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TITLE: Generic names and mislabelling conceal high species diversity in global fisheries markets

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Abstract

Consumers have the power to influence conservation of marine fishes by selectively purchasing sustainably-harvested species. Yet, this power is hindered by vague labelling and seafood fraud, which may mask market biodiversity and lead to inadvertent consumption of threatened species. Here, we investigate the repercussions of such labelling inaccuracies for one of the world's most highly-prized families of fishes – snappers (Family: Lutjanidae). By DNA barcoding 300 'snapper' samples collected from six countries, we show that the lax application of this umbrella term and widespread mislabelling (40%) conceal the identities of at least 67 species from 16 families in global marketplaces, effectively lumping taxa for sale that derive from an array of disparately-managed fisheries and have markedly different conservation concerns. Bringing this trade into the open should compel a revision of international labelling and traceability policies, as well as enforcement measures, which currently allow such extensive biodiversity to be consumed unknowingly.

Introduction

In an era of rising seafood demand, impaired ocean health, and perturbing rates of illegal, unreported and unregulated (IUU) fishing (FAO 2016), consumers are increasingly urged to source species from responsibly-managed fisheries (Gutiérrez *et al.* 2012). While there is general accord that detailed and accurate information on fishery products is crucial to empower consumer choice and promote legal and sustainable seafood trade (Barendse & Francis 2015), these provisions have not necessarily been translated into policy. The European Union (EU) has arguably the most robust seafood labelling legislation, requiring declaration of the commercial designation, scientific name, production method, geographical origin and fishing-gear category on retail seafood products (Reg. [EU] 1379/2013), complemented with comprehensive traceability requirements ([EC] 178/2002; 1224/2009; [EU] 404/2011). In comparison, labelling regulations in other countries are lenient, often necessitating little more than a common name on seafood packaging (Table S1). Furthermore, the approved common names for fish in the seafood naming lists of different countries (Table S1) introduce confusion, since these lack harmonisation between regions and frequently group multiple species under generic market labels. As fisheries trade expands, supply chains lengthen, and a growing number of 'new' and exotic species enter world markets (Watson *et al.* 2016; Di Muri *et al.* 2018), it becomes increasingly clear that weak and/or poorly-enforced regulations promote the proliferation of seafood fraud, undermining sustainable fisheries management and offering avenues for laundering of IUU products into legitimate marketplaces (Jacquet & Pauly 2008). Yet, no studies have empirically tested the extent to which generic labels and non-compliance conceal market biodiversity, hamper consumer choice and potentially imperil species on a global scale.

Here, we tackle this critical issue using an iconic but diverse family of fishes as a case example – snappers (Family: Lutjanidae). Members of this family represent major fisheries resources throughout their circumtropical range (Fig. 1) and are among the world's most valued marine species (Amorim *et al*. 2018). However, in addition to several life-history traits that render them vulnerable to overexploitation, the taxon embodies all the complexities associated with modern seafood supply chains: caught mainly in poorly-managed and data-scarce fisheries in developing countries, exported primarily to the affluent global North, and permitted to be marketed under 'umbrella' terms that may mask the diversity of >100 species comprising the family, and sometimes also those from other families (Cawthorn & Mariani 2017) (Table S2). For instance, 'snapper' can refer to 56 Lutjanid species in the United States (US) (FDA 2017), and 112 Lutjanid species in the United Kingdom (UK) (DEFRA 2013). Canada's 'Fish List' allows 108 species to be called 'snapper' or 'Pacific snapper', including both Lutjanids and *Sebastes* spp. (rockfishes) (CFIA 2017). In Australia, 'snapper' appears in the standard names of 96 species (AFNC 2017), whereas New Zealand's (NZ's) designations exclude Lutjanids altogether and rather include Sparidae (seabream) and Berycidae (alfonsino) species (MPI 2013). Adding to this obscurity, 'snappers' are exceptionally prone to market fraud (77–100%; Table S3), expanding the diversity under this umbrella term further.

In this most geographically-widespread seafood authentication study conducted to date, we employ a forensically-validated DNA barcoding technique (Dawnay *et al*. 2007) to unravel the species diversity underpinning the global 'snapper' trade, using the results to map patterns in labelling inconsistencies, assess the likely origins of collected 'snapper' samples, and investigate the conservation impacts of 'snapper' misrepresentation. Illuminating this trade, and the ripple effects on sustainability outcomes, should identify the path towards addressing the issue and oblige stakeholders to take necessary actions.

Methods

Sampling

To evaluate the variety of species sold as 'snapper' on world markets, we chose six English-speaking countries for sample collection, namely Canada, US, UK, Singapore, Australia and NZ. We visited multiple sites in each country, covering 21 states/counties and 26 cities/towns (Fig. 1, Table S4). We screened 300 samples sold with 'snapper' in the description, including fresh, frozen and cooked products, ranging from portions to whole fish, obtained from fishmongers, fish markets, supermarkets and restaurants over a 12-month period (August 2016–July 2017). The ratio of samples from different outlets and in different forms was based on availability in the given country. We submitted photographs of each sample and product-associated metadata to the Barcode of Life Database (BOLD, www.boldsystems.org), under the project 'SNAP-TRACE' (Database S1). Duplicate tissue sub-samples were excised from each sample and stored in 95%-ethanol tubes until shipping to the UK laboratory with pre-approved import permits.

Species identification

We used a Chelex® resin protocol (Estoup *et al*. 1996) to extract sample DNA and amplified a ~650 base-pair fragment of the cytochrome oxidase I (COI) gene using the primers, reaction mixtures and cycling conditions described in Cawthorn *et al.* (2015). PCR products were purified and sequenced by Macrogen (Europe) and quality-trimmed sequences were uploaded to the BOLD 'SNAP-TRACE' project. Sequences were subsequently identified in

GenBank (www.ncbi.nlm.nih.gov), cross-referencing results in the BOLD 'Species-Level' and 'Public-Records' databases. We used a similarity threshold of ≥98% to assign sequences to potential species, as most analysed marine fishes have intra-specific COI divergences well below 2% (Ward 2009). Next, we aligned all COI sequences and constructed a maximum-likelihood (ML) tree (File S1). For each sample, we inferred a 'most likely' species from top matches across the three sequence databases and positions in the ML tree and/or BOLD 'Tree-Based Identification' (TBI) tool, but also recorded possible candidate species with <2% divergence (Database S1). Where top matches included two or more taxa with identical sequence similarities, and where explicit identification could not be resolved from the ML tree or BOLD TBI, both/all taxa were designated 'most likely' species. We considered both 'most likely' species and possible candidates (<2% divergence) when evaluating 'snapper' misrepresentation. However, we included only 'most likely' species in downstream analyses, weighting scores equally across taxa when identifications could not be resolved.

Market biodiversity and misrepresentation

To evaluate species diversity across countries and overall, we calculated Shannon (H') indices in PAST 3.x. As a check for potential bias introduced by variations in country-specific sample sizes, we repeated the analyses using rarefaction in PAST 3.x to compare expected diversity ($E[S_n]$) in a standard sub-sample of 13 (i.e. smallest sample size).

We used the seafood labelling regulations and naming lists of each sample-collection country (Tables S1, S2), as well as a decision tree (Fig. S1), to define 'snapper' misrepresentation on two levels, i.e. 'misnamed' and/or 'mislabelled' by species. Samples were considered misnamed if an incorrect version of an approved common name was used at the point-of-sale, but this did not implicate another species in the relevant country's naming list. Samples were deemed mislabelled when either the declared species, or species inferred from the declared common name, did not correspond with the top genetic match or any candidate species (Database S1). For Singapore, where no seafood naming list exists, samples were not considered misnamed, but were considered mislabelled when identified as non-Lutjanid species. We statistically analysed misrepresentation rates across countries and sectors using likelihood-ratio Chi-squared tests with the GTest function of the R package DescTools v 0.99.24.

Likely origin

We followed a three-step approach to trace samples to potential source fisheries, using FishBase (www.fishbase.org) to determine the FAO areas in which genetically-identified species are natively distributed. Firstly, where a catch (FAO) area was declared, we verified the occurrence of the identified species in that area and considered this the most likely geographical origin (assigned a score of 1). Where a country of origin was declared on fresh (unprocessed) samples without a catch area, we recorded only FAO areas within the declared country's exclusive economic zone (EEZ) in which the identified species occurs. Where no provenance information was provided, or where the declared origin was possibly the country of processing, we assumed equal probability of deriving from any FAO area in which the identified species occurs. In the latter two cases, fractional scores were equally assigned to each recorded area as proportions of 1. Scores were subsequently summed across sampling countries and areas. Lastly, to evaluate the state of fisheries in each area, we tabulated information on overall catch trends and percentages of overfished stocks (FAO 2016), IUU fishing rates (Agnew *et al.* 2009) and snapper fisheries management (Amorim *et al.* 2018; FishSource [www.fishsource.org]). We nevertheless highlight that, although catch trends can be useful indicators of stock status particularly in fisheries lacking formal assessment (i.e. majority of global fisheries), declining catches may result from numerous factors, including improved management and legislation, and do not necessarily reflect abundance or mismanagement (Pauly *et al*. 2013). Conversely, high IUU rates strongly correlate with weak governance and fisheries mismanagement (MRAG 2005; Agnew *et al*. 2009).

Conservation status

We evaluated the conservation status of genetically-identified species using the IUCN Red List (IUCN 2017), as well as scores of 'intrinsic vulnerability to fishing' (IV) based on ecological and life-history traits and expressed on a scale from 1 to 100 (IV increases from 1 and is considered high at ≥55) (Cheung *et al*. 2005). We chose these metrics over individual stock assessments (e.g. FAO, RAM database) since most identified species are not covered by such assessments and because catch locations required to match samples with populations/stocks were seldom declared (Database S1). For comparison, all valid members of the Lutjanidae family (112 species) were also evaluated. To statistically analyse IV scores, we conducted a two-way ANOVA, verified acceptable normality, and used Fisher LSD post-hoc testing.

Results

We identified at least 67 species, representing 16 families and five orders, sold as 'snapper' globally (Fig. 2). Approximately one-third of all samples comprised non-Lutjanids, 32% were misnamed and 40% were mislabelled (Fig. 3). Mislabelled samples encompassed no less than 50 species, with the most common non-Lutjanid substitutes including seabreams (Sparidae spp.), rockfishes (*Sebastes* spp.), threadfin breams (*Nemipterus* spp.), tilapia (*Oreochromis* spp.) and fusiliers (*Caesio* spp.)[1] (Fig. 2, Database S1). By country, the UK samples exhibited the highest species diversity (38 species; H' = 3.5; $E(S_{13}) = 11.2$) (Fig. 2), 42% of which were non-Lutjanid spp. (Fig. 3). Diversity indices were similar for the US, Canada, Singapore and Australia (H' = 2.0–2.5; $E(S_{13}) = 6.9–7.9$), but the US had the largest proportion of Lutjanids and a high frequency of certain species within the family (e.g. *Lutjanus campechanus*). NZ had the lowest diversity (5 species; H' = 1.0), with a predominance of Sparids rather than Lutjanids.

Misnaming and mislabelling rates differed by country and sector (Fig. 3), although variations in sample size should be considered in proportional comparisons. The UK had the highest incidence of misnaming (67%), mostly involving samples from fishmongers and markets. Additionally, >80% of UK samples did not carry mandatory information (scientific name, production method, geographical origin, fishing-gear category) required by EU regulations ([EU] 1379/2013) (Fig. S2). Mislabelling rates were highest in the UK and Canada (55%), followed by the US (38%), with restaurant samples most frequently implicated (Fig. 3). Paradoxically, although NZ had the highest proportion of non-Lutjanids (85%), it had the lowest mislabelling rates, given that non-Lutjanids are permitted to be called 'snapper' in the country. By designation, 'red snapper' was most frequently mislabelled overall, and in the US, UK and Canada (Fig. 4).

Samples were predicted to have the highest probability of originating from the Western-Central Atlantic (FAO 31), including the bulk of Lutjanids from the US, where overall catches are declining but IUU fishing is low (Fig. 5). This was followed by Indo-Pacific regions (FAO 57, 71, 61) and the Southwest Atlantic (FAO 41), where IUU fishing is

[1] Although Caesionidae are phylogenetically nested within Lutjanidae (see File S1), they cannot be called 'snapper' in the seafood naming lists of sample-collection countries.

exceptionally high and snapper fisheries are considered poorly managed. Non-Lutjanids appeared to mainly originate from the Southwest Pacific (FAO 81) where IUU fishing is low, although several other areas with high IUU levels were among probable sources (Fig. 5). For most countries, samples were most likely to derive from surrounding areas. The UK represents an exception, with a high number of diverse likely source fisheries.

Correctly labelled Lutjanids in our study set had similar IUCN status but higher mean IV than mislabelled Lutjanids ($p = 0.04$), with both groups exhibiting poorer conservation status than the Lutjanidae family as a whole (Fig. 6). The most notable conservation impact was observed for non-Lutjanids labelled in accordance with country-specific naming lists, with this group having higher mean IV (66.1) than correctly labelled Lutjanids (50.6) ($p < 0.01$).

Discussion

The data presented underscore that misleading generic names and widespread mislabelling conceal substantial biodiversity in global marketplaces, with far-reaching impacts on market-based efforts to conserve wild fishes. Overall, we discovered at least 67 species from 16 families lumped under the 'snapper' umbrella, potentially deriving from an array of disparately-managed fisheries and having different conservation concerns. Moreover, over half of these are reef-dwelling species and are likely threatened by habitat loss/degradation, overfishing and insufficient protection (Newton *et al*. 2007; Mouillot *et al*. 2016). While inconclusive in proving intent, or assigning blame within supply chains, our study also reveals several substitutions with lower-value species (e.g. *Oreochromis* spp., *Nemipterus* spp., *Pagellus* spp., *Sebastes* spp., *Pollachius virens*) that hint at economic motives (Sumaila *et al*. 2007).

Seafood naming lists are in place to reduce confusion in fish nomenclature, yet our results raise questions as to whether these are achieving their goals – which at minimum should alert consumers to a product's true nature. Members of the Lutjanidae are ecologically diverse, vary in vulnerability and value, and are frequently caught in poorly-managed fisheries, with no stock assessments, and high IUU fishing rates (Wagey *et al*. 2009; Amorim *et al*. 2018). Even when legal, grouping these species under single market names drastically reduces consumer power to make informed choices. Allowing members of other families to be labelled as 'snapper' (Canada, Australia, NZ) exacerbates confusion, and may distort fisheries statistics (Cawthorn & Mariani 2017) and promote unintentional mislabelling in importing countries (Wong & Hanner 2008).

The high rates of 'snapper' misrepresentation uncovered here indicate shortcomings in industry management and policy enforcement. This is perhaps most aptly illustrated by the UK, which follows the world's most stringent seafood labelling regulations, but where misnamed and mislabelled non-Lutjanids appeared more frequently than in a country like Singapore, with minimal labelling requirements and no seafood naming list. Beyond labelling legislation, country-specific variations in misrepresentation rates may have stemmed from various geographical, social and economic factors. Australia, Singapore and the US are in key Lutjanid-producing regions, which might increase local supply and familiarity with these species, and partially explain the lower mislabelling rates in at least Australia and Singapore. The US is the single largest market for 'snappers', fed primarily by imports that may derive from over 60 partner countries (Cawthorn & Mariani 2017). The US Presidential IUU Task Force recently declared 'red snapper' (*L. campechanus*) a 'high-risk' species for IUU fishing and fraud (NOAA 2015), mandating full-chain traceability for imports of this species (NOAA 2016), although overlooking the many species traded under other 'snapper' designations. In light of this action, the current US mislabelling rates of 'snapper' (38%) and specifically 'red snapper' (36%) are lower than in previous studies (Table S3) but remain problematic considering the volumes traded. In non-Lutjanid-producing countries like the UK and Canada, a heavy reliance on imports and lack of species familiarity potentially contributed to the high mislabelling rates (55%) observed. Additionally, our results suggest that the UK faces momentous traceability challenges in the context of 'snappers', given the wide species diversity sold under this label, the many different likely source fisheries, and the high IUU rates in numerous source fisheries.

Considering the conservation impacts of this hidden trade more closely, we demonstrate that countries that allow non-Lutjanids to be labelled as 'snappers' essentially conceal the identities of species with high vulnerability to fishing (e.g. *Pagrus auratus* [Australia, NZ], *Centroberyx gerrardi* [NZ], several *Sebastes* spp. [Canada]). Logan *et al*. (2008) have similarly shown that the permitted use of 'Pacific red snapper' masks the sale of overfished *Sebastes* spp. Nonetheless, we find the repercussions arising from unauthorised mislabelling more difficult to disentangle. Whereas substitutions within the Lutjanid family might favour more resilient species, non-Lutjanid substitutes vary widely in their IUCN ratings and vulnerabilities, but may include threatened species (e.g. VUL *Lachnolaimus maximus*) and those from unassessed stocks from poorly-managed fisheries. Moreover, even when substitutes are not endangered, mislabelling can indirectly impact conservation efforts by (1) misrepresenting the abundance of potentially-dwindling labelled species, and (2) allowing overharvesting of substitute species to go unmonitored when disguised under different names (Pitcher *et al*. 2002). The case of 'red snapper', the most frequently marketed and mislabelled samples in this study, exemplifies the former point. Following decades of overexploitation, stocks of this highly-prized taxon (*L. campechanus*) are overfished in both the US South Atlantic and Gulf (SEDAR 2015; 2017). While limited supply juxtaposed against high consumer expectations may promote substitution of red snapper, the widespread misuse of this market name likely belies the true stock status and sustains demand. Perhaps most disconcertingly, these high mislabelling rates indicate failings in traceability systems in global snapper supply chains and, when traceability is inadequate, the chances of substitutes originating from IUU sources are vastly increased (Helyar *et al*. 2014).

Given the extent to which snappers are marketed globally, our findings call for a co-ordinated revision of international policies and practices that permit this extensive biodiversity to be consumed unknowingly. We recommend several actions to promote more transparent and sustainable snapper trade. At the national level, ambiguities in seafood naming lists might be reduced by adopting a 'one species, one name' approach, as in Australia (AFNC 2017), and by omitting references to 'snapper' for non-Lutjanids. Nevertheless, recognising the confusion with colloquial names in global marketplaces, we suggest that country-specific labelling regulations be aligned with those of the EU in requiring scientific names on seafood, as well as mandating additional criteria (geographical origin, production- and harvest-methods) to benefit consumer choice. Internationally, the Codex Alimentarius Commission could play a leading role in establishing standards and guidelines for responsible seafood labelling as part of its 'food fraud initiative' (CAC 2017). Along with more robust legislation, post-regulatory monitoring regimes will likely require consolidation and strengthening to overcome known barriers to enforcement, such as split or unclear governmental-agency mandates, inadequacies in agency funding, human-resource allocations, laboratory capacity and inspection rates, corruption and bribery of officials, and minimal penalties for non-compliance (Hofherr *et al.* 2016; Friedman 2017). Improving supply-chain traceability is imperative and could be facilitated by emerging technologies (e.g. electronic interoperable systems, DNA-based verification), however, such measures will require co-operation from both domestic fisheries and exporting nations. Developing countries, principal suppliers of snappers, often suffer from weak governance and insufficient financial and technical resources to achieve end-to-end traceability, opening doors for illicit conduct (Cawthorn & Mariani 2017). Fostering strategic partnerships between supply-chain actors, non-governmental organisations and foreign governments could assist in building infrastructure, expertise, and monitoring- and enforcement-capacity in developing-world fisheries, whilst preventing stricter regulations from becoming trade barriers and jeopardising livelihoods in such nations (Willette & Cheng 2018). Lastly, we recommend that all policies be complemented by appropriate public awareness campaigns on seafood sustainability, fraud and potential substitutes, creating bottom-up pressure for transparent labelling and a marketplace less susceptible to trickery through mislabelling.

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Author contributions

DMC conceived and designed the experiments, performed the experiments, analysed the data, prepared figures and tables, and wrote the paper. **CB** analysed the data and reviewed drafts of the paper. **SM** conceived and designed the experiments, contributed reagents/materials, and reviewed drafts of the paper.

DNA sequence deposition

DNA sequences and accompanying metadata have been submitted to the Barcode of Life Database (BOLD, www.boldsystems.org) Barcoding Applications Campaign, under the project 'SNAP-TRACE'. Sample IDs and BOLD process IDs are included in Database S1.

Supporting Information

Additional Supporting Information may be found in the online version of this article at the publisher's web site:

Database S1. Database of (A) product-associated metadata recorded during sample collections, (B) species identifications made through DNA barcoding and evaluations of misnaming and mislabelling, and (C) conservation status of genetically-identified species based on IUCN ratings and 'intrinsic vulnerability' scores.

Table S1 Comparison of seafood labelling requirements and seafood naming lists in different world regions.

Table S2 Species across various families permitted to labelled as 'snapper' according to the relevant seafood naming lists of different countries.

Table S3 Rates of 'snapper' mislabelling reported in various studies around the world.

Table S4 Full sampling protocol, including sample numbers collected at state/county- and city/town-levels.

Figure S1 Decision tree used to evaluate misnaming and species mislabelling of 'snapper' samples.

Figure S2 Numbers and percentages of samples collected from UK fishmongers / fish markets and supermarkets that lacked mandatory labelling information required by current EU regulations (Regulation [EU] No. 1379/2013).

Figure S3 Numbers and percentages of samples not mislabelled and mislabelled according to the seafood naming lists of sample-collection countries, by city/town.

File S1 Phylogenetic analysis: Methodology, maximum-likelihood tree, taxonomic notes.

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Main text figure legends

Figure 1 Sampling locations overlaid on the global species-richness map for the family Lutjanidae, with a breakdown of sample numbers collected per country, site and sector. Species-richness point data (GPS co-ordinates) for all assessed Lutjanidae species (n = 98) were derived from AquaMaps (Kaschner *et al.* 2016) and were plotted along with GPS co-ordinates of individual sampling sites in ArcGIS Online (www.arcgis.com).

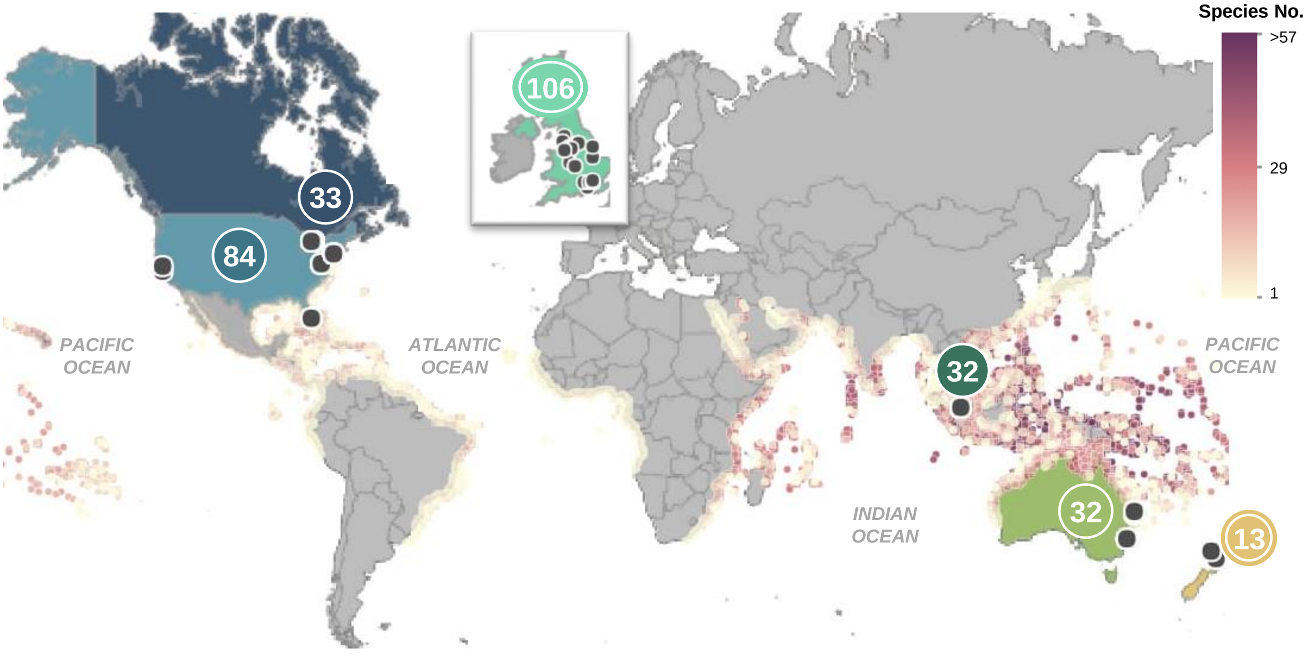
Figure 2 Proportional diversity of species and families identified in the global 'snapper' sample set (n = 300) (right) linked with the countries of sample collection (left), where the left-panel shows the relative contributions of individual families, the number of species and families, the Shannon diversity (H') indices and expected diversity ($E[S_n]$) indices estimated by rarefaction (i.e. number of taxa expected at the smallest sample size of 13) for each country. CAN = Canada; US = United States; UK = United Kingdom; AUS = Australia; NZ = New Zealand; SGP = Singapore.

Figure 3 Proportions of samples (numbers and percentages) identified as being (A) correctly named vs. misnamed, (B) not mislabelled vs. mislabelled by species, and (C) Lutjanidae vs. non-Lutjanidae spp., by country, sector and overall. CAN = Canada; US = United States; UK = United Kingdom; AUS = Australia; NZ = New Zealand; SGP = Singapore; FM/M = Fishmongers and fish markets; SUP = Supermarkets; RES = Restaurants; X^2 = Chi-squared; df = degrees of freedom.

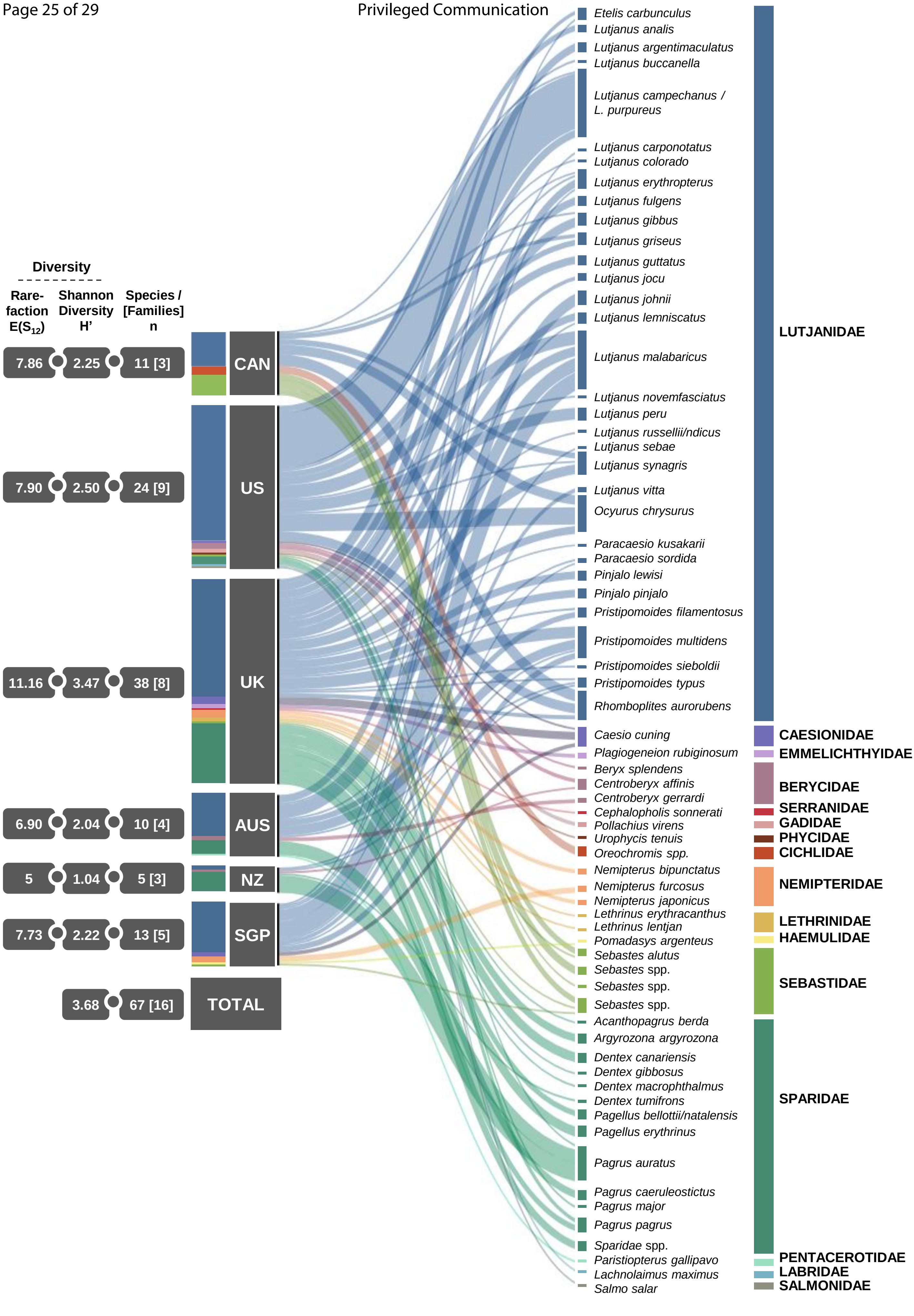
Figure 4 Numbers and percentages of samples not mislabelled and mislabelled according to the seafood naming lists of sample-collection countries, by designation and country.

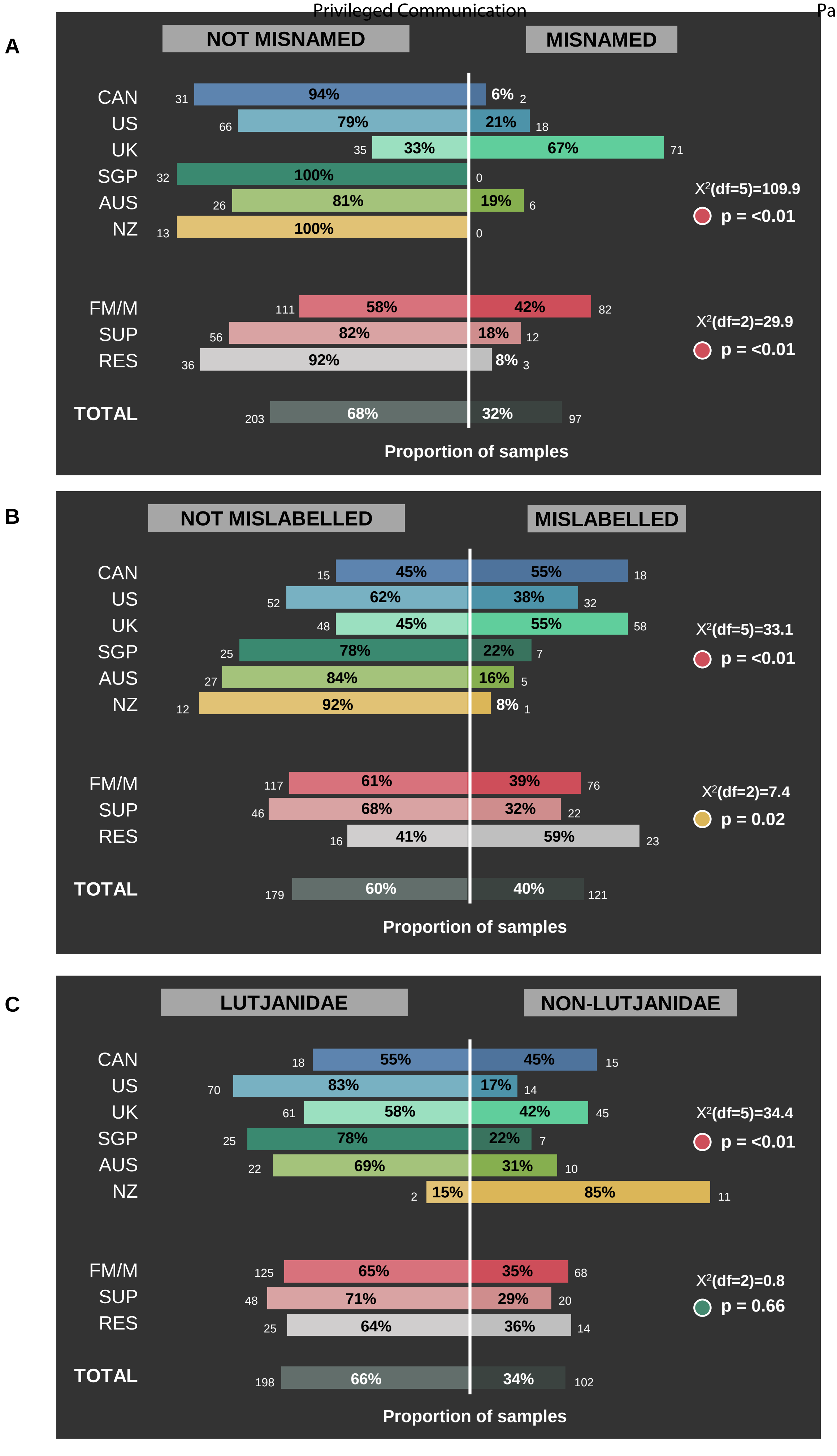
Figure 5 Likely geographical origins of 'snapper' samples and the status of prospective source fisheries. The main circular diagram uses bands of varying width to indicate the proportions of Lutjanids (LUT, white segments) and non-Lutjanids (NL, black segments) identified from each country (left) that were linked with different FAO major fishing areas (right). The top left-hand map shows FAO area boundaries, exclusive economic zones (EEZs) and sampling locations. The top right-hand panel indicates overall fisheries landing trends, percentages of overfished (O-F) stocks, estimated rates of IUU fishing, and the status of snapper fisheries management for each FAO fishing area. The FAO boundaries map was created in ArcGIS Online (www.arcgis.com) and the circular diagram was generated with Circos software (Krzywinski *et al*. 2009). W = well managed; P = poorly managed.

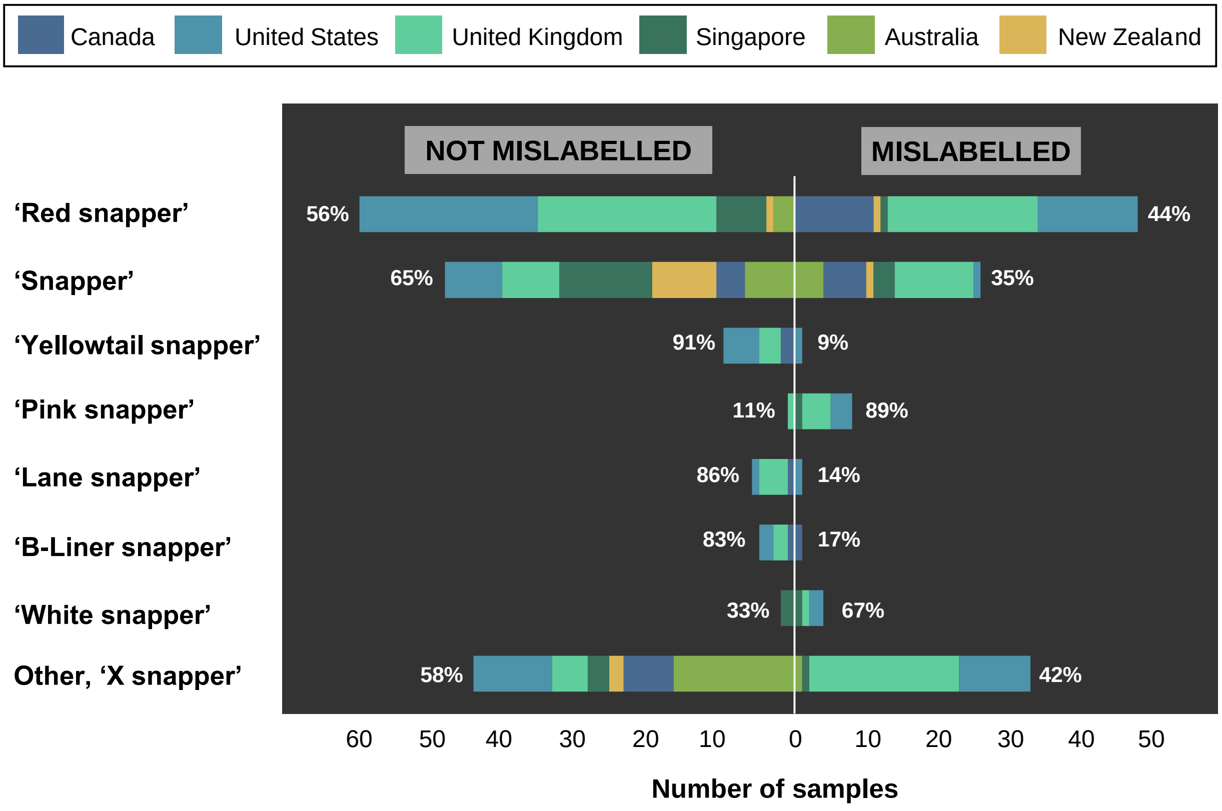
Figure 6 Conservation status of valid species within the Lutjanidae family (row 1) and genetically-identified species (rows 2–5) inferred from IUCN ratings and 'intrinsic vulnerability' scores estimated by fuzzy logic modelling. (A) shows the percentage of individuals falling into each IUCN category and (B) shows individual and mean 'intrinsic vulnerability' scores (out of 100), where a significant interaction was found between 'family' and 'labelling status' ($F_{[1,291]} = 22.93$, $MS_E = 2480.4$, $p < 0.01$) and lower-case letters indicate differences (5% level) determined through LSD post-hoc tests (between $MS_E = 108.17$, df = 219). IUCN ratings indicate global extinction risk based on population trends, whereas the fuzzy logic model integrates ecological and life-history characteristics to estimate vulnerability to fishing and proxy extinction risk. Four samples identified only to family level and one sample very likely to be farmed (*Salmo salar*) were excluded from this analysis. LUT = Lutjanidae spp.; NL = Non-Lutjanidae spp.; NA/DD = Not Assessed/Data Deficient; LC = Least Concern; NT = Near Threatened; VUL = Vulnerable; EN = Endangered; UNK = Unknown; INC = Increasing; STB = Stable and DEC = Decreasing.

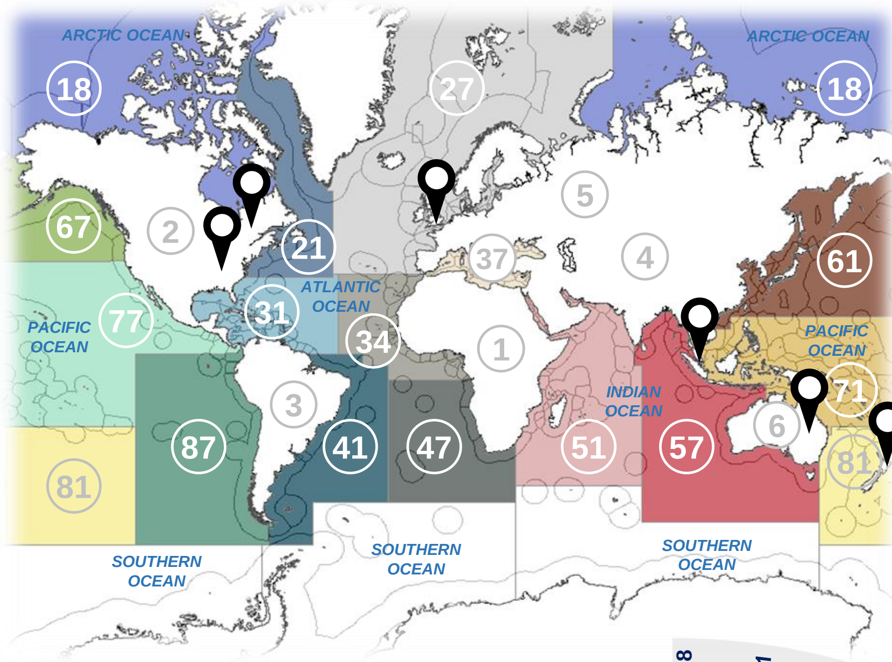


Country	State / county	City / town	Fishmonger / market (FM/M)	Supermarket (SUP)	Restaurant (RES)	Total
	n		*Sample n*			
Canada (CAN)	1	2	**15**	**8**	**10**	**33**
United States (US)	4	5	**39**	**27**	**18**	**84**
United Kingdom (UK)	11	14	**84**	**19**	**3**	**106**
Singapore (SGP)	1	1	**28**	**2**	**2**	**32**
Australia (AUS)	2	2	**21**	**6**	**5**	**32**
New Zealand (NZ)	2	2	**6**	**6**	**1**	**13**
GRAND TOTAL	**21**	**26**	**193**	**68**	**39**	**300**

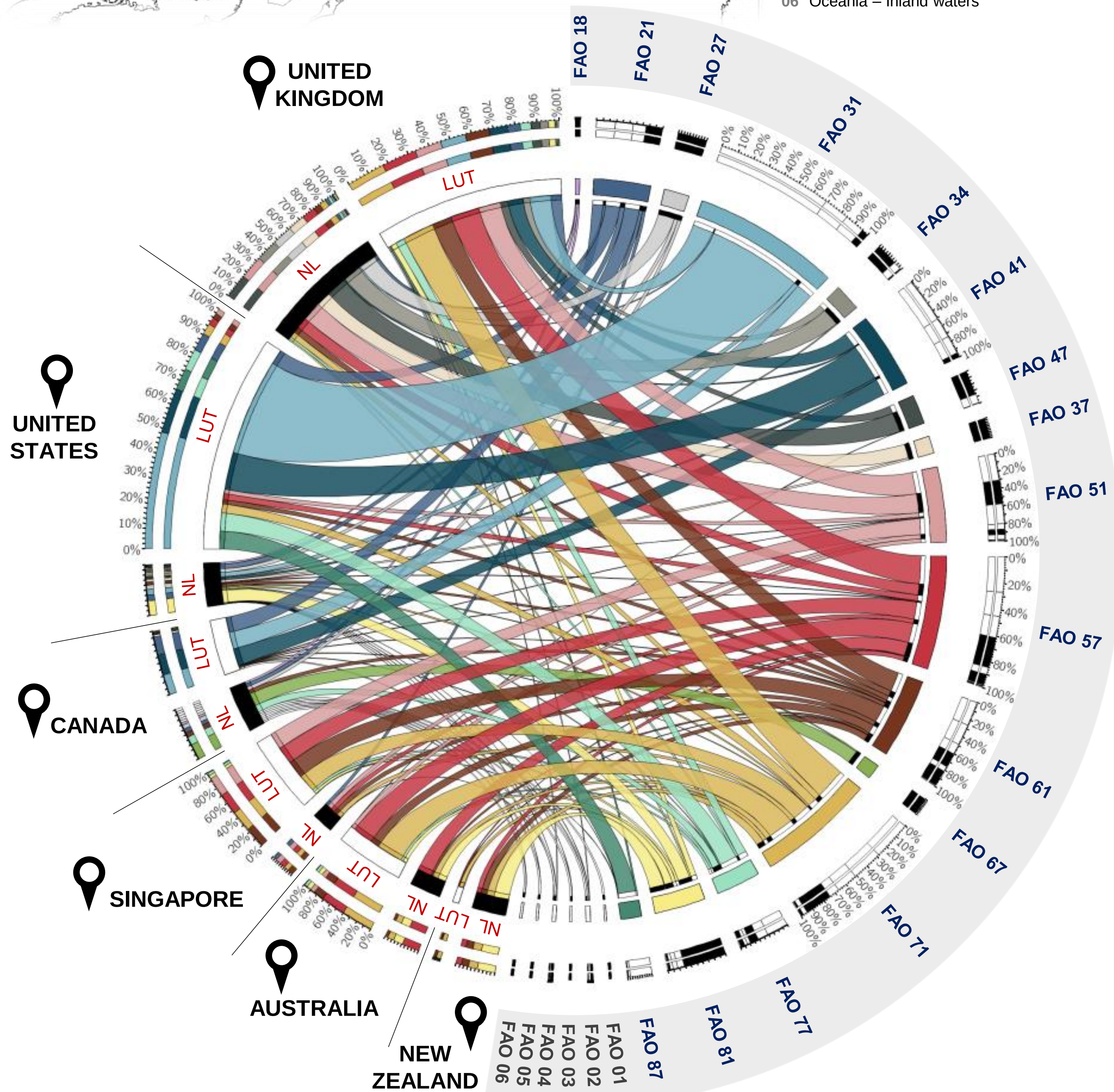

Diversity
Rare-faction E(S_{12})
Shannon Diversity H'
Species / [Families] n
7.86
2.25
11 [3]
CAN
7.90
2.50
24 [9]
US
11.16
3.47
38 [8]
UK
6.90
2.04
10 [4]
AUS
5
1.04
5 [3]
NZ
7.73
2.22
13 [5]
SGP
3.68
67 [16]
TOTAL
Etelis carbunculus
Lutjanus analis
Lutjanus argentimaculatus
Lutjanus buccanella
Lutjanus campechanus / L. purpureus
Lutjanus carponotatus
Lutjanus colorado
Lutjanus erythropterus
Lutjanus fulgens
Lutjanus gibbus
Lutjanus griseus
Lutjanus guttatus
Lutjanus jocu
Lutjanus johnii
Lutjanus lemniscatus
Lutjanus malabaricus
Lutjanus novemfasciatus
Lutjanus peru
Lutjanus russellii/ndicus
Lutjanus sebae
Lutjanus synagris
Lutjanus vitta
Ocyurus chrysurus
Paracaesio kusakarii
Paracaesio sordida
Pinjalo lewisi
Pinjalo pinjalo
Pristipomoides filamentosus
Pristipomoides multidens
Pristipomoides sieboldii
Pristipomoides typus
Rhomboplites aurorubens
Caesio cuning
Plagiogeneion rubiginosum
Beryx splendens
Centroberyx affinis
Centroberyx gerrardi
Cephalopholis sonnerati
Pollachius virens
Urophycis tenuis
Oreochromis spp.
Nemipterus bipunctatus
Nemipterus furcosus
Nemipterus japonicus
Lethrinus erythracanthus
Lethrinus lentjan
Pomadasys argenteus
Sebastes alutus
Sebastes spp.
Sebastes spp.
Sebastes spp.
Acanthopagrus berda
Argyrozona argyrozona
Dentex canariensis
Dentex gibbosus
Dentex macrophthalmus
Dentex tumifrons
Pagellus bellottii/natalensis
Pagellus erythrinus
Pagrus auratus
Pagrus caeruleostictus
Pagrus major
Pagrus pagrus
Sparidae spp.
Paristiopterus gallipavo
Lachnolaimus maximus
Salmo salar
LUTJANIDAE
CAESIONIDAE
EMMELICHTHYIDAE
BERYCIDAE
SERRANIDAE
GADIDAE
PHYCIDAE
CICHLIDAE
NEMIPTERIDAE
LETHRINIDAE
HAEMULIDAE
SEBASTIDAE
SPARIDAE
PENTACEROTIDAE
LABRIDAE
SALMONIDAE

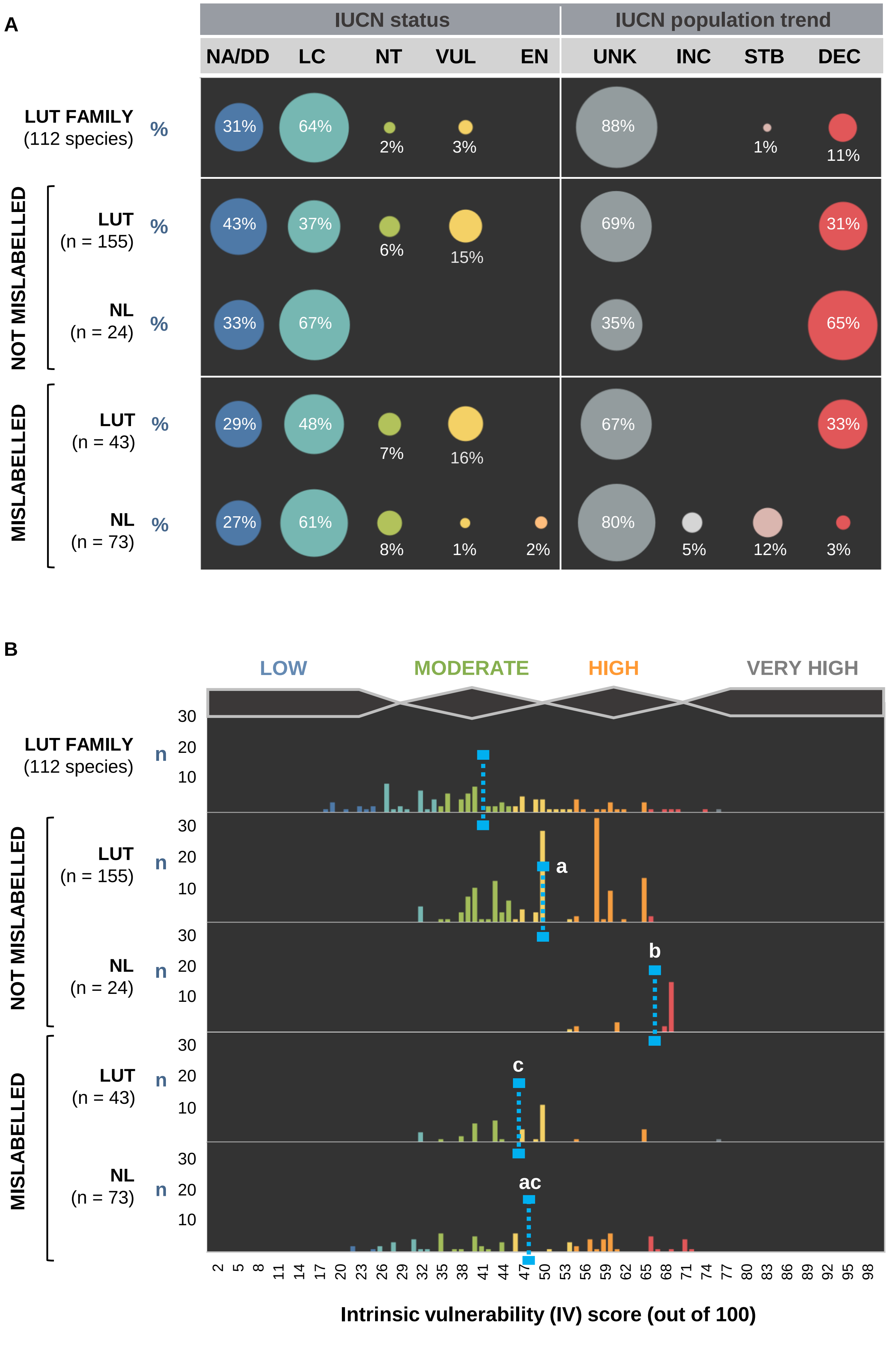

A
NOT MISNAMED
MISNAMED
CAN 31 94% 6% 2
US 66 79% 21% 18
UK 35 33% 67% 71
SGP 32 100% 0
AUS 26 81% 19% 6
NZ 13 100% 0
X2(df=5)=109.9
p = <0.01
FM/M 111 58% 42% 82
SUP 56 82% 18% 12
RES 36 92% 8% 3
X2(df=2)=29.9
p = <0.01
TOTAL 203 68% 32% 97
Proportion of samples
B
NOT MISLABELLED
MISLABELLED
CAN 15 45% 55% 18
US 52 62% 38% 32
UK 48 45% 55% 58
SGP 25 78% 22% 7
AUS 27 84% 16% 5
NZ 12 92% 8% 1
X2(df=5)=33.1
p = <0.01
FM/M 117 61% 39% 76
SUP 46 68% 32% 22
RES 16 41% 59% 23
X2(df=2)=7.4
p = 0.02
TOTAL 179 60% 40% 121
Proportion of samples
C
LUTJANIDAE
NON-LUTJANIDAE
CAN 18 55% 45% 15
US 70 83% 17% 14
UK 61 58% 42% 45
SGP 25 78% 22% 7
AUS 22 69% 31% 10
NZ 2 15% 85% 11
X2(df=5)=34.4
p = <0.01
FM/M 125 65% 35% 68
SUP 48 71% 29% 20
RES 25 64% 36% 14
X2(df=2)=0.8
p = 0.66
TOTAL 198 66% 34% 102
Proportion of samples


Canada
United States
United Kingdom
Singapore
Australia
New Zealand
NOT MISLABELLED
MISLABELLED
'Red snapper'
'Snapper'
'Yellowtail snapper'
'Pink snapper'
'Lane snapper'
'B-Liner snapper'
'White snapper'
Other, 'X snapper'
56%
44%
65%
35%
91%
9%
11%
89%
86%
14%
83%
17%
33%
67%
58%
42%
60
50
40
30
20
10
0
10
20
30
40
50
Number of samples



FAO fishing areas		Catch trend	O-F %	IUU %	Snapper
18	Arctic				
21	Atlantic, NW	↓	31	9	
27	Atlantic, NE	↓	21	9	
31	Atlantic, W central	↓	44	10	W / P
34	Atlantic, E central	≈	47	37	
37	Med. & Black Sea	↓	59		
41	Atlantic, SW	≈	50	32	P
47	Atlantic, SE	↓	50	7	
51	Indian, W	↑	32	18	
57	Indian, E	↑	15	32	P
61	Pacific, NW	≈	24	33	
67	Pacific, NE	≈	14	3	
71	Pacific, W central	↑	23	34	P
77	Pacific, E central	≈	9	15	W / P
81	Pacific, SW	↓	12	4	
87	Pacific, SE	≈	41	19	
01	Africa – Inland waters				
02	America, North – Inland waters				
03	America, South – Inland waters				
04	Asia – Inland waters				
05	Europe – Inland waters				
06	Oceania – Inland waters				




A
IUCN status
IUCN population trend
NA/DD LC NT VUL EN
UNK INC STB DEC
LUT FAMILY (112 species) %
31% 64% 2% 3%
88% 1% 11%
NOT MISLABELLED
LUT (n = 155) %
43% 37% 6% 15%
69% 31%
NL (n = 24) %
33% 67%
35% 65%
MISLABELLED
LUT (n = 43) %
29% 48% 7% 16%
67% 33%
NL (n = 73) %
27% 61% 8% 1% 2%
80% 5% 12% 3%
B
LOW MODERATE HIGH VERY HIGH
LUT FAMILY (112 species) n
NOT MISLABELLED
LUT (n = 155) n
NL (n = 24) n
MISLABELLED
LUT (n = 43) n
NL (n = 73) n
30 20 10
a
b
c
ac
2 5 8 11 14 17 20 23 26 29 32 35 38 41 44 47 50 53 56 59 62 65 68 71 74 77 80 83 86 89 92 95 98
Intrinsic vulnerability (IV) score (out of 100)