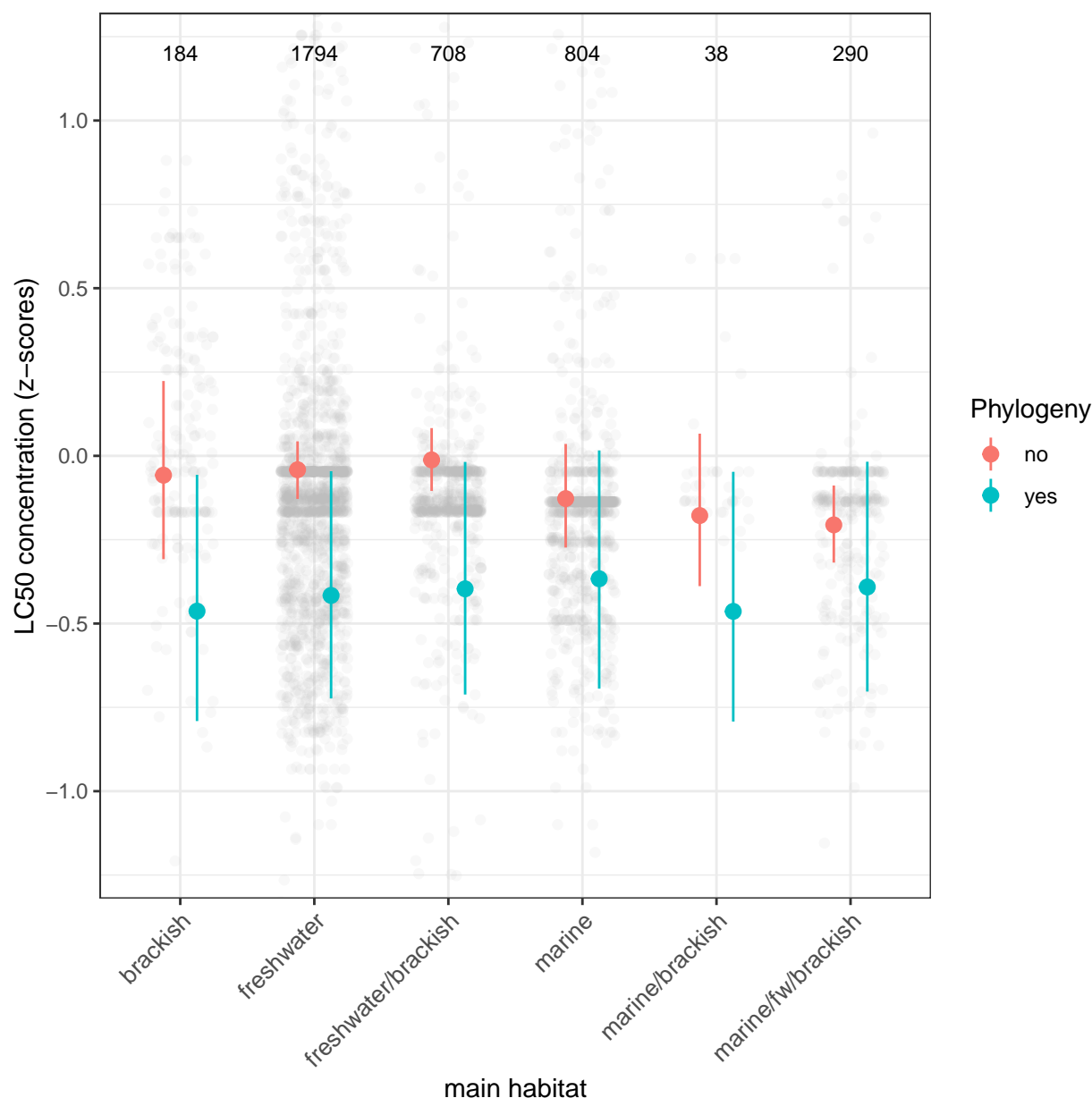


Figure S4. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is main habitat, and random effects are included for study (`ref_number`). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 7: Table S7 Pairwise comparisons from of the Bayesian regression models fitted to the data for the effect of main habitat. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum length of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	Main_habitat	brackish	freshwater	-0.034	-0.156	0.0998	
yes	Main_habitat	brackish	(freshwater/brackish)	-0.0468	-0.176	0.0913	
yes	Main_habitat	brackish	marine	-0.066	-0.215	0.0848	
yes	Main_habitat	brackish	(marine/brackish)	0.00173	-0.177	0.173	
yes	Main_habitat	brackish	(marine/fw/brackish)	0.0501	-0.194	0.0946	
yes	Main_habitat	freshwater	(freshwater/brackish)	-0.0127	-0.0746	0.0421	
yes	Main_habitat	freshwater	marine	-0.0318	-0.125	0.0569	
yes	Main_habitat	freshwater	(marine/brackish)	0.0352	-0.107	0.183	
yes	Main_habitat	freshwater	(marine/fw/brackish)	0.0162	-0.0989	0.067	
yes	Main_habitat	(freshwater/brackish)	marine	-0.0187	-0.118	0.082	
yes	Main_habitat	(freshwater/brackish)	(marine/brackish)	0.0479	-0.108	0.192	
yes	Main_habitat	(freshwater/brackish)	(marine/fw/brackish)	-	-0.0935	0.0906	
				0.00295			
yes	Main_habitat	marine	(marine/brackish)	0.0669	-0.0879	0.22	
yes	Main_habitat	marine	(marine/fw/brackish)	0.0159	-0.0645	0.102	
yes	Main_habitat	(marine/brackish)	(marine/fw/brackish)	0.0505	-0.19	0.101	
no	Main_habitat	brackish	freshwater	-	-0.155	0.149	
				0.00923			
no	Main_habitat	brackish	(freshwater/brackish)	-0.0256	-0.184	0.13	
no	Main_habitat	brackish	marine	0.04	-0.134	0.212	
no	Main_habitat	brackish	(marine/brackish)	0.0707	-0.123	0.252	
no	Main_habitat	brackish	(marine/fw/brackish)	0.0862	-0.0767	0.25	
no	Main_habitat	freshwater	(freshwater/brackish)	-0.0162	-0.0793	0.0465	
no	Main_habitat	freshwater	marine	0.0486	-0.0496	0.147	
no	Main_habitat	freshwater	(marine/brackish)	0.0787	-0.0655	0.214	
no	Main_habitat	freshwater	(marine/fw/brackish)	0.0952	0.0101	0.173	*
no	Main_habitat	(freshwater/brackish)	marine	0.0652	-0.0382	0.162	
no	Main_habitat	(freshwater/brackish)	(marine/brackish)	0.0947	-0.0479	0.241	
no	Main_habitat	(freshwater/brackish)	(marine/fw/brackish)	0.111	0.031	0.196	*
no	Main_habitat	marine	(marine/brackish)	0.0301	-0.123	0.193	
no	Main_habitat	marine	(marine/fw/brackish)	0.0461	-0.0545	0.15	
no	Main_habitat	(marine/brackish)	(marine/fw/brackish)	0.0167	-0.125	0.174	

While the phylogeny adjusted model suggest no clear differences between the main habitats, the model without phylogeny adjustment suggests that species living in freshwater are more less sensitive to toxic substances than those capable of living in different salinities (Figure S4, Table S7). Let's examine the sensitivity of species living in different salinities by combining some of the habitat types.

Water Salinities Differing in Sensitivity

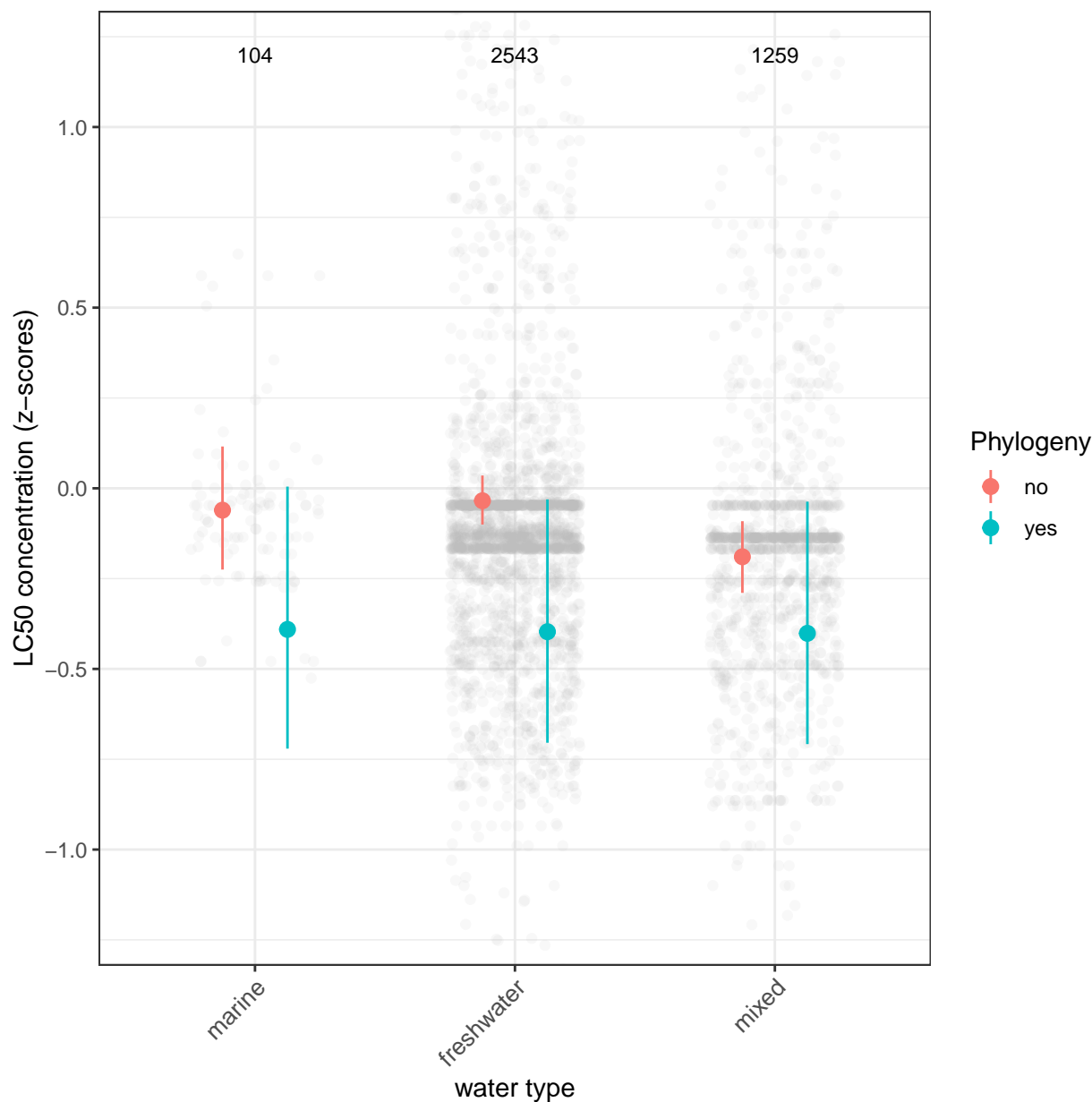


Figure S5. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is water type, and random effects are included for study (`ref_number`). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 8: Table S8 Pairwise comparisons from of the Bayesian regression models fitted to the data for the effect of water type. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum length of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	marineFreshMix	marine	freshwater	0.00298	-0.112	0.115	
yes	marineFreshMix	marine	mixed	0.00648	-0.108	0.119	
yes	marineFreshMix	freshwater	mixed	0.00323	-0.0651	0.0735	
no	marineFreshMix	marine	freshwater	-0.0158	-0.115	0.0815	
no	marineFreshMix	marine	mixed	0.0753	-0.0291	0.179	
no	marineFreshMix	freshwater	mixed	0.0908	0.0267	0.156	*

The same pattern is observed when comparing species living in different salinities. The phylogeny adjusted model suggests no clear differences between the species living in different salinities, while the model without phylogeny adjustment suggests that species living in freshwater are less sensitive to toxic substances than those living in mixed environments (Figure S5, Table S8).

Feeding Types Differing in Sensitivity

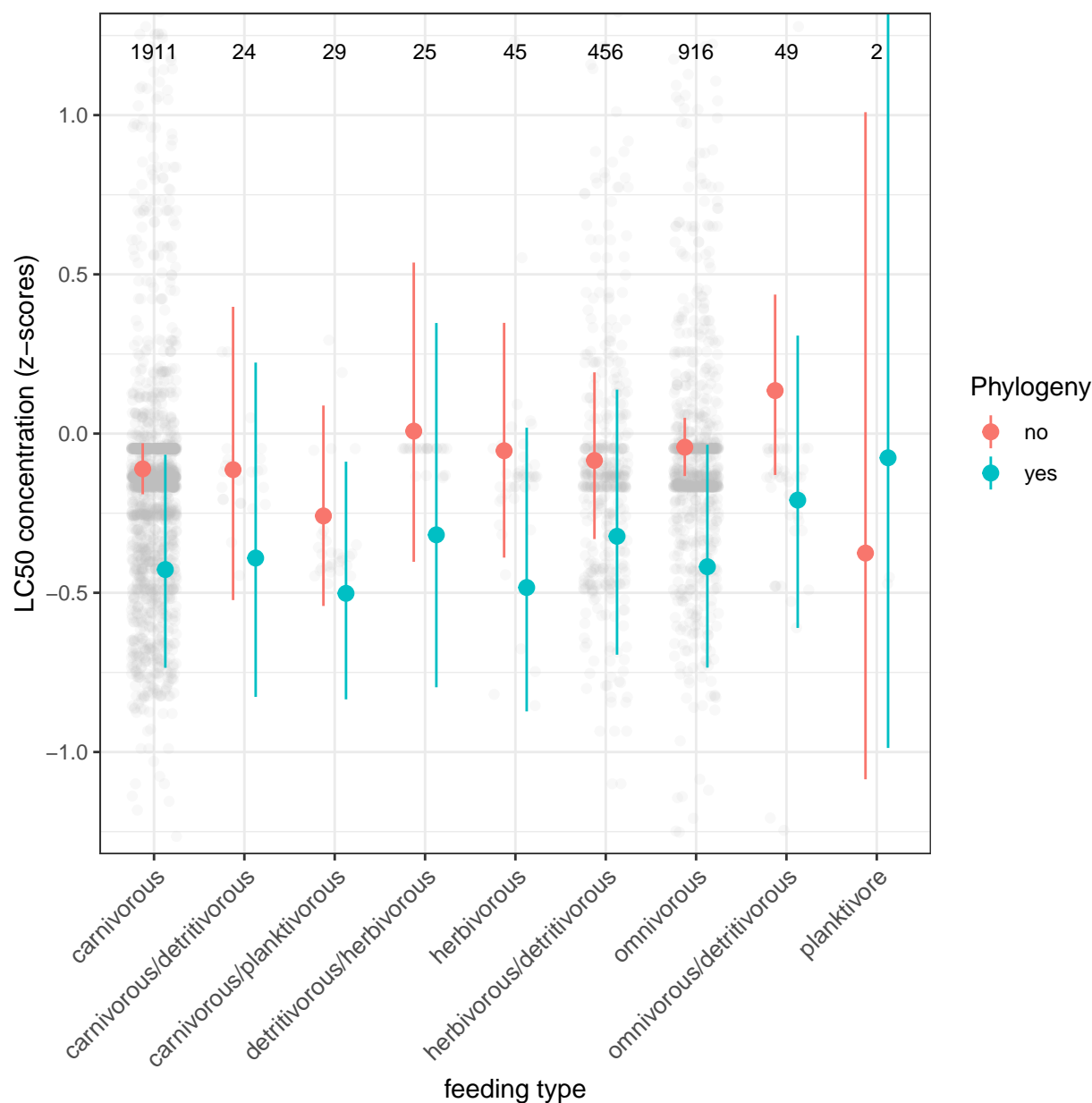


Figure S6. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is feeding type, and random effects are included for study (`ref_number`). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 9: Table S9 Pairwise comparisons from of the Bayesian regression models fitted to the data for the effect of feeding type. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum length of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	Feeding	carnivorous	(carnivorous/detritivorous)	-0.0286	-0.313	0.247	
yes	Feeding	carnivorous	(carnivorous/planktivore)	-0.0554	-0.0839	0.194	
yes	Feeding	carnivorous	(detritivorous/herbivorous)	-0.0731	-0.361	0.222	
yes	Feeding	carnivorous	herbivorous	0.04	-0.161	0.27	
yes	Feeding	carnivorous	(herbivorous/detritivorous)	-0.0716	-0.222	0.0725	
yes	Feeding	carnivorous	omnivorous	-	-0.0771	0.0621	
				0.00662			
yes	Feeding	carnivorous	(omnivorous/detritivorous)	-0.144	-0.303	0.00206	
yes	Feeding	carnivorous	planktivore	-0.222	-0.93	0.511	
yes	Feeding	(carnivorous/detritivorous)	(carnivorous/planktivore)	-0.0836	-0.228	0.413	
yes	Feeding	(carnivorous/detritivorous)	(detritivorous/herbivorous)	-0.049	-0.452	0.343	
yes	Feeding	(carnivorous/detritivorous)	herbivorous	0.0666	-0.268	0.44	
yes	Feeding	(carnivorous/detritivorous)	(herbivorous/detritivorous)	-0.045	-0.342	0.25	
yes	Feeding	(carnivorous/detritivorous)	omnivorous	0.0222	-0.255	0.31	
yes	Feeding	(carnivorous/detritivorous)	(omnivorous/detritivorous)	-0.116	-0.433	0.188	
yes	Feeding	(carnivorous/detritivorous)	planktivore	-0.194	-0.972	0.566	
yes	Feeding	(carnivorous/planktivore)	(detritivorous/herbivorous)	-0.128	-0.438	0.206	
yes	Feeding	(carnivorous/planktivore)	herbivorous	-0.0138	-0.273	0.232	
yes	Feeding	(carnivorous/planktivore)	(herbivorous/detritivorous)	-0.127	-0.335	0.0689	
yes	Feeding	(carnivorous/planktivore)	omnivorous	-0.0624	-0.213	0.0942	
yes	Feeding	(carnivorous/planktivore)	(omnivorous/detritivorous)	0.2	-0.409	0.0018	
yes	Feeding	(carnivorous/planktivore)	planktivore	-0.279	-1.02	0.446	
yes	Feeding	(detritivorous/herbivorous)	herbivorous	0.115	-0.235	0.453	
yes	Feeding	(detritivorous/herbivorous)	(herbivorous/detritivorous)	-0.021	-0.312	0.323	
yes	Feeding	(detritivorous/herbivorous)	omnivorous	0.0667	-0.225	0.353	
yes	Feeding	(detritivorous/herbivorous)	(omnivorous/detritivorous)	-0.0721	-0.38	0.251	
yes	Feeding	(detritivorous/herbivorous)	planktivore	-0.147	-0.906	0.632	
yes	Feeding	herbivorous	(herbivorous/detritivorous)	-0.112	-0.368	0.136	
yes	Feeding	herbivorous	omnivorous	-0.0474	-0.253	0.164	
yes	Feeding	herbivorous	(omnivorous/detritivorous)	-0.187	-0.42	0.0689	
yes	Feeding	herbivorous	planktivore	-0.262	-1.02	0.475	
yes	Feeding	(herbivorous/detritivorous)	omnivorous	0.065	-0.0806	0.219	
yes	Feeding	(herbivorous/detritivorous)	(omnivorous/detritivorous)	-0.0717	-0.268	0.138	
yes	Feeding	(herbivorous/detritivorous)	planktivore	-0.149	-0.874	0.603	
yes	Feeding	omnivorous	(omnivorous/detritivorous)	-0.139	-0.281	0.00146	
yes	Feeding	omnivorous	planktivore	-0.216	-0.943	0.504	
yes	Feeding	(omnivorous/detritivorous)	planktivore	-0.0776	-0.799	0.673	
no	Feeding	carnivorous	(carnivorous/detritivorous)	-0.0263	-0.272	0.267	
no	Feeding	carnivorous	(carnivorous/planktivore)	-0.0894	-0.111	0.286	
no	Feeding	carnivorous	(detritivorous/herbivorous)	-0.0653	-0.312	0.194	

Phylogeny Predictor		group1	group2	estimate	l-95% CI	u-95% CI	Notable
no	Feeding	carnivorous	herbivorous	-0.0325	-0.239	0.175	
no	Feeding	carnivorous	(herbivorous/detritivorous)	-0.0153	-0.17	0.132	
no	Feeding	carnivorous	omnivorous	-0.0386	-0.101	0.019	
no	Feeding	carnivorous	(omnivorous/detritivorous)	-0.134	-0.283	0.00511	
no	Feeding	carnivorous	planktivore	0.164	-0.49	0.841	
no	Feeding	(carnivorous/detritivorous)	(carnivorous/planktivore)	0.0852	-0.261	0.414	
no	Feeding	(carnivorous/detritivorous)	(detritivorous/herbivorous)	-0.0685	-0.45	0.286	
no	Feeding	(carnivorous/detritivorous)	herbivorous	-0.0356	-0.379	0.3	
no	Feeding	(carnivorous/detritivorous)	(herbivorous/detritivorous)	-0.0186	-0.33	0.274	
no	Feeding	(carnivorous/detritivorous)	omnivorous	-0.0411	-0.327	0.215	
no	Feeding	(carnivorous/detritivorous)	(omnivorous/detritivorous)	-0.137	-0.442	0.16	
no	Feeding	(carnivorous/detritivorous)	planktivore	0.156	-0.565	0.876	
no	Feeding	(carnivorous/planktivore)	(detritivorous/herbivorous)	-0.155	-0.475	0.16	
no	Feeding	(carnivorous/planktivorous)	herbivorous	-0.121	-0.407	0.159	
no	Feeding	(carnivorous/planktivore)	(herbivorous/detritivorous)	-0.104	-0.345	0.142	
no	Feeding	(carnivorous/planktivorous)	omnivorous	-0.128	-0.336	0.0723	
no	Feeding	(carnivorous/planktivore)	(omnivorous/detritivorous)	-0.223	-0.454	0.02	
no	Feeding	(carnivorous/planktivorous)	planktivore	0.0748	-0.635	0.735	
no	Feeding	(detritivorous/herbivorous)	herbivorous	0.0352	-0.287	0.358	
no	Feeding	(detritivorous/herbivore)	(herbivorous/detritivorous)	-0.0516	-0.244	0.339	
no	Feeding	(detritivorous/herbivorous)	omnivorous	0.0263	-0.224	0.282	
no	Feeding	(detritivorous/herbivore)	(omnivorous/detritivorous)	-0.0657	-0.347	0.227	
no	Feeding	(detritivorous/herbivorous)	planktivore	0.236	-0.471	0.95	
no	Feeding	herbivorous	(herbivorous/detritivorous)	-0.0153	-0.246	0.264	
no	Feeding	herbivorous	omnivorous	-	-0.221	0.199	
				0.00649			
no	Feeding	herbivorous	(omnivorous/detritivorous)	-0.102	-0.343	0.148	
no	Feeding	herbivorous	planktivore	0.196	-0.505	0.887	
no	Feeding	(herbivorous/detritivorous)	omnivorous	-0.0233	-0.18	0.122	
no	Feeding	(herbivorous/detritivore)	(omnivorous/detritivorous)	-0.118	-0.317	0.0905	
no	Feeding	(herbivorous/detritivorous)	planktivore	0.182	-0.507	0.86	
no	Feeding	omnivorous	(omnivorous/detritivorous)	-0.0945	-0.241	0.0543	
no	Feeding	omnivorous	planktivore	0.205	-0.453	0.875	
no	Feeding	(omnivorous/detritivorous)	planktivore	0.294	-0.359	1	

No clear trend emerges from comparing the sensitivity of species with different feeding types to toxic substances (Figure S6, Table S9). Next we will examine the sensitivity of species with different feeding types by combining some of the feeding types.

Simple Feeding Types Differing in Sensitivity

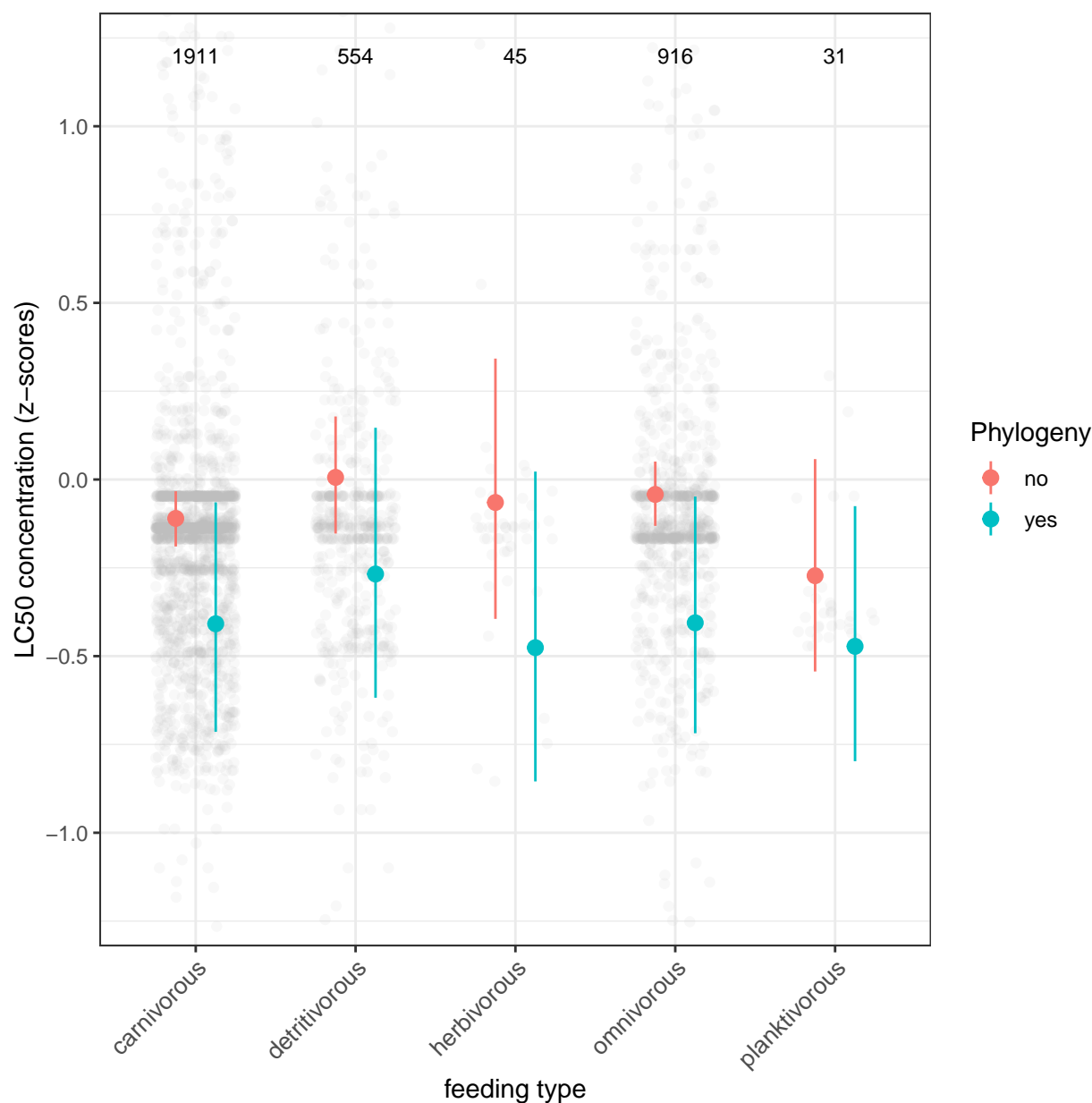


Figure S7. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is feeding type, and random effects are included for study (`ref_number`). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 10: Table S10 Pairwise comparisons from of the Bayesian regression models fitted to the data for the effect of feeding type. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum length of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	FeedingSimple	carnivorous	detritivorous	-0.0939	-0.194	0.0058	
yes	FeedingSimple	carnivorous	herbivorous	0.0459	-0.167	0.268	
yes	FeedingSimple	carnivorous	omnivorous	-0.00117	-0.0693	0.0674	
yes	FeedingSimple	carnivorous	planktivorous	0.0452	-0.0852	0.185	
yes	FeedingSimple	detritivorous	herbivorous	0.142	-0.0905	0.363	
yes	FeedingSimple	detritivorous	omnivorous	0.0925	-0.00287	0.191	
yes	FeedingSimple	detritivorous	planktivorous	0.139	-0.0179	0.321	
yes	FeedingSimple	herbivorous	omnivorous	-0.0477	-0.268	0.156	
yes	FeedingSimple	herbivorous	planktivorous	-0.000454	-0.259	0.249	
yes	FeedingSimple	omnivorous	planktivorous	0.0463	-0.104	0.198	
no	FeedingSimple	carnivorous	detritivorous	-0.0656	-0.156	0.0285	
no	FeedingSimple	carnivorous	herbivorous	-0.0261	-0.228	0.189	
no	FeedingSimple	carnivorous	omnivorous	-0.0386	-0.101	0.0207	
no	FeedingSimple	carnivorous	planktivorous	0.0984	-0.101	0.281	
no	FeedingSimple	detritivorous	herbivorous	0.0397	-0.184	0.261	
no	FeedingSimple	detritivorous	omnivorous	0.0267	-0.0697	0.126	
no	FeedingSimple	detritivorous	planktivorous	0.165	-0.0472	0.366	
no	FeedingSimple	herbivorous	omnivorous	-0.0128	-0.221	0.2	
no	FeedingSimple	herbivorous	planktivorous	0.126	-0.147	0.401	
no	FeedingSimple	omnivorous	planktivorous	0.137	-0.0595	0.332	

Simple feeding types do not appear to differ in their sensitivity to toxic substances (Figure S7, Table S10).

Geographical Regions Differing in Sensitivity

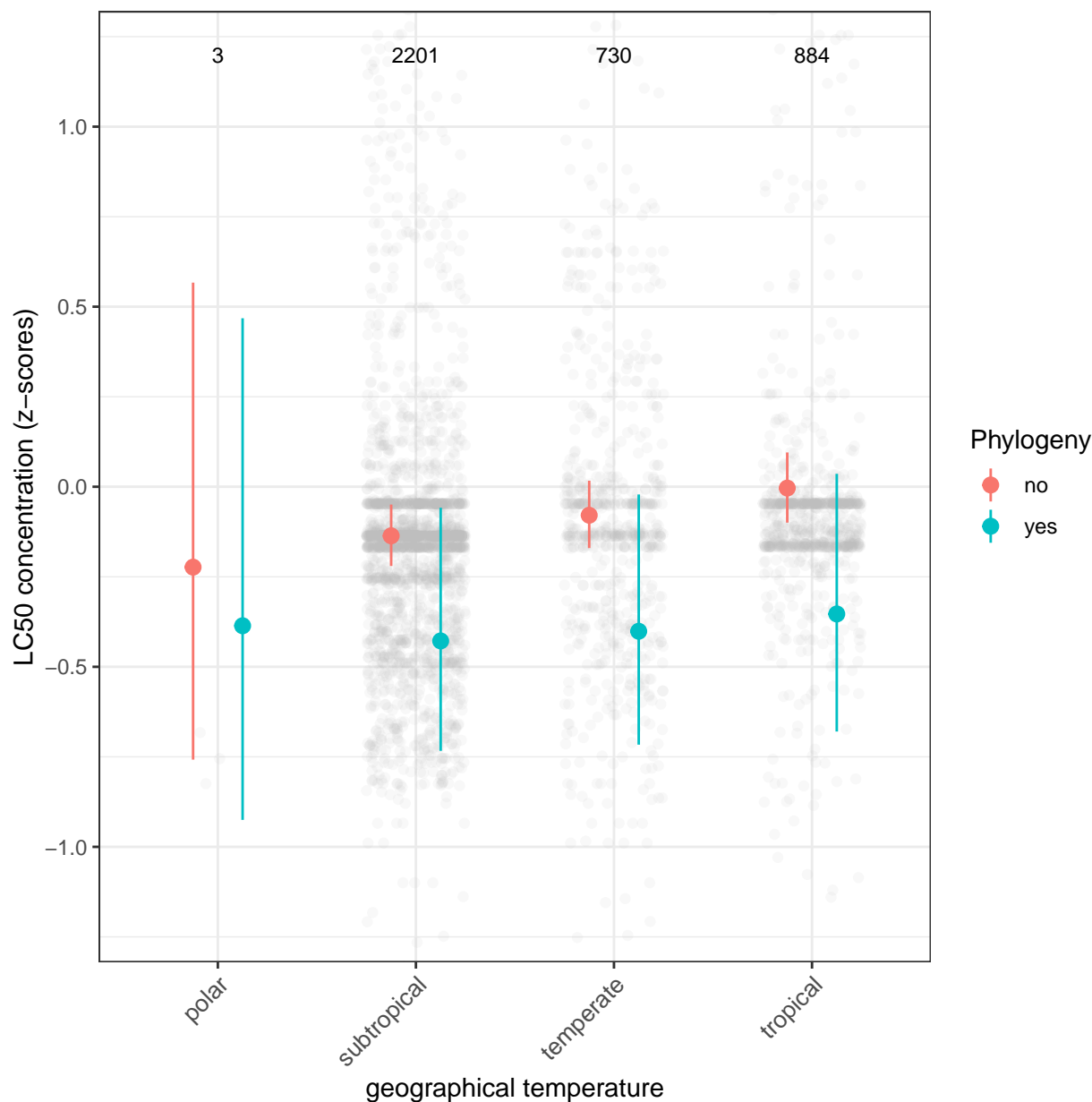


Figure S8. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is geographical temperature, and random effects are included for study (`ref_number`). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 11: Table S11 Pairwise comparisons from of the Bayesian regression models fitted to the data for the effect of geographical temperature. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum length of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	geogTemp	polar	subtropical	0.0285	-0.372	0.443	
yes	geogTemp	polar	temperate	0.0113	-0.392	0.415	
yes	geogTemp	polar	tropical	-0.0208	-0.446	0.375	
yes	geogTemp	subtropical	temperate	-0.0181	-0.0684	0.0331	
yes	geogTemp	subtropical	tropical	-0.0502	-0.119	0.0167	
yes	geogTemp	temperate	tropical	-0.0323	-0.108	0.0435	
no	geogTemp	polar	subtropical	-0.0531	-0.455	0.342	
no	geogTemp	polar	temperate	-0.0869	-0.482	0.311	
no	geogTemp	polar	tropical	-0.128	-0.513	0.291	
no	geogTemp	subtropical	temperate	-0.0326	-0.0959	0.0263	
no	geogTemp	subtropical	tropical	-0.0747	-0.145	-0.00655	*
no	geogTemp	temperate	tropical	-0.0422	-0.114	0.029	

There is no clear evidence that the geographical region where the species live would affect their sensitivity to toxic substances (Figure S8, Table S11) Nevertheless, when comparing the tropical species to subtropical the non-phylogeny adjusted model suggests that tropical species are more sensitive to toxic substances.

Water Column Types Differing in Sensitivity

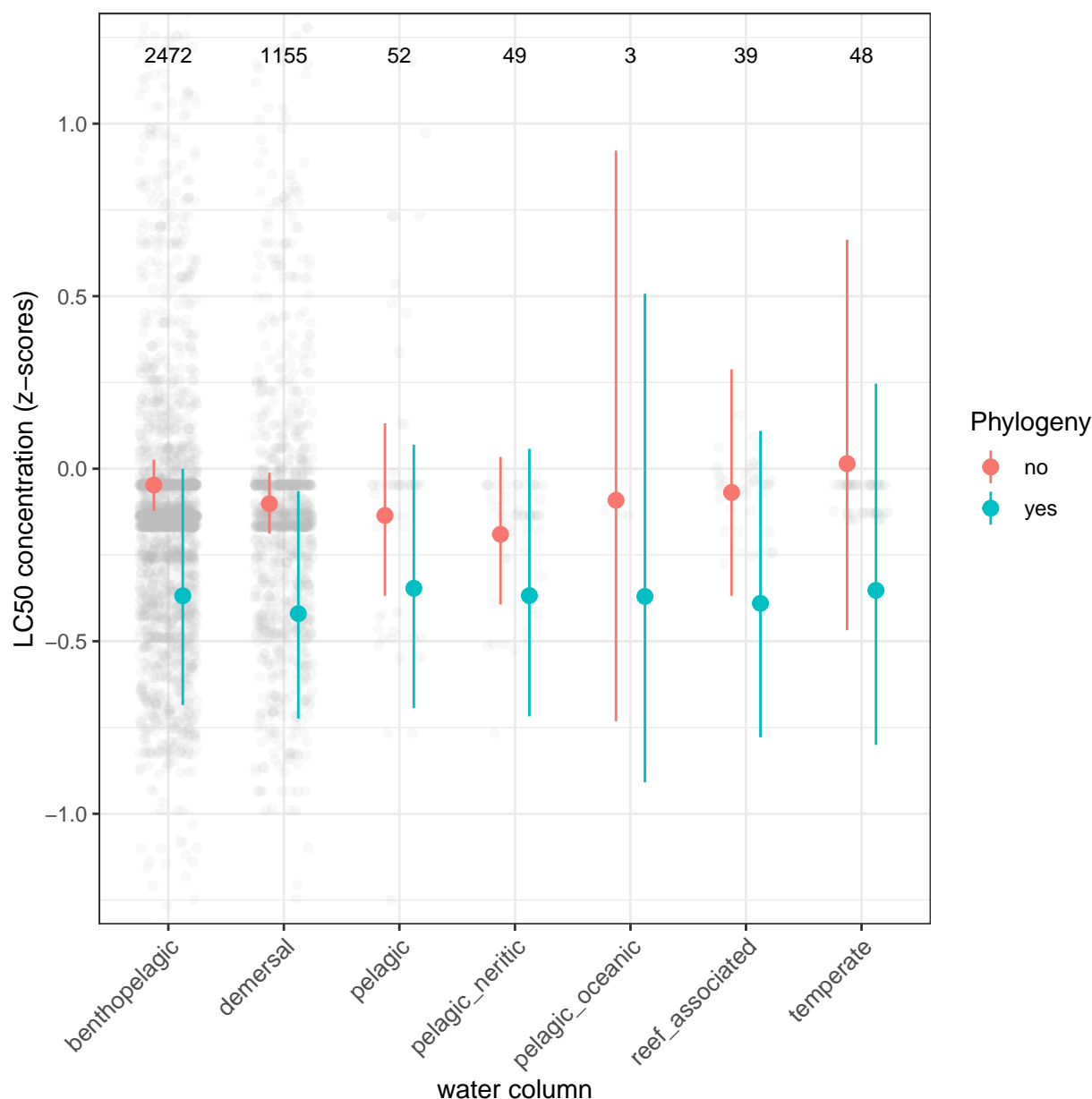


Figure S9. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is water column, and random effects are included for study (`ref_number`). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 12: Table S12 Pairwise comparisons from of the Bayesian regression models fitted to the data for the effect of water column. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum length of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	waterColumn	benthopelagic	demersal	0.0352	-0.0191	0.0834	
yes	waterColumn	benthopelagic	pelagic	-0.0157	-0.123	0.0917	
yes	waterColumn	benthopelagic	pelagic_neritic	-0.00197	-0.138	0.134	
yes	waterColumn	benthopelagic	pelagic_oceanic	0.000626	-0.397	0.412	
yes	waterColumn	benthopelagic	reef_associated	0.015	-0.182	0.218	
yes	waterColumn	benthopelagic	temperate	-0.0126	-0.303	0.257	
yes	waterColumn	demersal	pelagic	-0.0501	-0.161	0.0663	
yes	waterColumn	demersal	pelagic_neritic	-0.0376	-0.177	0.1	
yes	waterColumn	demersal	pelagic_oceanic	-0.0344	-0.43	0.376	
yes	waterColumn	demersal	reef_associated	-0.0191	-0.218	0.181	
yes	waterColumn	demersal	temperate	-0.0474	-0.329	0.217	
yes	waterColumn	pelagic	pelagic_neritic	0.0134	-0.147	0.186	
yes	waterColumn	pelagic	pelagic_oceanic	0.0144	-0.396	0.443	
yes	waterColumn	pelagic	reef_associated	0.03	-0.193	0.257	
yes	waterColumn	pelagic	temperate	0.0037	-0.295	0.3	
yes	waterColumn	pelagic_neritic	pelagic_oceanic	-0.000828	-0.421	0.427	
yes	waterColumn	pelagic_neritic	reef_associated	0.0164	-0.217	0.253	
yes	waterColumn	pelagic_neritic	temperate	-0.0113	-0.31	0.303	
yes	waterColumn	pelagic_oceanic	reef_associated	0.017	-0.417	0.47	
yes	waterColumn	pelagic_oceanic	temperate	-0.0114	-0.479	0.488	
yes	waterColumn	reef_associated	temperate	-0.027	-0.353	0.329	
no	waterColumn	benthopelagic	demersal	0.0307	-0.0261	0.0864	
no	waterColumn	benthopelagic	pelagic	0.0506	-0.0943	0.201	
no	waterColumn	benthopelagic	pelagic_neritic	0.0832	-0.0448	0.218	
no	waterColumn	benthopelagic	pelagic_oceanic	0.0239	-0.432	0.486	
no	waterColumn	benthopelagic	reef_associated	0.0114	-0.174	0.197	
no	waterColumn	benthopelagic	temperate	-0.0348	-0.339	0.272	
no	waterColumn	demersal	pelagic	0.0196	-0.132	0.173	
no	waterColumn	demersal	pelagic_neritic	0.0525	-0.0822	0.188	
no	waterColumn	demersal	pelagic_oceanic	-0.00738	-0.453	0.459	
no	waterColumn	demersal	reef_associated	-0.0188	-0.204	0.166	
no	waterColumn	demersal	temperate	-0.0648	-0.375	0.231	
no	waterColumn	pelagic	pelagic_neritic	0.0324	-0.163	0.216	
no	waterColumn	pelagic	pelagic_oceanic	-0.0286	-0.494	0.444	
no	waterColumn	pelagic	reef_associated	-0.038	-0.267	0.191	
no	waterColumn	pelagic	temperate	-0.0853	-0.405	0.265	
no	waterColumn	pelagic_neritic	pelagic_oceanic	-0.0576	-0.537	0.408	
no	waterColumn	pelagic_neritic	reef_associated	-0.071	-0.287	0.149	
no	waterColumn	pelagic_neritic	temperate	-0.116	-0.457	0.197	
no	waterColumn	pelagic_oceanic	reef_associated	-0.0107	-0.509	0.469	

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
no	waterColumn	pelagic_oceanic	temperate	-0.056	-0.609	0.492	
no	waterColumn	reef_associated	temperate	-0.0461	-0.4	0.31	

There is no clear pattern between the water column type and the sensitivity to toxic substances (Figure S9, Table S12).

Migration Types Differing in Sensitivity

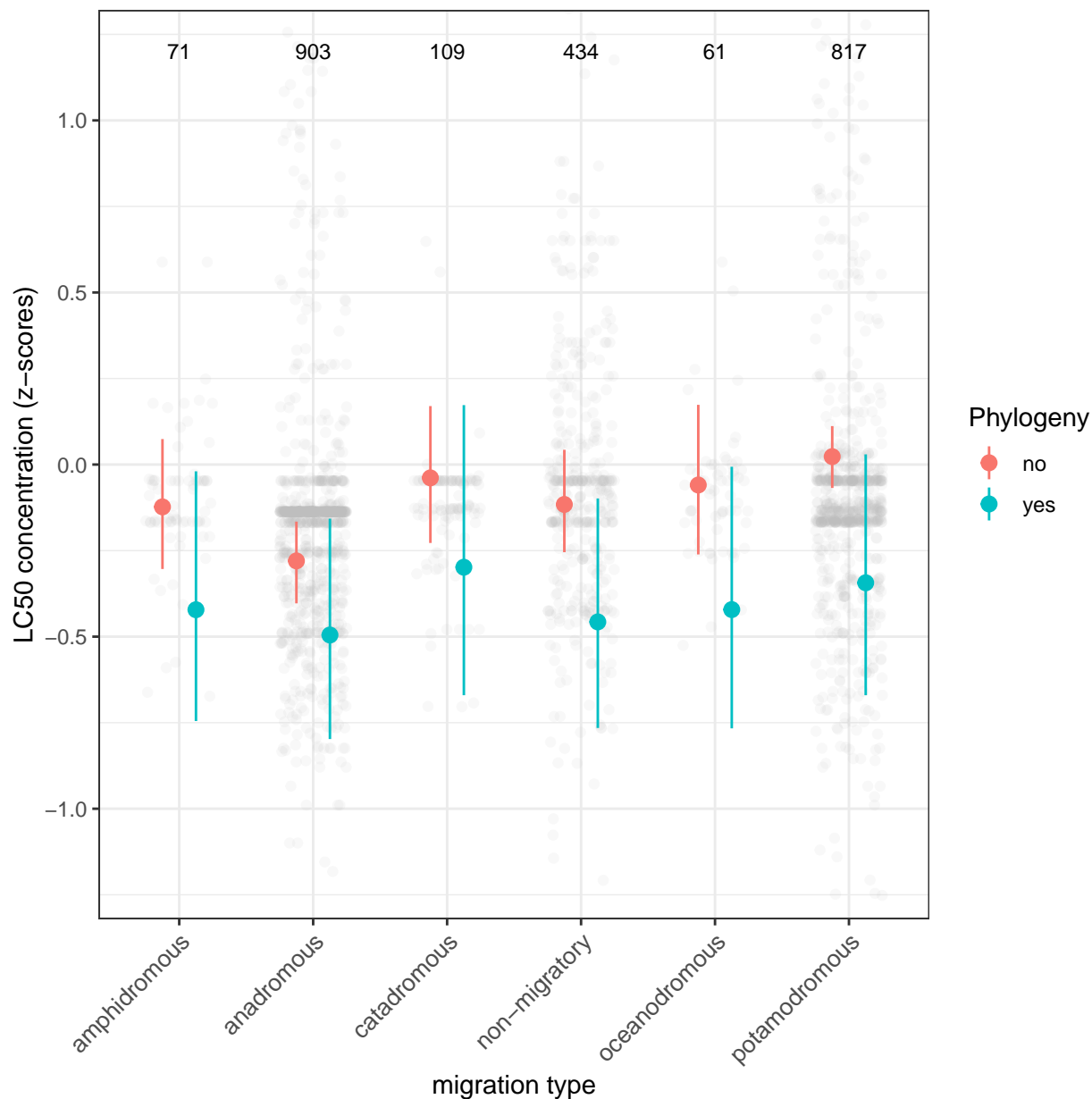


Figure S10. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is migration type, and random effects are included for study (`ref_number`).

The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 13: Table S13 Pairwise comparisons from of the Bayesian regression models fitted to the data for the effect of migration type. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum length of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
yes	Migration	amphidromous	anadromous	0.0528	-0.111	0.218	
yes	Migration	amphidromous	catadromous	-0.0856	-0.294	0.116	
yes	Migration	amphidromous	(non-migratory)	0.0253	-0.12	0.174	
yes	Migration	amphidromous	oceanodromous	0.000141	-0.184	0.178	
yes	Migration	amphidromous	potamodromous	-0.0527	-0.172	0.0631	
yes	Migration	anadromous	catadromous	-0.137	-0.338	0.066	
yes	Migration	anadromous	(non-migratory)	-0.0289	-0.141	0.0874	
yes	Migration	anadromous	oceanodromous	-0.0522	-0.243	0.122	
yes	Migration	anadromous	potamodromous	-0.107	-0.239	0.0358	
yes	Migration	catadromous	(non-migratory)	0.111	-0.0794	0.302	
yes	Migration	catadromous	oceanodromous	0.0856	-0.0959	0.266	
yes	Migration	catadromous	potamodromous	0.0314	-0.151	0.217	
yes	Migration	(non-migratory)	oceanodromous	-0.0251	-0.184	0.151	
yes	Migration	(non-migratory)	potamodromous	-0.0789	-0.19	0.0386	
yes	Migration	oceanodromous	potamodromous	-0.0543	-0.209	0.105	
no	Migration	amphidromous	anadromous	0.0955	-0.0425	0.232	
no	Migration	amphidromous	catadromous	-0.0493	-0.204	0.106	
no	Migration	amphidromous	(non-migratory)	-0.00492	-0.137	0.119	
no	Migration	amphidromous	oceanodromous	-0.0381	-0.203	0.121	
no	Migration	amphidromous	potamodromous	-0.082	-0.196	0.0328	
no	Migration	anadromous	catadromous	-0.144	-0.276	-0.0199	*
no	Migration	anadromous	(non-migratory)	-0.0996	-0.228	0.0128	
no	Migration	anadromous	oceanodromous	-0.133	-0.277	0.00748	
no	Migration	anadromous	potamodromous	-0.177	-0.265	-0.0985	*
no	Migration	catadromous	(non-migratory)	0.0433	-0.0972	0.191	
no	Migration	catadromous	oceanodromous	0.011	-0.131	0.169	

Phylogeny	Predictor	group1	group2	estimate	l-95% CI	u-95% CI	Notable
no	Migration	catadromous	potamodromous	-0.0341	-0.153	0.0861	
no	Migration	(non-migratory)	oceanodromous	-0.0315	-0.18	0.103	
no	Migration	(non-migratory)	potamodromous	-0.0779	-0.166	0.0183	
no	Migration	oceanodromous	potamodromous	-0.0452	-0.171	0.0863	

If phylogeny is not considered anadrosmous species appear to be more sensitive to toxic substances than catadromous or potamodromous species (Figure S10, Table S13).

Maximum Ages Differing in Sensitivity

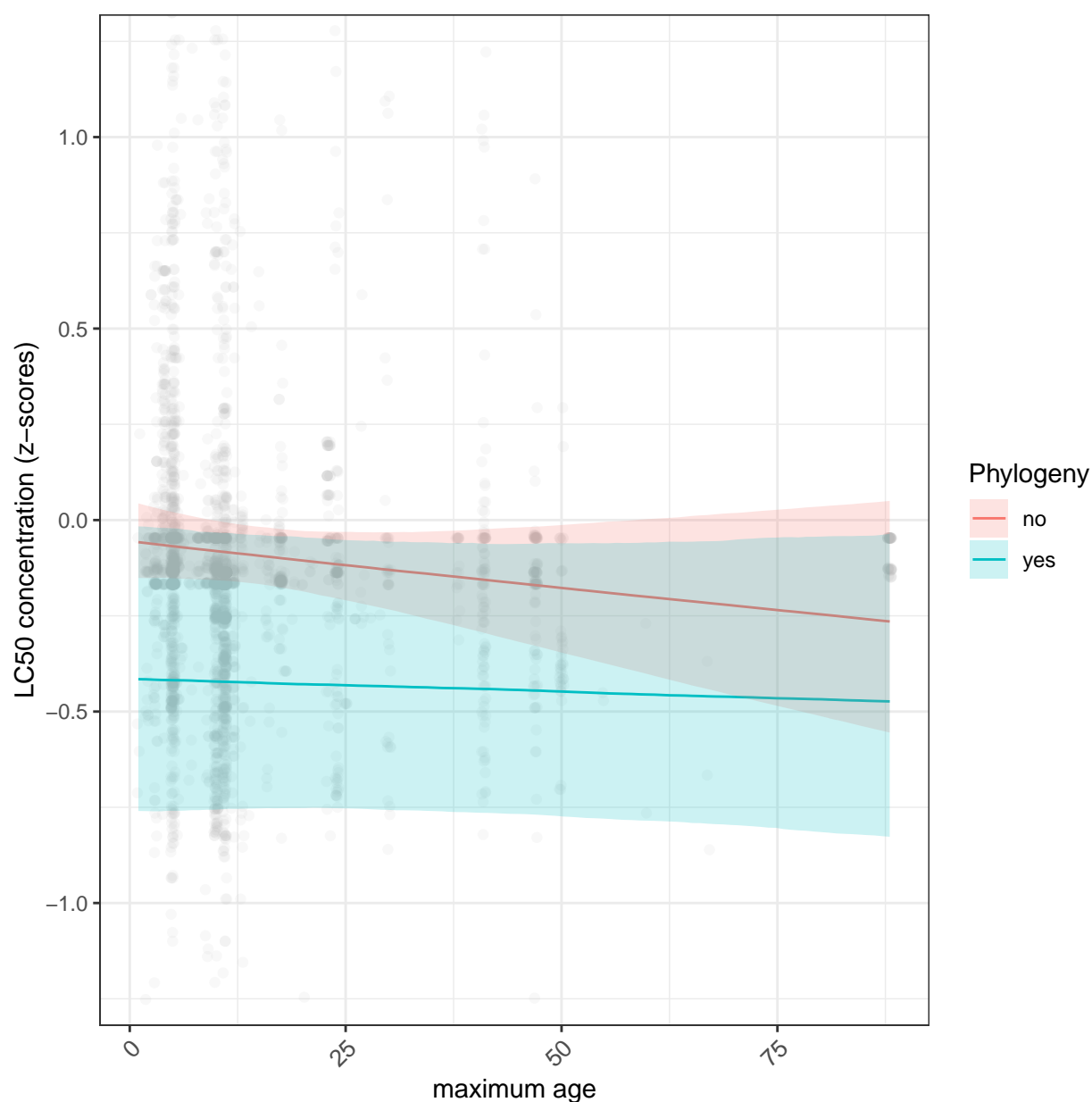


Figure S11. The conditional effects of the model fitted using the **brms** package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (tox_conc_z) response variable. The predictor variable is maximum age, and random effects are included for study (ref_number). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The shaded areas denote 95% credibility intervals (CI). The blue/red lines are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.

Table 14: Table S14 Model estimates with 95% credibitly intervals of the Bayesian regression model fitted to the data for the effect of maximum age. The models are fitted with and without phylogeny adjustment. The response variable is the z-scores of LC50 concentration (tox_conc_z) and the predictor variables include log transformed maximum lenght of species. The random effects are included for study (ref_number) and species (sp). The models are fitted with a log-normal family. The lower and upper credibility intervals (95% CI) show the range within which the true marginal mean is expected to fall with 95% probability.

Phylogeny	Predictor	Covariate	Estimate	Est.Error	l-95% CI	u-95% CI	Notable
yes	maxAge	Intercept	0.31	0.15	0.00	0.61	*
yes	maxAge	maxAge	0.00	0.00	0.00	0.00	
yes	maxAge	log_maxLength	0.00	0.02	-0.04	0.04	
no	maxAge	Intercept	0.62	0.07	0.48	0.75	*
no	maxAge	maxAge	0.00	0.00	0.00	0.00	
no	maxAge	log_maxLength	-0.02	0.02	-0.06	0.02	

There is no clear pattern between the maximum age of the species and their sensitivity to toxic substances (Figure S11, Table S14).

Combining Results Figures

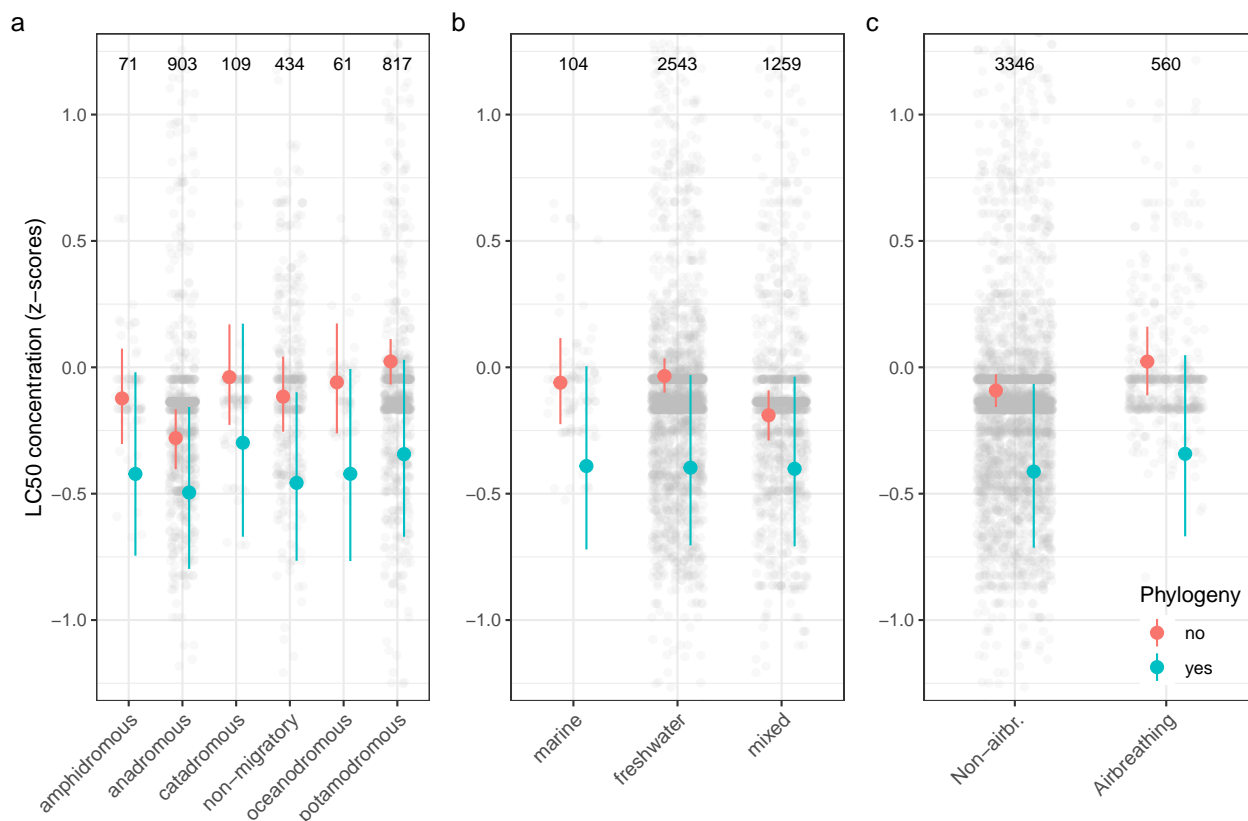


Figure S12. The conditional effects of the model fitted using the `brms` package. The model is a Bayesian regression model with a log-normal family, fitted on the z-scores of LC50 concentration (`tox_conc_z`) response variable. The predictor variable is either migration type (a), salinity (b) or air-breathing (c), and random effects are included for study (`ref_number`). The red denotes model with phylogeny excluded (ie. random effects include species only) while the blue indicates the phylogeny adjusted model. The whiskers denote 95% credibility intervals (CI). The blue/red points are the posterior means. The gray points are the log transformed original data points (i.e. representing one value for a species toxicity measurement for a chemical in a study). The number of data points for each order is shown on the top of the plot. Not all points are shown as the y axis is limited to -1.2 to 1.2 for readability.