

Fish identification tools for biodiversity and fisheries assessments

Review and guidance for decision-makers



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Mosaic by Johanne Fischer

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Edited by

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Preparation of this document

This document is a result of the contributions and deliberations of the workshop “Fish Identification Tools for Biodiversity and Fisheries Assessments” (Vigo, Spain, 11–13 October 2011) convened by the University of Vigo and the FAO FishFinder Programme. Although not a “Proceedings” as such, it does reflect the presentations and discussions of participants regarding user perspectives and user requirements, definition of criteria for the characterization of identification tools, description of identification tools and scenarios as well as recommendations for research and development. However, it also contains observations and summaries added after the workshop with the intent to make this document more accessible to the reader. A draft version of this document was circulated to workshop participants, and this finalized version incorporates substantive comments and corrections received from them.

The workshop participants consisted of 15 invited experts from 10 countries, two FAO officers and one FAO consultant. The first part of the workshop was dedicated to 14 plenary presentations on fish identification methods and tools. The workshop then proceeded to provide definitions for the criteria used to characterize each identification tool addressed by the workshop. Each expert reviewed the summary description and visual characterization of the ID tools prepared by FAO and the workshop then evaluated the results in a non-comparative manner. It was agreed that the visual characterization would serve as an approximate qualitative indication of the strengths and weaknesses of each method. After the workshop, a comparative review was undertaken by the editor and some adjustments were made to the figures.

The subsequent development and description of relevant scenarios took place in three subgroups: one focusing on research and development, the second on conservation, responsible use and trade, and the third on education, awareness building, consumer considerations and non-consumptive uses. The scenarios were intended to illustrate a variety of user requirements for species identification and recommending appropriate identification tools for each of these scenarios. The workshop concluded with a statement containing a number of recommendations by workshop participants.

The papers contained in Annex 3 to this work have been reproduced as submitted by the participants, without editorial intervention by FAO.

Abstract

This review provides an appraisal of existing, state-of-the-art fish identification (ID) tools (including some in the initial stages of their development) and shows their potential for providing the right solution in different real-life situations. The ID tools reviewed are: Use of scientific experts (taxonomists) and folk local experts, taxonomic reference collections, image recognition systems, field guides based on dichotomous keys; interactive electronic keys (e.g. IPOFIS), morphometrics (e.g. IPez), scale and otolith morphology, genetic methods (Single nucleotide polymorphisms [SNPs] and Barcode [BOL]) and Hydroacoustics.

The review is based on the results and recommendations of the workshop “Fish Identification Tools for Fishery Biodiversity and Fisheries Assessments”, convened by FAO FishFinder and the University of Vigo and held in Vigo, Spain, from 11 to 13 October 2011. It is expected that it will help fisheries managers, environmental administrators and other end users to select the best available species identification tools for their purposes.

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Abbreviations and acronyms

AIS	aquatic invasive species
BMU	Beach Management Unit (Kenya)
CBD	Convention on Biological Diversity
CBD-GTI	CBD-Global Taxonomy Initiative
CITES	Convention on International Trade in Endangered Species of Wild Fauna and Flora
CoF	Catalog of Fishes
CoL	Catalogue of Life
FCO	fisheries control officer
GM	genetically modified
ID	identification (tool)
IEK	interactive electronic key
IPOFIS	integrated photo-based online fish-identification system
IRS	image recognition system
IUU	illegal, unregulated and unreported (fishing)
NGO	non-governmental organization
RFMO	regional fisheries management organization
SNP	single nucleotide polymorphism
UNEP-WCMC	United Nations Environment Programme – World Conservation Monitoring Centre
WoRMS	World Register of Marine Species

Recommendations

At the conclusion of the workshop “Fish Identification Tools for Biodiversity and Fisheries Assessment”, held in Vigo, Spain, from 11 to 13 October 2011, the participants prepared the following statement and recommendations.

In recent decades, biodiversity research has been prioritized and new fish identification techniques have been developed. However, the actual transfer and application of fish identification technologies in projects and management schemes has lagged. It is an important objective of the present document to encourage and promote the informed use of appropriate identification techniques in all areas, specifically:

- Take initiatives to strengthen the links and enhance communication between scientists, stakeholders and end users.
- Strengthen the taxonomic community through additional training opportunities, the creation of jobs for taxonomists, research funding and infrastructure to ensure the stability of nomenclature and development of reliable diagnostic data sets.
- Strengthen the fish identification expertise of officers and others who need to identify fish in the execution of their jobs in order to ensure that the identification is authoritative and current.
- Develop more local, scientifically reviewed and curated reference collections of fish specimens (in fishery agencies, institutes) and encourage their use.
- Develop more local, scientifically reviewed and curated fish photographic reference collections (in fishery agencies, institutes) and encourage their use.
- Encourage users to assist in the population of reference databases.
- Promote the appropriate use of fish identification techniques by publicizing the range of techniques available to address diverse fishery and biodiversity questions (promote the right tool for the job).
- Encourage collaboration and increased integration of methodological approaches used by taxonomists and other scientists to increase accuracy, repeatability and the creation of enhanced tools.
- Improve access to fish identification tools.
- Make available more open-access fish identification tools or tools in the public domain.
- Create central repositories of metadata (e.g. web-links, experts) and/or clearing houses.
- Develop and improve identification tools for early life history stages of aquatic organisms.
- Strengthen the development of new and user-friendly fish identification tools through improved investment.
- Develop legally binding standards and guidelines for fish identification for fishery compliance purposes.
- Make available primary data (such as barcodes and images) that support development and maintenance of automatic and semi-automatic identification tools for improved cost-effectiveness.

- Ensure that scientific documents report on the species identification methods the authors have used.
- Increase awareness among the public and policy-makers of the importance of accurate fish identification through the use of user-friendly media and advocacy.
- Identify and address gaps in information for the identification of aquatic species.

1. Introduction

The current review intends to provide an overview of existing, state-of-the-art fish identification (ID) tools (including those in the initial stages of their development) and to show their potential for providing the right solution in different real-life situations. The content of this review is based on the results and recommendations of the workshop “Fish Identification Tools for Fishery Biodiversity and Fisheries Assessments”, convened by FAO and the University of Vigo and held in Vigo, Spain, from 11 to 13 October 2011. It is expected that the review will help fisheries managers, environmental administrators and other end users to select the best available species identification tools for their purposes. The experts involved in this review also hope that it will help renew public interest in taxonomy and promote the need for taxonomic research including user-friendly species ID tools.

Although the need for taxonomic expertise has never been as pronounced as it is today, this has not translated into training more taxonomists and providing more funding for necessary developments in taxonomy. Instead, more and more individuals without a taxonomic background, such as fishery inspectors and observers, customs officers, data collectors, traders and others, have been tasked with the complex and often difficult assignment of identifying aquatic species. These less-experienced users are often faced with confusing and inadequate information on the species they encounter and how to identify them reliably. Products such as the species catalogues and field guides produced by the FAO FishFinder Programme can help in countries and regions for which they exist, and web resources, such as FishBase¹ and the Catalog of Fishes² offer guidance to resolve issues regarding the correct scientific name for a species. Nonetheless, greater efforts are needed to ensure a correct identification of aquatic resources under management and conservation regimes.

In recent decades, many new and promising techniques for the identification of fishes have emerged, in particular based on genetics, interactive computer software, image recognition, hydroacoustics and morphometrics. However, with few exceptions, such advances in academic research have not yet been translated into user-friendly applications for non-specialists and still require further investments to mature into globally applicable tools.

Public consciousness about the need to conserve biodiversity has recently been growing. In all parts of the world, policy-makers, funding agencies and scientists have made it a priority to advance policies and knowledge for this purpose. This interest was prompted by the realization that taxonomic resources around the world are declining at a rapid pace and that this is having a negative impact on human well-being and survival.

The Census of Marine Life³ has just finished an ambitious and large-scale ten-year project that includes an inventory of aquatic species. A number of large national and international funding organizations (Convention on Biological Diversity [CBD],⁴ DIVERSITAS⁵, European Environment Agency,⁶ European Commission,⁷ Global Biodiversity Information Facility,⁸ Global Ocean Observing

¹ www.fishbase.org/search.php

² <http://researcharchive.calacademy.org/research/ichthyology/catalog/collections.asp>

³ www.coml.org/

⁴ www.cbd.int/

⁵ www.diversitas-international.org/

⁶ www.eea.europa.eu/

⁷ http://ec.europa.eu/index_en.htm

⁸ www.gbif.org

System,⁹ Intergovernmental Platform on Biodiversity and Ecosystem Services,¹⁰ International Union for Conservation of Nature,¹¹ United Nations Environment Programme – World Conservation Monitoring Centre [UNEP-WCMC]¹² and many others) are currently supporting broad worldwide attempts to summarize all knowledge on aquatic organisms and provide global species inventories (All Catfish Species Inventory,¹³ Continuous Planktonic Recorder project,¹⁴ UNEP-WCMC Species Database,¹⁵ Fish Barcode of Life Initiative¹⁶ and Marine Biodiversity and Ecosystem Functioning EU Network of Excellence¹⁷ among many others). The FAO Commission on Genetic Resources for Food and Agriculture¹⁸ has been mandated to cover all components of genetic resources relevant to food and agriculture, and it is now preparing a global review of aquatic resources.

The CBD uses the following definition: “‘Biological diversity’ means the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems”.¹⁹ This definition clarifies that biological diversity does not only apply to the number of species in an ecosystem but also considers the difference between subspecies, populations and other meaningful units below the species level.

The CBD-Global Taxonomy Initiative (CBD-GTI)²⁰ recognizes a “taxonomic impediment” to the sound management of biodiversity consisting in “the knowledge gaps in our taxonomic system (including those associated with genetic systems), the shortage of trained taxonomists and curators, and the impact these deficiencies have on our ability to conserve, use and share the benefits of our biological diversity”. The CBD-GTI also states that “simple-to-use identification guides for the non-taxonomist are rare and available for relatively few taxonomic groups and geographic areas. Taxonomic information is often in formats and languages that are not suitable or accessible in countries of origin, as specimens from developing countries are often studied in industrialized nations. There are millions of species still undescribed and there are far too few taxonomists to do the job, especially in biodiversity-rich but economically poorer countries. Most taxonomists work in industrialized countries, which typically have less diverse biota than in more tropical developing countries. Collection institutions in industrialized countries also hold most specimens from these developing countries, as well as associated taxonomic information.”²¹

It has become clear that taxonomic information is not a luxury – it is a real need in a world with a still-growing human population generating enormous pressure on natural resources. More and more organisms are shipped around the world and marketed continents away from their origins, thus generating an increased need for global fish identification tools to provide reliable information to consumers, customs officers and fishery inspectors. However, worldwide, there exist more

⁹ www.ioc-goos.org/

¹⁰ www.ipbes.net/

¹¹ www.iucn.org/

¹² www.unep-wcmc.org/

¹³ <http://silurus.ansp.org/>

¹⁴ www.sahfos.ac.uk/

¹⁵ www.unep-wcmc-apps.org/isdb/Taxonomy/

¹⁶ www.fishbol.org/index.php

¹⁷ www.marbef.org/

¹⁸ www.fao.org/nr/cgrfa/en/

¹⁹ CBD, Article 2. Use of Terms.

²⁰ www.cbd.int/gti/

²¹ www.cbd.int/gti/problem.shtml

than 32 500 species of finfishes²² and the amount of information required to separate them all is extremely difficult to process; therefore, fish identification is usually conducted at local or regional scales. The increasing globalization of fishery products thus introduces new challenges to the identification of aquatic organisms. In addition, new emerging applications require accurate species identification (e.g. marine hydrokinetic energy and ocean observatories).

The collection of species- and population-specific information for the purpose of sustainable fishery management has a long tradition. For many decades, FAO has been collecting global statistical catch data and analysing the results in two of its flagship publications: (i) *The State of World Fisheries and Aquaculture* and the *Review of the state of world marine fishery resources*. While progress has been made in the reporting of fishery data, much improvement is still needed for a more reliable and comprehensive assessment of the stock status of many commercially exploited aquatic species. Not only the taxonomic resolution of catch data could be better for many areas and species, but there is a real concern about the proportion of possible misidentifications in the catch statistics received by FAO, with severe implications for the ability to manage aquatic organisms sustainably. With its FishFinder Programme,²³ FAO has contributed to improving fish identification everywhere and produced more than 200 species identification guides including taxonomic descriptions for more than 8 000 species and an archive of more than 40 000 scientific illustrations. Although the programme struggles owing to funding constraints and competing priorities at FAO, it continues generating products to assist with fish identification in many parts of the world, including the guidance provided in this publication.

²² The cumulative species description curve for fishes is not yet close to its asymptote and, hence, the number of species will continue to increase.

²³ www.fao.org/fishery/fishfinder/en

2. User perspectives

User considerations provide the background and scope against which the different species ID tools are evaluated. The following summaries describe the user requirements from three different perspectives.²⁴ The first introduces the views of a taxonomist and ichthyologist, the second illustrates the difficulties and urgent needs for correct species identification experienced by a fisheries control officer on the high seas, and the third explains requirements of the fishing industry and consumers for non-ambiguous species identification and labelling. Notwithstanding the pronounced differences of these three perspectives, they are unified in their conviction that improving the identification of aquatic species will have considerable positive impacts for biodiversity research, fisheries management and law enforcement as well as trade and consumer safety.

2.1 FISH TAXONOMY IN BIODIVERSITY AND FISHERY ASSESSMENT AND MANAGEMENT

A stable naming and indexing system is essential to global communication about organisms, and such a system is maintained by the International Code of Zoological Nomenclature. The science of taxonomy, among other things, provides the methods and the manuals for the identification of organisms. Although largely based on observations of characters that local fishers may also use, taxonomic research offers the tools for a regionally and globally valid identification. Some examples of fundamental taxonomic tools for the use in fisheries include FishBase²⁵, the book *Fishes of the North-eastern Atlantic and the Mediterranean*²⁶ and a series of catalogues and regional checklists provided by FAO.²⁷ Although surveying, mapping, taxonomic characterization, and naming of the global marine and freshwater fish fauna are fundamental to a healthy fishery, the importance of taxonomic work is not fully recognized in the fisheries sector, particularly not in the boreal regions where “everything is known”. However, a lack of pertinent taxonomic information or lack of user experience can actually or potentially lead to undesired consequences for fishery management, and fish taxonomists are urgently needed to provide reliable name standards and identification tools for fishery purposes.

In many regions of the world, fish stocks are being exploited without much taxonomic assistance. However, it is impossible to develop conservation plans and long-term management without knowing what species are involved, and preferably also whether subpopulations exist, and how to identify them. Important faunal guides have been published by South Africa, Japan and Australia, but in these regions new species continue to be discovered, both from fresh material and from old museum specimens.

Taxonomic resources may also play a role in prospecting for new resources as is done particularly in aquaculture. Involving taxonomists in aquaculture is always recommended in order to prevent expensive errors based on the erroneous identification of species, e.g. to avoid a “new” species being imported to locations where it (or a very similar form) already exists but is known under an incorrect name.

²⁴ See Annex 3 for full papers submitted by workshop participants.

²⁵ Froese, R. & Pauly, D., eds. 2013. *FishBase* [online]. [Cited 19 June 2013]. www.fishbase.org

²⁶ Whitehead, P.J.P., Bauchot, M.-L., Hureau, J.-C., Nielsen, J. & Tortonese, E., eds. 1984–86. *Fishes of the North-eastern Atlantic and the Mediterranean*. Paris, UNESCO.

²⁷ See www.fao.org/fishery/fishfinder/publications/en

A mistaken identification, the use of outdated names, or the application of misleading names can have considerable economic consequences; therefore, trust and reliability are essential attributes for taxonomic experts and taxonomic tools. However, taxonomy is often practised by people without the necessary training, not least persons only interested in naming new species. Ideally, a taxonomic expert should hold a PhD in systematic biology including training in nomenclature and alpha taxonomy and should have considerable prior experience with the species group in question.

Many users of taxonomic services consider a photograph sufficient to work on. That may sometimes be true, but it may also turn out to be a bad cornerstone in an operation involving considerable sums of money. Specimen and DNA samples should be adequate for the level of precision required for the identification, and that usually entails more than a snapshot taken on a rocking ship.

In conclusion, taxonomy is paramount for describing biodiversity but it is underfunded. Precise identification of species and populations can be effected by several tools, and this is necessary for fishery management plans and reporting.

2.2 A FISHERY INSPECTOR'S VIEW OF FISH IDENTIFICATION

Fisheries enforcement around the world is unique to its own area of operations. The task faced by a fisheries control officer (FCO) is a mammoth one. Therefore, FCOs will develop their skills in accordance with the fishing activities of their respective countries. Some of the duties that FCOs are responsible for are as follows:

- monitoring and recording fish landings in commercial and fishing harbours;
- monitoring slipways where recreational boats land their catches;
- conducting coastal patrols (land patrols on foot or by vehicle);
- conducting aerial patrols;
- conducting fisheries patrols at sea by means of inshore and offshore patrol vessels;
- effecting arrests of illegal, unregulated and unreported (IUU) fishers and fishing vessels;
- collating evidence;
- identifying fish;
- testifying in court;
- obtaining statements from expert witnesses such as scientists in areas of fish identification;
- assisting investigators with cases;
- ensuring continuous follow-up on the outcomes of their respective cases.

In order for an FCO to ensure effective enforcement of fisheries regulations, it is essential for the FCO to have an understanding of fish identification. Fish identification is important in fisheries enforcement, and the ability to identify fish is of critical importance as it will assist in strengthening the case of the FCO against the accused.

However, there exists a lack of training in the field of fish identification for FCOs, and many FCOs do not possess this skill. The lack of the necessary tools and experience in the field of fish identification is a crucial factor that needs to be addressed.

2.3 IDENTIFICATION AND COMMERCIAL NAMES OF FISHERY PRODUCTS: A VIEW FROM THE INDUSTRY

Today, the correct identification of fish species and their precise, updated and taxonomic ordering are the basis for the bulk of the international fish trade. Proper and sufficient consumer information about products and prevention of fraud, wrongdoing or deceit will lead to a larger market trust and stimulate development. In most countries where the market for fish products has evolved more – the European Union (Member Organization), the United States of America, Australia and Japan – there are legal regulations covering these points. How detailed or specific should this information be? Is it problematic to group some species for commercial purposes and thus not allow consumers to distinguish the products by species? The answers depend on the customs and culture as well as on the technical and operational conditions in different countries. In particular, one should consider the following aspects when contemplating species identification for fishery products: commercial and operational, legislative, taxonomical and technical.

The commercial and operational aspects will take into account the cultural tradition of each country or region that influences the way fish species are perceived. These aspects must also consider the type of fisheries, i.e. small-scale fisheries with small volumes of catch and large industrial fisheries landing tens of thousands of tonnes of fish. What should be done in the case of mixed-species catches that are difficult to separate? Another difficulty consists in the fact that about 50 percent of the catches are traded under the form of fillets, portions and elaborated product. However, legislation in the European Union (Member Organization) currently applies only to non-processed fish and not to elaborated fish products, a situation that may be amended by the current review of the Common Marketing Organization.

At present the use of scientific fish species names is not legally prescribed. Therefore, different countries can use different official names for the same species. The denomination of genera and their species is not harmonized either. Different States can legally designate a common commercial name for a specific genus and afterwards they may separately develop specific names for the different species pertaining to this genus. However, the names might not be complete for all species under one genus and might not apply to all countries in which the genus in question occurs. In the texts currently under discussion at the European Commission, mention is made of FishBase as an official source for the consideration of the scientific names;²⁸ but this does not address invertebrates. Therefore, the agreed recognition of a unique international taxonomic reference system is required for the establishment of criteria and recommendations regarding the use of synonyms and new classifications.

As for the technical aspects concerning the identification of species, simple highly operational tools for non-experts would be desirable, in particular for work conditions on-site and preferably close to the catch and origin of the species. In addition, tools are needed to allow a quick, reliable and economic identification of highly processed fishery products at markets. Such tools would be used to check and verify the correct labelling of the product both by commercial agents and the local authorities. The necessary mechanisms must be developed to guarantee the integrity of the information throughout the product chain.

In conclusion, the fisheries industry is highly interested in the international harmonization of species-naming conventions, in the easy identification of species at the catch site (origin) and in the correct species identification of processed fish in markets.

²⁸ The Catalog of Fishes (<http://research.calacademy.org/ichthyology/catalog>), run by William Eschmeyer, is an equally authoritative source for taxonomically correct fish names.

3. Species identification tools

3.1 SPECIES ID TOOLS INCLUDED IN THIS REVIEW

This review covers most methods that are currently used for the identification of aquatic species. They include traditional, long-trusted and tested tools, such as the use of trained taxonomists, reference collections or field guides based on dichotomous keys, as well as more recently developed tools, some of which are still in the experimental stage, e.g. image recognition systems (IRSs), interactive electronic keys, computer-based morphometric identification (IPez) and genetic methods. In addition, the use of local (folk) expertise, scales, otoliths and hydroacoustics are reviewed. A few methods are not assessed in detail as they are either too generic, e.g. identification of fishes by browsing images (using the web), or because they are of limited application, e.g. the use of bones, animal sounds or electric signals (Table 1).

TABLE 1.

Species identification tools considered by workshop participants

CATEGORY	METHODS REVIEWED BY WORKSHOP	METHODS NOT REVIEWED BY WORKSHOP
WHOLE ORGANISMS		
Expert authority	<ul style="list-style-type: none"> • Scientific expert (taxonomist) onsite • Folk local experts 	
Images/specimen only	<ul style="list-style-type: none"> • Local reference collections • Image recognition systems 	Image browsing (addressed under web tools)
Identification keys, text- and/or image-based	<ul style="list-style-type: none"> • Field guides based on dichotomous keys: printed or electronic products; may use text or images for characters and taxa • Interactive electronic keys, e.g. IPOFIS • Polythetic keys; morphometrics, e.g. IPez 	
BODY PARTS		
Anatomy	<ul style="list-style-type: none"> • Scales • Otoliths 	Bones (addressed under web tools)
Genetics	<ul style="list-style-type: none"> • With SNPs • With BOL 	
EXTRINSIC AND OTHER ATTRIBUTES		
Acoustics	<ul style="list-style-type: none"> • Hydroacoustics 	Sounds produced by organisms
Electrics		Electric signals ^{Note}

^{Note} Some finfishes produce species-specific electric signals for communication or for orientation in turbid waters. These can be used for species identification (e.g. *Arnegard & Hopkins. 2003. Electric signal variation among seven blunt-snouted Brienomyrus species [Teleostei: Mormyridae] from a riverine species flock in Gabon. Central Africa Environmental Biology of Fishes 67: 321-339*).

3.2 CRITERIA FOR THE EVALUATION OF SPECIES IDENTIFICATION TOOLS

Each of the 12 species ID tools included in this review is evaluated using the ten criteria described in Table 2. A definition for each criterion is provided along with quantitative or qualitative benchmarks for a “low” or “high” expression. This forms the basis for the visual characterization of the ID tools in chapter 3.3 which consists in the depiction of “low” to “high” ranges for each criterion resulting in a unique visual pattern of criteria expressions for each ID tool and allowing their systematic comparison.

TABLE 2.
Criteria for the evaluation of species ID tools

CRITERION	DEFINITION	Low	High
EXPERTISE	Knowledge, training and experience required by the user (operator) to apply the method	No specialized or scientific knowledge	Advanced science degree
COSTS	Funds and equipment required to use the method	Hundreds USD (mid-level = thousands USD)	Hundreds of thousands USD
TIME	Response time (for obtaining an identification)	Minutes	Months
ACCURACY	Probability of correct identifications	50%	100%
RESOLUTION	Ability to assign a specimen/sample to a certain taxon (usually to species, genus, family), or to a given, well-determined group (population/stock/strain), or identifying the actual parents or even the individual (in exceptional cases). IMPORTANT: If the identification can only be done on a family/genus level, the number of species contained in the family/genus should be given)	Family	Populations and, in some cases, individuals ¹²
USABILITY	Ease of use and learnability; preparatory time and effort, handling	Very poor	Very good
REPRODUCIBILITY	Probability to deliver the same result if applied by different people and/or at different times	0%	100%
APPEAL	The ability to attract users and funds. This can comprise ethical and aesthetic considerations, perceived confidence	Low	High
RESEARCH AND DEVELOPMENT (R&D)	State of development of the tool and derived products including their availability and transferability, i.e. application in different geographical regions, ecosystems and for different species groups	At initial development state and/or only applicable to a few species/ regions	Fully established and globally accessible

3.3 EVALUATION OF SPECIES IDENTIFICATION TOOLS

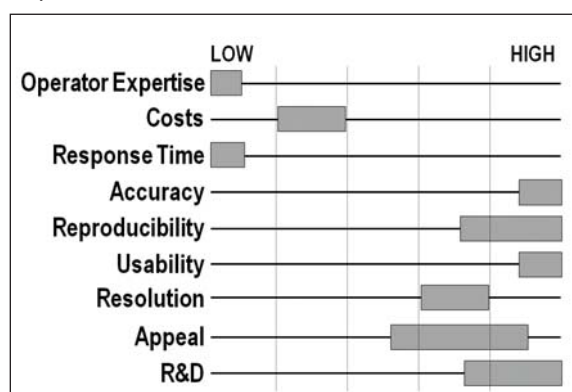
The following summary descriptions are based on material submitted by the experts and were reviewed during and after the workshop. The methods presented here are described in more detail in Annex 3.

3.3.1 On-site taxonomist

Trained taxonomists, preferably with a PhD in systematic biology and postdoctoral experience, are familiar with a large number of species and have specialist competence in a special group (e.g. a family or a fauna). They know about nomenclatural rules and morphometric methods for species identification and have a high awareness of the level of accuracy of their identifications. Moreover, they usually identify species relatively quickly. There may be conceptual differences between individual taxonomists that could lead to limited repeatability of certain identifications, but the accuracy should still be high. Taxonomists are most helpful with fresh or preserved whole specimens.

Characterization of the method – user perspective

FIGURE 1.
Depiction of the ID Tool “taxonomist”



Expert decisions by taxonomists on-site are ready-to-use and require no further expertise to employ. Usually, a consultancy or salary cost applies. The time needed for species identification can be expected to be very brief in most situations with a very high level of accuracy. The reproducibility will be 100 percent with the same taxonomist and close to that if a second taxonomist is consulted. The transferability has limitations as a taxonomist

may be more or less specialized in a certain taxonomic group or geographical area. The use of a taxonomist is very user friendly and only requires enabling access to the fish to be identified. The resolution level should not be expected to go beyond the species level, and, in some cases, it could be limited to the identification of a small group of similar species, depending on how well known the targeted fauna is. The appeal of hiring a taxonomist should be high where such experts are readily available and considering the capacity-building/training abilities of the taxonomist (in particular in areas where expertise in species identification is lacking). Taxonomy is an established science, and further development is limited to options for improving methods of assessing diagnostic characters, e.g. complementing the taxonomist with low-resolution microscopes and such. However, there is a severe lack of taxonomists in many regions limiting the access to this ID tool.

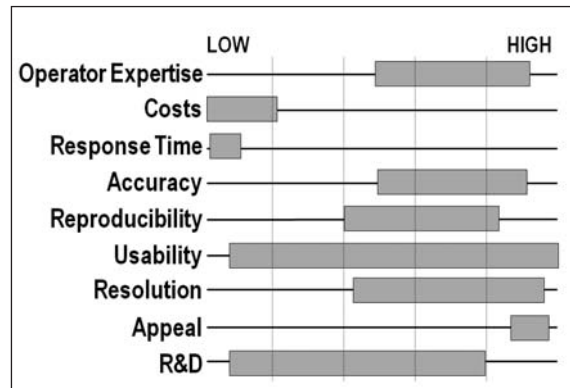
3.3.2 ID-tool: Local (folk) expert

Folk taxonomies are systems of categorization created by non-scientists in order to organize, name, and understand the natural world. Folk taxonomies frequently diverge on some points from the phylogeny established by the scientific study of taxonomy but they also tend to align with scientific classifications on other points. Sometimes, folk taxonomies lump together many biological species under a single name, or place species from several different biological orders in the same group,

sometimes there is one-to-one correspondence, and sometimes folk taxonomies differentiate where scientific taxonomies do not. Differentiation between types in folk taxonomies is determined by a wide variety of attributes, some of which may not be immediately obvious to outsiders; morphology and behaviour are important but so are the cultural significance and practical utility of the species constituting each group.²⁹

Characterization of the method – user perspective

FIGURE 2.
Depiction of the ID Tool “local expert”



Because folk taxonomies do not follow scientifically established norms and classification, their use requires a high level of expertise by the person or team making use of fishers' knowledge, in particular if the folk taxonomy in question has not been studied. In addition, the correct selection of cooperating resource users is crucial. The costs for this approach are relatively low and include mainly compensation of the folk experts. Good results can be achieved in a

short time (hours to days) provided that the folk taxonomy of the location in question is sufficiently known. While the resolution of the fish identification by folk taxonomists tends to vary (at population level for some, and at group level for others), their accuracy can be high, in particular regarding the organisms they are most familiar with (e.g. target species and those that stand out because of colour, size or form). The usability of this method is very high for most geographic locations in which the folk taxonomy has been studied and where the local experts are willing to collaborate. The likelihood of exactly reproducing the species identifications using this approach may vary depending on the expertise of individual resource users and on the proficiency of the person or team collecting the information from resource users. Using resource users' knowledge is very appealing, not only because of the relatively low costs and time requirements but also because it fosters participatory approaches and can yield much relevant information on fisheries beyond the identification of fish. The approach has been extensively described in scientific literature, but much research is still outstanding relating to the systematic study of the folk taxonomy of many locations.

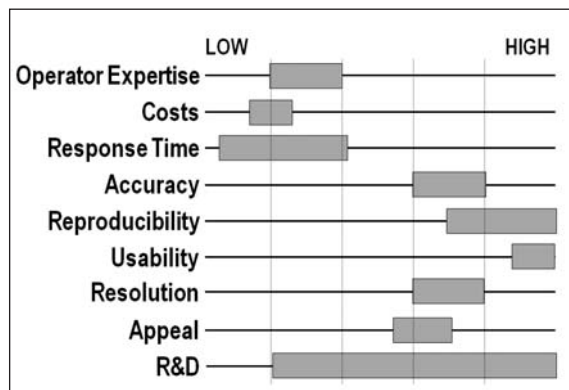
3.3.3 Local reference collection

Reference collections consist of preserved specimens of whole fish, otoliths, disarticulated bones, scales, pharyngeal bones, or similar body parts used in identification work. Local reference collections are mainly found in research institutions (and fisheries agencies) and are dedicated to a restricted geographical area (or a special purpose research). Local reference collections may be a sufficient tool for identification work in a restricted area and reduce the need for expert consultancy, keys, field guides and other methods. They are especially useful for smaller institutions in field-like situations and can be used also for continuous training of new staff.

²⁹ This paragraph is based on http://en.citizendium.org/wiki/Folk_taxonomy (accessed 19 June 2013)

Characterization of the method – user perspective

FIGURE 3.
Depiction of the ID Tool “local reference collection”



Reference specimens in local collections are ready-for-use and can be compared directly with the organism for which identification is needed to yield a result. The expertise required is relatively low and only a limited amount of introductory training usually is sufficient for an operator. No costs are incurred other than those necessary for the maintenance of the collection. The time needed for identifying a species may vary depending on the size of the collection and the amount of similar species in the area; however, normally, it should not exceed one day. Transferability is limited because the fauna will differ between geographic regions and the local collection usually only contains the fauna of the relevant geographical area. Local reference collections are typically housed in the area and the identification work is simple; therefore, it usually takes only a relatively short response time. The tool is characterized by its immediate usability as well as a potentially high level of accuracy and reproducibility. The resolution can be expected at species level. The ease of use, the involvement of local staff in maintaining the collection as well as the dispensability of complex tools makes it appealing. However, due to a lack of local reference collections in many parts of the world this tool is not widely available.

3.3.4 Image recognition system

In this method, the user provides a photograph (image) of the fish as input and a software (IRS) identifies the fish to a taxonomic level. The identification process is based on the automatic characterization of image visual properties (e.g. colour, texture and shape) using computer vision techniques, i.e. image retrieval and/or classification approaches that exploit feature vectors and similarity functions. Image processing methods are used to encode visual properties into feature vectors, and similarity functions are used to compute the similarity of two images by taking into account their feature vectors.

Characterization of the method – user perspective

FIGURE 4.
Depiction of the ID Tool “image recognition system”

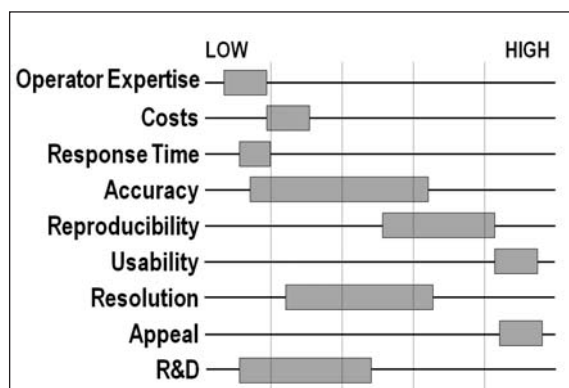


Image recognition systems allow an automatic identification of a fish to a taxonomic level. A limited amount of training may be needed for introduction to the method. It should take very little effort to achieve the desired identifications, meaning a high and immediate usability and the highest possible level of reproducibility. The cost is limited to the acquisition of appropriate computer hardware (maybe a portable device) and software for

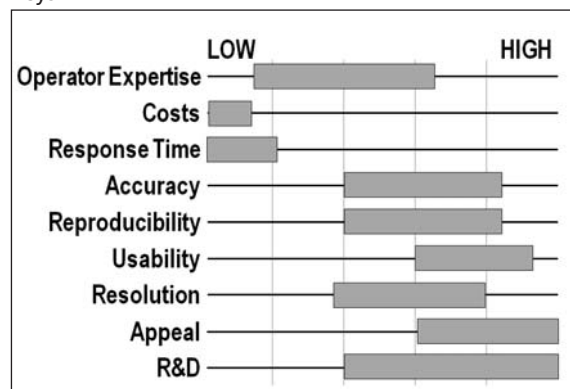
the use of the IRS. The time needed for species identification may vary with the size of the image data set but should normally not exceed one minute. However, the transferability and resolution are somewhat limited because the fauna will differ between geographic regions, and, therefore, the characterization of fish image properties (e.g. colour, texture and shape) may vary for the same species from different regions. In this sense, development needs are high. Much research is also still required on image processing and machine learning to broaden the scope of use and the accuracy of this identification method. The appeal of IRSs is high in terms of attracting both users and funding. With the rapid evolution of portable devices (e.g. tablet computers) the development, dissemination and use of computer-based fish identification tools is becoming increasingly relevant.

3.3.5 Field guides based on dichotomous keys

Diagnostic taxonomic keys are a common traditional means to identify organisms, and they form an important part of most field guides. A taxonomic key is an ordered sequence of alternative choices, as provided by diagnostic (morphological) characters of organisms, that leads to a reliable identification of an organism or class of organisms. Diagnostic characters used in a key are defined and may be illustrated for clarity. The formal or taxonomic scope of a key is usually restricted to printed material or presented in digital format.

Characterization of the method – user perspective

FIGURE 5. Depiction of the ID Tool “Field guides/dichotomous keys”



Taxonomic keys represent a logical and practical tool developed by an expert for others to identify organisms. Keys may be available in print (e.g. field guides) or as digital tools (computerized, e.g. IPOFIS) on mobile instruments and computers. There is little or no cost to using a key apart from purchasing the species identification field guide containing the key. The resolution of a key depends on the complexity of the fauna, and keys are usually

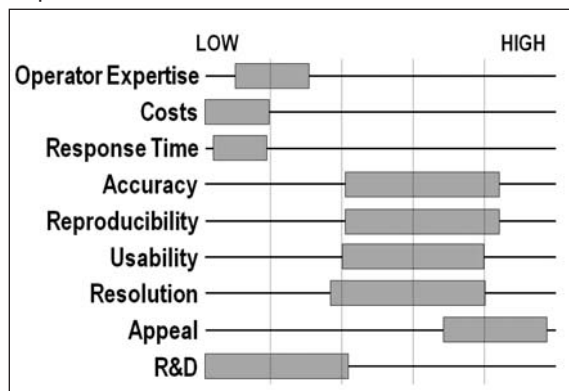
effective to species level. The time taken to identify an organism depends on various factors such as complexity of scope of the key but mostly should be less than one hour. Reproducibility and transferability of keys are extremely wide and keys have been applied to many situations in the field and in the lab. Keys are logical choice systems that are easy to use by both unskilled and highly skilled individuals. Once established, a key can be continually improved by user recommendations. Field guides based on dichotomous keys have wide acceptance and may generally be considered highly reliable in regions with well-known faunas such as Europe and North America, and they are convenient to use in field situations. In regions with numerous undescribed taxa, such guides will definitely fail. There is still a need for development of good field guides for aquatic species in many regions and countries.

3.3.6 Integrated Photo-based Online Fish-Identification System (IPOFIS) exemplifying Interactive Electronic Keys (IEKs)

An IPOFIS is a photo-based online fish identification system that integrates three methods: visual inspection, dichotomous keys, and a multiattribute query procedure. Each fish species is represented by multiple colour photographs of different individuals and close-ups of important identification features. The system efficiently organizes and presents these photographs and associated morphometric information in an interactive format that facilitates fast and accurate identification.

Characterization of the method – user perspective

FIGURE 6.
Depiction of the ID Tool "IPOFIS"



An IPOFIS is designed to be applied by users with no scientific training. Costs are relatively low and are generally limited to online access on a computer. The time required for fish identification generally ranges from 3 to 30 minutes, depending on how distinctive the specimen is. In informal trials, accuracy of identification by minimally experienced users has been good to excellent (~75–100 percent), and for a particular specimen of

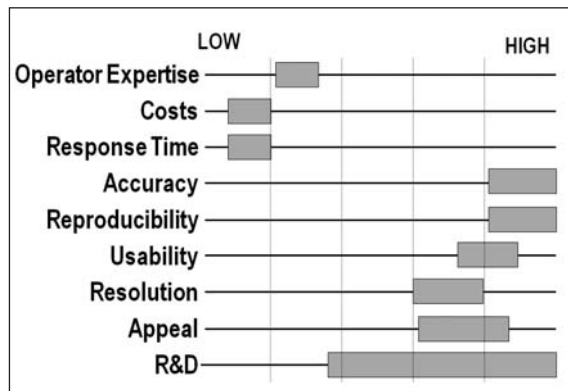
fish examined by different users, nearly all of the users arrived at the same identity. Transferability is limited because fish faunas differ between geographic regions and each fish faunal region requires its own IPOFIS, although the general concept is broadly applicable. Resolution is normally to species. The system has great appeal because of easy access via the web, simplicity of use, availability of multiple identification methodologies, and incorporation of numerous colour photographs of fish as they appear in life. This appeal is evidenced by high rates of use and substantial positive feedback from users. In terms of development, the general concept has been established and examples of appropriate software design and architecture are available, but a full IPOFIS has been completed for only one region, the State of Wisconsin in the north-central United States of America. The data and photographic needs of an IPOFIS are large, and the costs to develop a new IPOFIS will be substantial.

3.3.7 IPez (morphometric software)

IPez is an automated, computer- software-based species identification system for marine and freshwater fish species. It uses a large number of morphometric measurements and it is based on machine learning techniques.

Characterization of the method – user perspective

FIGURE 7.
Depiction of the ID Tool "IPez"



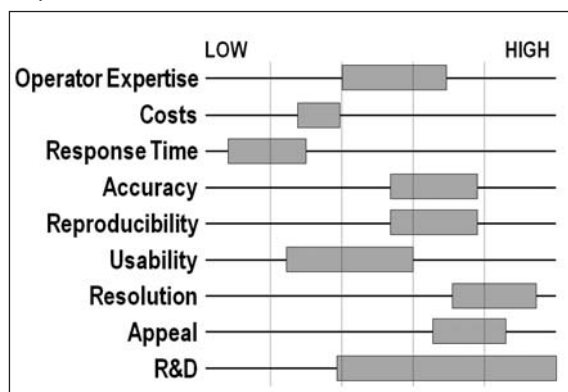
has an inbuilt alert in the event of uncertainty (in which case, the possible taxa will be listed in the order of probability). The system is fully operative but so far it is limited to about 1 300 species. Currently, efforts are under way to increase the number of species for the IPez database.

3.3.8 Scales

Fish scales have been extensively used in fish species identification since the early 1900s. Not only is their count important in key classification; also descriptions of their shape and particular features have been used in keys to recognize families or distinguish between close species. Moreover, alternative methods of shape analysis, based on landmark data, have found wide applicability in biology because of the natural links between homologies and measurements, the statistical properties of the resulting shape spaces and good statistical power. Fish-scale shape is especially useful for discrimination among genera, species and also sympatric populations.

Characterization of the method – user perspective

FIGURE 8.
Depiction of the ID Tool "scales"



identification varies, but the digitalization of scales is an easy job, allowing the review of large samples within a week. The transferability is good as the method does not depend on geographic regions, but its application is limited to species/populations with known scale morphology. The accuracy of this ID tool usually exceeds 70 percent (see references in Annex 3) and the resolution is high, allowing identification at population level. In addition, the method is appealing as scales offer a cheap, rapid and reliable identification of fish using easily extractible body

One day of training is needed in order to learn how to use the system. The user needs a computer, and the time required for fish identification will usually be lower than five minutes and depends on the user's expertise. The software can generate results with 100 percent accuracy provided it has been fed with baseline measures of at least 15 to 20 individuals of different sizes per species. The system allows for identification at a species level and

Knowledge of concepts of morphometric analysis is needed in order to understand the method used. However, analysis could be carried out as a routine, in which case a short training course (of about a week) is needed in order to learn the protocols of methodology. Costs for the equipment required (computer and microfiche reader or a microscope plus a digital camera) should be below 10 000 USD. Time from sampling to

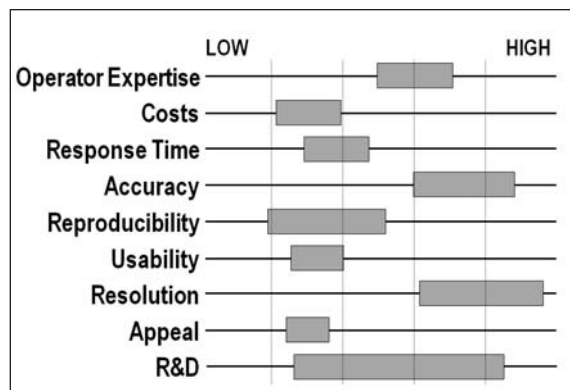
parts (scales) in a non-destructive manner (thus allowing rare and endangered species to be returned to the water). Research and development of the method should be improved as a baseline is needed for many species, including many that are commercially exploited.

3.3.9 Otoliths

The use of otoliths for species and stock identification is well established. While this method is more laborious than the use of fish scales and also requires more knowledge and training, its superior accuracy (exceeding 80 percent for congeneric species) can justify the additional effort. The main limitation of this ID tool consists in its destructiveness (the extraction of otoliths kills the fish) and in the fragility of the otoliths (they easily break during extraction and manipulation). In addition, the morphometric analysis is difficult because of the concave form of otoliths and overall variability of shape.

Characterization of the method – user perspective

FIGURE 9.
Depiction of the ID Tool “otolith”



Knowledge of the concepts of morphometric analysis is needed in order to utilize this method. However, analysis could be carried out as a routine, in which case a short training course (about a week) is needed in order to learn the protocols of the method. The equipment required is not expensive and should be less than 10 000 USD for a microscope and a digital camera. Time from sampling to identification could vary but otolith digitalization is an

uncomplicated job. The transferability is boundless as the method does not depend on geographic regions. However, reproducibility can be low because the shape is influenced by recent feeding habits as well as genetic and environmental characteristics. Resolution to species and even population is possible and the accuracy will normally be over 80 percent (for populations it could exceed 70 percent). However, reproducibility can vary because this is a destructive method that does not allow rare and endangered species to be returned to the water, and one must also consider the fragility of otoliths (a tendency to break during extraction and manipulation). These characteristics reduce its appeal. Development should be improved, as a baseline is needed, especially for commercial species.

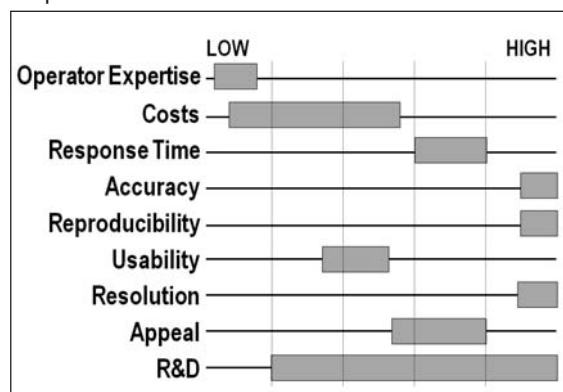
3.3.10 Genetic identification through single nucleotide polymorphisms (SNPs)

Single nucleotide polymorphisms (SNPs) are single mutational differences among individuals at specific loci in the genome that are typically distributed throughout the genome of individuals and are highly abundant. At the population level for example, the frequencies of the various mutational differences can yield population-specific genetic signatures. Importantly, the SNPs to be applied can be readily tailored to accommodate a wide range of differing levels of genetic differentiation, also at spatial scales relevant for fishery policy and management. To enable the use of SNPs for fish population identification, a genetic baseline has to be created. Specimens of a given species are collected across a geographical range and SNPs identified that reveal population-specific genetic signatures. Once the baseline is

created, various questions relevant for fisheries management, including control and enforcement, can be addressed. Examples are the identification of stocks (genetic stock identification), but also the assignment of fish to the source population (origin assignment). A major asset of DNA-based analytical procedures is that they can be applied throughout the food supply chain, from whole specimens to trace samples (e.g. scales and fins), through to highly processed fish products. In addition, DNA analysis is readily used not only on contemporary fish samples but also on archived historical material (e.g. bones and/or scales from museums, and archived otoliths from fishery agencies).

Characterization of the method – user perspective

FIGURE 10.
Depiction of the ID Tool “SNPs”



reference databases (baselines) are currently only available for very few marine and anadromous fish species. Costs have recently declined and the method is considered cost-effective.

The initial large investment is to identify SNPs in the target species, which requires considerable investment in time and high throughput sequencing (typically carried out by commercial sequencing facilities). However, once SNPs are optimized, various genotyping platforms are available and very large numbers of samples can be analysed extremely quickly (from days to weeks). The development of the technology is highly advanced but SNPs

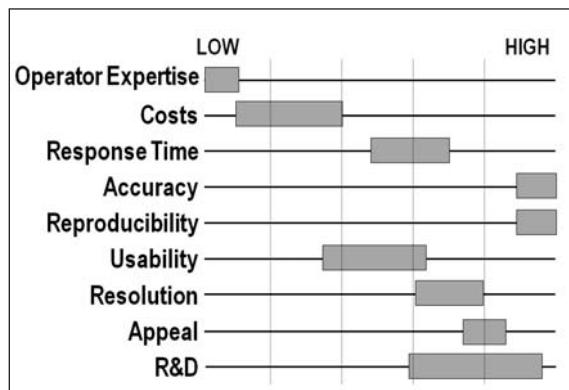
3.3.11 Genetic identification using barcoding

Barcoding is defined as the use of a standardized short region of DNA to verify species identity, which typically for fish is the CO1 region of mitochondrial DNA, with the generation of publicly accessible and highly comparable data. All publicly accessible data are available from one website (Barcode of Life Database), and information on specimen vouchers, photographs and other biological information is available from the same site. Currently, the practice relies on high throughput DNA sequencing, which is typically undertaken by commercial sequencing centres. Effort is currently being put into the development of hand-held barcoding devices for use in the field.

Characterization of the method – user perspective

An end user (e.g. fishery inspector) typically takes a tissue sample and delivers it to a laboratory for analytical purposes (however, as stated above, hand-held barcoding devices for use in the field are under development). Expertise is required for matching the DNA sequence of the sample to the Barcode of Life Database reference sequences. DNA sequencing and matching can be carried out within hours, so the response time depends greatly on the available infrastructure. DNA barcoding is now well established, leads typically to accurate results, and has helped to identify many new and cryptic species, including fish. DNA sequencing costs are low and constantly dropping. DNA barcoding is also amenable to forensics and, therefore, highly suitable for fishery control and enforcement. A major asset of DNA-based analytical procedures is that they can be applied throughout the

FIGURE 11.
Depiction of the ID Tool “barcoding”



barcodes for approximately 25 percent of global fish species (as of October 2011).

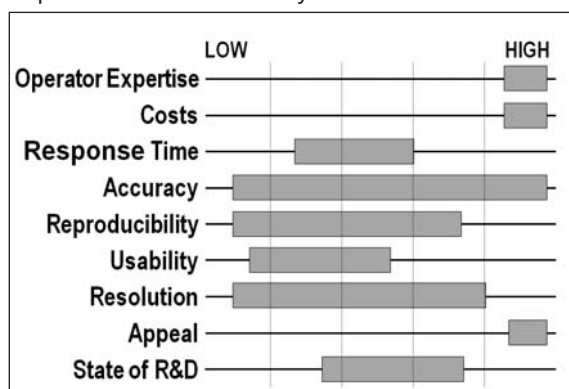
food supply chain, from whole specimens to trace samples (e.g. scales and fins), through to highly processed and cooked fish products. In addition, DNA analysis is readily used not only on contemporary fish samples but also archived historical material (e.g. bones and/or scales from museums, and archived otoliths from fishery agencies). The development of the technology is highly advanced, and the DNA barcode database contains DNA

3.3.12 Acoustic fish identification

Active acoustic technologies use sound to sample distributions, densities, individual lengths and, potentially, species through the entire water column. A pulse of sound is sent into the water, and then reflected echoes are used to derive the location and size of individual and aggregations of fish and zooplankton. Two current technologies used include echo sounders with single or multiple discrete frequencies, and broadband sonars that transmit a continuous frequency band. Analytic techniques compare echo amplitudes from single animals or aggregations as a function of frequency. In addition to identification algorithms, trawl samples are regularly used to verify the identity of acoustic targets.

Characterization of the method – user perspective

FIGURE 12.
Depiction of the ID Tool “hydro-acoustics”



identification can occur in near real time or may take weeks if integrated with trawl catch data. The resolution of the identification ranges from categorizing acoustically similar groups to allocating all reflected energy to species. Objective analysis of acoustic data continues to increase with the development of identification algorithms. Automated processing increases reproducibility of results. As the procedures used to collect and process fisheries acoustic data have been standardized internationally, the transferability of results is moderate to high. Because of the high expertise and costs required the usability of the method is rather low; however, there are many uses for processed acoustic data (e.g. species-specific abundances). The resolution of the data extends from functional groups of species to identified

Specialized training in theory and instrument operation is required in order to acquire, process and identify species using acoustic data. Capital investment to purchase equipment is high. A vessel capable of fishing is the traditional platform used for an acoustic survey. Technical support costs are incurred annually for maintenance and instrument calibration. Acoustic data are acquired in real time. Data processing and species

individuals. Given the familiar quantities (i.e. density) and continuous, whole-water-column coverage as well as the non-invasive nature of the method and wide area coverage, the appeal of species-specific acoustic data is high. Acquisition and processing of acoustic data is well developed. Objective, automated species identification continues as an active research topic.

3.4 WEB-BASED FISH IDENTIFICATION AND INFORMATION RESOURCES³⁰

The internet offers a broad array of information and tools for the identification of fishes by experts and non-experts. Web resources can be of particular use for checking information on a species and for corroborating a first identification. FishBase,³¹ SeaLife Base,³² FAO FishFinder³³ online publications and many other (often local or regional) sites include descriptions of diagnostic characters and distribution maps as well as bioecological and fishery data.

Another important use of web resources consists in confirming the validity of scientific names (in particular for older publications, field guides or keys). The Catalog of Fishes³⁴ (CoF) is the most authoritative site for taxonomic names of finfishes but FishBase and FishWisePro³⁵ may be used if the name is not found in the CoF. SeaLifeBase, World Register of Marine Species (WoRMS),³⁶ Catalogue of Life (CoL),³⁷ and the Integrated Taxonomic Information System (ITIS)³⁸ are good sources for taxonomic information on invertebrate aquatic species.

There is a growing number of websites offering assistance with the identification of aquatic organisms. However, a general platform that could direct users to the best identification tool for their purposes does not yet exist. Perhaps, in the future, IdentifyLife³⁹ could provide such a platform but this project is still in its initial phase.

The following list provides an overview of identification tools on the web.

1. Identification by specialists: Answers are provided by participants of discussion fora based on photographs; these are usually knowledgeable amateurs who can also provide contacts to experts (e.g. FishBase forum⁴⁰).
2. Identification by images (drawings, pictures, videos): Browsing species images on specialized websites (where experts assign images to species) can lead to the identification of an unknown species; however, this usually requires experienced users who can significantly narrow down the number of images that have to be viewed in order to find the species at hand (e.g. FishBase; World Atlas of Marine Fishes⁴¹ [not online]).
3. Dichotomous keys online: Dichotomous keys are available on the web under various formats, from the simple transcription of text up to more elaborated interfaces (e.g. Lucid Phoenix⁴²) with intermediate developments that take advantage of markup languages (html, xml) and their navigating capacities.

³⁰ See also detailed paper in Annex 3.

³¹ www.fishbase.org

³² www.sealifebase.org

³³ www.fao.org/fishery/fishfinder/en

³⁴ <http://research.calacademy.org/ichthyology/catalog>

³⁵ www.fishwisepro.com/

³⁶ www.marinespecies.org/

³⁷ www.catalogueoflife.org/

³⁸ www.itis.gov/

³⁹ www2.identifylife.org/

⁴⁰ www.fishbase.us/FBForum/index.php

⁴¹ Kuitert, R.H. & Debelius, H. 2006. *World atlas of marine fishes: 4,200 marine fishes from around the world with more than 6,000 photographs*. Frankfurt, Germany, IKAN-Unterwasserarchiv; University of California. 720 pp.

⁴² www.lucidcentral.com/en-us/software/lucidphoenix.aspx

More and more online keys are available based on electronically accessible taxonomic revisions for the taxon in question (mostly for genera or families) and from FAO FishFinder catalogues.

4. Polythetic keys online: The principle of a polythetic key consists in the selection of predefined distinctive characteristics and resulting computation of a list of possible species based on a similarity index. However, frequently the differences between the most probable species are so small that the user may not succeed in identifying the species, and making these keys is labour-intensive. Polythetic keys are mainly used for bacteria identification (API systems). The best example for finfish is the use of morphometrics measurements and meristics as in IPEZ⁴³ (see above) and the FishBase morphometrics tool,⁴⁴ both accessible on the web.
5. Interactive electronic keys (IEKs): This tool has been included in this review (see section 3.3.6), and the IPOFIS online site in Wisconsin⁴⁵ represents a good example.
6. Image Recognition Systems (IRSs): For fish identification this tool is still in the early development phase and has been included in this review (see section 3.3.4).

Other tools

Identification of fish bones is done by archaeozoologists. Current projects include Phenoscape⁴⁶ (ontological data for all fish bones); OsteoBase⁴⁷ (searchable online database of fish bone illustrations); Fish Remains⁴⁸ (for Hawaiian fishes), Catfish bones,⁴⁹ Archaeological Fish Resource⁵⁰ and Archaeological fish-bone images.⁵¹

Other resources

Some websites that include identification keys are global projects, e.g. DiscoverLife,⁵² KeyToNature⁵³ and its national websites, and the recent site of the European Union (Member Organization) IdentifyLife.⁵⁴

A few general platforms lead to further identification information (and also the information systems dedicated to Catalogue of Life⁵⁵ [CoL]);

- Encyclopedia of Life⁵⁶ (EOL);
- European Distributed Institute of Taxonomy⁵⁷ (EDIT);
- ScratchPads⁵⁸ (online virtual research environment for biodiversity).

⁴³ www.ipez.es/

⁴⁴ www.fishbase.org/Identification/Morphometrics/centimeters/index.php

⁴⁵ <http://wiscfish.org>

⁴⁶ <http://phenoscape.github.io/>

⁴⁷ www.mnhn.fr/osteo/osteobase/ (Muséum national d' Histoire naturelle, Paris, France)

⁴⁸ <http://hbs.bishopmuseum.org/frc/about.html>

⁴⁹ <http://catfishbone.ansp.org/>

⁵⁰ <http://fishbone.nottingham.ac.uk/>

⁵¹ <http://fish.library.usyd.edu.au/index.jsp?page=home>

⁵² www.discoverlife.org/

⁵³ www.keytonature.eu/

⁵⁴ www.identifylife.org/

⁵⁵ www.catalogueoflife.org/

⁵⁶ <http://eol.org/>

⁵⁷ www.e-taxonomy.eu/

⁵⁸ <http://scratchpads.eu/>

4. Selecting an identification tool

The process of selecting the best tool or combination of tools for a defined set of circumstances can be critical to the success of the activity in question and should not be underestimated. The following section is intended to provide practical guidance with regard to the best ID tools for specific purposes; this is achieved through evaluating the ID tools against a set of selection criteria and through providing extensive reference to the 24 scenarios described in chapter 5 which exemplify various conditions and situations requiring the identification of aquatic species.

4.1 USERS

The possible users for the identification of aquatic species are a diverse group with regard to their background and specific interest or objectives. In the following, a distinction is being made between the “end user” and the “operator”. The end user is defined as the person or group of individuals who ultimately requires the information on the species. In contrast, the operator is the individual who has been tasked with providing the information and will actually perform the species identification. The potential operators of fish ID tools can range from highly specialized taxonomists to laypersons without any experience or formal training.

In particular, fish identification is required for:

1. Conservation, responsible use and trade, and law enforcement, e.g. resource use (fisheries and aquaculture), environmental assessment, and responsible trade mechanisms (e.g. certification, non-detriment findings [Convention on International Trade in Endangered Species of Wild Fauna and Flora – CITES]). Typical end users in this sector are fishery managers, environmental fishery statisticians, stock assessment scientists, law enforcement officers, fishers, fish farmers and fish traders.
2. Education, awareness building, consumer considerations and non-consumptive uses, e.g. formal education (schools, universities, courses, etc.), aquaria and museums, consumer information, tourism (e.g. diving, sports fishing, and touring). Typical end users in this sector are consumers, environmental non-governmental organizations (NGOs), tourism planners, aquatic tour guides, divers and aquarium staff.
3. Research and development, e.g. scientific assessments and surveys, development of fishing and sampling methods, basic research. Typical end users in this sector (apart from the public or private research funding sources) are bioaquatic and fishery scientists and engineers, ichthyology curators and marine military officers.

4.2 SELECTION CRITERIA

Each of the presented species ID tools has its particular strengths and weaknesses, and its best uses depend on the requirements and available resources for the fish identification. The selection of the best species ID tools should start at the planning level of an activity and consider budgetary and staffing implications. Recommended criteria for such selection are:

1. **Response time:** How quickly is a result needed? Many situations require an immediate identification, i.e. within a few minutes. Sometimes, a few

hours are acceptable, and in other cases a much longer response time will be tolerable, e.g. from weeks to months.

2. **Accuracy:** How much tolerance is there for incorrect identifications; or what are the consequences if not all specimens are identified correctly? In some cases, the accuracy might be secondary to other considerations, e.g. children visiting an aquarium, whereas in other scenarios an incorrect identification could have serious legal implications, e.g. a port inspector suspecting that a vessel has been engaged in IUU fisheries.
3. **Resolution:** How specific should the information be? Is it enough to pinpoint the order or family of a specimen or is it necessary to determine the species or even population? A hobby diver, for example, might be thrilled to be able to tell the families or even higher levels apart, whereas a biologist studying population dynamics will require identification beyond the species level.
4. **Type:** Ideally, identification can be done through examination of a fresh and whole specimen. However, there are many situations in which the identification has to be based on frozen or otherwise processed organisms or parts of their bodies or on photographs of variable quality or even based on oral descriptions or from memory. This has implications for other criteria (e.g. response time and accuracy) and limits the number of appropriate ID tools.
5. **Resources (costs, expertise):** What funds, qualified staff and equipment are available for the activity? Resources available for species identification can range from very low, i.e. one or a few unskilled operators and no equipment other than a book, to very high, i.e. a research vessel fully equipped with a variety of gear and acoustic devices, state-of-the art computer facilities, a scientific laboratory and highly specialized scientific and technical operators.

Once the availability of resources and specific requirements for species identification have been established, the ID tools can be selected by matching the description of each tool with the criteria above. Table 3 summarizes the major strengths and weaknesses of the reviewed ID tools relative to the evaluation criteria used in Chapter 3 to help with a first selection of possible ID tools for a defined purpose. It is important to consider that each ID tool has unique attributes and advantages that are not reflected in the table. Therefore, a thorough evaluation of the user requirements and the characteristics of the available ID tools is necessary before choosing a fish identification method.

The ideal all-purpose fish ID tool would require only little expertise of the operator and be low-cost (and low-technology) as well as user-friendly. It would also have a very fast response time and high accuracy, resolution and reproducibility. Last, it could be easily applied for all species groups and in all geographic areas (high transferability) and would be scientifically fully established and available to users. Currently, such a tool does not exist - although an on-site taxonomist comes close and with IPEZ another excellent and affordable all-purpose fish ID tool is becoming available. However, the specific requirements can vary greatly from case to case and for certain situations and sets of conditions some fish ID tools will be more adequate than others.

TABLE 3. Summary of major strengths and weaknesses of the different identification tools based on the evaluation boxes in Chapter 4 (see Table 2 for definition of criteria)

Criteria	ID Tool	Onsite Taxonomist	Folk Local Experts	Local Reference Collection	IRS	Field Guides	IEK	IPEz	Scales	Otoliths	SNPs	Barcode	Hydro-acoustics
Expertise low (user/operator requires little specialized knowledge)		++	(-)	+	++	(+)	+	+	-	-	++	++	-
Low costs (hundreds [++] to thousands [+] USD)		+	++	++	+	++	+	+			(-)	(-)	-
Response time low (minutes [++], hours [+])		++	++	(+)	++	+	+	++		(+)	(-)	(-)	(+)
Accuracy high (close to 100% [++], > 80% [+])		++	(+)	(+)	(-)	(+)	(+)	++			++	++	(+)
Reproducibility high (close to 100% [++], > 80% [+])		(++)		+	(+)	(+)	(+)	++		-	++	++	
Usability high (ease of use, effort, etc.)		++	(+)	+	++	(++)	(+)	+		-			
Resolution high (population [++], species [+])		+	(+)	+		(+)	(+)	+	++	(++)	++	+	(+)
Appeal high (attracts users and funds)		(+)	++		++	(+)	+	(+)	+	-	+	+	++
R&D high (established and globally accessible)		(+)	(-)	(+)	-	(+)	-	(+)	(-)	(-)	(-)	(+)	

Notes: ++ = very strong; + = strong; - = weak; parenthesis indicate a high variability (depending on circumstances).

CAVEAT: Many ID tools have unique characteristics that cannot be addressed in a summary table. Therefore, this table should not be used as the only basis for selecting an ID tool.

4.2.1 Response time

Time can be of the essence in a number of situations and an immediate or very quick response time for species identification is required for many fishery applications, e.g. catch recording and reporting (scenarios 5.1, 5.3, 5.4 and 5.5) or vessel inspections (scenario 5.9). Often, for these situations, a combination of two ID tools can be recommended; the first for a quick identification with some tolerance of error, and a more time-consuming follow-up identification with an ID tool of very high accuracy. Other scenarios exemplifying a requirement for a very quick response time of the species identification are the assessment of introduced species by beach management units (scenario 5.2), the correct identification of fingerlings for aquaculture purposes (scenario 5.6), pre-harvest surveys by commercial fishing vessels (scenario 5.7), and the labelling of traded fish (scenario 5.22). It is noteworthy that a number of research scenarios have a high tolerance for long response times (e.g. scenarios 5.13, 5.14, 5.16 and 5.17).

ID tools providing very quick (within minutes) results in the field are on-site taxonomists, local folk experts and field guides (dichotomous keys). For situations with access to mobile devices, IRSs, morphometrics (IPez) and IEKs could be excellent tools if available for the region. Finally, if a microscope is on location, a species identification using scales can be a quick way of obtaining reliable results, provided a baseline has been established for the species in question. Genetic methods have a long response time, and this can diminish their usefulness for applications requiring a quick response time. However, they can be excellent ID tools for a highly accurate and legally valid follow-up identification.

4.2.2 Accuracy

Due consideration must be given to the required level of accuracy of a species identification. In most cases, the accuracy should be high; a very high accuracy is required in particular for the purpose of law enforcement (scenarios 5.8, 5.9, 5.10, 5.11 and 5.12), the tracing of introduced (“exotic”) species (scenarios 5.2, 5.19 and 5.23) and the supply of fish farmers with fingerlings (scenario 5.6). In a few cases, the required accuracy levels are not high, for example for large-scale marine biodiversity studies (scenario 5.17), provision of basic catch data for fishing gear engineers (scenario 5.16) and species identification by hobby divers (scenario 5.24).

Species ID tools generating highly accurate results are the hiring of a taxonomist, morphometrics (IPez), and both genetic tools (barcode and SNPs). Five other species ID tools have the potential to give accurate results depending on the expertise of the operator, i.e. dichotomous keys (field guides), IEKs, folk local experts, reference collections, and acoustics. However, their application by inexperienced users can result in unacceptable levels of misidentifications.

4.2.3 Resolution

In most cases, the identification should be performed at a species level. However, there are a growing number of applications where identification of an organism is required at a higher level of resolution (e.g. population level).

About one-third of the scenarios require the identification at a population level, e.g. tracing the geographic origin of catches (scenarios 5.11 and 5.21), studies of population dynamics (scenario 5.13) or distinguishing between similar species or between natural and genetically modified organisms (scenarios 5.20 and 5.23). On the other hand, a relatively low resolution of the identification can be sufficient if it just serves the satisfaction of general curiosity, e.g. species identification by hobby

divers (scenario 5.24), or where general data are required for other applications, e.g. the provision of basic catch data for fishing gear engineers (scenario 5.16).

The only species ID tools that can be used for fish identification at population level are SNPs, scales and otoliths. While SNPs are highly accurate, the response time is usually quite long as the probes have to be shipped to a laboratory for processing. On the other hand, the use of otoliths and scales provides a quick but – depending on the circumstances – sometimes less accurate identification. However, these three tools are not readily available for all species or in all geographic areas, and further efforts in the development of relevant species- and population-specific baseline information are required as well as, in the case of SNPs, more laboratories in all regions.

A resolution at species level can be achieved by most ID tools, e.g. taxonomists, morphometrics (IPez), dichotomous keys (field guides), reference collections and IEKs (IPOFIS). The genetic barcode technique can be a valid tool for the identification of most species; however, it will not recognize hybrids and, therefore, it should be used with caution when dealing with cultured species.

Folk local experts often but not always distinguish between species, and only experienced operators will be able to recognize where several species are being grouped and treated as one by the folk taxonomy in question. Identification through acoustic devices can also be used for species identification and even down to an individual level depending on locations and baseline data.

4.2.4 Type

There are many scenarios where identification has to be performed on body parts or processed specimen (frozen, dried, smoked, filleted, etc.), on photographs of varying quality or on oral descriptions. This is far more difficult to achieve than identification on whole, fresh bodies. Situations where such impediments are likely to be encountered are during catch inspections at high seas, ports or customs (scenarios 5.8, 5.9, 5.11 and 5.12), for trade scenarios such as labelling and catch certification (scenarios 5.21 and 5.22) as well as where hobby divers wish to identify interesting species after their dive (scenario 5.24) and similar situations.

Under these circumstances, many traditional fish ID tools will not work well. For frozen and otherwise processed specimens, product guides and the expertise of the inspector, observer or data collector can be helpful for a first assessment. For fish with known scale patterns, the microscopic scale exam can also provide a quick and easy identification. However, for the species identification based on fish products genetic tools will often be the only assured way of obtaining sufficiently accurate results, although this means a reduction in response time.

4.2.5 Resources

Species identification is not a luxury but a necessary activity for many applications and all geographic regions. However, expertise, equipment, personnel and funds are not everywhere and always within easy reach, and this will restrict the choices of ID tools. Workshop participants focused mainly on scenarios where the resources available would be moderate to low and only developed four scenarios requiring high resources for taxonomic identification. Three of these were research and development applications, i.e. the study of populations, a military study on distinguishing submarines from marine animals, and the provision of data for

ecosystem modelling (scenarios 5.13, 5.14 and 5.15). The only other resource-intensive activity was the non-invasive, pre-harvest survey of fishery resources by fishing vessels (scenario 5.7).

Ten scenarios were characterized by particularly low resource requirements including two research and development applications, i.e. a study on climate change impact on species diversity and the production of a fish inventory for gear development purposes (scenarios 5.16 and 5.17). Education and enhancement of consumer awareness usually do not require costly equipment provided that the trainers or presenters hired for the purpose are highly qualified as described for the taxonomic training of students and hobby anglers, and educating administrators and the public on genetically modified salmon and their identification (scenarios 5.18, 5.19 and 5.20). Non-consumptive uses might also require just limited resources, in particular when an identification of higher taxonomic groups (family, order) is sufficient, as was the case for hobby divers in scenario 5.24. The voluntary labelling of fresh fish by the owner or employees of a fish shop or fish restaurant also considered that resources might be scarce (scenario 5.22). Finally, catch reporting by fishers (scenario 5.1) as well as the identification of fishery products or live fishes by customs officers (scenarios 5.10 and 5.12) were also discussed based on the assumption of low funding and expertise and a minimum of equipment.

There are many ID tools that are not costly and do not require expensive equipment or much expertise by the operator. Very low-cost tools are the use of folk experts, reference collections and dichotomous keys (field guides). Slightly more expensive but still qualifying as low costs are the hiring of a taxonomist and the use of software-based tools such as IRS, IEKs (IPOFIS) and morphometrics (IPez).

5. Description of scenarios

The following 24 scenarios were developed to assist with the selection of the most appropriate ID tool for different situations under which the identification of aquatic species is required.

Each scenario is briefly described, operators and end users are identified and the scenario is characterized using the five criteria presented above. Finally, for each scenario, one or more identification tools are recommended.

Conservation, responsible use and trade, and law enforcement

1. Catch reporting by fishers (logbooks)
2. Assessment of introduced fish species in a lake
3. Monitoring catch during exploratory fishery
4. Reporting catches of lake fisheries (exotic species)
5. Reporting catches of marine artisanal fisheries
6. Fingerlings of aquaculture species are correctly identified by suppliers
7. Reduction of by-catch through pre-harvest survey
8. Port inspections of fishery catches
9. Vessel inspection at high sea
10. Live fish inspection by customs (CITES)
11. Verification of origin of catches
12. Fish product inspection by customs (CITES)
13. Distribution and characteristics of populations

Research and development

14. Provision of data for the ecosystem modelling of living marine components
15. Development of application to distinguish living objects from submarines
16. Fish inventory for gear development to minimize by-catch
17. Changes in species diversity due to climate change

Education, awareness building, consumer considerations and non-consumptive uses

18. Taxonomic training of students
19. Anglers track the spread of aquatic invasive species (AIS)
20. Assessment of genetically modified fish in waters and markets
21. Corroboration of the geographic origin of fishes as documented in catch certificates
22. Traded fish is labelled correctly
23. Investigating the alleged presence of exotic and GM species
24. Divers identify marine organisms

5.1 CATCH REPORTING BY FISHERS (LOGBOOKS)

Tag: Conservation, responsible use and trade, and law enforcement

Operators: fishers		End users: fishery managers and scientists		
Response time	Accuracy	Resolution	Type	Resources
<i>minutes</i>	<i>high</i>	<i>species</i>	<i>whole fresh</i>	<i>low/moderate</i>
ID TOOLS: Field guide, local expert				

Description: The fishing crew on a commercial vessel has been requested to survey the catch for the purpose of reporting requirements and complying with fishery regulations (e.g. bycatch requirements, moratoria, quotas). This is done by an observer and/or crew members who have received relevant training and have ample experience. Computer access for this purpose is not available and the resolution required is high (species). Taking samples for follow-up identification is not foreseen on a routine basis.

Constraints: Monitoring of the catch interferes with the normal fishery work flow (a very stressful environment).

5.2 ASSESSMENT OF INTRODUCED FISH SPECIES IN A LAKE

Tag: Conservation, responsible use and trade, and law enforcement

Operators: taxonomists (teachers), fishery officers		End users: fishery officers, scientists		
Response time	Accuracy	Resolution	Type	Resources
<i>minutes</i>	<i>very high</i>	<i>species (hybrids)</i>	<i>whole fresh</i>	<i>moderate</i>
ID TOOLS: Field guide, taxonomist (as teacher), reference collection. (scales)				

Description: The Kenya Ministry of Fisheries trains Beach Management Units (BMUs) of Lake Victoria in identifying different species of *Oreochromis*. This is an activity of a national project to assess the status of introduced *O. niloticus* and *O. leucostictus* and native *O. esculentus* and *O. variabilis* in Lake Victoria. The BMUs are contracted to collect data. Qualified trainers who speak the local languages and are familiar with the local folk taxonomy are available, as is transportable equipment, and the ID tool should be able to differentiate among *Oreochromis* species at various ages and sizes.

Constraints: A confusing amount of different common names can complicate fish identification. The rural and remote setting make working difficult, e.g. inconsistent electricity, difficult travel. These species are difficult to distinguish morphologically, and local fishers may not differentiate among all of them.

Other remarks: mDNA techniques, e.g. FBOL and cyt b, may not be useful owing to the recent divergence of *Oreochromis* species.

5.3 MONITORING CATCH DURING EXPLORATORY FISHERY

Tag: Conservation, responsible use and trade, and law enforcement

Operators: fishers, observer-on-board		End users: fishery managers and scientists		
Response time	Accuracy	Resolution	Type	Resources
<i>minutes</i>	<i>high</i>	<i>species</i>	<i>whole fresh</i>	<i>moderate</i>
ID TOOLS: (a) <i>Immediate ID:</i> Local experts (fishers); field guide, IPez (b) <i>Follow-up ID:</i> Taxonomist, reference collection, scales/otoliths, internet-based information sources				

Description: A regional fisheries management organization (RFMO) has defined its existing bottom fishing area (footprint) and/or some protected zones. For fisheries outside the footprint area and within protected zones, an exploratory fishery protocol applies requiring, *inter alia*, the identification and recording of all species brought on board to the lowest possible taxonomic level. The obligatory observer on board and some crew members have undergone basic fish identification training; all crew members assigned to this task have ample experience with fishing in the geographic area. Unknown and vulnerable species will be sampled and sent to a lab for further identification.

Constraints: Potential conflict with profit-oriented fishing activity (e.g. time constraints); unknown species could be encountered; know-how required for sampling, taking probes and usable photographs.

5.4 REPORTING CATCHES OF LAKE FISHERIES (EXOTIC SPECIES)

Tag: Conservation, responsible use and trade, and law enforcement

Operators: fishery officers		End users: fishery managers and scientists		
Response time	Accuracy	Resolution	Type	Resources
<i>minutes (days in suspicious cases)</i>	<i>high</i>	<i>population/species</i>	<i>whole fresh</i>	<i>moderate</i>
ID TOOLS: (a) <i>Native species:</i> field guide, local expert, (IPez) (b) <i>Tilapia first ID:</i> local expert (officer) (c) <i>Tilapia final ID:</i> SNPs				

Description: A lake in Nicaragua contains various introduced species of the tilapia group. Many of these have hybridized, and identification at a subspecies level is necessary. The officers have undergone biological training or are experienced fishers with extensive experience in fish identification.

Constraints: The tilapia species and their hybrids are difficult to distinguish (however, experienced officers may detect even subtle differences).

5.5 REPORTING CATCHES OF MARINE ARTISANAL FISHERIES

Tag: Conservation, responsible use and trade, and law enforcement

Operators: fishery officers		End users: fishery managers and scientists		
Response time	Accuracy	Resolution	Type	Resources
<i>minutes (days in suspicious cases)</i>	<i>high</i>	<i>species</i>	<i>whole fresh</i>	<i>low/moderate</i>
ID TOOLS: (a) <i>Immediate ID (minutes):</i> Field guide, local expert (b) <i>Follow-up ID:</i> Taxonomist, reference collection, Ipez, scales, IPOFIS and other internet-based information sources				

Description: Fishery officers collect catch data from artisanal fisheries on a beach in Kenya for reporting purposes. The beach is an attractive landing point and the number of boats is high. The fishery officers have biological training or are experienced fishers with extensive experience in the identification of local fish. The identification has to be at the species level.

Constraints: High number of landings; the officers have to develop a sound sampling technique to produce realistic catch reports. Possible reluctance of collaboration by fishers.

5.6 FINGERLINGS OF AQUACULTURE SPECIES ARE CORRECTLY IDENTIFIED BY SUPPLIERS

Tag: Conservation, responsible use and trade, and law enforcement

Operators: fish farmers		End users: fish farmers		
Response time	Accuracy	Resolution	Type	Resources
<i>minutes</i>	<i>very high</i>	<i>species</i>	<i>whole fresh</i>	<i>low/moderate</i>
ID TOOLS: (a) <i>Immediate ID:</i> Field guide, reference collection (b) <i>Follow-up ID:</i> SNPs, scales, otoliths				

Description: The Kenya Ministry of Fisheries Development and Marketing is trying to popularize fish farming and identified ten farmers in the Kilifi District to produce and supply *O. niloticus* fingerlings (seed) to potential fish farmers in Coast Province. Species surveys of local waters are completed and farmers have been trained in the use of transportable equipment and techniques to differentiate among tilapia species, also for specimen at fingerling size.

Constraints: Confusing amount of different common names can complicate fish identification. The rural and remote setting make working difficult, e.g. inconsistent electricity, difficult travel. These species are difficult to distinguish morphologically and local fishers may not differentiate among all of them. Hybridization is common and may be difficult to detect visually or by some genetic methods (e.g. BCOL).

Other remarks: Hybrid *Oreochromis*, although difficult to detect, might actually be a better product than pure *O. niloticus*. Genetic identification and farm evaluation of the best lineage might be beneficial.

5.7 REDUCTION OF BYCATCH THROUGH PRE-HARVEST SURVEY

Tag: Conservation, responsible use and trade, and law enforcement

Operators: fishers			End users: fishing industry	
Response time	Accuracy	Resolution	Type	Resources
<i>minutes</i>	<i>high</i>	<i>genus / family</i>	<i>image</i>	<i>high</i>
ID TOOLS: Hydroacoustics				

Description: For purse seine fisheries, pre-harvest identification offers the prospect of avoiding catches of non-target species or sizes. The avoidance of unwanted and discarded bycatch benefits the environment and also increases the profitability of fishing activities by saving fuel and time. The vessel is equipped with sophisticated technology, and one crew member has received training in the remote identification of fish. The resolution of the identification can be low (genus, family).

Constraints: Fishers might need some convincing as this will delay the fishing operation.

5.8 PORT INSPECTIONS OF FISHERY CATCHES

Tag: Conservation, responsible use and trade, and law enforcement

Operators: port inspectors, customs agents			End users: law enforcement	
Response time	Accuracy	Resolution	Type	Resources
<i>minutes</i>	<i>high</i>	<i>species</i>	<i>whole fresh, frozen</i>	<i>low/moderate</i>
ID TOOLS: (a) <i>Immediate ID:</i> Field guide, local expert, IPEz, scales, otoliths (b) <i>Follow-up ID:</i> Genetic tools				

Description: Port inspectors and customs agents are required to identify fish and fish products landed in the port of Vigo, Spain. Material may be live, fresh or frozen and may be of extremely high value, e.g. tuna or lobsters. Inspectors have undergone a three-day training course on fish identification and the use of taxonomic keys for relevant species as well as taking samples and learning about shipping requirements for frozen products. Technical resources include taxonomic keys (guides) and photographs of species of special concern, e.g. tuna.

Constraints: Time pressure to prevent spoilage; remote analysis (DNA) will cause delays; difficulties in identifying frozen material; proper custody and handling of biological material needs to be rigorous.

Other remarks: If the inspection requires DNA analysis, DNA extraction and analysis may be done locally to reduce time to identification. Training courses on fish ID tools for inspectors should be highly publicized to increase consumer confidence and to deter illegal activities.

5.9 VESSEL INSPECTION ON THE HIGH SEAS

Tag: Conservation, responsible use and trade, and law enforcement

Operators: fishery inspectors			End users: law enforcement	
Response time	Accuracy	Resolution	Type	Resources
<i>minutes (days in suspicious cases)</i>	<i>high/very high</i>	<i>species</i>	<i>whole/parts; fresh/processed</i>	<i>low</i>
ID TOOLS: (a) <i>Immediate ID:</i> Field guide, IRS (whole fish); product guides and expertise of inspector (for products) (b) <i>Short-term ID (hours):</i> Scales, IPOFIS, IPEz (c) <i>Final ID:</i> Taxonomist; barcoding (parts and products)				

Description: National enforcement officers board a vessel for inspection on the high seas. The inspectors have undergone one week of training in fish identification. They board a vessel for a routine inspection of the fishing gear, stored catches, logbook and stowage.

Constraints: The inspector only has a few hours to conclude the inspection; language barriers are frequent in international waters; catch will be frozen or processed.

Other remarks: If possible, e.g. back in fishing ports, existing Internet resources can be used for follow-up (e.g. FishFinder and FishBase).

5.10 LIVE FISH INSPECTION BY CUSTOMS (CITES)

Tag: Conservation, responsible use and trade, and law enforcement

Operators: customs officers			End users: law enforcement	
Response time	Accuracy	Resolution	Type	Resources
<i>minutes/hours (weeks)</i>	<i>very high</i>	<i>species/population</i>	<i>whole fresh</i>	<i>low/moderate</i>
ID TOOLS: (a) <i>Immediate ID:</i> Field guides, IPEz, IRS (b) <i>Follow-up ID:</i> Taxonomist, IPOFIS and other internet-based information sources; barcoding (species); SNPs to distinguish farmed or bred species from wild catches (CITES)				

Description: Customs officers at a large airport (Frankfurt, Germany) are used to dealing with live aquatic species imported for pet shops. CITES has imposed international trade regulations on a number of such fishes and these species have to be quickly identified. The officers have received two weeks' training and are experienced and competent.

Constraints: Time pressure for first ID as survival of the individuals (and profit) may depend on quick transferral from transport container to suitable aquaria. Corruption may be a problem in some countries.

5.11 VERIFICATION OF ORIGIN OF CATCHES

Tag: Conservation, responsible use and trade, and law enforcement

Operators: fishery inspectors			End users: <i>law enforcement</i>	
Response time	Accuracy	Resolution	Type	Resources
<i>hours /days</i>	<i>high/very high</i>	<i>population</i>	<i>processed body parts</i>	<i>low/moderate</i>
ID TOOLS: (a) <i>First ID:</i> Scales, otoliths (b) <i>Final ID:</i> SNPs				

Description: The control authority of the Russian Federation needs to verify the landing declaration regarding origin of catch from a large vessel. The inspectors have undergone one week's training in fish identification and have ideally accumulated many years of experience. The resolution required may be at a population/stock level.

Constraints: Frozen and processed fish.

5.12 FISH PRODUCT INSPECTION BY CUSTOMS (CITES)

Tag: Conservation, responsible use and trade, and law enforcement

Operators: customs officers			End users: law enforcement	
Response time	Accuracy	Resolution	Type	Resources
<i>hours (days)</i>	<i>high</i>	<i>population/species</i>	<i>processed body parts</i>	<i>low/moderate</i>
ID TOOLS: (a) <i>Immediate ID:</i> Product guide; expertise by the officer (b) <i>Follow-up ID:</i> Barcoding (species); SNPs to distinguish farmed or bred species from wild catches (CITES)				

Description: A customs officer (any country) inspects a box of dried or otherwise processed fish products, e.g. shark fins that are being imported from a neighbouring country. The officer suspects that some parts are derived from species whose international trade is regulated by CITES. The officer calls a highly competent colleague who has received basic, two weeks' training in fish identification and who attempts a first identification (at species level). Based on the conclusions, a follow-up identification may be necessary (at species and/or population level).

Constraints: The customs officers work under time constraints as the delays caused by their investigation will affect profits. In addition, identification is extremely difficult because of the often highly processed products. It must be pointed out that corruption of customs officers can be a problem in some countries.

5.13 DISTRIBUTION AND CHARACTERISTICS OF POPULATIONS

Tag: Conservation, responsible use and trade, and law enforcement

Operators: scientists			End users: fishery managers	
Response time	Accuracy	Resolution	Type	Resources
<i>weeks/months</i>	<i>high</i>	<i>population</i>	<i>whole fresh</i>	<i>high</i>
ID TOOLS: Hydroacoustics, scales/otoliths, SNPs (local folk experts in the design phase of the study)				

Description: A fishery manager of Lake Victoria needs to know how Nile perch are distributed, and if inshore and offshore populations differ. The study is funded by the Global Environment Facility with access to the necessary equipment and expertise.

Constraints: Possible sampling bias.

Other remarks: Access to local knowledge should be used to refine the sampling design and thus ensure the representativeness of samples; this could be crucial to the success of the project.

5.14 PROVISION OF DATA FOR THE ECOSYSTEM MODELLING OF LIVING MARINE COMPONENTS

Tag: Research and development

Operators: scientists			End users: project manager, client	
Response time	Accuracy	Resolution	Type	Resources
<i>weeks/months</i>	<i>high</i>	<i>species</i>	<i>whole fresh</i>	<i>high</i>
ID TOOLS: Field guide, taxonomist, IEK, IRS, IPEz, barcoding, hydroacoustics				

Description: Field scientists provide data for an ecosystem-based simulation model to understand how the removal of a particular species will influence the abundance, distributions, diversity and energy transfer of forage fish to whales in the Antarctic. The project includes internationally supported infrastructure, state-of-the-art equipment, and excellent expertise for sampling, analysis and modelling, including a taxonomist.

Constraints: Taxonomic information on larval fish is incomplete.

Other remarks: Barcoding use should be restricted to ambiguous larval fish (reference source is available).

5.15 DEVELOPMENT OF APPLICATION TO DISTINGUISH LIVING OBJECTS FROM SUBMARINES

Tag: Research and development

Operators: scientists			End users: military	
Response time	Accuracy	Resolution	Type	Resources
<i>days</i>	<i>high</i>	<i>family</i>	<i>whole fresh</i>	<i>high</i>
ID TOOLS: Hydroacoustics, field guide, IPez, IPOFIS, IRS, IEK, (passive sonars)				

Description: Hydrotechnicians in the military are being asked to distinguish submarines from biologics in the Baltic Sea. Classified project. No limit on funding.

Constraints: Military project influencing information gathering and dissemination (e.g. may influence access to submarine acoustic signatures).

5.16 FISH INVENTORY FOR GEAR DEVELOPMENT TO MINIMIZE BYCATCH

Tag: Research and development

Operators: fishers, scientists			End users: technical engineers	
Response time	Accuracy	Resolution	Type	Resources
<i>weeks/months</i>	<i>moderate/high</i>	<i>species/genus</i>	<i>whole fresh</i>	<i>low/moderate</i>
ID TOOLS: (a) Immediate ID: Local experts, field guide (b) Follow-up ID: Taxonomist, IPez, scales, otoliths, IPOFIS				

Description: A fish inventory is needed for the development of new or modification of existing fishing gear to minimize bycatch in a multispecies fishery in Indonesia. The inventory (baseline sampling) is done by a large fishing vessel operated by a local crew. The samples are identified on board and/or processed for later identification/verification of preserved samples. The scientific taxonomic knowledge on board is low but the fishers are experienced and have high local expertise.

Constraints: Availability of taxonomic keys limited.

5.17 CHANGES IN SPECIES DIVERSITY DUE TO CLIMATE CHANGE

Tag: Research and development

Operators: scientists and technicians			End users: scientists	
Response time	Accuracy	Resolution	Type	Resources
<i>weeks/months</i>	<i>moderate/high</i>	<i>species</i>	<i>whole fresh</i>	<i>low/moderate</i>
ID TOOLS: Field guides, IPez; taxonomist, (IRS, IPOFIS)				

Description: A project studies the potential effects of climate change on fish species diversity in the Humboldt Current. This is a modestly funded component of a larger project. Fish sampling is performed on board a survey vessel.

Constraints: Limited funds.

5.18 TAXONOMIC TRAINING OF STUDENTS

Tag: Education, awareness-building, consumer considerations and non-consumptive uses

Operators: biologists (teachers)			End users: students	
Response time	Accuracy	Resolution	Type	Resources
<i>minutes/hours</i>	<i>high</i>	<i>species/genus</i>	<i>whole fresh</i>	<i>moderate/high</i>
ID TOOLS: Field guides, IRS				

Description: Ichthyology students in college learn how to use dichotomous keys and IRS for fish identification and to understand the pros and cons of each method. Students, working in teams, are asked to identify ten unknown preserved and jarred specimens. To identify a specimen correctly, students have to write down the family, genus and species names of the specimen using both the traditional key-based method and IRS.

Constraints: Teachers require experience with both tools. One computer per student is necessary for IRS. Selection of appropriate specimens to highlight the pros and cons of each tool is necessary.

Other remarks: Similar procedures could be used to teach students how to identify fish species using other methods (e.g. IPEZ, reference collections, IPOFISH, genetic tools).

5.19 ANGLERS TRACK THE SPREAD OF AQUATIC INVASIVE SPECIES (AIS)

Tag: Education, awareness building, consumer considerations and non-consumptive uses

Operators: sport anglers			End users: government (society)	
Response time	Accuracy	Resolution	Type	Resources
<i>minutes/days</i>	<i>very high</i>	<i>genus</i>	<i>whole fresh</i>	<i>moderate/high</i>
ID TOOLS: Field guides; taxonomist (for training); online or phone ID tools				

Description: Government and conservation agencies in the Great Lakes region, the United States of America, mobilize and train sport anglers to identify the most common aquatic invasive species (AIS) in the region, such as Asian carp and round goby, that are threatening the integrity of aquatic ecosystems. Anglers can act as sentinels to track the spread of AIS as supplements to the agency surveys. Taxonomists need to develop identification materials in several languages and disseminate them to millions of anglers.

Constraints: Highly diverse ability of anglers to grasp fish identification concepts as well as disparate motivation to check for AIS.

Other remarks: Field guides developed for this purpose should make extensive use of photographs. Outreach activities are necessary, e.g. distribution of ID tools and posters at water access points and specialized stores, angler clubs, and among fisheries professionals. They should include a media campaign and promotion of ID tools as well as giving access to taxonomists for questions and follow-up identification. Similar outreach activities targeting fish farmers could help reduce AIS movement via fish farming activities.

5.20 ASSESSMENT OF GENETICALLY MODIFIED FISH IN WATERS AND MARKETS

Tag: Education, awareness building, consumer considerations and non-consumptive uses

Operators: fish geneticists			End users: policy makers	
Response time	Accuracy	Resolution	Type	Resources
<i>n/a</i>	<i>high</i>	<i>species</i>	<i>processed body parts</i>	<i>low</i>
ID TOOLS: SNPs				

Description: Following the approval for commercial growing and marketing of genetically modified (GM) Atlantic salmon in the United States of America, the European Commission initiates a series of one-day workshops for consumers to educate them on GM salmon and its identification as well as on the probability of GM salmon entering the waters and markets of the European Union (Member Organization). The presenters are highly specialized experts (genetic engineering, molecular biology, statistical analysis, Atlantic salmon) and use slides, brochures and pamphlets. The presentations should include an introduction to molecular genetic techniques with resolution below the species level that would specifically target the trans-gene, e.g. SNPs. The statistical methods required to find the trans-gene in a sample (trans-gene could occur in extremely low frequencies) will need to be presented as well.

Constraints: It may be difficult to find experts with required range of expertise; issue is highly politicized, which may be an obstacle for objectivity; the highly complex scientific content might be difficult to communicate to a non-expert audience.

Other remarks: Public debates or information exchange between opponents and proponents of GM technology could be another possibility to educate policy-makers.

5.21 CORROBORATION OF THE GEOGRAPHIC ORIGIN OF FISHES AS DOCUMENTED IN CATCH CERTIFICATE

Tag: Education, awareness building, consumer considerations and non-consumptive uses

Operators: scientist			End users: government of NGO	
Response time	Accuracy	Resolution	Type	Resources
<i>weeks</i>	<i>very high</i>	<i>species/population</i>	<i>any</i>	<i>moderate/high</i>
ID TOOLS: (a) For species: taxonomist, field guides (<i>whole</i>) or scales, barcoding (<i>products</i>) (b) For populations: SNPs, scales				

Description: A certification body asserts that a certification scheme is being applied according to the agreed rules. For that purpose, it employs a taxonomist to verify the declared geographic origin of fish from catch samples. The resolution required is on the species and population level.

Constraints: In the case of highly processed products, adequate identification methods will be limited.

5.22 TRADED FISH IS LABELLED CORRECTLY

Tag: Education, awareness building, consumer considerations and non-consumptive uses

Operators: fish shop/restaurant owner			End users: consumers	
Response time	Accuracy	Resolution	Type	Resources
<i>minutes</i>	<i>high</i>	<i>species</i>	<i>whole fresh</i>	<i>very low</i>
ID TOOLS: (a) <i>Immediate ID:</i> Field guide, local experts, (IRS) (b) <i>Follow-up ID:</i> IRS, IPez, internet and computer-based information sources				

Description: A fish shop or restaurant owner buys fresh fish directly from the fisher or at a local fish market and wants to ensure that the information received from the supplier is correct. The purchaser has had some basic training in fish identification and good experience. The information is required right away (possibly before the sale is concluded) and the resolution should be at a species level. A portable computer may be available.

Constraints: A high probability of erroneous identification owing to time constraints, in particular when dealing with processed fish.

5.23 INVESTIGATING THE ALLEGED PRESENCE OF EXOTIC AND GM SPECIES

Tag: Education, awareness building, consumer considerations and non-consumptive uses

Operators: fishery officers			End users: law enforcement	
Response time	Accuracy	Resolution	Type	Resources
<i>days/weeks</i>	<i>very high</i>	<i>population/species</i>	<i>whole fresh</i>	<i>moderate</i>
ID TOOLS: (a) <i>For populations:</i> scales, otoliths, SNPs (b) <i>For exotic species:</i> taxonomist, internet-based resources				

Description: A fishery agency in Colombia receives reports about the presence of exotic and genetically engineered species (e.g. *Danio rerio*) as well as fish farm escapees (e.g. *Oreochromis* species) in a river and investigates. The officers involved have received basic training and have experience in the identification of local fish. A short-term survey in different parts of the river is carried out using available fishing and sampling gear. Sampled fish are identified and native species are released; all other species are brought to the base where they are identified to population level to detect the origin of the fish.

5.24 DIVERS IDENTIFY MARINE ORGANISMS

Tag: Education, awareness building, consumer considerations and non-consumptive uses

Operators: fishers			End users: fishing industry	
Response time	Accuracy	Resolution	Type	Resources
<i>hours/days</i>	<i>moderate/high</i>	<i>genus/family</i>	<i>whole fresh or photos/descriptions</i>	<i>low - moderate</i>
ID TOOLS: (a) <i>Onsite:</i> images (water-resistant) (e.g. with outlines of orders) combined with local expert (b) <i>After the dive:</i> Analysis of photographs taken during the dive using field guides and local expertise; consultation of experts at internet fora.				

Description: Divers identify fish encountered during their dives. The dive master is a local expert with some biological training and assists with on-site identifications. Most of the identification takes place just after the diving session and is based on oral descriptions and/or digital pictures taken during the dive. A high resolution (species level) of the identification is mostly not necessary.

Constraints: Identification may not be possible if the information is too general or vague or if the photos are unfocused. Common names are highly variable even among neighbouring locations/countries that share the same language. Underwater, oral communication is not possible without additional technology.

Other remarks: Picture-based keys (dichotomous/interactive) are problematic to use with photographs as these often do not contain the complete details required; thus, small and cryptic species may only be identified to the family level. It is important that divers understand that they share the seascape with other users, in particular local small-scale fishers and aquaculturists, and that the fishing gear, cages, pens and other aquaculture devices must be respected. A local expert can help divers to memorize the species by adding interesting information and tales, e.g. on striking biological or ecological features, or possible threats to species. Hobby divers can be trained to perform visual census surveys for ecological assessments (e.g. for the baseline studies for marine protected areas) – picture analysis sessions can be adjusted for such purposes.

6. Conclusions

This review has demonstrated a great potential for new identification methods - in particular those based on species images, morphometrics and genetics - which can be useful for a broad array of applications and situations. However, in spite of these findings and although only few question the urgent need for improved species identification in the context of sustainable resource management and biodiversity conservation, there is still a shortage of funding for the adequate research and development of these new ID tools, and this is hindering their use.

The following summarizes observations and suggestions made by workshop participants which are directed at managers and decision-makers who are responsible for research projects and programmes that rely on the sampling and identification of aquatic organisms.

The scenarios have demonstrated that different user groups have different requirements with regard to fish identification and that application of existing and development of new species ID tools should be targeting specific purposes (e.g. fishery inspectors would benefit from IRSs). In addition, training in the operation of different identification tools is very important and it would be beneficial if, for example, curricula for the training of fisheries inspectors routinely included the identification of fish using different tools. New technologies such as computer imaging, genetic tools and web identification should be part of such training.

In many geographic regions, there is a need for taxonomic products such as the field and pocket guides produced by the FAO FishFinder Programme. In particular, it was suggested that field guides should include complete and accurate lists of local names – a prerequisite for involving local fishers in the sampling and reporting of catches.

Early life-history stages often cannot be accurately identified owing to a lack of descriptions and guides. The identification of larvae and juveniles is particularly difficult and may require more specialized training as well as the development of special ID tools, including the creation of a photographic identification database for early life stages.

Experts at the workshop recognized the high value of web-based taxonomic resources. In particular, concerns were expressed about the sustainability of the current funding for two of the most important web-based taxonomic reference tools for fishes, i.e. the Catalog of Fishes and FishBase. The key role of the FishFinder Programme was highlighted for providing identification keys, taxonomic and bio-ecological descriptions, geographic distribution maps, FAO names and local vernacular names as well as fishery information. It is of great importance for the appropriate assessment and management of fisheries and biodiversity that these programmes and projects are maintained at a high scientific level.

The photo-based IEK presented to the workshop (IPOFIS) met with much approval, and experts thought that such local and regional inventories of expert-reviewed picture sets of aquatic species could be most useful for all regions. It was noted that such photographic inventories should cover all life stages and colour variations of a species, and include striking biological and/or ecological features. They could be used for the creation of different print and electronic products for species identification.

The creation of systems like IPOFIS is entirely possible today (although lengthy and costly). In contrast, functional automatic fish image IRSs for local and possibly also regional and global use are still far from becoming a reality. Such an application, for example, for mobile phones, would be an important step for a wide

number of applications if they became acceptably accurate; in particular, fisheries management would benefit from IRSs for target species.

IPez is a new identification tool based on morphometrics that has been developed specifically to allow non-experts to identify fish with a high degree of accuracy after only a short period of introductory training. It still requires the addition of more fish species to its database to become fully operational, but it already is showing great promise in terms of becoming an excellent and very affordable tool for the identification of fishes, for example, in the context of fisheries management.

Genetic tools are recognized as highly promising for applications where accuracy and resolution are of the essence. The experts noted that genetic identification can also be used for quality assurance, i.e. to determine the accuracy of fish identification by other methods (e.g. local users), as well as for the validation of taxonomic keys. This will require the development of simple and accurate genetic sampling and analysis protocols. However, the broad and routine use of genetic identification tools everywhere depends on the existence of a genetic reference collection and, consequently, genetic baselines for all commercial fishes in all regions are needed and should be developed. Moreover, in the future, transgenic fishes might be marketed and the development of improved markers for detection of transgenic organisms is advisable in order to meet consumer needs.

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Annex 2 - Workshop agenda

“FISH IDENTIFICATION TOOLS FOR BIODIVERSITY AND FISHERY ASSESSMENTS”

Convenors: FAO and University of Vigo. Vigo, 11–13 October 2011

Tuesday, 11 October 2011

09:00 – 09:20 Opening of the Workshop

Introduction

09:20 – 09:40 Objectives of the workshop (Johanne Fischer / Monica Barone)

09:40 – 10:00 The need for fish taxonomy in biodiversity and fishery assessment and management (Sven Kullander)

10:00 – 10:20 A practitioner’s view of fish identification (Keith Govender)

10:20 – 10:40 Identification and commercial names of fishery products. A view from the industry (Juanjo de la Cerda)

Taxonomy

Session Coordinator: Johanne Fischer

10:40 – 11:00 On the use and abuse of taxonomic keys (Paul Skelton)

11:00 – 11:20 Folk taxonomy (Alpina Begossi)

11:35 – 11:55 Web-based fish identification and information resources (Nicolas Bailey)

11:55 – 12:15 A photo-based computer system for identifying Wisconsin fishes (John Lyons)

12:15 – 12:45 General discussion

Genetics

Session Coordinator: Devin Bartley

14:30 – 14:50 Genetic methodologies for identification of fish: concerns for the FAO Fisheries and Aquaculture Department (Devin Bartley)

14:50 – 15:10 Genetic identification in support of fisheries management: principles and context (Gary Carvalho & Jann Martinsohn)

15:10 – 15:30 Genetic identification in support of fisheries management: principles into practice (Jann Martinsohn & Gary Carvalho)

15:30 – 16:00 General discussion

Morphometrics and Image Recognition

Session Coordinator: Cástor Guisande

16:15 – 16:35 Fish identification using scales (and otoliths) (Ana Ibáñez)

16:35 – 16:55 Image recognition systems for fish identification (Ricardo Torres)

16:55 – 17:15 Fish identification using morphometrics: IPEZ (Cástor Guisande)

17:15 – 17:35 Acoustic fish identification (John Horne)

17:35 – 18:05 General discussion

Wednesday, 12 October 2011

Elaboration of Report

09:00 – 12:30 Plenary discussion on user requirements and scenarios

14:00 -18:00 Discussion and drafting in three subgroups

Thursday, 13 October 2011

Elaboration of Report

09:00 – 13:00 Discussion and drafting (subgroups/plenary)

14:00 – 18:00 Adoption of summaries and recommendations (plenary)

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The need for fish taxonomy in biodiversity and fishery assessment and management

Sven O. Kullander

A stable naming and indexing system is essential to the global communication about organisms. Taxonomic research and animal names maintained under the International Code of Zoological Nomenclature underlie all communication about different "kinds" of fish. Support for taxonomic research consequently is of significant concern for fisheries and application of standards and statistics in fishery administration.

Taxonomy, among other things, provide the methods and the manuals for the identification of organisms. Although largely based on observations of characters that local fishermen may also use, taxonomic research provides tools for identification valid regionally and globally, and builds on continuous taxonomic research. Examples of fundamental tools for use in fisheries include FishBase (Froese & Pauly, 2011), the book *Fishes of the North Atlantic and the Mediterranean* (Whitehead et al., 1984–1986), and a series of catalogues and regional checklists provided by FAO.

Identification tools provided by taxonomic research traditionally consists of determination keys, images, field guides, and other textual information. Field/identification guides, including keys, have wide acceptance and may generally be considered highly reliable in regions with well-known faunas such as Europe and North America, and are convenient to use in field situations. In regions with numerous undescribed taxa, such guides will definitely fail.

Barcoding, i.e., short standard DNA-sequences, play little role in whole-fish identification in well-known regions, and have limited use in other areas if not tied to taxonomic baseline data. Barcode identification will be most important in laboratory conditions, in the identification of derived products, for faster detection of new species, and for species tracking when used with nextgen sequencing.

The formats available for tools for presenting taxonomic information will improve and amplify with the present rapid development of electronic communication. Taxonomic sites dedicated for smartphone presentations are already underway.

The ability to use taxonomic research requires some amount of training. Users may be confused by the terminology used in describing characters, as well as in occasional changes of scientific names, and by other aspects of nomenclature. Training in basic taxonomy is useful for all biology, but opportunities are limited.

There are several examples where lack of pertinent taxonomic information or lack of user experience actually or potentially lead to undesired consequences for fishery management.

The blue skate (*Dipturus batis*) was shown by Iglésias et al. (2010) to include more than one species. Unfortunately those authors chose to put two previously unused names on those two species. Instead, they should have investigated which species was originally intended as *R. batis*, which is quite possible using old literature. However, the problem should not have arisen in the first place, and exemplifies the need for continuous taxonomic research.

Trisopterus capelanus in the Mediterranean has long been considered a subspecies of *T. minutus* in the North-East Atlantic. Genetic and morphological data show that *T. capelanus* is a distinct species more closely related to *T. luscus* than to *T. minutus* (Delling et al., 2011). Evidence pointing to this has been built up gradually over the years but largely ignored by fisheries biologists, and there were no taxonomists available to work on the Gadidae.

The name of the turbot, *Psetta maxima*, is another case of confusion. It is placed either in the genus *Psetta* or the genus *Scophthalmus* depending obviously on chance. It is closely related to the brill *Scophthalmus rhombus*, so it would be natural to call the turbot *Scophthalmus maximus* (Bailly & Chanet, 2010). But where is the turbot taxonomist to finally justify it. In the meantime everybody suffer.

Apparently, North America and Europe need fish taxonomists to make revisions and set standards for scientific names, and provide reliable name standards and identification tools for fishery. This is an urgent need.

In the rest of the world, fish stocks are being exploited without much taxonomic assistance. It is impossible to develop conservation plans and long term management without knowing what species are involved, and preferably also if subpopulations exist, and how to identify them. Important faunal guides have been published by South Africa, Japan and Australia, but still in these regions, new species continue to be discovered, both from fresh material and from old museum specimens.

The surveying, mapping, taxonomic characterization, and naming of the global marine and freshwater fish fauna is fundamental to a healthy fishery, but the importance of taxonomic work is not fully recognized in the fisheries sector, particularly not in the boreal regions where "everything is known".

Taxonomic resources may also play a role in prospecting for new resources as is done particularly in aquaculture. Involving taxonomists in aquaculture is always recommended to prevent such mistakes as importing aquaculture stock of a species to where it or a very similar form is already present but the names used by aquaculturists are not correct.

Because an incorrect identification, use of outdated names, or application of misleading names can have considerable economic consequences, trust and reliability are essential to expect from taxonomic experts and taxonomic tools. Unfortunately, taxonomy is often practised by persons without the necessary training, not least persons only interested in naming new species. Taxonomic expertise should be based on a PhD in systematic biology including training in nomenclature and alpha taxonomy. It should also be based on considerable prior experience with the group in question.

Many users of taxonomic services consider a photo sufficient to work on. That may often be the case, but it may be a bad cornerstone in an operation spending millions of Euros. Specimen and DNA samples should be adequate for the identification precision requested, and that may take more than a snapshot on a swaying ship.

In conclusion: Taxonomy is paramount for describing biodiversity but is underfunded. Precise identification of species and populations can be effected by several tools, and is necessary for fishery management plans and reporting.

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Identification and commercial names of fishery products - a view from the industry

Juanjo De la Cerda

There are many aspects related to identification and taxonomy of fish species that have great importance for the industry.

Today in a growing number of countries - EU countries and others - the trade names of marketed unprocessed fish are regulated basing on an Official List that relates the scientific names of species and the possible trade names that can be applied to these. Several different mechanisms are developed by the States to keep this list updated.

It should be noted that the ultimate goal of these regulations should be to provide the consumer with adequate and understandable information allowing them to choose with full knowledge and in their experience and habits – to avoid being confused by the offer - and this sometimes is not an easy task as consumer culture and assessment of fish species vary significantly between different territories or geographical areas.

The availability, from the concerning international organization of some horizontal guidelines or recommendations that homogenize the criteria when it comes to managing groups of species - genus – or species not identified as a whole (.sp - .spp) would greatly facilitate better management.

In each case, control and surveillance markets services, deal with regulatory compliance, but their action is usually based on checking the adequacy of labelling so that the scientific and commercial names are related according to the list above rather than on the positive identification of fish species. In most cases any possible fraud control is not performed with the intensity that would be desirable.

The availability of quick and economic techniques that would permit the identification of species from the fillets, portions of fish or other preparations in the market, would certainly contribute significantly to market transparency and would lead to greater consumer confidence.

Going even further, the possible identification of not only the species but also, the geographical origin of the product would be desirable, because sometimes the different organoleptic characteristics, which can be based on the origin, determine also the potential commercial value.

As a last step, the possible incorporation of these standards on processed products, would be desirable, knowing that the original species identification is difficult in many cases and cannot always be matched with a different perception of value by the consumer.

In exploratory fishing or surveys, the availability of tools to identify images or morphological keys for non-experts, would facilitate the classification and the possible direct marketing of products without adding further non-productive costs for proper classification.

A practitioner's view of fish identification

Keith Govender

Fisheries enforcement around the world is unique to its own area of operations. A Fisheries Control Officer's (FCO's) task is a mammoth one. FCO's will therefore develop their skills in accordance with the fishing activities of their respective countries. Some of the duties that FCO's are responsible for are as follows:

- Monitor and record fish landings in commercial and fishing harbours
- Monitor slipways where recreational boats land their catches
- Conduct coastal patrols (and patrols by foot or vehicle)
- Conduct aerial patrols
- Conduct fisheries patrols at sea by means of inshore and offshore patrol vessels
- Effect arrests of illegal, unregulated and unreported (IUU) fishermen and fishing vessels
- Evidence collation
- Fish identification
- Testifying in a court of law
- Obtaining statements from expert witnesses such as scientists in areas of fish identification
- Assisting investigators with cases
- Continuous follow-up on the outcome of their respective cases

The above mentioned are but just a few of the duties of an FCO. In order for an FCO to ensure effective enforcement of fisheries regulations, it is essential for the FCO to have an understanding of fish identification. The above mentioned presentation will indicate to the audience the importance of fish identification in fisheries enforcement. The presentation will talk to the advantages of being able to identify fish when FCO's are engaged in their daily duties and it will also talk to the various methods that FCO's may utilize to identify fish.

The lack of training in the field of fish identification for FCO's will also be discussed. This is an important aspect for discussion as there are many FCO's who do not possess this skill. The lack of the necessary tools and experience in the field of fish identification is a crucial factor and the ways in which we can resolve these will also be discussed.

During the presentation, a present case will also be discussed that will aid the discussions on the importance of fish identification and enabling experts to be able to identify the fish. It is of critical importance to possess this type of expertise as it will assist in strengthening the case of the FCO against the accused.

Genetic identification in support of fisheries management: Principles and context

Gary Carvalho and Jann Martinsohn

Genetics in fisheries

Fisheries genetics - the application of genetic principles and methods to fisheries biology and management - has stimulated a resurgence of interest in the factors underpinning the dynamics and resilience of exploited species. Topics such as connectivity among marine populations (Cowen et al., 2006, Treml et al., 2008), the spatial and temporal scale of population differentiation (Jørgensen et al., 2005, Ruzzante et al., 2006), effective population size (Hauser et al., 2002, Waples and Yokota, 2007), fisheries-induced evolution (Olsen et al., 2004), and the analysis of adaptive variation in the wild (Conover et al., 2006), not only enhance our understanding of the mechanisms shaping fish abundance and distribution, but contribute conceptually to ecological and evolutionary theory. Whereas classical fisheries approaches focused typically on the factors driving short-term demographic changes in populations ("quantitative" change), genetic approaches examine the extent to which changes in the composition of populations ("qualitative" change) influence both short-term alterations in phenotypic traits and longer-term response to natural and anthropogenic perturbations (Frankham, 2005). Although the notion that population dynamics and genetic structure are inextricably linked was emphasized long ago (Elton, 1924), traditional fisheries biology makes scant reference to genetic factors in fish population ecology, as evidenced by recent texts in the area (e.g. (Jennings et al., 2001); but see (Hallerman, 2003)). Yet, as is clear from the recent escalation of publications in the field, the incorporation of such "qualitative" thinking into fish and fisheries biology has generated new insights into the temporal and spatial scale of change in fish populations and communities (Conover et al., 2006, Larsen et al., 2007), culminating in a significant shift in how we view both the marine environment and some of its key inhabitants.

Biological levels of genetic identification- species and populations

In relation to fisheries management, both the species and population level are relevant when in relation to their identification. For species, it might be self-evident,



FIGURE 1. THREE ESSENTIAL QUESTIONS, RELEVANT FOR FISHERIES MANAGEMENT AND CONSERVATION, WHICH CAN BE TACKLED BY GENETIC IDENTIFICATION APPROACHES. A) WHAT SPECIES? B) WHERE FROM? C) WILD OR CULTURED? GENETIC SPECIES IDENTIFICATION IS SHOWN HERE IN THE CONTEXT OF PRODUCT AUTHENTICATION IN A CONTROL AND ENFORCEMENT CONTEXT BUT CAN ALSO BE USED FOR FISHERIES MANAGEMENT E.G. WHEN PERFORMED ON ICHTHYOPLANKTON. THE GENETIC DISTINCTION BETWEEN WILD AND FARMED FISH WILL BECOME MORE RELEVANT IN THE NEAR FUTURE, DUE TO THE STEEP RISE IN AQUACULTURE ACTIVITY WORLDWIDE. SEE TEXT FOR DETAILS. FISH SYMBOLS COURTESY OF THE INTEGRATION AND APPLICATION NETWORK, UNIVERSITY OF MARYLAND CENTER FOR ENVIRONMENTAL SCIENCE. MAP: ©

EUROPEAN UNION, 2010.

that before being able to tailor management policies to promote sustainability, it is necessary first to identify those biological entities: that is, the biological properties attributable to each species, which will influence significantly patterns of recruitment, distribution, growth, size structure and consequent population dynamics. It is also essential that species-level identification can be made across life history stages, and even from fragments of tissue or remains, including processed fish products for example. Genetic techniques are suited ideally for such purposes because DNA, the genetic material that comprises the genetic code of all living organisms can be obtained from very small tissue samples, and often from highly degraded material. Within a species such genetic identification at the species level is also consistent across morphologically or ecologically divergent individuals.

The population as a target for biodiversity assessment and fishery assessments

Perhaps what is less well appreciated is genetic identification below the species level that is at the level of the population- a crucially important biological level to identify, monitor and accommodate within sustainable fisheries practices. The idea that species should be managed at some sub-specific level can be traced back to the turn of the century, when two pioneering fishery biologists, F. Heincke and J. Hjort, established the local self-sustaining population as opposed to the typological species as the preferred unit of study for fisheries management (Sinclair, 1988). Five primary drivers demand information at such scales. First, it is generally recognised that populations (hereafter used interchangeably with the term “sub-populations”) are the natural unit of evolutionary change, and as such, provide the genetic resources required for adaptive response to natural and man-made changes in the environment (Bonin et al., 2007). It is therefore at the level of populations that genetic and ecological diversity should be described for conservation measures, which necessitates discrimination between populations in relation to their distribution and abundance across regional waters. To preserve the evolutionary legacy and future evolutionary potential of a given marine fish species, it is important to secure viable populations covering the full geographical and environmental range (Nelson and Soulé, 1987). The existence of biologically differentiated populations, so-called “biocomplexity” (Michener et al., 2001), even in marine pelagic fishes (Ruzzante et al., 2006), has been credited with a major role in conferring resilience and in buffering overall productivity of fish population complexes (Hilborn et al., 2003). Thus, a key aim of sustainable fisheries management is to identify the spatial and temporal scale of population structuring, and to devise tools to monitor its dynamics and contribution to overall fisheries production. Even apparently small genetic differences among populations of marine fishes at presumably neutral genetic markers could translate into important adaptive variation distributed among populations (Conover et al., 2006). Second, it is at the population level that policy legislation and associated enforcement must take place. In addition to output management tools (catch limits, Total Allowable Catches (TAC), minimum landing sizes) there is a growing need to develop control through input management tools (capacity and effort limitation). Such a policy requires information on the relative dynamics and abundance of fish stocks from particular regions. Third, overfishing, eutrophication and habitat disturbance have made it increasingly important to know which populations act as sources and sinks, and how they might be connected by larval and adult exchange. Fourth, there is an increasing requirement for traceability of fish and fish products, both for consumer protection (Logan et al., 2008) and for regulatory enforcement (Primmer et al., 2000), in particular with respect to illegal, unreported and unregulated (IUU) fishing (McCluskey and Lewison, 2008). For example, in the UK, the Marine Stewardship

Council encourages consumers to eat particular landings of cod that are taken from ‘stocks maintained within safe limits’. A traceability system based on regional stocks is necessary to preclude fraudulent allocations. Fifth, there is increasing awareness that spatially-defined management in the form of Marine Protected Areas (MPAs) is a key addition in the arsenal of methods to promote sustainability and for biodiversity conservation (Polunin, 2002, Jones et al., 2008). The decisions governing the choice of reserve size, number, spacing and location depends heavily on species-specific patterns of connectivity, dispersal and biologically-significant population structuring. Thus, taking into account the pivotal role of population structuring in management, conservation and enforcement, and as fisheries stocks continue to collapse or show little recovery, it is no surprise that there continues to be considerable investment in genetic studies targeted at stock discrimination.

It is important to realise at the outset that genetic identification systems will necessarily be different for species and populations in terms of their nature, evolutionary characteristics and applications (Figure 2). However all such genetic methods share a common baseline: molecular genetic methods employ inherited, discrete and stable markers to identify genotypes that characterize individuals, populations or species. Heritability of such markers is crucial to ensure consistency of genetic signal across generations; their discrete nature into quantifiable entities, whether they be gene frequencies or DNA sequences, facilitates comparability across data sets and ease of quantification; stability ensures relative independence from environmental factors.

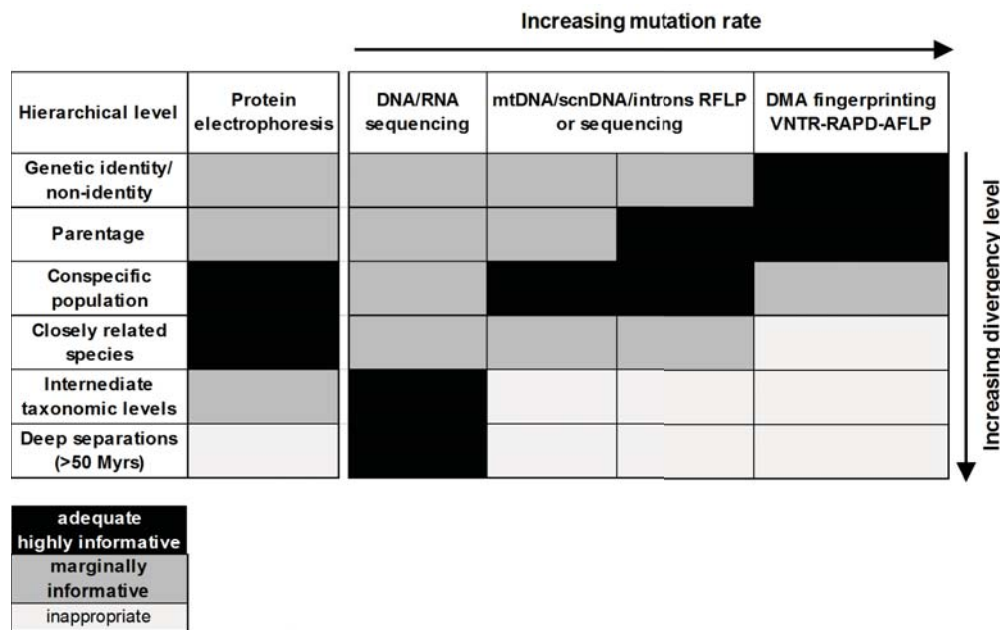


FIGURE 2. BROAD CLASSIFICATION OF MOLECULAR MARKERS AVAILABLE DEPENDING ON THE LEVEL OF EVOLUTIONARY DIVERGENCE. [AFLP: AMPLIFIED FRAGMENT LENGTH POLYMORPHISM; MTDNA: MITOCHONDRIAL DNA; RAPD: RANDOM AMPLIFIED POLYMORPHIC DNAs; RFLP: RESTRICTION FRAGMENT LENGTH POLYMORPHISM; SCNDA: SINGLE COPY NUCLEAR DNA; VNTR: VARIABLE NUMBER OF TANDEM REPEATS]. AFTER FÉRAL 2002.

“DNA barcoding”, a form of DNA sequencing which utilises a common or few short standard DNA sequences is most commonly used at the species level; for populations, current technologies utilise primarily microsatellites (a form of DNA fingerprinting using VNTR- variable number of tandem repeats- highly variable population markers) or, most recently, single nucleotide polymorphisms (SNPs),

that relies on a form of DNA sequencing to identify single mutational differences among common regions of the genome within and among populations.

In this synopsis we give brief consideration to the primary genetic tools that can be used at both the species and population levels, but focus on those that we present as the most widely used and that hold the greatest promise for their effective incorporation into biodiversity assessment and fishery assessments. Although individuals within populations are the ultimate target for analysis, we will restrict our analysis here to how individuals can be identified or traced back to species and populations, rather than the tools used to explore genetic relationships among individuals.

Approaches and rationale

Traceability in the “ocean to fork” sense relies on efficient, reliable, cost-effective technologies, enabling the independent control of compliance with rules. In the fisheries sector, this encompasses the ability to determine whether labels on fish and fish products identify the correct species, correct origin, and whether fish derive from aquaculture or the wild. Ideally, such methods should be adapted to end-users such as staff of control authorities, be applicable on whole fish as well as processed products, and swiftly lead to results. Moreover, if they are to be utilised for enforcement, these methods should be validated applying forensic standards and generate levels of confidence based on statistical analysis certainty, which are considerably higher than that required for purely scientific inference (Murphy and Morrison, 2007).

Historically, a plethora of methods have been used to identify fish species or for analyses supporting origin assignment. These include the description of features determined by morphology, which are used to identify a species. Markers, determined by the environment such as parasite load (MacKenzie and Abaunza, 1998), can be used to determine where a fish comes from (origin assignment). However, most morphological markers are also influenced by environmental factors (e.g. temperature), which complicates their interpretation, in contrast to molecular genetic markers (see below) which are transmitted across generations independently of environmental factors. With the advent of molecular biology, molecular and genetic markers are increasingly employed both for species identification and origin assignment. It is important to understand that traceability tools for species identification and origin assignment require comprehensive reference data sets (“baselines”): When control authorities wish to test whether a fish fillet derives from the species indicated on the product label, their analytical data must be comparable to a set of validated data for species identification. This has been achieved to a great extent by the DNA barcoding approach (see below). Likewise, if the origin of a fish (product) is under investigation, fish deriving from different geographical regions must have been formerly analysed and distinct features, robust “population-level signatures”, characterising these groups must be recorded. We now consider some fundamental principles on the use of advanced analytical technologies based on genetics, genomics and chemistry for traceability of fish species identification and origin assignment.

Broadly speaking, the analysis of genetic markers can be separated into DNA-analysis, revealing DNA sequence variation, and protein analysis, that reveals differences in amino acids. For traceability purposes, for example, samples of fish (or products) have to be collected, followed by DNA or protein extraction from tissue, nowadays a routine process facilitated by commercial kits. Protein analysis, such as isoelectric focusing (IEF) and related techniques (Rehbein, 2003), or assays based on antibodies binding to proteins with high specificity (Taylor et al., 1994), can provide high species resolution and are still applied for fish food authenticity

control. However their application is progressively replaced by DNA-based technologies (see below).

Recently, the use of DNA markers has increasingly become the standard approach in fisheries genetics and fish food research (Hauser and Carvalho, 2008, Rasmussen and Morrissey, 2008). Both for fish species identification and population structure studies, which ultimately underlie origin assignment, the genome of the mitochondria - sub-cellular organelles - and the nuclear genome have been useful (Kochzius, 2008). Particularly, the use of the mitochondrial cytochrome oxidase I (COI) gene for species identification by "DNA barcoding" has a high potential for routine fish species identification purposes (Ward et al., 2009). For the analysis of species identifying DNA markers, a panoply of different technologies has been employed which is reviewed in detail elsewhere (Teletchea, 2009).

Species-level identification

For species identification, DNA microarrays ("DNA-Chips") can here be of great value. Microarrays consist of a surface with thousands of covalently attached DNA oligonucleotides. This allows monitoring of thousands of different (i.e. species identifying) DNA sequences simultaneously with one array (size about 1x1cm). Theoretically, just one chip would enable the screening for all major economic fish species simultaneously (Kochzius et al., 2008). While the development of DNA-microarrays is laborious, the running costs are moderate. Other high-throughput and parallel processing methodologies for fish species identification have also been developed (Dooley et al., 2005). Such technologies might ultimately lead to the development of handheld analytical devices, enabling field use, which is critical with respect to the response time (the period between starting an investigation and the receipt of analytical results). For example, inspectors in the fisheries sector carry huge responsibility: if they decide to put landings "on hold" because of suspect content, there can be severe consequences for fishermen and stakeholders. Engineering of such machines is carried out in support of forensic genetic analysis at crime scenes (Liu et al., 2008). However, while recent publications show that progress has been made in this area (Arnaud, 2008), currently no cost-effective handheld analytical device supporting fisheries control and enforcement or traceability is available.

One of the most commonly employed species-level genetic identification systems is DNA barcoding. Although the approach utilises technologies that have been available for some time within the general field of "molecular systematics", initially based primarily on protein variation or allozyme electrophoresis, there are attributes of the approach of DNA barcoding that are highly distinctive and that enhance its utility within fisheries applications. Hebert et al (2003) proposed a new approach to species identification, which offered great promise. The new approach is based on the premise that the sequence analysis of a short fragment of a single gene (cytochrome c oxidase subunit 1), enables unequivocal identification of all animal species. Hence, analogously to the barcodes used in commercial products, the DNA barcode would provide a standardised tool for fast, simple, robust and precise species identification. Such a 'barcode region' would also have to evolve at a rate that would distinguish species from each other while remaining more or less identical for all members of the same species. Finally it would have to be flanked by conserved DNA regions so as to make the polymerase chain reaction (PCR), a method of targeted gene replication. With the exception of certain groups of Cnidaria and sponges, studies have now confirmed that the target segment of COI ordinarily provides clear-cut discrimination of most animal species. An international consortium (Consortium for the Barcode of Life, CBOL) was established in 2004 to build support for global implementation of DNA barcoding. The critical

mass of institutional and community participation required to progress the DNA barcoding effort for species identification now exists: the International Barcode of Life (iBOL) project. With the central goal of building a library of DNA barcodes for 5 million specimens and 500 K eukaryotic species by 2015, iBOL promises rapid progress toward a global identification system accessible to all. DNA barcoding differs in many ways from conventional taxonomic identification tools and approaches, over which it offers several advantages. It permits the identification of species from fragments, and from any life-history stage, as well as the standardisation of a universal master key in a format that reduces ambiguity and enables direct comparison of specimens to a global reference database.

Fish and fisheries resources comprise a key target group from which it is anticipated that DNA barcoding will bring larger and more immediate benefits. Such a system will offer a simple – and increasingly rapid and inexpensive – means of unambiguously identifying not only whole fish, but fish eggs and larvae, fish fragments, fish fillets and processed fish. This capability will yield more rigorous and extensive data on recruitment, ecology and geographic ranges of fisheries resources, and improved knowledge of nursery areas and spawning grounds, with evident impacts at the fisheries management and conservation levels. For example, the possibility of rigorous identification of fish species from eggs and larvae could be particularly fruitful, since phenotypic identification of early life stages can be especially difficult. A study testing the application of molecular techniques in species identification of fish eggs revealed that over 60% of the eggs were misidentified when phenotypic characters were used. 81 Eggs from haddock and whiting may have been reported as cod's eggs in previous surveys, possibly leading to an inflation of stock assessments of cod in the Irish Sea (Fox et al., 2005). Moreover, early stage haddock eggs were detected in the Irish Sea, indicating the presence of a spawning stock of this species previously unknown to that region. In a context of environmental change, induced, for instance, by global warming, the ability to rigorously identify fish species at all life history stages from egg to adult is particularly useful to assess changes in geographic distribution ranges, spawning grounds and nursery areas.

Potential forensic applications of fish DNA barcoding include the monitoring of fisheries quotas and by-catch, inspection of fisheries markets and products, the control of trade in endangered species, and improvements in the traceability of fish products.

In Australian waters, for example, sharks are illegally captured, largely for their fins alone. Quality sharks' fins can sell for \$6,000-\$8,000/kg in Hong Kong, and it is estimated that globally more than 100 million sharks are killed every year. Sharks are a particularly susceptible animal, since they are slow growing, long lived, undergo a long gestation and have low fecundity. Many species are morphologically very similar, and many are protected. A tool enabling precise identification of shark species from fins, from the fisheries boat to the soup in the restaurant, could be of great utility for law enforcement and conservation of endangered species. Such a tool could also be used for detection of fraudulent species substitutions in fish markets and fish food products, a practice that is generating concern among consumers. A striking example comes from the Red Snapper (*Lutjanus campechanus*), which is one of the most economically important fisheries in the Gulf of Mexico, and which has been subject to stringent fishing restrictions due to stock depletion. Marko and colleagues used sequences of the mtDNA gene cytochrome b, in an approach very similar to DNA barcoding, to show that as much as 77% of the *L. campechanus* fillets were mislabelled in USA markets. This level of mislabelling may adversely affect estimates of stock size and contribute to the false impression among consumers that the supply of fish is keeping up with demand.

Thus, DNA barcoding provides a standardised tool for describing and monitoring fish species diversity, not only in the wild, but also throughout the food supply chain in relation to legal enforcement and consumer protection. Moreover, a globally-accessible, standardised DNA barcoding data base means that non-experts may utilise the information to examine species identity, but importantly also allows a coordinated and extensive effort to document biodiversity from throughout species distributions.

Population-level identification

Here we will focus on those DNA markers most amenable to identification in fisheries. Microsatellites, also called Short Tandem Repeats (STRs) in forensics, are tandem sequence repeats of one to six nucleotides (e.g. 'cgtacgtacgtacgtacgta') in the genome. Their high polymorphism is characterised by variable repeat numbers (between 5 and 100) even between individuals. Microsatellites are the standard marker for human identity testing by DNA profiling and for forensic genetic crime scene investigation (Butler, 2005). They have also been extensively used in fish population studies, and their potential value as traceability markers for origin assignment is very high. However, despite the widespread application of microsatellites, there are drawbacks, particularly scoring error and lack of comparability among laboratories (Dewoody et al., 2006). Nevertheless, numerous examples exist where microsatellites are used for fish population/stock analysis, management, and also origin assignment (Manel et al., 2005, Hauser and Carvalho, 2008), including Atlantic salmon (Primmer et al., 2000), Pacific salmon (Fisheries and Oceans Canada, DFO) and cod (Nielsen et al., 2001).

Meanwhile, Single Nucleotide Polymorphisms (SNPs) entered the realm of fisheries genetics, offering a great potential for origin assignment (Hudson, 2008). SNPs are genome sites where more than one nucleotide (A, C, G or T) is present in a species. They are the most abundant polymorphism in the genome (Brumfield et al., 2003), but per locus normally only two alleles exist (biallelic markers), thus they are less variable than Microsatellites, where often many alleles exist. The lack of potential information per SNP marker is outweighed by their high abundance. Compared to other genetic markers, where routine genotyping and transfer of protocols between laboratories proves difficult, the information retrieved from SNPs is categorical, and data can be standardized across laboratories for forensic applications (Sobrino et al., 2005). However, a substantial research effort targeting all commercial marine fish species will be necessary before SNPs can be employed routinely for origin assignment. Despite this, available studies on marine fish using SNPs are encouraging. SNPs as markers to distinguish stocks of Atlantic cod (*Gadus morhua*) provided a high resolution power for stock identification, comparable to that of microsatellite loci (Wirgin et al., 2007). Another example is the North Pacific Anadromous Fish Commission (NPAFC) that is developing SNP arrays for Pacific salmon (www.npafc.org). The application of SNPs to population genetics is not without some problems, including so-called "ascertainment bias"-the selection of loci based on an unrepresentative sample of individuals. For example if SNPs have been developed from a few individuals (small ascertainment depth), SNPs with high heterozygosities are preferentially found, providing a false impression of overall genomic polymorphism. Likewise, if SNPs are developed from a biased sample of individuals (e.g. not covering the full range of populations), comparative analysis with respect to population-specific indices of variability can be biased. However, in the context of mixed stock analysis (MSA) for example, ascertainment bias is not expected to create problems. Population-biased ascertainment could result in marginally lower power for MSA in populations not included in the ascertainment sample; however, the high number of markers employed

would most likely compensate for this.

Among the most recent application of SNP markers to fisheries were the outputs deriving from an EU Seventh Framework Project, FishPopTrace (<http://fishpoptrace.jrc.ec.europa.eu/>). Among the most striking scientific results is the provision of several hundred novel genetic markers in, hake, herring and sole. Although these fish represent a major part of the European catch, many aspects of their biology remain unknown. This holds also for the number, location and independence of biological populations. The lack of high resolution genetic data has complicated sustainable management, which should rely on the basal biological independent units rather than geographically defined “stocks”. However, access to new genetic methods, the so-called next generation sequencing, has changed the picture in a matter of just a few years. From a dozen genetic markers a few years ago, we now have knowledge about thousands of small genetic differences (genetic variation) at numerous genes, allowing the design of hundreds to thousands of new genetic markers. The unique combinations of the variation make it feasible to assign the fish to specific populations and in some conditions to identify unique individuals.

It is now possible to correctly assign fish to populations from more areas and with higher certainty than previously possible, reaching standards which can be used in a court of law. Based on use of the most highly distinct genes among populations it has been possible to develop “minimum assays with maximum power” with from 10-30 SNPs. These assays have been developed to target some of the most pertinent needs for traceability tools in European fisheries management. For example, fast, efficient and forensically robust tools are now available to discriminate between cod from Canada, North Sea, Baltic Sea and Northeast Arctic populations, between North Sea and North Atlantic herring, between sole from the Irish Sea and Thames and between hake from the Mediterranean and Atlantic areas.

One major advantage of using SNPs is the ability to alter the number of markers in relation to the biology of the species (levels of genetic differentiation) and scale of geographic structuring of interest. Thus by varying the numbers used on a SNP-chip, it is possible, for example, to assign individuals back to their source population across different geographic scales with high levels of certainty and reproducibility. Such outputs are especially significant since previous types of genetic markers either detect levels of population differences that are too low, or there are inherent difficulties in comparing data generated from different laboratories. The use of a marker system such as SNPs, which is essentially based on the presence or absence of large numbers of single genetic variants means that data can be compiled from sources in a much more reliable and high throughput way. The approach thereby enables the generation of baseline and ongoing additions for subsequent genetic monitoring. Moreover it is imperative that any such tools can be used in a legal context, necessitating forensic validation. This has been achieved for SNP markers within FishPopTrace across a range of policy-driven IUU scenarios (see Traceability of Fish Populations and Fish Products: Available from- . <http://fishpoptrace.jrc.ec.europa.eu/>).

Anticipated developments in the near future

Although there is always an element of uncertainty in forecasting the nature and direction of technologies and their application, the following trends are likely:

At the species level: although a range of tailored protein or DNA-based tools can be employed to discriminate species from a variety of sources, there is a widely recognised need to secure standardisation, high cost-effectiveness and accessibility of data generated. Although DNA barcoding depends upon the availability of a publicly accessible data base, it is globally available and enjoys strict quality

control, both in the technical aspects of generating the DNA sequences, and also importantly in their deposition into data bases. The high throughput nature of DNA barcoding also means that the costs have declined in recent years, and such work can be either outsourced to a central facility, or be undertaken by commercial sequencing companies, meaning that local infrastructure and expertise can be minimal.

At the population level: large data bases of microsatellite data exist for many commercial fish species. Although such resources will continue to be developed and utilised, a primary limitation is their comparability across laboratories and data sets. The ability to type an allele (genetic variants at a specific region of the gene) at a genetic locus depends essentially on quantifying the size of that allele in terms of the number of component nucleotide bases (bp), which critically depends on the electrophoretic equipment and size standards used in individual laboratories. The general lack of calibration across laboratories poses large problems for creating comparable databases for population identification, traceability and forensic applications. SNPs in contrast are essentially binary – at a specific gene locus, there are only 2 possible conditions – the absence or presence of a variant (in diploid genomes, as with most fish), and such characters can be more readily quantified and compared based merely in their frequencies in populations. Individual SNP loci are less informative than microsatellites, but the ease of ascertainment due to their high abundance can generate equal or higher statistical power with higher quality data and better genomic coverage, making SNPs the best candidate for future genetic markers for ecology, evolution and conservation. Importantly also, establishing base line data bases to examine changes over time in distribution and abundance of specific spawning populations, means that SNPs are ideally suited for ongoing additions to the data base. Genetic monitoring can then become attainable. Thus, wherever possible, SNPs might be expected to increasingly dominate the available approaches for fish population identification, as indeed is becoming the case with the management of Pacific salmon in the USA.

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Genetic identification in support of fisheries management: Principles into practice

Gary Carvalho and Jann Martinsohn

Scientific advice is undeniably indispensable to sound fisheries management and fisheries science is already taken into account in the process of reaching management decisions in many countries around the world. However, modern analytical technologies based on genetics and genomics to address marine biological questions including those relevant to fisheries management, still remain almost exclusively harboured by the academic realm. This stands in stark contrast to the current genetic and genomic technological revolution, which is only paralleled by that in the IT sector. There is significant scope to exploit such advances within the environmental and fisheries context.

The prevailing under-utilisation of molecular technologies, in particular DNA-based technologies, is indeed unexpected. As shown by many, yet sparse, examples, some of which are mentioned in the section before, such technologies are not only theoretically available to support the fisheries sector, but have already been used both for fisheries control and enforcement, as well as management and conservation purposes. Moreover, while genetic population characterisation of marine fish remains a challenge and needs for many species significant further research, species identification is at a stage where it should become standard and routine internationally for management bodies and control authorities. The ease with which DNA-barcoding can be applied is exemplified in a test carried out by high school students of the Manhattan Trinity School in collaboration with the Ontario University of Guelph: 60 samples of seafood taken from New York sushi restaurants and seafood markets, were tested for their authenticity. DNA-barcoding revealed that approximately 25% of fish samples with identifiable DNA were mislabelled (Schwartz, 2008). In a similar way, it is anticipated that with appropriate investment and development, research projects such as FishPopTrace (<http://fishpoptrace.jrc.ec.europa.eu>) will in the near future considerably increase knowledge about the genetic population structure of marine fish. This will greatly facilitate the uptake and integration of genetic approaches into fisheries management and help to tackle the fundamental question “To what extent do biological units match management units”?

The feasibility of applying DNA-based technology for fisheries control and enforcement is shown by a collaboration between the Danish fisheries inspectorate and the Danish Technical University (DTU). Inspectors are equipped with tissue sampling kits and can send samples for genetic analysis to a laboratory of the DTU if suspicion about the identity or origin of fish landings arises (Personal communication: Lars B. Erikson - Danish Fisheries Inspectorate). Moreover genetic origin assignment, long thought to be hardly possible for marine fish, was applied in a recent enforcement case: A fisher who claimed his catch was from the Baltic Sea, where he was legally entitled to fish. A DNA analysis, comparing microsatellite marker allele distribution between Baltic and North Sea cod proved beyond reasonable doubt that the fish in question could not have been caught in the Baltic and had been caught in the North Sea, where the fisherman had engaged in illegal fishing. Based on this evidence the court decided to confiscate the catch and the fisher was fined (Personal communication: Danish Directorate of Fisheries, 2006)

There are also examples for the application of genetic principles in fisheries management.

Pacific Salmon management is meanwhile to a large extent based on SNP analysis on a yearly basis, and even challenging management questions such as mixed stock analysis are addressed using a genetic approach (Seeb et al., 2011, Barclay et al., 2009).

Also in Europe there are, even though currently rather timid, attempts to integrate genetics into fisheries management. One example is the Western Baltic cod stock exploitation. Western Baltic cod is fished with very high intensity, beyond the MSY but has not yet collapsed. Eastern Baltic cod is doing well. It was observed that over the years the fishing pattern has changed so that a larger proportion is fished right at the border between Eastern and Western Baltic. So the question arises whether instead of fishing Western Baltic cod, Eastern Baltic cod is exploited in this border region. Genetic testing, using only 20 SNP markers can unambiguously differentiate between Eastern and Western Baltic cod and it has been suggested to apply genetic testing to determine which stock is really exploited. This example exemplifies that by using genetic approaches fisheries management can identify basal biological units in order to secure sustainable fisheries.

Capacity building

Yet, despite such, largely anecdotal, success a coherent and consistent approach to fully integrate genetics into fisheries management on an international level is not yet in place. This includes control and enforcement, where genetic testing could strongly support traceability schemes. Since illegal fishing or fisheries fraud is barely impaired by borders, the apparent little uptake of DNA technologies is of particular note. Similarly, it is appropriate to stress that developing countries are most exposed to the risks emerging from IUU. For example, along the West African coastline, total estimated catches were reported to be 40% higher than reported catches (MRAG and Development:DFID), 2009). Many countries, including those from the developing world, urgently require access to affordable valuable traceability tools for fish and fish products and, eventually, the use of forensic genetic tests as emphasized for example by the FAO (Personal communication: Michele Kuruc - FAO Fisheries and Aquaculture Department). However, such uptake places demands not only on the availability of appropriate technologies, but crucially is constrained by complex socio-economic and political issues.

What are the principal reasons for the insufficient transfer of genetic technologies into traceability applications readily available for management and authorities, and how can existing obstacles be overcome? – To a large extent it is the consequence of a prevailing gap between science and fisheries management (Waples et al., 2008) and a similar problem is observed in wildlife forensics (Ogden, 2010).

A further considerable impediment is the current absence of a central data hub, where DNA data relevant to fisheries management is stored, professionally managed and easily accessible, similar to the European Bioinformatics Institutes (EBI) DNA databank (Brooksbank et al., 2009). However, a great opportunity opened for species identification by the DNA-barcoding approach (see also section before), since reference DNA-sequences for currently nearly 8300 fish species (September 2011) are compiled in a public database (www.boldsystems.org). In contrast, an analogous database including baseline data for fish population structure analysis and origin assignment is unavailable. This lack is basis for the recommendation of the ICES Working Group on Applied Genetics in Fisheries and Mariculture (WGAGFM) to create a meta-database cataloguing existing data in the field of fish and shellfish population genetics (Verspoor et al., 2009).

Additional requirements have to be fulfilled to build a functional infrastructure ensuring the use of modern molecular technologies globally. Not only should data be easily accessible, but it must also be validated, data quality must be verified, and standardized formats must be applied. For the purpose of fisheries control and enforcement, a network of test laboratories, certified to carry out analysis for control and enforcement purposes, and applying protocols, validated through inter-laboratory trials, as well as forensic standards should be established. Such institutions should also be committed to share information and expertise. In many countries it won't even be necessary to create new laboratories as facilities with appropriate expertise and capacity already exist. However, these typically operate independently, and respond to ad hoc queries. To ensure inter-operability and consistency, both on the national and international level, accreditation schemes for routine and reference laboratories should be put in place, as for instance observed in the GMO detection area (Zel et al., 2006, Zel et al., 2008). Another crucial component of capacity building is training. For fisheries management and conservation measures this concerns specifically sampling. In fact it should be explored how routine sampling activities and surveys currently carried out for stock assessment purposes can additionally be used for genetic analysis purposes.

For control and enforcement training should be tailored for and targeted at inspectors, enforcement officers, including guidance in core sampling procedures and for laboratory personal. Such an approach will be followed by the European Commission in November 2011, by providing a forensic genetic training course to EU member countries and partner countries with access to the Mediterranean and Black Sea. Additionally the existence of "focal points", institutions, endowed with the necessary expertise and authority to produce technical guidelines and standards to be followed by laboratories, to pursue targeted dissemination activities in order to inform stakeholders would be crucial.

Ideally the transfer of genetics into fisheries management, including control and enforcement should be accompanied by a sound Cost Benefit Analysis (CBA) to estimate cost-effectiveness and to provide a valuable reference and decision-support tool for stakeholders and policy analysts (Pearce et al., 2006). However, the recent decline in costs, especially for DNA analysis, and the examples of applications, strongly indicates that the methods discussed here are cost-effective. Moreover, advanced technologies feature an added value in that they are beneficial to fisheries management beyond traceability: they typically allow detection and monitoring of discrete fish assemblages, the dynamics of which underpin resilience and recovery (Waples et al., 2008).

Future trends

To attain sustainable exploitation levels of fish, and to build a healthy and thriving fisheries sector major efforts, on national and global level, will be needed.

Aquaculture is often regarded as an increasingly important contributor to the global food supply and food security, and also as providing an alternative to wild capture fisheries, thereby helping to preserve fish stocks, biodiversity and ecosystem services (Science, 2011, Godfray et al., 2010, Hishamunda and Ridler, 2006). However there are strong concerns about the environmental impact of aquaculture (Focardi et al., 2005, BurrIDGE et al., 2010), including the risk of fish escaping from farms into the wild ('farm escapees'), a genuine concern as shown by the high number of salmon escaping from aquaculture worldwide (Naylor et al., 2005). Specifically the risk of the potential genetic impact of fish farm escapees on wild populations (genetic introgression) has been addressed by scientists (Utter and Epifanio, 2002) as well as regulators (e.g. (Fisheries, 2010)). While this is currently still largely a scientific matter (e.g. AquaGen: <http://aquagen.jrc.ec.europa>).

eu) there are already examples where genetics were used to identify farm escapees and trace them back to the farm of origin (Glover et al., 2008).

DNA-based technology development is advancing at a staggering pace (Metzker, 2010), and the fisheries industry, including control authorities, can and should profit from this phenomenon. Also new approaches such as proteomics and gene expression profiling are increasingly looked at in the context of fisheries management.

Gene expression, the process by which information encoded by a gene is used in the synthesis of a gene product, can differ between species (interspecies level), but also changes in response to the environment, and is subject to adaptive evolution on an intraspecies level. Microarrays have been used to analyse gene expression in fish to investigate questions related to ecology, evolution and environment. Gene expression variation has also been assessed in natural populations of marine fish (Larsen et al., 2007). Microarrays used in the study of population differences in gene expression target thousands of genes simultaneously ("transcriptomics" – reviewed in (Nielsen et al., 2009)). Such microarrays have now been developed for a large number of marine fishes, e.g. gilthead sea bream (*Sparus aurata*) (Ferraresso et al., 2008), Atlantic halibut (*Hippoglossus hippoglossus*) (Douglas et al., 2008) and Senegalese sole (*Solea senegalensis*) (Cerdeira et al., 2008). They are presently particularly used for aquaculture species as they help to elucidate transcriptional changes under specific farming conditions or during infections. This can improve knowledge about reproduction, development, nutrition and immunity thereby supporting the optimization of production under culture conditions. Proteomics, the investigation into the sets of proteins expressed by the genome of an organism under given environmental conditions, has recently been employed to understand protein diversity across and within human populations (Biron et al., 2006).

Analysis of gene expression is in principle applicable to develop suitable markers for population studies, be it for origin assignment (if different expression patterns between populations of fish occupying different regions/environments can be established, this can be used for traceability) or to distinguish between wild and farmed fish. This has recently been demonstrated in a study on European hake (*Merluccius merluccius*), where proteomics have been used to establish differential protein expression patterns in hake from the Mediterranean Sea, the Cantabrian Sea, and the Atlantic Ocean (Gonzalez et al., 2010). However while assessing the potential of such novel tools is also part of explorative research of projects such as FishPopTrace, they are not yet used in fisheries management or at an applicable stage for control and enforcement.

To maximise the power of fish product origin verification a holistic approach taking into account different and complementing technologies is advisable. For control and enforcement this has been done in recent high-level workshops held by the FAO and the European Commission, involving regulators, policy makers, control authority personnel and scientists. The latter event was highly successful in that it contributed to the mentioning of genetics as a potentially powerful technique in support of fisheries control and enforcement in a new EU law (European, 2009). Similar events addressing fisheries management in general and involving fisheries scientists, managers and geneticists are needed to advance the field and to improve sustainable fisheries management schemes worldwide.

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Use and Abuse of Taxonomic Keys

Paul Skelton

The use of taxonomic keys is a well tried and tested method to identify organisms in biology. A taxonomic key is an ordered sequence of alternative choices as provided by diagnostic (morphological) characters of organisms that leads to a reliable identification of an organism or class of organism. The effectiveness and efficiency of a particular key depends on its construction and terminology, factors that depend on the knowledge, expertise, and skill of the individual building the key. The target user group for a particular key is equally important in terms of key construction – inappropriate terminology can render a key ineffective.

User group definition is a vital first step in good key construction. Generally in biology there are three levels of potential user groups – a basic level where elementary or little technical skill or knowledge is available and identification is intended for curiosity or general interest purposes only; an intermediate level where technical skills and knowledge are basic or general and the purpose of identification is broadly requisite at a technical level (eg. subsistence fishery monitoring); and lastly at a specialist technical level where identification is for scientific purposes and a high degree of accuracy and precision is required.

The principles for effective key construction are the same across the different user group spectrum. The major differences involve terminology and character description. The actual form and structure of a key can vary from strict dichotomy to polychotomy depending often on the complexity of the target group of organisms and the target user group level.

The broad principles of good key design includes (a) that characters used must be diagnostic at the relevant level of universality, (b) the characters used should be differential at the relevant level of universality, (c) redundant characters should be included where possible to aid choice, (d) terminology should be consistent and uniformly used, (e) positive attributes are preferable to negative attributes, (f) character descriptions should be clear and unambiguous, with comparative levels clearly defined and illustrated where necessary, (f) geographic and non-specimen features used in the key only when needed for unambiguous identification. Keys generally use telegraphic style of statement and can vary in terms of format (eg. indented). The coverage and scope of a key should be clearly defined in advance. In general keys should aim to cover a single level of universality (eg. families, genera, sub-genera or species) rather than stretch over the entire range. Excessively long keys frequently resort to trivial or ineffective character differentiation.

Common problems in usage of keys leading to misidentifications include excessive technical jargon, obtuse character clarity, overlapping characters, under-estimated character variation and mistaken characterization, the non-discrimination of cryptic or complex species groups, and incomplete coverage including omission of sexual or ontogenetic (life history) dimorphism.

Taxonomic keys are considered as aids to identifying organisms, and in at least technical scientific context, identifications made should be confirmed by comparison with verified specimens or through vouchered specimens submitted to an authority.

Traditional keys are generally single-access, requiring a fixed sequence of leads from the beginning of the key. An alternative is multi-access keys where entry is defined by user character choice and the key format is in tabular or as a matrix. Multi-access keys generally use high-tech computer systems and can include interactive elements such as audio-visual or supplemental text.

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Folk taxonomy: Applications in fisheries

Alpina Begossi

Introduction

Folk taxonomy is an area of inquiry that deals with the understanding of how populations perceive, identify, and classify organisms. Such discipline has had a notorious growth after the eighties, and especially after the development of a body of knowledge created and based on data collected on native communities from B. Berlin (1982), Brown (1984), Hunn (1982), Medin and Atran (1999), among other researchers. Berlin's contributions are manifold, but his five hierarchical categories in folk taxonomy are very adequate from data gathered on native knowledge, which are as follows: unique beginner, life form, generic, specific, and varietal.

Life form in an intermediate rank, and Brown (1984) contributed with analysis on life forms (that should be equivalent to family, class or order in taxonomy) in folk taxonomy, among others. Hunn (1982) have proposed that organisms are not perceived and identified by people at random, but based on their salience, that can be identified or perceived mostly by the utility of organisms.

Folk taxonomy in fisheries

Fishers have shown a great deal of knowledge on the fish they know, especially on target species (Begossi et al., 2011, Ruddle, 2000; Silvano et al, 2006). Their knowledge includes fish behavior, the marine environment and habitats and ecosystems interactions (Ruddle, 2000). In our study here we are most concerned to folk taxonomy, a sub-sample of the total body of local ecological knowledge.

Our results from Brazilian coastal and riverine fisheries have shown that fishers perceive, identify and classify the fish they target, which embody especially commercial fish, as well as the fish that shown some kind of salience, such as the colorful Labridae (Begossi and Figueiredo, 1995).

Fish nomenclature has received more detailed attention by the use of binomials in Amazonian riverine communities rather than in coastal communities of the Atlantic Forest. A high number of binomials denotes a fine-grained identification and nomenclature; in the case of the comparison between Amazonian riverine and coastal marine communities, our hypothesis is that the diversity of forms (and taxonomical orders) is much greater in the marine environment rather than in the riverine environment, where the necessity of binomials responds to the necessity of more detail in the diagnostic variables necessary to differentiate fish species. On the other hand, in the Atlantic Forest coast, the generic denomination is common and sufficient to discriminate among the different forms and fish species (Begossi et al. 2008). Some families of difficult identification in taxonomy are also difficult to identify in folk taxonomy, such as the Loricariidae (Begossi and Garvello, 1990).

Diagnostic variables used by fishers are of importance in the interaction between folk and scientific taxonomy, since it is a form of understanding how and why fishers separate the fish species. Some results are shown in this regard, such as on the use of morphological variables to identify fish (examples through species of the families Serranidae and Sciaenidae) (Table 1).

Prototypes are found in folk taxonomy (Oliveira and Begossi in prep.); since groups (or species) are difficult to differentiate, a prototype can usually be the most easily identifiable species, or the most easily recognized, or even the most abundant among species.

The methods used to study folk taxonomy include interviews, some using pictures of a fish collected or obtained at landing point, and systematic sampling of

the fish landed. Methods are applied in the field, and fishers can be very helpful in the process of fish collection, mostly done at landing points.

The application of folk taxonomy to fish inventories is extremely helpful: fishers can be engaged in research projects, in fish collection, in helping in analyzing diagnostic variables that differentiate species and in helping identifying the organisms.

Shortcomings and recommendations: fishers seem to be most concentrated on knowledge on target species. Therefore, it is wise to identify target species in order to work on folk biology. Moreover, knowledge among fishers is heterogeneous, and it is important to identify the fishers that retain such folk knowledge. Our research has been selecting fishers that inhabit an area for at least 10 years, that fish for at least 10 years, and that are at least 40 years old. Empirical experience is a key factor. It is important also do avoid conducting studies based on insufficient informants, or on a small number of them. The 'noble sauvage' idea, or a romantic view of local knowledge and of folk taxonomies is also something to avoid or to take care. For those shortcomings, it is recommended to consult Ruddle and Hviding (2008) and Ruddle and Davis (2011).

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TABLE 3. DIAGNOSTIC VARIABLES: A COMPARISON (FROESE AND PAULY 2011, FIGUEIREDO AND MENEZES, 1980; MENEZES AND FIGUEIREDO, 1980).

Species Comparison	Folk Taxonomy	Taxonomy
<p><i>Epinephelus marginatus</i> (dusky grouper, DG, garoupa)</p> <p><i>Mycteroperca bonaci</i> (black grouper, badejo)</p>	<p>Body, Eye, Scale, Color</p> <p>Example DG:</p> <ul style="list-style-type: none"> • Body form wide • Big eye • Thick scale • Color 	<p>Fins, rays and spines, color, gill rakers, color:</p> <p>Example DG:</p> <ul style="list-style-type: none"> • 7-10 rays anal fin, • 10-11 spines dorsal and • 14-18 rays dorsal fin, plus Color
<p><i>Macrodon ancylodon</i> (king weakfish, pescada banana)</p> <p><i>Cynoscion leiarchus</i> (smooth weakfish, pescada branca)</p> <p><i>Nebris microps</i> (small-eye croaker, pescada azeitona, PA)</p>	<p>Body, fin, head, teeth, color</p> <p>Ex: PA</p> <ul style="list-style-type: none"> -small eye -round head -Round body - different fin 	<p>Fins, rays and spines, color, gill rakers, color:</p> <p>Example PA:</p> <ul style="list-style-type: none"> -teeth -7-13 rays -eyes -mouth

A photo-based system for identifying Wisconsin (USA) fishes

John Lyons

Ongoing improvements in digital photography and online image storage and access capabilities provide exciting opportunities for new and innovative web-based approaches to the challenging task of fish identification. In my presentation I summarize the development and application of a photo-based fish identification website (<http://wiscfish.org>) for the state of Wisconsin (USA) that illustrates some of these new approaches (Lyons et al. 2006). This website has been widely and heavily used over the last eight years and has received almost uniformly positive reviews.

The Wisconsin fish identification website contains over 4,000 color photos of 175 species and was designed for a variety of users with different levels of expertise, ranging from members of the public with no training in fish identification to professional fisheries biologists and ichthyologists needing to distinguish between very similar species. Consequently, emphasis is placed on the photos as the primary source of identification information with text technical details available but secondary and jargon minimized. At the heart of the website are 175 species pages, one for each of the 148 species native to Wisconsin, the 15 established nonnative species, and the 12 nonnative species potentially encountered as strays or as likely future invaders. Each page has 16-35 photos with at least three different images of typical adults in side view; top, bottom, and head-on views of these adults; close-up views of their flank, head, and mouth and their caudal, dorsal, anal, pelvic, and pectoral fins; and three to nine views of specific features useful in identification. Additional side-views and close-ups are provided for juveniles (non larvae) and breeding adults if they differ substantially in appearance from non-breeding adults as well as side-views and close-ups of hybrids for those species that commonly hybridize. Nearly all photos are of live or recently preserved (within 15 minutes) individuals to illustrate colors and pigment patterns as they would appear in nature. All images have descriptions and often include arrows or other notations highlighting identification features. Each page also has two text tables, one that lists quantitative and qualitative attributes of each species related to shape, size, pigmentation, color, scale distribution and number, fin characteristics and position, and key distinguishing features, and another that provides detailed comparisons with similar-appearing species. Technical terms in the text are linked to a photo-based glossary.

Three approaches are available for identifying species—traditional dichotomous keys (i.e., “single access keys”, “decision trees”), a multi-character query tool (i.e., “multi-entry key”), and a visual comparison of photos (i.e., “mug shot”, “eye-balling”, “slide show”). A series of dichotomous keys are provided for users to distinguish among families and among species within each family. Although comprised of text, the phrases (i.e., “leads”) in each couplet within each key are illustrated by multiple photos, and species names in terminal couplets are linked to the appropriate species page. The query tool allows users to specify simultaneously multiple attributes of an unidentified fish in terms of six morphological categories: snout shape, fin spines, tail shape, body shape, body pigment patterns, and miscellaneous features. Choices within each category are limited to easily seen characters that are illustrated with photos. Specifying a character within a category returns a list of only those species with that character, and specifying characters in multiple categories usually rapidly reduces the list of possible species to a small number. The visual comparison approach allows the user to view photos of different species and decide which photo best matches their fish. This approach, although conceptually simple, is cumbersome for large numbers of species and is best used after either

the dichotomous keys or the query tool has substantially reduced the number of potential species to consider.

The Wisconsin website required substantial resources to develop, far more than were originally anticipated. All told, the website took about 5 years to complete and included over 6,000 hours of work by professional biologists, software programmers, and technical editors plus about \$100,000 for equipment, supplies, and contract services. Photography was the most challenging aspect, involving more than 200 field days throughout and outside of Wisconsin by two or more highly experienced biologists to obtain high-quality photographs plus hundreds of additional hours to select and label photos for inclusion in the website.

User feedback has highlighted two features of the Wisconsin website that have made it especially popular and effective. First, the availability of multiple photos of each species, with an emphasis on “typical” specimens as they look in life and close-ups of key identification features, is often cited as one of the most valuable aspects of the site. Photo-based identification systems are increasingly common on the web, but most have only one or two views of each species, lack close-ups, and sometimes portray only colorful breeding specimens rather than the more frequently encountered non-breeders. Although there is a significant up-front cost in photographing multiple specimens and obtaining close-ups, the Wisconsin experience suggests that the value of these additional photos is worth their expense. Second, the query approach to identification appears to be more effective than the dichotomous key approach, particularly among those new to fish identification. Classroom trials with university undergraduate biology students and observations of website use by the general public indicate that dichotomous keys are often confusing and intimidating to non-specialists. The query approach seems to be more intuitive and appealing and yields more accurate results for most users, perhaps because query tools are a common feature of the online search engines and databases that many of us use routinely in our daily lives. Web-based fish identification systems should consider diversifying beyond traditional dichotomous keys to include query-based options.

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Fish identification using scales and otoliths

Ana L. Ibáñez

Synopsis of the fish identification method and approaches.

Species identification is a basic procedure in the conservation of biodiversity and natural resources management, including fisheries. Fish scales have been extensively used in fish species identification since the early 1900s (Goodrich, 1909) and not only their count is important in key classification also descriptions of their shape and particular features have been used in keys to recognize families (e.g. Maitland, 2004; Daniels, 1996) or particular ornamentations to easily distinguish between close species (Chervinski, 1984, 1986; Ibáñez & Gallardo-Cabello, 2005; Ibáñez et al., 2011). As well Fourier analysis of fish scales shape has been used to discriminate between stocks (Jarvis et al. 1978; Riley and Carline, 1982; Richards and Esteves 1997a & 1997b; Poulet et al. 2005) and more recently, Watkinson and Gillis (2005) used wavelet analysis as an alternative to Fourier analysis, to improve discrimination. Alternative methods of shape analysis, based on landmark data have also found wide applicability in biology because of the natural links between homologies and measurements (the landmark coordinates; c.f. Fourier and wavelet approaches), the statistical properties of the resulting shape spaces (Dryden and Mardia 1998) and good statistical power. These Geometric Morphometrics methods (GM) preserve geometry throughout the analysis and, like Fourier and wavelet analyses, offer graphical visualisations of the statistical results that can give support to biological interpretation. The landmark-based methods vary fundamentally from others in that they employ biological equivalences between structures: matching or 'homologous' landmarks and to this extent the resulting metrics are founded in biology. In practical terms the Fourier and other 'landmark free' approaches work well and offer the immediate advantage of capturing the subtleties of outline detail. GM methods have advanced to incorporate these outline features (e.g. Bookstein et al. 2005) and offer all of the advantages of outline measurement methods while incorporating all available homology information. Nevertheless, the extent to which outline variations between landmarks are informative depends greatly on the features of the structure being measured, the adequacy of sampling of form that can be achieved by landmarks alone and on the question at hand. In the case of fish scales, a reasonable representation of form is achieved using very few landmarks (until now we had used seven and five) and there are definite advantages in achieving a succinct description of form by using a few variables because the resulting multivariate spaces are readily visualised and 'noise' is minimised relative to 'signal' in discriminant analysis.

There is some progress on the knowledge of the use of scale shape in stock discrimination. Recently, Ibáñez et al. (2007) applied geometric morphometric methods to scales in order to identify genera, species and stocks among the Mugilidae. Garduño-Paz et al. (2010) used fish scales morphometrics and could discriminate between sympatric phenotypes of Artic charr *Salvelinus alpinus*. Fish scales allometric growth and their influence in species discrimination were reviewed (Ibáñez and O'Higgins, 2011) and results showed that if size is not included in the analysis, identification rates are far better than those from random and taking into account the size classification improved somewhat for which it is possible to use them even without knowing the size of specimens or finding differences in size between geographical areas for the purpose of stocks discrimination (Ibáñez and O'Higgins,

2011). Also is known the effectiveness of fish scales of the different parts of the body in the discrimination (Ibáñez et al., 2009).

As scale shape could be used to discriminate stocks this condition also reflex populations connectivity. Fish scale shape was used to identify geographic variants among Lutjanidae (*Lutjanus argentiventis*, *L. guttatus* and *L. peru*) with specimens collected from three different geographic areas, north to south of the tropical Pacific coast of Mexico: Puerto Vallarta (PV), Manzanillo (MA) and Caleta de Campos (CC). PV and MA were recognized as one population different from the CC geographic area. Consistency for the three species show non fortuitous events. Separation between geographical areas seems to be caused by a geographic barrier between North-Equatorial Current and California Current. In other species from *Scomberomorus sierra* genetic studies have seen differentiation between specimens from these areas.

The predominance of currents seems to leave a footprint in accrete growing process of fish scales that modify scale shape. Changes in fish scale shape have been recorded for juveniles of the cyprinid roach, *Rutilus rutilus* reared on a fish farm in the UK when fish suffer compensatory growth owing to the type of holding facility movements, which are surrogates of food availability, density, temperature and other variables (Ibáñez et al., in press). Nevertheless, further studies are needed to explore the influence of extrinsic (e.g. habitat, food type) and intrinsic (e.g. growth) factors determining variation in fish scales shape and also compensatory-growth-fish-scale-fish.

Strengths and limitations of the method (e.g. reliability, applicable to all species or to subsets, combination with other methods, etc.)

Strengths: Scales offer a cheap, rapid and reliable on-the-spot means of identification of fish that have been caught, even when no other material is available. The method is non destructive, thus allowing rare and endangered species to be returned to the water. Fish scales are by far transportable. The method is fast allowing screening of many individuals for traceability of fish. As scales have two dimensions deformation is avoided reducing error and images digitalization is easier.

Limitations: Scale shape changes along the body and they don't discriminate equally. Nevertheless, analyses ignoring anatomical sampling region still achieve good classification by species. It is obvious but this method works only for fish with scales.

Requirements for their use in terms of:

Technology: Only a flat microfiche projector or a microscope with digital camera and a computer is needed to digitalize images and run the analysis. A digital image could be taken whether on the flat screen of a microfiche projector or taking a digital image using a microscope and a digital camera. Later, in order to do the geometric morphometric analysis, a computer is needed to run the analysis where most of the software is free at website (<http://life.bio.sunysb.edu/morph/>) and to run discriminant analysis with any statistical software.

Prior knowledge/training: Knowledge of basic concepts of geometric morphometric analysis is needed in order to understand the method used. Nevertheless, all analysis could be carried out as a routine in which case a short training (around a week) is needed in order to learn the protocols of methodology.

Costs: General approximations of minimum and maximum cost vary depending if microfiche or microscope is used (see table).

Kit	Item	Minimum	Maximum
		USD	USD
1.-	Computer	800	2,500
	Microfiche reader	370	700
	Digital camera	250	700
	Tripod	20	60
	Total	1,440	3,960
2.-	Computer	800	2,500
	Microscope + digital cámara	6,700	6,700
	Total	7,500	9,200

Time from sampling to identification: Scales digitalization: During four hours ten specimens could be processed. It is recommended to use big samples with more than thirty fish, bigger samples will diminish variation.

Morphometric analysis: During four hours fifty specimens could be processed for landmark location on key features of each scale. Geometric morphometric methods utilise the coordinates of landmark configurations as the basis for comparisons of form (size and shape). Shape variables are derived from generalized procrustes analysis (GPA) which involves best fitting of landmark configurations (i.e. through translation, rotation, reflection and isometric scaling) (Dryden and Mardia, 1998). Subsequently these shape variables are used as inputs to multivariate analyses in order to investigate form variations and discrimination. Afterwards all morphometric information is captured discrimination analysis could be done. With all information at hand this process could take several hours.

Other information: Although only one scale will be used in analysis it's recommended to digitalize three fish scales because it's frequent to find regenerate scales and these must be discarded from the analysis.

Scales from the central region perform best for identification purposes. It is recommended to remove the scale from the shoulder region above the lateral line and stored dry in paper envelopes or in coin pages.

Fish identification using otoliths

The use of otoliths for stocks identification is well established, and while their use is more laborious and prior knowledge and training is needed, their efficacy is clear (Hong- Yi et al., 2010; Farias et al., 2009; Petursdottir et al., 2006). The rate of correct identification among congeneric species using otoliths is over 80% (Stransky and MacLellan, 2005; Torres et al., 2000). The limitation of the use of otoliths in discrimination is that is a destructive method, thus not allowing rare and endangered species to be returned to the water and also due to their fragility break during extraction and manipulation. Also as otoliths are concave deformation could occur rising error. In otoliths, shape is influenced by recent feeding history (Gagliano & McCormick, 2004) and both, genetic and environmental characteristics play a substantial role in determining the shape of the otolith (Vignon & Morat, 2010).

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Using content-based image retrieval tools in fish identification tasks

Ricardo da Silva Torres

Introduction

Several biodiversity information systems (BISs) have been created to manage data on species (e.g., field observation records and experimental data). BISs are concerned with determining the spatial distribution of one or more living species, and the spatio-temporal correlations and trends of these distributions. This requires combining data on species (when and where they are observed, by whom and how) with geographic data that characterize the ecosystems where the species are observed [10].

Drawings and photos of species also may be used in the context of BISs. They are adopted by scientists to help them identify species, given existing image archives. Usually, however, those photos are stored apart in the system's data files, and treated as auxiliary documentation, usually retrieved by species' name. This scenario opens a new area of investigation related to the management of images' content (e.g., shape, color, texture), aiming at supporting the automatic identification of species.

Content-Based Image Retrieval (CBIR) systems have been created in the last 20 years aiming at efficiently and effectively processing queries based on image content [7, 11]. Basically, those systems try to retrieve images similar to a user-defined specification or pattern (e.g., shape sketch, image example). Their goal is to support image retrieval based on content properties (e.g., shape, color, texture), usually encoded into feature vectors. One of the main advantages of the CBIR approach is the possibility of an automatic retrieval process, instead of the traditional keyword-based approach, which usually requires very laborious and time-consuming previous annotation of collection images.

This document describes ongoing initiatives with the objective of using CBIR tools in the construction of BISs. We present some of those tools as well as some of the achieved results regarding their use in tasks related to the identification of fish species.

The remaining of this document is organized as follows: Section 2 gives an overview on CBIR concepts; Section 3 describes developed tools and outlines achieved results; Section 4 discusses about strengths, limitations, and challenges related to the developed methods.

Content-based Image Retrieval

This section describes the basic architecture of a CBIR system and presents a brief overview on image descriptors.

Architecture of CBIR Systems

Figure 1 shows a typical architecture of a content-based image retrieval system. Two main functionalities are supported: data insertion and query processing.

The data insertion subsystem is responsible for extracting appropriate features from images and storing them into the image database (see dashed modules and arrows). This process is usually performed off-line.

The query processing, in turn, is organized as follows: the interface allows a user to specify a query by means of a query pattern and to visualize the retrieved similar images. The query-processing module extracts a feature vector from a query pattern and applies a metric (such as the Euclidean distance) to evaluate the similar-

ity between the query image and the database images. Next, it ranks the database images in a decreasing order of similarity to the query image and forwards the most similar images to the interface module. Note that database images are often indexed according to their feature vectors by using structures such as M-tree [4] or BP-tree [2] to speed up retrieval and similarity computation. Note that both the data insertion and the query processing functionalities use the feature vector extraction module.

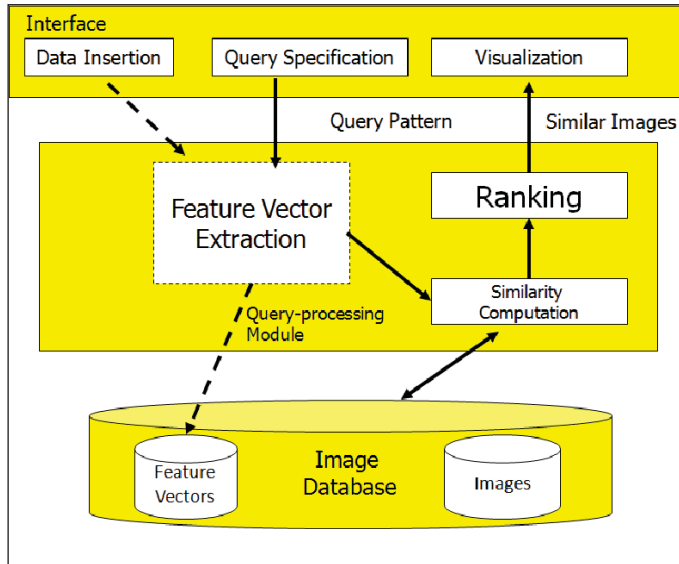


FIGURE 1. TYPICAL ARCHITECTURE OF A CONTENT-BASED IMAGE WHICH CAN BE ANNOTATED IMAGE MARKS (SHOWN IN THE FIG-RETRIEVAL SYSTEM [7]. URE) AND/OR COMPLETE IMAGES ([19])

Image Descriptors

A typical CBIR solution requires the construction of an image descriptor, which is characterized by [7]: (i) an extraction algorithm to encode image properties into feature vectors; and (ii) a similarity measure to compare two images. The similarity measure is a matching function, which gives the degree of similarity for a given pair of images as represented by their feature vectors, often defined as an inverse function of the distance (e.g., Euclidean), that is, the larger the distance value, the less similar the images are.

Color Descriptors

Color property is one of the most widely used visual feature in content-based image retrieval (CBIR) systems. Researches in this field can be grouped into three main subareas: (a) definition of adequate color space for a given target application, (b) proposal of appropriate extraction algorithms, and (c) study/evaluation of similarity measures. Several color description techniques have been proposed [1,14,23,27,29,30]. They can be grouped into two classes based on whether or not they encode information related to the color spatial distribution.

Texture Descriptors

There is no widely accepted definition of texture. However, this image property can be characterized by the existence of basic primitives, whose spatial distribution creates some visual patterns defined in terms of granularity, directionality, and repetitiveness. There exists different approaches to extract and represent textures. They can be classified into space-based, frequency-based models, and texture signatures [12].

Shape Descriptors

In pattern recognition and related areas, shape is an important characteristic to identify and distinguish objects [16, 31]. Shape descriptors are classified into boundary-based (or contour-based) and region-based methods [31]. This classification takes into account whether shape features are extracted from the contour only or from the whole shape region. These two classes, in turn, can be divided into structural (local) and global descriptors. This subdivision is based on whether the shape is represented as a whole or represented by segments/sections. Another possible classification categorizes shape description methods into spatial and transform domain techniques, depending on whether direct measurements of the shape are used or a transformation is applied [28]2 . More details about existing shape representation techniques can be found in [5, 16, 18, 31].

CBIR-related tools and achieved results

This section presents some of the CBIR-related tools created recently, as well as discusses their use in tasks concerning fish identification.

Content-Based Image Search Component (CBISC)

Overview

CBISC [6,9,15] provides an easy-to-install search engine to query images by content. It can be readily tailored for a particular collection by a domain expert, who carries out a clearly defined set of pilot experiments. It supports the use of different types of vector-based image descriptors (metric and non-metric; color, texture, and shape descriptors; with different data structures to represent feature vectors), which can be chosen based on the pilot experiment, and then easily combined to yield improved effectiveness. Besides, it encapsulates a metric index structure [4] to speed up the search process, that can be easily configured for different image collections. Queries are submitted to CBISC via HTTP requests. Two special requests are supported by this image search component:

- **ListDescriptors:** This request is used to retrieve the list of image descriptors supported by the CBISC. No arguments are required for this verb.
- **GetImages:** This request is used to retrieve a set of images by taking into account their contents. Required arguments specify the query image, the descriptors to be used, and the kind of query (either K-nearest neighbor query (KNNQ) or range query (RQ)).

Use of CBISC in fish identification tasks

CBISC was used as one of the modules of a BIS dedicated [10] to fish descriptions on over 200 species found in the Commonwealth of Virginia, USA, including data related to taxonomic classification, common names, fish morphology, metabolism, diet habits, etc. We have evaluated the use of the BIS as a tool to support the identification of Virginia freshwater fish.

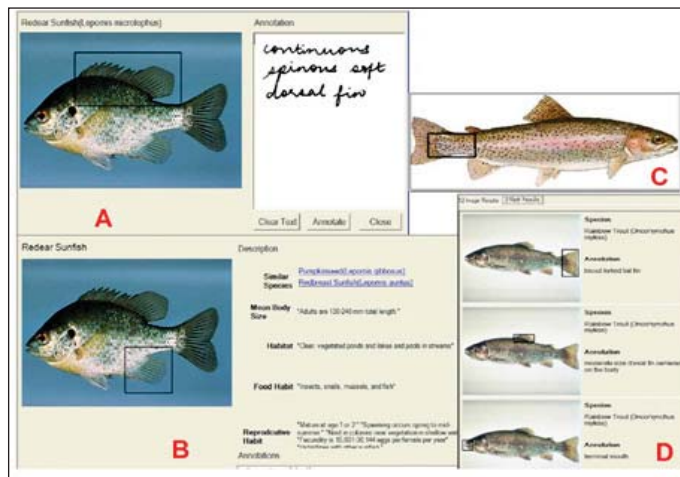
We configured the CBISC to use the Beam Angle Statistics (BAS) [3] shape descriptor. Seven subjects from the Department of Fisheries and Wildlife Sciences at Virginia Tech were recruited. Given a preserved and jarred fish specimen, users were asked to identify its corresponding family, genus, and species using both the traditional key-based method, and by performing queries on the created BIS.

Results show that the fish identification process based on our information system is more effective, easier, and less time consuming than that based on the traditional key-based approach [10].

Superimposed Image Description and Retrieval Application (SuperIDR)

Overview

SuperIDR [20–22] is a tablet-PC tool that supports image description and retrieval by combining text and visual descriptions. It allows users to select and mark parts of images and associate them with text annotations. Annotations can be entered using either pen-based or keypad-based input. Later, users can perform queries using part of an image or a textual description. With SuperIDR, users can navigate through the collection by species or taxonomic organization. Users can also open two images to analyze similarities and differences between specimens side by side. Figure 2 shows screenshots of the SuperIDR tool.



A) Annotation screen – pen input is used to mark the fish image and “write” the annotation; B) Species description screen shows details of species and annotations; C) Content-based image search, where the query is the marked region; D) Image search results.

Use of SuperIDR in fish identification tasks

Different experiments were conducted in the context of using SuperIDR in fish identification tasks. In [21], for example, 28 students who were taking the Ichthyology course at Virginia Tech used the SuperIDR tool to identify 40 unknown specimens. To correctly identify a specimen, students (grouped in teams) had to write down the family, genus, and species names of the specimen. Experiment results show that using SuperIDR yields a higher likelihood of identifying a specimen correctly than using traditional methods. In this experiment, BIC [29] descriptor was used to characterize fish image color information.

In a more recent work [22], a qualitative study was conducted to identify contexts and strategies of working with subimages in fish species identification tasks. Six experienced students used the SuperIDR in their work/study environments. We asked them to complete a text diary entry on every use. We also asked them to identify six unknown fish specimens using SuperIDR in specific task sessions. Findings include the identification of new ways of querying and searching for subimages and associated information, as well as the proposal of recommendations for the design of digital libraries with superimposed information.

Strengths, limitations, challenges, and research opportunities

Image descriptors vary with the application domain and expert requirements. Thus, in order to identify appropriate image descriptors for new fish image collections, experts must perform a set of experiments, prior to the use of the presented tools. The experimental results are analyzed to evaluate image descriptors in terms

of efficiency (response/recognition time) and effectiveness (response/recognition accuracy).

The BAS descriptor [3] was chosen in the experiment involving the CBISC tool after a set of preliminary tests with end-users showed that it would be a good descriptor for the target collection. In fact, shape information was identified as being very effective to differentiate Virginia fish at taxonomic family level. The use of contour-based shape descriptor such as BAS requires the prior segmentation (extraction) of the object of interest for each collection image. Segmentation is a hard problem for specific domains. For heterogeneous image collections, with different acquisition protocols (e.g., different background color and presence of illumination changes), the segmentation problem is even harder.

The use of the BIC descriptor [29] in the SuperIDR tool avoided the use of segmentation. On the other hand, color information was not as effective as shape for identifying Virginia fish. Biologists involved in our experiments described fish morphological features that could be used in the design of new descriptors. That venue is being addressed with the investigation of appropriate local descriptors (e.g., SIFT-like descriptors) that can be used for characterizing specific fish morphological features.

Descriptors are typically domain and usage-dependent. Thus, a given image can be associated with very many descriptors. Different CBIR descriptors produce different rankings. Further, it is intuitive that different descriptors may provide different but complementary information about images, so that the combination of multiple descriptors may improve the effectiveness performance of a CBIR system. An approach for improving CBIR systems consists in using rank aggregation techniques [8,13,24–26]. Basically, rank aggregation approaches aim to combine different rankings in order to obtain a more accurately one. One possible research venue consists in investigating the use of rank aggregation approaches in fish identification tasks.

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IPez: An expert system for the taxonomic identification of fishes

Cástor Guisande González

Synopsis

Species identification for fishery purposes has been the subject of a major Food and Agriculture Organization (FAO) program since the 1960s. Optimization of the world-wide community efforts in generating and sharing taxonomically related knowledge in a global network is a current challenge calling for an urgent solution. Therefore, to develop an automated species identification system would be very useful, because it would improve catch statistics through fast accurate species identification.

Meristic and morphometric characters are powerful tools for measuring discreteness and relationships among fish species. For this reason, analysis of morphometric and meristic characters has been widely used by ichthyologists to differentiate between different species and among different populations within a species (Cadrin 2000; Wainwright 2007). However, despite automated species identification might be a good option to the burden of routine fish taxonomic identification, there is not an automated taxonomic identification system for fishes based on morphological characters. In fact, automated species identification based on morphological characteristics has not become widely employed in any discipline of the biology (Gaston and O'Neill 2004).

IPez is an automated species identification system (Guisande et al., 2010), which have several strengths that are explained as follows.

Strengths

- It combines 3 methods of identification. 1) An automated identification system based on morphometry and machine learning techniques, 2) the classical routine species identification based on taxonomic catalogues and 3) information about the geographical distribution of the species.
 - High identification success. It is only necessary to measure between 15 and 20 individuals of different sizes of each species to achieve 100% identification success.
 - Short time for identification. Maximum time to identify 1 individual is around 5 minutes, which is the time to introduce the 32 to measurements. However, IPez uses a hierarchical system, which means that if the order, family and/or genera are known, the number of measurements necessary for the identification is lower.
 - It is an expert system. The measurements to be inserted for identifying each level (order, family, genus or species) may change as more species are introduced into the database. The program will adapt to the new situation involving the new species, by searching for the measurements that give a better differentiation of the different taxa within each level. When the program updates, all the modifications are automatically incorporated.
 - Fast retraining. In IPez, a new species being added to the training set causes only local changes to the network and, therefore, it is no necessary to retrain the entire network.
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- Easy to update. There are changes in fish taxonomy and nomenclature

almost every week. The program allows the database to be updated in an automatic way, and the size of the file with all the information necessary for the automated identification is only 7 megabytes, and the size of file with all common names and synonyms is only of 21 megabytes. Therefore, it is very easy to update IPez.

- It is able to handle very efficiently the scaling up required for a large number of species. One of the main problems of species identification systems is that with more species, the acquisition of sufficient computing power may rapidly become limiting. As mentioned above the size of the files needed for identification in IPez are rather small. Moreover, it is important to stress that the computing time needed by IPez for the identification of one individual is less than 1 second, and it will always be less than 1 second, irrespective of the number of species included in the database.
- It does not require internet. Sometimes it is necessary to identify fish species in places where there is not internet access or it is very expensive (in the middle of the sea, in some field areas, etc.). Once these two files mentioned above have been updating, it is not necessary internet for automated fish identification of the fish species.

Limitations

One important problem for automated species identification systems is what to do about the identification of novel species (species that are not yet included in the database). In most cases, novel species will tend to be identified as belonging to a similar species, included in the database. As mentioned above, IPez allows checking if the taxonomic characteristics of the species identified, which are shown in a photograph, match the characteristics of the animal we have in our hands. This does not completely solve the problem of novel species, but it is easier to check errors in identification with the specimens than with the digital imagery of the specimens.

The way to really solve this problem is to include as many species as possible into the data base of IPez

Requirements

Technology. It is necessary just a computer.

Prior knowledge/training. From the experience of several training workshops carried out in different cities, after half day of work, people without any experience on fish taxonomy were able to identify correctly fish species.

Cost. The species are identified at no cost.

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Use of active acoustics for biodiversity and fishery assessments

John K. Horne

Synopsis of identification methods and approaches

Acoustic species identification remains a longterm goal of commercial fishers, researchers, and resource managers that use sound to locate, map, and count aquatic organisms (Horne 2000). Interpreting acoustic data for species identification requires an understanding of how pressure waves interact with aquatic organisms to reflect sound. The amount of energy reflected from an animal depends on the acoustic frequency and the net angle between the transducer and the location and orientation of the animal within the beam.

Any interface that has a density different than the surrounding water will reflect sound. Measureable acoustic reflections originate from environmental features such as thermoclines or bubbles, and biological organisms ranging from zooplankton to whales. Challenges associated with using active acoustics to collect biodiversity and fishery assessment data progress from detecting animals, to discriminating among animal categories, and finally to identifying species. Techniques used to acoustically identify species exploit unique characteristics from returned or backscattered echoes.

Single or mixed species assemblages of fish and invertebrates are common in both marine and freshwater ecosystems. Fish are complex acoustic targets due to anatomy and behaviour. The length, shape, and material properties of animals influence the amount of sound it will reflect. Locomotory and aggregative behaviours influence the intensities and variability of returned echoes through changes in animal orientation, packing density, and vertical distributions within the water column.

The first step in acoustic identification of fish species characterizes echo amplitudes from individual animals, aggregation of animals, or the energy within a sample volume. Characterization of echoes from an individual target measures the width of echoes at specific points relative to the peak amplitude. Echoes from fish aggregations are characterized using metrics that quantify the structure of the aggregation (e.g. height, length, area). Image analysis techniques are used to group contiguous pixels or voxels into discrete aggregations and then characterized using morphologic indices and measures of the aggregation relative to features in its environment (e.g. distance off bottom).

Objective discrimination and identification of fish species within acoustic data utilizes a variety of techniques. Once indices have been used to describe individuals or ensembles of fish, echoes or contiguous pixels are grouped using statistical tools. Examples identifying single or multiple species using single frequencies have used discriminant functions (e.g. Rose and Leggett 1988), ordination (e.g. Scalabrin and Masse 1993), classification and regression trees (e.g. Fernandes 2009), and neural networks (e.g. Haralabous and Georgakarakos 1996). When separating species using multiple frequencies, traditional amplitude-based approaches have examined differences in average backscatter values between pairs of frequencies (Kang et al. 2002), categorized maximum backscatter amplitudes (Kloser et al. 2002), or standardized relative backscatter amplitudes to a common frequency (i.e. frequency response, Korneliussen and Ona 2003). Recent work has implemented an algorithm that combines several techniques to characterize backscatter from a single species (Korneliussen 2010). Application of multifrequency approaches has increased objectivity of target classification and has maximized the amount of information derived from acoustic data.

Exploiting the dependence of echo amplitudes on incident angles for species

identification is a current research topic that has been stimulated by the desire to use multibeam sonars for population abundance estimate surveys. Multibeam sonars have beam widths that are an order of magnitude larger than the scientific echosounders that are commonly used in population abundance surveys. Using a wide angled beam increases the range of angles between the transducer and the target and therefore potentially increases the amount of information available to identify targets (cf. Cutter and Demer 2007). Unfortunately within the frequencies typically used in fisheries acoustic surveys, there is rarely a unique echo amplitude, or target strength, for a single animal within an acoustic beam. Echo amplitudes can differ by several orders of magnitude depending on a combination of biological and physical factors.

One approach used to understand the dependence of acoustic frequency and angle on echo intensities is backscatter modeling. Backscatter models estimate the amount of energy reflected as a function of animal length, morphology, material properties, orientation, and acoustic frequency (e.g. Horne 2003). Organism representations in backscatter models have evolved from “simple” geometric shapes (e.g. spheres, cylinders, prolate spheroids), to anatomical images obtained using radiographs, computed tomography (i.e. CT) scans, or magnetic resonance imaging (MRI). The choice of backscatter model and associated representation of the fish or organism of interest is difficult. Numerous models are available, each with advantages and constraints. The challenge is to choose a model and representation that provide accurate target strength estimates. Backscatter model predictions are validated using empirical backscatter measures of individual animals under controlled conditions or acoustic measures that are combined with direct samples from nets.

Strengths and limitations of methods

Acoustic technologies are continuous, non-invasive samplers that measure organism densities through the entire water column. As a remote sensing tool, acoustic data records are combined with direct methods (e.g. data from trawl catches) to validate species compositions and length-frequency distributions. Standard procedures for all acoustic surveys include one or more direct sampling technologies used to match species compositions to observed acoustic patterns and for length frequency distributions. Off-the-shelf scientific instruments and analytic packages are widely available, but specialized training is required to ensure appropriate acquisition and interpretation of data.

Anticipated developments in the near future

Increasing use of acoustic technologies for fish diversity and fishery assessments maintains the demand for hardware and analytic innovation. Hardware developments include adapting multibeam and broadband (i.e. wide frequency) sonar technologies for ecosystem research, species identification, and species-specific population abundance estimates. Multibeam sonars have traditionally been used to image fish aggregations in the water column for commercial purse seine or trawl fisheries. Initial scientific applications include investigations of fish schooling and vessel avoidance behaviours. Current or developing investigations are using multibeam sonars for population abundance estimates, fish essential habitat selection for choice of marine protected areas, and associated species identification research through angle-dependent backscatter amplitudes. Unique maximum echo amplitudes at species or length-specific frequencies are being exploited to adapt broadband sonars for scientific investigations. Maximum amplitude peaks or characteristic profiles across a range of frequencies potentially increase the use of broadband sonars when fish communities are composed of multiple species or

life history stages.

Current development in acoustic data analysis focuses on the use of multiple frequency data for species identification. Statistical approaches use supervised or unsupervised classification to define limits for backscatter returns from aggregations of animals. Additional species discriminators use metrics describing aggregations of animals or the orientation of aggregations relative to their environment. Metrics can be grouped in four categories: morphological (e.g. geometry of the aggregation), bathymetric (e.g. position of the aggregation in the water column), energetic (e.g. properties of the backscattered signal), and positional (e.g. distance of the aggregation from a coast). Probabilistic methods provide an alternate approach to species identification when analyzing multifrequency acoustic data (e.g. Anderson et al. 2007). Single and multiple species categories are allocated a probability of membership to each category based on analytic algorithms and supplementary empirical samples. This approach has the potential to provide automated, objective species identification and is predicted to become the norm in acoustic data processing.

Integration of acoustic instruments with other direct and indirect sampling technologies to enhance species identification continues. These integrated sampling packages that may contain acoustic, optic, and direct samplers (e.g. pumps, nets), are being installed on alternate platforms in an effort to bring the sensors closer to species of interest and to increase duration of sampling. Alternate sampling platforms currently exploited include autonomous underwater vehicles (i.e. AUV's), sea gliders, and wave gliders. Instrument miniaturization reduces space and weight constraints in these smaller platforms and helps to reduce power requirements. Battery size and weight are still the limiting factors when determining vehicle deployment length and sampling duty cycles. Power requirements exceed those of data storage or computer control requirements in autonomous platforms. The need for species identification from acoustic-based monitoring is predicted to increase with increases in ecosystem based resource management, ocean observatories, and renewable energy applications.

Requirements

The current international standard for fisheries acoustic technology is multifrequency, splitbeam echosounders. A splitbeam echosounder positions individual targets in three dimensional space using time lag differences (i.e. phase) of echo arrivals in separate quadrants of the acoustic beam. These instruments are commonly integrated with other acoustic (e.g. acoustic Doppler current profiler (i.e. ADCP), sonar) technologies on government or academic institutional research vessels. Data processing procedures and software packages are internationally reviewed, well documented, and commercially available. Standard operating procedures for both marine and freshwater environments have been published and are revised as hardware or analytic innovations are validated by the community.

Acoustic data acquisition, processing, analysis, and interpretation all require prior knowledge and training. Training through vendors on equipment operation and initial data processing is available, but formal theoretical training is limited and is the largest constraint to expanding the user base.

Acoustic technologies are typically considered capital intensive. Single frequency, splitbeam echosounders range in price from approximately \$50,000 to \$60,000 USD (2011 prices). Multifrequency systems with four to six frequencies are becoming the standard when conducting ecological research and population abundance surveys. Development of new and adapting existing technologies for use in aquatic research continues over approximately ten year product cycles. A sampling platform is typically a boat with the transducers installed in the hull or

made portable using a tow body or pole mount. Supporting personnel for maintenance and calibration of equipment is an ongoing, annual cost. Data processing and analytic software containing specific algorithms and a programming shell are available in third party software packages but represent additional costs ranging from \$16,000 to over \$30,000 USD (2011 prices). The alternate approach is to program processing and analytic algorithms in a computer programming language of choice (e.g. MatLab, C#, R).

Time from sample acquisition to species identification ranges from a minimum of real time to a maximum of the time it takes to process and interpret data and biological samples back in the laboratory (typically weeks to months if continental shelf survey). On average, species identification is possible after direct samples (e.g. nets) are acquired. The actual time required depends on the complexity and behavior of the fish community in the region of interest. If species are anatomically and spatially or temporally separate, then time required for species discrimination and identification is reduced. All prior biological knowledge of the system is used to aid species identification within acoustic data.

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Web-based fish identification and information resources

Nicolas Bailly

Brief summary

The specimen identification tools available on the web are presented in 6 different categories that were historically created along the development of taxonomy and systematics. The old ones were progressively implemented on computers and then on the web, the last two ones could be developed only with informatics:

- Identification by specialists
- Identification by images (drawings, pictures, videos)
- Dichotomous keys
- Polythetic keys
- Interactive keys
- Image analysis

I have limited the identification tools listed below to those based on entire specimen morphology. Other tools are or may be available on the web but concern only parts of a specimen like internal anatomy or DNA barcode, that will be presented by other participants.

The closure of an identification is done by the necessary back-checking of the species account and the current valid name, steps which are now very easy through the web.

In addition, other selected websites and projects that are related to identification are listed in the annex that gathers a number of selected websites mainly as typical examples since there are many websites dedicated to fish.

Identification by specialist

The first method of identification is to present the specimen to a specialist who knows already how to differentiate the species among possible others. This is the most efficient method in a limited context (geographic and/or taxonomic)!

After a first positive identification, the specialist has accumulated experience over years by observing and manipulating many specimens, and visually recording the variability, e.g., juvenile/adult, male/female, normal/reproduction phases and other colour pattern changes, still/moving, wild/museum specimens, etc. To some extent, this specialist is able to picture potential non yet observed variability, but would have hard time to translate it in words and sometimes even as illustrations.

This is the first method used by our ancestors where knowledge was transmitted orally and by shared experience (e.g., group hunting or gathering). And most probably, predator-prey relationships based on visual detection in general are using the same mechanisms, being either genetically inherited or acquired by training from parents. The knowledge transfer from a senior to a junior taxonomist still includes that pathway, e.g., from a supervisor to a PhD student (hence the importance that current retiring taxonomists have the opportunity to pass on their knowledge).

It corresponds to our brain capacity to treat and store species patterns and their variations as visual memories (like when you iron-impress an image on a tee-shirt), and to process new images against these memories, which our most elaborated computers and softwares have still hard time to mimic (see below and other presentation on image analysis).

So how could it be on the web? For the user, the challenge is to bring the specimen to the specialist. Through internet, the only possibility is to post pictures

in forum-like websites. There are many of those around the world, global like FishBase, or restricted to a region (more rarely to a taxon) and/or to some domains like diving, angling, aquarium hobby, ... The answers come from the forum community (usually non-taxonomists) but who know the species well (the so-called “amateurs”). The accuracy of the answers may be quite good in a limited context, and is correlated to the quality of the pictures. But no forum will deal properly with deep-sea fishes, areas where many new species are still described (mainly in freshwaters in Amazona and South-East Asia), taxa including many small species that are not targeted by any domain or to a restricted extent (gobies, blennies, gobiesocids, ...), and areas or taxa that include species morphologically similar that require measures and/or counts (Carcharhinus spp., skates, flying fishes, clupeids, ...).

As far as I know, there is no such forum exclusively answered by specialists (who usually do not appreciate the picture identification exercise). For the FishBase forum, we may ask help from colleagues, but only when pictures present high quality (e.g., P.R. Last for sharks and rays around Australia), or may represent new records or new species (e.g., G.R. Allen for damselfishes).

Potential development for fisher communities:

Establish a specialist forum with those colleagues who are authors in FAO catalogues, but then some rewarding mechanism must be put in place, trying to be as imaginative as possible (e.g., FAO could help colleagues to get specimens from all around the world through their connections with fisheries department that could be involved to get collection permits and to follow national regulations?)

Develop the same as smart phone and tablet applications. I will not repeat that point below, but it is valid for all (see the annex for a few example applications).

Identification by pictures

The second method, which is related to the first one, is to compare visually (= screen) the specimen, its picture, or the memory of it the user is keeping in mind, to a number of well-identified reference images. The capacity of our brain to manipulate visual memories is again involved.

Before the Internet, it was the role of field guides that represent pictures and/or drawings with highlights of diagnostic characters, and images regrouped in plates where similar species are displayed together. Usually one picture per species is given except when the sexual dimorphism is marked like in the labroid lineage (wrasses, parrotfishes, cichlids) and others (dragonets, killifishes, anthiids, ...). If available some juvenile remarkable patterns are presented too (e.g., damsel-, angel-, butterfly-fishes, ...). Also were developed posters and plasticized cards.

The challenge is to gather at least one image per species in the geographic area or for the taxon targeted, but also to report natural and geographical colour variations, and/or artificial colour ones in different situations: dead/alive, in/out of the water, fresh/preserved, etc. Note that the recent World Atlas of Marine Fishes gathers “only” 6,000 pictures for 4,200 species over the 16,000 currently valid in the sea (and they are among the more productive fish photographers at the moment). One issue for divers is the colour at depth, e.g., a red fish at 20 m depth looks black; a tool is implemented in FishBase to mimic the colour changes with depth. Also dead fish colour pattern may change, which has quite an importance for statistics inspectors in fishery landing areas in tropical countries, and for the type of pictures to be used.

The difficulty of the method is when the user really does not know what the fish could be, e.g. in which family, because too many pictures would need to be

screened (hoping that the species is included in the picture set!). It may work in low species richness areas, but in mega-diverse waters, e.g., the coral triangle for marine environment, or Amazon for freshwaters, it is a challenge. For example for a diver, there are 10 times more commonly visible species in the whole Mediterranean than in the Philippines alone; this ratio is probably alike for small coastal fisher communities and exploited species. In such cases, a pre-sorting mechanism is needed in order to find first, e.g., the family: general outlines of the supra-generic taxa are usually utilized (class, order, family, subfamily). Even if the user has to explore several families because some body shapes are spread across many phylogenetic lineages (e.g., the anguilliform shape, not to speak that this one may be mistaken for snakes ...), it retains only a few of them.

On the Internet, FishBase is probably the most advanced website for that matter with one image (picture, drawing) for half of the ca. 32,000 species, with two main contributors, J.R. Randall and FAO and its drawers. The user can restrict one's research by family/genus, by continent or ocean/ country or a combination of those. FishBase has also implemented the possibility to enter the number of fin rays, a method that was proposed in the famous Smith's ichthyofauna (but I think this method may lead to mistakes when applied by non specialists, fin rays being not that easy to count correctly, e.g., macrourids, and the discriminating power being very sensible to mistakes just for one ray already). Still the species are presented in the FishBase identification by picture page by alphabetical order; remains to implement a mechanism to display similar species close to each other on the web page. Many websites gather pictures as well, but as image repositories, they are not displayed in the view of identification, and the identification must be checked.

There are many websites presenting the species of one geographic area (e.g., Italy, Australia, US states, Tropical Eastern Pacific, ...), but they do not necessarily propose a picture browsing functionality. In that case, users need to check the species pages one by one. But many of them are not complete.

Potential developments:

- Browsing capacities over webpages do not reach yet the user-friendliness offered by books from a "mechanical" point of view. The extensive use of tablets and touch-screens should address this issue in the near future.
- Screening a large number of images through the internet require a proper and fine tuned programming to overcome possible limitations of the available bandwidth (with a particular thought to Africa still not well connected in general).
- There are many possibilities to develop better and user-friendly navigating and browsing tools, e.g., when you scroll over a picture, you display other pictures of the species presenting colour variations. This require high programming efforts and systematics knowledge in a same team (if not in a same person). Outsourcing the programming is more likely to lead to disasters from the past 20 years experience.
- The existing pre-sorting mechanisms could be much improved as well.

Dichotomous keys

The third method is the use of dichotomous keys. It is the main rationalized identification method. Dichotomous keys are decision trees with nodes and branches. Each node proposes a couplet of questions, each of the alternative leading to the next node through a branch. The terminal nodes are species (or any other rank as targeted by the key). There is a lot of literature on the theoretical aspects of key elaboration (e.g., Pankhurst, Dallwitz, Thiele, Hagedorn, Vignes-Lebbe, ...).

Note that nodes may be polytomic (originating more than two branches).

Keys are not easy to elaborate when the number of taxa is large (e.g., the macrourid key in the Gadiformes FAO catalogue by T. Iwamoto). Also the user needs to understand the vocabulary utilized to describe the characters and their states. So a textual key must be adapted to the targeted public: e.g., character states must be illustrated by small images and schemas along the key, as it is well designed in the FAO catalogues. The advantage of the web is that characters can be more illustrated than on paper.

Dichotomous keys are available on the web under various format, from the simple transcription of the text up to more elaborated interfaces like LucId Phoenix, with intermediate developments that take advantages of the markup languages (html, xml) and their navigating capacities. The keys may have been paper-published first, or directly created on the web. It is worth to mention that more and more keys are available from their original paper printed format through the increasing availability of scientific papers, in our case mainly taxonomic revisions that usually contain a key for the taxon revised (genus to family ranks in majority), and from FAO catalogues.

Again, FishBase (and now SeaLifeBase) is well in advance proposing 1600 keys transposed in a simple html format with internal links to jump from one question to the next couplet or the picture of the identified species, with character illustrations; 1200 of them are also converted into the LucId Phoenix format. Many other websites present but only one key for the area or the taxon targeted by the website.

Potential developments;

- Improving the navigation along the key taking advantages of new web technology developments;
- But maybe the most important is to have a metadatabase of available keys both printed and web ones with a query interface: users enter the geographic area, the taxon, and their skill level, and is redirected to the key the most appropriate, including existing websites.
- There is a need to develop more illustrations of characters, but it is a time-costly operation that can be done only by or under the direction of specialists.
- Theoretically, there is a need to study how different keys could be linked together, and how to reuse parts from several keys to create new ones in order to increase drastically the number of available keys for poorly studied areas.

Polythetic keys

The fourth method is the use of polythetic keys. The principle is to collect the state of a predefined number of characters that are known to be discriminating across the targeted species (or taxa) set. Then a similarity index is computed that orders the list of possible species. Note that some polythetic keys work on paper, without the similarity computation.

The difficulty of the method is that at the top of the list, the differences between the similarity indices may be very small letting the user in a position of doubt (which after all may be better than a dichotomous key where the last question will definitely lead to a result even if the character used may present some uncertainty or even overlap). Also gathering data to elaborate the keys is quite labour-intensive.

They are mainly used for bacteria identification (API systems) where several culture tests are conducted simultaneously, but rarely for metazoan and macroalgae. The best examples in our domain are the use of morphometrics measure-

ments and meristics counts as in IPez (see the corresponding presentation) and the FishBase morphometrics tool.

I found very few uses of polythetic keys on the web in our domain other than these two ones. One I found was only proposed at the end of the process for species in a genus. In any case, it would be most probably limited to some (student) prototypes if it exists, not representing a large production like for the dichotomous keys, or for a large number of species like for the two morphometrics tools above.

Potential developments

- Testing the existing tools in real environment.
- Reducing the number of characters used to compute the similarity in order to simplify the tools.

Interactive keys

The fifth method makes use of interactive keys (computer-aided identification), also called multi-access or multi-entry (but this is rather to be applied to polythetic keys; however, one may find interactive for dichotomous keys just because of the use of html links, which is not the interactivity we are talking about). They were designed along the development of computers where they are only available since the mid-70s (Pankhurst, Dallwitz, etc.). The principle is that all the possible questions on characters are available from the beginning of the identification process, the choice being given to users to answer first the question they are more comfortable with. After each answer, the list of remaining possibilities is given as well as the eliminated taxa, and the user chooses the next question until only one species remains. Characters may be illustrated as well.

In graph theory terms, it is a generalized polytomic network where all dichotomous keys may be potentially derived; in a way, the user interactively selects on the fly the one he is more comfortable with. Various functionalities were developed: hiding the characters dependent on a first question, proposing the couplet the most discriminating at each step, facilitating the identification of the most common species, of the easiest to identify, or any other constraint, etc.

On the user side, this is the best approach when pictures are not enough. On the system producer side, it is labour-intensive because the standardization of characters over a large group is quite difficult. Also, each species or taxon must be described as completely as possible even documenting the state of the non-diagnostic characters, whereas in dichotomous keys, only diagnostic/discriminating characters are used at each step of the key.

Various systems are available for free or as commercial products (Delta, XPER2, LucId, NaviKey, MEKA, ...), and almost of them propose now web interfaces, after a pre-internet phase where they were only standalone packages that continue to be distributed. Some of these systems can generate true static dichotomous keys under various constraints. The Standard Descriptive Data ontology has been developed by TDWG to be able to exchange descriptive data between the various systems that present different functionalities.

However, very few actual operating keys were developed with these systems so far for fishes and even for other aquatic organisms (Crustacea was the group the most used so far, but mainly for small groups). For fishes, it may be explained by the good performance of the identification by pictures for the most common species. Most of the published interactive keys are for plants and insects.

Potential developments

- Could be the basis for a multi-system identification strategy.
- Improve the semi-automatic extraction of characters and state from literature.

Image analysis

In general, the use of image analysis softwares does not give good results with picture taken in the wild, but embarked systems on trawlers are better. See the other presentation. Since most of the well identified reference images are taken perpendicularly to the body side of the fish, the difficulty is to obtain the same picture in the wild for the specimen to identify, which is quite demanding underwater, and requires a strict procedure on land. One option would be to reconstruct such images from videos.

Other tools

Other tools are available on the web but concern only parts of a specimen, e.g., otoliths or barcoding that will be presented elsewhere.

However, the OsteoBase project currently in progress at MNHN on fish bones is noticeable. Already 33 species have illustrations for skull bones and some vertebrae, that are searchable through an efficient browsing system. The public targeted is mainly the archeozoologists who identify the diet of past human communities from their dump sites. This project is collaborating with Phenoscope that gathers an ontology for all fish bones. Similar projects, some of them being older, are Fish Remains, Catfish bones, Archaeological Fish Resource and Archaeological fish-bone images (not given in annex).

Closing the identification

It is crucial to check the species information after reaching a possible identification. Whatever tool is used, the identifier must check the species account concerning the main diagnostic characters, the distribution (is the species actually recorded from the area where the specimen was found), and some biological and ecological data to confirm the identification. This step is too often neglected by many identifiers. On the web, this is easily done through FishBase, SeaLifeBase, and many scope restricted information systems.

The final step is to check the current valid name primarily in Catalog of Fishes (CofF) because the utilized tool may have been developed for a while, e.g., the printed dichotomous keys just translated in web format but with no update of the current valid names. FishBase and FishWise may be used if the name is not found in CofF as they record more combinations and typos and/or in a different way, which widen the name search capacities for fish in general. SeaLifeBase, WoRMS, and CoL, ITIS and other sources may be used for non-fish.

In both cases, the use of the web speeds up this final necessary step.

Other resources

A few websites gathers or lists identification keys:

- The web site of the interactive keys tools.
- Dedicated global projects: DiscoverLife, KeyToNature and its national websites, IndentifyLife (which was launched in June 2011) among a few others.

A few general platforms lead to further identification information (and also the information systems dedicated to taxonomic groups that are listed in those): Biodiversity Informatics (TDWG, formerly Taxonomic Database Working Group), World Register of Marine Species (WoRMS), Catalogue of Life (CoL),

Encyclopedia of Life (EOL), European Distributed Institute of Taxonomy (EDIT), ScratchPads, etc.

The challenges

None of these methods is better than another in general. It is context dependent: number of possible species, skill level of the identifier, specimen available or not, good picture or not, etc.

There is no general platform that would redirect a user to the identification tool he could use depending on the context. IdentifyLife may be that platform in the future with a metadatabase of available identification tools online, but it is only a starting project.

The great challenge in identification with the tools that are now available on the web is to propose a best strategy to the user to select the most efficient, or better, to jump from one tool to the other as necessary or if more efficient. There is already a start in FishBase where different tools are proposed or successively used. But this interoperability is mostly based on html navigation links. The development of ontologies and the semantic web may help in that way.

However, what are missing from a practical point of view for developing more websites are available standardized descriptions, species pictures, and character/ states illustrations, which is a content challenge.

The technology is well in advance compared to the lack of data content like in too many cases in Biodiversity Informatics.

This review provides an appraisal of existing, state-of-the-art fish identification (ID) tools (including some in the initial stages of their development) and shows their potential for providing the right solution in different real-life situations. The ID tools reviewed are: Use of scientific experts (taxonomists) and folk local experts, taxonomic reference collections, image recognition systems, field guides based on dichotomous keys; interactive electronic keys (e.g. IPOFIS), morphometrics (e.g. IPez), scale and otolith morphology, genetic methods (Single nucleotide polymorphisms [SNPs] and Barcode [BOL]) and Hydroacoustics. The review is based on the results and recommendations of the workshop “Fish Identification Tools for Fishery Biodiversity and Fisheries Assessments”, convened by FAO FishFinder and the University of Vigo and held in Vigo, Spain, from 11 to 13 October 2011. It is expected that it will help fisheries managers, environmental administrators and other end users to select the best available species identification tools for their purposes.

