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REVIEW

Oryzias javanicus as a Bioindicator in Southeast Asian Intertidal Waters: Integrating Bibliometric Mapping with Ecotoxicological Evidence

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ABSTRACT

This study assesses the suitability of *Oryzias javanicus* as a bioindicator for Southeast Asian intertidal waters by combining bibliographic network mapping with laboratory and field ecotoxicology to reveal how mechanistic, reproductive, developmental, and pathology endpoints align with estuarine research in Malaysia, Indonesia, and Thailand. The objectives were to map the structure and evolution of Oryzias research; extract biological insights on life stage, population structure, and habitat use relevant to monitoring; evaluate ecotoxicological endpoints that provide decision ready indicators; assess the alignment of these endpoints with sustainability goals in intertidal systems; and derive SWOT and TOWS strategies. The mapping resolved four clusters with a clear chronology. Environmental exposure and early life stages anchor the estuarine use case, while organ pathology and disease consolidate outcome measures. More recent work concentrates on mechanistic biomarkers and endocrine endpoints that are compatible with regulatory testing. Across clusters, *O. javanicus* functions as the hub that links field exposures with laboratory inference. The discussion synthesizes these signals into a three module monitoring design. First, quarterly embryo to juvenile assays target metals, herbicides, pharmaceuticals, nanoparticles, and microplastics with LC_{50} and cardiac endpoints. Second, semi-annual adult histopathology and reproductive assessments track chronic risk and fecundity. Third, an annual disease and microbiome panel captures co-occurring microbial hazards. SWOT and TOWS analyses highlight strengths in regional validation and euryhalinity, identify weaknesses in omics resources, and convert them into strategies for reference lines, mixture realistic assays, and habitat coupled metrics.

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1. Introduction

Small euryhaline fishes in the genus *Oryzias* occupy creeks, mangroves, and estuaries across tropical Asia, making them natural sentinels for land–sea interfaces where pollutants and salinity regimes fluctuate. Foundational systematics clarified species boundaries and diversity in the group, supplying the taxonomic scaffolding for ecological and toxicological work[1–3]. Regional surveys then documented distribution and identification keys for Thai ricefishes and demonstrated co-occurrence of congeners across salinity gradients in Peninsular Malaysia, positioning *Oryzias javanicus* as a tractable estuarine model[4,5]. Early cytogenetic studies and later barcoding efforts further stabilized species diagnosis and life-stage studies, which are essential for reproducible biomonitoring[6,7]. Recent rediscovery and reproductive isolation data for *O. hubbsi* underscore that species limits within Southeast Asian *Oryzias* remain relevant to monitoring design and data comparability[8].

Among the *Oryzias* genus, the Japanese medaka (*Oryzias latipes)*, a freshwater species native to Japan, has been extensively studied in environmental toxicology, and its developmental biology is well characterized. Consequently, it has been designated as one of the model organisms under the OECD test guidelines. However, as a freshwater species, the Japanese medaka is not suitable for ecotoxicological studies targeting coastal or marine environments[9,10].

In contrast, *O. javanicus*, distributed across coastal areas of Southeast Asia, inhabits estuarine and intertidal environments, making it a practical bioindicator for pollutant assessment in these ecosystems[11]. This species tolerates both freshwater and brackish conditions and allows evaluation of a wide range of endpoints from embryonic stages to adults, rendering it a valuable model organism for chemical management and ecosystem conservation in coastal and estuarine waters[12]. Ecologically, *O. javanicus* is embedded in intertidal assemblages that are structured by tidal, diel, and lunar cycles, providing predictable access for standardized sampling and exposure assessment. Studies from southwest Thailand, Lombok, and Banten Bay show consistent community organization in mangrove creeks and forests, implying that sentinel signals from *O. javanicus* can be interpreted alongside assemblage trends and nursery functions[13]. Community-level and bioindicator applications already link fish burdens to local chemistry in estuaries of the Malaysian west coast and to lead or cadmium exposure in Indonesian sites, demonstrating field–lab translation potential[14–16]. Population genetic work across the Indonesian Archipelago and brackish Thai systems reveals geographic structure within *O. javanicus* and congeners, a consideration for establishing regional reference lines and for interpreting site effects[17–20].

Ecotoxicology with *O. javanicus* spans classic priorities and emerging contaminants, yielding a multi-tier indicator suite from LC_{50} to histopathology and mechanistic biomarkers[21,22]. Acute and early-life assays define sensitivity to mercury and cadmium and document inducible defenses such as metallothionein, which anchor risk screening in intertidal settings[23–25]. Herbicide and antifouling exposures link endocrine and behavioral outcomes to management contexts in agriculture and marinas, while pharmaceuticals and microplastics extend the model to wastewater and urban leakage scenarios[26–31]. Developmental toxicity from zinc oxide nanoparticles has been replicated across laboratories and venues, strengthening confidence in embryo-based early-warning endpoints[32,33]. Disease-model studies on *Streptococcus agalactiae*, aeromoniasis, and vibriosis suggest a practical One-Health interface where chemical and microbial risks can be co-monitored in the same sentinel[34–36].

Against this background, the present study integrates bibliographic network mapping with biological and ecotoxicological evidence to evaluate *O. javanicus* as a bioindicator for Southeast Asian intertidal waters. The objectives are fivefold: first, to map the structure and temporal evolution of *Oryzias* research and identify the core clusters that link field exposure, development, endocrine endpoints, and pathology; second, to extract biological insights on life stages, habitat use, and population structure that affect indicator performance; third, to evaluate ecotoxicological endpoints that are decision ready for metals, herbicides, pharmaceuticals, nanomaterials, and microplastics; fourth, to assess alignment with sustainability and intertidal habitat management, including assemblage and nursery functions; and fifth, to derive SWOT and TOWS strategies that convert the evidence base into standardized, mixture-realistic surveillance modules for mangrove and creek systems in Malaysia, Indonesia, and Thailand[5,13,31].

2. Methodology

2.1. Data Source and Search Strategy

We used Elsevier's Scopus database because it indexes multidisciplinary journals and proceedings relevant to ichthyology, ecology, and ecotoxicology. The search was performed in the Scopus advanced interface and the results were exported on 06 October 2025. We queried the Article Title, Abstract, and Author Keywords fields with the following Boolean string:

("*Oryzias javanicus*" OR "Javanese medaka" OR ("*Oryzias*" AND (*javanicus* OR "Java medaka")))

No year limit was imposed at the query stage. Document types included articles, reviews, conference papers, notes, and short communications to capture method reports and first records that often introduce new endpoints or field sites. The initial retrieval returned N = 105 records.

2.2. Screening and Eligibility

Screening proceeded in two passes.

Phase 1 Pass: Bibliographic de-duplication and relevance. We removed exact duplicates and records that were outside scope after reading titles and abstracts. Exclusions at this stage were:

1. studies on non-target *Oryzias* species without comparative relevance to *O. javanicus*;
2. papers where *Oryzias* appeared only in references or author affiliations;
3. articles focused solely on aquaculture husbandry without environmental or toxicological context.

Phase 2 Pass: Geographic and habitat relevance. Because the study evaluates *O. javanicus* as a bioindicator for Southeast Asian intertidal waters, we next screened the records using a country/territory filter in Scopus and full-text checking. We first inspected the 'country/territory' field in Scopus to identify papers whose primary field sites were located in Malaysia, Indonesia, Thailand, the Philippines, or Myanmar. At the time of export, the country panel in the dataset showed the following distribution of hits: Malaysia (24), Indonesia (13), Thailand (7), Philippines (1), and Myanmar (1), with smaller counts for other countries. We then read the full texts to confirm that these records involved intertidal or coastal habitats relevant to *O. javanicus*. Papers from outside these five countries were retained only when they contained (i) experimental or field exposures that mimic Southeast Asian intertidal conditions, (ii) comparative data directly involving *O. javanicus*, or (iii) taxonomic, physiological, or ecological information that could be directly applied to *O. javanicus* populations in Southeast Asia. After completing Phases 1 and 2, the final dataset used for analysis comprised N = 44 records.

2.3. Data Extraction and Harmonisation

For each record we extracted: authors, year, title, source, document type, study country, study habitat (estuary, mangrove creek, coastal lagoon, river mouth), focal life stage, contaminants or stressors, endpoints (for example LC_{50}, histopathology, reproductive indices, behaviour, microbiome, metabolome), and all Author Keywords and Index Keywords.

To reduce sparsity and synonym inflation we harmonised terms by manual thesaurus mapping before network building. Examples include merging "*Oryzias javanicus*," "Javanese medaka," and "Java medaka" under a single controlled label; unifying contaminants (for example "ZnO nanoparticles" → "zinc oxide nanoparticles"; "Cu" → "copper"); standardising anatomical terms ("gonad" and "gonads" → "gonad"; "liver/kidney/brain" kept as separate targets); and collapsing generic measurement terms ("concentration (composition)" → "concentration"). Stop-terms with little semantic value in this corpus (for example "article," "method," "study," "South East Asia" as a region label when a country tag existed) were removed. All taxon names were left in their scientific form and italicised at the reporting stage.

2.4. Keyword Co-Occurrence Network and Clustering

We constructed co-occurrence networks from the union of Author and Index Keywords using binary counting. To focus on stable signals while retaining breadth typical of small-to-medium bibliographies, we set the minimum keyword occurrence to 3. Keywords that met the threshold were normalised using association strength and laid out with the default VOSviewer attraction–repulsion routine. Clusters were identified by modularity optimisation with the resolution parameter = 1.00.

Network diagnostics recorded for quality control were number of nodes after thresholding, average degree, modularity, and silhouette-like separation checked visually at multiple random seeds. To test robustness, we ran sensitivity analyses by varying the minimum occurrence to 2 and 4 and confirmed that the thematic cores and their bridges were conserved.

2.5. Temporal Overlay

To visualise knowledge progression we computed the average publication year for each keyword (weighted by binary presence in documents). The same network topology was coloured by this average in an overlay map with a continuous scale matching the year range of the corpus. This produced the left–right and centre–periphery temporal patterns discussed in the Results, with earlier nodes in cooler tones and newer signals in warmer tones.

2.6. Country and Habitat Profiling

We used Scopus “Affiliation Country/Territory” and “Study Area” information supplemented by full-text reading to code each record’s primary study country and habitat class. For multi-site papers, the Southeast Asian intertidal site determined the tag. We then generated simple frequency profiles to verify that the narrowed dataset reflects the regional focus: most records are from Malaysia, Indonesia, and Thailand, with sparse contributions from the Philippines and Myanmar. Habitat tagging confirmed that estuaries, mangrove creeks, and river mouths dominate the final set.

2.7. Endpoint Taxonomy

To support cross-study comparison we created an endpoint taxonomy with five families:

1. Acute and sub-acute metrics (LC_{50}, Mortality, Behaviour);
2. Reproductive and endocrine (Gonad histology, Fecundity indices, Sex difference, Endocrine disruptor flags);
3. Organ pathology (Liver, Kidney, Brain histopathology);
4. Mechanistic markers (Oxidative stress,Enzyme inhibition, Metabolome/microbiome changes);
5. Developmental (Embryo development, Heart rate, Malformations). Each article could map to multiple families. This taxonomy underlies the bridges described between clusters in the Results.

2.8. Software and Reproducibility

Bibliographic records were exported from Scopus as CSV with full citation data and keywords. Text cleaning and thesaurus mapping were performed in a reproducible worksheet (available upon request). VOSviewer was used for network and overlay construction; parameter files were archived with the export. All counts reported in the Results reflect the final curated set of N = 44. A PRISMA-style flow was kept internally with tallies at each step: retrieval 105, de-duplication and relevance screen 78, geographic and habitat screen.

2.9. Ethical and Quality Considerations

This bibliometric synthesis uses published materials only. To reduce selection bias, we preserved conference and short-format items when they reported first records, methodological advances, or site baselines. To mitigate language bias, non-English abstracts were screened with English metadata; where clarity was insufficient, the item was excluded during Pass 1. Finally, all species names and sensitive ecological terms were verified against the original papers during harmonisation to avoid propagation of indexing errors.

3. Results

Figure 1 presents the keyword co-occurrence network for the *Oryzias* literature, and **Figure 2** overlays the same network with average publication year. Four major clusters emerge and they align with distinct research foci. The temporal colours in **Figure 2** help track how each cluster matured across the record.

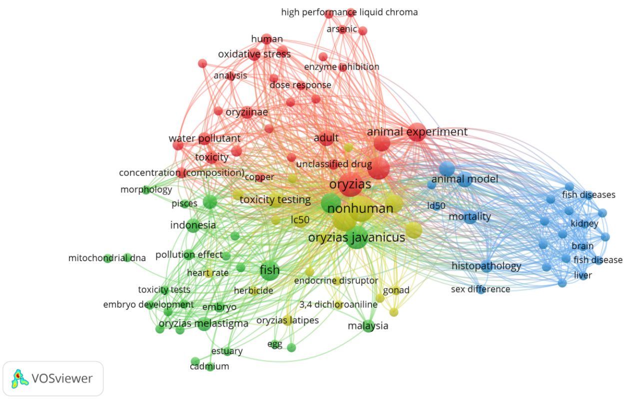

Figure 1. Keyword co-occurrence network for *Oryzias* research based on author and index keywords. Node size reflects frequency, edge thickness reflects co-occurrence strength, and colors denote four communities: red, toxicity mechanisms and analytics; green, environmental exposure and early life stages; yellow, endocrine and regulatory endpoints; blue, disease and organ pathology.
Note: Based on 101 items with 4 major clusters, with 2 minimum number of occurrences of a keyword, out of 424 keywords with 101 met the threshold.

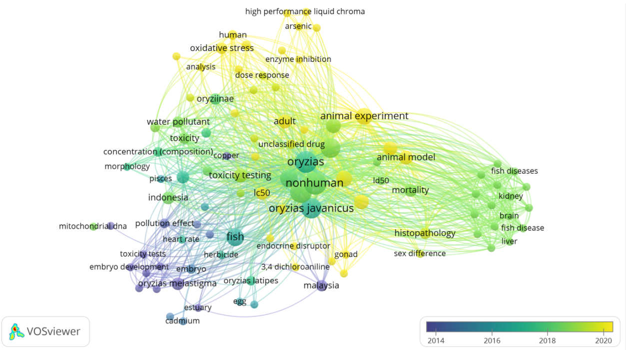

Figure 2. Temporal overlay of the same network shown in **Figure 1**. Node color encodes the average publication year on a blue to yellow scale, which highlights early emphasis on developmental and habitat terms, mid-period consolidation of pathology endpoints, and later growth in mechanistic biomarkers and endocrine testing.
Note: Based on 101 items with 4 major clusters, with 2 minimum number of occurrences of a keyword, out of 424 keywords with 101 met the threshold.

3.1. Cluster 1. Toxicity Mechanisms and Chemical Analytics (Red in Figure 1, Yellow to Yellow-Green in Figure 2)

The red community in **Figure 1** concentrates terms that mark controlled exposures and mechanistic assays, including “Animal experiment,” “Adult,” “Dose response,” “Enzyme inhibition,” and “Oxidative stress.” Analytical and compound terms such as “High performance liquid chroma,” “Arsenic,” “Copper,” and “Water pollutant” anchor this space. The node “*Oryzias*” sits near the community’s centroid and connects strongly to “Animal experiment,” “Adult,” and “Oxidative stress,” confirming that *Oryzias* species serve as tractable adult models for mechanistic toxicology. Bridges from this cluster to disease outcomes and to endocrine endpoints run through “Animal model,” “Toxicity testing,” and “LC_{50},” which appear at the interface with the blue and yellow communities.

In **Figure 2**, most of these nodes are yellow to yellow-green, which places their main growth between about 2017 and 2020. The later coloration of “Oxidative stress,” “Enzyme inhibition,” and “Dose response” indicates an expansion in biomarker-driven studies and analytic chemistry in the most recent period.

3.2. Cluster 2. Environmental Exposure and Early Life Stages in Estuarine Systems (Green in Figure 1, Blue-Green to Green in Figure 2)

The green community in **Figure 1** (left) assembles habitat and life-stage language around “Nonhuman,” “*Oryzias javanicus*,” and “Fish,” with environmental anchors such as “Estuary,” “Pollution effect,” and “Indonesia.” It also contains contaminants and pesticides that dominate field-relevant testing, for example “Cadmium,” “Copper,” “Herbicide,” and “3,4-dichloroaniline,” together with developmental markers “Embryo,” “Embryo development,” “Egg,” “Heart rate,” and “Mitochondrial DNA.” This structure shows that much of the *O. javanicus* work couples estuarine exposure contexts to early life-stage endpoints.

As seen in **Figure 1**, connectivity to Cluster 1 runs through shared chemicals and “Toxicity testing,” while connections to the endocrine and disease clusters run through “Gonad,” “Mortality,” and “Histopathology.” In **Figure 2**, the colour gradient moves from blue-green nodes such as “Mitochondrial DNA,” “Embryo development,” and “*Oryzias melastigma*,” which appear earlier in the time series, to greener and yellow nodes like “pollution effect,” “Herbicide,” and “3,4-dichloroaniline,” which mature later. This pattern suggests an early focus on species and developmental baselines followed by broader contaminant testing in Malaysian and Indonesian estuaries.

3.3. Cluster 3. Endocrine and Reproductive Toxicity with Regulatory Endpoints (Yellow in Figure 1, Yellow-Green in Figure 2)

The yellow community in **Figure 1** centers on decision-oriented endpoints. Core nodes include “LC_{50},” “Toxicity testing," "Endocrine disruptor," "Gonad," and the chemical "3,4-dichloroaniline," with "Malaysia" acting as a regional anchor. The proximity of "LC_{50}" and "Toxicity testing" to "*Oryzias javanicus*" shows that the species is widely used to generate quantitative metrics required in hazard assessment. Links to "Gonad" and to "Sex difference," which sits at the interface with the blue pathology community, indicate frequent use of reproductive tissues and sexual dimorphism as readouts.

In **Figure 2**, the community is predominantly yellow-green, placing most activity in the 2016 to 2020 window. Its position between the red and blue communities in **Figure 1** reflects its bridging role from mechanistic laboratory assays to organ pathology.

3.4. Cluster 4. Disease, Pathology, and Organ-Specific Responses (Blue in Figure 1, Green to Yellow-Green in Figure 2)

The blue community in **Figure 1** gathers clinical and organ endpoints such as "Fish diseases," "Mortality," and "Histopathology," together with the organ targets "Liver," "Kidney," and "Brain." The nearby "Animal model" and "Sex difference" nodes show that disease studies use structured experimental designs and often consider sex as a biological variable. Thick edges connect this community to the red mechanistic cluster via "Animal experiment", and to the yellow endocrine cluster via "Histopathology," making it the central outcome hub of the network.

In **Figure 2**, these nodes are mainly green with some yellow-green, indicating sustained growth from around 2016 onward. Earlier blue-green neighbours at the left margin connect back to developmental topics from Cluster 2, which suggests a methodological progression from embryo effects to organ pathology across the timeline.

4. Discussion

4.1. The Biological Insights of the Mappings

The network shows that *O. javanicus* anchors a coherent research program that integrates life history, population structure, and organ biology. The dense bridging of "*Oryzias*," "Nonhuman," and "*O. javanicus*" to both mechanistic and organ-level terms reflect how this euryhaline species connects laboratory inference with estuarine ecology. Baseline systematics and distribution work provide the long spine of that integration. Early taxonomic syntheses of Asian ricefishes and the description of congeners established the comparative canvas on which model use later expanded [1]. Regionally resolved accounts from Thailand and Peninsular Malaysia then clarified the presence of closely related species across salinity gradients and helped explain why *O. javanicus* is a practical sentinel for estuarine and mangrove margins [4,5]. Cytogenetic and mitochondrial reports strengthened the species framework for developmental and population studies, which the map registers as early, blue-green signals around "Embryo development" and "Mitochondrial DNA" [6,7].

Population genetic structure along the Indonesian Archipelago indicates measurable divergence within *O. javanicus*, which bears directly on experimental reproducibility and local adaptation to stressors [17]. Complementary work on mitochondrial and nuclear markers in Thai brackish congeners, including *O. minutillus*, shows that brackish populations can maintain distinct haplogroups and that geographic mosaics are common in Southeast Asia's coastal networks [19,20]. The network's ecological flank also ties *O. javanicus* to community context. Mangrove and creek assemblage studies clarify diel and tidal organization and the likely co-occurrence of *Oryzias* with stressors and pathogens, consistent with the strong links from "Fish" to "Estuary," "Pollution effect," and "Fish diseases" [11–13,37]. Together these foundations explain why developmental, reproductive, and organ-specific endpoints are so central in the map. They are nested in a biologically coherent species complex with well-described habitats, population structure, and community interactions that make inference generalizable across sites and years [17,38].

A complementary insight from the mapping is that the *Oryzias* platform continues to widen taxonomically and geographically. Rediscovery of *O. hubbsi* and clarification of reproductive isolation with *O. javanicus* show that speciation boundaries remain an active subject, which matters for biomonitor choice and for interpreting cross-study variation when nontarget *Oryzias* occur in samples [8]. The map therefore captures a field where biological scaffolding and model traits evolved in tandem with toxicology questions, and where population and community context now inform experimental design as a matter of routine[17,20].

4.2. The Ecotoxicological Perspectives

The red and yellow clusters converge on a clear toxicology agenda. Studies span metals, pesticides, pharmaceuticals, and microplastics, with reproducible translation from acute metrics to tissue and cellular mechanisms. Acute and sub-acute metals work established sensitivity ranges in early life stages and juveniles and demonstrated classic inducible defences such as metallothionein, which the network expresses through bridges from "LC_{50}" to "Histopathology" and "Enzyme inhibition"[23–25]. Estuarine co-exposures are well represented: cadmium and copper produce short-time effects and developmental toxicity consistent with field composition data and with the early embedding of "Cadmium," "Copper," and "Concentration" in the green environmental cluster[14–16].

Endocrine and reproductive endpoints form a second pillar. Diuron exposure impairs gonadal architecture and functions as an endocrine disruptor, while mercury produces gonadal lesions detectable histologically, explaining the map's strong path from "Endocrine disruptor" and "Gonad" to "Histopathology" and "Sex difference"[26]. Antibiotics and personal-care compounds add a pharmaceutical dimension. Erythromycin induces sex-contextual responses, and fluoxetine perturbs neurotransmission and endocrine axes in aquatic animals, consistent with the proximity of "Dose response," "Enzyme inhibition," and "Unclassified drug" to the mechanistic core[28,29]. Engineered nanomaterials further widen the stressor space. Zinc oxide nanoparticles cause developmental and embryonic toxicity with clear dose responses across experiments in *O. javanicus*, and these findings replicate across independent groups and journals, strengthening their evidentiary weight[32,33].

Microplastics studies demonstrate system-level responses that bridge the mechanistic and disease clusters in the map. Polystyrene particles shift the gut microbiome and metabolome and produce multi-organ histological alterations and neurotoxicity, aligning with the right-hand blue community containing "Liver," "Kidney," and "Brain" and with the central mechanistic terms related to oxidative stress[30,31]. Complementary acute assays with copper pyrithione confirm behavioral and survival thresholds relevant to risk characterization for antifouling agents, supporting the network's emphasis on LC_{50}-type endpoints[27]. The coherence across chemicals, organs, and biomarkers is the most striking ecotoxicological feature of the mapping. *O. javanicus* yields internally consistent signal chains that run from exposure concentration to organismal performance and then down to tissue and cellular markers, which increases confidence in inferred mechanisms across contaminant classes[23,26,32,33].

4.3. The Connections to Sustainability Using Java Medaka as a Bioindicator

Several elements in the map support a sustainability narrative built around *O. javanicus*. First, the species occupies boundary waters where land-sea interactions and human pressures concentrate, which is reflected by the green cluster's anchors in "Estuary," "Pollution effect," "Malaysia," and "Indonesia." This makes the species sensitive to watershed decisions, coastal land use, and aquaculture practices that influence contaminant mixtures and salinity regimes[5,11,12]. Second, *O. javanicus* offers a multi-tier indicator suite. Field-adjacent exposures reproduce histological lesions, reproductive impairments, and organ-specific pathology under laboratory control, so early warning at the biomarker level can be coupled to population-relevant outcomes like reduced fecundity or increased juvenile mortality[26,27].

Third, the model helps connect chemical stewardship to ecosystem services in mangrove and creek systems. Assemblage shifts linked to tidal and lunar cycles imply that stressors encountered by *Oryzias* co-vary with nursery functions for other taxa, so medaka biomarker trends are likely to co-vary with broader service indicators such as juvenile fish recruitment and pathogen dynamics[13,37]. Fourth, the species supports a One-Health style interface. Reports on bacterial infections, susceptibility to *Streptococcus agalactiae*, and potential for vibriosis modelling indicate that chemical and microbial risks can be co-monitored using the same sentinel, a point that the blue disease cluster makes explicit[34–36]. Finally, the growing record on pharmaceuticals and microplastics strengthens the link to circular-economy and wastewater governance. Where fluoxetine and erythromycin occur, and where plastic leakage is significant, *O. javanicus* provides practical metrics to test mitigation scenarios, from wastewater polishing to antifouling alternatives and plastic reduction, with measurable improvements in biomarkers and tissue histology as targets[28,29,31].

4.4. SWOT

1) Strengths

The biological platform is compact, inexpensive, and regionally validated. The species tolerates a wide salinity range, enabling both freshwater and brackish testing that reflects real estuarine gradients[38]. Endpoints span LC_{50}, behaviour, histology, and reproductive biology, enabling multi-layer causal chains under controlled conditions, which are well documented across metals, pesticides, pharmaceuticals, nanomaterials, and microplastics[23,26,30,33]. Population and mitochondrial studies provide a genetic frame that can be leveraged to control for cryptic structure and to build local reference strains[17–20].

2) Weaknesses

Comparative genomic resources and standardized omics pipelines remain thinner than for zebrafish, which can limit deep pathway inference and cross-lab comparability for transcriptomic or proteomic biomarkers. Reported sensitivity can vary with salinity, age, and local lineage, complicating the transfer of LC_{50} values without explicit context[17,23]. Field-to-lab translation sometimes lacks paired exposure assessment at the site level, producing uncertainty about realistic mixture proportions, which is visible in the network's broad "Unclassified drug" and compound-agnostic terms.

3) Opportunities

The rise of studies on endocrine disruption, pharmaceuticals, and nanomaterials suggests clear paths for method unification and regulatory engagement in tropical Asia, with *O. javanicus* positioned to provide standardized developmental and reproductive endpoints aligned to decision needs[26,29,32]. Microplastics and metabolome–microbiome coupling are fertile ground for system-level indicators that connect to circular-economy interventions[31]. Mangrove and estuarine conservation programs can integrate *Oryzias* biomarkers with assemblage monitoring to quantify benefits of restoration and riparian protection[11–13].

4) Threats

Habitat loss in mangroves and modification of intertidal creeks may undermine the very conditions that make *O. javanicus* a sentinel, and can introduce selection that shifts sensitivity profiles over short timescales[11,12]. The proliferation of complex contaminant mixtures, including antibiotics and personal-care products, raises mixture-interaction questions that single-compound tests do not capture well, risking underestimation of cumulative effects[17,29]. Competition for funding with globally standard models could slow development of advanced genomic resources required for next-generation mechanistic inference.

4.5. TOWS

1) SO strategies (use strengths to exploit opportunities).

Deploy standardized multi-tier test batteries that couple LC_{50}, reproductive histology, and oxidative-stress biomarkers for priority contaminants in tropical estuaries, leveraging the species' euryhalinity and existing dose-response baselines for metals, herbicides, pharmaceuticals, and nanomaterials[23,26,29,33].

Embed *O. javanicus* assays into mangrove restoration monitoring, using histopathology and embryo-development endpoints as early-warning metrics alongside fish assemblage indicators to quantify restoration gains[12,13].

2) WO strategies (mitigate weaknesses by taking opportunities).

Establish regional reference lines characterized by whole-genome or high-density marker panels derived from documented population structure to reduce variability in sensitivity and to support inter-lab calibration across Malaysia, Indonesia, and Thailand[17–20].

Build mixture-exposure protocols that reflect measured site chemistries from wastewater and mariculture settings and validate outcomes against microbiome and metabolome shifts, closing the gap between single-compound tests and environmental realism[28,30].

3) ST strategies (use strengths to neutralize threats)

Apply the well-validated reproductive and organ-pathology endpoints to evaluate antifouling and agricultural alternatives that claim lower risk, using *O. javanicus* to filter options before field deployment where mangrove habitats remain vulnerable[26,27].

Pair sentinel testing with habitat-protection metrics by aligning biomarker recovery with creek and mangrove integrity indices, ensuring that chemical management and habitat conservation proceed together to buffer against sensitivity drift and local lineage replacement[11,13].

4) WT strategies (minimize weaknesses and avoid threats)

Create a shared regional repository of protocols, reference histology, and dose-response curves across life stages and salinity classes to reduce heterogeneity in LC_{50} and pathology scoring, which will guard against misinterpretation when land-use changes alter background conditions[23,39].

Prioritize funding for genomic and transcriptomic resources so that Southeast Asian laboratories can resolve mechanisms for mixture effects and endocrine disruption in the same depth now common for zebrafish, thereby future-proofing the model against competition and enabling policy-relevant pathway analysis for tropical contaminants[26,29,32].

4.6. The Use of Java Medaka as a Bioindicator in Southeast Asian Intertidal Waters

Java medaka *O. javanicus* is well suited to intertidal monitoring because it is native, abundant, and euryhaline across creek–estuary gradients that typify Southeast Asian shorelines. Field records from Peninsular Malaysia and Thailand show the species co-occurs with sister taxa along salinity transitions, which allows site selection across freshwater–brackish mosaics without moving outside its ecological niche[4,5]. Mangrove and creek assemblage studies from Lombok, Banten Bay, and southwest Thailand document predictable tidal and diel use of channels by small fishes, including *Oryzias*, confirming that intertidal creeks provide consistent access for standardized sampling[11–13]. This natural history matters for biomonitoring because it couples exposure to riverborne and coastal sources, including agricultural runoff, antifouling inputs, aquaculture effluents, and urban discharge.

As a sentinel, *O. javanicus* supports a multi-tier suite of endpoints that link environmental contamination to organismal condition. Early work established sensitivity of embryos and juveniles to priority metals and set LC_{50} baselines for mercury and cadmium that remain useful for site ranking[23]. Site-adjacent studies then tied fish burdens to estuarine sediments and water, for example copper and zinc in west-coast Malaysian estuaries, and specific lead-indicator applications, which demonstrate translation between field chemistry and fish responses[14,15]. Short-time cadmium and copper tests, and cadmium body burdens, further strengthened acute-exposure interpretation for intertidal settings where pulses follow storms and tidal pumping[16,40].

Histopathology and reproductive biology give the model high value for chronic and sub-chronic surveillance. Diuron exposure produced clear gonadal alterations consistent with endocrine disruption, while mercury caused gonadal impairment detectable by routine histology, offering tissue-level indicators that managers can track over seasons[26,29]. Copper pyrithione assays added behaviour and survival thresholds relevant to marinas and shipyards in mangrove-fringed estuaries[27]. These endpoints align well with intertidal management questions because they translate into fecundity risk, recruitment bottlenecks, and potential population-level consequences in nursery habitats.

The bioindicator role extends to contaminants of emerging concern. In intertidal waters receiving wastewater and aquaculture effluents, pharmaceuticals and microplastics are now routine. Java medaka exhibits organ-level pathology and neurotoxicity after polystyrene exposure and shows microbiome–metabolome shifts that integrate diet, waterborne exposure, and gut health, giving managers system-level signals that are difficult to obtain otherwise[30,31]. Antidepressant and antibiotic exposures demonstrate additional sensitivity of neuro-endocrine endpoints in realistic coastal scenarios and argue for including pharmaceutical tracers in creek-scale monitoring[17,19]. Developmental toxicity from zinc oxide nanoparticles, repeatedly demonstrated in embryos, extends early-warning capacity to engineered particulates common in urbanized catchments[32,33].

Disease ecology is an added strength in intertidal programs. *O. javanicus* is a workable host for *Streptococcus agalactiae* challenge and a candidate model for aeromoniasis and vibriosis, allowing joint chemical–pathogen risk tracking where creek temperatures, salinity, and pollutants co-vary with disease pressure[34–36]. Parasite and bacterial diversity reports from Thai mangroves show how pathogen exposure can be profiled alongside contaminant endpoints within the same sentinel, which is efficient for resource-limited coastal management[19].

Two caveats should guide intertidal deployment. First, population structure varies across the Indonesian and Thai coasts, so reference lines and within-project genotyping or barcoding are prudent to reduce unexplained variance in sensitivity and life-history traits[7,17,18,20]. Second, species replacement or cryptic co-occurrence is possible in mixed *Oryzias* habitats, as highlighted by observations of congeners across salinities and the rediscovery of *O. hubbsi*, which underscores the need for periodic taxonomic checks in long-running monitoring[8,38]. With these controls, programs can standardize three complementary modules for intertidal creeks and mangroves: 1) quarterly embryo-to-juvenile assays for metals, pesticides, nanoparticles, and pharmaceuticals with LC_{50} and cardiac endpoints; 2) semi-annual adult histopathology and reproductive assessments keyed to spawning periods; and 3) an annual disease–microbiome panel aligned to wet and dry seasons. Because sampling is low-cost and field access is reliable at neap tides, Java medaka offers a practical and scientifically mature bioindicator for Southeast Asian intertidal waters that can tie chemical stewardship, habitat protection, and public health into one tractable monitoring frame[11–13,23,31,41].

5. Conclusions

The bibliographic mapping resolves *O. javanicus* research into four tightly linked clusters and a clear chronology. Mechanistic toxicology and analytical chemistry anchor the red community, environmental exposure and early life stages structure the green community, regulatory endocrine endpoints define the yellow community, and organ pathology and disease form the blue community. The overlay shows a progression from early developmental and habitat work to a mid-period consolidation of pathology and, most recently, to biomarker-rich mechanistic and endocrine studies. Regional anchors for Malaysia and Indonesia keep the network rooted in estuarine and mangrove systems where stressors, salinity, and community dynamics intersect. The six sectional discussions translate this structure into practice. Biologically, the model is coherent across taxonomy, population structure, life stage, and community context. Ecotoxicologically, it yields reproducible chains from exposure to organism and tissue mechanisms across metals, herbicides, pharmaceuticals, nanoparticles, and microplastics. For sustainability, *O. javanicus* offers a One-Health-aligned indicator that links wastewater control, antifouling choices, estuarine restoration, and nursery-habitat services. The SWOT highlights strong regional validation and multi-tier endpoints alongside weaknesses in genomic resources and sensitivity variance; the TOWS converts these into concrete actions: standardize reference lines and protocols, design mixture-realistic assays, pair biomonitoring with habitat protection, and invest in omics to future-proof the model. Finally, intertidal deployment is feasible and cost-effective: routine embryo–juvenile tests, seasonal adult histopathology and reproduction, and an annual disease–microbiome panel provide an integrated surveillance suite. Together, the mapping and discussions support *O. javanicus* as a mature Southeast Asian sentinel that connects field exposures to regulatory endpoints and management decisions in estuarine and mangrove ecosystems.

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Conflicts of Interest

The authors declare no conflict of interest.

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