

STOCK STRUCTURE OF KAWAKAWA (*Euthynnus affinis*) IN INDONESIAN WATERS INFERRED FROM PARASITE COMMUNITIES

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Abstract

Tuna is a commercially important fish in Indonesia. While large oceanic tunas have been extensively studied, smaller neritic species such as *Euthynnus affinis* (kawakawa) remain relatively understudied despite being widely consumed. This study examined kawakawa collected from four locations: Palabuhanratu and Prigi (southern Java, within Fisheries Management Area [FMA] 573, Indian Ocean), Pekalongan (northern Java, within FMA 712, Java Sea), and Pemangkat (FMA 711, Karimata Strait). Sampling was conducted between December 2020 and March 2021. Each fish was dissected to recover and identify parasites to the species level. A total of 17 parasite species were identified from 140 fish collected from the viscera and gills. Of these, 11 species belonged to the class Trematoda, two to Chromadorea, two to Palaeacanthocephala, one to Crustacea, and one to Copepoda. Five species were present in all four locations: *Didymocystis* sp., *Didymosulcus* sp. C, *Kollikeria* sp. B, *Lecithochirium* sp., and *Anisakis simplex*. Non-metric multidimensional scaling (NMDS) based on Jaccard and Bray–Curtis distances indicated that Palabuhanratu and Prigi shared similar parasite communities, distinct from those of Pemangkat and Pekalongan, which were more alike. Notably, kawakawa from Palabuhanratu were significantly larger (53.8 ± 3.6 cm; 2779 ± 489 g, $p < 0.05$) than those from Prigi (37.5 ± 1.9 cm; 988 ± 159 g), suggesting that parasite community composition in this coastal region may not depend on the size or age of the host. Overall, parasite community composition revealed spatial patterns indicative of kawakawa population structure. Palabuhanratu and Prigi, both located within FMA 573 and facing the Indian Ocean, exhibited similar parasite assemblages, suggesting connectivity among kawakawa populations within this management area. In contrast, Pemangkat and Pekalongan, despite being located in different seas and Fisheries Management Areas (FMAs), showed comparable parasite communities, indicating ecological connectivity between FMA 711 and FMA 712.

Keywords: tuna, kawakawa, parasite communities, fisheries management area.

1. Introduction

Tuna species have long been recognized for their high commercial and ecological value. Since the early 2000s, neritic tunas have been increasingly exploited as important fishing targets and have become a subject of concern in several international fisheries forums (Noegroho, 2020). As the availability of large oceanic tuna species, such as *Thunnus albacares* and *Katsuwonus pelamis*, continues to decline, neritic tunas have become an increasingly important alternative source of protein for domestic consumption. In Indonesia, this group includes *Thunnus tonggol*, *Auxis thazard*, *Auxis rochei*, *Scomberomorus commerson*, *Scomberomorus guttatus*, and *Euthynnus affinis*, which together represent an important component of small pelagic fisheries (Herrera & Pierre, 2009). However, several neritic tuna species have also shown signs of overexploitation, raising concerns regarding their long-term sustainability (Jaya et al., 2022; MMAF, 2017).

Among neritic tuna species, *Euthynnus affinis* (commonly known as kawakawa) is one of the most frequently captured and consumed species in Indonesia. Kawakawa is a piscivorous predator that feeds primarily on small pelagic fishes, including skipjack, anchovies, lanternfish, flying fish, and mackerel (Chiou et al., 2004). In Indonesian waters, kawakawa is commonly harvested using purse seine, mini purse seine, drift gillnet, and encircling gillnet fisheries. Although kawakawa is classified as Least Concern on the IUCN Red List (Collette et al., 2011), effective management remains challenging because recent studies have reported indications of overfishing in coastal waters of Java Island, particularly in the Java Sea (Mardijah et al., 2022).

To address overexploitation and promote sustainable fisheries, the Indonesian government established eleven Fisheries Management Areas (FMAs) as a spatial framework for managing marine resources. Each FMA is governed by a management council comprising regional stakeholders, including fishing ports, provincial fisheries departments, and local universities. Based on fish production data from the Research Institute for Marine Fisheries (RIMF) during 2018–2020, kawakawa was consistently caught in all FMAs, although production levels fluctuated over time (RIMF, 2021). However, although FMAs provide a useful management framework, their boundaries are administratively defined and may not correspond to the actual biological distribution or stock structure of fish populations. The spatial dynamics of kawakawa stocks across these FMAs remain poorly understood, particularly regarding whether their movements and population structure align with current management boundaries. Such information is essential for designing effective management strategies that reflect true ecological connectivity among regions. It is possible that kawakawa migrate seasonally—from the Natuna Sea (FMA 711) to the Java Sea (FMA 712), and from the Java Sea to the Indian Ocean (FMA 573)—following the movement of water masses through the Sunda Strait. The Java Sea, bounded by Borneo to the north and the islands of Sulawesi, Flores, and Bali to the east, is influenced by the convergence of waters from the South China Sea and the Makassar Strait (Simanjong et al., 2018). These mixing processes create oceanographic fronts that alter seawater characteristics and drive seasonal shifts in pelagic fish abundance and fishing activity, which may influence the migration patterns of kawakawa (Simbolon & Wahyuningrum, 2013; Hermawan et al., 2021; Sepri et al., 2021; Ningsih et al., 2018).

To elucidate this hypothesis, the present study aims to infer kawakawa stock structure based on the parasite communities found within their bodies. In fisheries science, stock identification refers to determining the biological subpopulations within a species that can be independently managed (Ricker, 1975; Wells & Richmond, 1995). Various methods have been applied for this purpose, including genetic, otolith, and parasitological approaches (Taillebois et al., 2017). Parasites serve as useful biological tags because their composition reflects the host's movement, ecology, and environmental exposure (Lester & Moore, 2015). Many marine fish migrate considerable distances between feeding and spawning grounds, acquiring or losing parasites along the way through host switching or speciation (Mosquera et al., 2000). As a result, geographical variation in parasite assemblages can provide valuable insights into fish migration pathways and stock structure (Bailey et al., 1988; Lester, 1990). The use of parasites as biological tags in marine fish studies is well established and cost-effective (Sinderman, 1961; Gibson, 1972; Mackenzie, 1983, 1990; Begg & Waldman, 1999; MacKenzie et al., 2008). In Indonesia, studies have reported parasite assemblages of kawakawa from West Java (Pambudi et al., 2021), East Java (Pardede et al., 2020), and Aceh (Hidayati et al., 2016), although these primarily focused on species occurrence without assessing their potential as biological markers. Lestari et al. (2017) demonstrated the usefulness of parasites in identifying the stock structure of *Thunnus albacares* and *T. obesus* in Indonesian waters, suggesting that similar approaches could be applied to kawakawa.

The goal of this study is to determine whether kawakawa captured from different FMAs host distinct parasite communities. Specifically, the objectives are to (1) identify the parasite species infecting kawakawa across the sampling locations and (2) compare the similarity of parasite communities among these locations. To achieve these objectives, we applied several statistical analyses to compare the length and weight of kawakawa, as well as to characterize parasite communities using univariate and multivariate approaches following Lester and Moore (2015). If parasite communities are similar among FMAs, this would suggest that kawakawa populations are not restricted by management boundaries and may intermingle across areas, potentially complicating stock management efforts. Conversely, if parasite communities differ among FMAs, this would indicate that the current management divisions correspond well to the biological stock structure of kawakawa.

2. Method

2.1 Study Location and Sample Collection

Samples of kawakawa were collected from four locations. The sampling sites were selected based on kawakawa production records, accessibility, specimen availability, and the absence of previous parasitological studies. The locations included Palabuhanratu (6°59'47.156" S, 106°32'61.884" E) and Prigi (8°17'22" S, 111°43'58" E), which are situated within the Indian Ocean (FMA 573); Pekalongan (6°51'55" S, 109°41'55" E), located in the Java Sea (FMA 712); and Pemangkat (1°6'9.88" N, 109°57'38.06" E), located in the Natuna Sea (FMA 711) (Fig. 1).

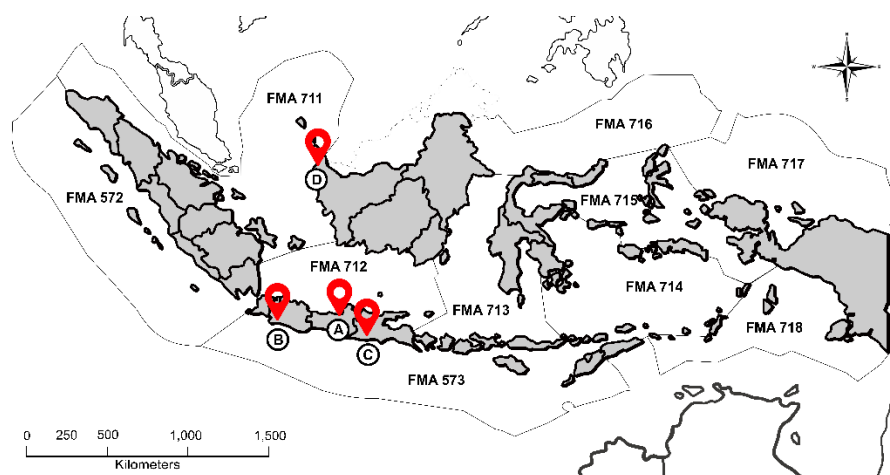


Figure 1. Research locations (A=Pekalongan, B=Palabuhanratu, C=Prigi, D=Pemangkat). Source: MMAF, 2014 modify by adding labels of research location.

Kawakawa specimens were collected from December 2020 to March 2021 directly from fishing vessels during landing, as well as from local fish markets and distribution companies where the catch origin could be traced. During sampling, gills and viscera were removed, placed in individually labeled plastic bags, and frozen until subsequent examination for parasites.

2.2 Parasite Identification

In the laboratory gills and viscera were thawed and dissections were carried out according to the methods of Lester et al. (2001). The gill arches were opened, and the external and internal gill surfaces were examined under a dissecting microscope to find parasites. The viscera were separated into the stomach, pyloric caeca, intestine, and liver. Each organ was placed in a petri dish and examined under a stereomicroscope. Any parasites found were removed and preserved in 70% alcohol. Identification was initially assigned up to the morphospecies level using. After identification, we determined the occurrence of parasites and then calculated the prevalence.

2.3 Statistical Analysis

We calculated mean abundance (mA) with standard error (SE) and prevalence (P, %) following Bush et al. (1997). Mean abundance was defined as the total number of individual parasites divided by the total number of hosts examined (infected and uninfected). Prevalence was defined as the number of hosts infected with a particular parasite species divided by the total number of hosts examined, multiplied by 100%. Ecological community metrics, including species richness, Shannon diversity index (H), Simpson's dominance, and Pielou's evenness, were calculated for each location using the *vegan* package in R (Oksanen et al., 2022).

Univariate analyses were conducted on host length, weight, and parasite species. For host length and weight, we applied the non-parametric Kruskal-Wallis test, followed by Dunn's post hoc test when significant differences were detected ($p < 0.05$). For comparisons among locations for each parasite species, Fisher's exact test was used. Multivariate analyses of parasite community composition were performed using Jaccard and Bray-Curtis dissimilarities

with non-metric multidimensional scaling (nMDS). The non-parametric ANOSIM was used to confirm differences detected by Jaccard and Bray-Curtis analyses. All analyses were conducted in R (Version 4.5.1; R Core Team, 2025) using the packages *dplyr* (Wickham et al., 2023), and *tidyr* (Wickham et al., 2023).

3. Results and Discussion

A total of 140 kawakawa were collected from the four sampling locations. The FL of specimens ranged from 35 to 62 cm, while body weight varied between 771 and 2,779 g. Summary statistics of length and weight for each location are presented in Table 1. On average, the largest individuals were obtained from Palabuhanratu, with a mean FL of 53.8 cm and mean body weight of 2,779 g, whereas the smallest were from Prigi (mean FL = 37.5 cm, mean weight = 988 g). Size and weight distributions differed among locations, suggesting variation in population structure or fishing selectivity.

Table 1. Summary of length and weight (number of fish (N), mean, standard deviation (SD), minimum (Min), and maximum (Max)) of kawakawa (*Euthynnus affinis*) collected from four locations between December 2020 and March 2021.

Location	N	Length (cm)				Weight (g)			
		Mean	SD	Min	Max	Mean	SD	Min	Max
Palabuhanratu	40	53.8	3.6	42.0	62.0	2779	489	1354	4094
Pekalongan	33	42.6	3.6	37.5	48.9	1281	341	819	1944
Pemangkat	32	44.3	1.2	41.9	47.0	1189	114	965	1445
Prigi	35	37.5	1.9	35.0	44.5	988	159	771	1596

The Kruskal-Wallis test indicated significant differences in both fish length ($\chi^2 = 108.22$, $df = 3$, $p < 0.001$) and weight ($\chi^2 = 96.80$, $df = 3$, $p < 0.001$) among the four locations. Dunn's post hoc comparisons showed that Palabuhanratu differed significantly from all other locations, as did Prigi, whereas no significant differences were observed between Pemangkat and Pekalongan. The box-and-whisker plots (Fig.2) further illustrate these patterns, with Palabuhanratu (red) exhibiting the largest and heaviest fish, while Prigi (purple) had smaller individuals.

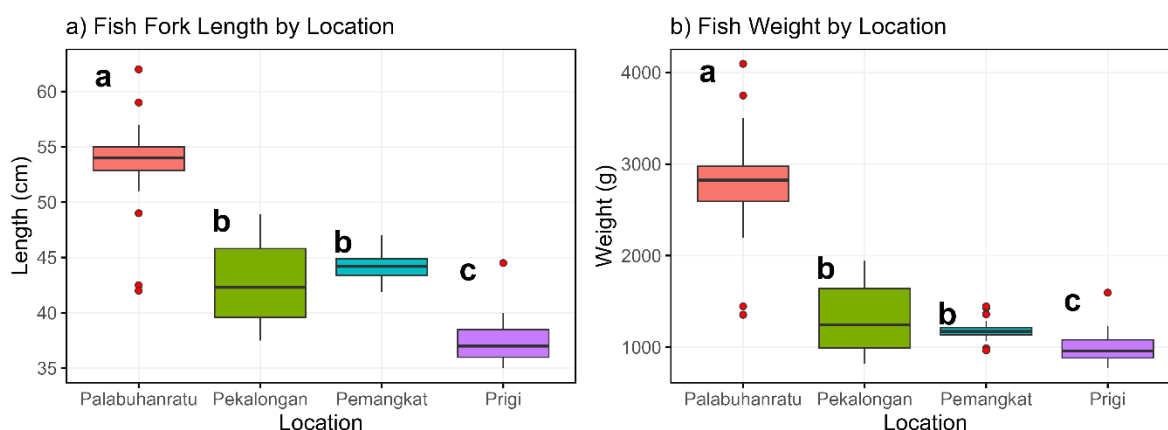


Figure 2. Box-and-whisker plots of kawakawa (*Euthynnus affinis*) fish length (cm) and weight (g) across four locations. Colors indicate locations: red = Palabuhanratu, green = Pekalongan, blue = Pemangkat, purple = Prigi. Different letters denote statistically significant differences among groups ($p < 0.05$) based on Dunn's post hoc test.

A total of 16 parasite taxa were identified from kawakawa across the four sampling locations, consisting of trematodes, nematodes, acanthocephalans, crustaceans, and copepoda (Table 3). Trematodes were the most diverse group, represented by species of *Didymocystis*, *Didymocodium*, *Didymosulcus*, and *Kollikeria*, infecting mainly the gill arches, stomach, intestine, and pyloric caeca. Among these, *Kollikeria* spp. showed the highest mean abundance and prevalence, particularly *Kollikeria* sp. B, which was recorded in all locations with prevalence ranging from 43.8% in Pemangkat to 75.0% in Palabuhanratu. Nematodes such as *Anisakis simplex* and *Camallanus* sp. were found primarily in the liver, stomach, and intestine, with *A. simplex* exhibiting notably high prevalence in Palabuhanratu (80.0%). Acanthocephalans (*Bolbosoma* sp. and *Rhadinorhynchus* sp.) occurred mainly in the stomach and intestine, with moderate infection levels in Pekalongan and Palabuhanratu. Crustacean ectoparasites, including *Pseudocycnus appendiculatus* and *Caligus* sp., were detected on the gill filaments, with higher infection rates in Palabuhanratu and Prigi. Overall, parasite composition and infection intensity varied considerably among locations, with Palabuhanratu and Prigi showing the greatest diversity and abundance of parasite taxa.

Table 3. Parasite species identified in the study, including the organ or site of infection. Species metrics are presented as mean abundance (mA \pm standard deviation) and prevalence (P%). Location abbreviations: Pm = Pemangkat, Pk = Pekalongan, Pg = Prigi, Pb = Palabuhanratu. N indicates the number of hosts examined per location.

Parasite Species	Organ-Site	Species Metrics	Locations			
			Pm (N=32)	Pk (N=33)	Pg (N=35)	Pb (N=40)
Trematoda						
<i>Didymocystis</i> sp.	Gills arch	mA	0.3 \pm 0.6	0.5 \pm 1.1	1.0 \pm 1.3	2.3 \pm 4.5
		P (%)	18.8	18.2	42.9	50.0
	Stomach	mA	1.3 \pm 2.2	0	0.6 \pm 1.0	1.2 \pm 1.8

<i>Didymocodium euthynni</i>		P (%)	40.6	0	25.7	40.0
<i>Didymosulcus</i> sp. A	Gills arch	mA	0.7±1.3	0	1.0±1.2	0.9±1.2
		P (%)	28.1	0	45.7	45.0
<i>Didymosulcus</i> sp. B	Gills arch	mA	0	0	0.3±0.7	0.1±0.4
		P (%)	0	0	17.1	10.0
<i>Didymosulcus</i> sp. C	Gills arch	mA	0.2±0.6	1.2±2.2	0.7±1.0	0.5±1.1
		P (%)	12.5	36.4	48.6	20.0
<i>Kollikeria</i> sp. A	Stomach	mA	0	0	2.4±2.7	3.3±4.0
		P (%)	0	0	54.3	75.0
<i>Kollikeria</i> sp. B	Intestine	mA	7.1±14.2	2.5±3.6	11.7±26.4	12.7±18.1
		P (%)	43.8	45.5	54.3	75.0
<i>Kollikeria</i> sp. C	Pyloric caeca	mA	0.8±2.1	8.0±19.5	0	0
		P (%)	18.8	39.4	0	0
<i>Kollikeria</i> sp. D	Stomach	mA	0	0	0.6±1.4	1.8±2.3
		P (%)	0	0	20.0	50.0
<i>Hirudinella ventricosa</i>	Stomach	mA	0.8±1.4	0.4±0.9	0	0
		P (%)	37.5	18.2	0	0
<i>Lecithochirium</i> sp.	Stomach	mA	1.7±1.9	0.6±1.1	0.1±0.5	0.6±1.0
		P (%)	59.4	24.2	8.6	30.0
Chromadorea						
<i>Camallanus</i> sp.	Intestine	mA	1.1±2.2	0.0	0.0	0.0
		P (%)	31.3	0.0	0.0	0.0
<i>Anisakis simplex</i>	Liver, stomach	mA	0.3±0.8	2.0±3.3	1.8±3.3	10.0±15.5
		P (%)	9.4	39.4	42.9	80.0
Palaeacanthocephala						
<i>Bolbosoma</i> sp.	Stomach	mA	0.0	0.0	0.3±0.7	0.3±0.6
		P (%)	0.0	0.0	20.0	25.0
<i>Rhadinorhynchus</i> sp.	Stomach, intestine	mA	0.0	0.0	2.1±3.7	0.7±1.0
		P (%)	0.0	0.0	45.7	37.5
Crustacea						
<i>Pseudocycnus appendiculatus</i>	Gills filament	mA	0.0	0.0	1.1±1.2	1.1±1.7
		P (%)	0.0	0.0	57.1	45.0
Copepoda						
<i>Caligus</i> sp.	Gills filament	mA	0.0	0.0	0.0	0.6±0.9
		P (%)	0.0	0.0	0.0	42.5

Table 4 summarizes the community metrics of parasite assemblages across the four sampling locations. Species richness was highest in Palabuhanratu (14 species) and Prigi (13 species), intermediate in Pemangkat (10 species), and lowest in Pekalongan (7 species). Shannon diversity (H) showed a similar trend, with the highest values observed in Palabuhanratu (1.95) and Prigi (1.89), suggesting greater diversity and more balanced parasite communities in these locations. Simpson dominance values were also relatively high across sites (0.68-0.79), indicating that a few parasite species tend to dominate the assemblages, though this effect was strongest in Palabuhanratu. Pielou evenness values ranged from 0.73 to 0.77, showing that despite differences in richness, the distribution of individuals among species was uniform across all locations. Collectively, these metrics suggest that parasite communities in Palabuhanratu and Prigi are more diverse and richer compared to those in Pemangkat and especially Pekalongan, although dominance and evenness patterns remain broadly comparable.

Table 4. Community metrics of parasite assemblages at each location, including species richness, Shannon diversity (H), Simpson dominance, and Pielou evenness.

Community Metrics	Locations			
	Pemangkat	Pekalongan	Prigi	Palabuhanratu
Species richness	10	7	13	14
Shannon diversity (H)	1.78	1.48	1.89	1.95
Simpson dominance	0.73	0.68	0.74	0.79
Pielou evenness	0.77	0.76	0.73	0.74

Fisher's Exact test results (Table 5) revealed significant differences in the distribution of several parasite species among locations. Among the species occurring in all four sites, *Didymocystis sp.*, *Didymosulcus sp. C*, *Kollikeria sp. B*, and *Lecithochirium sp.* showed significant variation ($p < 0.05$), suggesting that their prevalence differs meaningfully among locations. In contrast, parasite species found in three locations (*Didymocodium euthynni* and *Didymosulcus sp. A*) did not exhibit significant differences, indicating a relatively consistent distribution across sites. For species present in only two locations, most did not differ significantly between the paired sites, with the exception of *Kollikeria sp. D* ($p < 0.05$), which was unevenly distributed between Palabuhanratu and Prigi. These results indicate that while some widespread parasite species vary strongly in their prevalence across regions, others remain relatively stable, and only a limited number of two-location species show significant geographic structuring.

Table 5. Fisher’s Exact test results for parasite species among locations. Parasites not detected in a location, those found in only a single location, and *Anisakis simplex* were excluded from the analysis.

Locations	Parasite Species	p-value
All Locations	<i>Didymocystis</i> sp.	< 0.05
	<i>Didymosulcus</i> sp. C	< 0.05
	<i>Kollikeria</i> sp. B	< 0.05
	<i>Lecithochirium</i> sp.	< 0.05
Three Locations	<i>Didymocodium euthynni</i>	0.37
(Except Pekalongan)	<i>Didymosulcus</i> sp. A	0.27
Two Locations		
Pemangkat & Pekalongan	<i>Kollikeria</i> sp. C	0.10
	<i>Hirudinella ventricose</i>	0.10
Palabuhanratu & Prigi	<i>Didymosulcus</i> sp. B	0.50
	<i>Kollikeria</i> sp. A	0.09
	<i>Kollikeria</i> sp. D	<0.05
	<i>Bolbosoma</i> sp.	0.78
	<i>Rhadinorhynchus</i> sp.	0.49
	<i>Pseudocycnus appendiculatus</i>	0.36

The NMDS plots for both Jaccard distance (Fig. 3a) and Bray-Curtis distance (Fig. 3b) revealed consistent patterns of community overlap. Palabuhanratu (red) and Prigi (purple) showed substantial overlap, while Pemangkat (blue) and Pekalongan (green) also clustered closely together. Some partial overlap was observed between these two groups. This similarity between Jaccard and Bray-Curtis results suggests that parasite presence/absence alone provides comparable information to abundance data. ANOSIM further supported these patterns, with significant differences among locations for both Jaccard ($R = 0.41$, $p = 0.001$) and Bray-Curtis ($R = 0.29$, $p = 0.001$). Pairwise ANOSIM results (Fig. 4) indicated particularly low R values between Palabuhanratu and Prigi, and between Pemangkat and Pekalongan, reinforcing the NMDS interpretation that these location pairs share more similar parasite communities. Collectively, these findings highlight two main clusters: Palabuhanratu–Prigi and Pemangkat–Pekalongan.

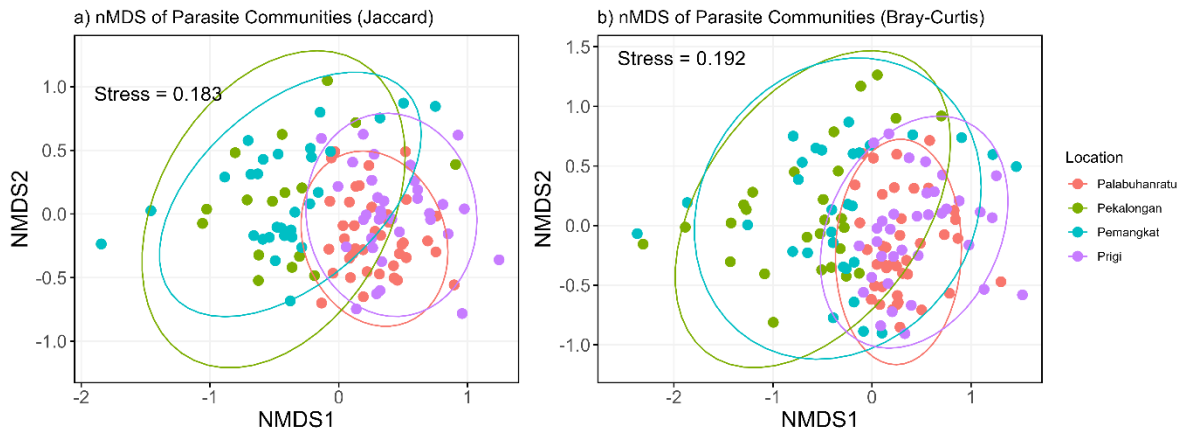


Figure 3. Non-metric multidimensional scaling (NMDS) plots of parasite community composition in kawakawa (*Euthynnus affinis*) based on (a) Jaccard distance (presence/absence) and (b) Bray–Curtis distance (abundance). Ellipses represent 95% confidence intervals. Colors indicate sampling locations: red = Palabuhanratu, green = Pekalongan, blue = Pemangkat, and purple = Prigi.

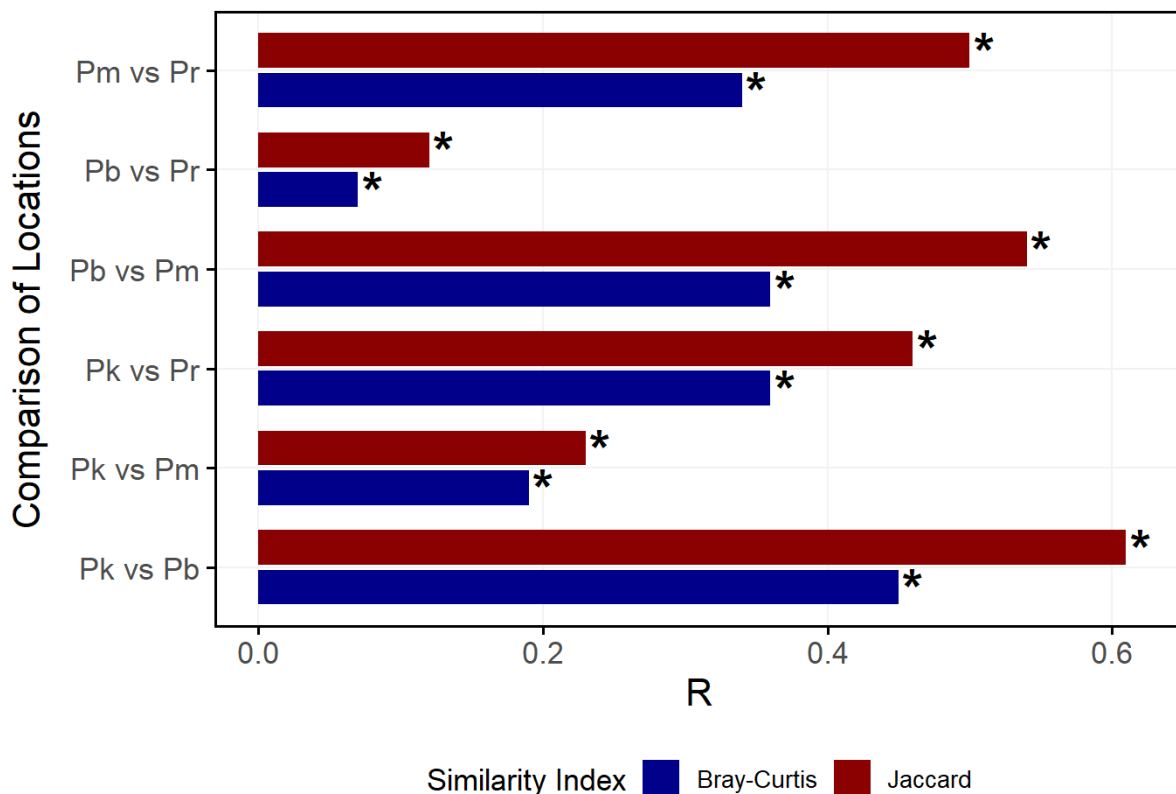


Figure 4. Barplot of pairwise ANOSIM results based on Jaccard distance (presence/absence; red) and Bray-Curtis distance (abundance; blue). Asterisks (*) indicate statistically significant differences at $p < 0.05$. Location codes: Pk = Pekalongan, Pm = Pemangkat, Pb = Palabuhanratu, and Pr = Prigi.

The results of this study show that the parasite communities of kawakawa exhibit notable similarities between Palabuhanratu and Prigi, as well as between Pemangkat and Pekalongan. This pattern reinforces the close ecological relationship between Palabuhanratu and Prigi, both situated along the southern coast of Java and facing the Indian Ocean (Fig. 1). These two sites also belong to the same marine ecoregion (Spalding et al., 2007), further supporting the spatial coherence of the FMA 573 region. Although the distance between Palabuhanratu and Prigi is relatively modest (~584 km) compared to that between Pemangkat and Pekalongan (~899 km), spatial proximity alone does not fully explain the observed similarity in parasite assemblages.

For example, the genus *Rhadinorhynchus* was identified only in samples from Palabuhanratu and Prigi, despite previous reports of its occurrence along the Banten coast (western Java; Pambudi et al., 2021), East Java (Pardede et al., 2020), and the coast of Vietnam (Amin et al., 2019). Both Palabuhanratu and Prigi are more strongly influenced by oceanic processes, particularly the Indian Ocean Dipole (IOD), which modulates sea surface temperatures (Abidin et al., 2020). In contrast, the Java and Natuna Seas are more affected by the El Niño–Southern Oscillation (ENSO) (Puryajati et al., 2021; Wirasatriya et al., 2018). Such large-scale climatic oscillations can influence the distribution and availability of kawakawa (Syamsuddin et al., 2018), thereby indirectly shaping the composition, richness, and abundance of their parasite communities. The resemblance in parasite fauna among certain sites suggests that the host fish may have developed under comparable environmental conditions or shared overlapping life histories (Lester, 1990).

Although Palabuhanratu and Prigi exhibited similar parasite assemblages, notable differences in host body size were observed among sites (Fig. 2). Kawakawa collected from Prigi were consistently smaller, even compared to those from Pemangkat and Pekalongan, suggesting that Prigi may be located closer to a nursery ground for juvenile fish. Fish length was measured to assess maturity stage, as body size can indicate the length at first maturity (L_m)—the point at which gonadal development begins (Jamal et al., 2011). According to the Indian Ocean Tuna Commission (2014), the L_m of kawakawa ranges from 38 to 50 cm fork length (FL). The mean fork length of kawakawa from Prigi was near the lower end of this range (37.5 ± 1.9 cm; 988 ± 159 g), whereas individuals from Palabuhanratu were significantly larger (53.8 ± 3.6 cm; 2779 ± 489 g), suggesting that older kawakawa may aggregate along the Palabuhanratu coast.

The relationship between host size and parasite prevalence has been widely documented in both marine and freshwater systems. Al-Zubaidy (2007) observed such patterns in Red Sea fishes, while Luque et al. (1996) and Alves and Luque (2001) reported similar findings in coastal regions of Brazil. Larger hosts often harbor higher parasite loads due to cumulative exposure, broader diets, and longer lifespans, which increase opportunities for infection (Kennedy, 1975; Luque & Chaves, 1999). This is consistent with the diversity and abundance of helminths found in our samples (Table 3), indicating that diet and regional distribution may influence parasite composition (George-Nascimento, 1987). Nevertheless, despite differences in host body size, our results show similar parasite community composition and diversity between Palabuhanratu and Prigi.

Pemangkat and Pekalongan, although located in different seas, approximately 899 km apart, and belonging to different FMAs, exhibited broadly similar parasite communities. However, the degree of similarity between these two sites was weaker than that observed between Palabuhanratu and Prigi, as indicated by the ANOSIM results (Fig. 4), where the Pemangkat–Pekalongan pair showed a higher R-value. Community diversity indices further revealed that Pekalongan had lower species richness, Shannon–Wiener diversity (H), and Simpson's dominance index than Pemangkat (Table 4). In Pekalongan, three parasite species detected in Pemangkat—*Didymocodium euthynni* (stomach), *Didymosulcus* sp. A (gill arch), and *Camallanus* sp.—were absent (Table 3).

The absence of *Camallanus* sp. is particularly noteworthy, as this genus has previously been reported off the coast of Banten Province, west of Java Island (Pambudi et al., 2021). Its absence in our Pekalongan samples may therefore reflect sampling coincidence rather than true absence from the local population. Other external factors, such as seasonal variation and environmental conditions, may also influence *Camallanus* sp. infection, as observed in other fish hosts (Mgwede & Msiska, 2018).

Lecithochirium sp. exhibited a markedly higher prevalence in Pemangkat (59.4%) compared to Pekalongan (24.2%) (Table 3). Members of this genus are common digeneans inhabiting the stomachs of marine fishes (Yamaguti, 1971; Shih et al., 2004) and are known for considerable morphological variability, likely driven by ecological and physiological factors of their hosts (Surekha & Lakshmi, 2005). Habitat preference and adaptive capacity may explain the higher abundance of *Lecithochirium* sp. in kawakawa from Pemangkat (Bauer, 1970; Grabda, 1981). Although *Lecithochirium* has not been reported in kawakawa within Indonesian waters, it has been recorded from Fiji (Bray & Nahhas, 2002). Host specificity can occur at multiple levels—including species, organ, and geographic scales—depending on the parasite's adaptive traits and environmental constraints. The high prevalence of *Lecithochirium* sp. across all locations suggests a high infection success rate in kawakawa, indicating that this host provides a favorable environment for the parasite's establishment and reproduction (Olsen, 1974).

Among the detected parasite species, *Anisakis simplex* was the most prevalent (80%), occurring mainly in the liver and being most abundant in samples from Palabuhanratu (Table 3). *Anisakis simplex* is a common nematode parasite infecting a wide range of pelagic and demersal fishes (Mladineo & Poljak, 2014). Positive correlations between fish size and *Anisakis* abundance have been reported previously, which may explain its higher occurrence in Palabuhanratu (Vasconcelos et al., 2017). This species was detected in all four locations, supporting its wide distribution, as it has also been reported from Muncar in East Java (Pardede et al., 2020), Banten in western Java (Pambudi et al., 2021), and Aceh in northern Sumatra (Hidayati et al., 2016). The distribution of *Anisakis* largely depends on the presence of definitive hosts (e.g., marine mammals), local food-web structure, and the parasite's ability to complete its life cycle (Palm, 1999; Smith, 1984). Its consistent occurrence across all sites suggests that *Anisakis* may have a preference for kawakawa as an intermediate or paratenic host (Rokicki et al., 2009; Olsen, 1974). The prevalence of *Anisakis* is also influenced by the feeding habits of the host and the water layer it inhabits (Palm et al., 2007). The widespread occurrence of *Anisakis* indicates both ecological connectivity among kawakawa populations

and potential zoonotic risks, as *Anisakis* species are known causes of seafood-borne allergies and anisakiasis in humans (Murata et al., 2021). Although muscle tissue was not examined in this study, previous research has shown that *Anisakis* occurs primarily in the digestive tract of tunas rather than in the muscle (Anshary et al., 2014; Yani & Susaniati, 2017). This suggests a relatively low food safety risk for cooked products, although caution remains warranted, particularly for raw or undercooked fish.

From a management perspective, parasite community structure can provide ecological insight into population connectivity and stock delineation. Although the Indian Ocean Tuna Commission (IOTC, 2006) considers kawakawa a single stock in the Indian Ocean, our results suggest that regional sub-structuring may occur, particularly between Java coastal waters and the Natuna Sea. Integrating parasite data with otolith microchemistry and population genetics (e.g., Taillebois et al., 2017) could strengthen stock identification and support more effective spatial management. Given reports of kawakawa overexploitation in the Java Sea (Mardlijah et al., 2022) and its vulnerability to climate change (Koropitan & Siregar, 2021), such multi-approach assessments are increasingly urgent for sustainable management.

5. Acknowledgments

This study was funded by the Marine Fisheries Education Centre, the Ministry of Marine Affairs and Fisheries Republic of Indonesia, and the National Research and Innovation Agency of Indonesia to Pratiwi Lestari as scholarship for master's degree. Local staff of fishing ports in Prigi, Palabuhanratu, Pekalongan, and Pemangkat assisted with the fish collections.

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APPENDIX

Table A. Pairwise ANOSIM results based on Jaccard distance (presence/absence) and Bray-Curtis distance (abundance).

Comparison of Locations	Jaccard		Bray-Curtis	
	R	p-value	R	p-value
Pekalongan vs Palabuhanratu	0.61	0.001	0.45	0.001
Pekalongan vs Pemangkat	0.23	0.001	0.19	0.001
Pekalongan vs Prigi	0.46	0.001	0.36	0.001
Palabuhanratu vs Pemangkat	0.54	0.001	0.36	0.001
Palabuhanratu vs Prigi	0.12	0.001	0.07	0.007
Pemangkat vs Prigi	0.50	0.001	0.34	0.001