Food Chemistry 185 (2015) 165–181

Contents lists available at ScienceDirect

Food Chemistry

journal homepage: www.elsevier.com/locate/foodchem

Analytical Methods

Fish species substitution and misnaming in South Africa: An economic, safety and sustainability conundrum revisited

Donna-Mareè Cawthorn [a,*], John Duncan [b], Chris Kastern [b], Junaid Francis [b], Louwrens C. Hoffman [a,1]

[a] Department of Animal Sciences, University of Stellenbosch, Private Bag X1, Matieland 7602, South Africa
[b] World Wildlife Fund South Africa – Southern African Sustainable Seafood Initiative (WWF-SASSI), PO Box 23273, Claremont 7735, South Africa

ARTICLE INFO

Article history:
Received 10 September 2014
Received in revised form 16 March 2015
Accepted 29 March 2015
Available online 2 April 2015

Keywords:
Authentication
DNA barcoding
Fish species
Mislabelling
Seafood
Sustainability

ABSTRACT

While fish species mislabelling has emerged as a global problem, the tracking of improvements or deteriorations in seafood trading practices is challenging without a consistent basis for monitoring. The aim of this study was to develop a robust, repeatable species authentication protocol that could be used to benchmark the current and future incidences of fish mislabelling in South Africa. Using this approach, 149 fish samples collected from restaurants and retailers in three provinces (KwaZulu-Natal, Western Cape and Gauteng) were identified using DNA barcoding, supplemented in certain cases with mitochondrial control region sequencing. Overall, 18% of samples were incorrectly described in terms of species, with similar misrepresentation rates in restaurants (18%) and retail outlets (19%). While there appears to be some improvement in the transparency of local seafood marketing compared to previous studies, the results remain of concern and signal the need for enhanced seafood labelling regulations, monitoring and law enforcement.

© 2015 Elsevier Ltd. All rights reserved.

1. Introduction

Modern consumers are increasingly aware of their health and social responsibilities and are seeking greater assurance on the origin, composition and environmental impacts of their food. Consumers have, however, also voiced concerns relating to the reliability of information received on product labels, with reports of 'food counterfeiting' likely fuelling such concerns (Eden, Bear, & Walker, 2008). Although 'food fraud" has been carried out since antiquity, these practices seem to have escalated in recent years. High-value, protein-rich foods are especially prone to substitution or mislabelling, as exemplified by the Chinese melamine saga of 2008 (Sharma & Paradakar, 2010), the 2013 meat scandals in South Africa and the EU (Cawthorn, Steinman, & Hoffman, 2013; Premanandh, 2013) and the many documented cases of seafood fraud. While the former two examples were generally sporadic, seafood mislabelling has been a persistent and widespread problem, apparently intensifying in synchrony with the ever-declining state of the world's fish stocks. Evidence for the latter derives from studies conducted over a broad geographic scale that have exposed high levels of fish mislabelling in, amongst others, the Americas, Europe and South Africa (Ardura et al., 2010; Cawthorn et al., 2012a; Filonzi et al., 2010; Hanner et al., 2011; Von der Heyden, Barendse, Seebregts, & Matthee, 2010; Warner et al., 2013). Factors appearing to contribute to the upsurge in fish mislabelling include the associated financial incentives, globalisation of seafood supply chains, the highly processed nature of fish products, as well as lax law enforcement. Regardless of the motives, the repercussions of fish mislabelling are manifold and include financial, health and conservation concerns.

South Africa is a nation largely defined by its productive oceans and diverse aquatic life, which in turn support a range of commercial and artisanal fishermen. The country's domestic marine harvest has averaged over 690,000 tonnes per annum over the last decade, placing its fisheries among the most important in Africa (FAO, 2013). However, the region has neither escaped the wrath of overexploitation nor has it evaded the burden of illegal seafood trade and corruption (Hauck & Kroese, 2006). Similar to the global trend of overexploited marine fisheries, many of South Africa's wild fish stocks are considered overfished, particularly within the inshore zone (DAFF, 2012).

Although fish mislabelling has been suspected in South Africa for decades (Smith & Smith, 1966), little was done prior to 2010 to elucidate its true prevalence. Between 2010 and 2012, a comprehensive DNA sequence library was established to facilitate the

* Corresponding author. Tel.: +27 21 808 4916; fax: +27 21 808 4750.
E-mail address: DonnaC@sun.ac.za (D.-M. Cawthorn).

[1] South African Research Chair in Meat Science hosted by the University of Stellenbosch in partnership with the University of Fort Hare, funded by the Department of Science and Technology (DST) and administered by the National Research Foundation (NRF).

http://dx.doi.org/10.1016/j.foodchem.2015.03.113
0308-8146/© 2015 Elsevier Ltd. All rights reserved.

authentication of commonly-traded fish species in South Africa (Cawthorn, Steinman, & Witthuhn, 2011a, 2012b). Through this work, 'DNA barcoding' was shown to hold particular promise in explicitly distinguishing the species origin of raw, processed, whole or partial fish specimens (Cawthorn, Steinman, & Witthuhn, 2011a). DNA barcoding, based on the sequencing of a short, standardised region of the cytochrome *c* oxidase I (COI) gene, has garnered increasing attention as a broadly applicable tool for identifying an array of animal species, including fishes (Hebert, Cywinska, & Ball, 2003; Hebert, Ratnasingham, & deWaard, 2003). The utility of the method for fish species identifications is grounded on the premise that the COI sequence shows considerably greater inter- than intra-species variation, allowing for the differentiation of *ca.* 97% of fish species (Ward, 2009) and often being more discriminatory than alternative DNA markers used for this purpose (Cawthorn et al., 2011a, 2012b; Nicolè et al., 2012). Although some potential limitations of DNA barcoding have previously been recognised (Rubinoff, Cameron, & Will, 2006), the method has more recently been validated for use in forensic and regulatory fields (Dawnay et al., 2007; Handy et al., 2011). Momentum for the initiative has further been aided by, *inter alia*, the establishment of the Consortium for the Barcode of Life (CBOL) – an international alliance that promotes global standards for DNA barcoding, the development of the Barcode of Life Database (BOLD, www.barcodinglife.org) – an online data management system that serves as a global repository for barcode sequences (Ratnasingham & Hebert, 2007), as well as the emergence of numerous campaigns seeking to barcode all life on earth. The Fish Barcode of Life Initiative (FISH-BOL, http://www.fishbol.org) is one such campaign aiming to assemble a COI-reference library for all fishes (Ward, Hanner, & Hebert, 2009), with over 10 000 of the *ca.* 32 000 fish species being barcoded to date (2014).

COI barcoding (Cawthorn et al., 2012a) and other DNA markers (Von der Heyden et al., 2010) have recently been used to reveal disturbing rates of fish mislabelling (21–50%) in South Africa, with both studies generating considerable media attention (Joseph, 2009; Yeld, 2012) and likely leaving some industry role players infuriated and even humiliated. Such responses, however, typify those surrounding any major food scandal, where the immediate effects are often perceived as negative but the ensuing ones are largely positive. Research of this kind raises awareness around pertinent concerns, compelling the entire industry to resolve the issues. While weaknesses are exposed that are inherent to modern food supply chains (e.g. complexity, traceability), areas are highlighted that need improvement, prompting authorities to step up checks and revise regulations.

Apart from this media attention, several other developments have emerged of late with the potential to alter local seafood marketing transparency. For one, new food labelling regulations came into effect in South Africa in 2012 (DoH, 2010), urging suppliers to re-assess the accuracy of their product marketing. In response to observed cases of confounded fish naming, Von der Heyden et al. (2010) and Cawthorn et al. (2012a) advised the compilation of a 'standardised seafood naming list' in South Africa (as used in the US, UK, Canada), which is currently under development. A further factor relates to the efforts of the Southern African Sustainable Seafood Initiative (WWF-SASSI, www.wwfsassi.co.za), a World Wide Fund for Nature programme established in 2004 with the aim of fostering public awareness around marine conservation issues and driving responsible fishing through a market-based approach. This programme now works across the seafood supply chain with key suppliers and retailers to address shortcomings in traceability systems and to revise seafood labelling to include more comprehensive species information.

In order to gauge the success of the abovementioned initiatives and to understand if enhanced consumer and industry awareness are being translated into tangible improvements, it is critical to consistently monitor the operating of the seafood supply chain. To this end, the aim of this study was to assess the current extent of fish misnaming or mislabelling in South Africa at the final supply chain link (consumer level) and to reconcile the results with previous studies. Further, the study aimed to benchmark the present state with a rigorous, statistically relevant protocol that can be repeated on a pre-determined basis to aptly track changes in seafood trading practices.

2. Materials and methods

2.1. Study and sampling design

The overall research design was to survey restaurants and retail outlets in three South African provinces to evaluate the extent of fish misnaming or mislabelling prevailing on the market. A chi-square (χ^2) test power analysis was used to estimate the number of samples required from each outlet type and province to ensure the statistical relevance of results.

2.1.1. Selection of geographic regions

The regions chosen for sample collection included the coastal provinces of KwaZulu-Natal (KZN) and the Western Cape (WC), as well as the Gauteng province (GP). KZN and WC were selected as these are among the most populated South African provinces, are both major fishing provinces in the country and have been shown to have access to a wide variety of locally-caught fish species (Cawthorn, Steinman, & Witthuhn, 2011b). Gauteng was included to assess commercial fish trading practices in an inland province, since it represents a principal seafood market in South Africa and has the largest population density and highest per capita income of all the country's provinces.

2.1.2. Selection of outlets

Restaurants and retail outlets were selected for sample collection since these represent the main channels through which consumers obtain fish products in South Africa. Outlets in each province were designated for the study prior to sample collection, with the intent to balance the sample sizes from high and low income regions. The basis for selection of restaurants was that these should have a dedicated seafood section on the menu and/or serve at least three different fish species. Where seafood restaurant franchises were chosen for sample collection, efforts were made to include the same outlets in each province to promote result comparability. The retail outlets selected included predominantly supermarkets (stores selling a range of food and grocery products) and to a lesser extent fish markets (outlets selling primarily fish), with the prerequisite being that these sell at least three different fish species. In order to standardise the sampling protocol for supermarkets, six established supermarket chains were identified in South Africa that market fresh and frozen fish products and similar sample numbers were collected from each chain in each province.

2.1.3. Priority fish species

This study focused on the species authentication of finfish (teleost spp.). Samples were collected only from those specimens that could not be visually confirmed as the species being sold, whether this was due to processing or suspected mislabelling. A minimum of one and a maximum of two samples were obtained from each outlet in each province.

Two categories were defined for fish sample collection. For 'category A' samples, the following four 'priority' species were selected for collection: (i) kingklip (*Genypterus* spp.); (ii)

kabeljou/kob (*Argyrosomus* spp.); (iii) hake (*Merluccius* spp.) and (iv) tuna (*Thunnus* spp.). These are among the top ten most frequently marketed fish species in South Africa (Cawthorn et al., 2011b) and have all been shown to be prone to mislabelling or substitution (Cawthorn et al., 2012a; Von der Heyden et al., 2010). The purpose of designating priority species was to ensure that sufficient numbers of popular fish types were assessed to facilitate result comparability and identification of mislabelling trends. Only one of the four priority species was collected per outlet, with attempts to obtain equivalent numbers of each across the provinces. In order to target a broader taxonomic coverage and to randomise the species obtained for 'category B' samples, any fish marketed as 'linefish' or 'catch of the day' was collected, with the common name being sought and recorded in each case.

When only group or generic names were used to describe the fish on sale, the vendors in the respective outlets were asked to identify the specific type or species and the common and/or species names were noted. When present on sample packaging, the scientific name of the enclosed fish sample was recorded. For restaurant and retail samples where no scientific names were given, these were inferred from the common or market names specified for the applicable specimens.

2.2. Sample collection

A total of 150 samples were collected for analysis over a *ca.* nine-month period (May 2013–January 2014), comprising 75 samples from restaurants ($N = 25$ per province) and 75 from retail outlets ($N = 25$ per province). Overall, these samples were derived from 48 different restaurants and 62 retail outlets. Ninety of the 150 samples were 'category A' priority species ($N = 37$ hake, $N = 31$ kingklip, $N = 16$ tuna and $N = 6$ kabeljou samples) and the remaining 60 samples represented a variety of species sold as 'linefish' or 'catch of the day' ('category B'). In restaurants, samples were taken either while sitting in the outlet to consume the meal or by opting to obtain the fish as a 'take away'. In retail outlets, fresh samples were preferably procured from fresh fish counters ($N = 56$), however, frozen samples ($N = 19$) were collected in cases when no fresh fish was available. Once collected, samples were packaged separately, labelled and stored at −20 °C until DNA extraction.

2.3. DNA extraction and Polymerase Chain Reaction (PCR)

DNA was extracted from each sample using the SureFood® PREP DNA extraction kit (#S1012, supplied by AEC-Amersham, Cape Town, South Africa) following the manufacturer's instructions. Extracted DNA was used as a template for PCR amplification of a *ca.* 652 base pair (bp) fragment of the COI gene using the primer cocktail and thermal cycling conditions in Table 1. PCR reactions were performed in a Labnet MultiGene™ Thermal Cycler and the 25 μl reaction mixtures contained 12.5 μl Qiagen TopTaq Master Mix (supplied by Whitehead Scientific, Cape Town, South Africa), 0.25 μl (100 nM) of each primer and 2 μl of DNA template. In the limited cases where DNA amplification failed with the COI cocktail or where closely-related species could not be resolved by COI sequencing, a *ca.* 450 bp fragment of the mitochondrial control region (CR) was amplified to confirm identifications (Table 1). Reaction mixtures for the CR PCR (25 μl final volume) comprised 12.5 μl Qiagen TopTaq Master Mix, 0.5 μl (200 nM) of each primer and 1 μl of DNA template.

2.4. DNA sequencing and sequence analysis

PCR products were purified with the NucleoFast 96 PCR Clean-up Kit (Macherey–Nagel, supplied by Separations, Gauteng, South Africa), following the manufacturer's instructions. DNA sequencing was performed using BigDye chemistry and analysis on an ABI 3100 Genetic Analyser (Applied Biosystems, Foster City, USA). Primers for M13-tailed PCR products were used for sequencing COI amplicons, whereas PCR amplification primers were used as sequencing primers for CR amplicons (Table 1). COI sequence divergences or distances (D) were calculated in the Barcode of Life Database (BOLD; www.barcodinglife.org) using the Kimura 2-parameter (K2P) model. A neighbour-Joining (NJ) tree was created in MEGA 4.0, with Bootstrapping of 1000 replicates (Supp. Fig. 1).

All generated COI and CR sequences were compared with reference nucleotide sequences in GenBank (www.ncbi.nlm.nih.gov) to establish the most likely identify of the specimens. For COI sequences, the identifications made in GenBank were cross-referenced in BOLD. A top match with a sequence similarity of $\geqslant 98\%$ was used for designating potential species identifications (Barbuto et al., 2010). Since most analysed marine fish species exhibit intra-specific COI divergence values considerably lower than 2% (generally < 0.4%), this can be regarded as a relatively loose criterion (Costa et al., 2012; Steinke et al., 2009; Ward et al., 2005). Species identifications made in BOLD and/or GenBank were compared to the market names, expected scientific names or specified scientific names (when provided) under which the queried specimens had been sold.

2.5. Assessment of species authenticity and potential mislabelling

The accuracy of fish species mislabelling was evaluated using a multiple-step approach, as used in similar fish mislabelling studies (Hanner et al., 2011; Wong & Hanner, 2008). Since both GenBank and BOLD rely on FishBase (www.fishbase.org) as the taxonomic

Table 1
PCR amplification and sequencing primers used for fish species identifications in this study.

Primer	Primer sequence (5′–3′)	mtDNA target	PCR cycling regime	Amplicon size (bp)	Reference
Fish DNA barcoding primer cocktail (C_FishF1t1/C_FishR1t1)					
VF2_t1	TGTAAAACGACGGCCAGTCAACCAACCACAAAGACATTGGCAC	COI	94 °C – 2 min; 35 × (94 °C – 30 s, 52 °C – 40 s, 72 °C – 60 s); 72 °C – 10 min	652	Ivanova, Zemlak, Hanner, and Hebert (2007)
FishF2_t1	TGTAAAACGACGGCCAGTCGACTAATCATAAAGATATCGGCAC				
FishR2_t1	CAGGAAACAGCTATGACACTTCAGGGTGACCGAAGAATCAGAA				
FR1d_t1	CAGGAAACAGCTATGACACCTCAGGGTGTCCGAARAAYCARAA				
M13F *	TGTAAAACGACGGCCAGT				Messing (1983)
M13R *	CAGGAAACAGCTATGAC				
Control region primers					
L15998	TACCCCAAACTCCCA AAGCTA	CR	94 °C – 5 min; 35 × (94 °C – 45 s, 54 °C – 45 s, 72 °C – 60 s); 72 °C – 10 min	450	Alvarado Bremer (1994).
CSBDH	TGAATTAGGAACCAGATGCCAG				

COI = cytochrome *c* oxidase 1 (COI); CR = control region.
* Sequencing primers for M13-tailed PCR products.

authority for valid fish species names, the top species matches (highest percentage similarities) made by sequencing were initially compared with the scientific names and corresponding common names within this database. Where discrepancies were found between the market names of queried samples and the currently accepted fish names in FishBase, the scientific and common names were cross-checked in Van der Elst (2000), Smith et al. (2003) and the WWF-SASSI database (www.wwfsassi.co.za). The three aforementioned sources were consulted in the absence of published authoritative lists specifying acceptable market names for seafood species traded in South Africa (such as those available in the US Food and Drug Administration (FDA) seafood list (www.fda.gov) and the Canadian Food Inspection Agency (CFIA) fish list (www.inspection.gc.ca)).

It is important to emphasise that the designation of potentially misnamed or mislabelled specimens in this study was based solely on the comparison of literal information with the species name obtained by DNA sequencing. Thus, it is plausible that some misrepresentations may appear less serious than others and may not even be viewed as surprising given common consumer knowledge and expectations. However, as suggested by Wong and Hanner (2008), such a literal and rigid approach is crucial to ensure that the determination of mislabelling is assessed consistently for all samples, especially when a single market name may be applied to multiple species or when different name categories exist for a single species (e.g. common, market and vernacular names).

3. Results and discussion

3.1. DNA sequencing interpretations

DNA sequencing results obtained from the fish samples collected from restaurants and retail outlets in three provinces are presented in Tables 2 and 3, respectively. Of the 150 acquired samples, the DNA from 147 (98%) was successfully amplified with the COI primer cocktail. The resulting PCR products were sequenced to produce full length DNA barcodes averaging 651 base pairs (bp) in length, with no detectable insertions, deletions or stop codons. Only three samples, constituting products marketed as 'dorado' (SAS-K16), 'pangasius' (SAS-K24) and 'kingklip' (SAS-K42), did not amplify with the COI primers (Tables 2 and 3). This amplification failure could most likely be attributed to DNA degradation or the presence of PCR inhibitors in the samples, with the former being especially probable given that two of the latter three samples represented cooked samples obtained from restaurants (SAS-K16 and -K24) (Table 2).

For the 147 samples yielding interpretable COI barcodes, maximum sequence similarity values of $\geqslant$99% were achieved in BOLD and/or GenBank and the top species identifications in the two databases corresponded precisely (Table 2 and 3). For only one specimen (SAS-K48), sold as 'red steenbras' (expected species *Petrus rupestris*) but identified in GenBank as opah (*Lampris guttatus*), a 'no species match' result was delivered in BOLD (Table 3).

A total of 131 of the 147 (89%) sequenced samples could be readily discriminated at the species level (either matching the species under which they were sold or being assigned to an alternative species), with all showing >5% COI divergence from their nearest neighbouring species. The remaining 16 samples analysed, representing members of the genus *Thunnus* (tuna), exhibited overlapping COI barcodes. A review of the COI NJ tree (Supp. Fig. 1) revealed that these samples clustered into two groupings, but the mean divergence between the groupings was small (*ca.* 0.2%). Additionally, comparison of the COI sequences of these putative species with those in GenBank and BOLD returned 99–100% matches for at least four different *Thunnus* species in each case (Tables 2 and 3). Such results reiterate previous findings relating to the challenges of explicitly identifying closely-related (and potentially introgressed) members of this genus with COI barcoding and genetic-distance analyses (Viñas & Tudela, 2009; Wong & Hanner, 2008). For the discrimination of recently-speciated taxa, of which the genus *Thunnus* represents an example, it is considered preferable to analyse fast-evolving gene regions rather than slowly-evolving ones, as the latter often exhibit insufficient mutations to make clear distinctions. The non-coding CR is reported to be the most variable segment in the mitochondrial genome and has been shown to be more apt than the COI marker for differentiating *Thunnus* spp. (Pedrosa-Gerasmio et al., 2012; Viñas & Tudela, 2009). Although sample sizes were small and species variety was limited in this study, the latter appeared to hold true for the *Thunnus* spp. evaluated. All specimens sold as one or other type of tuna were clearly assignable to the species level based on their CR sequences, with sequence similarities of $\geqslant$99% returned in GenBank for all 16 samples (Tables 2 and 3). Interpretable CR sequences were also recovered from two of the three samples that failed to amplify with the COI primers (SAS-K24 and -K42) (Tables 2 and 3). Thus, considering the 147 generated COI results and the additional two aforesaid CR results, credible species identifications were made for 149 of 150 (99%) samples collected (N = 90 'category A' and N = 59 'category B' samples), with these assigned to 32 different species in eight families.

3.2. Misnaming and mislabelling of fish samples

Overall, taking all provinces and outlets into account, a total of 27 of 149 (18%) samples were genetically identified as different species to those indicated at the point of sale or inferred from the names under which they were sold (Fig. 1(1a)). This misrepresentation rate is lower than those observed in similar studies in North America (25–41% mislabelling) (Hanner et al., 2011; Warner et al., 2013; Wong & Hanner, 2008) (Table 4). Compared to previous studies from South Africa, the current results are also lower than the *ca.* 50% fish mislabelling rate reported by Von der Heyden et al. (2010) and the 21% determined by Cawthorn et al. (2012a) (Table 4). While this perceived improvement in labelling appears encouraging, it should be acknowledged that the sample acquisition strategies in both of the preceding studies differed to the one used in the present work. This emphasises the importance of using a rigid and repeatable protocol for such studies in order to ensure uniformity, promote comparability and to assist in tracking mislabelling trends.

In view of these results, cognisance should also be taken of the increasing complexity and obscurity of seafood supply chains, implying that fraud can manifest at any point from the fishing vessel to the consumer's plate. Since this study was limited to fish sold in restaurants and retail outlets, it cannot be categorically determined where the observed transgressions occurred. While fish mislabelling rates in South Africa have formerly been found to be higher at the retail level than at the wholesale level (Cawthorn et al., 2012a), the possibility of some of the current misdescription transpiring prior to fish receipt by the respective restaurants or retailers cannot be discounted. However, if this was the case, the receiving outlets would ultimately be liable for this in terms of the South African regulations effected in April 2011 under the Consumer Protection Act (DTI, 2009).

On a per province basis and including all outlets visited in each, fish misrepresentation rates equated to 12 of 49 (24.5%) samples in KZN, 10 of 50 (20%) in GP and 5 of 50 (10%) in WC (Fig. 1(2–4a)). The reasons for these inter-provincial variations could include differences in levels of income, awareness and regulatory control. KZN has a larger proportion of low income groups than WC and GP and since much of its populace may be comparatively less

Table 2
Identification results based on cytochrome *c* oxidase I (COI) and control region (CR) sequencing for 74 fish samples collected from seafood restaurants in South Africa, where *N* indicates the number of fish samples that were correctly labelled or potentially mislabelled. Cases of suspected mislabelling are indicated in bold typescript.

Fish marketed as: (expected species)	Province (*N*)	Code	Gene target	GENBANK			BOLD	
				Species identification	Similarity	Accession number	Species identification	Similarity
Angelfish (*Brama brama*)	GP (*N* = 1)	SAS-G9	COI	*Brama brama*	100%	EF609300	*Brama brama*	100%
Bluenose (*Hyperoglyphe antarctica*)	**WC (*N* = 1)**	**SAS-W10**	**COI**	***Hyperoglyphe moselii***[a]	**100%**	**DQ107610**	***Hyperoglyphe moselii***[a]	**100%**
				***Schedophilus velaini* (violet warehou)**	**100%**	**AB751624**	***Schedophilus velaini* (violet warehou)**	**100%**
Cape salmon (*Atractoscion aequidens*)	GP (*N* = 1)	SAS-G18	COI	*Atractoscion aequidens*	100%	HM007696	*Atractoscion aequidens*	100%
Barracuda (*Sphyraena* spp.)	**KZN (*N* = 3)**	**SAS-K9**	**COI**	***Scomberomorus commerson* (Spanish/king mackerel)**	**99%**	**HM007790**	***Scomberomorus commerson* (Spanish/king mackerel)**	**99.7%**
		SAS-K19		***Scomberomorus commerson* (Spanish/king mackerel)**	**99%**	**HM007790**	***Scomberomorus commerson* (Spanish/king mackerel)**	**99.8%**
		SAS-K25		***Scomberomorus commerson* (Spanish/king mackerel)**	**100%**	**HM007791**	***Scomberomorus commerson* (Spanish/king mackerel)**	**100%**
Dorado (*Coryphaena hippurus*)	KZN (*N* = 4)	SAS-K2	COI	*Coryphaena hippurus*	99%	HM007705	*Coryphaena hippurus*	99.7%
		SAS-K5		*Coryphaena hippurus*	99%	HM007705	*Coryphaena hippurus*	99.7%
		SAS-K18		*Coryphaena hippurus*	99%	HM007705	*Coryphaena hippurus*	99.8%
		SAS-K14		*Coryphaena hippurus*	99%	HM007705	*Coryphaena hippurus*	99.8%
	KZN (*N* = 1)	**SAS-K7**	**COI**	***Argyrozona argyrozona* (Carpenter/silverfish)**	**100%**	**HM007754**	***Argyrozona argyrozona* (Carpenter/silverfish)**	**100%**
	KZN (*N* = 1)	SAS-K16	COI CR	No interpretable sequence with COI or CR primers			No interpretable sequence with COI primers	
	GP (*N* = 2)	SAS-G11	COI	*Coryphaena hippurus*	99%	HM007705	*Coryphaena hippurus*	100%
		SAS-G7		*Coryphaena hippurus*	100%	HM007705	*Coryphaena hippurus*	100%
	WC (*N* = 2)	SAS-W3	COI	*Coryphaena hippurus*	100%	HM007705	*Coryphaena hippurus*	100%
		SAS-W19		*Coryphaena hippurus*	99%	HM007705	*Coryphaena hippurus*	100%
Hake (*Merluccius* spp.)	KZN (*N* = 6)	SAS-K6	COI	*Merluccius capensis*	100%	HM007691	*Merluccius capensis*	100%
		SAS-K11		*Merluccius capensis*	100%	HM007691	*Merluccius capensis*	100%
		SAS-K15		*Merluccius capensis*	99%	HM007691	*Merluccius capensis*	100%
		SAS-K20		*Merluccius capensis*	99%	HM007691	*Merluccius capensis*	99.7%
		SAS-K8		*Merluccius paradoxus*	100%	HM007683	*Merluccius paradoxus*	100%
		SAS-K23		*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
	GP (*N* = 6)	SAS-G8	COI	*Merluccius capensis*	100%	HM007691	*Merluccius capensis*	100%
		SAS-G10		*Merluccius capensis*	100%	HM007691	*Merluccius capensis*	100%
		SAS-G13		*Merluccius capensis*	100%	HM007690	*Merluccius capensis*	100%
		SAS-G21		*Merluccius capensis*	100%	HM007691	*Merluccius capensis*	100%
		SAS-G0		*Merluccius paradoxus*	100%	HM007683	*Merluccius paradoxus*	100%
		SAS-G6		*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
	WC (*N* = 4)	SAS-W4	COI	*Merluccius capensis*	100%	HM007691	*Merluccius capensis*	100%
		SAS-W18		*Merluccius capensis*	99%	HM007690	*Merluccius capensis*	100%
		SAS-W20		*Merluccius capensis*	100%	HM007691	*Merluccius capensis*	100%
		SAS-W16		*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
Kabeljou (*Argyrosomus* spp.)	**GP (*N* = 1)**	**SAS-G15**	**COI**	***Atractoscion aequidens* (Cape salmon/geelbek)**	**100%**	**HM007696**	***Atractoscion aequidens* (Cape salmon/geelbek)**	**100%**
	WC (*N* = 2)	SAS-W14	COI	*Argyrosomus inodorus*	100%	HM007712	*Argyrosomus inodorus*	100%
		SAS-W11		*Argyrosomus japonicas*	100%	HM007719	*Argyrosomus japonicas*	100%
Kingklip (*Genypterus capensis*)	KZN (*N* = 6)	SAS-K1	COI	*Genypterus capensis*	99%	HM007736	*Genypterus capensis*	99.8%
		SAS-K3		*Genypterus capensis*	99%	HM007736	*Genypterus capensis*	100%
		SAS-K10		*Genypterus capensis*	100%	HM007735	*Genypterus capensis*	100%

(*continued on next page*)

Table 2 (*continued*)

Fish marketed as: (expected species)	Province (*N*)	Code	Gene target	GENBANK			BOLD	
				Species identification	Similarity	Accession number	Species identification	Similarity
		SAS-K12		*Genypterus capensis*	99%	HM007736	*Genypterus capensis*	100%
		SAS-K17		*Genypterus capensis*	99%	HM007736	*Genypterus capensis*	99.8%
		SAS-K22		*Genypterus capensis*	100%	HM007735	*Genypterus capensis*	100%
	GP	SAS-G2	COI	*Genypterus capensis*	99%	HM007736	*Genypterus capensis*	100%
	(*N* = 6)	SAS-G5		*Genypterus capensis*	100%	HM007735	*Genypterus capensis*	100%
		SAS-G19		*Genypterus capensis*	99%	HM007735	*Genypterus capensis*	99.8%
		SAS-G20		*Genypterus capensis*	99%	HM007737	*Genypterus capensis*	99.8%
		SAS-G25		*Genypterus capensis*	99%	HM007738	*Genypterus capensis*	99.7%
		SAS-G12		*Genypterus capensis*	100%	HM007738	*Genypterus capensis*	100%
	WC	SAS-W7	COI	*Genypterus capensis*	99%	HM007744	*Genypterus capensis*	100%
	(*N* = 4)	SAS-W17		*Genypterus capensis*	99%	HM007736	*Genypterus capensis*	100%
		SAS-W13		*Genypterus capensis*	99%	HM007736	*Genypterus capensis*	99.8%
		SAS-W22		*Genypterus capensis*	100%	JF493517	*Genypterus capensis*	100%
Monk fish (*Lophius vomerinus*)	WC (*N* = 1)	SAS-W29	COI	*Lophius vomerinus*	100%	HM007766	*Lophius vomerinus*	100%
Pangasius/catfish (*Pangasius* spp.)	KZN (*N* = 1)	SAS-K24	COI	No interpretable sequence with COI primers			No interpretable sequence with COI primers	
			CR	*Pangasius* spp.	98%	AY297093		
	GP (*N* = 1)	SAS-G22	COI	*Pangasianodon (Pangasius) hypophthalmus* [b] (Striped (sutchi) catfish)	99%	JF292409	*Pangasianodon (Pangasius) hypophthalmus* [b] (Striped (sutchi) catfish)	99.8%
Panga (*Pterogymnus laniarius*)	**GP (*N* = 1)**	**SAS-G4**	**COI**	***Pangasianodon (Pangasius) hypophthalmus*** [b] **(Striped (sutchi) catfish)**	**99%**	**JF292409**	***Pangasianodon (Pangasius) hypophthalmus*** [b] **(Striped (sutchi) catfish)**	**100%**
Red roman (*Chrysoblephus laticeps*)	**KZN (*N* = 1)**	**SAS-K21**	**COI**	***Argyrozona argyrozona* (Carpenter/silverfish)**	**100%**	**HM007754**	***Argyrozona argyrozona* (Carpenter/silverfish)**	**100%**
	GP (*N* = 1)	SAS-G24	COI	*Chrysoblephus laticeps*	100%	HM007750	*Chrysoblephus laticeps*	100%
Rockcod (*Epinephelus* spp.)	GP (*N* = 1)	SAS-G17	COI	*Epinephelus marginatus* (Yellowbelly rockcod/Dusky grouper)	99%	HQ611093	*Epinephelus marginatus* (Yellowbelly rockcod/Dusky grouper)	100%
Sea bass (any of numerous fishes of the family Serranidae)	**GP (*N* = 1)**	**SAS-G3**	**COI**	***Sciaenops ocellatus* (Red drum) (FAO name) Family – Sciaenidae**	**99%**	**EU180148**	***Sciaenops ocellatus* (Red drum) (FAO name) Family – Sciaenidae**	**100%**
Seabream (any of numerous fishes of the seabream family Sparidae)	**WC (*N* = 1)**	**SAS-W2**	**COI**	***Seriolella brama* (Common warehou)**	**99%**	**HM007732**	***Seriolella brama* (Common warehou)**	**99.7%**
Silverfish (*Argyrozona argyrozona*)	**GP (*N* = 1)**	**SAS-G16**	**COI**	***Chrysoblephus laticeps* (Red roman)**	**99%**	**HM007751**	***Chrysoblephus laticeps* (Red roman)**	**99.8%**
Tuna (*Thunnus* spp.)	KZN (*N* = 1)	SAS-K13	COI	*Thunnus obesus*	100%	GU451764	*Thunnus obesus*	100%
				Thunnus atlanticus	99%	GU225688	*Thunnus atlanticus*	100%
				Thunnus albacares	99%	KF528374	*Thunnus albacares*	99.85%
				Thunnus tonggol	99%	JN086154	*Thunnus maccoyii*	99.85%
			CR	*Thunnus obesus*	99%	DQ126580	–	–
	WC (*N* = 1)	SAS-W23	COI	*Thunnus obesus*	99%	KF597025	*Thunnus obesus*	99.42%
				Thunnus atlanticus	99%	GU225688	*Thunnus atlanticus*	99.41%
				Thunnus albacares	99%	JN086153	*Thunnus albacares*	99.22%
				Thunnus maccoyii	99%	GU256523	*Thunnus maccoyii*	99.13%
				Thunnus tonggol	99%	HQ425780	*Thunnus tonggol*	98.96%
			CR	*Thunnus obesus*	99%	DQ126561	–	–

Table 2 (*continued*)

Fish marketed as: (expected species)	Province (*N*)	Code	Gene target	GENBANK			BOLD	
				Species identification	Similarity	Accession number	Species identification	Similarity
	KZN	SAS-K4	COI	*Thunnus albacares*	100%	JN086153	*Thunnus albacares*	100%
	(*N* = 1)			*Thunnus atlanticus*	100%	GU225688	*Thunnus atlanticus*	100%
				Thunnus obesus	99%	GU451764	*Thunnus obesus*	100%
				Thunnus maccoyii	99%	AY302574	*Thunnus maccoyii*	99.85%
				Thunnus tonggol	99%	DQ107634	*Thunnus tonggol*	99.84%
			CR	*Thunnus albacares*	99%	KC165915	–	–
Yellowfin tuna	GP	SAS-G1	COI	*Thunnus albacares*	100%	JN086153	*Thunnus albacares*	100%
(*Thunnus albacares*)	(*N* = 1)			*Thunnus atlanticus*	100%	GU225688	*Thunnus atlanticus*	100%
				Thunnus obesus	99%	GU451764	*Thunnus obesus*	100%
				Thunnus maccoyii	99%	AY302574	*Thunnus maccoyii*	99.85%
				Thunnus tonggol	99%	DQ107634	*Thunnus tonggol*	99.84%
			CR	*Thunnus albacares*	99%	KC165915	–	–
	GP	**SAS-G23**	**COI**	***Thunnus obesus***	**100%**	**GU451792**	***Thunnus obesus***	**100%**
	(*N* = 1)			***Thunnus albacares***	**99%**	**KF528374**	***Thunnus albacares***	**99.69%**
				Thunnus atlanticus	**99%**	**GU225688**	***Thunnus atlanticus***	**99.69%**
			CR	***Thunnus obesus*** **(Bigeye tuna)**	**99%**	**DQ126561**	–	–
	WC	SAS-W1	COI	*Thunnus albacares*	100%	JN086153	*Thunnus albacares*	100%
	(*N* = 3)			*Thunnus atlanticus*	100%	GU225688	*Thunnus atlanticus*	100%
				Thunnus maccoyii	99%	GU256523	*Thunnus maccoyii*	100%
				Thunnus obesus	99%	HQ611138	*Thunnus obesus*	100%
				Thunnus tonggol	99%	HQ425780	*Thunnus tonggol*	99.85%
			CR	*Thunnus albacares*	100%	JN572753	–	–
		SAS-W9	COI	*Thunnus albacares*	100%	JN086153	*Thunnus albacares*	100%
				Thunnus atlanticus	100%	GU225688	*Thunnus atlanticus*	100%
				Thunnus obesus	99%	JN086152	*Thunnus obesus*	100%
				Thunnus maccoyii	99%	GU256523	*Thunnus maccoyii*	99.84%
				Thunnus tonggol	99%	HQ425780	*Thunnus tonggol*	99.84%
			CR	*Thunnus albacares*	99%	JN572746	–	–
		SAS-W24	COI	*Thunnus albacares*	100%100%99%99%	DQ107652	*Thunnus albacares*	100%
				Thunnus atlanticus	99%	GU225688	*Thunnus atlanticus*	99.84%
				Thunnus obesus		HQ611138	*Thunnus obesus*	99.84%
				Thunnus maccoyii		GU256523	*Thunnus maccoyii*	99.69%
				Thunnus tonggol		HQ425780	*Thunnus tonggol*	99.69%
			CR	*Thunnus albacares*	99%	KC165909	–	–
White stumpnose	**WC**	**SAS-W12**	**COI**	***Chrysoblephus gibbiceps***	**100%**	**JF493183**	***Chrysoblephus gibbiceps***	**100%**
(*Rhabdosargus globiceps*)	**(*N* = 1)**			**(Red stumpnose)**			**(Red stumpnose)**	
Yellowtail	WC	SAS-W6	COI	*Seriola lalandi*	99%	HM007728	*Seriola lalandi*	100%
(*Seriola lalandi*)	(*N* = 5)	SAS-W8	COI	*Seriola lalandi*	99%	HM007728	*Seriola lalandi*	100%
		SAS-W21	COI	*Seriola lalandi*	100%	JF494499	*Seriola lalandi*	100%
		SAS-W25	COI	*Seriola lalandi*	99%	HM007728	*Seriola lalandi*	100%
		SAS-W28	COI	*Seriola lalandi*	99%	HM007728	*Seriola lalandi*	100%

[a] *Hyperoglyphe moselii* and *Schedophilus velaini* refer to the same species, although *S. velaini* is the currently accepted name.
[b] *Pangasius hypophthalmus* is an accepted synonym for *Pangasianodon hypophthalmus*.

Table 3
Identification results based on cytochrome *c* oxidase I (COI) and control region (CR) sequencing for 75 fish samples collected from retail outlets in South Africa, where N indicates the number of fish samples that were correctly labelled or potentially mislabelled. Cases of suspected mislabelling are indicated in bold typescript.

Fish marketed as: (expected species)	Province (*N*)	Code	Gene target	GENBANK			BOLD	
				Species identification	Similarity	Accession number	Species identification	Similarity
Angelfish (*Brama brama*)	WC (*N* = 1)	SAS-W46[b]	COI	*Brama brama*	100%	EF609300	*Brama brama*	100%
Butterfish(*Ruvettus pretiosus*/*Lepidocybium flavobrunneum*)	GP (*N* = 1)	SAS-G35[2]	COI	*Ruvettus pretiosus*	100%	HQ945988	*Ruvettus pretiosus*	100%
Cape salmon (*Atractoscion aequidens*)	**KZN (*N* = 1)**	**SAS-K49**	**COI**	***Argyrosomus japonicus* (Dusky kob)**	**99%**	**HM007719**	***Argyrosomus japonicus* (Dusky kob)**	**99.4%**
Dorado (*Coryphaena hippurus*)	KZN (*N* = 2)	SAS-K28[b]	COI	*Coryphaena hippurus*	100%	HM007705	*Coryphaena hippurus*	100%
		SAS-K38[b]		*Coryphaena hippurus*	99%	HM007705	*Coryphaena hippurus*	99.8%
	WC (*N* = 2)	SAS-W42[b]		*Coryphaena hippurus*	99%	JQ839746	*Coryphaena hippurus*	99.3%
		SAS-W47[b]		*Coryphaena hippurus*	99%	KF814117	*Coryphaena hippurus*	99%
Hake (*Merluccius* spp.)	KZN (*N* = 4)	SAS-K29[a]	COI	*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
		SAS-K34[a]		*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
		SAS-K35[b]		*Merluccius paradoxus*	100%	HM007683	*Merluccius paradoxus*	100%
		SAS-K41[a]		*Merluccius paradoxus*	100%	HM007683	*Merluccius paradoxus*	100%
	GP (*N* = 6)	SAS-G31[b]	COI	*Merluccius capensis*	100%	HM007690	*Merluccius capensis*	100%
		SAS-G36[a]		*Merluccius capensis*	100%	HM007691	*Merluccius capensis*	100%
		SAS-G34[a]		*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
		SAS-G38[a]		*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
		SAS-G45[a]		*Merluccius paradoxus*	99%	HM007683	*Merluccius paradoxus*	99.8%
		SAS-G46[b]		*Merluccius paradoxus*	100%	HM007683	*Merluccius paradoxus*	100%
	WC (*N* = 5)	SAS-W44[b]	COI	*Merluccius capensis*	100%	HM007691	*Merluccius capensis*	100%
		SAS-W58[a]		*Merluccius capensis*	99%	HM007691	*Merluccius capensis*	100%
		SAS-W45[b]		*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
		SAS-W53[b]		*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
		SAS-W61[b]		*Merluccius paradoxus*	100%	HM007684	*Merluccius paradoxus*	100%
Hake (*Merluccius capensis*)	WC (*N* = 1)	SAS-W56[a]	COI	*Merluccius capensis*	100%	HM007690	*Merluccius capensis*	100%
Deep water hake (*Merluccius paradoxus*)	GP (*N* = 1)	SAS-G48[b]	COI	*Merluccius paradoxus*	99%	HM007684	*Merluccius paradoxus*	99.8%
Hake (*Merluccius hubbsi*)	KZN (*N* = 2)	SAS-K32[a]	COI	*Merluccius hubbsi*	99%	EU074469	*Merluccius hubbsi*	100%
		SAS-K51[a]		*Merluccius hubbsi*	99%	EU074469	*Merluccius hubbsi*	99.8%
	WC (*N* = 2)	SAS-W70[a]		*Merluccius hubbsi*	100%	EU074469	*Merluccius hubbsi*	100%
		SAS-W71[a]		*Merluccius hubbsi*	100%	EU074469	*Merluccius hubbsi*	100%
John dory (*Zeus faber*)	**WC (*N* = 1)**	**SAS-W60[b]**	**COI**	***Zeus capensis* (Cape dory)**	**100%**	**HM007763**	***Zeus capensis* (Cape dory)**	**100%**
Kabeljou (*Argyrosomus* spp.)	GP (*N* = 1)	SAS-G26[b]	COI	*Argyrosomus japonicus*	100%	HM007718	*Argyrosomus japonicus*	100%
	WC (*N* = 2)	SAS-W54[b]		*Argyrosomus japonicus*	100%	HM007718	*Argyrosomus japonicus*	100%
		SAS-W55[b]		*Argyrosomus japonicus*	100%	HM007719	*Argyrosomus japonicus*	100%
Linefish (*Seriola quinqueradiata*)	WC (*N* = 1)	SAS-W59[a]	COI	*Seriola quinqueradiata*	100%	HQ641665	*Seriola quinqueradiata*	99.8%
Kingklip (*Genypterus blacodes*)	**GP (*N* = 1)**	**SAS-G47[a]**	**COI**	***Genypterus capensis* (kingklip)**	**100%**	**HM007736**	***Genypterus capensis* (kingklip)**	**100%**
	WC (*N* = 1)	**SAS-W74[a]**	**COI**	***Genypterus capensis* (kingklip)**	**100%**	**HM007735**	***Genypterus capensis* (kingklip)**	**100%**
Kingklip (*Genypterus capensis*)	KZN (*N* = 5)	SAS-K36[a]	COI	*Genypterus capensis*	99%	HM007735	*Genypterus capensis*	99.7%
		SAS-K27[b]		*Genypterus capensis*	100%	HM007736	*Genypterus capensis*	100%
		SAS-K33[b]		*Genypterus capensis*	100%	HM007737	*Genypterus capensis*	100%
		SAS-K37[b]		*Genypterus capensis*	99%	HM007735	*Genypterus capensis*	99.8%
		SAS-K42[b]	COI	No interpretable sequence with COI primers			No interpretable sequence with COI	

Table 3 (*continued*)

Fish marketed as: (expected species)	Province (*N*)	Code	Gene target	GENBANK			BOLD	
				Species identification	Similarity	Accession number	Species identification	Similarity
							primers	
			CR	*Genypterus capensis*	99%	GQ324561	–	–
	GP (*N* = 3)	SAS-G37[a]	COI	*Genypterus capensis*	100%	HM007736	*Genypterus capensis*	100%
		SAS-G30[b]		*Genypterus capensis*	100%	HM007738	*Genypterus capensis*	100%
		SAS-G39[b]		*Genypterus capensis*	100%	HM007735	*Genypterus capensis*	100%
	WC (*N* = 5)	SAS-W40[b]	COI	*Genypterus capensis*	100%	HM007736	*Genypterus capensis*	100%
		SAS-W41[b]		*Genypterus capensis*	99%	HM007738	*Genypterus capensis*	99.8%
		SAS-W48[b]		*Genypterus capensis*	100%	JF493517	*Genypterus capensis*	100%
		SAS-W50[b]		*Genypterus capensis*	100%	JF493517	*Genypterus capensis*	100%
		SAS-W43[b]		*Genypterus capensis*	100%	HM007735	*Genypterus capensis*	100%
Red roman (*Chrysoblephus laticeps*)	**KZN (*N* = 1)**	**SAS-K43[b]**	**COI**	***Chrysoblephus puniceus* (slinger seabream)**	**100%**	**HQ611087**	***Chrysoblephus puniceus* (slinger seabream)**	**100%**
	KZN (*N* = 1)	SAS-K45[b]	COI	*Chrysoblephus laticeps*	99%	HM007751	*Chrysoblephus laticeps*	99.7%
	GP (*N* = 1)	SAS-G29[b]	COI	*Chrysoblephus laticeps*	100%	HM007751	*Chrysoblephus laticeps*	100%
Red snapper (*Lutjanus* spp.)	GP (*N* = 1)	SAS-G33[b]	COI	*Lutjanus sanguineus* (Humphead snapper)	100%	JF493848	*Lutjanus sanguineus* (Humphead snapper)	100%
Red steenbras (*Petrus rupestris*)	**KZN (*N* = 2)**	**SAS-K39[b]**	**COI**	***Seriola lalandi* (yellowtail amberjack)**	**100%**	**HM007727**	***Seriola lalandi* (yellowtail amberjack)**	**100%**
		SAS-K48[b]		***Lampris guttatus* (Opah)**	**99%**	**JF931910**	No species match in BOLD	
Silver steenbras [white musselcracker] (*Sparodon durbanensis*)	**KZN (*N* = 1)**	**SAS-K46[b]**	**COI**	***Lethrinus lentjan* (Pink ear emperor)**	**99%**	**JF493749**	***Lethrinus lentjan* (Pink ear emperor)**	**99.8%**
White steenbras (*Lithognathus lithognathus*)	**KZN (*N* = 1)**	**SAS-K40[b]**	**COI**	***Pristipomoides multidens* (goldbanded jobfish)**	**99%**	**KF430626**	***Pristipomoides multidens* (goldbanded jobfish)**	**99.8%**
Rockcod (*Epinephelus* spp.)	**KZN (*N* = 1)**	**SAS-K50[b]**	**COI**	***Chelidonichthys capensis* (Cape gurnard)**	**100%**	**HM007757**	***Chelidonichthys capensis* (Cape gurnard)**	**100%**
Santer (*Cheimerius nufar*)	WC (*N* = 1)	SAS-W35[b]	COI	*Cheimerius nufar*	100%	JF493134	*Cheimerius nufar*	100%
Silverfish (*Argyrozona argyrozona*)	KZN (N = 1)	SAS-K47[2]	COI	*Argyrozona argyrozona*	99%	HM007754	*Argyrozona argyrozona*	99.8%
	GP (*N* = 1)	SAS-G42[b]	COI	*Argyrozona argyrozona*	100%	HM007754	*Argyrozona argyrozona*	100%
Slinger (*Chrysoblephus puniceus*)	KZN (*N* = 1)	SAS-K30[b]	COI	*Chrysoblephus puniceus*	100%	HQ611087	*Chrysoblephus puniceus*	100%
Snoek (*Thyrsites atun*)	KZN (*N* = 2)	SAS-K31[a]	COI	*Thyrsites atun*	99%	HQ611109	*Thyrsites atun*	99.8%
		SAS-K44[a]		*Thyrsites atun*	100%	HQ641670	*Thyrsites atun*	100%
	GP (*N* = 2)	SAS-G28[a]	COI	*Thyrsites atun*	100%	HQ641670	*Thyrsites atun*	100%
		SAS-G40[a]		*Thyrsites atun*	99%	HQ641670	*Thyrsites atun*	99.7%
Tuna (*Thunnus* spp.)	GP (*N* = 1)	SAS-G52[b]	COI	*Thunnus albacares*	100%	DQ107652	*Thunnus albacares*	100%
				Thunnus atlanticus	100%	GU225688	*Thunnus atlanticus*	99.84%
				Thunnus obesus	99%	HQ611138	*Thunnus obesus*	99.84%
				Thunnus maccoyii	99%	GU256523H	*Thunnus maccoyii*	99.69%
				Thunnus tonggol	99%	Q425780	*Thunnus tonggol*	99.69%
			CR	*Thunnus albacares*	99%	KC165915	–	–
Longfin tuna (*Thunnus alalunga*)	**GP (*N* = 2)**	**SAS-G41[b]**	**COI**	***Thunnus albacares***	**100%**	**KF528374**	***Thunnus albacares***	**100%**
				Thunnus atlanticus	**100%**	**GU225688**	***Thunnus atlanticus***	**100%**
				Thunnus obesus	**99%**	**HQ611138**	***Thunnus obesus***	**100%**
				Thunnus maccoyii	**99%**	**GU256523**	***Thunnus maccoyii***	**99.84%**
				Thunnus tonggol	**99%**	**DQ107632**	***Thunnus tonggol***	**99.84%**
			CR	***Thunnus albacares* (Yellowfin tuna)**	**99%**	**KC165851**	**–**	**–**

(*continued on next page*)

Table 3 (*continued*)

Fish marketed as: (expected species)	Province (*N*)	Code	Gene target	GENBANK			BOLD	
				Species identification	Similarity	Accession number	Species identification	Similarity
		SAS-G43[b]	**COI**	***Thunnus albacares***	**100%**	**HM007769**	***Thunnus albacares***	**100%**
				Thunnus obesus	**99%**	**JN086152**	***Thunnus obesus***	**99.84%**
				Thunnus atlanticus	**99%**	**GU225688**	***Thunnus atlanticus***	**99.84%**
				Thunnus maccoyii	**99%**	**GU256523**	***Thunnus maccoyii***	**99.69%**
				Thunnus tonggol	**99%**	**HQ425780**	***Thunnus tonggol***	**99.69%**
			CR	***Thunnus albacares*** **(Yellowfin tuna)**	**99%**	**KC166035**	**–**	**–**
Yellowfin tuna (*Thunnus albacares*)	GP (*N* = 2)	SAS-G32[b]	COI	*Thunnus albacares*	100%	JN086153	*Thunnus albacares*	100%
				Thunnus atlanticus	100%	GU225688	*Thunnus atlanticus*	100%
				Thunnus maccoyii	99%	GU256523	*Thunnus maccoyii*	100%
				Thunnus obesus	99%	HQ611138	*Thunnus obesus*	100%
				Thunnus tonggol	99%	HQ425780	*Thunnus tonggol*	99.85%
			CR	*Thunnus albacares*	99%	JN572786	–	–
		SAS-G44[a]	COI	*Thunnus albacares*	100%	JN086153	*Thunnus albacares*	100%
				Thunnus atlanticus	100%	GU225688	*Thunnus atlanticus*	100%
				Thunnus maccoyii	99%	GU256523	*Thunnus maccoyii*	100%
				Thunnus obesus	99%	JN086152	*Thunnus obesus*	100%
				Thunnus tonggol	99%	HQ425780	*Thunnus tonggol*	99.85%
			CR	*Thunnus albacares*	99%	KC165917	–	–
	WC (*N* = 3)	SAS-W51[b]	COI	*Thunnus albacares*	100%	JN086153	*Thunnus albacares*	100%
				Thunnus atlanticus	100%	GU225688	*Thunnus atlanticus*	100%
				Thunnus obesus	99%	JN086152	*Thunnus obesus*	100%
				Thunnus tonggol	99%	HQ425780	*Thunnus tonggol*	99.85%
			CR	*Thunnus albacares*	99%	JN572789	–	–
		SAS-W52[a]	COI	*Thunnus albacares*	100%	JN086153	*Thunnus albacares*	100%
				Thunnus atlanticus	99%	DQ107588	*Thunnus atlanticus*	100%
				Thunnus maccoyii	99%	GU256523	*Thunnus maccoyii*	100%
				Thunnus obesus	99%	JN086152	*Thunnus obesus*	100%
				Thunnus tonggol	99%	HQ425780	*Thunnus tonggol*	99.84%
			CR	*Thunnus albacares*	99%	AF301205	–	–
		SAS-W73[a]	COI	*Thunnus albacares*	100%	JN086153	*Thunnus albacares*	100%
				Thunnus atlanticus	100%	GU225688	*Thunnus atlanticus*	100%
				Thunnus obesus	99%	JN086152	*Thunnus obesus*	100%
				Thunnus tonggol	99%	HQ425780	*Thunnus tonggol*	99.85%
				Thunnus maccoyii	99%	GU256523	*Thunnus maccoyii*	99.84%
			CR	*Thunnus albacares*	99%	AF301205	–	–
Yellowtail (*Seriola lalandi*)	GP (*N* = 2)	**SAS-G27**[b]	**COI**	***Seriola quinqueradiata*** **(Japanese amberjack)**	**100%**	**HQ641666**	***Seriola quinqueradiata*** **(Japanese amberjack)**	**99.7%**
		SAS-G51[b]	**COI**	***Seriola quinqueradiata*** **(Japanese amberjack)**	**100%**	**AB517556**	***Seriola quinqueradiata*** **(Japanese amberjack)**	**100%**

[a] Latin name indicated on product labelling.
[b] Expected Latin name inferred from common name provided.

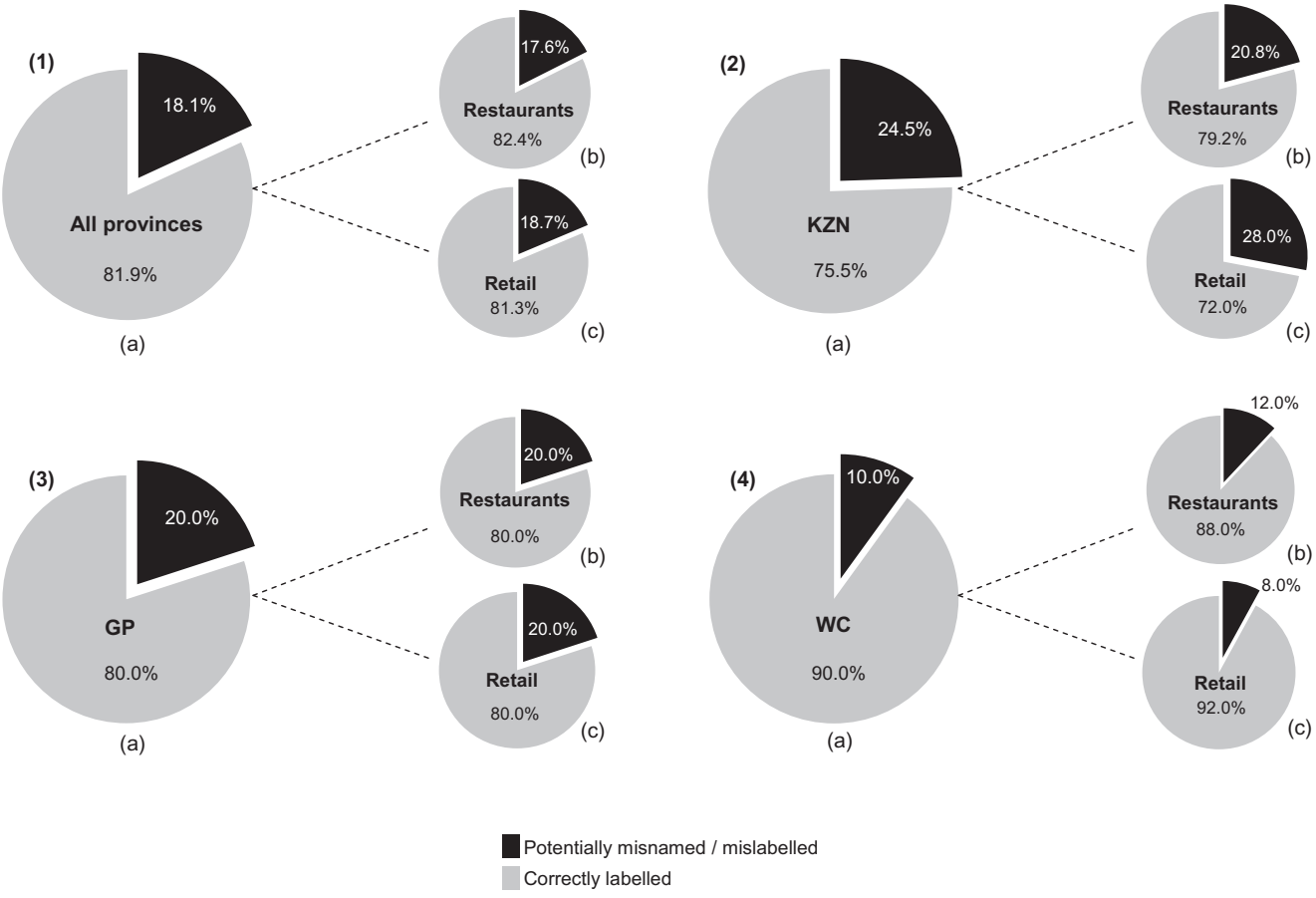

Fig. 1. The proportions (in percentages) of correctly labelled and potentially misnamed or mislabelled fish samples (1) overall, (2) in KZN, (3) in GP and (4) in WC, where (a) depicts all samples from restaurants and retail outlets, (b) depicts restaurant samples and (c) depicts retail outlets samples.

interested in market transparency than in cost savings, opportunities may arise for suppliers in the province to boost profits through deceitful substitutions. The WC, on the other hand, is the province where most food mislabelling studies have emerged to date (Cawthorn et al., 2012a, 2013; D'Amato, Alechine, Cloete, Davison, & Corach, 2013; Von der Heyden et al., 2010), likely leading to an increased localised focus on food authenticity issues.

In total, 21 of the 59 (36%) 'category B' specimens procured as 'linefish' or 'catch of the day' were deemed to be incorrectly described (Table 4), with misdescriptions including a range of fish types (Fig. 2). Conversely, only six of 90 specimens (7%) collected as 'category A' priority species were found to be different species compared to those expected (Table 4), including 1 'kabeljou', 2 'kingklip' and 3 'tuna' samples (Fig. 2). Within the latter category, all 37 samples collected as 'hake' from restaurants and retailers were assigned to an anticipated *Merluccius* species. Yet, it was notable from a conservation viewpoint that four hake samples collected from retailers were labelled and confirmed as the unsustainable and WWF-SASSI red-listed Merluccius hubbsi (Argentine hake) (Table 3), an imported species trawled in the Southwest Atlantic. This hake resource was declared to be in a state of emergency in 1998 and despite restrictive fishing measures being imposed for M. hubbsi in Argentina and Uruguay, their stocks remain overexploited, while overexploitation of Brazilian stocks has more recently been detected (Vaz-dos-Santos, Rossi-Wongtschowski, & Figueiredo, 2009). The remaining 33 hake samples were all correctly identified as one of the two South African hake species, *Merluccius capensis* or *Merluccius paradoxus* (Tables 2 and 3). This finding may be partially attributed to the fact that the South African hake trawl is Marine Stewardship Council (MSC)-certified, a prerequisite for which is strict compliance with the MSC Chain of Custody (CoC) traceability component. While it is accepted that a portion of hake sold in South Africa is not derived from the local fishery, that hake caught in the domestic MSC-certified trawl would be expected to be fully traceable through the supply chain and also correctly described when appearing on the market.

3.2.1. Restaurant samples

Discrepancies were discovered between the declared market names and the genetically identified species for 13 of 74 (18%) samples collected from restaurants (Table 2, Fig. 1), which is lower than the 38% fish mislabelling rate reported by Warner et al. (2013) for restaurants in the US (Table 4). Interestingly, all 13 cases of restaurant-level misdescription in this study were related back to instances where the waiter or manager had supplied the incorrect name to qualify the fish on sale, while no such cases were detected for samples where the common names appeared on the menu. This could indicate a lack of adequate restaurant personnel training, or could imply that substitutions are more easily perpetuated when a fish is merely described as 'linefish' or 'catch of the day'.

The provincial breakdown of fish species misdescription in restaurants was calculated as 5 of 24 (20.8%) samples in KZN, 5 of 25 (20%) in GP and 3 of 25 (12%) in WC (Fig. 1). The aforementioned results can be related back to observations made during sample collection, when it was noted that the waitrons and/or managers in KZN and GP restaurants were often less capable of

Table 4
Comparison of seafood mislabelling rates found in this study with those from similar studies conducted in South Africa and worldwide.

Country of study	Gene target	Species assessed	Outlets	No. samples identified	No. (%) mislabelled	Comments	Reference
South Africa (3 provinces)	COI (CR, some cases)	Various finfish –	Restaurants (n = 48)	74	13 (18%)	Mislabelling most pronounced for fish sold under generic term 'linefish' or 'catch of the day', particularly for 'barracuda' and 'steenbras'.	This study
			'Category A'	43	2 (5%)		
			'Category B'	31	11 (36%)		
		'Category A' = kingklip (*Genypterus* spp.), kabeljou/kob (*Argyrosomus* spp.), hake (*Merluccius* spp.), tuna (*Thunnus* spp.)	Retail outlets (n = 62)	75	14 (19%)		
			'Category A'	47	4 (9%)		
			'Category B'	28	10 (36%)		
		'Category B' = any linefish/'catch of the day'	Total (N = 110)	298	27 (18%)		
			'Category A'	90	6 (7%)		
			'Category B'	59	21 (36%)		
South Africa (4 provinces)	COI (CR, some cases)	Various finfish species	Wholesalers/distributors	108	10 (9%)	Mislabelling most pronounced for 'barramundi', 'yellowtail', 'bluenose', 'kingklip', 'red snapper' and 'musselcracker'.	Cawthorn et al. (2012a)
			Retail outlets	140	43 (31%)		
			Total	248	53 (21%)		
South Africa (2 provinces)	16S rRNA (CR for kingklip)	Various finfish species	Seafood wholesalers & restaurants	178	89 (50%)	Mislabelling most pronounced for 'kob' (84%), also potentially for kingklip (ca. 30%).	Von der Heyden et al. (2010)
Canada (5 metropolitan areas)	COI	Various finfish species	Retail outlets, take-out, restaurants	236	89 (41%)	Mislabelling most pronounced for 'cod' and 'red snapper'.	Hanner et al. (2011)
North America (Canada & US)	COI	Various seafood products	Commercial markets & restaurants	91	23 (25%)	Mislabelling most pronounced for 'red snapper'.	Wong and Hanner (2008)
United States (21 states)	COI mostly	46 different fish types	Restaurants (n = 148)	243	93 (38%)	Mislabelling most pronounced for 'snapper' and 'tuna, followed by 'Halibut', 'grouper', 'cod' and 'Chilean seabass'.	Warner et al. (2013)
			Retail outlets (n = 408)	731	130 (18%)		
			Sushi venues (n = 118)	241	178 (74%)		
			Total (N = 674)	1215	401 (33%)		
Brazil (Southern region)	COI	Fresh, frozen or cooked fish samples	Retail outlets	23	6 (20%)		Carvalho et al. (2015)
			Restaurants	7	2 (29%)		
			Total	30	8 (27%)		
Italy (Northern & Central)	COI/Cyt *b*	Processed fish products representing 27 teleost species	Retail outlets	69	22 (32%)	Substitutions of economic, nutritional & conservation concern.	Filonzi et al. (2010)
UK		Processed white fish products	Supermarkets	371	21 (6%)		Helyar et al., 2014
Australia (Hobart, Tasmania)		Fresh (unprocessed, uncooked) fish samples	Retail outlets	38	0 (0%)		Lamendin et al., 2015

Note: retail outlets generally refer to a combination of supermarkets/grocery stores, fishmongers and seafood markets.
COI = cytochrome *c* oxidase I (COI) gene; CR = mitochondrial control region; 16S rRNA = 16S ribosomal RNA gene, Cyt *b* = cytochrome b gene.

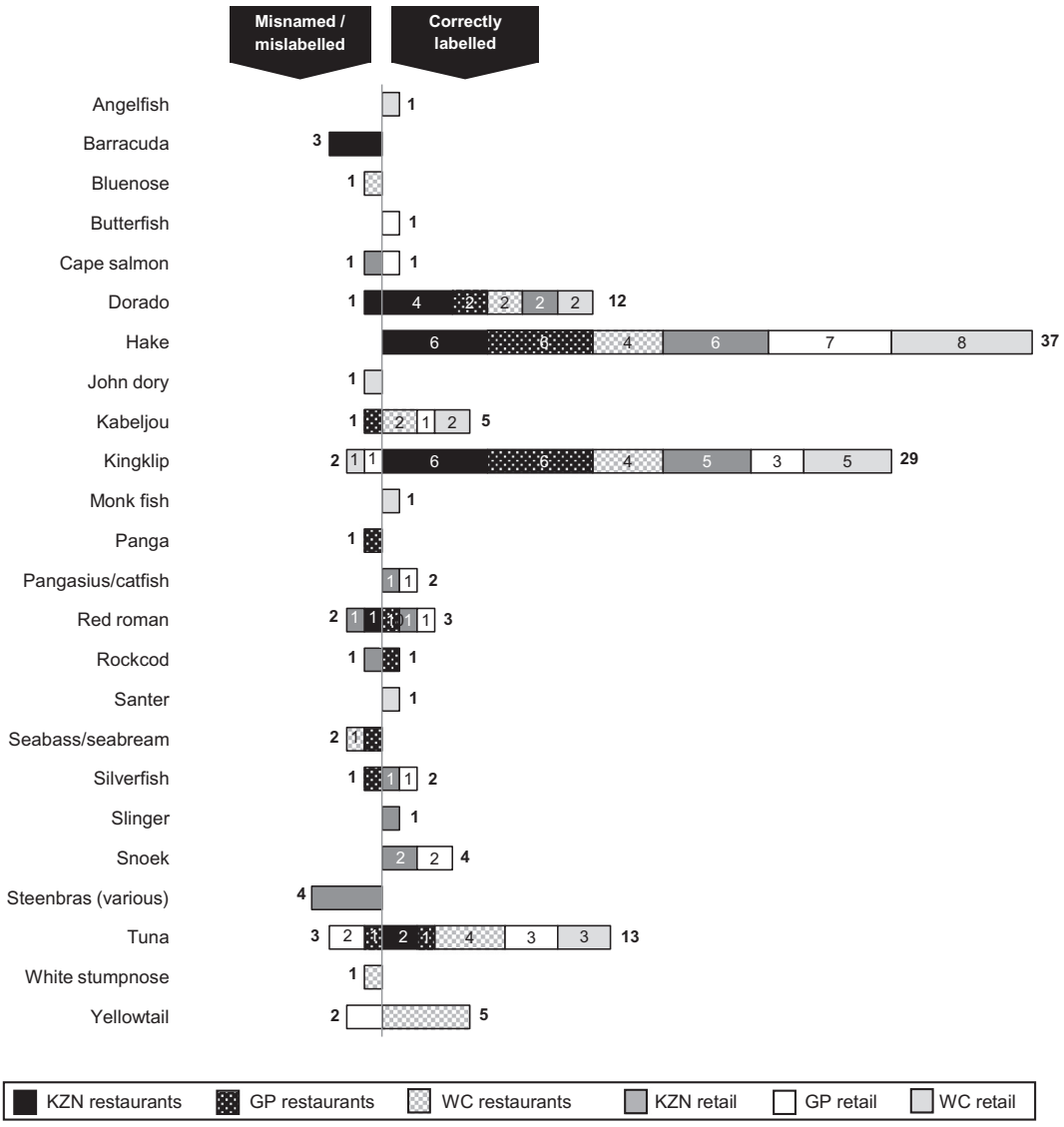

Fig. 2. The frequency of correct and potentially incorrect labelling for the individual fish specifies collected in this study Table 1. PCR amplification and sequencing primers used for fish species identifications in this study.

clearly indicating the fish type/species on sale than those in the WC.

A total of 11 'category B' specimens collected in restaurants were found to be misrepresented in some way, while such a scenario related to only two 'category A' specimens. Encouragingly, apart from hake, all kingklip samples ($N = 16$) from restaurants appeared to be correctly described, being identified as the locally-caught *Genypterus capensis*. Such results can be viewed as positive compared to those reported by Von der Heyden et al. (2010), who showed that *ca.* 30% of the 'kingklip' samples acquired from the domestic market (including in restaurants) potentially had their origin in New Zealand and were more likely to be *Genypterus blacodes* (pink cusk-eel/ling).

Certain cases of restaurant species misrepresentation observed in this study were seemingly less blatant than others and may have even been accidental. For example, a sample sold in GP as 'panga', which would be anticipated to refer to the sparid species 'panga seabream' (*Pterogymnus laniarius*), exhibited 99–100% sequence similarity with *Pangasianodon hypophthalmus* (striped catfish) (Table 2). Such a finding may indicate possible confusion between the common and scientific names, but still implies that an unsuspecting consumer would be receiving a potentially farmed species from Asia rather than a wild-caught marine one from local waters.

The most common incidence of perceived species misdescription in restaurants involved three samples sold in KZN as 'barracuda' (Table 2, Fig. 2). In all cases, the waitrons/managers of the respective restaurants were asked to verify the latter description by writing down the name and to confirm that they were not possibly referring to 'barracouta' (a market name often used locally for snoek (*Thyrsites atun*)). Directly interpreted, 'barracuda' would be expected to be one or other species belonging to the genus *Sphyraena*. However, all three queried samples showed $\geqslant$99% COI sequence similarity in GenBank and BOLD with *Scomberomorus commerson* (Spanish mackerel). In South Africa, *S. commerson* is frequently called king mackerel, couta, cuda or katonkel (Van der Elst, 2000) and the potential thus exists that the latter cases could have arisen due to confounded nomenclature considering the plethora of vernacular names associated with the species.

An observed instance of congeneric species swopping involved a sample sold as 'yellowfin tuna' (expected species *Thunnus*

albacares) in GP, but which exhibited a top match with *Thunnus obsesus* (bigeye tuna) with COI and CR sequencing. A further sample served as 'bluenose' in the WC and anticipated to be 'bluenose warehou' (*Hyperoglyphe antarctica*) was identified as its family member violet warehou (*Hyperoglyphe moselii*, accepted name *Schedophilus velaini*) (Table 2).

It has been repeatedly recognised that the use of single vernacular names or generic market labels to describe various fish types can hamper consumer choice, since this groups together species for sale that have markedly different values, sustainability statuses and even health concerns (Cawthorn et al., 2012a; Logan, Alter, Haupt, Tomalty, & Palumbi, 2008). In one restaurant in GP, the linefish of the day was described merely as 'seabass' (Table 2) and when requested to narrow the description, the manager was unable to do so, adding only that it was imported. In a South African context, the term 'seabass' may refer to any of numerous species within the family Serranidae, while the name may also be applied to the European species *Dicentrarchus labrax* (family Morinidae). The sample in question, however, was identified as *Sciaenops ocellatus* (red drum), which is in fact a member of the Sciaenidae family. Similarly, a sample sold in the WC under the group name 'seabream' (which could also not be qualified according to type or species) showed $\geqslant$99% sequence similarity with *Seriolella brama* (common warehou). The term 'seabream' is expected to encompass various perch-like species within the Sparidae family (Van der Elst, 2000), although some sources include Bramidae species (pomfrets) under this definition. In spite of the fact that 'seabream' may be used as a vernacular name for *S. brama* in Australia, the aforementioned species belongs to the family Centrolophidae, rather than either of the formerly mentioned families.

Other detected cases of species misrepresentation in restaurants were more difficult to explain and appeared less likely to be accidental. Such cases not only involved fish within different genera and sometimes even different families to those anticipated, but also those carrying different conservation concerns. For example, a fish sold in KZN as 'dorado' (expected species *Coryphaena hippurus*) presented 100% sequence similarity with silverfish/carpenter (*Argyrozona argyrozona*) (Table 2). Apart from the different morphological characteristics, textures and tastes of these two species, the former is a more sustainable WWF-SASSI green-listed species, while the latter is of conservation concern and is either orange- or red-listed depending on the source fishery. Another sample sold in KZN as 'red roman' (expected species *Chrysoblephus laticeps*) was also identified as *A. argyrozona*, while the opposite was found for a GP restaurant, where the sample indicated as 'silverfish' (expected species *A. argyrozona*) turned out to be red roman (*C. laticeps*) (Table 2). Both the red roman and silverfish in the latter cases were served in the whole state and given their unique external features, their identities should have been readily apparent to those selling them. Lastly, a fish ordered in a popular WC restaurant as white stumpnose (expected species *Rhabdosargus globiceps*) exhibited 100% COI sequence similarity with red stumpnose (*Chrysoblephus gibbiceps*). Although WWF-SASSI sustainability assessments of both of the aforesaid endemic species are under review, current data suggest that white stumpnose is regionally overexploited, but that red stumpnose is severely overfished throughout its range and is estimated to have declined to 1–5% of the original population size (Griffiths & Lamberth, 2002).

3.2.2. Retail outlet samples

Since most South African food labelling regulations (e.g. DOH, 2010; DTI, 2003) relate to pre-packaged products and are likely more applicable to retailers than to restaurants, it might be anticipated that fish mislabelling would be lower in the former than in the latter. Nonetheless, this anticipation was not corroborated by the results of this study. Of the 75 retail samples sequenced, 14 (19%) were identified as different species to those declared on the packaging or implied by the common name provided, with four being 'category A' specimens and 10 being 'category B' specimens (Table 3, Fig. 1). Of these 14 cases of misdescription, eight were related back to samples for which the common names had been provided by the vendor behind a fresh fish counter only (no common name supplied on labelling), four were fresh samples with the common name printed on the label and two were pre-packaged frozen products with the common and scientific names on the packaging. Although this level of misdescription (19%) remains of concern, it suggests an improvement on the *ca.* 31% mislabelling rate previously found for retail outlets in South Africa (Cawthorn et al., 2012a) (Table 4). In relation to international studies, this value corresponds with the seafood mislabelling rates determined for retail outlets in the US (18%) and Brazil (20%) (Carvalho, Palhares, Drummond, & Frigo, 2015; Warner et al., 2013), falls below the rate of 32% found for Italian retailers (Filonzi et al., 2010), but is considerably higher than those rates reported for retailers in the UK (6%) and Tasmania (0%) (Helyar et al., 2014; Lamendin, Miller, & Ward, 2015) (Table 4).

Per province, the frequency of misdescription in retail outlets was calculated as 7 of 25 (28%) samples in KZN, 5 of 25 (20%) in GP and only 2 of 25 (8%) in WC (Fig. 2). These values follow a similar pattern to those seen by Cawthorn et al. (2012a), where the greatest proportion of fish mislabelling in retail outlets was also found in KZN (56%), followed by GP (30%) and WC (25%) (Fig. 1). Such comparative results, although derived from studies using somewhat different sample acquirement approaches, indicate a reduction in retail-level mislabelling in all evaluated provinces, particularly the WC. However, the prevalence of such practices is still high in KZN and GP relative to WC, indicating that the former two provinces should be flagged as targets for improvement.

In certain circumstances, the determination of whether a species is mislabelled or not depends largely on the geographic area in which it is sold. In this study, a sample sold by a GP retailer as 'red snapper' showed 100% sequence similarity with *Lutjanus sanguineus* (humphead snapper) (Table 3). According to the 'seafood list' published in the US (FDA, 2014), 'red snapper' is the legally designated market name only for *Lutjanus campechanus*, a highly-valued but overexploited species from the Atlantic coast and Gulf of Mexico that has been a target for substitution in North America (Hanner et al., 2011). However, 'red snapper' is also the vernacular name for various other Lutjanidae species in different parts of the world (e.g. Australia, India, Malaysia, Mauritius). In the absence of a 'seafood list' in South Africa specifying acceptable names for locally-traded species, this sample can likely not be considered mislabelled. Nonetheless, it is notable that the common name for *L. sanguineus* in South Africa is 'blood snapper' and thus comprehensible that the term 'red snapper' might be preferably selected to appeal to local consumers.

Eight of the 14 (57%) cases of misdescription determined at the retail level were apparently subtle in nature, involving substitutions with congeneric species. For instance, a sample sold by a WC retailer as 'John dory' (expected species *Zeus faber*) was identified as Cape dory (*Zeus capensis*), while one sold as 'red roman' (expected species *C. laticeps*) was rather found to be slinger seabream (*Chrysoblephus puniceus*) (Table 3). In a previous study, *ca.* 25% of samples sold by South African retailers as 'kingklip' (expected species *G. capensis*) were substituted with *G. blacodes*, the closely-related counterpart from Australia or New Zealand (Cawthorn et al., 2012a). In contrast to these findings, two frozen samples from the current study that were labelled as kingklip, but specified on the packaging to be *G. blacodes*, exhibited 100% sequence similarity with *G. capensis* (Table 3). Although 'kingklip' is the accepted FAO name for *G. capensis*, these

samples would be considered mislabelled purely based on the fact that the enclosed species did not match the label designation. Similarly, the CR sequences from two samples marketed in GP as 'longfin tuna' (expected species *T. alalunga*) rather corresponded with those from *T. albacares* (yellowfin tuna) (Table 3), an unexpected finding given that yellowfin tuna generally demands a higher price than longfin. The reason for such findings is unclear, but could point to mistaken species identification by suppliers or retailers, insufficient information being provided to vendors to describe the fish on sale or the possibility of by-catch species being processed as part of a targeted catch.

The common name 'yellowtail' was provided for two samples collected in retail outlets in GP, which, when sold in South Africa, would be expected to refer to the well-known *Seriola lalandi*. Yet, both samples exhibited a top match with *Seriola quinqueradiata* (Japanese amberjack) (Table 3), which is likely to be a farmed species imported from Asia. As pointed out previously (Cawthorn et al., 2012a), in the absence of a 'seafood list' detailing the species that can rightfully constitute a 'yellowtail' in South Africa, fish purveyors may opt to capitalise on the use of a locally-accepted name rather than to risk marketing a foreign one to a generally uninformed consumer base.

Other marketing distortions observed at the retail level involved substitution of species from different genera. For instance, a specimen sold in a KZN seafood market under the generic term 'rockcod' (expected to be of the genus *Epinephelus*) instead showed 100% sequence similarly with *Chelidonichthys capensis* (Cape gurnard) (Table 3). Although Cape gurnard may have a superior sustainability rating than rockcod species, it also has a lower commercial value. In the same outlet, a sample described as 'Cape salmon' (expected species *A. aequidens*) exhibited $\geqslant$99% sequence similarity with *A. japonicas* (locally referred to as dusky kob). In South Africa, 'daga salmon' is also a recognised vernacular name for *A. japonicas*. While not likely to be the case for vendors familiar with locally-traded fish species, the possibility of confusion between the latter term and Cape salmon cannot be overlooked. Nevertheless, when caught in the wild, these two species have different conservation concerns and given that *A. japonicas* is increasingly being farmed in South Africa, their accurate description should be considered paramount.

Perhaps the most blatant and disconcerting cases of mislabelling from a legitimacy and sustainability viewpoint involved four fish samples sold in KZN under the generic term 'steenbras' (Table 3). Further questioning of the relevant vendors was generally required in order to ascertain the type of 'steenbras' being marketed in each case. Two of these specimens were subsequently established by the suppliers to be 'red steenbras', which refers to a specially-protected species (*Petrus rupestris*) that may not be caught, bought or sold in South Africa. These samples were, however, identified by COI sequencing as yellowtail (*S. lalandi*) and opah (*Lampris guttatus*) (Table 3), species that are morphologically distinct from red steenbras and belong to different families. Two additional samples from the same supermarket chain in KZN were further qualified as 'silver steenbras' (expected species *Sparodon durbanensis*) and 'white steenbras' (expected species *Lithognathus lithognathus*), both of which are illegal to buy or sell in South Africa. Nonetheless, the sample denoted as 'silver steenbras' was substituted with *Lethrinus lentjan* (Pink ear emperor), a species reported in South African waters but for which little information exists on the stock status. On the other hand, the fish found to be masquerading as 'white steenbras' was *Pristipomoides multidens* (goldbanded jobfish). This Lutjanid species does not appear to occur around South Africa (Froese & Pauly, 2014), but may have gained entry into KZN through Mozambican borders. It may indeed be argued from a conservation perspective that the substitution of protected or over-exploited species with potentially more sustainable ones is not undesirable. However, apart from being deceptive, such acts serve only to confuse consumers and to hinder sustainable seafood campaigns in their efforts to provide effective tools for responsible purchasing decisions. For instance, the marketing of 'steenbras' (even if they are not what they are said to be) creates the skewed public impression that these species are readily available and thus must be in plentiful supply, which severally belies the true status of the stocks.

3.3. Credible seafood labelling in South Africa – where to from here?

The legislation relating to the labelling of seafood products in South Africa, as well as the regulatory authorities responsible for implementing these, have been comprehensively discussed by Cawthorn et al. (2012a). While not being repeated in detail, some key points that have emerged in the current work are highlighted, with recommendations for resolution.

3.3.1. Standardised seafood naming lists

The observation that almost half of the cases of misrepresentation in this study could be linked with confused naming practices reiterates the strong and immediate need for the development of a 'standardised seafood naming list' in South Africa. Whether initiated as a guidance document or legislated from the start, this list should contain the scientific names and preferably one agreed-upon market name for each species (or species group, where relevant) of local and imported fresh, frozen and canned seafood traded in the country. The inclusion of pictorial illustrations, defining features and DNA profiles would likely further aid users in verifying the identities of the fish being marketed. In line with global trends, WWF-SA recently undertook to initiate the collation of such list in consultation with a working group comprising stakeholders from government, the commercial fishing industry, suppliers, retailers, restaurateurs, consumer bodies, research institutions and NGOs. The South African Bureau of Standards (SABS) has subsequently agreed to advance the initiative through the compilation of South African National Standard 1647 (SANS 1647).

While it is envisioned that the standardised naming list will aid in reducing domestic seafood misrepresentation, it is recognised that such lists are not without complications and these alone are unlikely to eliminate mislabelling altogether. While undoubtedly beneficial in terms of locally-sourced and traded fish, problems can arise with these lists during international trade. Different countries often have different 'seafood lists' and, due to a lack of harmonisation, different 'acceptable market names' can be applied to different species. Such complexities need to be considered in compiling the local list, with emphasis on clearly defining the labelling requirements for commonly-imported foreign species with closely-related local counterparts (e.g. imported *S. quinqueradiata* vs. local *S. lalandi* and imported *G. blacodes* vs. local *G. capensis*).

3.3.2. Comprehensive labelling requirements

The ambiguities associated with colloquial names in the global marketplace signal a clear need for the utilisation of scientific names in seafood product labelling, as also increasingly called for in the monitoring of international wildlife trade (Gerson et al., 2008). The inclusion of scientific names would not only promote uniformity in seafood trade, but would assist law enforcers to detect fraud or the commercialisation of illegal species. For the consumer, however, the need for accurate information on labels exists not only for the species, but should extend to the origin and production method if they are to be fully capable of making sustainable seafood choices. Regulators in the EU have recognised these factors by effecting legislation requiring that the commercial designation, scientific name, geographical origin and production method (wild or farmed) be declared on fish product labels (EC,

2001). At a minimum, it is advised that South Africa adopt the same mandatory labelling provisions into national policy.

3.3.3. Improved traceability

Lack of traceability is a common feature of many seafood supply chains and one that can be strongly associated with the perpetuation of fraud. The requirement for suppliers to ensure full traceability of fish products is mandated by law in the EU (EC, 2001, 2002) and is also among the key provisions of the recently promulgated Food Safety Modernisation Act in the US. Nonetheless, corresponding regulations in South Africa are weak, fragmented and poorly executed. As a direct result, traceability in local seafood supply chains is voluntary or largely absent. With little accountability for the fish arriving at the marketplace, cases of misrepresentation as seen in this study are bound to occur. In order to enhance transparency, the establishment of concrete legislation on food traceability in South Africa is pivotal and should be placed high on the agendas of local policy makers. Until such time as local regulation is improved, the industry should consider incorporating such systems into their own company policies, which will not only assist the management of supply chain and reputational risks, but will equip them in responding to emerging incidents through rapid and precise recalls.

3.3.4. Enhanced monitoring and enforcement

Regardless of the intervention applied, improvement in the accuracy of seafood labelling in South Africa will rely critically on intensified effort and buy-in from both the industry and government. The necessity for more stringent regulations is clear, but accompanying this is the crucial need to evaluate the current procedures used for monitoring seafood trade in South Africa, specifically addressing whether these are adequate to deter deceitful activities. While DNA testing (particularly DNA barcoding) could undoubtedly provide an advanced level of precision to the monitoring of fish mislabelling in this country, such methods will likely hold limited benefit if they are not consistently applied. Thus, any monitoring initiatives aimed at stamping out fish mislabelling in South Africa should be based on a 'pro-active rather than reactive' approach, underpinned by a structured, rigorous and on-going authentication programme. The use of such an approach, when backed up by validated analytical methods, would not only aid in identifying the links where mislabelling occurs, but may provide the basis for the prosecution of unlawful activities.

4. Conclusions

The global seafood and fishing industries are delicately interlinked, with the former influenced by consumer demand and the latter determining the types of fish made available for consumption. Mislabelling, however, threatens to sever this link by eliminating the consumer's ability to effect patterns of seafood exploitation through educated choices. This study was aimed at benchmarking the current prevalence of fish species misdescription in South Africa and at evaluating strategies that can be applied to reduce such instances. The results obtained from this research indeed suggest some improvement in the transparency of local seafood marketing and underscore the efforts made towards this over the last two years. Nonetheless, the fact that almost one in five fish remain incorrectly described on the South African market points to a clear problem requiring correction. Even though substantial reductions in mislabelling have been witnessed for specific provinces and fish species, the present work has elucidated the regions where fish misdescription prevails (e.g. KZN, GP) and the species remaining prone to such practices (e.g. steenbras, barracuda, tuna). The findings have strongly reinforced the need for a locally-applicable 'standardised seafood naming list' and more comprehensive fishery product labelling and traceability regulations. Nevertheless, neither factor on its own nor a combination of these is likely to significantly reduce fish mislabelling in South Africa without effective enforcement and appropriately discouraging penalisation. In this context, DNA barcoding has been confirmed as an extremely powerful tool for the identification of fish species traded in South Africa and its adoption into industry and governmental monitoring programmes is strongly advocated. For in the end, the assurance that the fish sold in South Africa is legal, sustainable and accurately labelled should not be considered a luxury, but rather a necessity.

Acknowledgements

The authors are indebted to WWF-SASSI for providing the primary source of funding for the running costs of this study. Dr Donna Cawthorn was funded by the Stellenbosch University and the Claude Leon Foundation post-doctoral fellowship. This work is based on the research supported by the South African Research Chairs Initiative of the Department of Science and Technology (DST) and National Research Foundation (NRF) of South Africa. Any opinion, finding and conclusion or recommendation expressed in this material is that of the authors and the NRF does not accept any liability in this regard. Gratitude is expressed to Mr. L.B. Fitzhenry (Stellenbosch University) for aiding with sample collection and to J. du Plessis (FACTS) for technical support.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.foodchem.2015.03.113.

References

Alvarado Bremer, J.R. (1994). *Assessment of morphological and genetic variation of the swordfish (Xiphias gladius Linnaeus): Evolutionary patterns of nucleotide substitution in the mitochondrial genome* (Ph.D. thesis). Canada: University of Toronto.

Ardura, A., Pola, I. G., Ginuino, I., Gomes, V., & Garcia-Vazquez, E. (2010). Application of barcoding to Amazonian commercial fish labelling. *Food Research International, 43*, 1549–1552.

Barbuto, M., Galimberti, A., Ferri, E., Labra, M., Malandra, R., Galli, P., et al. (2010). DNA barcoding reveals fraudulent substitutions in shark seafood products: The Italian case of "palombo" (*Mustelus* spp.). *Food Research International, 43*, 376–381.

Carvalho, D. C., Palhares, R. M., Drummond, M. G., & Frigo, T. B. (2015). DNA barcoding identification of commercialized seafood in South Brazil: A governmental regulatory forensic program. *Food Control, 50*, 784–788.

Cawthorn, D. M., Steinman, H. A., & Hoffman, L. C. (2013). A high incidence of species substitution and mislabelling detected in meat products sold in South Africa. *Food Control, 32*, 440–449.

Cawthorn, D. M., Steinman, H. A., & Witthuhn, R. C. (2011a). Establishment of a mitochondrial DNA sequence database for the identification of fish species commercially available in South Africa. *Molecular Ecology Resources, 11*, 979–991.

Cawthorn, D. M., Steinman, H. A., & Witthuhn, R. C. (2011b). Evaluating the availability of fish species on the South African market and the factors undermining sustainability and consumer choice. *Food Control, 22*, 1748–1759.

Cawthorn, D. M., Steinman, H. A., & Witthuhn, R. C. (2012a). DNA barcoding of the cytochrome *c* oxidase I (COI) gene reveals a high incidence of fish species misrepresentation and substitution on the South African market. *Food Research International, 46*, 30–40.

Cawthorn, D. M., Steinman, H. A., & Witthuhn, R. C. (2012b). Evaluation of the 16S and 12S rRNA genes as universal markers for the identification of commercial fish species in South Africa. *Gene, 491*, 40–48.

Costa, F. O., Landi, M., Martins, R., Costa, M. H., Costa, M. E., Carneiro, M., et al. (2012). A ranking system for reference libraries of DNA barcodes: Application to marine fish species from Portugal. *PLoS ONE, 7*, e35858.

DAFF (Department of Agriculture, Forestry and Fisheries) (2012). *Status of the South African marine fishery resources*. Available at <www.nda.agric.za/doadev/fisheries/indexpage_DOCS/STATUS%20REPORT%202012FINAL%20DRAFT.pdf>. Accessed 20.04.14.

D'Amato, M. E., Alechine, E., Cloete, K. W., Davison, S., & Corach, D. (2013). Where is the game? Wild meat products authentication in South Africa: A case study. *Investigative Genetics, 4*, 1–13.

Dawnay, N., Ogden, R., McEwing, R., Carvalho, G. R., & Thorpe, R. S. (2007). Validation of the barcoding gene COI for use in forensic genetic species identification. *Forensic Science International, 173*, 1–6.

DOH (Department of Health) (2010). Foodstuffs, Cosmetics and Disinfectants Act, 1972 (Act 54 of 1972), regulations relating to the labelling and advertising of foodstuffs (R. 146/2010). South African Government Gazette, 32975, 3–53.

DTI (Department of Trade and Industry) (2003). Compulsory Specification for frozen fish, frozen marine molluscs and frozen products derived therefrom, VC 8017:2003, Ed. 3 (R. 979/2003). South African Government Gazette, 25172, 3–50.

DTI (Department of Trade and Industry) (2009). Consumer Protection Act. Act no. 68 of 2008. R. 467/2009. South African Government Gazette, 32186, 1–186.

EC (European Commission) (2001). Commission Regulation (EC) No 2065/2001 of 22 October 2001 laying down detailed rules for the application of Council Regulation (EC) No 104/2000 as regards informing consumers about fishery and aquaculture products. *Official Journal of the European Communities, L278*, 6–8.

EC (European Commission) (2002). Regulation (EC) No 178/2002 of the European Parliament and of the council of 28 January 2002 laying down the general principles and requirements of food law, establishing the European Food Safety Authority and laying down procedures in matters of food safety. *Official Journal of the European Communities, L31*, 1–24.

Eden, S., Bear, C., & Walker, G. (2008). The sceptical consumer? Exploring views about food assurance. *Food Policy, 33*, 624–630.

FAO (Food and Agriculture Organization of the United Nations) (2013). *FAO yearbook of fishery and aquaculture statistics 2011*. Rome: FAO, pp. 9.

FDA (Food and Drug Administration) (2014). *The seafood list – FDA's guide to acceptable market names for seafood sold in interstate commerce*. Available at <www.fda.gov/food/guidanceregulation/guidancedocumentsregulatoryinformation/seafood/ucm113260.htm>. Accessed 21.03.14.

Filonzi, L., Chiesa, S., Vaghi, M., & Nonnis Marzano, F. (2010). Molecular barcoding reveals mislabelling of commercial fish products in Italy. *Food Research International, 43*, 1383–1388.

Froese, R. & Pauly, D. (2014). *FishBase: World Wide Web electronic publication, version 02/2014.* Available at <www.fishbase.org>. Accessed 21.03.14.

Gerson, H., Cudmore, B., Mandrak, N. E., Coote, L. D., Farr, K., & Baillergeon, G. (2008). Monitoring international wildlife trade with coded species data. *Conservation Biology, 22*, 4–7.

Griffiths, M. A., & Lamberth, S. J. (2002). Evaluating the marine recreational fishery in South Africa. In T. J. Pitcher & C. E. Hollingworth (Eds.), *Recreational fisheries: Ecological, economic and social evaluation* (pp. 227–251). Oxford: Blackwell Science Ltd..

Handy, S. M., Deeds, J. R., Ivanova, N. V., Hebert, P. D. N., Hanner, R. H., Ormos, A., et al. (2011). A single-laboratory validated method for the generation of DNA barcodes for the identification of fish for regulatory compliance. *Journal of AOAC International, 94*, 201–210.

Hanner, R. H., Becker, S., Ivanova, N. V., & Steinke, D. (2011). FISH-BOL and seafood identification: Geographically dispersed case studies reveal systemic market substitution across Canada. *Mitochondrial DNA, 22*, 106–122.

Hauck, M., & Kroese, M. (2006). Fisheries compliance in South Africa: A decade of challenges and reform, 1994–2004. *Marine Policy, 30*, 74–83.

Hebert, P. D. N., Cywinska, A., & Ball, S. L. (2003). Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London B: Biological Sciences, 270*, 313–321.

Hebert, P. D. N., Ratnasingham, S., & deWaard, J. R. (2003). Barcoding animal life: Cytochrome c oxidase subunit I divergences among closely related species. *Proceedings of the Royal Society B, 270*, S96–S99.

Helyar, S. J., Lloyd, H. A. D., de Bruyn, M., Leake, J., Bennett, N., & Carvalho, G. R. (2014). Fish product mislabelling: Failings of traceability in the production chain and implications for Illegal, Unreported and Unregulated (IUU) fishing. *PLoS ONE, 9*(6), e98691.

Ivanova, N. V., Zemlak, T. S., Hanner, R., & Hebert, P. D. N. (2007). Universal primer cocktails for fish DNA barcoding. *Molecular Ecology Notes, 7*, 544–548.

Joseph, N. (April 27, 2009). Fishy behaviour at restaurants. IOL News.

Lamendin, R., Miller, K., & Ward, R. D. (2015). Labelling accuracy in Tasmanian seafood: An investigation using DNA barcoding. *Food Control, 47*, 436–443.

Logan, C. A., Alter, S. E., Haupt, A. J., Tomalty, K., & Palumbi, S. R. (2008). An impediment to consumer choice: Overfished species are sold as Pacific red snapper. *Biological Conservation, 141*, 1591–1599.

Messing, J. (1983). New M13 vectors for cloning. *Methods in Enzymology, 101*, 20–78.

Nicolè, S., Negrisolo, E., Eccher, G., Mantovani, R., Patarnello, T., Erickson, D. L., et al. (2012). DNA barcoding as a reliable method for the authentication of commercial seafood products. *Food Technology and Biotechnology, 50*, 387–398.

Pedrosa-Gerasmio, I. R., Babaran, R. P., & Santos, M. D. (2012). Discrimination of juvenile yellowfin (*Thunnus albacares*) and bigeye (*T. obesus*) tunas using mitochondrial DNA control region and liver morphology. *PLoS ONE, 7*, e35604.

Premanandh, J. (2013). Horse meat scandal – A wake-up call for regulatory authorities. *Food Control, 34*, 568–569.

Ratnasingham, S., & Hebert, P. D. N. (2007). The barcode of life database. *Molecular Ecology Notes, 7*, 355–364.

Rubinoff, D., Cameron, S., & Will, K. (2006). A genomic perspective on the shortcomings of mitochondrial DNA for "barcoding" identification. *Journal of Heredity, 97*, 581–594.

Sharma, K., & Paradakar, M. (2010). The melamine adulteration scandal. *Food Security, 2*, 97–107.

Smith, J. L.B., & Smith, M.M. (1966). *Fishes of the Tsitsikamma Coastal National Park*. South Africa: National Parks Board Trust. pp. 102

Smith, J.L.B., Smith, M.M., & Heemstra, P.C. (2003). *Smiths' sea fishes*. South Africa: Struik Publishers. p. 1047

Steinke, D., Zemlak, T. S., Hebert, P. D. N., & Adamowicz, S. A. (2009). DNA barcoding of Pacific Canada's fishes. *Marine Biology, 156*, 2641–2647.

Van der Elst, R. (2000). *A guide to common sea fishes of Southern Africa*. South Africa: Struik Publishers. pp. 1–398.

Vaz-dos-Santos, A. M., Rossi-Wongtschowski, C. L. D. B., & Figueiredo, J. L. D. (2009). *Merluccius hubbsi* (Teleostei: Merlucciidae): Stock identification based on reproductive biology in the south-southeast Brazilian region. *Brazilian Journal of Oceanography, 57*, 17–31.

Viñas, J., & Tudela, S. (2009). A validated methodology for genetic identification of tuna species (genus *Thunnus*). *PLoS ONE, 4*, e7606.

Von der Heyden, S., Barendse, J., Seebregts, A. J., & Matthee, C. A. (2010). Misleading the masses: Detection of mislabelled and substituted frozen fish products in South Africa. *ICES Journal of Marine Science, 67*, 176–185.

Ward, R. D. (2009). DNA barcode divergence among species and genera of birds and fishes. *Molecular Ecology Resources, 9*, 1077–1085.

Ward, R. D., Hanner, R., & Hebert, P. D. (2009). The campaign to DNA barcode all fishes, FISH-BOL. *Journal of Fish Biology, 74*, 329–356.

Ward, R. D., Zemlak, T. S., Innes, B. H., Last, P. R., & Hebert, P. D. N. (2005). DNA barcoding Australia's fish species. *Philosophical Transactions of the Royal Society B, 360*, 1847–1857.

Warner, K., Walker Timme, B. L., & Hirshfield, M. (2013). *Oceana Study Reveals Seafood Fraud Nationwide*. Available at <http://oceana.org/en>. Accessed 28.11.14.

Wong, H. K., & Hanner, R. H. (2008). DNA barcoding detects market substitution in North American seafood. *Food Research International, 41*, 828–837.

Yeld, J. (December 6, 2012). Are you getting the fish you're paying for? The Star.