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Lipid and mercury profiles of 61 mid-trophic species collected off south-eastern Australia

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Abstract:

Total mercury (Hg) concentrations and lipid composition data, including fatty acid profiles, for 61 mid-trophic species (fish, cephalopods, crustaceans) collected from continental slope waters off south-east Australia were examined. Overall, Hg concentrations were greatest in fish (0.01–0.30 μg g^{-1} ww) (with highest content found in barracouta (*Thyrsites atun*) and whiptails (*Coelorinchus fasciatus*)), compared with cephalopods (0.01 and 0.17 μg g^{-1} ww) and crustaceans (<0.04 μg g^{-1} ww). Lipid composition varied between species and within habitat (mesopelagic, bathypelagic and benthic). Mean total lipid content ranged from 0.5 to 13.2% ww, and in most species was dominated by triacylglycerols and phospholipids. In fish and squid, fatty acids were generally dominated by monounsaturated fatty acids, whereas crustaceans were higher in polyunsaturated fatty acids. Multidimensional scaling analyses separated species into groupings according to their fatty acid composition that could be interpreted with taxonomic, trophic and habitat information. Discriminant function analyses indicated the most influential (predictor) fatty acids for each group. Biochemical profile classifications can be used in wider trophodynamic studies to understand contaminant transfer, trophic relationships and community dynamics in marine environments.

Keywords: deep-sea, ecosystem dynamics, fatty acids, lipids, mercury, mid-trophic prey, mid-water.

1. Introduction

A great challenge to marine biologists and ecologists is to adequately assess the status of large, complex and highly dynamic marine ecosystems. To date, conventional stomach analyses remains the most used technique to explore dietary trends despite several inherent constraints (Hyslop 1980), most notable of which is the differential digestion of certain prey groups. Stomach analysis only provides a snap-shot in time that may not necessarily represent long-term dietary trends. In response to these shortcomings, biochemical markers (such as trace metal analyses, lipid and fatty acid composition and stable isotopes) are increasingly being used, individually and/or in combination, to provide less biased, temporally integrated signatures of biogeochemical processes and trophic relationships (Kidd et al. 1995; Parrish et al. 2000; Iverson et al. 2004). The basis of these approaches is that a consumer incorporates the 'marker' or 'signature' of their food source into their somatic tissue with minimal or predictable changes (Parrish et al. 2000). Such techniques have been used in a range of marine species to address questions regarding energy transfer (Parrish et al. 2000), animal physiology (Dalsgaard et al. 2003), community health (Adams et al. 2001) and metal bioaccumulation (Kidd et al.1995). Despite the potential use of these markers, biochemical data in many regions and on many mid-water and mid-trophic level species, are scarce.

In the last decade, signature lipid techniques have evolved as powerful qualitative and quantitative tools (Iverson et al. 2004) for reconstructing spatial and temporal differences in diets both within and among species (Iverson et al. 1997; Phillips et al. 2001). The basis of the technique is built on the fact that storage lipids, particularly fatty acids (FAs), are heavily influenced by diet (Cowey et al. 1976), and certain fatty acids (e.g. polyunsaturated fatty acids (PUFAs)) must be biosynthesised at lower trophic levels before being transferred up the food web. Numerous studies have successfully used this approach to reconstruct feeding histories for a wide range of predators around the world (Iverson et al. 1997; Raclot et al. 1998; Turner and Rooker 2005). To use fatty acid analyses in foraging ecology and dietary studies, an understanding of the characteristics of prey fatty acid signatures and the extent to which they differ in a given ecosystem is necessary (Iverson et al. 1997). Lipid profiling techniques are also helpful when evaluating the productivity of marine systems, as a source of energy storage and transfer. Furthermore, lipids are an important determinant of organic contaminant accumulation in aquatic organisms (Landrum and Fisher 1998). Therefore, discerning the role of lipids in trophic transfer has been identified as a critical area of research (Clark and Mackay 1991).

Mercury, in particular methyl mercury (MeHg), is a marine contaminant and is a concern in conservation ecology and public health (Fitzgerald and Clarkson 1991). It has been well established that there is a progressive increase of MeHg concentrations with increasing trophic position in marine food webs (Wiener et al. 2003). Since most MeHg is transferred up the food chain (Mason et al. 1995), information on the feeding ecology ofmarine consumers is needed to determine the source(s) of MeHg and examine patterns of bioaccumulation in marine predators. Many other biotic, ecological and physiological factors play important roles in the bioacummulation of MeHg (Mason et al. 1995). For example, in certain biota, biochemical and physiological detoxifying mechanisms (e.g. metallothioneins) allow some species (e.g. molluscs) to accumulate and tolerate high amounts of heavy metals (Dietz et al. 2000). In addition, spatial variation in mercury concentrations can be attributed to environmental factors, such as pH, water temperature and dissolved organic carbon (DOC) concentrations, which control the biogeochemical processes and transformation of MeHg in the ecosystem (Bodaly et al. 1993).

The deep sea is a unique environment, usually associated with low productivity (Gordon 2001), and supports biota that are longer lived, have slower growth rates (Gordon et al. 1995) and tend to feed at higher and a greater range of trophic levels than species from pelagic and coastal areas (Cronin et al. 1998). As a result, deeper-dwelling species are believed to be exposed to higher levels of contaminants (Gordon et al. 1995) and many accumulate fewer lipids (Drazen 2007) than their shallower counterparts, largely as a result of their environmental limitations (e.g. food availability and temperature). The continental slope and seamounts off southern Australia are important areas for several commercially valuable demersal fisheries, including orange roughy, ling and blue grenadier. In these waters, mid-trophic fishes dominate the biomass (Koslow et al. 1994) and are key to understanding how this ecosystem functions and how predatory fish can be managed sustainably. As highlighted above, biochemical techniques have a great potential to address complex ecological questions. Presently, however, only limited trace metal, lipid and FA composition data on relatively few marine species are available for the waters off south-east Australia (Dunstan et al. 1988; Davenport 1995; Turoczy et al. 2000; Davenport and Bax 2002) with most studies on near-shore and/or top-order species.

In this study, we determined total mercury concentrations and detailed lipid and FA compositional profiles of a range of mid-trophic species collected from continental slope waters off south-east Australia. Such biochemical information is useful for understanding ecological patterns of mercury distribution and lipid bioenergetics in demersal food webs, as well as aiding concurrent studies using the signature lipid approach to examine the diet of high-order predators. For example, these data will be incorporated into a study examining the efficacy of using FA signature analysis of demersal sharks to identify prey species and foraging trends (Pethybridge 2010). In the present study, we also examine the body distribution of mercury and lipid content in various tissues in four species, with results justifying the use of whole-prey items in such trophic studies. Although not the primary focus, this study will also provide pertinent information on mercury content and nutritional lipid profiles to the fish consuming public, food scientists and aquaculturists to address areas such as dietary formulation, nutrient labelling and product developments.

2. Materials and methods

Sample collection and preparation

We sampled 157 individuals from 61 species (43 fish, 14 cephalopods and 4 crustaceans; (Table 1). Species selected were from a wide range of vertical distributions and are some of the most abundant in the mid-water column around south-eastern Australia and important in the diet of numerous mesopelagic and bathydemersal predators. The majority of samples were collected during an orange roughy trawl survey onboard the *Adriatic Pearl* in July 2005 from a mid-water opening and closing (MIDOC) net. Other species (primarily deep-sea fish and squid species) were collected by the *Adriatic Pearl* between April and July 2006. All samples were collected in waters south and east of Tasmania, from 44°5 to 41°2′S and 146°1 to 149°0′E, 500–1500 m depth. All captured specimens were separated, identified to species level, weighed (g), and measured (cm) before being stored at –80°C for up to 2 years. Before analyses, the whole bodies of specimens were homogenised using mixers and hand-held blenders. To justify the usage of whole-prey samples, we investigated the tissue distribution of mercury and lipid content in selected individuals (two fish and two squid), where representative sub-samples of the liver/digestive gland, mantle/muscle and stomach fluid were analysed. To understand the accumulation patterns of mercury and lipid compositional differences in relation to habitat,

profiles were compared among habitat type of fish (coastal, mesopelagic, bathypelagic, benthic).

Mercury analyses

Total mercury (Hg) analyses were carried out on two aliquots of dried material ranging from 10 to 50 mg and concentrations were determined by flameless atomic absorption spectrometry using an Advanced Mercury Analyser AMA 254 (Altec, Prague). The mercury analyser was regularly calibrated using standard solutions of mercury (prepared in 0.1% (m/v) $K_2Cr_2O_7$ and 0.6% (v/v) HNO_3) for the calibration intervals. Calibration curves were linear within the range of concentration of our samples. Detailed procedure is described by Cossa et al (2002). The accuracy and repeatability of the method were established using a certified reference material, consisting of dogfish muscle (DORM-2, National Research Council of Canada). The certified value (4.64 ± 0.26 μg g^{-1}) was reproduced at 98% (4.54 ± 0.32 μg g^{-1}), i.e. within the confidence limits of the certified reference material. Repeatability varied from 3 to 7% depending on the concentration of the sample. The detection limit, defined as three times the standard deviation of blank replicates, was 0.007 μg g^{-1} (dry weight). Metal concentrations are reported as total Hg per gram of wet weight (Hg μg g^{-1}ww).

Lipid and fatty acid profiling

Total lipid was extracted quantitatively by the modified Bligh and Dyer (1995) method using a one-phase methanol:chloroform:water solvent mixture (2:1:0.8). Approximately 1.0 g of muscle and 0.5 g of liver were weighed to three decimal places before extraction. Total lipid content and lipid class composition of samples were determined by an Iatroscan Mark V TH10 thin layer chromatograph (TLC) (Iatron laboratories, Kyoto) coupled with a flame ionisation detector (FID). An aliquot of the total lipid extract (1.0 μL) was spotted on to silica gel chromarods using disposable micropipettes. All samples were developed for 25 min in a polar solvent system (60:17:0.1 v/v/v hexane:diethyl-ether:acetic acid) lined with pre-extracted filter paper. A non-polar solvent system (96:4 v/v hexane:ether) was used to separate hydrocarbons from wax esters and diacyglyceryl ethers from triacylglycerol (Volkman and Nichols 1991). All samples were run in duplicate along with standards. Peaks were quantified using DAPA Scientific Software (Kalamunda, Western Australia). Total lipid content represents the sum of the individual lipid classes determined using the Iatroscan TLC-FID. Iatroscan results have been previously shown to be reproducible to ± 10% (Volkman and Nichols 1991).

For fatty acid analyses, an aliquot of the total lipid extract (TLE) was transmethylated at 100°C for 2 h in a 10:1:1 (v/v/v) mixture of methanol: hydrochloric acid: chloroform to produce fatty acid methyl esters (FAME). After samples were cooled, 1 mL of water was added and the mixture was extracted with hexane and chloroform (4:1 v/v) and centrifuged. This process was repeated three times with the upper organic phase being removed and placed in 1.5 mL vials after each extraction. FAME were reduced to dryness under a nitrogen stream and silyated by the addition of N-O-bis-(trimethylsilyl)-trifluoroacetamide (BSTFA) and heated at 60°C overnight. Gas chromographic analyses were performed with an Agilent Technologies 6890N gas chromatograph (Palo Alto, CA) equipped with an HP-5 cross-linked methyl silicone fused silica capillary column (50 × 0.32 mm i.d.), an FID, a split injector and an Agilent Technologies 7683 Series auto-sampler. Helium was the carrier gas. Selected FAME samples were analysed further using gas chromatography–mass spectrometry (GC-MS) to verify component identifications. GC-MS analysis was performed on a Finnigan Thermoquest system fitted with an on-column injector and using Thermoquest Xcalibur software (Austin, TX). The GC was fitted with a capillary column similar to that described above. In this paper, the FA nomenclature uses the term *x*:*y*ω*z* (also termed omega, ñ and n), where *x* denotes the number of carbon atoms, *y*

the number of double bonds and *z* the position of first double bond from the terminal methyl group.

Statistical analyses

All results are expressed as mean ± standard deviation. To study interspecies, size and habitat effects on biometric parameters and Hg concentrations, variance (ANOVA) and covariance (ANCOVA) analyses were performed after checking assumptions of normality and homoscedasticity of the data. If assumptions were met, a parametric Student *t*-test was applied. If assumptions were not met, the non-parametric Mann–Whitney *U*-test was performed. In each test, $P < 0.05$ was considered significant. Lipid class and fatty acid profiles were compared among species and major prey groups using principal components analysis (PCA) and non-metric multidimensional scaling (MDS) ordinations generated from a Bray–Curtis similarity distance matrix on proportional data of 24 fatty acids. A backwards stepwise discriminant function analysis (DFA) was then used to determine how reliably the FA profiles of individual fish could be assigned to species cluster groups and which fatty acids were most influential. Only fatty acids present at >0.2% were considered. All analyses were performed on percentage composition data. All statistical investigations used SPSS (SPSS Inc., Chicago, IL) and multivariate statistical analyses used PRIMER 6 software (PRIMER-E, Plymouth, UK).

3. Results and discussion

Mercury bioavailability and routes of bioaccumulation

As a group, fish had the greatest concentrations of Hg, followed by squid and crustaceans (Table 1). Mean Hg concentrations in the 43 fish species ranged from 0.01 to 0.30 µg g^{-1}ww and were generally low (<0.1 µg g^{-1}ww), with the exception of 8 species (Table 1). The highest Hg content was found in larger sized fish, such as barracouta (*Thyrsites atun*), grenadier (*Coelorinchus fasciatus*) and orange roughy (*Hoplostethus atlanticus*) (0.30, 0.28, 0.17 µg g^{-1} ww respectively). Similar concentrations to those reported in this study were recorded in pelagic fish, including *T. atun* and *Coelorinchus australis* collected from inshore waters off Tasmania (Thomson 1985). Mercury content in cephalopods varied between 0.04 and 0.24 µg g^{-1}ww, with higher levels recorded in a large oceanic species, *Todarodes filippovae* (0.18–0.26 µg g^{-1}ww), a demersal cranchiid (*Teuthowenia pellucida*; 0.14 – 0.17 µg g^{-1}ww), and a benthic *Octopus* species (0.09–0.16 µg g^{-1}ww). Mercury concentrations in whole arrow squid (*Notodarus gouldi*) were similar to those recorded previously in mantle tissue (Thomson 1985). Higher concentrations were observed in whole *T. filippova* than in the mantle of a slightly larger sized ommastrephid, the warty squid (*Moroteuthis ingens*, 0.09 µg g^{-1}ww) collected off Macquarie Island (McArthur et al. 2003). Few other studies have investigated mercury in whole cephalopods; however, similar ranges have been observed in whole squid from the north-eastern Atlantic (Bustamante et al 2006). In crustaceans, mercury is believed to be an immunosuppressant (Bennett et al 2001) and is generally low in concentration (Andersen and Depledge 1997; Martins et al 2001), as we found in this study where mean Hg content ranged between 0.01 and 0.04 µg g^{-1}ww. All prey taxa had lower Hg content than the local regulatory limit (0.5 µg g^{-1}ww), set by Food Standards Australian and New Zealand (FSANZ 2007). For the major prey groups of fish and cephalopods, size was positively related to mercury (Fig. 1), with higher concentrations found in largest fish ($R^2 = 0.60$, $P = 0.07$) and squid ($R^2 = 0.76$, $P = 0.04$). Such correlations have been observed in other studies (Monteiro et al. 1991; Joiris et al. 1995) and ultimately relate to prey-size choice restrictions by the predators' mouth size and morphology (Karpouzi and Stergiou 2003).

The environmental chemistry of mercury is complex, and subtle changes in chemical, physical, biological and oceanographic conditions can cause substantial shifts in its physical form and valence state over time scales ranging from hourly to seasonal (Krabbenhft et al. 1998). In this study, vertical habitat distribution was correlated with mercury with slightly higher concentrations observed in bathypelagic species as opposed to mesopelagic species (ANOVA, $F_{2, 53} = 4.08$, $p = 0.02$). Similar depth relationships have been observed in other ecosystems (Monteiro et al. 1996; Choy et al. 2009) and seem to arise from the elevated availability of monomethylmercury in sub-thermocline low-oxygen waters (Mason and Fitzgerald 1990; Cossa et al. 1994, 2009), which generally occur below 200 m. Another contributing factor may be the decline in metabolic rates with depth as shown in some fishes (Torres et al 1979), crustaceans (Childress et al. 1990) and cephalopods (Seibel et al. 1997), which would likely affect their capacity to process, metabolise and excrete or sequester contaminants.

Lipid content and composition

Whole-body, total lipid content and lipid-class composition data varied considerably between prey species (Table 1). Most species contained low amounts of lipid (<3.0% body mass), with notably higher concentrations of lipid in myctophids, *S. barnardi*, *S. boops*, *P. normari* and *D. danae* (9.2–13.2% ww), and some squid (*S. circumantarctica*, 11.0% and *T. filippovae* 8.8–10.1% ww). Total lipid content of a species indicates its calorific or energetic importance to a predator. This observation is supported by studies on the calorific content (a measure of the combined energy derived from carbohydrates, proteins and lipids) of mesopelagic fish and crustaceans off south-eastern Tasmania (Blaber and Bulman 1987). In terms of ecosystem functioning and trophodynamics, removal of those species with high lipid content (e.g. by commercial fishing) may potentially affect predators to a greater extent than removal of lipid-poor species. However, where low-lipid prey species are dominant and abundant, predators will likely consume more of such species.

The varying lipid content stored by marine organisms is also considered to reflect differing requirements for energy storage during times of reduced food availability (Bakes et al. 1995). In general, lipid content is thought to decrease with increasing depth of occurrence as a consequence of the selective pressure for reduced locomotory capacity (Seibel and Drazen 2007). However, no such relationship was found in this study, largely due to the high intraspecific and interspecific variability within our data.

In most species, triacylglycerols (TAG) were the major lipid class present with values averaging 49 ± 27% as percentage total lipid, and reaching as high as 91% and 94% in pelagic species (*T. tasmania* and *T. atun* respectively). Phospholipids (PL) were generally the next most prominent lipid class, averaging 33 ± 20% and reaching as high as 78% in the crustacean *S. debilis*, 63% in the squid Sepiolidae sp. and 62% in hake *M. novaezealandia*. As a group, fish had higher TAG levels than squid, but lower PL. With the exception of three fish species (*H. atlanticus*, *Nannobrachium* sp, and *Nemichthys* sp.), and two crustaceans (*Acanthephyra* sp. and *Sergia potens*), wax esters (WE) were not important constituents (most species <2.0%) of lipid composition of deep-sea species, nor was there any trend to support the hypothesis that WE content increases with increasing depth (Body et al. 1985, 1995). Among most fish species, %TAG correlated with total lipid content (Fig. 1), similar to other studies (Weber et al. 2003), suggesting that variability in lipid composition is simply a reflection of the variability in total lipid content. Sterols (ST) and free fatty acids (FFA) were less abundant components, composing between 1.4 and 14% and <5% of total lipid, respectively, in most species. Slightly higher FFA levels were observed in crustaceans, suggesting greater tissue degradation than for other

groups (Jeckel et al. 1989). The low lipid content of many species examined in this study, and their reliance on TAG rather than WE, suggests that lipid does not play a large role in either the long-term storage of energy or buoyancy regulation in these species.

Principal components analysis separated prey into groups, according to their average lipid class profiles (Fig. 2). No distinct groupings related to taxonomy were apparent from lipid-class profiles, but species were separated into those rich in TAG (>75%), rich in WE (>65%), rich in PL (>45%), and those with an even distribution of PL and TAG or WE (20–40% of each). No cephalopods grouped with WE-rich species, demonstrating that cephalopods use TAG rather than the hydrophobic WE for energy storage and buoyancy. This is likely to be an adaptive response to the 'live fast, die young' life history pattern of cephalopods and may also be related to the fact that cephalopods have a protein-based metabolism and are physiologically very different from their fish and crustacean counterparts that rely on lipids as an energy source.

Fatty acid profiles

The variation in the fatty acid composition became quite large both between and within species, with increasing sample size (Tables 2 – 5). Forty-eight different FAs occurred in the marine prey reported here, but only seven FAs frequently represented more than 5% of the total FAs (Tables 2 – 5). In fish and squid, FAs were generally dominated by monounsaturated fatty acids (MUFAs, mean 43 ± 11%, Tables 3 – 4, and 40 ± 10%, Table 5, respectively), whereas crustaceans were higher in polyunsaturated fatty acids (PUFA, mean 40 ± 13%, Table 4). Saturated fatty acids (SATs) were rather consistent among species groups (mean 25 ± 6% total lipids) and were dominated by 16:0 (mean 17 ± 4%), and 18:0 (mean 5 ± 2%). Only the waryfish, *Scopelosaurus* sp., had higher SAT levels (37.5%) than other FA groups. The principal MUFAs in most prey groups included oleic acid (18:1ω9, mean 17 ± 6% of total fatty acids) followed by 20:1ω9 (mean 9 ± 6%), and 20:1(ω11 and ω7, mean <5%). Species particularly rich in MUFAs included: pencil smelt, *Nansenia* sp. (61 ± 3%); viperfish, *Chauliodus sloani* (57%); rudderfish, *Tubbia tasmanica* (56%); and redbait, *Emmelichthys nitidus* (55%). MUFA composition provides further insight into trophodynamics, making it possible to distinguish between carnivory and herbivory (Drazen et al. 2008). For example, high ratios of 18:1ω9/18:1ω7 such as those reported in this study (range, 2–21%) suggest carnivory as the predominant mode of foraging in most species analysed here.

In most prey species, PUFAs were present at similar levels to SAT and were dominated by docosahexaenoic acid (DHA, 22:6ω3, 11 ± 8%), eicosapentaenoic acid (EPA, 20:5ω3, 6 ± 3%) and docosapentaenoic acid (DPA) (22:5ω3, 4 ± 6%) in the range previously determined for these and other species obtained from different regions (Raclot et al. 1998; Phleger et al. 1999). Large variations were observed within groups and between species. For example in crustaceans, DHA varies from 2% (*Systellaspis debilis*) to 24 ± 1% (*Acanthephyra sp*), while in cephalopods it is between 4% (jewel squid, *Histioteuthis atlantica*) and 28% (Gould's squid, *Notodarus gouldi*), and in fish between 6% (*E. nitidus*) and 20% (spookfish, *Winteria telescopa*). Interspecific variation in FA profiles is likely to reflect major differences related to phylogeny, habitat (depth) usage and ecological roles (including diet). The greatest within-species variation occurred in the jewel squid (*Histioteuthis macrohista*), where MUFA ranged from 30 to 54%. Intraspecific variations reflect the extent of morphological (size) disparity between samples and are likely related to dietary differences. The differences are, in this case, likely due to the different size of individuals analysed.

EPA and DHA are useful as biomarkers as they cannot be synthesised by marine predators and must be obtained from the diet (Phleger et al. 2000). In microalgae, at the base of the marine

food chain, EPA is typically found in higher proportions in diatoms (Volkman et al. 1989), while flagellates contain higher DHA relative to EPA (Brown et al. 1993). In this study, cephalopods were rich in EPA (6–15%) and relatively low in arachidonic acid (AA, 20:4ω6 1–3%), which is consistent with other studies (Dunstan et al. 1988) reflecting a phytoplankton-based food chain (EPA-rich, AA-poor). Crustaceans had moderate levels of AA (1–7%), while fish had lower concentrations (0.4–2.3%). Crustaceans contained higher levels of EPA and DHA, which are characteristic of hyperiid amphipods (Phleger et al. 2000; Nelson et al. 2000), demonstrating their lower trophic status. Levels of PUFA may gradually increase over time with predatory feeding in the sea, and high PUFA levels in the lipids of highly migratory fishes are often observed (Medina et al. 1995). For all prey and within all prey groups, no correlations were found between habitat depth distribution and FA composition.

Many fatty acids are readily transferred from prey to predators with little or no modification (Sargent et al. 1993; Navarro et al. 1995). Thus, the variation in the composition of long-chain ($\geq C_{20}$) PUFAs (particularly EPA and DHA) found in this study is likely to be indicative of dietary variation. Variations between species in percentages of branched fatty acids (1 ± 2%) and fatty alcohols (0.6 ± 0.7%, generally dominated by 18:1ω9Alc, 18:0 glyceryl ether diol (GED, derived from DAGE) and 20:1GED) were also observed (unpubl. data). Although the degree to which organisms accumulate or actively modify fatty alcohols from the diet is poorly understood, relationships between them have been related to changes in diet (Wilson 2004).

Human nutritionists have focussed our attention on the numerous health benefits of maintaining sufficient levels of long-chain PUFAs in our diet (Arts et al. 2001). The high concentrations of DHA found in some fish and invertebrate oils (e.g. Gould's squid (*Nototodorus gouldi*) 28%, shrimp *Acanthephyra* sp. 24% and spookfish *Winteria telescopa* 20%) are as high as some of the oils currently marketed as sources of this fatty acid (Nichols et al. 1998). Ratios of ω3/ω6 PUFAs varied between species (6 ± 4), with dragonfish (*Astronesthes* sp.) having the lowest ratios (2) and the squid *Lycoteuthis lorigera* the highest (14), which are within the range reported for other marine fishes (4.7–14.4, Henderson and Tocher 1987). The ω3/ω6 ratio has been suggested to be a useful indicator for comparing relative nutritional values of fish oils (Pigott and Tucker 1990). An increase in the dietary ω3/ω6 fatty acid ratio in favour of ω3 fatty acids is more effective in preventing coronary heart disease (Kinsella et al. 1990). Thus, for some mid-trophic species there exists potential for commercial utilisation. This would be particularly important for the aquaculture industry, which is the biggest user of fish oils (Pike 2005), and where it is necessary to have an oil rich in long-chain ω3 PUFAs. However, there remain many questions over the sustainability of such operations.

Distribution of mercury, lipids and FAs in tissues

The distribution of Hg, lipid content and lipid class composition were recorded in the tissues of two squid (Grimaldi squid, *Lycoteuthis lorigera*, and arrow squid, *Todarodes filippova*) and two fish (lanternfish, *Diaphus danae*, and dragonfish, *Stomias boa*) (Table 6). In fish, Hg content did not drastically change throughout the body. In squid, higher mean Hg concentrations were recorded in the digestive gland (0.20 Hg μg g^{-1} ww) than in any other body part (0.05–0.13 μg g^{-1} ww). This distribution of Hg throughout the body suggests tissue-specific binding for storing of methylmercury. Mercury is cumulatively stored in the muscle throughout an organism's lifespan (Mormede
and Davies 2001), whereas the liver is more dynamic in its processing role. Higher Hg concentrations observed in the liver may also be related to its greater lipid content, as has been suggested for some deep-sea fish (Martins et al. 2006). However, in this study, interspecific variation in lipid content was not correlated with mercury concentrations (Fig. 1*a*), confirming

that Hg does not have a high affinity for lipids, but does for proteins and amino acids (Bloom 1992).

Total lipid content (as % ww) was slightly greater for whole animals than the average sum of all other tissues and was consistently higher than in the muscle/mantle tissue (Table 6). In squid, lipid content of whole specimens was lower than that recorded in the digestive gland, whereas in fish, higher contents were found in whole specimens. It has been suggested that the lipid content of the squid digestive gland is a proximal indicator of the trophicity, or lipid potential, of the collection region (Abolmasova et al. 1990; Semmens 1998). An increase in the lipid content of this organ would therefore be correlated with an increase in the availability of dietary lipid in a given region. Of the major lipid classes, TAG dominated in the liver/digestive gland while PL was higher in muscle/mantle tissues. Dominant lipid classes reported for whole specimens were similar to those of the liver/digestive gland, and were consistently similar to those of the average and, thus, were deemed representative. FA profiles of whole ommastrephid squid, *T. filippova*, were compared with those reported for the digestive gland and mantle tissue by Pethybridge (2004) (Table 5). In this comparison, marked differences in the FA composition between the squid mantle and the digestive gland were detected, the most obvious being the high level of PUFAs (especially EPA and DHA), mainly incorporated into PL, in the mantle compared with the digestive gland. Such results are common in squid (Phillips et al. 2001), and demonstrate that dietary PUFAs are transferred to the mantle where they perform a structural role.

A large number of studies have investigated mercury and lipid content partitioning in marine organisms (Navarro et al. 1995; Wilson 2004; Bustamante et al. 2006). In most of these studies, as shown in the present study, the liver/digestive gland in most organisms has higher and more variable concentrations of mercury and lipid than in the muscle/mantle. Differences between the biochemical compositions of tissues arise from the different body functions, such as buoyancy regulation (gas bladders, liver), energy storage (liver, muscle) movement (muscle), and detoxification (kidney, liver). For lipid distribution, this is partly reflected in the lipid-class composition of tissues, such as TAG rich digestive tissue, which can be reflective of energy storage, whereas PL-rich muscle indicates a greater role in maintaining membrane structure (Sargent 1989). Lipid content particularly varied within the digestive tissues (including the liver) as these organs are greatly influenced by short-term dietary changes and/ or by life-history stages. In general, whole-animal profiles are a representative mix of both tissues, but are more similar to that of the liver/digestive gland (Table 6). Variability increased with increasing sample size, largely due to a greater disparity in the sizes of specimens. Studies on the partitioning of mercury and lipid are informative to animal physiology and to human consumption, but not to marine predators that devour whole prey. To study biochemical patterns, such as energy transfer or mercury bioaccumulation, through marine food chains, whole bodies of animals should be selected as they are more representative of the entire dietary (biochemical) intake of a predator (e.g. prey are usually ingested whole).

Interspecies variation: implications for food web and higher-order dietary studies

In this study, biochemical composition differed between species and was also highly variable within species groups (myctophid fish, bathypelagic fish, mesopelagic fish, *Histioteuthis* squid, bathypelagic squid, mesopelagic squid and crustaceans) and to a lesser extent, between individuals of the same species (Tables 1–5). Sources of variability in mercury and lipid composition are likely to include a suite of biological and environmental factors, such as diet, temporal and regional fluxes in water chemistry, animal size, sex and age, metabolism and physiology and the ability of an organism to detoxify or eliminate contaminants.

FA profiles provide an initial basis for biomarker studies of continental-slope food webs and provide insight into the diet of the examined taxa (Tables 2–5). Different groups were present when comparing major FA constituents (SAT, MUFA and PUFA) and overall FA compositions (including all FA 40.2%, Fig. 3). Ordination analysis showed groupings for the FA profiles of fish and cephalopods. In general, within major prey groups, individual species were well separated on the basis of their FA signatures. Large-scale taxonomic differences were also observed, with most myctophid fish grouping separately from all other fish due to slightly higher SAT, significantly higher levels of 20:1ω11 and DHA, and significantly lower levels of 20:1ω7 and DPA (*t*-test, $P<0.05$). High levels of 22:1ω11 and 20:1ω9 may be indicative of a diet containing copepods (Dahl *et al.* 2000). Squid were grouped together according to their higher levels of 20:1ω9, 22:1ω9, 16:1ω7, DHA and EPA, whereas crustaceans grouped due to higher levels of EPA, AA and 18:1ω7. In most fish and invertebrates, FA profiles related to both functional patterns of feeding and taxonomic relationships. Other food-web studies that have used lipid profiling techniques have shown similar patterns. For example, Phillips et al. (2001) reported that 20:1ω9, along with 18:1ω9, were major fatty acids in the squid, *Moroteuthis ingens*, at Heard and Macquarie Islands, and highlighted the existence of a copepod–myctophid–*M. ingens* food chain.

Discriminant function analysis (DFA) indicated the best ‘marker’ fatty acids for each prey group (Table 7). When treated separately, cluster analysis produced several groupings within the prey groups of squid and fish (Fig. 4), especially in the relative proportions of PUFA and MUFA. The choice of cut-off point that defined groupings is somewhat arbitrary, but comparison between the cluster results and the biological and ecological information available enables a useful basis for a description of the different feeding patterns observed. Assuming that the dietary differences attributed to each of these trophic guilds was great enough to be reflected in variations in dietary FAs, then species with similar diets, and therefore FA compositions, should theoretically group together.

Summary

Investigating the biochemical properties of mid-trophic prey groups, including fish and invertebrates, can provide invaluable insight into commonly overlooked aspects of the marine ecosystem. Specifically, the data reported here will have application in wider trophodynamic studies for demersal and temperate Australian food chains, particularly for top-level predators. It will also provide insight into metabolic processes, life-history strategies, habitat usage and buoyancy mechanisms of these documented species.

Lipids are the currency by which energy is transferred from lower to higher trophic levels. It is this transfer of lipids, particularly the constituent fatty acids, that can be traced from prey to predator, elucidating dietary relationships. In this study, some distinct differences in the FA composition of the examined taxa allowed for their separation, indicating that FA profiles can be useful as biomarkers in demersal food-web studies. Likewise, species differences in mercury concentrations were related to differences in size, habitat and feeding strategies, and therefore, can be used to delineate feeding relationships and transfer patterns within the food web. However, assessing the diet and foraging ecology of a species using contaminant or fatty acid tracers requires more than the comparison of predators and potential prey profiles. It necessitates knowledge of various factors, including habitat, physiology and general biology of a species. Future research should investigate the extent to which such variables influence lipid and mercury dynamics.

This study represents the first major study using lipid and mercury tracers to investigate broad trophic relationships of marine organisms on the continental shelf of south-eastern Australia. For most species examined, this is the first such biochemical data. The mid-trophic species selected in this study, including commercial and non-commercial species, are critically important owing to their role in energy and contaminant transfer and bioavailability. The breadth of prey and their chemotaxonomic separation are also highly relevant, given the general preference for dietary studies to investigate predators occupying only the higher trophic levels. Increasingly, management approaches are assessing ecosystem function and health and include the use of whole-ecosystem and dynamic-system models. Good examples are the Ecopath (with Ecosim or Ecotracer) framework (Christensen and Walters 2004) and biogeochemical models such as ATLANTIS (Fulton et al. 2004). The mid-trophic prey compositional data presented in this study may be useful to establish new models, particularly in tracking energy transfer, contaminant bioaccumulation, and complex food-web dynamics.

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Table 1. Total mercury concentrations (range, maximum – minimum, µg·g^{-1} wet weight, ww), total lipid content (percent composition, ww), lipid class composition (mean percent of total lipid ± SD) and sampling data for whole prey samples from south east Australia.

Family / Species	Spp Code	Water Column	Food	N	Length TL or ML (cm)	Hg range (µg g^{-1}ww)	Total lipid %	Lipid Class (Mean ± SD % body mass)				
								WE	TAG	FFA	ST	PL
TELEOST												
Bathylagidae (Deep-sea smelts)												
Bathylagus antarcticus	Bsp	MP	N	1		-	5.3	0.7	79.1	3.5	2.2	14.5
Centrolophidae (Trevallas)												
Tubbia tasmanica	Tt	BP	N	2	32–34	0.14–0.17	2.2–2.6	0.7±0.1	91.3±1.3 #	2.2±0.5	1.4±0.3	4.2±0.4
Chauliodontidae (Viperfish)												
Chauliodus sloani *	Cs	MP	N	3	19.4	0.08–0.09	1.0–1.2	0.4±0.2	31.1±1.7	2.6±0.8	10.6±1.9	56.3±2.1
Emmelichthyidae (Rovers)												
Emmelichthys nitidus	En	MP	N	3	18–25	0.08–0.10	4.7–6.3	0.4±0.2	80.3±1.2	7.2±0.4	3.8±0.2	8.2±0.8
Epigonidae (Cardinalfishes)												
Epigonus lenimen	El	BP	N, ZB	1	20.1	0.11	2.8	6.7	62.7	2.1	2.3	24.9
Epigonus robustus	Epi	BP	N	1		-	4.0	8.1	68.3	3.1	2.8	17.7
Gempylidae (Snake mackerels)												
Thyrsites atun	Ta	BP	N	5	60–69	0.22–0.30	4.8–6.9	0.0±0.0	94.0±1.6	0.6±0.2	1.4±0.3	2.9±0.4
Gonostomatidae (Bristlemouths)												
Maurolicus australis	Ma	MP	N	3	4–6	0.04–0.06	4.1–4.8	10.3±0.6	50.8±1.4	2.2±0.7	4.7±0.9	32.0±1.1
Howellidae (Oceanic basslets)												
Howella sp.		MP	N	2	6–9	0.05–0.07	6.0–6.6	0.0±0.0	83.6±2.0	0.9±0.3	5.6±0.8	9.8±1.4
Macrouridae (Whiptails)												
Coelorinchus fasciatus	Cf	BP	N, ZB	*1*	21.6	0.28	5.7	-	-	-	-	-
Lepidorhynchus denticulatus	Ld	BP	N	5	10–31	0.05–0.11	1.5–1.9	0.0±0.0	50.9±1.3	7.6±0.6	11.5±1.0	29.9±1.2
Merlucciidae (Merluccid hakes)												
Macruronus novaezelandiae	Mnz	BP	N	2	30–40	0.11–0.13	0.7–0.8	0.4±0.2	16.9±0.7	1.6±0.2	19.5±0.5	61.6±1.4
Microstomatidae (Pencil smelts)												
Nansenia spp.	Nsp	BP	N	2	18–19	0.06–0.07	3.4–5.0	<1.0	94.5	0.9	1.3	3.3
Myctophidae (Lightfish)												
Diaphus danae *	Dd	MP	Z	3	8–14	0.04–0.05	9.6–10.2	1.1±0.2	76.3±1.2	1.5±0.4	1.5±0.1	19.7±1.0
Diaphus hudsoni *	Dh	MP	Z, ZB	4	4–8	0.02–0.5	6.2–7.9	0.0±0.0	36.3±0.9	3.9±0.4	8.9±0.7	50.9±2.4
Diaphus metoploclampus	Dm	MP	Z	1	8.2	0.05	8.7	0.0	58.1	2.7	4.1	35.1
Electrona paucirastra	Ep	MP	Z	3	7–10	0.02–0.04	4.4–5.9	0.4±0.0	49.4±1.7	4.1±0.5	7.2±0.6	38.8±1.3
Electrona risso *	Er	MP	Z	4	6–9	0.02–0.04	6.1–6.5	0.0±0.0	62.8±1.6	3.1±0.2	6.4±0.7	27.6±0.7
Hygophum hanseni *	Hh	MP	Z	2	4–7	0.02–0.03	8.4–8.8	0.0±0.0	78.1±0.9	1.9±0.2	4.8±0.5	15.2±0.3
Lampanyctus australis *	La	MP	Z	4	10–12	0.03–0.06	8.0–9.7	2.4±0.9	84.4±1.8	1.3±0.5	4.1±0.6	7.8±0.9
Lampanyctodes hectoris		MP	Z	3	2–6	0.04–0.07	2.6–3.5	0.0±0.0	49.6±0.9	2.8±0.9	9.9±1.0	37.6±0.6
Lampichthys procerus *	Lp	MP		4	6–12	0.02–0.05	5.1–5.9	0.0±0.0	72.3±2.6	2.9±1.0	8.1±1.1	16.5±1.9

Metelectrona ventralis	Mv	MP		3	8–11	0.02–0.05	6.7–8.1	0.1±0.0	74.9±1.6	1.8±0.5	4.4±0.7	18.8±1.2
Nannobrachium sp	Nan	MP	Z	4	11–15	0.07–0.08	6.2–6.9	95.3±3.4	1.8±0.4	0.3±0.2	2.9±0.7	0.6±0.2
Protomyctophum normani	Pn	MP		2	3–5	0.02–0.03	11.8–12.6	1.4±0.5	32.1±1.3	7.8±1.3	12.7±1.1	46.0±1.7
Symbolophorus boops	Sbo	MP	Z, ZB	3	12–18	0.03–0.06	9.2–10.5	0.6±0.3	76.5±1.9	1.2±0.2	4.0±0.3	17.6±1.3
Symbolophorus barnardi *	Sba	MP	Z, ZB	4	8–13	0.01–0.03	10.5–13.2	0.5±0.2	44.0±2.0	6.9±1.7	10.8±1.6	37.8±1.9
Nemichthyidae (Snipe-eel)												
Nemichthys sp	Nem	B	Z,N	1	8.1	0.04	6.7	96.9	1.1	0.3	1.3	0.3
Notacanthidae (Deepsea spiny eels)												
Notacanthus sexspinis	Ns	B	N	1		-	6.1	0.6	81.6	1.4	1.8	14.6
Notosudidae (Waryfishes)												
Scopelosaurus sp cf ahlstromi.	Sa	BP	Z	1	28.7	0.10	4.5	0.0	80.8	1.1	5.6	12.5
Opisthoproctidae (Spookfishes)												
Winteria telescopa	Wt	BP	N	1		-	1.3	-	-	-	-	-
Oreosomatidae (Oreos)												
Allocyttus verrucosus		BP	N	1	19.2	0.12	1.2	27.3	6.5	0.6	4.6	61.0
Percichthyidae (Temperate Basses)												
Apogonops anomalus	Aa	BP	N, Z	4	9–11	0.03–0.05	1.9–3.8	1.4±0.4	66.9±2.3	7.3±0.8	3.2±0.6	21.1±1.4
Phosichthyidae (Lightfishes)												
Ichthyococcus sp.		MP	N,Z	1	10	0.06	4.8	4.8	58.0	4.1	7.3	25.8
Photichthys argenteus *	Pa	MP	N	8	8–23	0.02–0.05	0.9–1.8	1.6±0.5	18.7±2.8	6.0±1.7	14.4±3.0	59.3±3.2
Woodsia meyerwaardeni *	Wm	MP	N	5	7–10	0.03–0.04	1.9–2.5	0.0±0.0	74.3±0.3	2.2±1.0	2.3±0.9	21.1±2.0
Platytroctidae (tubeshoulders)												
Persparsia kopua *	Pk	MP	N	3	11–18	0.03–0.04	1.0–2.1	0.5±0.2	43.5±2.2	5.3±1.9	9.8±0.7	40.9±1.7
Sternoptychidae (hatchetfish)												
Argyropelecus gigas *	Ag	MP	N	3	8–9	0.02	1.5–1.7	9.9±1.3	42.3±0.2	1.9±0.3	3.6±0.3	42.2±0.9
Stomiidae (Barbeled dragonfishes)												
Astronesthes sp	Ast	MP	N	1		-	-	-	-	-	-	-
Stomias boa	Sb	MP	N, Z	3	18–20	0.05–0.07	1.8–2.2	0.0±0.0	69.9±1.0	2.4±0.6	3.2±0.1	24.4±1.2
Malacosteus sp.cf niger		MP	N, Z	2	15–17	0.03–0.04	3.9–4.8	0.6±0.2	10.7±2.8	9.4±3.0	12.0±2.4	67.3±0.8
Trachichthyidae (Slimeheads)												
Hoplostethus atlanticus		BP	N	2	46–50	0.12–0.17	1.1–1.5	95.0 ±1.5	0.6±0.0	2.1±0.2	0.9±0.1	1.4±0.0
Tetragonuridae (Squaretails)												
Tetragonurus cuvieri		BP	Z	3	32–33	0.06–0.09	5.1	-	-	-	-	-
CRUSTACEAN												
Euphausiidae (krill)												
Euphausia sp.	E	MP	Z	1	<1.2	0.01	4.9	1.2	22.6	7.3	11.7	56.8
Oplophoridae (Deepsea shrimp)												
Systellaspis debilis	Sd	BP	Z	2	12–13	0.02	1.7–1.9	4.8±1.1	0.9±0.2	6.9±1.2	7.4±1.4	77.9±2.4
Acanthephyra sp.	Asp	BP	Z	5	5–15	0.01–0.04	3.6–5.6	83.7±3.9	0.9±0.3	8.1±1.6	1.8±0.9	11.1±1.9
Sergestidae (Belachan Shrimp)												
Sergia potens *	Sp	MP	Z	5	10–13	0.02–0.03	2.4–3.0	53.3±2.9	1.7±0.2	2.4±0.7	4.9±1.1	32.5±1.8

CEPHALOPODA

Ancistrocheiridae (Sharpear Squid)												
Ancistrocheirus lesueuri	Al	BP	N	1	21	0.09	9.0	4.6	19.4	2.2	5.5	67.5
Brachioteuthidae (armed squid)												
Slosarczykovia circumantarctica	Slc	BP	N	1	9	0.11	11.0	3.0	42.1	1.3	6.8	46.8
Cranchiidae (bathyscaphoid squid)												
Helicobranchia pfefferi	Hp	BP	N	1	15	0.07	4.7	5.0	55.0 #	1.9	8.3	29.8
Teuthowenia pellucida *	Tp	BP	N	2	11–17	0.14–0.17	6.0–7.1	5.2 ±0.2	63.2±3.8#	1.9±0.3	2.8±0.4	18.9±2.0
Histioteuthidae (Jewel squid)												
Histioteuthis atlantica	Ha	BP	N	3	11–16	0.08–0.10	3.9–4.5	1.2±0.6	45.9±2.9	3.4±0.4	10.6±0.9	38.9±1.6
Histioteuthis macrohista	Hm	BP	N	3	3–6	0.06–0.09	4.5–5.8	2.2±0.4	52.6±2.7	2.6±0.4	6.0±0.9	36.6±2.4
Lycoteuthidae (Grimaldi squid)												
Lycoteuthis lorigera *	Ll	BP	N	3	70–160	0.04–0.06	3.0–3.4	1.0±0.3	32.2±4.6	1.2±0.5	10.7±1.6	54.9±2.3
Octopoda (octupus)												
Octopus sp	Oct	B	N	2	5–6	0.09–0.16	1.8–2.2	0.0	30.7	3.8	3.2	62.3
Ommastrephidae (flying squid)												
Mastigoteuthis (cf idioteuthis)	Mi	MP	N	2	12	0.05–0.06	2.9–3.4	0.0±0.0	42.4±1.9	1.8±0.2	6.4±1.5	49.4±2.0
Mastigoteuthis sp	Msp	MP	N	1	8	0.10	4.8	1.0	45.1	3.1	6.1	44.7
Nototodarus gouldi	Ng	MP	N	3	11	0.08–0.12	5.8- 6.7	2.1±0.5	40.2±2.3	2.3±1.0	5.5±0.9	49.9±3.6
Todarodes filippovae	Tf	MP	N	5	190–270	0.18–0.26	8.8 – 10.1	4.2±0.9	61.2±5.3	2.8±1.3	3.9±1.2	27.9±2.7
Octopoteuthidae (squid)												
Octopoteuthis megaptera	Om	MP	N	1	11–16	0.10	2.3	0.6	29.8	4.8	5.2	59.6
Sepiolidae (Dumpling squid)												
Sepiolidae sp.	Ssp	MP	N	3	4–7	0.04–0.05	3.4 – 4.4	1.1±0.4	27.4±3.2	5.1±1.9	3.1±1.0	63.3±4.0

Habitat : D – Deep-sea, BD - Bathydemersal, P – Pelagic, BP – Bathypelagic, CS – Continental Slopes, MP – Mesopelagic, (dm) – undergoes diel vertical migrations, (nm) – non migratory. Food: Z – zooplankton, ZB – zoobethos, N – nekton. Abbreviations: N – number; TL – total length; ML – mantle length; Hg – total mercury; WE – wax ester; TAG - triacylglycerol; FFA – free fatty acid; ST – sterol; PL – phospholipid. # represents the possible occurrence of DAGE (diacylglyceryl ether). * indicates that the species has a high biomass (Koslow et al. 1994).

Table 2. Fatty acids (percent of total fatty acids) in 12 myctophid and 2 meso-pelagic fish caught off east Tasmania. Values are mean ± SD.

Species	*Dd*	*Dh*	*Dm*	*Ep*	*Er*	*Hh*	*La*	*Lp*	*Mv*	*Nan*	*Pn*	*Sba*	*Sbo*	*Ta*	*En*
Size (cm)	10.4	4.0 – 8.2	8.2	7.4 – 9.8	8.3	4.5 – 6.5	10.2 – 12.0	10.2	10.6	11.3 – 14.7	3.3 – 4.8	8.0 – 13.4	12.1 – 17.5	60.1 – 69.3	20.3
Number	1	3	1	3	1	2	4	1	1	2	2	5	2	3	1
14:0	4.2	1.7 ± 0.6	2.9	2.5 ± 0.5	1.2	2.2 ± 1.0	1.9 ± 0.4	2.7	4.8	0.8 ± 0.0	0.1 ± 0.1	0.7 ± 0.3	2.8 ± 0.8	4.3 ± 0.6	1.4
15:0	0.9	0.8 ± 0.4	0.5	0.5 ± 0.1	0.8	0.5 ± 0.1	0.5 ± 0.1	0.2	0.4	0.1 ± 0.1	0.4 ± 0.1	0.5 ± 0.3	0.7 ± 0.7	0.4 ± 0.1	0.4
16:0	22.3	21.2 ± 1.5	17.9	15.7 ± 1.0	23.0	20.3 ± 2.1	10.3 ± 1.6	17.0	19.4	24.9 ± 2.5	14.9 ± 0.7	18.9 ± 1.3	21.5 ± 3.7	13.6 ± 1.2	17.8
17:0	1.1	1.3 ± 0.4	0.8	0.6 ± 0.1	0.1	0.6 ± 0.3	0.9 ± 0.1	0.5	0.2	0.0 ± 0.0	0.1 ± 0.1	0.9 ± 0.3	1.0 ± 0.3	0.6 ± 0.0	1.1
18:0	5.8	5.8 ± 1.0	4.4	4.1 ± 0.1	4.5	5.2 ± 0.7	5.2 ± 0.6	4.2	3.6	7.7 ± 1.1	3.8 ± 0.6	5.9 ± 0.4	6.6 ± 1.7	4.1 ± 0.4	7.2
∑SAT	**34.2**	**30.7 ± 1.8**	**26.6**	**23.5 ± 1.0**	**29.6**	**28.9 ± 2.7**	**28.7 ± 1.1**	**24.8**	**28.6**	**33.5 ± 1.9**	**19.4 ± 0.6**	**27.0 ± 2.3**	**32.6 ± 2.8**	**23.3 ± 1.3**	**28.5**
16:1ω7	3.3	0.8 ± 0.5	2.8	2.9 ± 1.4	4.1	0.3 ± 0.1	4.5 ± 0.4	3.7	5.1	1.6 ± 0.6	4.1 ± 0.3	1.9 ± 0.5	6.2 ± 1.0	2.8 ± 0.3	3.7
17:1ω8	0.6	0.3 ± 0.3	0.6	0.5 ± 0.2	0.2	0.5 ± 0.2	0.9 ± 0.0	0.5	0.3	0.4 ± 0.0	0.7 ± 0.1	0.7 ± 0.2	0.9 ± 0.2	0.3 ± 0.0	0.5
18:1ω9	17.7	17.0 ± 1.4	11.9	14.5 ± 1.3	22.1	17.6 ± 4.0	21.5 ± 1.5	23.8	21.0	28.3 ± 2.9	21.4 ± 0.6	17.5 ± 1.8	13.3 ± 1.1	16.6 ± 3.8	27.7
18:1ω7	2.2	2.1 ± 0.1	1.6	1.7 ± 0.7	2.4	2.1 ± 0.2	1.1 ± 0.3	2.8	3.4	1.7 ± 0.2	2.1 ± 0.2	2.7 ± 0.6	1.3 ± 0.2	3.0 ± 0.3	4.4
18:1ω5	0.3	0.2 ± 0.2	0.5	0.4 ± 0.0	0.0	0.3 ± 0.0	0.4 ± 0.1	0.2	0.2	0.5 ± 0.3	0.6 ± 0.3	0.2 ± 0.1	0.3 ± 0.1	0.3 ± 0.1	0.4
20:1ω11	1.3	2.0 ± 0.3	3.3	0.8 ± 0.2	1.1	1.5 ± 0.8	1.6 ± 0.4	2.2	2.0	2.8 ± 0.5	3.0 ± 1.0	2.2 ± 0.4	3.5 ± 1.0	0.3 ± 0.1	0.4
20:1ω9	5.6	4.8 ± 0.6	5.9	14.5 ± 2.9	6.2	8.7 ± 2.1	12.8 ± 1.6	8.9	6.9	8.8 ± 1.5	11.6 ± 4.7	8.2 ± 0.5	9.7 ± 1.8	10.6 ± 1.5	11.3
20:1ω7	0.3	0.5 ± 0.1	0.4	0.2 ± 0.4	0.1	0.2 ± 0.1	0.0 ± 0.0	0.2	0.2	0.0 ± 0.0	0.3 ± 0.1	0.1 ± 0.1	0.2 ± 0.0	0.0 ± 0.0	0.0
22:1ω11+13	2.8	1.0 ± 0.3	1.1	9.5 ± 1.2	7.1	3.5 ± 1.2	6.3 ± 0.6	1.8	4.5	1.2 ± 0.9	3.2 ± 1.6	0.9 ± 0.3	4.8 ± 0.2	4.0 ± 2.1	5.2
22:1ω9	0.7	1.4 ± 0.1	0.3	0.8 ± 0.7	0.9	0.6 ± 0.2	0.3 ± 0.0	0.7	1.3	0.2 ± 0.2	0.3 ± 0.2	0.4 ± 0.3	0.3 ± 0.1	1.3 ± 0.3	0.9
24:1ω9	2.3	4.0 ± 1.1	0.3	1.0 ± 1.2	2.3	1.6 ± 0.7	0.2 ± 0.0	2.0	1.6	0.8 ± 0.1	2.6 ± 0.6	1.5 ± 1.0	0.2 ± 0.0	0.3 ± 0.1	0.4
∑MUFA	**38.0**	**35.3 ± 1.7**	**29.4**	**46.7 ± 3.1**	**46.5**	**41.2 ± 5.1**	**51.4 ± 0.7**	**47.7**	**47.2**	**45.4 ± 2.0**	**50.3 ± 3.6**	**37.2 ± 1.4**	**41.3 ± 1.7**	**40.1 ± 4.2**	**54.9**
18:2ω6	1.0	1.0 ± 0.1	0.9	1.4 ± 0.3	1.3	1.1 ± 0.3	1.6 ± 0.3	1.0	0.5	0.7 ± 0.1	0.8 ± 0.3	1.2 ± 0.2	1.6 ± 0.2	1.6 ± 0.1	1.3
20:2ω6	0.0	0.4 ± 0.0	0.4	0.3 ± 0.2	1.0	0.5 ± 0.2	0.7 ± 0.1	0.3	0.6	0.1 ± 0.1	0.9 ± 0.2	0.3 ± 0.1	0.4 ± 0.6	0.1 ± 0.1	0.3
20:4ω6 (AA)	0.4	0.7 ± 0.2	0.6	0.8 ± 0.4	0.6	0.8 ± 0.2	1.2 ± 0.1	0.5	0.4	0.7 ± 0.2	0.8 ± 0.4	1.6 ± 0.3	1.6 ± 0.2	0.5 ± 0.1	0.6
22:4ω6	0.2	0.3 ± 0.0	0.7	1.5 ± 0.2	0.2	0.6 ± 0.4	1.6 ± 0.2	0.3	0.6	0.1 ± 0.1	0.2 ± 0.1	1.2 ± 0.2	0.1 ± 0.0	0.3 ± 0.0	0.2
22:5ω6	0.3	0.5 ± 0.1	0.8	0.2 ± 0.1	0.2	0.3 ± 0.2	0.2 ± 0.2	0.2	0.1	0.1 ± 0.1	0.1 ± 0.1	0.3 ± 0.2	0.0 ± 0.0	0.3 ± 0.0	0.3
18:4ω3	1.5	1.6 ± 0.6	0.7	1.0 ± 0.0	1.3	0.9 ± 0.4	1.1 ± 0.2	0.4	0.5	0.3 ± 0.0	0.4 ± 0.1	0.8 ± 0.3	1.5 ± 0.1	0.0 ± 0.0	0.0
20:4ω3	1.2	1.0 ± 0.3	0.8	1.6 ± 0.2	0.6	1.1 ± 0.4	1.3 ± 0.2	1.1	1.7	0.6 ± 0.0	1.3 ± 0.6	0.7 ± 0.2	1.6 ± 0.1	2.5 ± 0.1	1.0
20:5ω3 (EPA)	5.2	5.2 ± 1.3	3.0	4.2 ± 0.4	4.1	4.8 ± 1.1	7.2 ± 1.4	5.1	3.2	3.7 ± 0.7	4.3 ± 0.5	5.5 ± 1.1	6.5 ± 0.5	4.1 ± 0.5	2.5
22:4ω3	0.0	0.2 ± 0.0	3.1	0.9 ± 0.6	0.2	0.8 ± 0.5	1.3 ± 0.1	0.2	1.1	0.2 ± 0.1	0.4 ± 0.1	0.4 ± 0.4	1.4 ± 0.7	0.5 ± 0.3	0.1
22:5ω3 (DPA)	0.9	1.0 ± 0.1	7.2	0.3 ± 0.1	0.6	1.2 ± 1.6	0.1 ± 0.0	1.4	1.2	0.4 ± 0.1	0.8 ± 0.2	0.2 ± 0.1	0.1 ± 0.0	2.0 ± 0.3	1.0
22:6ω3 (DHA)	13.2	19.8 ± 1.1	19.2	9.8 ± 0.5	10.6	13.3 ± 4.1	13.2 ± 1.1	10.4	9.6	8.0 ± 1.7	18.9 ± 4.7	17.9 ± 1.6	7.4 ± 0.7	16.9 ± 2.6	5.8
∑PUFA	**23.9**	**31.6 ± 0.4**	**37.5**	**22.0 ± 0.4**	**20.7**	**25.3 ± 5.7**	**29.4 ± 1.2**	**21.3**	**19.7**	**14.7 ± 1.2**	**28.8 ± 2.1**	**30.1± 1.4**	**22.1 ± 0.4**	**32.0 ± 3.8**	**13.2**
br17:1+7Me17:1	0.9	1.3 ± 0.7	0.7	0.4 ± 0.2	0.8	0.7 ± 0.3	0.4 ± 0.0	0.5	0.8	0.0 ± 0.0	0.6 ± 0.2	0.7 ± 0.3	0.8 ± 0.1	0.3 ± 0.0	0.3
iso-SAT	0.8	0.6 ± 0.0	0.6	0.8 ± 0.1	0.5	0.7 ± 0.2	0.9 ± 0.1	0.7	0.6	0.6 ± 0.1	0.6 ± 0.1	0.6 ± 0.1	1.0 ± 0.2	0.6 ± 0.1	0.7
ω3/ω6	11.0	10.1	9.9	4.2	5.4	7.4	5.0	7.5	7.5	8.4	9.1	5.6	5.0	4.7	3.8
other *	1.2	1.5 ± 0.6	2.5	4.0 ± 0.9	1.8	2.1 ± 1.3	1.5 ± 0.6	3.1	2.1	1.4 ± 0.8	0.6 ± 0.3	3.0 ± 1.0	1.7 ± 0.9	3.7 ± 0.9	2.4

N = number. SAT, saturated faty acids; MUFA, monounsaturated fatty acids; PUFA, polyunsaturated fatty acids. AA, arachidonic acid; EPA, eicosapentaenoic acid; DPA, docosapentaenoic acid; DHA, docosahexaenoic acid. *other FA include those <0.5%: 20:0, 21:0, 22:0, 24:0, 14:1ω7, 16:1/16:2, 16:1ω5, 16:1ω9, 17:1ω6, 18:1ω7t, 19:1, 20:1, 22:1ω7c, 21:5ω3, 18:3ω6, 20:3ω6, 22:3ω6, 22:5ω6. Species codes as defined in Table 1.

Table 3. Fatty acids (percent of total fatty acids) in 14 demersal fish species, caught off east Tasmania. Values are mean ± SD.

Species	*Aa*	*Nsp*	*Ag*	*Sb*	*Tt*	*Pk*	*Sa*	*Nem*	*Wm*	*Mnz*	*Ld*	*Ma*	*Pa*
Size (cm)	10.3	17.6 – 19.0	8.1 – 9.3	18.4 – 20.3	34.1	14.2 - 18	28.7	8.1	7.2 – 10.1	30.2 – 40.4	12.4 – 30.6	4 – 5.7	10.5 – 22.9
Number	1	2	2	2	1	2	1	1	3	3	4	2	3
14:0	1.1	1.2 ± 0.1	0.1 ± 0.1	2.5 ± 0.3	2.1	3.1 ± 1.0	2.5	1.9	2.3 ± 0.1	1.7 ± 0.0	2.1 ± 0.5	4.8 ± 1.1	2.3 ± 0.7
15:0	0.1	0.3 ± 0.2	0.6 ± 0.1	0.7 ± 0.1	0.4	1.0 ± 0.2	1.0	0.0	0.4 ± 0.2	0.4 ± 0.1	0.8 ± 0.2	0.8 ± 0.1	0.7 ± 0.3
16:0	12.6	13.0 ± 0.2	17.4 ± 4.6	12.9 ± 2.0	11.1	15.1 ± 3.6	21.5	12.9	26.9 ± 1.5	18.3 ± 0.7	18.3 ± 4.2	19.1 ± 2.5	15.8 ± 1.9
17:0	0.6	0.5 ± 0.3	0.7 ± 0.0	0.8 ± 0.1	0.6	1.0 ± 0.1	1.6	2.1	0.9 ± 0.1	0.5 ± 0.3	1.1 ± 0.3	0.9 ± 0.1	0.9 ± 0.6
18:0	3.8	6.3 ± 0.9	3.1 ± 0.7	4.0 ± 1.4	6.1	5.4 ± 0.6	7.8	4.0	6.2 ± 0.9	8.1 ± 0.0	6.1 ± 1.4	4.2 ± 0.2	4.5 ± 0.6
∑SAT	**18.4**	**21.9 ± 0.8**	**22.9 ± 3.1**	**21.3 ± 1.4**	**20.6**	**26.0 ± 1.9**	**37.5**	**22.1**	**37.2 ± 1.6**	**29.3 ± 0.8**	**28.8 ± 3.4**	**30.2 ± 2.4**	**24.2 ± 1.5**
16:1ω7	2.1	0.6 ± 0.1	3.5 ± 0.2	3.5 ± 0.6	2.1	3.4 ± 1.2	2.1	3.5	3.6 ± 0.2	1.5 ± 0.3	4.3 ± 1.4	2.5 ± 0.1	0.5 ± 0.2
17:1ω8	0.4	0.2 ± 0.1	0.5 ± 0.0	0.6 ± 0.2	0.6	0.6 ± 0.0	0.6	1.5	0.8 ± 0.1	0.3 ± 0.2	1.2 ± 0.5	0.6 ± 0.0	0.3 ± 0.1
18:1ω5	0.6	0.1 ± 0.1	0.6 ± 0.1	0.3 ± 0.0	0.1	0.4 ± 0.0	0.4	0.4	0.7 ± 0.2	0.1 ± 0.0	0.3 ± 0.2	0.6 ± 0.0	3.1 ± 0.5
18:1ω7	2.6	2.4 ± 0.5	2.3 ± 0.3	1.8 ± 0.9	3.6	2.7 ± 0.3	1.0	0.8	1.3 ± 0.7	2.5 ± 0.2	0.3 ± 0.2	2.5 ± 0.3	3.4 ± 0.4
18:1ω9	14.6	15.3 ± 2.3	15.2 ± 0.9	25.7 ± 4.4	34.9	16.3 ± 1.3	13.4	5.5	21.5 ± 2.1	25.5 ± 1.9	6.9 ± 2.0	18.4 ± 1.4	18.8 ± 0.9
20:1ω11	0.4	0.2 ± 0.1	0.1 ± 0.0	0.3 ± 0.1	0.2	1.2 ± 0.0	0.8	0.6	0.3 ± 0.0	0.1 ± 0.0	0.3 ± 0.1	0.0 ± 0.0	0.9 ± 2.1
20:1ω7	0.3	1.3 ± 0.3	0.5 ± 0.2	0.5 ± 0.0	1.3	0.6 ± 0.1	1.3	0.2	0.2 ± 0.0	0.1 ± 0.0	0.2 ± 0.2	0.5 ± 0.1	0.1 ± 0.2
20:1ω9	18.3	29.4 ± 2.9	12.6 ± 4.9	11.3 ± 0.4	7.8	5.6 ± 1.2	8.5	19.6	6.9 ± 0.6	9.1 ± 0.2	9.8 ± 3.9	15.9 ± 0.1	9.4 ± 0.5
22:1ω11+13	10.8	8.3 ± 1.4	5.3 ± 1.9	4.2 ± 0.5	2.6	2.4 ± 0.6	1.1	4.3	1.9 ± 0.3	1.4 ± 0.4	5.9 ± 1.0	3.9 ± 0.6	2.2 ± 1.4
22:1ω9	0.2	1.1 ± 0.1	1.5 ± 0.5	0.5 ± 0.3	0.2	1.6 ± 0.6	0.3	2.0	0.2 ± 0.0	0.4 ± 0.2	0.6 ± 0.1	0.8 ± 0.5	0.5 ± 0.2
24:1b/24:1ω9	0.8	1.9 ± 0.2	2.0 ± 0.1	1.8 ± 02	2.2	0.2 ± 0.0	0.6	0.3	0.7 ± 0.1	0.3 ± 0.0	0.7 ± 0.2	0.3 ± 0.1	1.4 ± 0.6
∑MUFA	**51.2**	**61.3 ± 2.9**	**44.3 ± 4.3**	**51.0 ± 4.9**	**55.9**	**36.7 ± 2.2**	**30.5**	**39.0**	**38.4 ± 1.8**	**26.4 ± 1.7**	**30.7 ± 4.2**	**46.2 ± 1.5**	**39.7 ± 1.4**
18:2ω6	1.0	0.4 ± 0.2	1.0 ± 0.1	1.6 ± 0.2	1.2	1.0 ± 0.2	1.4	1.7	1.2 ± 0.1	1.0 ± 0.1	1.7 ± 0.5	1.0 ± 0.2	1.9 ± 0.7
20:2ω6	0.5	0.4 ± 0.0	0.0 ± 0.0	0.6 ± 0.1	0.4	0.3 ± 0.0	1.0	1.1	0.7 ± 0.0	0.5 ± 0.3	0.5 ± 0.1	0.1 ± 0.0	0.2 ± 0.1
20:4ω6 (AA)	1.0	0.4 ± 0.2	1.0 ± 0.1	1.1 ± 0.6	1.6	2.3 ± 0.9	1.0	2.2	1.0 ± 0.2	2.2 ± 0.1	1.3 ± 0.6	0.6 ± 0.1	2.4 ± 0.9
22:3ω6	0.3	0.6 ± 0.0	0.3 ± 0.0	0.2 ± 0.1	0.1	0.3 ± 0.1	0.4	0.5	0.1 ± 0.0	0.4 ± 0.2	0.6 ± 0.1	0.4 ± 0.1	0.1±0.0
22:4ω6	1.1	0.4 ± 0.2	0.1 ± 0.2	0.9 ± 0.4	0.5	0.4 ± 0.1	0.5	0.5	0.8 ± 0.2	0.5 ± 0.0	2.2 ± 0.8	0.3 ± 0.1	0.6 ± 0.3
18:4ω3	0.7	0.3 ± 0.1	0.9 ± 0.2	1.2 ± 0.1	0.5	1.3 ± 0.4	0.9	0.3	1.1 ± 0.1	0.4 ± 0.0	1.4 ± 0.2	0.5 ± 0.3	1.0 ± 0.4
20:4ω3	1.2	0.6 ± 0.2	1.3 ± 0.3	1.9 ± 0.6	0.3	0.9 ± 0.1	1.5	2.1	0.6 ± 0.1	0.8 ± 0.1	1.7 ± 0.9	1.1 ± 0.0	1.5 ± 0.4
20:5ω3 (EPA)	4.3	0.9 ± 0.2	4.7 ± 0.6	4.9 ± 0.8	3.2	6.6 ± 1.0	3.6	4.4	4.7 ± 0.3	4.0 ± 0.1	6.2 ± 1.9	3.0 ± 0.1	5.8 ± 1.0
22:4ω3	1.4	0.2 ± 0.0	0.1 ± 0.0	0.1 ± 0.1	0.0	0.0 ± 0.0	2.9	2.2	1.4 ± 0.3	1.0 ± 0.2	1.6 ± 0.5	0.0 ± 0.0	1.2 ± 0.8
22:6ω3 (DHA)	15.8	7.7 ± 1.2	15.5 ± 4.4	14.2 ± 1.4	8.6	19.3 ± 3.6	11.7	17.5	8.6 ± 1.1	11.2 ± 3.0	16.5 ± 5.6	11.5 ± 1.0	14.8 ± 3.4
22:5ω3 (DPA)	0.3	1.1 ± 0.4	1.0 ± 0.1	0.5 ± 0.3	1.0	1.8 ± 0.4	0.9	1.2	0.3 ± 0.1	2.5 ± 0.1	0.8 ± 1.1	0.8 ± 0.1	0.5 ± 0.7
∑PUFA	**27.6**	**13.0 ± 1.4**	**26.1 ± 3.4**	**27.6 ± 2.8**	**17.3**	**34.1 ± 2.4**	**25.8**	**33.5**	**20.4 ± 1.5**	**24.7 ± 1.8**	**34.5 ± 5.3**	**19.3 ± 0.9**	**30.0 ± 2.4**
br17:1/7Me17:1	0.3	0.6 ± 0.1	0.8 ± 0.2	0.8 ± 0.2	0.7	0.2 ± 0.2	0.7	0.5	0.9 ± 0.2	1.2 ± 0.1	1.0 ± 0.2	0.6 ± 0.0	0.6 ± 0.8
iso-SAT	0.4	0.4 ± 0.1	0.7 ± 0.1	0.8 ± 0.2	1.4	0.8 ± 0.1	1.1	0.3	0.7 ± 0.1	0.6 ± 0.1	0.9 ± 0.2	0.6 ± 0.2	0.8 ± 0.0
ω3/ω6	5.6	4.2	7.9	2.7	3.3	5.7	3.4	4.9	4.6	4.1	6.7	4.6	4.6
others *	2.5	4.2 ± 1.0	6.0 ± 1.8	3.9 ± 0.3	4.7	2.9 ± 0.6	7.6	5.7	3.1 ± 1.0	3.1 ± 0.3	4.0 ± 0.9	3.6 ± 0.9	5.7 ± 0.2

For abbreviations and footnotes, refer to Tables 1 and 2.

Table 4. Fatty acids (percent of total fatty acids) in 8 deep-sea fish and 4 crustacean species collected off southeast Tasmania. Values are mean ± SD.

	Deep-sea fish								Crustaceans			
Species	Cs	Bsp	*Cf*	*Wt*	*Epi*	*El*	*Ns*	*Ast*	*Asp*	*Sp*	*E*	Sd
Size (cm)	19.4		21.6			20.1			5.1 – 34.6	9.8 – 13.1	sml (>1cm)	12.6
Number	1	1	1	1	1	1	1	1	2	2	mass	1
14:0	3	2.3	1.1	1.6	1.6	0.9	1.3	2.1	1.7 ± 0.1	0.8 ± 0.3	0.9	1.8
15:0	0.3	0.4	0.0	0.0	1.0	0.1	0.0	0.2	0.1 ± 0.2	0.8 ± 0.2	0.6	1.3
16:0	13.2	15.3	20.0	14.7	16.8	14.3	23.7	20.5	6.9 ± 1.6	14.6 ± 2.9	19.5	21.8
17:0	0.4	0.3	0.3	0.6	0.5	0.6	0.7	0.7	0.5 ± 0.1	2.0 ± 0.4	1.2	1.9
18:0	2.9	3.7	1.9	1.3	2.9	3.8	2.1	3.9	1.3 ± 0.3	7.4 ± 1.0	2.2	8.2
20:0	0.1	0.3	0.4	0.3	0.4	3.0	0.9	0.7	0.4 ± 0.2	0.2 ± 0.0	0.0	0.0
∑SAT	**20.1**	**22.4**	**24.1**	**18.7**	**23.1**	**22.9**	**28.8**	**28.3**	**11.1 ± 2.4**	**26.0 ± 2.4**	**24.5**	**35.4**
16:1ω7	9.0	4.4	1.9	3.9	4.9	1.4	2.5	3.5	2.3 ± 0.5	5.1 ± 0.8	2.6	2.5
17:1ω8	0.4	0.3	0.5	0.2	1.4	0.4	0.8	0.9	0.2 ± 0.2	1.5 ± 0.5	0.7	1.3
18:1ω5	0.5	0.5	0.4	0.6	0.3	0.1	0.3	0.2	0.8 ± 0.0	0.4 ± 0.2	0.4	0.4
18:1ω7	4.1	3.4	2.4	1.2	3.1	3.5	3.6	4.0	3.0 ± 0.3	3.4 ± 0.7	4.0	3.5
18:1ω9	29.6	18.6	24.1	12.9	15.2	11.3	22.8	26.7	15.8 ± 0.4	9.3 ± 2.1	8.8	22.9
20:1ω9	6.2	8.8	7.8	17.8	18.8	13.1	15.1	8.6	14.0 ± 2.3	2.6 ± 0.5	1.1	2.4
20:1ω7	0.4	1.1	0.5	0.5	0.9	0.6	1.5	0.4	0.7 ± 0.0	0.3 ± 0.1	0.3	0.2
22:1ω11/13	3.6	4.6	5.9	8.0	8.4	6.8	6.7	5.0	3.8 ± 4.6	0.9 ± 0.2	0.4	1.1
22:1ω7	0.2	0.3	0.2	0.3	0.3	0.2	0.2	0.2	0.4 ± 0.0	0.0 ± 0.0	0.0	0.1
22:1ω9	1.2	2.6	0.2	1.0	0.9	0.5	0.2	0.4	3.7 ± 1.5	0.5 ± 0.1	0.9	0.4
24:1b/24:1ω9	2	1.1	0.6	0.5	0.3	0.7	0.5	0.6	0.4 ± 0.1	0.4 ± 0.1	0.6	0.4
∑MUFA	**57.4**	**46.2**	**44.5**	**47.0**	**54.9**	**39.1**	**54.5**	**50.8**	**45.4 ± 10.2**	**24.4 ± 2.1**	**19.9**	**35.4**
18:2ω6	1.8	1.2	1.1	0.9	0.9	0.8	0.8	1.1	0.6 ± 0.0	1.5 ± 0.4	1.6	2.1
20:2ω6	0.3	0.5	0.3	0.5	0.8	0.8	0.3	0.6	0.4 ± 0.3	0.4 ± 0.0	0.5	0.1
20:4ω6	0.4	1.1	0.8	1.4	1.3	1.0	0.9	1.2	0.6 ± 0.2	7.5 ± 2.6	6.2	1.8
22:3ω6	0.3	0.2	0.3	0.1	0.7	0.8	0.0	0.8	0.3 ± 0.1	0.3 ± 0.1	0.1	0.6
22:4ω6	0.2	0.4	0.8	0.3	0.6	0.5	0.3	0.4	0.2 ± 0.0	1.6 ± 0.8	0.4	0.2
22:5ω6	0.3	0.3	0.7	1.0	0.4	1.2	0.4	1.8	0.2 ± 0.0	0.0 ± 0.0	0.0	0.0
20:4ω3	0.5	0.9	0.5	1.0	1.5	1.1	0.5	0.8	1.0 ± 0.0	0.2 ± 0.0	0.4	1.0
18:4ω3	1	0.8	0.8	1.6	0.3	0.0	0.0	0.4	0.6 ± 0.1	0.0 ± 0.0	0.2	1.5
20:5ω3 (EPA)	5.5	7.8	2.6	2.4	2.3	4.7	3.3	1.5	4.7 ± 1..1	12.0 ± 2.5	14.8	11.0
22:4ω3	0.6	0.2	1.2	0.2	0.8	1.6	1.0	1.1	0.0 ± 0.0	0.3 ± 0.1	0.2	0.8
22:6ω3 (DHA)	8.9	12.3	17.6	20.0	6.8	19.0	6.5	6.2	24.3 ± 1.5	16.2 ± 1.9	22.1	2.2
22:5ω3 (DPA)	0.9	1.2	1.7	2.1	1.2	2.5	0.7	1.3	8.4 ± 0.1	2.4 ± 0.4	7.0	0.3
∑PUFA	**20.7**	**26.9**	**28.4**	**31.4**	**17.7**	**34.0**	**14.7**	**17.2**	**41.3 ± 3.0**	**42.4 ± 3.3**	**53.5**	**21.8**
br17:1/7Me17:1	0.4	1.9	0.8	0.3	0.4	1.0	0.4	0.9	0.6 ± 0.3	0.4 ± 0.2	0.3	2.5
iso-SAT	0.2	0.6	0.4	0.6	0.6	0.6	0.7	0.7	0.4 ± 0.0	0.3 ± 0.1	0.3	0.7
ω3/ω6	**5.3**	**6.3**	6.1	6.5	2.8	5.6	4.5	1.9	17.2	2.8	5.1	**3.4**
others *	1.1	1.9	2.1	2.4	3.7	3.0	1.3	2.7	1.7 ± 0.2	3.2 ± 0.8	1.6	4.3

For abbreviations and footnotes, refer to Tables 1 and 2.

Table 5. Fatty acids (percent of total fatty acids) in 14 whole cephalopods and in the digestive gland and mantle of *Todarodes filippovae*. Values are mean ± SD.

Species	*Ha*	*Hm*	*Slc*	*Ng*	*Ll*	*Hp*	Om	*Tp*	Mi	Msp	Oct	Al	Ssp	Tf	Tf (Pethybridge 2004)	
															DG	Mantle
Size (cm)	11.5-15.6	25-50	9.0	11.2	7-18	15.3	10.7-19.4	11.1	9.8	12.5	6.1	21.0	4.5-7.0	190-267	156-7	
Number	2	*3*	1	2	1	1	3	1	1	1	2	1	2	3	43	42
14:0	0.3 ± 0.3	1.4 ± 0.3	0.6	0.6 ± 0.3	0.6	0.3	0.5 ± 0.5	0.3	0.5	0.3	0.2 ± 0.3	0.3	0.2 ± 0.1	1.1 ± 0.1	1.3 ± 0.5	0.6 ± 0.3
15:0	0.2 ± 0.1	0.1 ± 0.1	0.2	0.3 ± 0.1	0.0	0.0	0.2 ± 0.1	0.1	0.2	0.1	0.1 ± 0.0	0.2	0.0 ± 0.0	0.2 ± 0.1	0.4 ± 0.2	0.5 ± 0.2
16:0	27.3 ± 3.2	18.4 ± 4.3	14.4	30.3 ± 2.9	15.8	17.1	15.3 ± 1.3	15.5	9.7	17.3	13.8 ± 5.4	18.6	20.6 ± 3.2	18.4 ± 3.4	14.8 ± 4.6	27.3 ± 3.8
18:0	5.3 ± 1.1	4.0 ± 2.1	6.2	7.6 ± 0.6	7.3	6.1	5.2 ± 0.3	3.3	3.5	5.3	4.3 ± 0.4	5.2	3.7 ± 1.0	5.1 ± 0.2	5.4 ± 0.7	5.8 ± 1.7
∑SAT	**33.1 ± 1.8**	**23.9 ± 7.2**	**21.4**	**38.9 ± 3.6**	**23.7**	**23.5**	**21.2 ± 1.4**	**19.3**	**13.9**	**22.9**	**18.5 ± 6.1**	**24.2**	**24.5 ± 3.7**	**24.8 ± 2.0**	**23.9 ± 6.9**	**36.2 ± 7.0**
16:1ω7	2.5 ± 1.0	3.3± 0.9	0.5	0.9 ± 0.5	0.7	5.1	1.3 ± 0.7	3.5	1.5	1.0	0.7 ± 0.1	1.4	2.1 ± 0.5	1.6 ± 0.6	1.6 ± 0.7	0.3 ± 0.1
16:1ω9	0.3 ± 0.1	3.0 ± 2.4	0.2	0.8 ± 1.1	1.3	0.3	0.3 ± 0.2	5.0	1.7	2.2	0.1 ± 0.2	2.3	0.2 ± 0.2	0.2 ± 0.1	0.5 ± 0.4	0.1 ± 0.2
17:1ω8	0.0 ± 0.0	0.6 ± 0.3	0.0	0.1 ± 0.1	0.0	0.4	0.5 ± 0.4	0.4	0.8	0.3	0.2 ± 0.2	0.4	0.5 ± 0.0	0.4 ± 0.2	0.4 ± 0.2	0.1 ± 0.1
18:1ω5	0.4 ± 0.1	0.6 ± 0.0	0.2	0.3 ± 0.2	0.5	0.6	0.3 ± 0.1	0.2	0.6	0.4	0.4 ± 0.0	0.5	0.4 ± 0.1	0.1 ± 0.1	0.0 ± 0.1	0.0 ± 0.0
18:1ω7	3.6 ± 0.4	1.8 ± 1.6	1.7	1.1 ± 0.3	3.0	4.3	2.4 ± 0.7	6.7	3.1	1.9	2.6 ± 0.6	3.1	2.8 ± 0.7	2.3 ± 0.2	2.9 ± 0.7	1.3 ± 0.4
18:1ω9	11.7 ± 3.4	14.3 ± 4.0	5.9	4.5 ± 0.8	13.6	14.6	9.1 ± 2.9	19.2	18.4	14.7	9.8 ± 2.3	13.4	13.2 ± 2.4	16.6 ± 1.4	22.0 ± 4.1	2.7 ± 0.9
20:1ω9	13.4 ± 1.3	13.1 ± 3.0	14.4	5.8 ± 2.3	15.0	14.2	13.5 ± 1.8	15.7	14.3	14.9	13.3 ± 4.7	14.1	10.8 ± 2.2	12.3 ± 4.0	13.8 ± 3.5	7.4 ± 1.6
20:1ω7	0.7 ± 0.5	0.8 ± 0.3	0.6	0.5 ± 0.4	0.0	1.0	0.8 ± 0.1	2.3	1.0	0.6	0.9 ± 0.0	0.8	0.6 ± 0.0	0.8 ± 0.0	0.7 ± 0.2	0.1 ± 0.1
20:1ω11	1.5 ± 0.1	1.3 ± 0.0	0.4	0.2 ± 0.2	0.5	0.8	0.3 ± 0.0	0.9	1.1	1.4	0.8 ± 0.1	0.4	0.3 ± 0.0	1.0 ± 0.4	0.0 ± 0.0	0.1 ± 0.1
22:1ω11+13	1.4 ± 0.0	5.4 ± 4.7	8.6	0.3 ± 0.5	3.1	4.9	7.2 ± 0.4	0.0	7.0	3.5	0.3 ± 0.4	1.6	1.8 ± 0.4	6.1 ± 1.4	3.4 ± 1.2	0.3 ± 0.3
22:1ω7	0.4 ± 0.1	0.3 ± 0.0	0.4	0.1 ± 0.1	0.0	0.3	0.3 ± 0.1	0.8	0.5	0.3	0.6 ± 0.5	0.4	0.1 ± 0.1	0.3 ± 0.1	0.1 ± 0.1	0.0 ± 0.0
22:1ω9	2.4 ± 0.1	1.3 ± 1.1	0.1	0.3 ± 0.5	4.6	0.0	0.1 ± 0.1	2.2	1.8	3.8	3.5 ± 2.8	2.3	1.5 ± 0.6	2.2 ± 0.5	2.3 ± 1.2	2.4 ± 0.6
24:1b/24:1ω9	0.3 ± 0.2	0.0 ± 0.0	0.3	0.1 ± 0.0	1.3	0.0	0.1 ± 0.2	0.2	0.0	0.0	0.2 ± 0.2	0.2	0.7 ± 0.3	0.5 ± 0.1	1.2 ± 0.6	0.9 ± 0.4
∑MUFA	**39.0 ± 5.2**	**45.8 ± 13.2**	**33.3**	**15.2 ±3.5**	**43.6**	**46.5**	**36.1 ± 3.0**	**57.2**	**51.3**	**45.0**	**33.3 ± 8.2**	**40.9**	**35.1 ± 5.8**	**43.9 ± 3.4**	**50.8 ± 14.8**	**15.4 ±1.8**
18:2ω6	0.7 ± 0.4	0.8 ± 0.3	0.3	0.5 ± 0.0	0.4	1.1	0.5 ± 0.2	0.5	0.9	0.4	0.7 ± 0.1	0.7	1.2 ± 0.7	0.7 ± 0.2	0.8 ± 0.3	0.1 ± 0.1
20:2ω6	1.1 ± 0.2	0.1 ± 0.1	0.7	0.2 ± 0.3	0.0	0.2	0.5 ± 0.4	0.5	0.0	0.0	0.3 ± 0.4	0.5	0.0 ± 0.1	0.1 ± 0.0	0.6 ± 0.9	0.1 ± 0.1
20:4ω6	3.0 ± 2.2	0.9 ± 0.2	1.7	1.8 ± 0.4	1.6	1.0	1.5 ± 0.1	1.0	1.0	1.4	2.8 ± 2.5	1.9	2.0 ± 0.8	0.9 ± 0.3	1.1 ± 0.5	1.1 ± 0.5
22:3ω6	0.0 ± 0.0	0.4 ± 0.3	0.6	0.1 ± 0.2	0.0	0.3	0.5 ± 0.1	0.6	0.0	0.3	0.4 ± 0.1	0.4	0.1 ± 0.0	0.2 ± 0.1	0.1 ± 0.1	0.1 ± 0.1
22:4ω6	0.8 ± 0.1	0.0 ± 0.0	0.8	0.2 ± 0.3	0.0	0.0	0.1 ± 0.1	1.0	0.0	0.0	0.5 ± 0.7	0.6	0.0 ± 0.0	0.0 ± 0.0	0.2 ± 0.2	0.1 ± 0.1
22:5ω6	0.5 ± 0.1	0.2 ± 0.1	0.3	0.4 ± 0.0	0.0	0.2	0.4 ± 0.1	0.2	0.3	0.4	0.2 ± 0.1	0.4	0.4 ± 0.1	0.2 ± 0.1	0.3 ± 0.2	0.2 ± 0.2
18:4ω3	0.7 ± 0.3	0.6 ± 0.5	0.4	0.6 ± 0.3	0.5	0.7	0.5 ± 0.1	0.3	0.8	0.4	0.4 ± 0.2	0.5	0.7 ± 0.3	0.7 ± 0.2	1.4 ± 0.6	0.3 ± 0.3
20:4ω3	1.1 ± 0.8	0.7 ± 0.6	0.7	0.6 ± 0.5	0.7	0.8	0.8 ± 0.2	0.5	1.3	0.7	0.7 ± 0.8	1.1	0.8 ± 0.1	1.3 ± 0.3	1.4 ± 0.6	0.2 ± 0.2
20:5ω3 (EPA)	11.8 ± 5.4	8.9 ± 2.0	11.4	9.3 ± 1.3	9.4	9.3	10.4 ± 1.7	6.6	9.5	9.3	14.2 ± 3.8	10.1	9.6 ± 3.2	5.9 ± 0.5	4.4 ± 1.6	10.3 ± 1.3
22:4ω3	0.5 ± 0.1	0.2 ± 0.1	0.5	0.4 ± 0.3	0.0	0.0	0.4 ± 0.1	0.5	0.0	0.1	0.2 ± 0.1	0.3	0.1 ± 0.0	0.2 ± 0.1	0.2 ± 0.1	0.2 ± 0.1
22:5ω3 (DPA)	1.6 ± 0.5	1.0 ± 0.1	1.5	1.6 ± 0.3	0.0	0.9	1.8 ± 0.4	2.0	1.3	0.8	2.3 ± 0.2	1.8	1.1 ± 1.7	1.8 ± 0.2	1.1 ± 0.9	0.6 ± 0.6
22:6ω3 (DHA)	4.0 ± 1.1	14.6 ± 4.0	24.6	27.6 ± 1.9	18.5	13.1	23.3 ± 2.6	7.8	17.8	16.8	23.3 ± 4.2	15.0	22.5 ± 4.1	16.5 ±1.7	12.8 ± 5.4	33.7 ± 5.3
∑PUFA	**25.9 ± 5.6**	**28.4 ± 5.2**	**43.4**	**43.2 ± 1.0**	**31.1**	**27.6**	**40.7 ± 3.7**	**21.4**	**32.9**	**30.6**	**46.1 ± 1.0**	**33.1**	**38.5 ± 5.4**	**28.6 ± 2.8**	**24.2 ± 12.2**	**46.6**
ω3/ω6	3.4 ± 0.4	11.0 ±0.4	9.0	13.2 ± 4.2	14.3	8.9	10.8 ± 2.5	4.6	13.7	11.1	10.0 ± 4.8	6.1	*9.9* ± 4.2	11.7 ± 1.4	6.8	26.9
br17:1/7Me17:1	0.4 ± 0.2	0.3 ± 0.1	0.4	0.4 ± 0.1	0.0	0.8	0.5 ± 0.1	0.3	0.3	0.3	0.3 ± 0.0	0.4	0.5 ± 0.0	0.8 ± 0.4	1.0 ± 0.3	0.1 ± 0.0
iso-SAT	0.2 ± 0.1	0.1 ± 0.1	0.1	0.2 ± 0.2	0.0	0.3	0.1 ± 0.0	0.3	0.2	0.3	0.0 ± 0.0	0.2	0.1 ± 0.0	0.2 ± 0.0	0.2 ± 0.1	0.1 ± 0.1
others *	1.6 ± 1.6	1.3 ± 0.8	1.3	1.8 ± 1.4	1.6	1.2	1.3 ± 0.2	1.4	0.8	0.8	1.7 ± 0.2	1.2	1.3 ± 0.8	1.5±0.9	1.8 ± 1.7	1.7

For abbreviations and footnotes, refer to Tables 1 and 2.

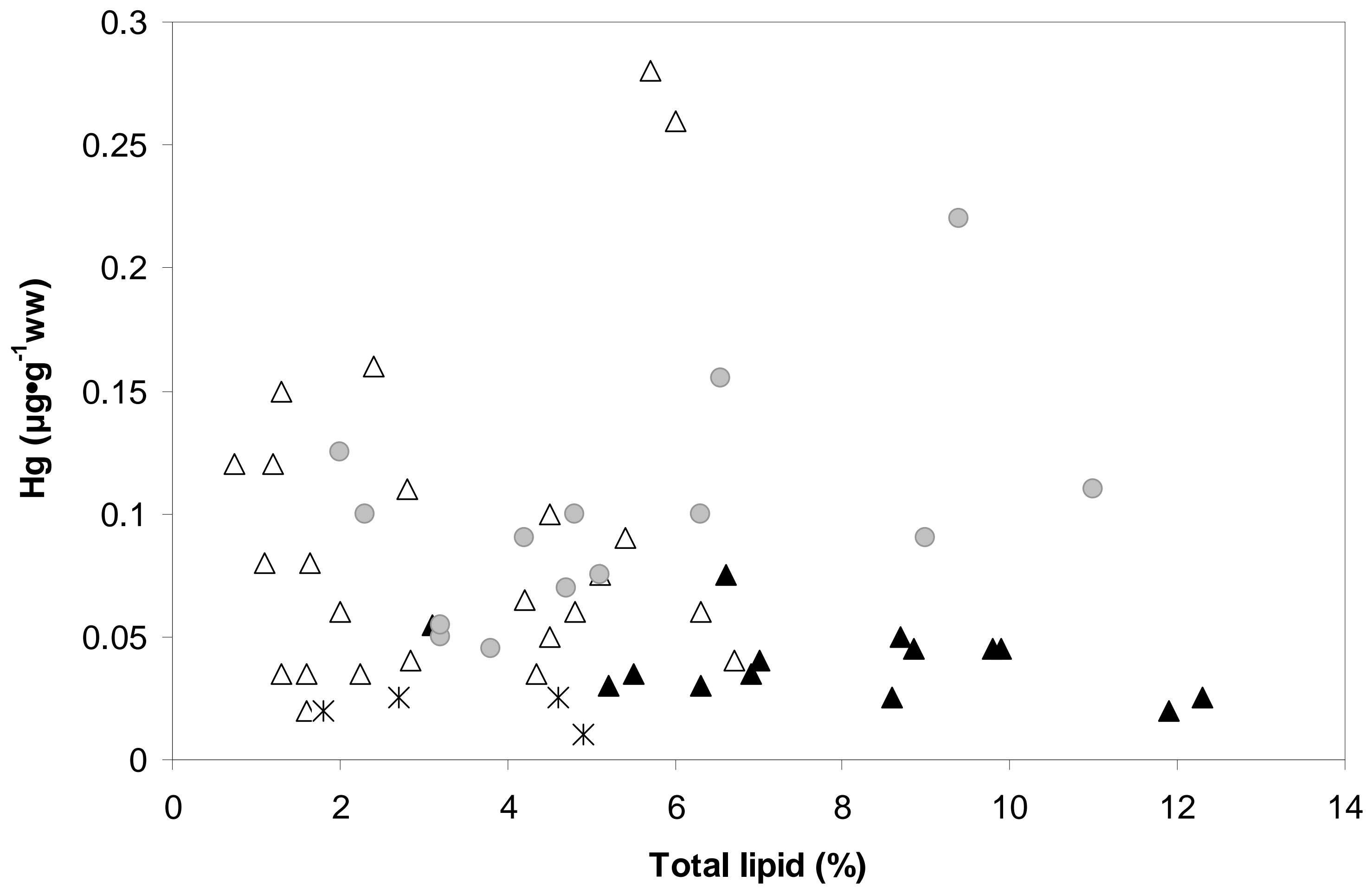
Table 6. Tissue distribution of mercury (Hg μg·g^{-1}ww), total lipid content (TLC % ww) and dominant lipid class (DLC) in squid, lanternfish and dragonfish

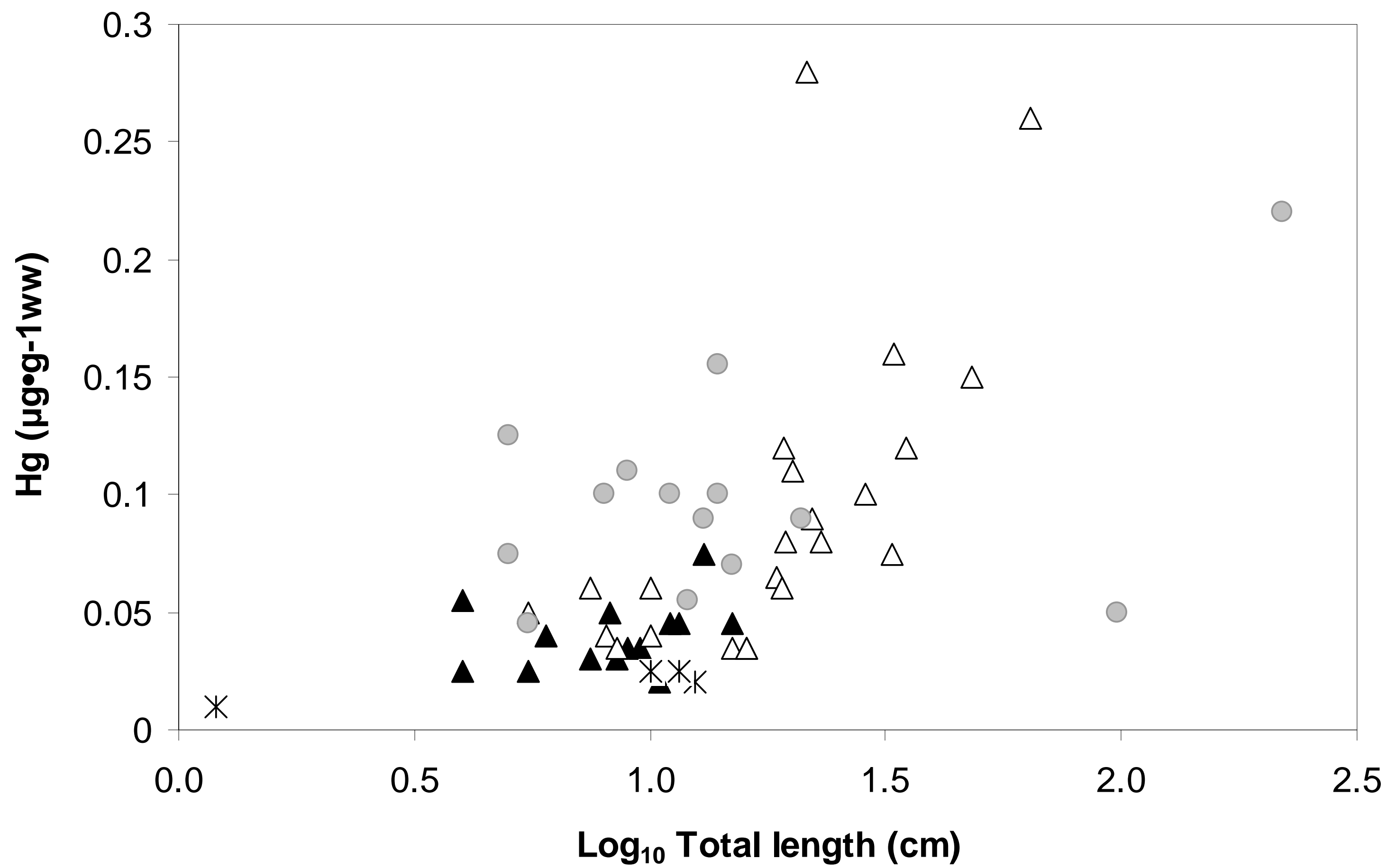
	Lycoteuthis lorigera (n = 1)		*Todarodes filippovae* (n = 1)		*Diaphus danae* (n = 1)		*Stomias boa* (n = 1)	
Total length (cm)	5.2		210		14.0		19.4	
Total weight (g)	10.9		340.2		26.1		16.6	
Water content (%) Whole	76		-		72		84	
Total mercury (Hg μg g^{-1}ww)								
Whole	0.11		0.22		0.03		0.04	
Liver/digestive gland	0.20		0.26		0.05		0.04	
Flesh/mantle	0.09		0.11		0.03		0.03	
Stomach	0.09		-		0.01		-	
Head tissue	0.06		-		0.02		-	
Average	0.11		0.20		0.03		0.04	
Lipid class composition								
	DLC (%)	TLC %	DLC (%)	TLC %	DLC (%)	TLC %	DLC (%)	TLC %
Whole	PL (52.3)	3.2	TAG (61.2)	9.8	TAG (76.3)	10.6	TAG (69.9)	2.1
Liver/digestive gland	TAG (58.7)	4.3	TAG (79.2)	14.8	TAG (86.5)	6.9	TAG (62.7)	1.6
Flesh/mantle	PL (87.1) 0.9		PL (87.4)	0.8	PL (70.9)	1.6	PL (73.1)	0.6
Stomach	PL (62.7)	3.1	– –	– –	TAG (38.8)	5.5	– –	– –
Average	PL	2.9	TAG	8.4	TAG	6.1	TAG	1.4

PL – polar lipids, TAG – triacylglycerols

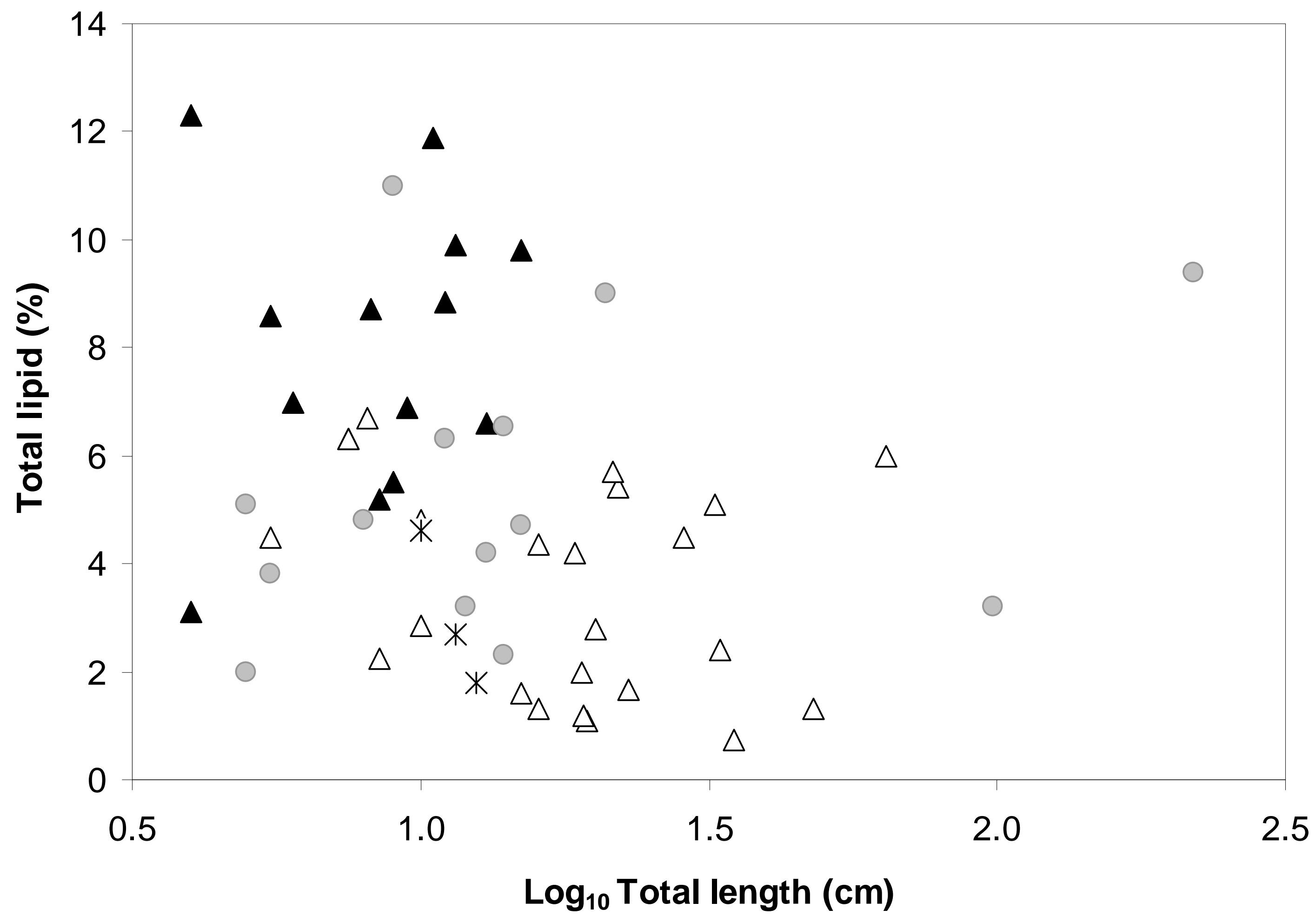
Table 7. Predictor fatty acids (FAs) for various prey groupings as identified by discriminant function analysis

Prey group		Predictor FAs (major contribution)	non-predictive FAs (minor contribution)
Fish	myctophids	20:1ω11, 24:1ω9, 16:0	18:1ω7, 22:1ω9, 20:4ω6, 20:1ω7
	mesopelagic	16:1ω7, 16:0, 18:1ω9, 20:4ω3, 14:0	22:6ω3, 22:5ω3
	bathypelagic	22:4ω3, 20:1ω9, 22:1ω11, 20:2ω6	20:5ω3, 22:1ω9
Squid	mesopelagic	22:6ω3, 22:1ω9	24:1, 20:2ω6, 22:4ω6, 22:4ω3, 16:1ω7
	bathypelagic	20:1ω7, 20:1ω9, 18:1ω7, 18:0	22:4ω3, 18:2ω6, 24:1
Octopus	benthic	20:5ω3, 22:6ω3, 20:1ω7	14:0, 16:1ω7, 18:1ω9, 22:1ω11, 24:1, 22:4ω3
Crustaceans	meso & bathypelagic	20:4ω6, 22:5ω3, 20:5ω3, 18:1ω7, 22:1ω9, 22:6ω3	16:0, 18:0, 22:1ω11, 18:4ω3, 22:4ω3

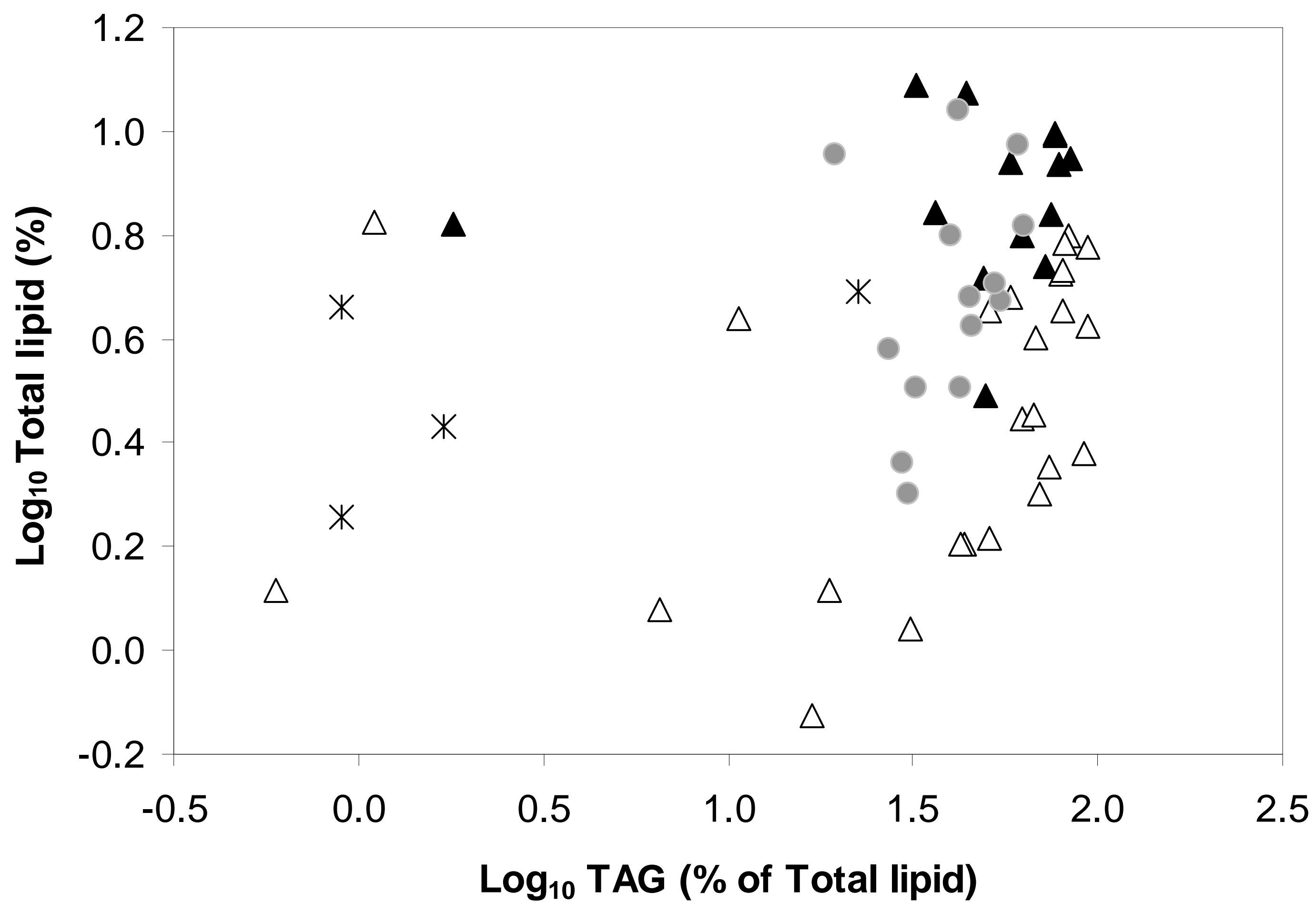

0.3
0.25
0.2
0.15
0.1
0.05
0
Hg (µg•g-1ww)
0
2
4
6
8
10
12
14
Total lipid (%)
A



B



C



D

Figure 1. Plots of: A) total lipid and total mercury, B) total mercury and total length, C) total lipid and total length, and D) TAG and total length in all prey species: * crustaceans ● cephalopods ▲ myctophid fish Δ other fish

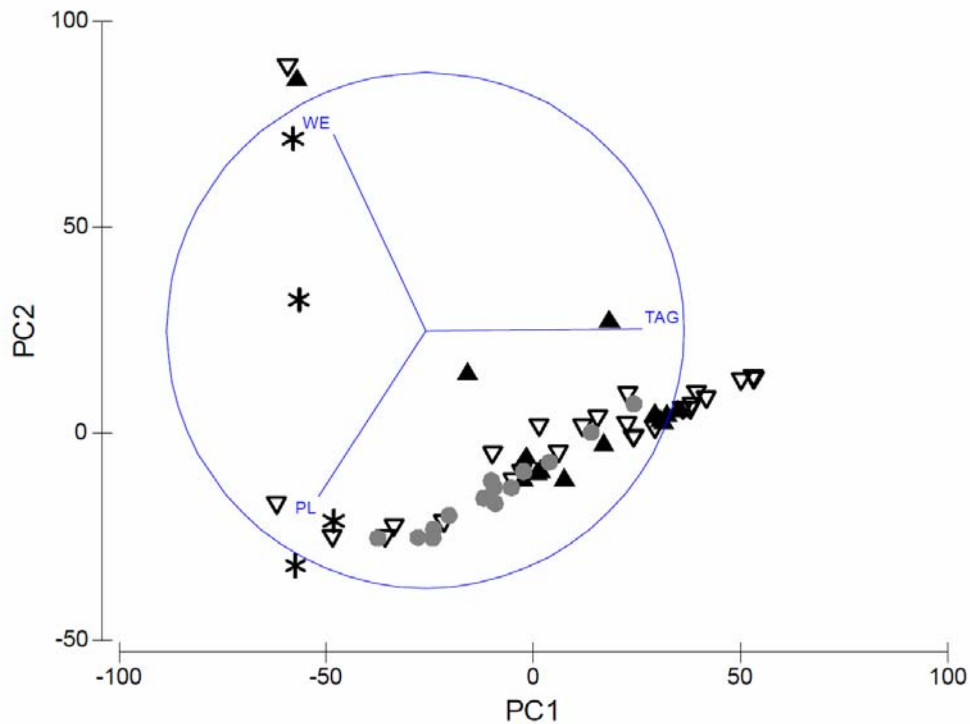


Figure 2. Scatter plot of principle component analysis (PCA) of the main lipid class (WE; wax esters, TAG; triacylglycerols, PL; phospholipids) composition of all prey species examined in this study collected from south east Australia. ● Cephalopods, ▽ Fish, ▲ Myctophid fish, * Crustaceans. WE dominant species include Ha, Nan, Asp. PL dominate prey include Av, Sd, Esp. TAG dominant prey include La, Nsp, Tt, Ta (Refer to Table 1 for species names). The correlation circle represents the relationships between treatments along the two axes. When two variables are far from the centre, then, if they are close to each other they are significantly positively correlated.

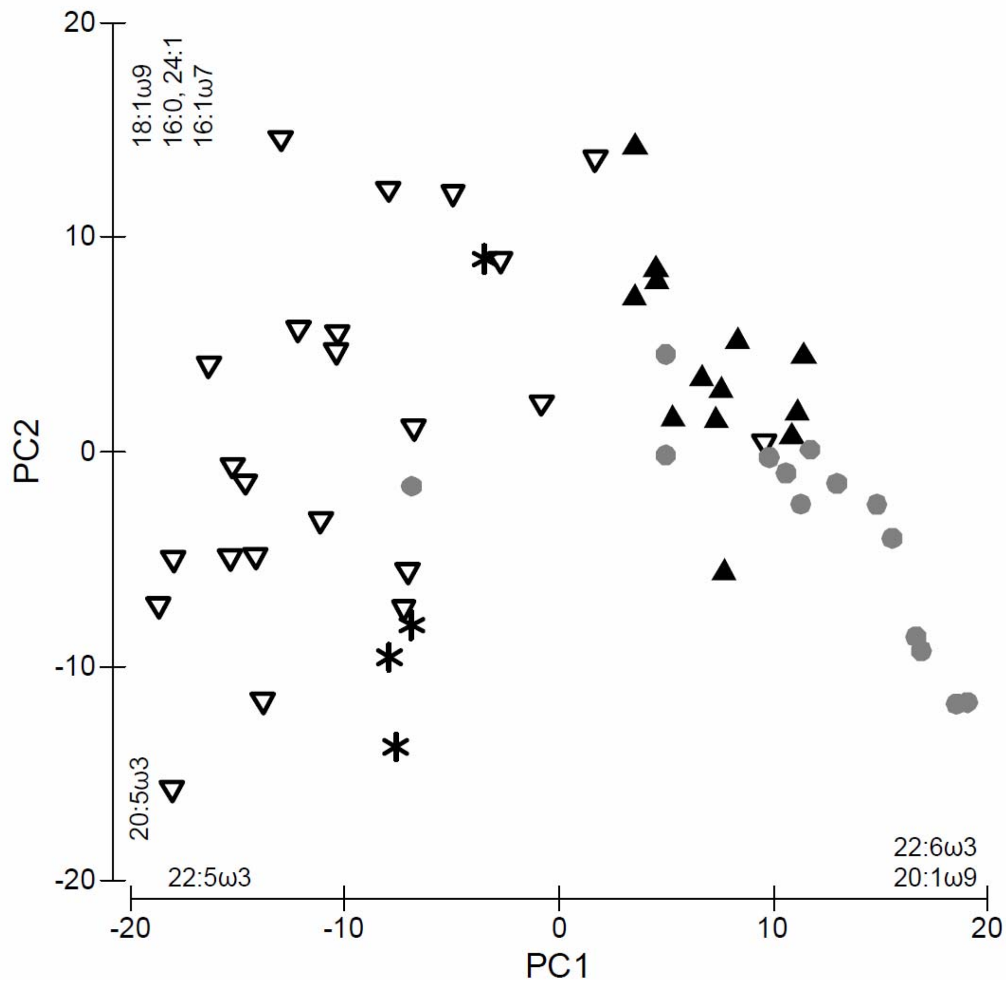


Figure 3. Principle component analysis (PCA) of all FA for all prey species. ● cephalopods, ▽ fish, ▲myctophid fish,* crustaceans.

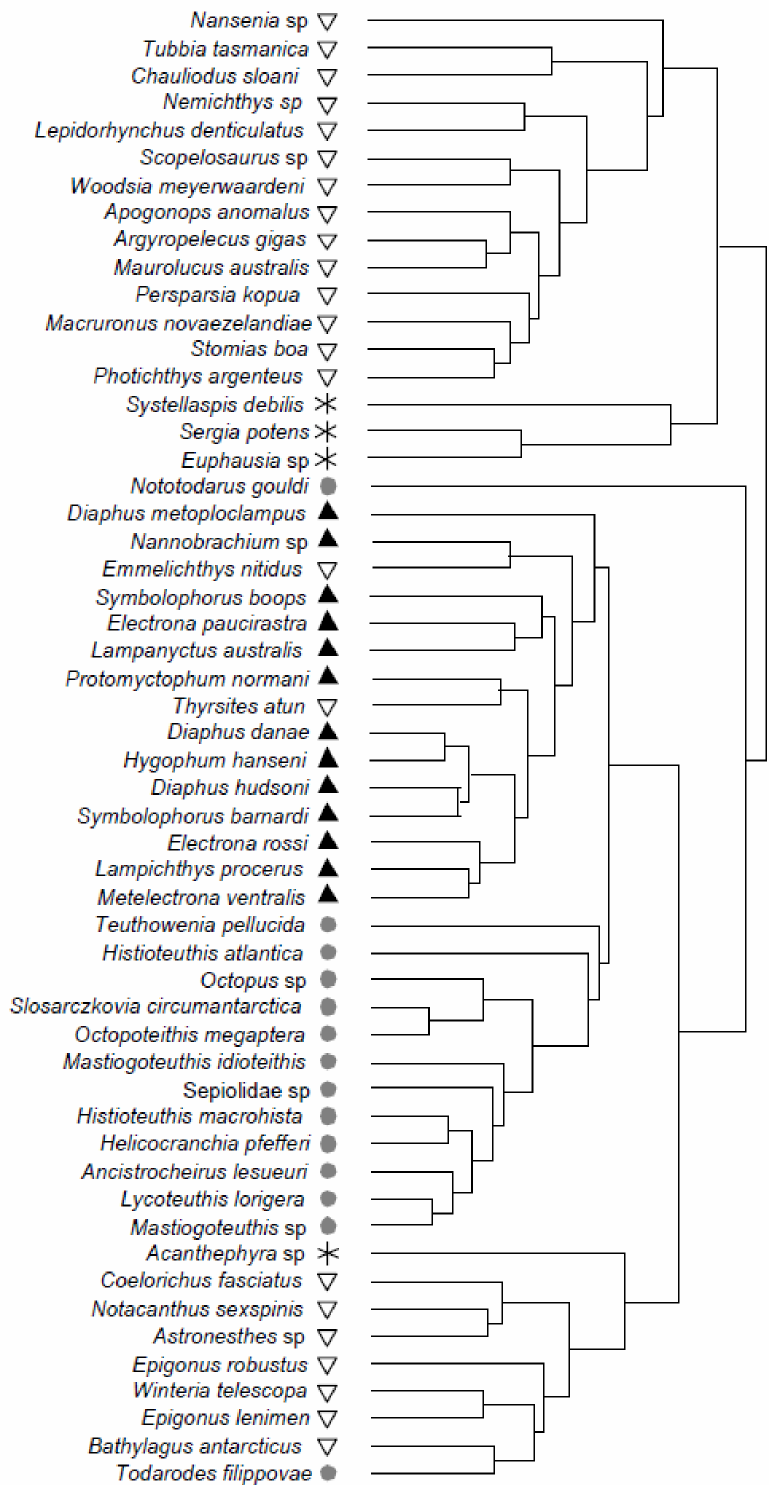


Figure 4. Hierarchical cluster dendogram based on Bray-Curtis similarity (complete linkage) for the average FA composition of 54 prey species, collected from continental slope waters off south-eastern Australia. Symbols refer to prey groups: ▲ myctophid fish; ∇ other fish; ● squid; *crustaceans.