



Species-specific sensitivity to PAHs reveals widespread biodiversity impact from the 2021 oil spill in the Eastern Mediterranean[☆]

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ABSTRACT

Marine oil spills are globally widespread, posing significant threats to marine wildlife. While the spatial and temporal distribution of oil concentrations in the environment can be modeled with high resolution, the impact of petroleum products on marine biodiversity has remained largely unquantified due to a critical missing component: the species-specific sensitivity of marine organisms to oil pollution, particularly to polycyclic aromatic hydrocarbons (PAHs), the most toxic fraction of crude oil. In this study, we address this knowledge gap by developing a predictive model that estimates the sensitivity of marine species to PAHs exposure based on taxonomic proximity and shared ecological traits. We apply this framework to assess the impact of the February 2021 oil spill on marine biodiversity along the Israeli Mediterranean coastline, integrating our sensitivity model with a high-resolution oil transport model (oil-CMS). Our model predicted PAH sensitivity of 88% of key local species, demonstrating that close to the spill core (i.e., the slick), as many as 75.4% of pelagic species were predicted to experience exposure to PAHs concentrations associated with harmful or lethal effects. This novel approach provides a scalable method for assessing biodiversity risks from oil pollution and emphasizes the urgent need to incorporate species-specific pollutant-sensitivity into marine environmental risk and impact assessments.

1. Introduction

In mid-February 2021, the entire ~190 km of the Israeli Eastern Mediterranean coastline was contaminated with a substantial amount of oil and tar that was spilled from a tanker outside Israel's national waters. Satellite imagery indicated a major slick initially identified 50 km west of Israel's shoreline (MoEP, 2021) with an estimated surface slick area of 12.21 km² (Herut et al., 2024). Oil and semi-solid tar pollutants drifted ashore, driven by strong south-westerly winds, identified 6 days earlier (Herut et al., 2024). The Israeli Ministry of Environmental Protection (MoEP) officially reported an estimated spill amount ranging from dozens to hundreds of tons (MoEP, 2021; Amir, 2022). Extensive

cleanup efforts resulted in the removal of approximately 1400 tons of tar and debris (Ministry of Environmental Protection, 2022; Spanier and Zviely, 2022). Applying the accepted 10:1 waste-to-spilled-oil ratio (Wadsworth, 2014) suggests that approximately 140 tons of oil was originally released, in agreement with the MoEP's reported range. Assuming that the collected material contained a minimum of 60% sand and debris, the net mass of beached tar is estimated at approximately 550 tons. Chemical analysis of the tar samples collected at the beaches indicated high concentrations of polycyclic aromatic hydrocarbons (PAHs) and heavy metals that are considered toxic to humans and environment (Herut et al., 2024). This spill, which was described as "one of the most severe ecological disasters in the region's history" (Amir,

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2022), emphasizes the increasing threats of oil pollution to the marine environment and risks for thousands of marine species (IUCN, 2022). Yet, no comprehensive impact assessment of the oil spill on marine biodiversity was carried out. To the best of our knowledge, this is the first study to integrate species-specific PAH sensitivity modeling with an oil transport model hindcast of an actual spill to assess impacts on biodiversity. Note that the term “biodiversity impact” is used here to denote the extent of potential lethal and sub-lethal effects on individuals across species, rather than an irreversible decline in species richness.

PAHs are considered to be the most toxic fraction of crude oil compounds (Honda and Suzuki, 2020). Previous toxicological studies have reported mortality and harmful effects of PAHs on early development including deformities and edemas (Barron et al., 2004). In addition, at sub-lethal concentrations, PAHs tend to accumulate in organisms' tissues and be transferred through the food web (i.e., trophic transfer), which can eventually impact human consumers (Meador et al., 1995; Zhang et al., 2015; Poliakova et al., 2000; Wang et al., 2025).

The increase in global oil and gas exploration raises deep concerns over the environmental impacts of oil spills (Cordes et al., 2016) based on dire experience (e.g. Bahía Las Minas oil spill; Jackson et al., 1989). Thus, several ecological tools were developed over the years to estimate the sensitivity of marine habitats to petroleum products and have been used in ecological studies and risk assessments. Such tools include Species Sensitivity Distribution (SSD) curves (Kooijman, 1987; Bejarano et al., 2017; Etterson, 2020), Environmental Sensitivity Index (ESI) maps (Jensen et al., 1990) and Quantitative Structure-Activity Relationship (QSAR) models (Gramatica et al., 2007). While these tools provide important insights regarding the potential ecological damage of oil spills, they are very limited in providing extensive species-explicit information related to the impact on marine biodiversity.

Previous models for predicting species-specific sensitivity to pollutants are typically limited to specific regions (e.g. coastal areas) and a narrow range of species, usually from the same small group of repeatedly standard lab-testing species (Rohr et al., 2016; Baird and Van den Brink, 2007). For example, more than 45% of *Deepwater Horizon* (DWH) studies were conducted on mahi-mahi (*Coryphaena hippurus*), red drum (*Sciaenops ocellatus*), and Sheepshead minnow (*Cyprinodon variegatus*), mostly on embryos or larval stages (Pasparakis et al., 2019). To date, PAH sensitivity of only a few dozen species has been studied, covering less than 0.01% of known marine species (IUCN, 2022).

Moreover, analytical measurement of total PAHs (Σ PAHs) requires significant resources and advanced analytical equipment, such as gas chromatography (GC) and high-performance liquid chromatography (HPLC) devices (Park et al., 2018) leading toxicological studies to focus on individual PAH compounds, keeping species-specific sensitivity to Σ PAHs under-examined. In addition, quantification of Σ PAHs lacks consistency across studies, with different sums of PAHs that include 16 priority PAHs (Σ PAH16) defined by the U.S. Environmental Protection Agency (EPA; Keith, 2015), 8 PAHs specified under the European Union Water Framework Directive (Koljančić and Španik, 2024) and extended compounds sets of 50 PAHs that were used in DWH studies (Σ PAH50). This lack of standardization creates challenges in comparing toxicity estimates across studies and constrains our ability to assess biodiversity sensitivity to PAH mixtures. As a result, our ability to systematically quantify the ecological consequences of frequent global oil spills (Dong et al., 2022) remains highly limited.

This study aims to bridge this gap and has two main objectives: First, to develop a quantitative model that estimates species-specific sensitivity to PAHs, considering taxonomic relatedness, developmental stage, and trophic level. And second, to apply this model to the Eastern Mediterranean Sea (EMS) 2021 spill as a case study and assess the risk to marine species present in the affected areas during the time of the spill. We hypothesized that species that are taxonomically related and share similar developmental stages and trophic levels could serve as a basis for reliable sensitivity estimation for thousands of species that currently lack this information. This data-driven approach will help address

current knowledge gaps and improve our understanding of the ecological impacts of hydrocarbon pollution on marine biodiversity.

2. Materials & methods

Assessing the potential impacts of oil pollution on marine biodiversity involves three key components: (1) estimating the spatial extent of the spill using an oil transport model that accounts for oceanographic and atmospheric conditions; (2) identifying the species most likely to be present during the spill event; and (3) evaluating species' sensitivity to Σ PAHs exposure using a quantitative, taxonomy-based model. The following sections detail the methodology applied to each component.

2.1. Spatio-temporal simulation of the oil spill

Quantification of the spatio-temporal distribution of surface oil concentrations and shoreline deposition that occurred primarily along the Israeli coast is conducted in five steps: (1) hourly four-dimensional ocean/sea currents are obtained from high-resolution ocean models for the region, (2) surface winds at the standard 10 m level are obtained from high-resolution atmospheric model, (3) surface wind correction is applied for the upper ocean layer to compute a combined forcing field for the oil transport model, (4) oil-spill transport model simulation is run to compute oil transport and fate, (5) post-processing of the model output is done to derive gridded fields of oil mass and concentrations. Σ PAHs values are estimated as 1.5% of the crude oil mass, representing a conservative estimate of the fraction of Σ PAHs within crude oil (Overton et al., 2016; Berenshtein et al., 2020). Additional analyses using higher Σ PAHs fractions (3% and 7%) are provided in the Supplementary Material (Section 1.5).

2.1.1. Ocean and wind data for the EMS

The oil spill model relies on gridded three-dimensional data of ocean state from external high-resolution numerical ocean circulation models. Two modeled products are integrated as hydrodynamic forcing in this study, one for the outer nested region and one for the inner (Berenshtein and Shenkar, 2025).

For the outer nest, modeled hydrodynamic fields are a product of Nucleus for European Modeling of the Ocean (NEMO; Clementi et al., 2019), implemented over the Mediterranean Basin with a horizontal grid resolution of $1/24^\circ$ (~ 4 km) with 141 vertical levels. The model includes data assimilation schemes of temperature and salinity vertical profiles, as well as those of satellite sea level anomaly observations. The dataset has been accessed and downloaded through the Copernicus Marine Environment Monitoring Service (CMEMS).

2.1.2. Ocean model data for the inner model domain

For the inner domain, hourly ocean state data were provided by the South Eastern Levantine Israeli Prediction System (SELIPS; Goldman et al., 2015) a sub-regional high-resolution circulation model operated by the Israel Oceanographic and Limnological Research (IOLR). SELIPS forecasts are produced daily, including fields of temperature, salinity, and currents velocity in the southeastern Levantine Basin, and are based on the Princeton Ocean Model (POM; Blumberg and Mellor, 1987). The model resolution is $0.01^\circ \times 0.00833^\circ$ (~ 1 km) with 27 sigma levels and a minimum depth of 5 m. Initial and boundary conditions for temperature, salinity, and velocity are derived from the ALERMO forecast system (Zafirakou-Koulouris et al., 2012).

Atmospheric fluxes of heat, fresh water, and momentum at the sea surface were computed in SELIPS from bulk formulas using the conditions taken from SKIRON, a regional atmospheric model forecast, including air temperature, specific humidity, air pressure, wind, total cloud cover and precipitation. Modeled heat flux was corrected using the remotely sensed sea surface temperature (SST) fields taken from CMEMS.

2.1.2.1. ICON-LAM winds. Oil reached the shoreline during a winter storm, when a deep upper-level trough developed over the Eastern Mediterranean. This generated a low-pressure system producing strong west-southwest surface winds (Herut et al., 2024). At the Israeli coast, wind gusts reached up to 25 m/s on the morning of 17 February 2021, as recorded at the Hadera coastal meteorological station. These winds appear to have played a major role in driving the oil slick rapidly “beaching” onshore, i.e., shoreline oil deposition.

Surface wind fields were simulated by the ICON-LAM model, a limited-area atmospheric circulation model of the non-hydrostatic ICON (Icosahedral Nonhydrostatic) model (Zängl et al., 2015; Pham et al., 2021). The ICON-LAM with a convection-permitting resolution of ~2.5 km horizontal grid is used operationally by the Israeli Meteorological Service (IMS, n.d). Hourly forecasts of 10-m altitude winds from the model were used to calculate surface wind correction for the upper-ocean layer velocity components. Combined 3-D hydrodynamic forcing was subsequently used by the oil transport model.

2.1.2.2. Wind drift correction. The movement of oil particles at the surface is influenced by advection from surface currents and by the additional displacement by wind-driven wave breaking and Langmuir circulation. Specifically, wind drift (u_{drift} ; eq. 1) was computed as the sum of the Stokes drift, representing the ocean surface waves, and an additional displacement component representing the surface wave breaking and Langmuir circulation (Le Hénaff et al., 2012; Arduin et al., 2009).

$$u_{drift} = 0.015 U_{10} + fr R U_{10} \quad (1)$$

where u_{drift} is the total wind-induced drift, U_{10} is the zonal wind velocity at an altitude of 10 m, fr is the fractional contribution of the wind velocity to the additional wind-driven displacement (wind-driven wave breaking and Langmuir circulation), and R represents the rotation matrix associated with the deflection angle. Following Arduin et al. (2009), given the oceanographic conditions of the domain, parameters were set to $fr = 0.006$ and $R = 55^\circ$.

2.1.3. Oil-CMS model

The Lagrangian particle-tracking Connectivity Modeling System (CMS, Paris et al., 2013) developed at the University of Miami, adapted to oil transport and fate (oil-CMS, Paris et al., 2012), was used for numerical simulation of the 2021 oil spill off the coast of Israel. The oil-CMS has been tested over the years in the aftermath of *Deepwater Horizon* (2010) blowout in the Gulf of Mexico (Le Hénaff et al., 2012; Lindo-Atichati et al., 2016; Perlin et al., 2019; Faillettaz et al., 2021; Vaz et al., 2021; Berenshtein et al., 2020).

The oil-CMS released 5000 multi-fractional oil droplets at 0000 UTC 11-February-2021 at 47 individual points, covering the area of the oil slick, a total of 235,000 droplets. The oil droplets undergo weathering processes during their transport and are tracked by the model for 18 days through 0000 UTC 03-March-2021. Their geographical locations, densities, and diameters were recorded hourly and saved as trajectory output. The amount of oil released at the slick location was set to 10, 100 and 1000 metric tons. Results for the 100-t scenario are presented in the main text, while the 10- and 1000-t scenarios are provided in the Supplementary Material (Supplementary Section 1.4). This amount was used to scale the oil droplets to achieve mass balance. This amount was later scaled in the post-process to represent released quantities of 10, 100 and 1000 metric tons.

Oil mass at the surface was estimated using trajectory files output and scaling which were further mapped into the 0.01×0.01 degree grid. All post-processing and spatial analyses were performed using MATLAB R2023b.

2.2. Species with the highest likelihood of being present during the EMS oil spill

Key species (Supplementary Table S5) were included in the analysis based on the high probability of their presence in the impacted area, which was considered as the upper water column (0-20 m) in the pelagic and coastal environment of the Israeli territorial waters. The list was based on the Marine BioBlitz-biological survey of the Israeli marine protected areas in the Mediterranean Sea (Lazarus et al., 2020), the National Monitoring Program (NMP) Biodiversity report of 2023 (Rahav et al., 2024), and experts' opinion (Drs. Nir Stern, Tamar Guy-Haim, and Gil Rilov). These species are characterized by a high probability of dwelling in the upper area of the water column, where PAHs concentrations are the highest (Brussaard et al., 2016). The list includes 62 species from 43 families, spanning across eight Phyla, found in the pelagic environment as zooplankton, covering early to adult life stages.

We compiled a database of 306 LC₅₀ and EC₅₀ records from 43 aquatic species including fish, crustaceans and mollusks, from different developmental life stages including gamete, embryo, veliger, pediveliger, early spat, nauplii, zoea, larvae, juvenile and adult (see Fig. 1 and Supplementary Table S1).

2.3. TESS – Taxonomy-based Estimation of Species Sensitivity model

2.3.1. Toxicological data collection

Toxicological data of Median lethal concentration (LC₅₀) and median effective concentration (EC₅₀) values of ΣPAHs (hereinafter referred to as “LC₅₀|EC₅₀”; Bejarano, 2014) were gathered from 36 scientific papers (see Supplementary Table S1) and the National Oceanic and Atmospheric Administration (NOAA)’s *Deepwater Horizon* Trustee Natural Resource Damage Assessment (NRDA) Toxicity Testing Program (DWH NRDA Trustees).

A complete dataset from the NOAA database containing 2636 LC₅₀|EC₅₀ records that were sampled from seawater, including the sum of 50 PAHs (list of compounds can be found in DIVER, 2020), toxicity tested against oil substances (i.e., slick types) and with no additional stressors applied to the experiment, was added to our database.

The endpoints of LC₅₀|EC₅₀ include mortality, deformities, abnormalities in development, fertilization, metamorphosis success and cardiac functions, CYP1A induction, clearance rates and low hatching rates. Importantly, these endpoints represent effects which are expected to lead to consecutive mortality, hence these EC₅₀ data were combined with LC₅₀ data. For comparison, we provide analysis that is based solely on LC₅₀ in Supplementary Fig. S1.

Test duration ranged from 1 to 72 h (acute effect tests) and 96 h to 20 days (chronic effect tests). ΣPAHs concentration refers to the sum of EPA ΣPAH16 and the ΣPAH50 used in the DWH oil spill analysis. Test substances ranged from light crude oils with API gravity above 31.1° to heavy crude oils with API gravity less than 20° (see Supplementary Table S2).

The different types of mixing methods include Water Accommodated Fraction (WAF), Breaking Wave WAF (BWAF), Mechanically dispersed oil, High-Energy Water Accommodated Fraction (HEWAF) and Low-Energy Water Accommodated Fraction (LEWAF).

Following the construction of the species-specific toxicity endpoints database, we found highly positively skewed distribution with extreme high values. Thus LC₅₀|EC₅₀ values that fell above the upper 95th percentile were considered as outliers and were excluded from the database (see Supplementary Table S7). This was done because extremely high values, outside the range of most studies, disproportionately impact the geometric mean. Since the primary objective of LC₅₀ and EC₅₀ analyses is to support the protection and conservation of natural resources, we adopted a conservative approach by focusing on the lower, more ecologically protective range of values, and assuming that the outliers do not represent the realistic toxicity endpoints.

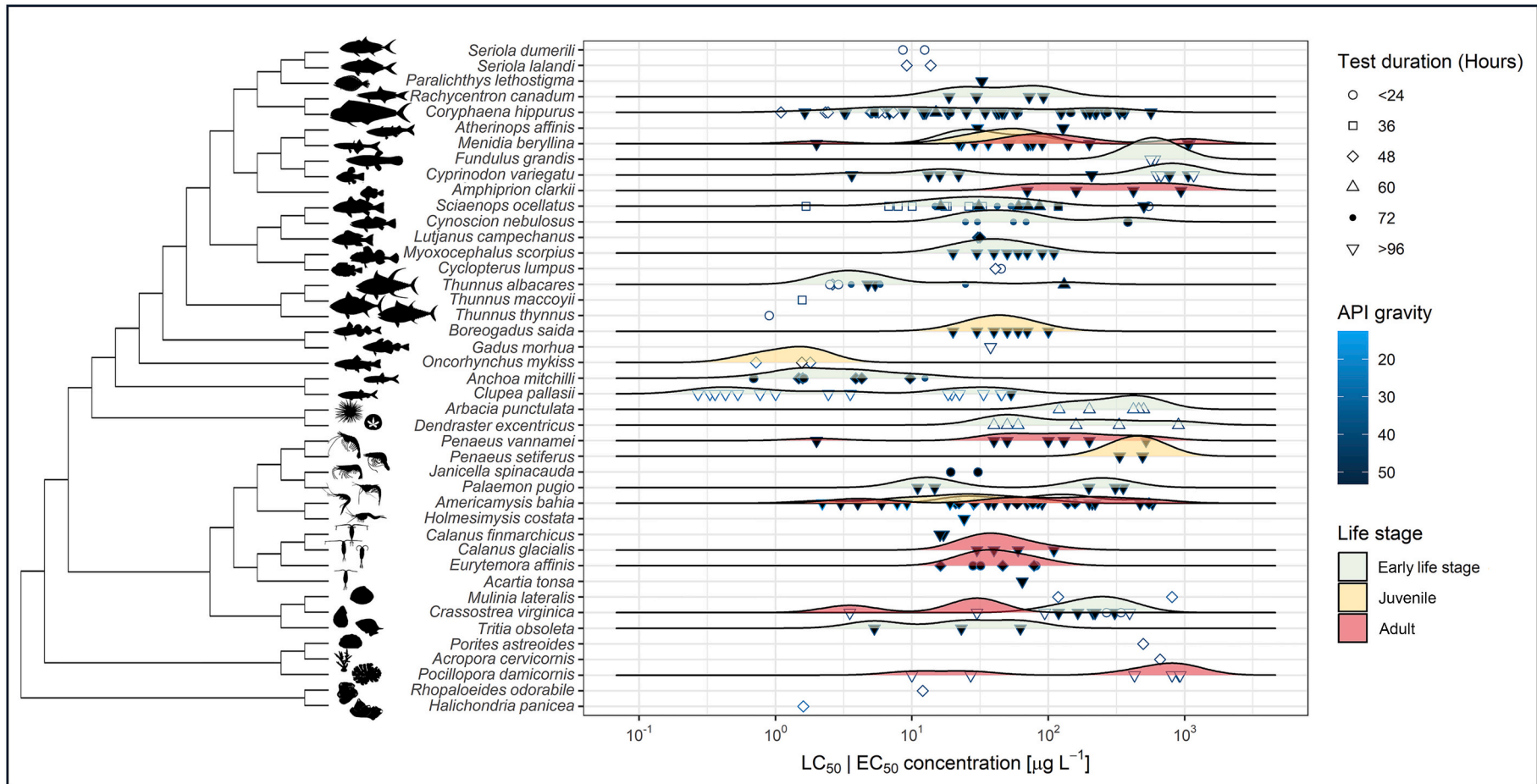


Fig. 1. Observed toxic response to PAH exposure. Species on the y-axis are sorted by their taxonomic relatedness as shown on the taxonomic tree on the left. Toxicity is represented by density function of median lethal concentration (LC_{50}) and median effective concentration (EC_{50}) values. Different colors of points represent the API gravity of the oil type used in the test and the shape of the points represent the test duration. The color of Probability Density Function (PDF) plot indicates organism's developmental stage.

2.3.2. Taxonomic data

Taxonomic hierarchy information was retrieved from The National Center for Biotechnology Information (NCBI) using Taxonomy function of R package myTAI (Drost et al., 2018). Missing taxonomic ranks were completed with available data from taxonomic database of World Register of Marine Species (WoRMS: <https://www.marinespecies.org/>). The 43 aquatic species in our database were classified into one kingdom, six phyla, eight classes, nine subclasses, 23 orders, 34 families and 38 genera as shown in Supplementary Fig. S2.

2.3.3. Trophic level data

Trophic level refers to the position of an organism in the food web with primary producers (e.g. phytoplankton and corals) at level 1, herbivores at level 2, carnivores at levels 3–4 and apex predators at level 5.

Larval stages such as veligers and fish larvae were assigned to trophic level 3 (secondary consumers) due to their diet of small crustaceans, primarily nauplii. Three coral species (*Acropora cervicornis*, *Pocillopora damicornis* and *Porites astreoides*), lacking trophic level information, were assigned to trophic level 2.5 due to their main diet of phytoplankton and small planktonic organisms. Early embryonic stages (gametes, embryos) were not assigned a value, as their nutrition derives from yolk sacs rather than active feeding.

Trophic level information was derived from scientific literature and three global databases: FishBase (<https://www.fishbase.se/>), SeaLifeBase (<https://www.sealifebase.org/>) and SeaAroundUs (www.seaaroundus.org/), as presented in Supplementary Table S3.

2.3.4. Sensitivity estimation

The TESS model follows a series of steps designed to predict the sensitivity of untested organisms to PAHs exposure (see scheme in Fig. 2). First, the target organism's developmental stage, taxonomic rank, and trophic level are identified. Next, the database is filtered to match the target organism's developmental stage. For this purpose, embryonic stages (gametes, cells and embryos) together with larval stages (early spat, larvae, zoea, nauplii) are grouped under “early life stages”.

The second step is to find the nearest neighbors in the taxonomic tree

and filter those with a matching developmental stage.

The third step is to filter organisms within the same trophic level. Finally, geometric mean (GM) of the $LC_{50}|EC_{50}$ values is calculated, according to:

$$GM = \sqrt[n]{\prod_{i=1}^n x_i} \quad (2)$$

where n is the total number of matching values, and x is the individual $LC_{50}|EC_{50}$ values that were found. Note that the algorithm is based on $LC_{50}|EC_{50}$ values derived from a toxicological database (see Section 2.3.1) and does not use a training dataset, in contrast to machine learning-based methodologies.

If no matching $LC_{50}|EC_{50}$ values were found, the algorithm returns to step 2 and searches for organisms in the next upper rank in the hierarchy of the taxonomic tree. The model starts at genus level and moves through family, order and class to phylum levels.

2.3.5. Statistical and model performance analysis

To evaluate the TESS model's performance, we compared each species' observed $LC_{50}|EC_{50}$ values, derived from the scientific literature and NOAA's database (see Fig. 3 and Supplementary Table S1), with predictions generated by the TESS model. For each species, the predicted value was calculated from the geometric mean of its closest relatives in the taxonomic tree, with similar developmental stage and trophic level, while its own values were excluded from the calculation. For example, for the embryos of southern blue fin tuna (*Thunnus maccoyii*) the known $LC_{50}|EC_{50}$ value was $1.56 \mu\text{g L}^{-1}$, when running the model to predict this species' $LC_{50}|EC_{50}$ based on embryos of yellow fin tuna (*Thunnus albacares*) and Atlantic blue fin tuna (*Thunnus thynnus*) only, we got $2.37 \mu\text{g L}^{-1}$, therefore the absolute error was $2.37 - 1.56 = 0.81 \mu\text{g L}^{-1}$.

Finally, we calculated Mean Absolute Error (MAE) of model's predictions. MAE refers to the averaged distance between the observed $LC_{50}|EC_{50}$ values and the model's results (defined here as predicted values) according to:

$$MAE = \frac{\sum_{i=1}^n |x_i - y_i|}{n} \quad (3)$$

where n is the number of observations, x and y are the observed and predicted values, respectively. Because the $LC_{50}|EC_{50}$ values range spans across more than one order of magnitude, logarithmic transformation was applied to the data.

Correlation between observed and predicted values was tested using Pearson's correlation coefficient on the log-transformed data. All raw data analysis, statistical computing and graphics were performed using R statistical software (R Core Team, 2013).

2.3.6. Randomization test

To test the validity of the TESS model's results and avoid type 1 error of chance correlation, we used a randomization test (also known as Y-Scrambling; Daghighi et al., 2022), where the main goal was to test if the model performance is linked to taxonomic relatedness or occurred by chance.

According to this technique, observed values are randomly shuffled so the taxonomic tree is reorganized, creating “fake” neighbors. In every iteration the model produces new predictions based on the “new” neighbors of the tree. Next, Pearson's correlation coefficient (r) between the generated predictions and the observed values is calculated. We ran the randomization test for 1000 iterations and then compared the randomly generated correlation coefficients (r) with those obtained by the TESS model.

2.3.7. Model performance compared to ICE models

The performance of the taxonomy-based model in species specific

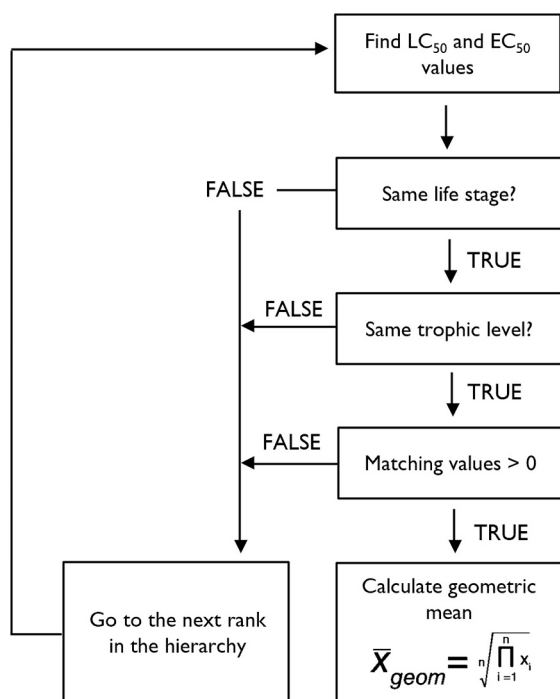


Fig. 2. Schematic diagram of the TESS model.

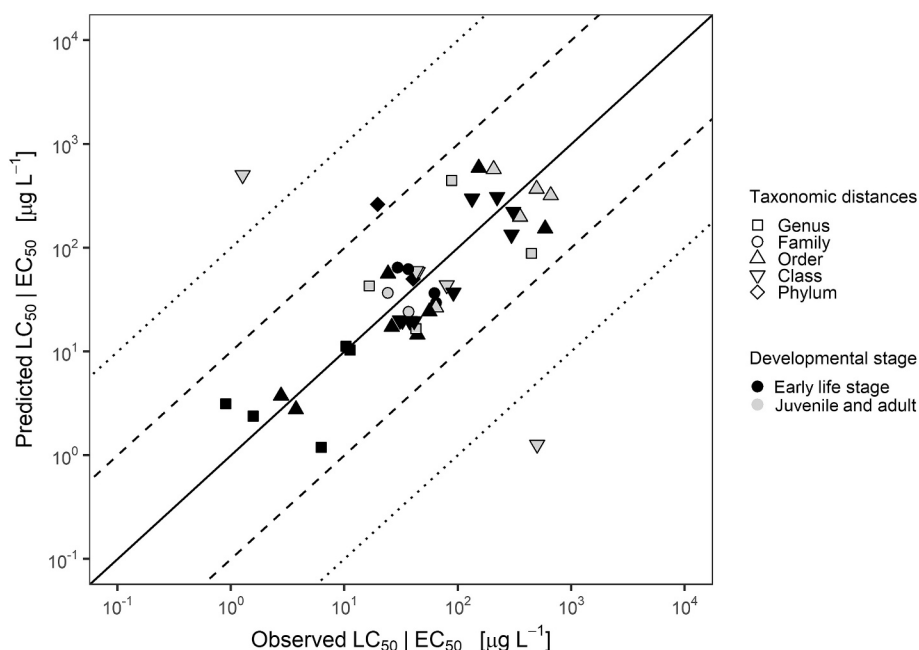


Fig. 3. Predicted vs. observed $LC_{50}|EC_{50}$ values. The black solid line indicates a full agreement between observed and predicted values. Dashed lines indicate 10-fold difference. Dotted lines indicate 100-fold difference.

sensitivity estimation was compared with Interspecies Correlation Estimation (ICE) models: (1) ICE model from The Chemical Aquatic Fate and Effects (CAFE) database (Bejarano et al., 2016) and (2) web-based ICE model (Web-ICE; Raimondo et al., 2010a). These types of models use the correlation between pairs of organisms in a series of toxicity values of different chemicals, i.e., predict one's sensitivity based on another surrogate organism (Raimondo et al., 2010b; Raimondo et al., 2022; Bejarano et al., 2016). We compared TESS model with ICE models because ICE models are widely used predictive tools for species toxicity based on taxonomic relatedness, making them appropriate benchmarks for comparison.

Predicted values of $LC_{50}|EC_{50}$ of $\Sigma PAHs$ were downloaded from CAFE database (Supplementary Table S2). The dataset contained 64 records from 15 species. Predicted and surrogate species were filtered to match the predicted species of the Taxonomy-based model.

The Web-ICE model is based on least squares log linear regressions of toxicity between paired species in a series of common chemicals in acute (96 h) exposure (Raimondo and Barron, 2020). The relationship between species pairs allows the prediction of one species' toxicity based on another surrogate species.

Complete dataset containing 2294 records of aquatic species pairs (predicted and surrogate species) was downloaded from U.S. Environmental Protection Agency website. Because the Web-ICE model does not consider species' life stages, fish species were classified as juveniles (Raimondo and Barron, 2020), crustacean species as juveniles or larvae only, and mollusk species as juveniles (Raimondo et al., 2022). Predicted and surrogate species were filtered to match the predicted species of the TESS model to create an accurate and reliable list for comparison.

Predicted sensitivity values were computed according to:

$$\log_{10}(\text{Pred}) = a + b \log_{10}(\text{Surrogate}) \quad (4)$$

where Pred is the predicted Taxa Toxicity, a is the intercept, b is the slope, and Surrogate represents the surrogate species' observed toxicity (Raimondo and Barron, 2020).

A single species can be predicted by several surrogate species, therefore only the best surrogate species (i.e., the species with the minimal difference between predicted and observed values) were used in the comparison between the models. Finally, MAE was computed for

each of the models.

2.4. Potential biodiversity impact estimation of the EMS oil pollution

The methodology for estimating the species impacted by the spill is based on the integration of three main datasets: (1) Spatio-temporally explicit PAHs concentrations from our oil spill simulation, (2) Presence of key species in the impacted region – based on surveys datasets (Supplementary Table S5), and (3) Species sensitivities to oil contamination (Supplementary Table S6). Oil mass concentrations in the contaminated grid cells area of simulated oil spill were computed based on the mass divided by the grid cell volume (Berenshtein et al., 2020).

The transformation from mass of crude oil to $\Sigma PAHs$ is based on reported mass fraction of 0.2–7% in crude oil (Neff et al., 2005) and ~1.5–3% in total petroleum hydrocarbons (Berenshtein et al., 2020). Here, we used a conservative value of 1.5% as follows:

$$C_{\Sigma PAHs} = f_{\Sigma PAHs} C_{oil,max} = 0.015 C_{oil,max} \quad (5)$$

Where $C_{\Sigma PAHs}$ is the estimated total PAH concentration, $C_{oil,max}$ is the maximum oil concentration, and $f_{\Sigma PAHs}$ is the assumed PAH mass fraction.

To assess the potential ecological damage of the oil spill on marine biodiversity, we quantified the number of sensitive key species, defined as species for which the predicted $LC_{50}|EC_{50}$ thresholds were lower than the PAHs concentrations estimated in each grid cell. We then calculated the proportion of affected species relative to the total number of species in the grid cell. Additional analysis of potential ecological damage for $\Sigma PAHs$ fractions of 3% and 7% in crude oil, is provided in the Supplementary Material (Supplementary Section 1.5).

3. Results

3.1. Species-specific PAH sensitivity

Our collated species-specific PAH sensitivity data demonstrates a wide range of sensitivities across the taxonomic spectrum, ranging from $0.27 \mu g L^{-1}$ PAHs (Pacific herring *Clupea pallasii*, endpoint: larvae skeletal defects response) to $1162.9 \mu g L^{-1}$ PAHs (Sheepshead minnow *Cyprinodon variegatus*; Fig. 1, Supplementary Table S1, more details are

in Supplementary Section 1.1). Nevertheless, closely related taxonomic species generally indicate similarity in PAH sensitivity for most species, for example, embryos of the greater amberjack *Seriola dumerili* (10.3 $\mu\text{g L}^{-1}$ PAHs) and yellowtail amberjack *Seriola lalandi* (11.2 $\mu\text{g L}^{-1}$ PAHs; Table 1).

Based on the TESS model, observed $\text{LC}_{50}|\text{EC}_{50}$ values were positively correlated with predicted values ($r = 0.55$, Pearson's correlation, $t = 4.2611$, $\text{df} = 42$, p -value < 0.001 , $\text{MAE} = 110.5 \mu\text{g L}^{-1}$). All species predictions aside from Rainbow trout *Oncorhynchus mykiss* and Red drum *Sciaenops ocellatus* were found in between the 1:1 line and the 10-fold difference range (Fig. 3). Randomization test indicated that the correlation between observed and predicted values is significantly higher than what is expected under random shuffling of the species-specific sensitivity data ($N = 1000$ iterations, $p < 0.001$, Fig. S4). The prediction accuracy of the TESS model was comparable and not statistically different from previously published PAH sensitivity ICE model for five common species that could be modeled ($\text{MAE}_{\text{TESS}} = 158.6 \mu\text{g L}^{-1}$, $\text{MAE}_{\text{ICE EPA}} = 122.4 \mu\text{g L}^{-1}$, Supplementary Section 1.3). The key difference between the modeling platforms is the number of modellable species out of the total 61 local key species: 7 species for the ICE model (11.5%), compared to 54 (88%) in the TESS model.

Table 1

Observed and predicted $\text{LC}_{50}|\text{EC}_{50}$ values ($\mu\text{g L}^{-1}$) for marine species across developmental stages, with the corresponding taxonomic distance applied in TESS model.

Organism	Developmental stage	Observed $\text{LC}_{50} \text{EC}_{50}$ ($\mu\text{g L}^{-1}$)	Trophic level	Predicted $\text{LC}_{50} \text{EC}_{50}$ ($\mu\text{g L}^{-1}$)	Taxonomic distance
<i>Crassostrea virginica</i>	Early life stage	82.22	3	308.4	Within same class
<i>Cyprinodon variegatus</i>	Early life stage	165.14	3	467.94	Within same order
<i>Cyprinodon variegatus</i>	Juvenile and adult	181.76	2.4	257.87	Within same class
<i>Cynoscion nebulosus</i>	Early life stage	63.15	3	29.52	Within same family
<i>Callinectes sapidus</i>	Early life stage	33.61	3	36.87	Within same order
<i>Fundulus grandis</i>	Early life stage	467.94	3	165.14	Within same order
<i>Seriola lalandi</i>	Early life stage	11.2	3	10.33	Within same genus
<i>Coryphaena hippurus</i>	Early life stage	22.37	3	17.19	Within same order
<i>Sciaenops ocellatus</i>	Early life stage	29.52	3	63.15	Within same family
<i>Sciaenops ocellatus</i>	Juvenile and adult	130.6	4.07	1.24	Within same class
<i>Menidia beryllina</i>	Early life stage	62.13	3	62.33	Within same family
<i>Litopenaeus setiferus</i>	Juvenile and adult	277.63	2.7	88.09	Within same genus
<i>Palaemonetes pugio</i>	Juvenile and adult	143.12	2.71	156.38	Within same order
<i>Rachycentron canadum</i>	Early life stage	43.9	3	13.73	Within same order
<i>Thunnus maccoyii</i>	Early life stage	1.57	3	2.37	Within same genus
<i>Thunnus albacares</i>	Early life stage	6.25	3	1.19	Within same genus
<i>Paralichthys lethostigma</i>	Early life stage	32.51	3	19.67	Within same class
<i>Acartia tonsa</i>	Juvenile and adult	64.38	2	37.08	Within same order
<i>Anchoa mitchilli</i>	Early life stage	2.95	3	3.73	Within same order
<i>Lutjanus campechanus</i>	Early life stage	30.97	3	19.72	Within same class
<i>Calanus glacialis</i>	Juvenile and adult	101.34	2.3	13.57	Within same genus
<i>Boreogadus saida</i>	Juvenile and adult	88.9	3.6	77.74	Within same class
<i>Myoxocephalus scorpius</i>	Early life stage	68.56	3	18.92	Within same class
<i>Amphiprion clarkii</i>	Juvenile and adult	257.87	2.9	181.76	Within same class
<i>Menidia beryllina</i>	Juvenile and adult	79.65	3.17	82.14	Within same class
<i>Americamysis bahia</i>	Juvenile and adult	36.72	2.3	24.1	Within same family
<i>Penaeus vannamei</i>	Juvenile and adult	88.09	2.7	277.63	Within same genus
<i>Arbacia punctulata</i>	Early life stage	297.19	3	133.66	Within same class
<i>Dendraster excentricus</i>	Early life stage	133.66	3	297.19	Within same class
<i>Gadus morhua</i>	Early life stage	45.86	3	19.32	Within same class
<i>Thunnus thynnus</i>	Early life stage	0.9	3	3.13	Within same genus
<i>Seriola dumerili</i>	Early life stage	10.33	3	11.2	Within same genus
<i>Janicella spinacauda</i>	Early life stage	24.2	3	43.45	Within same order
<i>Palaemonetes pugio</i>	Early life stage	56.16	3	28.52	Within same order
<i>Tritia obsoleta</i>	Early life stage	19.68	3	159.24	Within same phylum
<i>Americamysis bahia</i>	Early life stage	91.43	3	35.75	Within same class
<i>Mulinia lateralis</i>	Early life stage	308.4	3	82.22	Within same class
<i>Clupea pallasii</i>	Early life stage	3.73	3	2.95	Within same order
<i>Oncorhynchus mykiss</i>	Early life stage	6.4	3	21.43	Within same class
<i>Eurytemora affinis</i>	Early life stage	34.98	3	45.21	Within same phylum
<i>Pocillopora damicornis</i>	Juvenile and adult	207.03	2.5	418.33	Within same order
<i>Acropora cervicornis</i>	Juvenile and adult	210.92	2.5	414.45	Within same order
<i>Porites astreoides</i>	Juvenile and adult	829.69	2.5	208.97	Within same order
<i>Cyclopterus lumpus</i>	Juvenile and adult	75.89	3.89	84.15	Within same class
<i>Oncorhynchus mykiss</i>	Juvenile and adult	1.24	4.08	130.6	Within same class
<i>Atherinops affinis</i>	Early life stage	62.33	3	62.13	Within same family
<i>Holmesimysis costata</i>	Juvenile and adult	24.1	2.3	36.72	Within same family
<i>Calanus finmarchicus</i>	Juvenile and adult	13.57	2.7	101.34	Within same genus

3.2. Oil spill spatiotemporal simulation

The oil-CMS transport model indicated that a total area of 12,788 km^2 was contaminated by the oil spill. The simulated release of 100 metric tons of oil over an 18-day model run, accounting for ocean currents, temperature, salinity, and atmospheric surface winds, indicated that the oil spill spread toward the Israeli coast and the southern Lebanese coast. Average surface oil concentrations ranged from approximately 1000 $\mu\text{g L}^{-1}$ near the spill core to less than 1 $\mu\text{g L}^{-1}$ in areas distant from the spill (Fig. 4). Correspondingly, maximum PAHs concentrations ranged from 59.4 to 118.7 $\mu\text{g L}^{-1}$ near the spill core to as low as 0.006 $\mu\text{g L}^{-1}$ in remote areas.

3.3. Quantitative assessment of species-level potential impacts of the EMS oil spill

The taxonomy-based model generated predictions for 54 of the 61 local key species typically inhabiting the study area (Supplementary Table S6). Predicted $\text{LC}_{50}|\text{EC}_{50}$ values varied by more than two orders of magnitude between the most and the least sensitive species. Larvae of anchovy (*Engraulis encrasicolus*) were the most sensitive, with a

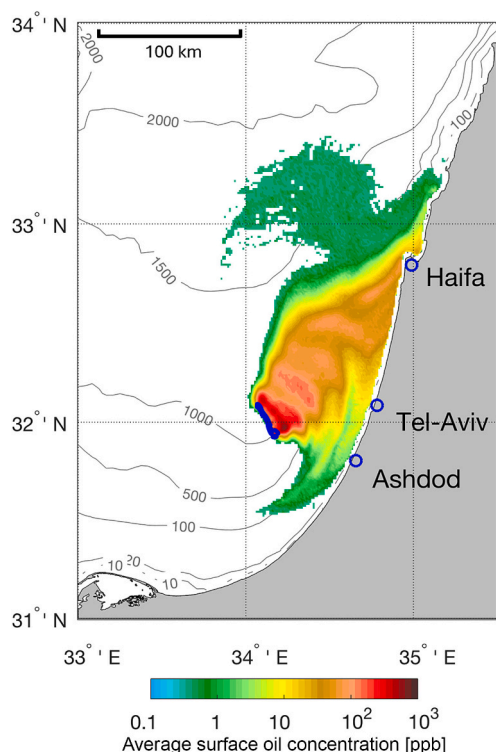


Fig. 4. The average surface oil concentration (in ppb) as modeled by oil-CMS from 11 to 28 in February 2021. Color indicates oil concentration in ppb. Location of the initial oil slick at 0000 UTC on 11 February 2021 is shown as a blue line around 32°N and 34.2°E. The amount of oil released at the slick location was set to 100 metric tons. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

predicted sensitivity of $2.77 \mu\text{g L}^{-1}$ PAHs, whereas the siphonophores

Sphaeronectes koellikeri and *Nanomia bijuga*, were the least sensitive, with predicted values of $407.5 \mu\text{g L}^{-1}$ PAHs. Most key species (87%) had predicted sensitivities ranging between 10 and $70 \mu\text{g L}^{-1}$ PAHs.

The application of these sensitivity predictions was applied in the simulated EMS oil spill scenario, assuming ΣPAHs fraction of 1.5% in crude oil. Results indicated that up to 46 of 61 pelagic key species (75.4%) were potentially affected in the core area near the oil slick (Fig. 5) with similar outcomes observed under a 3% ΣPAHs . Potentially affected species reached up to 83.6% under a 7% ΣPAHs fraction in crude oil (see Supplementary Section 1.5). The proportion of affected pelagic key species declined with increasing distance from the spill core and in accordance with decreasing PAHs concentration (Fig. 5A). Examination of impacts at the taxonomic class level shows that, at a maximum PAH concentration of $118 \mu\text{g L}^{-1}$, 28 of 31 Actinopterygii species (90.3%), 10 of 11 Hexanauplia species (91%), all Gastropoda species, and the planktonic crustacean groups Branchiopoda, Ostracoda, and Thecostraca were impacted (Fig. 5B). At intermediate PAHs concentrations of $50 \mu\text{g L}^{-1}$, all Gastropoda species examined (5 of 5; 100%) were affected (Fig. 5C). At lower concentrations of $15 \mu\text{g L}^{-1}$, impacts were limited to 3 of 32 Actinopterygii species (9.4%) (Fig. 5D).

4. Discussion

We introduce a novel taxonomy-based model that successfully predicts species-specific sensitivity to PAHs, filling critical data gaps for marine species with no prior PAH toxicity records. By integrating this model with the oil-CMS transport model, our framework provides for the first time a spatially explicit quantitative assessment of the impact of oil pollution on biodiversity.

The results indicate that toxicological data from aquatic organisms belonging to closely related taxonomic groups, trophic levels, and developmental stages can serve as a reliable predictor for species-specific sensitivity to PAHs with a certain quantifiable error. This pattern is expected, as closely related taxa tend to share morphological, physiological, and behavioral traits owing to their evolutionary

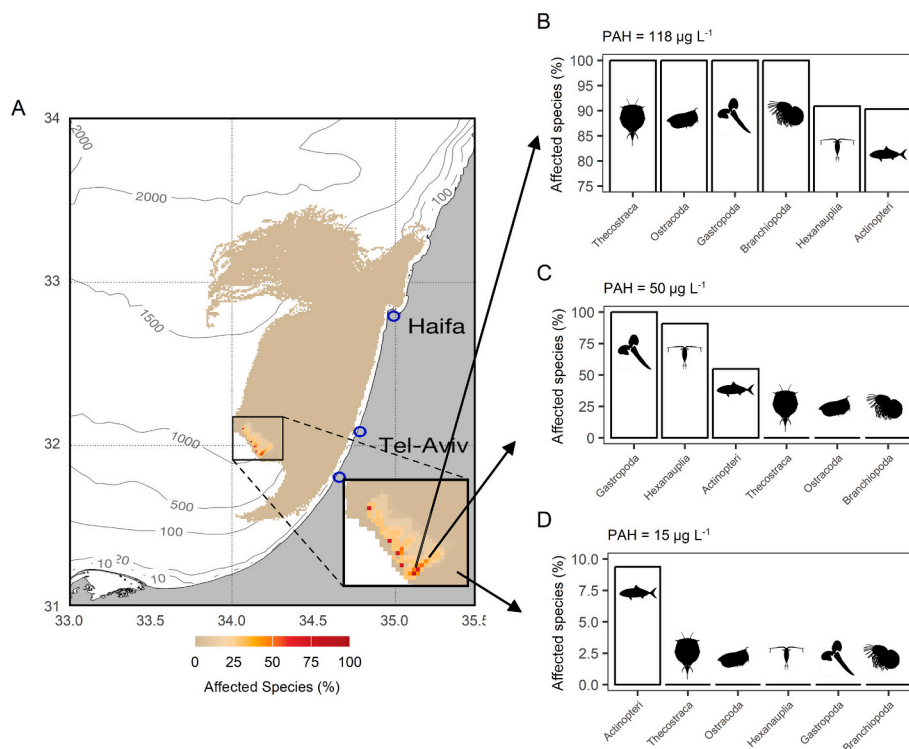


Fig. 5. Key species impacted in a 100 metric ton oil spill simulation. Color map (A) represents the percentage of the affected species out of the predicted species per grid cell in the domain. Column graphs (B,C,D) show the percentage of affected species in hierarchical taxonomic rank of class.

relationships (Strauss and Bond, 1990). Shared functional traits, such as body size, lipid content and metabolic enzyme activity (Martini et al., 2021), can strongly influence sensitivity to toxicants (Baird and Van den Brink, 2007; Guénard et al., 2011) as they govern pollutant uptake, metabolism and detoxification processes. For example, lipid content can modulate sensitivity to lipophilic compounds such as PAHs by acting as a reservoir for chemical accumulation, potentially reducing the fraction reaching sensitive target tissues (Gainer et al., 2018). In addition, enzymatic activity of the cytochrome P450 1A (CYP1A) subfamily, particularly CYP1A1, plays a central role in metabolic activation of PAHs into reactive intermediates (Incardona et al., 2004; Kumar et al., 2026).

Similarly, trophic position is linked with sensitivity to PAHs because it is strongly associated with body size (Romanuk et al., 2011; Woodward and Hildrew, 2002) and feeding habits (Baird and Van den Brink, 2007). Organisms at higher trophic levels (e.g., carnivores) tend to accumulate higher concentrations of PAHs than lower-level omnivores (Wang et al., 2025). Sensitivity to oil pollution also varies across life stages, with early developmental stages typically being more vulnerable than juveniles or adults due to physiological constraints (Petersen and Kristensen, 1998; Sørhus et al., 2021).

The oil-CMS transport model (Fig. 4) matched the dynamics observed in the field during the spill in terms of time and shore extent impact. Consistent with model results, tar landings were first reported on the morning of the 17 February 2021 along most of the Israeli EMS coastline and spread to the entire coastline by the following day (Ministry of Environmental Protection, 2022).

The integration of sensitivity with oil-CMS transport models indicated that the large area of the spill has a substantial impact on the local marine biodiversity: between ~20% and ~50% affected pelagic species in proximity to the oil slick and up to 75.4% near the core area (Fig. 5). During and following the EMS oil spill, numerous observations of dead marine animals attributable to tar exposure were reported, primarily involving sea turtles and seabirds (Ministry of Environmental Protection, 2022). Our findings suggest that the ecological damage was potentially more extensive than previously reported, affecting a broader range of species, particularly early life stages and small organisms, which are often excluded from oil spill assessments despite their important roles in long-term ecosystem functioning.

Comparison against ICE models (see Fig. S5 and Supplementary Section 1.3) indicated that the taxonomy-based method had a smaller MAE relative to the CAFE database and EPA-derived ICE model. The fundamental differences in model design make our framework particularly suitable for assessing PAH impacts in regions beyond North America, as ICE models are built largely on North American species (Liu et al., 2022). Indeed, ICE models were unable to generate predictions for EMS species, underscoring this limitation. Moreover, toxicity estimates derived from individual PAH, as applied in the ICE models, are inherently conservative relative to mixture-based evaluations, as they fail to capture the enhanced or synergistic effects arising from interactions between different PAHs (Hodson, 2017).

A data-driven approach, while very powerful, is fundamentally reliant on the availability and quality of its data. This study is primarily based on toxicity data and therefore mainly limited by the scant amount of oil pollution toxicological studies, particularly for ΣPAHs as a mixture. Developing a predictive model under such data limitations may lead to inaccuracies. Moreover, organisms within the same taxonomic group may exhibit different tolerances to PAHs (Honda and Suzuki, 2020). Although such cases are relatively uncommon, they introduce additional uncertainty. Here, for example, the sensitivity of 13 distinct pelagic fish species was predicted as a single $LC_{50}|EC_{50}$ value of $53.33 \mu\text{g L}^{-1}$ PAHs (Supplementary Table S6). This simplification arose because all species were adult-stage from the class of Actinopterygii and no toxicity data of other organisms within lower taxonomic ranks were available. Given that 72% of the observed values fall within the $0\text{--}100 \mu\text{g L}^{-1}$ range, the model's MAE of $110.5 \mu\text{g L}^{-1}$ PAHs is substantial and

may be particularly consequential for sensitive species and early life stages (French-McCay et al., 2023). Nevertheless, the option of assessing the impacted species from oil spills with a certain error is better than a complete lack of such capability.

The use of multiple data sources such as governmental (EPA) databases, NOAA's DWH Trustee Toxicity Testing Program and the broader scientific literature can introduce variability and lack of uniformity across the compiled dataset. This may lead to biases in toxicity estimates. For example, studies using ΣPAH50 may report higher $LC_{50}|EC_{50}$ values than those based on EPA ΣPAH16 as they sum a broader set of analytes, potentially leading to misinterpretation of lower apparent toxicity and reduced organismal sensitivity to PAHs.

Oil spill events such as the EMS spill typically persist for several days; accordingly, we included data from exposure durations ranging from hours to days, without explicitly distinguishing between acute and chronic effects. As a result, immediate, predominantly lethal responses associated with acute exposure - more commonly represented in available datasets - may obscure slower, long-term, cumulative, sub-lethal effects of chronic exposure (e.g., reduced growth and reproduction, low settlement rates). This limitation may lead to an underestimation of long-term, population-level risks and particularly their impact on long-lived species. While field observations of oiled animals (e.g., sea turtles and birds) provide clear evidence of exposure to oil, they do not necessarily indicate biological impact or causality. Establishing such links requires targeted validation through mortality surveys and/or biomarker-based approaches (e.g., PAH metabolites or CYP1A induction; Miller et al., 1998; Kim et al., 2013; Pei et al., 2022). Given these limitations, the TESS model should be considered a screening-level tool that supports environmental risk assessment and management decision-making rather than a definitive measure of ecological impact. It is not intended to replace empirical toxicological approaches which provide precise $LC_{50}|EC_{50}$ estimates.

These limitations in data availability emphasize the need for additional toxicological research, particularly on ΣPAHs as complex mixtures. Notably, while toxicity data are relatively abundant for certain taxonomic groups (e.g., fish and crustaceans), they remain scarce for others, like corals, which frequently serve as bioindicators for water contamination (Yang et al., 2020), underscoring the need to quantify PAH sensitivity across a broader range of taxa. This imbalance largely reflects the long-standing reliance on a limited set of model species used in ecotoxicological testing under EPA and EU regulatory frameworks. However, these species do not adequately represent the biodiversity of most marine ecosystems. Expanding and regionally tailoring species lists to reflect local ecological communities would therefore substantially improve our capacity to assess the impacts of PAHs and oil spills on marine biodiversity.

Future work will integrate taxon-specific abundance data into our modeling framework to estimate the number of individuals and biomass affected by oil pollution, both retrospectively and prospectively for hypothetical future scenarios. By advancing from species-level sensitivity to population and community-level impact assessments, this data-driven approach enhances our ability to understand the ecological consequences of petroleum pollution on marine biodiversity, while also supporting sustainable management, accountability, and the protection of marine and coastal ecosystems and the vital services they provide to humanity.

CRediT authorship contribution statement

Omri Lapidot: Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Formal analysis, Conceptualization. **Natalie Perlin:** Writing – original draft, Visualization, Software, Methodology, Formal analysis. **Eli Biton:** Writing – original draft, Software, Methodology. **Pavel Khain:** Writing – original draft, Methodology, Data curation. **Yoav Levi:** Writing – original draft, Software, Data curation. **Pinhas Alpert:** Writing – original draft,

Methodology, Data curation. **Debra Ramon**: Writing – original draft, Methodology, Conceptualization. **Nir Stern**: Writing – original draft, Methodology, Data curation. **Gil Rilov**: Writing – original draft, Data curation. **Tamar Guy-Haim**: Methodology, Data curation. **Yoav Lehahn**: Writing – original draft, Methodology. **Claire B. Paris**: Writing – original draft, Validation, Methodology. **Igal Berenshtein**: Writing – review & editing, Writing – original draft, Visualization, Supervision, Software, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Conceptualization.

Declaration of Generative AI and AI-assisted technologies in the writing process

During the preparation of this work the author(s) used chatGPT in order to improve language and readability of the manuscript. After using this tool/service, the author(s) reviewed and edited the content as needed and take(s) full responsibility for the content of the published article.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.marpolbul.2026.120090>.

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