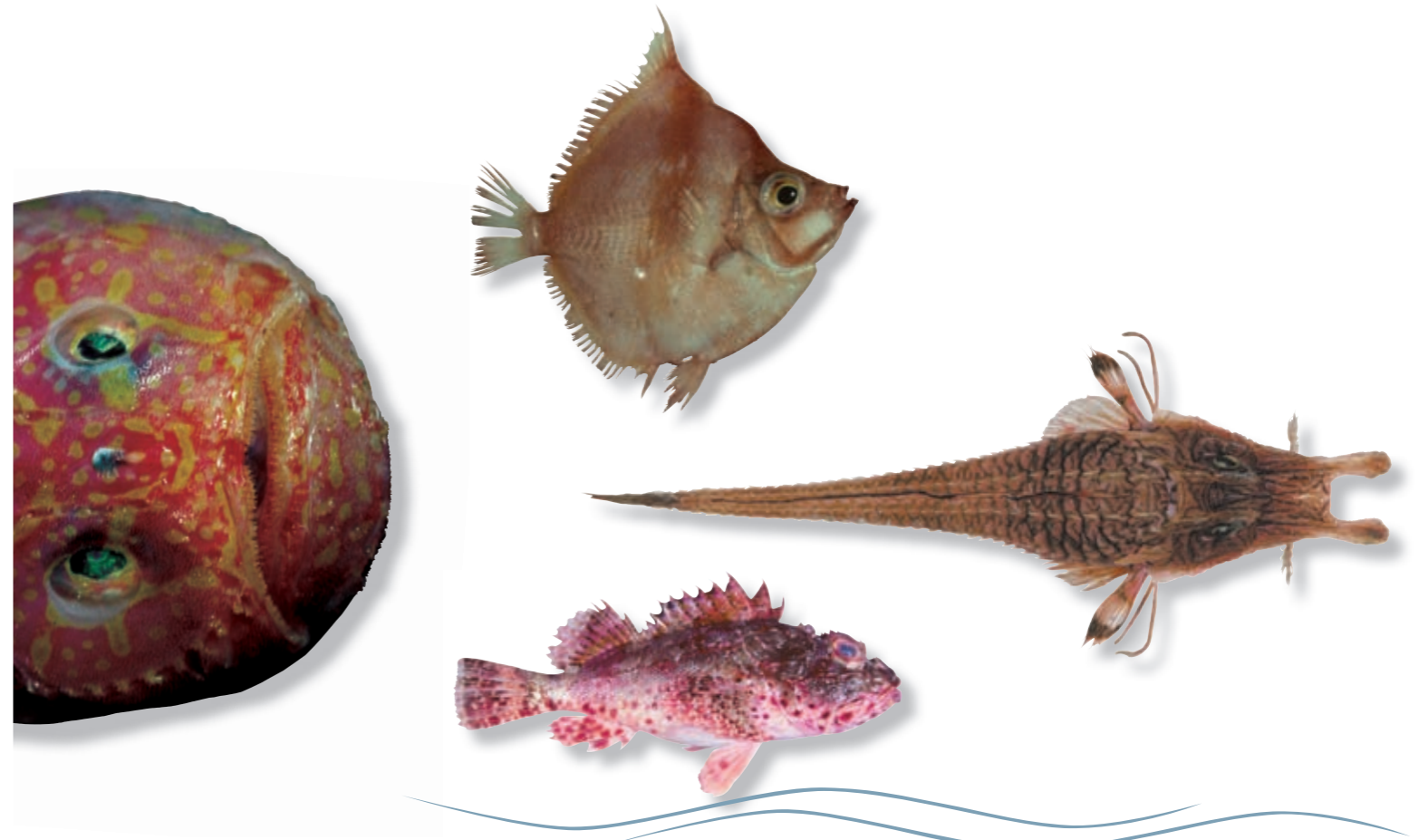




Validation of national demersal
fish datasets
 for the regionalisation of the
 Australian continental slope and
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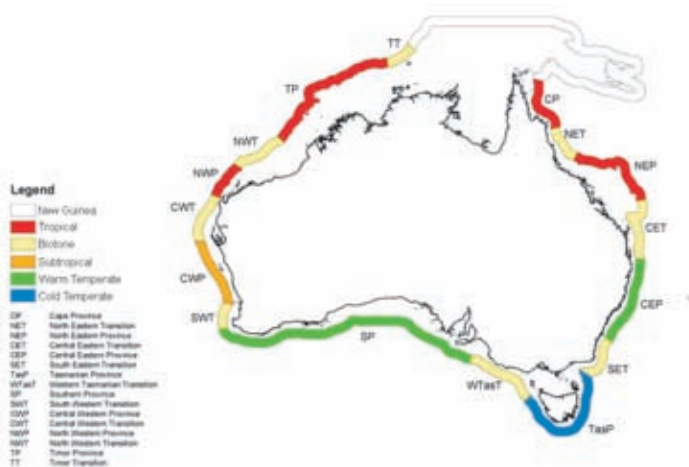
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1. Summary

Earlier studies of inshore bioregions identified the need for a large-scale, faunal-based bioregionalisation of offshore demersal habitats in the Australian Exclusive Economic Zone (EEZ). In this project, provincial and biomic regionalisations of the EEZ beyond the coastal zone were produced from validated national datasets for deepwater demersal fishes (defined for this study as fishes found at depths greater than 40 m).

In this project, critical information on the geographic and depth distributions of fishes were used to provide the first comprehensive biogeographic appraisal of Australia's deepwater demersal fish fauna, and the first anywhere at such a large scale. Of the almost 1500 species examined by the project, 21% do not have full scientific names and many of these will be new to science. The distributions of deepwater fishes provide a surrogate of marine faunal distributions across the Australian EEZ.

The study discovered evidence of strong patterns in the distribution of Australian deepwater fishes (faunal substructure), with some obvious parallels to the patterns inshore, as well as some marked differences. Eight deepwater provincial units were identified (the Cape, North Eastern, Central Eastern, Tasmanian, Southern, Central Western, North Western and Timor Provinces), as well as indicator species that characterise each province (see map in Figure 10).

Notably, the fauna is less complex offshore than inshore in temperate Australia, but more complex on the Australian slope than on the shelf in the tropical Indian and Pacific Oceans. A well-defined Tasmanian province adjoins a more pronounced, cool temperate inshore unit (the Maugean Province). Similarly, the Central Eastern Province off New South Wales coincides with an eastern warm temperate unit inshore, the Peronian Province. The offshore pattern in the Great Australian Bight appears less complex, with evidence for only a single province across this part of southern Australia, whereas there are separate inshore provinces (in south-western Australia and the South Australian gulfs). On the other hand, a strong secondary provincial structure, consisting of a suite of widespread southern Australian species, is evident in deepwater. A subtropical unit off western Australia weakly coincides with an equivalent inshore unit. However, the single tropical provinces inshore, off both the north-west and north-east coasts respectively (the Dampierian and Solanderian Provinces), are both represented offshore by two distinct deepwater provinces.

In each of the eight deepwater provinces, there are strong patterns of bathymetric zoning of the fauna, which indicate the presence of biomes at different depths. This means that the widespread stratified partitioning of provincial faunas by depth, detected earlier in the South-east Marine Region (SEMR) by CSIRO (2001), is widespread throughout the EEZ. In the present study, three biomes were identified on the continental slope (upper slope, mid-upper slope and mid-slope), as well as an ill-defined unit on the outer continental shelf. Biomic patterns on the continental shelf determined by other studies were unclear, and the data will need to be combined with coastal data in a more comprehensive analysis.

A well-developed faunal assemblage, known as the upper slope biome, occurs just below the continental shelf break in each deepwater province (ca 300–520 m). The depth ranges of this biome varied only slightly between provinces; it is slightly shallower in the east than in other areas off the Australian coast. A strong mid-slope band is evident at similar depths (ca 860–1140 m) in all provinces. An additional, less obvious biome was identified on the mid-upper slope between 590–830 m. This biome persisted in all provinces, except the Timor Province. Assemblages beyond the mid-slope could not be clearly evaluated due to a lack of data, but species confined to the deep slope indicate the existence of a lower slope biome, probably beyond 1600 m. Beyond the continental slope (ie, deeper than 2000 m), where the fauna is not well known but thought to become more homogeneous, geological data will be needed as surrogates for the biota.

The methods adopted for this project required the development of innovative, world-first solutions to facilitate rapid assessment of the accuracy and quality of literally thousands of literature records and

specimens, to allow construction of realistic bioregionalisations. Consultation, both within the project team and externally, was an essential part of refining the scientific approach throughout the project. New tools developed for visualising and analysing data will greatly enhance the national biological baseline and research capability. The mapping tools developed in this project could be customised to produce an interrogative database that would enable the user to produce sub-lists of the fish fauna at any geographic location in the Australian EEZ. For this to happen, the geographic data (converted to 1-dimensional string data) produced from inshore and offshore regionalisations would need to be amalgamated into a uniform data format. If developed, this database would enable managers and researchers to instantaneously determine the fish composition of any marine bioregional unit, from provincial to geomorphological scales, and between any depth intervals. The database could incorporate images and key characteristics of species, thus providing a unique means of characterising and accessing our marine biodiversity. This prototype could be expanded to include invertebrates and marine plants.

This project has greatly advanced our knowledge of Australian deepwater fishes, but serious knowledge gaps still exist in our EEZ region, mainly through inadequate research material and a lack of sampling coverage of some regions. Our knowledge of the bioregions will improve dramatically if and when these regions are surveyed. The highest priorities are two relatively accessible, but surprisingly little known regions: the continental shelf off south-west Australia, and the continental slopes off north-east and north-west Australia. Also, our interpretation of the fish data could have been improved if more objective methods of analysing the data were available. New spatial statistic methods may need to be derived, but modified forms of methods used in classical systematics, such as cladistics, could help to interpret the evolutionary history of the bioregions. Biogeographic interpretations have been undertaken for many marine groups of plants and animals in our region, but these patterns have never been assimilated to explain the present provincial or biomic structure of Australia's marine biota.

2. Introduction

In 1996, the Commonwealth's 'Ocean Rescue 2000' initiative commissioned a series of state and national research projects to produce scientifically credible bioregionalisations of the entire Australian EEZ (IMCRA 1996). These studies were to be used to facilitate plans for establishing a representative system of Marine Protected Areas (MPAs) throughout the EEZ (Blake 1995). The project culminated in the publication of the *Interim Marine and Coastal Regionalisation for Australia* (Version 3.3) report (IMCRA 1998). The IMCRA report (<http://www.deh.gov.au/coasts/mpa/nrsmmpa/imcra.html>) produced four modelled regionalisations represented as maps: a meso-scale regionalisation of the Australian continental shelf; demersal provinces and biotones of the continental shelf (Map 2); pelagic provinces and biotones; and proposed provinces for the external territories.

The IMCRA (1998) Map 2, a bioregionalisation of demersal provinces and biotones, was produced from a study of the distributions of Australian continental shelf fishes (IMCRA 1996). IMCRA identified three tropical provinces in the north, a subtropical province in the west, and three warm-temperate provinces and one cold-temperate province in the south. The fish species used in analyses to produce the IMCRA regionalisation occur primarily in coastal waters where the fauna is relatively well known. Demersal slope fishes were not included in the IMCRA analysis, so extrapolation of these biogeographic units beyond the inshore into the deepsea without evidence was considered unwise, as the factors controlling biotic distributions between them are not equally comparable. Hence, the IMCRA study identified the need for a companion project to investigate the biogeographic patterns of the less well-known fauna of the continental slope, to identify provinces and also the biomic structure at different depths within these provinces.

More recently (CSIRO 2001), this approach was adopted to produce provincial and biomic regionalisations of the South-east Marine Region (SEMR), this time using fish data from the continental slope. The SEMR study found bathymetrically distinct faunal assemblages on the slope, which represent biomes, separated by ecotones (transition zones). The study detected more than a single biological province in the region, but these findings were inconclusive due to interference from edge effects in the extreme east and west of the region. The study flagged the need for a national approach to develop an overarching framework for the whole Australian region, rather than using a piecemeal approach. In contrast, the SEMR analysis produced evidence of four biomes: near the continental shelf break, and on the upper, mid and lower slopes.

The present study was designed to construct a biogeographic framework from regionalisations of the continental slope of Australia's marine jurisdiction, based on the distributional patterns of the region's demersal fish fauna. Offshore demersal fishes are defined as those occurring below a depth of 40 m (ie, those living beyond the coastal zone). This upper depth limit, which was chosen to reduce edge effects near the shelf break, excludes most coastal species and includes a large suite of species occurring across deeper parts of the continental shelf. However, the main focus of the present study was to examine faunal structure of fishes on the continental slope.

The objectives were to:

1. Validate national datasets for demersal fishes on the continental shelf and the slope (from 40 m depth) to the edge of the Australian EEZ, including information on the geographic and depth distributions of species.
2. Use these data to produce provincial and biomic regionalisations of the Australian EEZ beyond the coastal zone (below 40 m).

The region covered was the EEZ waters adjacent to continental Australia and Tasmania. The region excludes Australian territorial waters—Macquarie, Heard, McDonald, Christmas, Cocos (Keeling), Lord Howe and Norfolk Islands. The principles and methods used were based on the earlier regionalisations of

south-eastern Australia's outer continental shelf and slope (CSIRO 2001), and the coast and continental shelf of Australia (IMCRA 1996). The current study investigated the provinces of the region's outer continental shelf and the biomes of the slope, based on the geographic and depth distributions of the deepwater demersal fishes. These demersal fish distributions were modelled from a variety of data sources, including survey and fisheries catches, museum collection records, and records in the literature.

In large-scale biogeographic studies, fishes can be used as surrogates for the rest of the marine biota when data are limited for other faunal groups. The use of physical information as a surrogate for the biota in rapid assessments of biodiversity, is limited because the distribution patterns of the biota cannot always be modelled on physical attributes alone. In Australian seas, biogeographic units at the provincial level are products of evolutionary history, with their origins often dating back to Gondwana, more than 80 million years ago. The geographic distributions of these faunal assemblages are modified by contemporary physical regimes, but their composition cannot be determined using physical information alone.

The determination of provincial units is basic and apical in a hierarchical sense when characterising biodiversity at megascales, or scales of entire regions such as the Australian EEZ. These provinces can be further subdivided into biomic assemblages or biomes (Hedgepeth 1957). For example, the faunal assemblages of lower continental slope biomes are very different from those of coastal biomes. The nesting of biophysical units, in a hierarchy of spatial/diversity complexity, with the province-level units at the top, forms the basis of this approach to bioregionalisation (see Lyne 2003).

Of all faunal groups represented in Australian seas, based on our present knowledge of the biota, fishes are the most suitable for rapid assessment of biodiversity at the provincial level. Australian fishes are a diverse group comprised of numerous families that have co-evolved in the Australian region over millions of years. Several invertebrate groups are likely to be equally biogeographically informative, but these are not adequately known along most of the continental slope.

The taxonomic knowledge and data coverage is much better for fishes than any other marine group. Compared to the inshore fauna, however, the taxonomy and distribution of Australian deepwater demersal fishes is less well known. Specimens recorded on research voyages or deposited in collections often have unreliable identifications. As a consequence, multiple species have been lumped under a single, widely used name, often using the name of similar animals occurring in other regions near Australia. Hence, to improve the quality of the data, this project needed an unprecedented level of alpha taxonomic research (delineating species) to validate datasets and the identity of collected fish specimens. Special web-based tools were developed, and a consortium of senior local and international ichthyologists assembled, to produce distributional maps of Australia's deepwater fishes. This group of scientists involved contained several members of the research teams involved in previous fish regionalisation projects.

This deepwater bioregionalisation project is multifaceted and has other peripheral objectives. The project included a 'gap analysis', which used bottom survey information to define poorly sampled faunal regions of the Australian EEZ. A companion database was produced to summarise the distribution of museum holdings, and the poorly sampled regions were identified by assessing the distribution of verifiable records. This identification of gaps in the region's biological inventory and collections will help to prioritise research needs and identify locations for targeted surveys to fill these gaps. Targeted 'infill' surveys should lead to a better data baseline and inventory of marine invertebrates, as well as fishes.

3. Methods

3.1 Consultation and reporting

The project team was required to develop innovative ways to rapidly assess the accuracy and quality of literally thousands of literature records and fish specimens, to enable the construction of realistic bioregionalisations.

Consultation, both within the project team and with various stakeholders and specialists, was an essential part of refining the scientific approach throughout the project. Numerous discussions were held with National Oceans Office staff to define the scope and optimal modus operandi within the time and financial constraints of the project. The National Oceans Office staff provided constructive feedback on issues raised by either them or the project team, and provided feedback on the draft progress reports.

Peter Last, Vincent Lyne, Martin Gomon and/or Gordon Yearsley represented the project team at various Bioregionalisation Working Group (BWG) meetings. Feedback received at these meetings was used to clarify the project and integrate it within the national bioregionalisation framework. For example, the decision to recognise a secondary structure beneath the core provinces eventuated through discussions between BWG members and project staff. These meetings also initiated useful discussions with other agencies (eg, with Peter Harris and other staff at Geoscience Australia).

The museum staff and ichthyologists involved with the project, and CSIRO Marine Research (CMR) specialists from other research areas, also provided valuable input to the collation, collection and analysis of data. The core project personnel are listed in Appendix 1.

3.2 Metadata and gap analysis

Two primary types of fish distribution data were sought for this study: (1) specimen or point data and (2) catch composition data.

Specimens held in museum collections provide valuable distributional information that can be accessed, and the accuracy of specimen identifications can be validated. However, most catch data cannot be validated unless the data are linked to specimens or images retained from the survey in question. It was important to obtain taxonomically reliable, historical catch data, where it exists, to supplement the point data available from specimens registered in scientific collections. Both types of data are obtained mainly from surveys by State and Australian Government research vessels, plus a few surveys from Australian commercial and foreign vessels.

Historical data varies in quality (mainly in taxonomic reliability), regional coverage and accessibility. It was therefore important to efficiently determine data gaps (areas with poor coverage of available, reliable data) so that future effort can be focused on obtaining data for these regions. All reliable existing digitised data were collated from demersal stations from the 40 m depth contour to the edge of the Australian EEZ. This demersal dataset was then partitioned into depth intervals and plotted on a map of the EEZ. Efforts to locate additional datasets were biased toward areas with poor survey coverage as demonstrated by this mapping process.

Commonwealth Scientific and Industrial Research Organisation (CSIRO) data

CSIRO has conducted some 240 research voyages across the EEZ since the 1970s. Before this project, catch information collected from data stations for about 100 of these voyages had been digitised and stored in CSIRO Marine Research's data warehouse. Access to these data is via an online application called 'Data Trawler'.

Before collating these data, the voyages with data stored in the CMR data warehouse were classified by the taxonomic quality of the data obtained (eg, the area fished, the presence or absence of a taxonomist on board, the age of the data). Voyages that delivered poor quality catch data were removed from the dataset. Complications were encountered because the fishing method was recorded for only about half of the stations, and the bottom depth was omitted for all stations. These parameters are required to classify fishing operations as either pelagic or demersal, so a method of back calculation for this classification was derived as follows.

For each station without a recorded gear code, bottom depth was estimated by matching the start and end coordinates of stations against bottom depths taken from a bathymetric dataset (with 1/15 degree intervals) prepared jointly by CMR and the University of Tasmania. Stations where the mean fishing depth and mean estimated bottom depth differed by less than 50 m were classified as ‘demersal’. For the remaining stations (where this interval exceeded 50 m), sources such as cruise reports and original catch composition records were checked to determine the fishing method, with stations usually labelled as demersal, pelagic, or unverified.

External agency data

Fisheries agencies across the nation were contacted to locate, and negotiate access to, datasets of potential relevance to this study. This proved to be a slow process, but was essential to improving the data coverage. Data obtained from external agencies were manipulated into a common format and then collated for mapping. The datasets accessed in this manner were crucial to supplementing the data available from CSIRO voyages. In addition to discovering and locating new data, numerous known datasets were not used (following discussion with state bodies) due to, for example, inadequate taxonomic reliability, access difficulties or poor geographic coverage.

Mapping

Data for demersal stations deeper than 40 m, from both CSIRO voyages and external agencies, were mapped at the resolution of 0.1 degrees to illustrate spatial coverage by depth (Appendix 2). These maps were examined to determine areas and depth strata with poor data coverage, and effort was subsequently made to obtain reliable data for these areas. The maps also provide a basis for planning future surveys by determining critical gaps in existing survey coverage and, therefore, gaps in our knowledge of demersal fish species and other demersal biota.

3.3 Producing the species database

Species list compilation

A provisional list of fish species (the Species Database, Appendix 3) containing all taxa known to occur in the Australian EEZ was compiled by combining the species list from CAAB (Codes for Australian Aquatic Biota, <http://www.marine.csiro.au/caab/>) with the species lists from draft versions of the revised (Volume 1) and new (Volume 2) editions of the Zoological Catalogue of Australia (Pisces) (unpublished, Australian Biological Resources Study).

Provisional data (depth, geographic range and broad habitat type) were added to the Species Database for each taxon, based on earlier bioregionalisations—IMCRA (1998) and the SEMR study (CSIRO 2001)—and specialist knowledge. Habitat types coded were ‘Freshwater’, ‘Coastal’ (to depths of 40 m), ‘Shelf’ (depths of 40 m to 200 m), ‘Pelagic’, and ‘Demersal slope and uncoded’. The usefulness of ‘uncoded’ species was unknown until further investigation. Retaining a full listing of the Australian fish fauna provides a baseline dataset that allows for compiling future species lists by general habitat type.

Genus list compilation

A copy of the Species Database was then reduced to include a subset of only those genera relevant to the continental slope study, which is the main focus of this project. Species coded as ‘Freshwater’, ‘Pelagic’,

'Coastal' or 'Shelf' were therefore deleted. Then the species list was converted to a list of genera only. This list of 509 fish genera was annotated by marking genera that, based on expert opinion, probably do not occur on the slope. The names of potential custodians (see below), project collaborators and potential external collaborators were also noted (see Appendix 15).

Custodians

A custodian (a taxonomic specialist) was appointed for each genus on the list of continental slope fish genera. The role of each custodian was to coordinate the examination of relevant specimens, and to collate and vet the data prior to entry in the Species Database. In addition to the custodians, project and external collaborators were assigned where appropriate.

Prioritisation of genera using the Biogeographic Information Index (BII)

Taxa vary in their usefulness for biogeographic analysis, depending on factors such as their geographic range, taxonomic complexity, and the quality and availability of data. Due to the species richness of fishes in Australian waters, not all local fishes could be included and it was necessary to identify a subset of the fish fauna for analysis. Genera within this subset would then be given priority in the validation of taxonomic and distributional information.

The Biogeographic Information Index (BII), which was developed during the IMCRA project (1996), was used to identify genera for the priority fauna subset. Genera listed on the Species Database were first ordered based on their biogeographic usefulness, using the following formula:

$$BII = C (2A + B) / \log (n + 1)$$

where: A = biogeographic potential; B = information content qualifier; C = value within each ecosystem and n = number of species in the genus. For details of the scoring criteria used for determining the BII of each genus see Appendix 4.

The genera on the Species Database were then ranked by the resulting BII score. A low BII score (less than 30) indicates a genus providing significant biogeographic information, ie, a genus with a high proportion of narrow-ranging endemic species. The 91 most informative genera for this purpose are listed in Appendix 5.

Of some 500 genera in the database, about 370 were coded as having demersal species occurring on the outer shelf and/or slope. The initial BII for these genera ranged from 4.35 to 249.14. The project focussed on examining specimens of genera with high potential for identifying bioregions (ie, with a BII score less than 30). The priority listing changed as custodians resolved taxonomic and nomenclatural issues within their respective taxa. For example, changes to the number of species within genera, or changes to their geographic ranges, resulted in changes to their BII score and thus their value to the study. After the data-entry phase of the project, the BII scores of the list of priority genera were recalculated and the list was updated for analysis. The additional priority genera are highlighted in Appendix 5.

Data entry to the Species Database

The Species Database was incorporated into the CAAB system, and made accessible to all project participants via the web. The CAAB system codes all Australian fish species with an eight digit number, and includes information on species names. While these names and codes are publicly accessible via the web, password-restricted access allowed participants to enter and edit data relating to this bioregionalisation project. However, access was restricted to genera for which they were the custodian. This maintained the integrity of data within the Species Database as, for each genus, a single collaborator was solely responsible for data management. For each species, a notes section was also available, where project participants other than the custodian could submit additional information. When this facility was used, an automated email response informed the custodian what information was added, and by whom.

Online data entry to the Species Database was facilitated by a standardised entry screen (Appendix 6), to

ensure consistent data capture. Mandatory fields captured data for string position (geographic range, see Section 3.4), depth, and the broad habitat occupied by each species.

Entry of string data (start and end points of each geographic range) allowed for up to three disjunct distributions (see Appendix 6). Each custodian was also required to record the source of the information (eg, a museum specimen or literature record). The custodian's confidence in the string start and end points was then entered on a scale from 1–5 (where 1 = excellent; 2 = good; 3 = satisfactory; 4 = poor; 5 = doubtful), followed by an overall 'string completeness' score (where 1 = ready for analysis; 2 = minor upgrade still needed; 3 = incomplete, species potentially useful; 4 = data deficient, species probably not useful). The only species used in the analysis were those with a string completeness score of 1 (ready for analysis). Data with varying levels of confidence could be included in future analyses; for example, an analysis could be broadened to include data with a string completeness confidence score of 2 (good).

Minimal and maximal depths were also entered on the Species Database for each species. The custodian's confidence in these depth ranges, and the completeness of depth data, were scored in the same manner as for the string data, and analysed using similar techniques. When available, additional data were entered about the distribution of the taxon (the biomes occupied, its core and extra-limital distributions), as well as general and other notes (see Appendix 6).

Point data mapping—OZFISHCAM

Mark McGrouther, collection manager at the Australian Museum in Sydney, had already produced a website of holdings of the country's largest fish collection. He made a major contribution to this project by assimilating electronic data from all major Australian fish collections (with the assistance of colleagues at the relevant museums). He mapped the catch localities for each catalogued taxon held in Australian collections (see 'total holdings' map in Appendix 7) and made these specimen (point) data searchable online.

This database was made available to the specialist taxonomic team via a web-based mapping interface, Online Zoological Fish Collections of Australian Museums (OZFISHCAM). The collection holdings in OZFISHCAM could be queried by species or genus name. Capture localities for specimen holdings were depicted by dot points on a map of Australia. The dots were colour coded, with different colours representing different museum collections. Clicking on a dot (representing the catch locality of a specimen, see Appendix 7) revealed a subset of the relevant collection data, and the acronym of the collection in which the specimens were held.

The project's point data OZFISHCAM database should not be confused with the Online Zoological Collections of Australian Museums (OZCAM) project, which aims to connect museum faunal databases throughout Australia. The OZFISHCAM point data mapping facility for fishes can be considered a case study for the OZCAM project, demonstrating the strengths and weaknesses of this type of approach. However, the level of information included in the fish collections database is far more detailed than that available to OZCAM, due to the negotiation of unrestricted access to fish collection data, that could include commercial-in-confidence data and sensitive, unpublished information.

The online database of collection records facilitated extremely rapid and simple assessment of station data coverage, and species localities. With potentially thousands of specimens to examine, individual contributors could tailor their research by examining data outliers and/or simply checking endpoints (string and depth) by validating the identification of just a few specimens. While the complexity of some genera, and the generally high level of misidentifications in collections, in many cases prevented such a simple approach, the use of the database was nevertheless extremely valuable and time efficient. Furthermore, it remains functional for ongoing use by Australian fish taxonomists.

Catch data mapping—CMR data warehouse and modelled distribution maps

A similar online mapping capability was developed by project participants, particularly Tony Rees at CMR, to display current species data from CMR's data warehouse (Appendix 8). For each species, results of the search were plotted at the resolution of 0.1 degree squares, depicting stations where that species

had been recorded. Individual catch localities on the map could be ‘clicked’ to list trawl and voyage data for that record.

Online access to individual maps allowed participants to view historical catch locations for fish species, and to compare these to other records. These other records included museum collection records, previous distributions described by the IMCRA (1998) study and/or the 2001 CSIRO SEMR study (see Appendix 9 map), distributions recorded in the literature, and/or the current distribution as recorded in the Species Database (see Appendix 10). Contributors could then assess the potential reliability of catch data based on the species being examined. CMR’s data warehouse was also extended by adding some catch data (where available) from target areas identified in the gap analysis. These data could be used to identify possible extensions in the range of some species.

Multiple maps display

The web-based mapping facilities were further developed to display on a single screen for each species the above two maps—the OZFISHCAM map of total museum collections (point data) and the CMR data warehouse map (catch data)—plus a map of IMCRA plus SEMR distribution data (where available), and an updated map of the current distribution data as entered by the custodian in the Species Database (Appendix 11).

Comparison of the four maps allowed the project participants to identify and locate species records from voyage data, and also specimens that were collected outside the current known distribution of any species. Participants, following validation of the identification, could also update the depth and/or string data in the Species Database. This capacity is probably a world first and will act as a *prima facie* assessment method for developing more integrated exercises such as OZCAM.

3.4 Modelled distributions based on string analysis

The geographic distributions of each fish species were converted to a 1-dimensional string (similar to those used in IMCRA 1996, and in the CSIRO SEMR study, 2001) along the 500 m depth contour (Figure 1). The string characterisation for this continental slope study (compared with IMCRA, where the north-east and north-west are connected via the Gulf of Carpentaria and Torres Strait) is complicated by the fact that Australia’s continental slope is contiguous with the slopes of Indonesia and Papua New Guinea. For the purposes of provincial and biomic analyses, a points index ranging from 0 to 281 was used to identify locations equidistant along the string.

The start point (0) of the string was near the northern tip of Queensland, just to the east of Cape York. North of Arnhem Land, the string was artificially diverted to run due east for points 265–281, to simplify the coding of distributional data in the Gulf of Carpentaria, because some offshore species can occur at depths shallower than 40 m. The string points used were the same as those used in the earlier SEMR study, but the numbers were changed so that the zero point was the first point, progressing in a clockwise direction, after Cape York.

The modelled distributions were thus graphical representations as inferred by taxonomic specialists from various available data. Four end points, demarcated as polygons (two string and two depth points), determined the boundaries of these (2-dimensional) modelled distributions.

3.5 Online map creation of modelled distributions

For every species that was ultimately considered to be a valid taxonomic unit, the basic information that was assembled, assessed for quality, and documented comprised a geographic range around the Australian continent (converted to a 1-dimensional string, or multiple strings), together with a depth range, plus associated confidence indicators.

Early in the project, it was decided to provide the collaborators and the species custodians (the taxonomic specialists) with an interactive tool that would enable them (by combining the values entered for the string start and end points with the values entered for minimum and maximum depths), to display the range of each species in graphical form (for instance, as a shaded area on a map). To do this, a previously created web-accessible mapping utility at CMR, the 'c-squares mapper', was employed together with an algorithm that would generate the appropriate area (expressed as a set of 0.5 x 0.5 degree cells) to be mapped, for data relevant to any species, at either the intermediate or final stages of compiling the Species Database.

The CMR c-squares mapper is a grid-based nomenclature system that allows a unique identifier to be generated for any 10 x 10 degree, 5 x 5 degree, 1 x 1 degree, or 0.5 x 0.5 degree cell, or smaller, on the surface of the globe, and the c-squares mapper enables sets of such squares to be visualised on one of a range of base maps, which can be selected by the user. For further description of the c-squares mapper and the nomenclatural method used for individual c-squares, see Rees (2003).

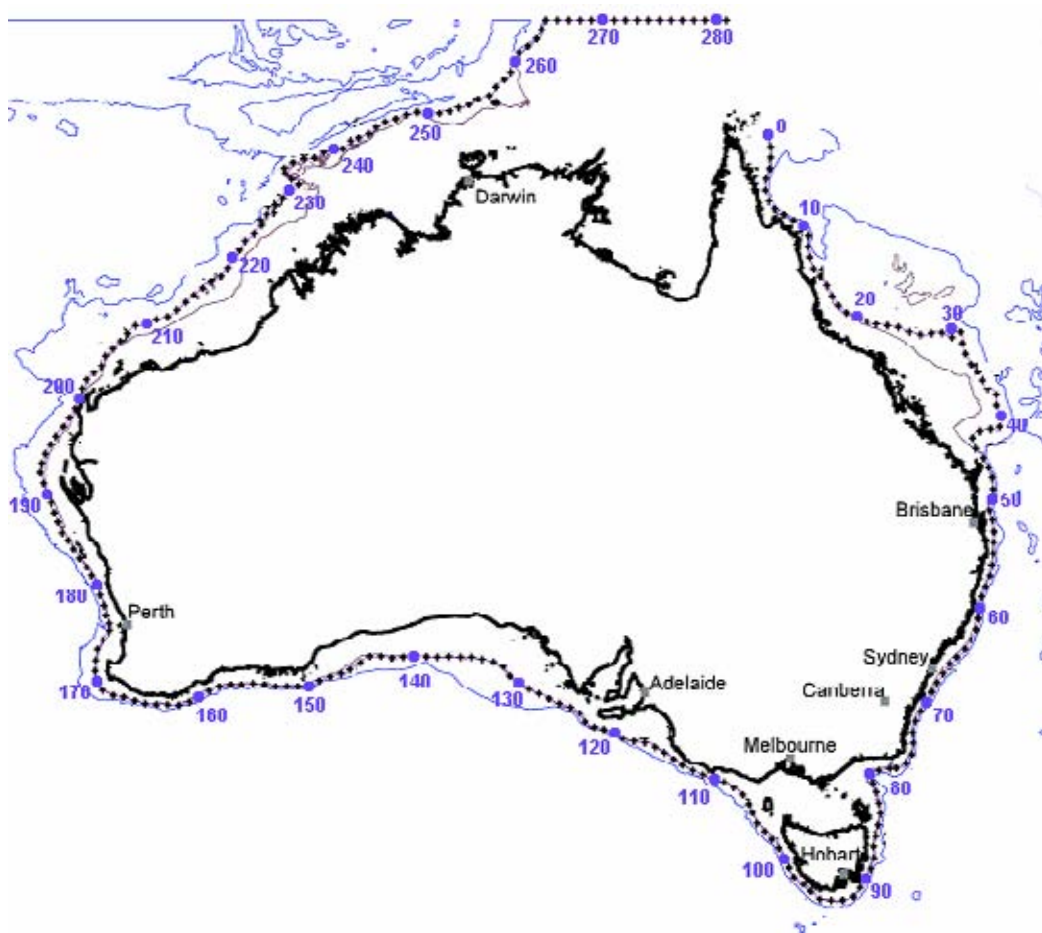


Figure 1. String route map based on the 500 m isobath.

The algorithm used for the present study comprised accessing a data table containing approximately 8500 rows, each corresponding to an individual 0.5 x 0.5 degree square over the ocean in the region surrounding Australia. For each square, maximum and minimum depths were then obtained from the high-resolution (1/15 degree) bathymetric dataset cited in section 3.2 (ie, between 49 and 64 points per square) and recorded in the table, along with an assigned string position. Initially this string position was

the closest point on the 500 m string to that point (by a nearest neighbour/least squares calculation), but it was subsequently adjusted (at the request of project scientists) to be the nearest neighbour by latitude down the east and west coasts of Australia (string points 0–93 and 169–265) and the nearest neighbour by longitude through the Gulf of Carpentaria (string points 265–281). In addition, minor manual adjustments were made in the vicinity of Bass Strait, so that data falling within the Strait was plotted to its nearest logical point (line of sight combined with a north/south and east/west split) instead of, in some cases, its mathematical nearest neighbour. Each cell was also assigned its equivalent code in c-squares notation, to enable the output to be directly generated in a format suitable for display using the c-squares mapper.

With this data table as a resource, it was then a relatively simple automated task for the software to receive as input one or more string start/end pairs and a depth range (minimum and maximum depth, in metres) and return in a single operation, a list of codes (= square IDs) for all the squares assigned to any position along the supplied string(s), and with a cell depth range overlapping the depth range of the supplied species. In practice, this list of codes was generated as a web-supplied variable (text string) that could then be submitted to the c-squares mapper via a standard ‘form submit’ button on an HTML page. This provided the person entering data with a rapid web-based tool to check the validity of newly entered or edited data, and to produce maps that could be compared instantaneously with other sources of information such as maps of catch data, specimen (museum) data, and the results of any previous analyses, which could also be called up to the user’s browser window via a ‘multiple maps’ option.

The final ‘latest modelled distribution’ maps (based on the expert-assessed species string and depth ranges) could be regenerated on demand via a web call, accessible to authorised project users only (at this time) via the CMR CAAB entry point. The source data (string and depth limits for each species assessed as part of this project) are also retained as a discrete dataset with the potential to be mapped in other ways. For example, the source data could also be used as input to a GIS/vector based system with access to relevant contour information, should there be a requirement in the future to produce polygon-based representations of the data as a replacement for (or supplement to) the present raster-based information.

3.6 Taxonomic elucidation

Several ichthyologists with specialist knowledge of Australian deepwater fishes were invited to participate in the taxonomic validation and clarification of priority groups. Fish groups were assigned to participants based on their areas of expertise and the time they could allocate to the project. Each specialist determined and then refined the distributional plots of species in their target groups by examining specimens in state museums and the CSIRO Marine Research collection in Hobart, and by checking literature records.

An initial workshop was held in Hobart with six interstate specialists (whose attendance was staggered from 28 October to 11 November 2002) and 7 project members from CMR (listed in Appendix 12). The workshop was a laboratory-based exercise to validate the identification of specimens held in the National Fish Collection, and to incorporate distributional data into species dossiers (see below). Genera were prioritised for examination based on their Biogeographic Information Index (BII) ranking as described above, and their representation in the Hobart collection. Distribution and depth data for species within priority genera were refined and keys to the fauna were drafted, where time permitted. These keys were used to assist in the identification process, thus improving data quality and saving time when examining additional material. Literature keys for priority genera were mostly unavailable or grossly inadequate for the Australian fauna. However, literature reviews of each group were an essential ‘first step’ in the process of taxonomic elucidation.

A species dossier folder was established for each family. This became the repository for all hardcopy documents and data relating to that family. The dossier included: a status report (eg, summaries of tasks completed and remaining), checklists of species, species lists from various museums, copies of published keys to species, the draft project key to species, species photographs, laboratory notes, and key literature.

Over the 14 months or so following the workshop, specialists travelled to various Australian museums to examine additional material of the priority genera, and to assemble or improve the accuracy of distributional plots. Specimens were examined at the following institutions: Australian Museum, Sydney (AMS); CSIRO Marine Research (CMR); Museum Victoria, Melbourne (NMV); Queensland Museum (QM); South Australian Museum (SAM); Western Australian Museum (WAM); and Museum and Art Gallery of the Northern Territory (MAGNT). Two overseas consultants (Tomio Iwamoto, California Academy of Sciences, and Kunio Amaoka, Hokkaido University) also visited the National Fish Collection in Sydney and other Australian museums to refine data for their assigned groups (whiptails and flatfishes respectively). A case study example of taxonomic elucidation (for the Bight stinkfish, *Foetorepus phasis*) is provided below.

The National Fish Collection at the Australian Museum has a scaling system for identifications, which records both the identifier and the level of confidence placed in the identification:

Level 1: Highly reliable identification

Level 2: Identification made with high degree of confidence at all levels

Level 3: Identification made with high confidence to genus, but less so to species

Level 4: Identification made with limited confidence

Level 5: Identification superficial.

Each level of confidence is based on a set of objective criteria. The reliability of identification for each specimen is recorded using this system at the National Fish Collection, and a similar system is now used at most other Australian museums.

By mid-January 2004, custodians had completed comparisons of specimens held in collections around Australia, and had completed the data entry form for species in their prescribed genera. Many additional species (several of which are new to science) were discovered during this process, and these were added to CAAB for use in the project.

Case study—Foetorepus phasis

The following constitutes a typical example of how research was undertaken by a custodian to delineate a species, and to determine string and depth endpoints, using the Bight stinkfish, *Foetorepus phasis* (family Callionymidae). However, due to the taxonomic complexity of many genera studied, and the paucity of reliable literature on many of Australia's deepwater fishes, the process, particularly the taxonomic component, was often more complex than the following example suggests.

After literature review and preliminary desktop assessment of diagnostic characters, specimens of the family Callionymidae were examined in the National Fish Collection. Based on these specimens (and on any reliable literature), diagnostic characters of *F. phasis* were confirmed and/or delineated, and draft string and depth endpoints were identified.

These draft endpoints were then compared with data available online in the bioregionalisation section of the CAAB database (ie, the multiple maps page, Appendix 11). The four maps shown at this page relate to catch records from CMR's data warehouse (top left), collection specimen records (top right), previous string and depth data from IMCRA (1996) and/or the (CSIRO 2001) SEMR study (bottom left), and the latest national bioregionalisation string and depth data (bottom right).

For *F. phasis*, the map displaying previous data (bottom left, Appendix 11) depicts the distribution of this species, extending from about Sydney to north of Perth, in depths of 124–639 m. Comparison with the mapped CMR records (top left, Appendix 11) shows that *F. phasis* was only recorded at one station in CMR's data warehouse, despite this apparently being a widespread species (occurring across southern Australia). This record, off the North West Shelf, potentially extends the range for the species, or conversely, is an erroneous identification.

Unvalidated records such as the single record from CMR's data warehouse, and the previously accepted string and depth endpoints for *F. phasis*, were then checked by examining specimens at relevant Australian museums. Examining specimens is an extremely time-consuming task, and researchers needed

quick access to specimen holdings data in the Australian museums network. Without the use of the rapid assessment tool made possible by the OZFISHCAM online database of collection records, this crucial aspect of the project would have been largely unachievable.

In the example of *F. phasis*, the collection-records map (top right of the four in Appendix 11) shows most data points in south-eastern Australia, with only three points west of the central Australian Bight. Rather than needing to examine all specimens provisionally identified as this species to determine, for example, the western string endpoint, the custodian was able to efficiently target the three outliers to determine which, if any, delineated the westernmost verifiable record of *F. phasis*. Generally, time efficiency was maximised by not examining specimens from the core range of a species distribution. However, for those genera with numerous misidentifications, it was necessary for the custodian to examine additional specimens, as a misidentified specimen may have extended the range for another species. The reduction in effort afforded by the OZFISHCAM point data mapping facility therefore varied greatly between genera, but in all cases provided a quick and reliable method for targeting specimens and saving time during museum visits.

By repeating this process for string and depth endpoints, and after examining specimens in various collections, the custodian was able to refine the distribution of *F. phasis*. The final map produced (which records the data used in the provincial analyses) is located on the fourth map (bottom right). This 'latest modelled distribution' map confirms that the three westernmost points on the collections map represented a different species, and that the CMR record of *F. phasis* from North-West Shelf is likely to be erroneous.

3.7 Data analysis and regionalisation

Analytical strategy

The hierarchical biodiversity framework that underpins this project (see Lyne 2003) demonstrates that provinces are the most important biological unit for spatial structuring and bioregionalisation. Biomes are also important biological units that are nested within each province. In this study the boundaries of the EEZ provinces and biomes were determined through multiple analyses, with the biomes defined (partitioned) at different depths within each province.

The primary determinants of the spatial scale equating to the provincial level (a major bioregion spanning hundreds or thousands of km), are past evolutionary processes associated with speciation, and modified by the contemporary environment. At the biomic level, species are keyed to depth-related processes (speciation and adaptation to different depth-related environments). Thus, the analyses of fish distribution data are aimed first at the provincial level, describing the largest scale spatial structures inherent in the data. At the biomic level, data analyses are aimed at partitioning the depth-related structures that are nested within the provinces at a lower level.

A variety of analytical methods could have been adopted and the governing considerations used in selecting the most appropriate one for this project included:

1. Recognising that insufficient information on deepwater fish distributions is available to undertake an integrated 3-dimensional analysis. This is obvious from considering the amount of data required to populate a 3-dimensional grid in latitude/longitude/depth space.
2. At the provincial scale, the biogeographic evolutionary processes in Australian seas (where the continental shelf is generally narrow) are more related to dispersion in geographical space (latitude/longitude) rather than depth. This does not necessarily imply that depth is not important in biogeographic structuring, rather it implicitly assumes that the depth structures at this level are nested within the provinces.
3. Distributional information contained in the data is limited to range information along the slope and by depth, and also to presence/absence data only.

4. Given the paucity of geographic spatial information in certain regions, geographic range information is characterised along a string running at the arbitrary 500 m isobath contour along the continental slope. Each species is also characterised by a depth range (which will remain invariant along its string range).
5. Quality criteria from biogeographic potential and confidence classifications on ranges are available.

The chosen analytical approach was to derive the provincial structures from a string analysis that combined data from a number of depth ranges. This provided the broadscale structure within which more detailed biomic analyses of the depth structuring were conducted for each derived province.

Four main analyses were used to investigate patterns in the distribution of demersal fish:

1. A summary of the raw data
2. Two-dimensional analysis of string data and depth information to identify major patterns in the data.
3. String range scaling—calculation of Jaccard Indices, combined with novel ‘bowler-hat’ analyses based on normalised string data, using species within specified depth ranges (see next point 4). This identified provinces.
4. Depth range scaling—calculation of Jaccard Indices by depth using species within specified string ranges representative of provinces derived from (2). This identified biomes at different depths within the provinces.

Each of these approaches was iterated, using different subsets of the data to either investigate broad-scale patterns, or trends within sections of strings or depth intervals. All the information was then integrated to produce a national bioregionalisation of demersal habitats on the continental slope.

Summarising the raw data—data formats

Patterns in the data were investigated using various subsets of the raw data (Group A data) and a more refined component consisting of the best quality, most reliable data (Group B data).

Group A (Raw data)

A1. ‘*Raw Data—All Data*’ uses all available data aggregated along the string route. This includes species with distributions on the shelf below 40 m (ie, all demersal fish).

A2. ‘*Raw Data—Max Depths >200 m*’ uses data only for slope species, defined as those whose maximum depth is greater than 200 m (ie, all slope species).

A3. ‘*Raw Data—Max Depths >200 m and String Range <130 units*’ uses data only for slope species whose maximum depth is greater than 200 m and whose string range is less than 130 units (ie, slope species excluding widely distributed species)

A4. ‘*Raw Data—Max Depths >200 m and String Range <60 units*’ uses data only for slope species whose maximum depth is greater than 200 m and whose string range is less than 60 units (ie, slope species with restricted ranges)

A5. ‘*Raw Data—Max Depths >200 m and String Range <25 units*’ uses data only for slope species whose maximum depth is greater than 200 m and whose string range is less than 25 units (ie, slope species with very restricted ranges)

Group B (High confidence data)

Five additional plots (B1–B5) used the Group A raw data subsets defined above, but were restricted to those species with distributions based on highly reliable information (ie, with confidence levels 1–3).

Two-dimensional analysis of string data

More than 1000 of the demersal fish species recorded on the Species Database were deemed suitable for analysis, with confidence levels of 1–3 characterising the required data quality in both geographic and depth distributions. The geographic and depth distributions were plotted on a string route map of the EEZ (Figure 1). From these data, 2-dimensional images were produced for all species that occur on the continental slope (ie, at depths >200 m). Then subsets of these data were determined by using the Biogeographic Information Index (BII) and string range (see section 3.3) to investigate spatial disjunctions across the region (see section 4.4).

East-west dissimilarity test

To assess the degree of overlap or segregation between species occurring in the north-east and north-west extremities of the EEZ region, we compared the species compositions at string ranges 0–10 and 250–260 (see section 4.4).

Jaccard analyses

The initial provincial structures reported here are based on exploratory analyses using the Jaccard analysis as a basis to determine local species composition changes and species richness. These analyses were used to plot the Jaccard Index against the string route/index.

The Jaccard Index is a measure of the species dissimilarity in adjacent areas. It is the ratio of the number of shared species to the number of distinct species in two communities.

Given two adjacent string units (a, b) that record the presence/absence of species, the Jaccard Index is defined as:

$$JI = (n10 + n01)/(n10 + n01 + n11)$$

where $n10$ is the number of species present in a but not in b,
 $n01$ is the number of species present in b but not in a,
 $n11$ is the number of species common to both a and b.

Thus, in the case where no species are unique to string units a or b ($n10 = n01 = 0$), JI is equal to zero and correspondingly, where the species are completely different ($n11 = 0$), JI is equal to one.

A version of the Jaccard Index based on non-integer numbers can also be used to characterise species distributional changes (other than presence/absence). For the moment we note that such an index based on adjacent units (e, w, where 'e' and 'w' are abundance sums of species) that record distributional information on species, can be defined as:

$$ji = (abxor)/(abxor + aband)$$

where

$$\begin{aligned} abxor &= \text{sum}(\text{abs}(e - w)) \\ aband &= \text{sum}(e * w) \end{aligned}$$

This version of the Jaccard is useful in investigating changes in species composition. A high Jaccard indicates faunal changeover, whereas uniformly low indices across a sequence of string points will flag the existence of regions of faunal consistency typical of major faunal units such as biogeographic provinces. Hence, these areas of evenness and change on a Jaccard plot are important in interpreting

distributional patterns. Similarly, several analyses using different data combinations are needed to bring out the full complement of patterns existing in the data. For the work reported here, changes of JI are displayed along the string route using the various formats of the data discussed here. For the purposes of this project both JI and *ji* give the same results because we are dealing with presence/absence data.

Species richness analyses

While the Jaccard Index is useful in showing relative changes in species composition between adjacent cells/grids (in the maps), it is independent of species numbers and does not indicate species richness.

One option in calculating species richness is to simply sum the number of other species that occur in each cell/grid over the range of the target species—we refer to this as a ‘top-hat’ distribution. This approach gives equal weight to each species, regardless of the location within the range of that species. In most cases, a species is less common at the extremities of its range than near the centre of its range. An alternative approach is to postulate a distribution which gives more weighting to positions away from these extremes. For the analyses reported here, a normalised distribution was used where it was assumed that the extremities of the range were two standard deviations away from the peak (centred at the middle of the range, but we did develop a two-sided distribution profile to allow for biasing of the ‘core range’ of the species towards one end of its range, when known). To emphasise the importance of more narrow-ranging, endemic species, this normalised distribution was scaled in an inverse relation to the length of the distributional range. A demonstration of this method, which is termed the ‘bowler-hat’ string scaling function, is presented in Figure 2.

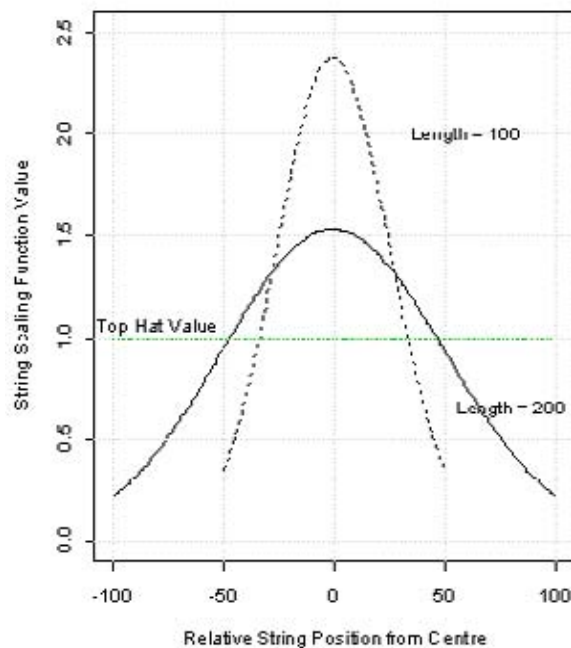


Figure 2. Diagrammatic plots of the string scaling function for three scenarios demonstrating the concept of ‘bowler-hat’ weighting toward more biogeographically informative, narrow-ranging species: 1) ‘Top-Hat Value’ shows the equal scaling of 1.0 applied to all string positions; 2) ‘Length = 200’ shows the normalised amplitude ‘Bowler-hat’ scaling for a string that is 200 units long, and 3) ‘Length = 100’ show the normalised amplitude ‘Bowler-hat’ scaling for a string that is 100 units long. Note that the centre of the string has been placed at ‘0’ for illustrative purposes.

String range scaling

The inverse relation attempts to determine the relationship between the ‘importance’ of a species (for biogeographic structuring) and its range. In the absence of any guiding principles, or studies, it is obvious heuristically that the shorter the range of a species, the greater its contribution to endemism at a particular location. For the analyses reported here, the scaling was based on the frequency of distribution of string ranges (Figure 3).

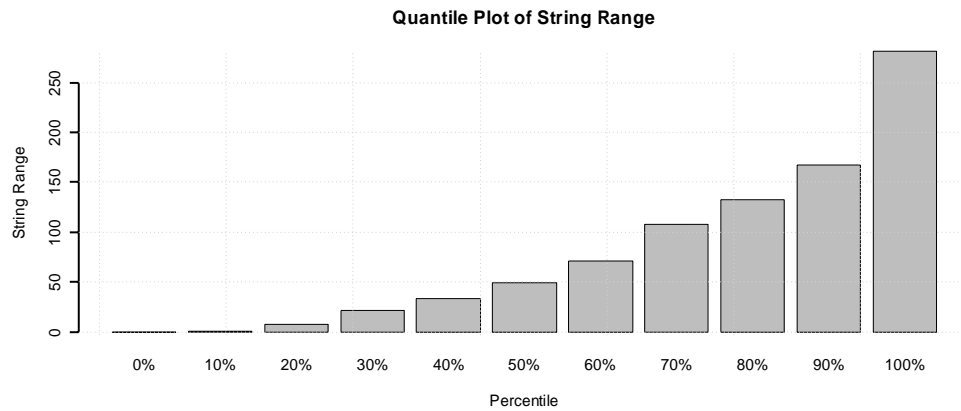


Figure 3. Frequency distribution of string ranges – cumulative plot of their quantile distributions. The ‘percentile’ is the percentage of all species whose string range is less than or equal to the maximum represented by the barplot at that point.

In Figure 3, the frequency of distribution of string ranges shows that approximately 50% of strings have lengths less than 50 string units, and that the relationship between frequency and string range is not linear. The significance of string range was mapped into a ‘string range index’ from 1 to 5, to reflect our subjective assessment of the importance of string range (with 1 most important). This mapping is shown in Figure 4. In other words, the ‘string range index’ equates to the likely information content of species, where 1 is the most biogeographically informative, narrow-ranging species.

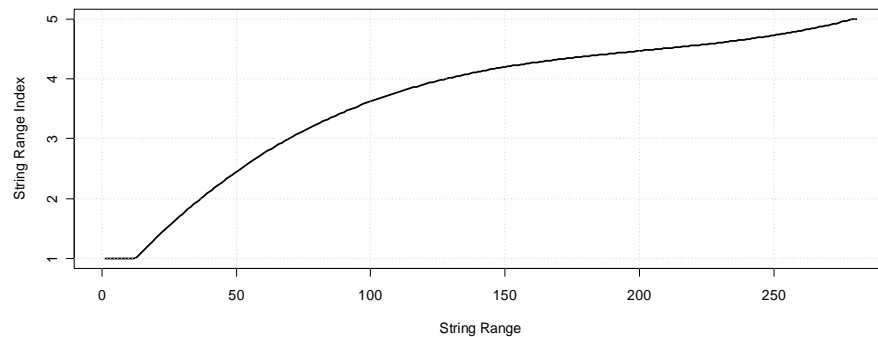


Figure 4. Delphi plot mapping of the significance of string range into an information index (from 1 to 5) based on the frequency distribution of string ranges (Figure 3). ‘String Range Index’ equates to the likely biogeographic information content of species, where 1 is most informative.

Thus, in calculating the bowler-hat distribution peaks, we used $(6 - \text{string range index})$ as the divisor for the normal distribution profile. The scaling was intended to emphasize the shorter-range species, but for very short-range species (less than about 12 string range units) the index was set at 1 to avoid unduly biasing the analyses.

Province strengths

The strengths of provincial units were assessed using the following equation:

Province strength = string length x no. endemics/total no. string points

where “string length” is defined as the number of string units representing the bioregion; “no. endemics” are the number of species confined solely to the province; and “total no. string points” refers to the total number of string units across the region (ie, 281 for the Australian continental slope along the 500 m isobath).

Provinces are the evolutionary products of palaeohistorical events modified by the contemporary environment. Therefore, strong provinces would be expected to have high numbers of endemics and/or a broad geographic coverage within the Australian region. Weak provinces have few endemics, which are often narrowly distributed. A data confidence level exceeding 3 was considered to indicate a well-defined or strong province.

Provincial boundaries were determined subjectively from visual inspection of overlays of several analyses.

Depth range scaling

As with the string range scaling, the 2-dimensional version of the bowler-hat distribution (in string-depth space) requires scaling of the depth data. In this case, the scaling is less obvious, as there is a relationship between the nominal depth of a species and its range (Figure 5). Except for some tropical deepwater species, the deeper the species’ nominal depth, the more extensive is its depth excursion. In other words, for a given depth, range is relatively less ‘important’ for deeper species (as it gives less information for biogeographic structuring).

The following formulations were used in determining the depth range indices:

- For species with nominal depths (taken as the mean depth of the species) greater than 500 m,
 - Index = (depth range)/200 for depth ranges under 1000 m
 - Index = 5 for depth ranges of 1000 m or more

For species with nominal depths (taken as the mean depth of the species) of 500 m or less,

- Index = (depth range)/100 for depth ranges under 500 m
- Index = 5 for depth ranges of 500 m or more
- For species with nominal depths (taken as the mean depth of the species) of 150 m or less,
 - Index = (depth range)/20 for depth ranges under 100 m
 - Index = 5 for depth ranges of 100 m or more
- The depth range index scaling was then rounded up to the nearest integer (from 1 to 5).

With these depth range index scalings, there is then no direct relationship between mean depth and the range of a species, and there are also discontinuities between the depth range scaling relationships. These need to be borne in mind when analysing bowler-hat distributions that use the depth-range-based weightings. For a given depth range change, this scaling increases the weighting to shallower depth species.

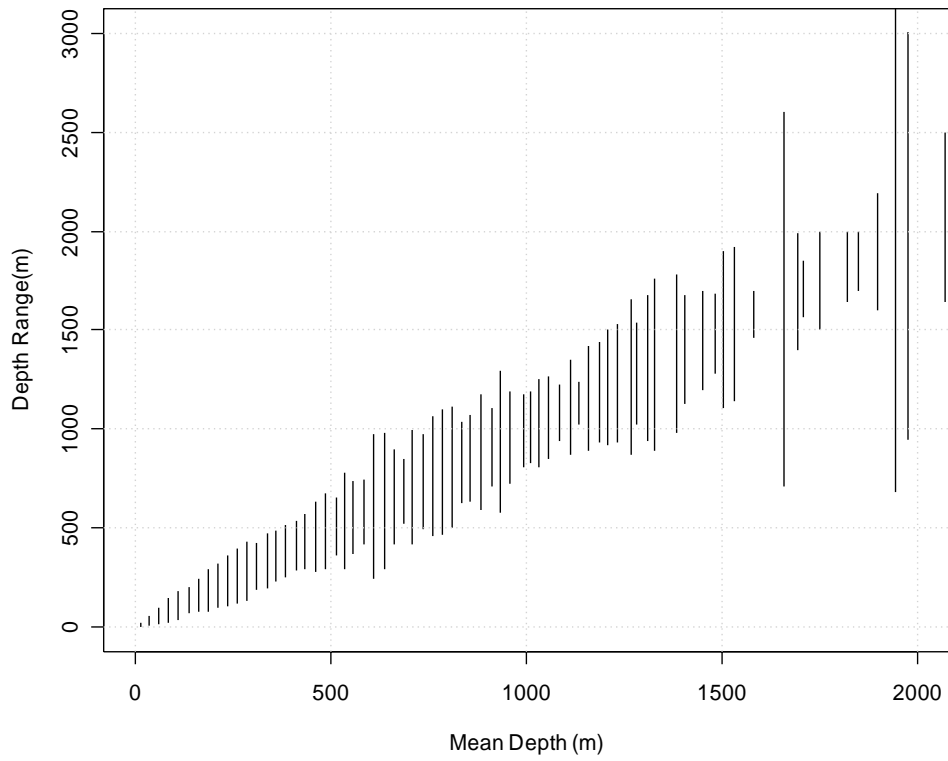


Figure 5. Relationship between mean depth and overall depth range for bathymetric classes of species. Demersal species were assigned to 25 m depth intervals based on their mean known depth distributions. Mean minimum and maximum ranges were determined for each depth interval based on all the species within that particular interval. Some coastal species (those with a depth <40 m) are included in this figure.

4. Results and Discussion

4.1 Faunal list and composition

This study produced a Species Database for deepwater fishes by combining species records from CAAB (Codes for Australian Aquatic Biota), draft (unpublished) versions of the new Pisces volumes of the Zoological Catalogue of Australia, additional depth data based on earlier bioregionalisations (the IMCRA and the CSIRO SEMR studies), and specialist taxonomic knowledge.

This Species Database comprised some 4525 fish species, from the following general habitat types:

Freshwater	203 species (4.5%)
Coastal (to depths of 40 m)	1121 species (24.7%)
Shelf demersal (depths from 40–200 m)	1090 species (24.1%)
Pelagic	559 species (12.4%)
Demersal slope and uncoded	1552 species (34.3%)

Appendix 3 provides a sample page of this Species Database, with colour-coded habitat types. The uncoded portion of the ‘Slope demersal and uncoded’ habitat type represents species for which depth data had not been captured in earlier regionalisations. Many of these species were later separated from the slope species because they were not relevant to this study, which focussed on species occurring on the continental slope.

The Species Database was used to produce a list of continental shelf and slope genera (see Appendix 15). Of these 509 genera, 375 were slope genera and considered to be potentially biogeographically informative, with the remaining 134 considered irrelevant to slope communities because they contained species found almost exclusively on the continental shelf.

The Biogeographic Information Index (BII) was used to prioritise the potentially informative genera for defining provinces and biomes. The BII for 369 of the target genera ranged from 4.4 to 249; knowledge of the other six genera was insufficient to allow BII calculations. An arbitrary value of 30 was selected as the cut-off point for inclusion, which corresponds to about 25% of the candidate groups. Genera with low BII values (less than 30) are considered more informative than those with high BII, and 91 genera with these low BII values are listed in Appendix 5. Table 1 lists the 20 most informative genera.

String and depth data were not collected for two of the priority genera (*Scolecenchelys* and *Branchiostegus*) due to unavailable specimens and/or insufficient time to resolve taxonomic issues. While informative genera were given priority status in some analyses, other less informative genera were also examined by specialist taxonomists. A better understanding of the composition of genera was obtained from taxonomic work as the project progressed (eg, the number of species in a genus). The BIIs were recalculated after the data entry phase of the project. As a result, an additional 15 genera were added to the list of most informative genera (an increase from 76 to 91), and these additional genera are listed in bold text in Appendix 5 and Table 1. The top three most informative taxa were ray genera, and eight of the top 10 most informative genera were sharks or rays.

4.2 Gap analysis

The knowledge gap analysis used data that was readily available from CSIRO Marine Research (CMR) and state fisheries bodies. Much of the historical data from CMR voyages were already digitised and centrally located in CMR’s data warehouse. Additional data exist, however, that had not been digitised, and/or had not been ascribed to the data warehouse. Considerable effort was made to locate these non-centralised datasets and assess their relevance to this project (project contributors and data owners were consulted to determine the accessibility and quality of data). Some datasets that were in the data warehouse prior to this project were excluded from the gap analysis because they were not relevant (eg, pelagic samples) or had low data quality.

Table 1. Twenty most informative genera based on Biogeographic Information Index (BII) scores. Species in plain text were demarcated during the first BII calculation; those in bold text were incorporated to the list based on recalculated BIIs after the completion of taxonomic elucidation.

Genus	Number of species*	BII score	Family	Family common name
<i>Dipturus</i>	23	4.35	Rajidae	skates
<i>Urolophus</i>	16	4.88	Urolophidae	stingarees
<i>Pavoraja</i>	8	5.24	Rajidae	skates
<i>Cephaloscyllium</i>	7	6.64	Scyliorhinidae	catsharks
<i>Etmopterus</i>	11	7.41	Squalidae	dogfishes
<i>Paraliparis</i>	28	7.52	Liparidae	snailfishes
<i>Asymbolus</i>	8	7.86	Scyliorhinidae	catsharks
<i>Scorpaena</i>	24	8.58	Scorpaenidae	scorpionfishes
<i>Trygonoptera</i>	6	8.87	Urolophidae	stingarees
<i>Squalus</i>	9	9.00	Squalidae	dogfishes
<i>Lepidotrigla</i>	19	9.22	Triglidae	searobins
<i>Antigonia</i>	13	9.60	Caproidae	deepsea boarfishes
<i>Squatina</i>	4	9.64	Squatinae	angel sharks
<i>Caelorinchus</i>	35	9.97	Macrouridae	whiptails
<i>Thamnaconus</i>	6	11.57	Monacanthidae	leatherjackets
<i>Pristiophorus</i>	5	11.57	Pristiophoridae	sawsharks
<i>Narcine</i>	5	11.57	Narcinidae	numbfishes
<i>Coryphaenoides</i>	10	12.00	Macrouridae	whiptails
<i>Centrophorus</i>	7	12.85	Squalidae	dogfishes
<i>Chimaera</i>	5	12.85	Chimaeridae	shortnose chimaeras

The data were mapped to show the geographic location of demersal stations within the Australian EEZ (Appendix 2). The stations were stratified by depth zones representing the continental shelf (40–200 m), the upper to mid-continental slope (201–1000 m) and the deeper continental slope and rise (>1000 m).

Examination of the maps of demersal stations revealed poor data coverage for four broad geographic regions in depths less than 1000 m:

1. the continental shelf off south-western Australia
2. inter-reefal areas of the Great Barrier Reef

3. the upper continental slope off Queensland (almost no data recorded from the extreme northern sector)
4. the upper continental slope and shelf-break off far north-western Australia.

These gaps reflect a general lack of faunal sampling effort in these relatively broad geographic regions. Data coverage is particularly poor on the continental slope off the far north-west. Some historical datasets exist (eg, Russian surveys in the 1960s and 1970s), but their data quality is mostly poor due to inaccurate taxonomy. In the far north-west, the Australian continental slope is narrow and merges with the slopes of Timor and eastern Indonesia. There is a need to clarify overlaps between the faunas of these neighbouring areas, and to identify local endemism. Some additional data were acquired for southern Queensland during the project, and current research on invertebrate and fish bycatch along the Great Barrier Reef should greatly improve our knowledge.

There is a major gap in knowledge along the lower continental slope in all regions, with the exception of the south-east. Virtually nothing is known of the biota on the continental rise and the abyssal plains—the number of samples collected at these depths can be counted on one hand.

The demersal station maps were used during the 2002 Hobart taxonomic workshop (Appendix 12) to prioritise areas that require further survey work to strengthen data coverage for the Australian fauna, both invertebrate and fishes. The most highly prioritised regions from this gap analysis are depicted in Figure 6. A research voyage to the northwestern continental slope was planned, but unfortunately has not yet been undertaken. A major knowledge gap, however, was partly filled in early 2003 by the NORFANZ voyage (Joint Australia and New Zealand survey of seamounts of the Tasman Sea, see Appendix 14). This voyage surveyed the Norfolk and Lord Howe Ridges (in Australian territorial waters), providing a regional perspective to the eastern Australian fauna, as well as some insight into possible differences between the faunas of these ridges.

The gap analysis showed that the taxonomic reliability of data collected during research voyages varied greatly. While this was expected, the extent of the anomalies only became apparent when the species distributions from CMR's data warehouse (using only reliable data) were compared with those from museum collections (the point data mapping facility, OZFISHCAM) and the distribution of particular species in the published literature. Further, the number of misidentifications recorded in collections, due largely to inadequate documentation of Australian continental slope fishes, suggested that identifications of slope fishes by non-taxonomists were unlikely to be accurate. It was decided that, apart from some already digitised datasets, no further effort would be made to track additional data; such as filling an apparent gap on the continental shelf off Victoria, so that more effort could be focused on correctly identifying and elucidating the taxonomy of specimens in the museum fish collections. The data gap off Victoria is probably an artefact: other data may exist that were not accessed by this project.

Because the quality of historical catch data (eg, in CMR's data warehouse) in its present form is highly variable, any analysis based solely on such catch composition data should be carefully considered. This is especially true of data from the outer continental shelf and the slope beyond. Large-scale assessment of the quality of the data was beyond the scope of this project, but with adequate resources it would be possible to assess and rank the data based on the year conducted, the region sampled, and the staff involved. The data could be further enhanced by examining samples retained from particular voyages to validate identifications, and by flagging species for which the identification was validated. This approach has been used successfully for data from some of the Russian vessel research voyages.

Robust biological data are needed in all sectors of the Australian Marine Jurisdiction. Infill surveys to fill these major gaps are needed, preferably before attempting a major marine planning exercise for the region. The three highest priority gaps are in the north-west, the north-east and on the continental shelf off Perth. Surveys of these regions should be undertaken to provide the baseline data necessary to make informed decisions about bioregional structure.

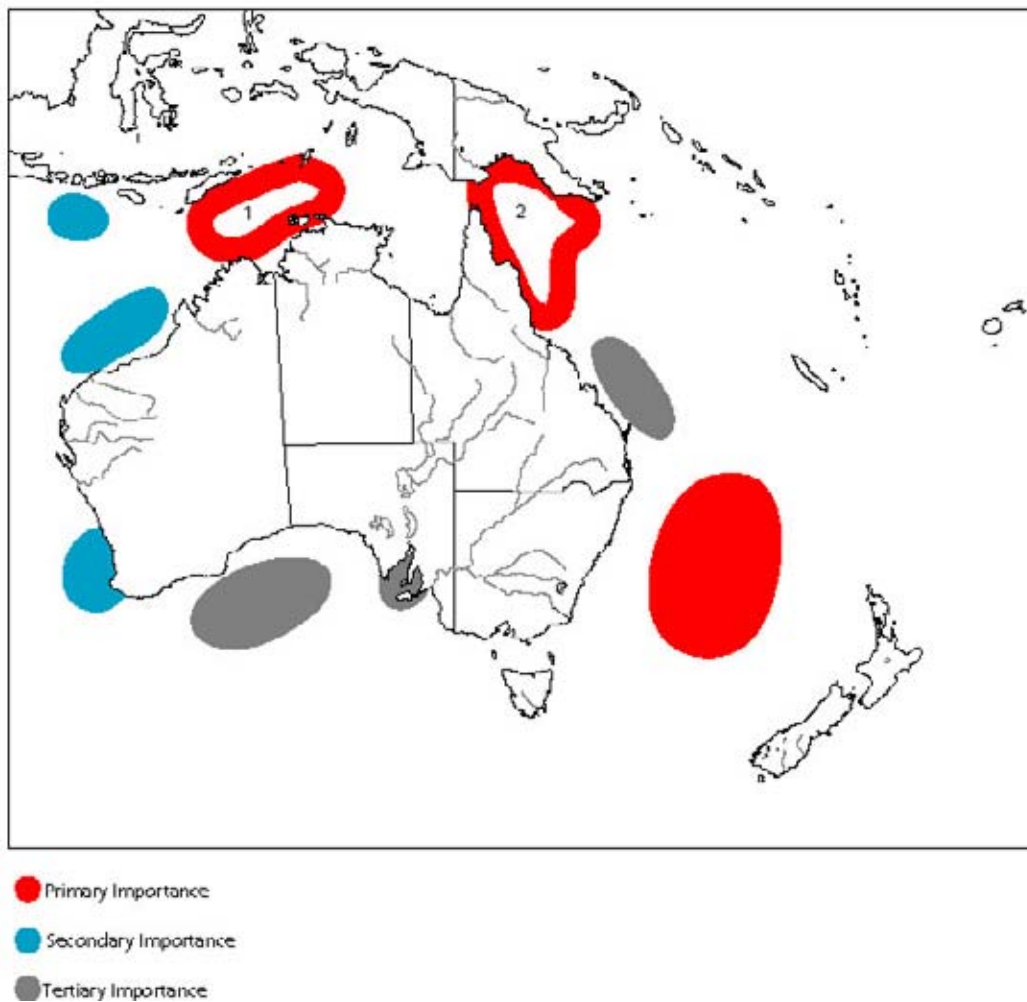


Figure 6. Map depicting prioritisation of areas that are desirable for inclusion in future infill surveys.

4.3 Taxonomic elucidation

A total of 1489 species from 494 genera (representing 121 families) were examined by specialist taxonomists. Most specimens were in state museum collections and the CMR collection; a few were literature examinations only. Of the species examined, 312 (21%) do not have full scientific names and many of these are new to science. The total number of specimens examined across all museums is difficult to determine exactly, but about 7000 specimens in the National Fish Collection were examined.

The process of taxonomic elucidation was complex. Comparison of the final distribution with the IMCRA/SEMR data, CMR's warehouse data, and collection records often showed how inaccurate historical data and many collection identifications are. In Australia, this is particularly true of continental slope fishes, which have not been well studied. CMR's data warehouse records were obviously poor for many species, and were therefore excluded in most cases. However, in instances involving well-known species where misidentifications were unlikely, CMR records were used with confidence.

The task of appraising Australian deepwater fishes at the species level was particularly challenging. It is important to note that the IMCRA bioregionalisation was based on continental shelf fishes, where the baseline taxonomy and distributions of species are generally much better known. Demersal slope fishes were not part of the IMCRA analysis.

To determine the status of some species, it proved necessary to examine specimens from across the entire geographic range of all representatives of the genus. Examining specimens in just one collection rarely provided enough data to accurately define their string and depth endpoints. More comprehensive examinations allowed custodians to recognise highly informative sister species and split the genus accordingly. In bioregionalisation studies, genera containing a high number of narrow-ranging endemic species are usually more informative than genera containing only a few, wide-ranging species. Therefore, lumping species due to poor taxonomic resolution hides regional endemism, and reduces the usefulness of data for biogeographic analyses.

For many genera studied here, these detailed examinations of specimens resulted in a surprisingly large increase in the number of species identified from Australian waters (Appendix 13), often with a corresponding reduction in the string and/or depth ranges of previously known species. The labour-intensive step of examining, and then updating or confirming the identification of specimens of useful genera was crucial to the project.

The deepsea boarfish genus, *Antigonia*, provides a useful example of this process of taxonomic elucidation. The study of this genus also flagged the importance of expert participation in data collection and the potential dangers of using non-validated data. Prior to this project, five species of the genus *Antigonia* were recorded from Australian seas (Figure 7a). Of these species, two were recorded as having disjunct populations, while the others were regionally distinct. After the process of taxonomic elucidation, *Antigonia* was considered to contain at least ten species (Figure 7b). Other potentially new species were known from only one specimen, and remain unresolved in this study.

Due to the nomenclatural complexity of genera such as *Antigonia*, and many other similar groups, numerous naming issues remain outstanding. Operational Taxonomic Units (OTUs) were recognised for these taxa but determining the correct scientific name (if one was available) to attach to each OTU was beyond the scope of this project. Also, some taxonomic issues still remain outstanding, particularly where specimen numbers were insufficient to gauge variation within species, including sexual dimorphism.

The taxonomic research conducted during this project added great value to all major Australian fish collections by dramatically increasing the reliability of identifications of target specimens. For example, the reliability of *Scorpaena* specimens held at the National Fish Collection was greatly improved. Prior to the study, 76 specimens were recorded as *Scorpaena* but 41 of these were actually other genera (ie, either they were misidentified or the species in question had been transferred to another genus). Of the 35 specimens that were correctly identified to genus, 16 were not accurately identified to species. Therefore only 19 of the original 76 specimens labelled as *Scorpaena* were accurately identified to species prior to this study. In addition, a further 13 *Scorpaena* specimens had been misidentified at the genus level and were listed under genera other than *Scorpaena*. The collection data were enhanced for all these specimens. Even the 19 that were correctly identified before the study were given a high-confidence, up-to-date identification.

Fig. 7a

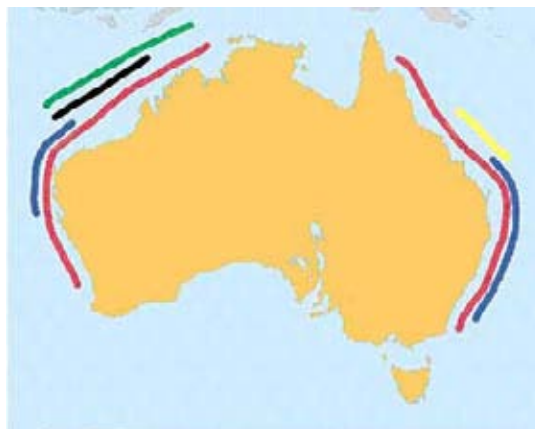


Fig. 7b



Figure 7. Example of increase in known species of a slope genus (*Antigonina*). Each colour represents a different species. (7a) Prior to this study, five species recorded from Australia, two of which were thought to have disjunct distributions (7b). Towards the end of the taxonomic elucidation process, *Antigonina* was considered to contain at least ten species, only one of which may be disjunct.

4.4 Regionalisations

The regionalisation process involved four independent steps:

1. Two-dimensional analyses of string and depth information to investigate major patterns in the data.
2. Analyses of the string data to produce a bioregionalisation at the provincial level.
3. Analysis of the depth data to determine the biomes within each province.
4. Summarising and integrating this information to produce a national bioregionalisation of demersal slope fishes.

Two-dimensional analyses

By early February 2004, custodians had finished recording the distributions of demersal fish species on the online Species Database, along with confidence levels to characterise data quality. Of 1324 species digitally recorded, more than 1000 were suitable for analysis (with confidence levels 1–3) in both

geographic and depth categories. Plots of the geographic and depth distributions showed that the shelf and slope assemblages are faunally distinct from each other (the overlap between them is less than 40% and 50% for the slope and shelf respectively).

Two-dimensional images were produced using data from all species that occur on the continental slope (ie, >200 m), and subsets of species were determined by calculating the Biogeographic Information Index (BII) and string range, to investigate spatial disjunctions across the region (Figures 8.1–6). The most complex pattern was obtained from the full dataset of species (Figure 8.1). Very strong pulses of faunal similarity (and distinctness from those adjacent) emerge (pink zones in figure 8) on the upper continental slope off NE Queensland (ca string points 20–40), off New South Wales (ca points 60–70), and off southern Australia (ca points 80–160). A similar pulse is evident on the mid-slope off southern Australia, with a reasonably prominent disjunction (blue zone) off the North-West Shelf (ca points 200–220). The width of the pulses off southern Australia suggests that the fauna is reasonably homogeneous across this region, indicating a large province. Conversely, the narrowness of the other pulses suggests that these are smaller provinces, where the fishes have a restricted distribution. There is a relatively little data for fish deeper than 1500 m, and fishes occurring at depths shallower than 40 m fall outside the scope of this project. Both groups are reflected by almost uniform red bands at these depths. As mentioned above, fishes found only on the continental shelf (at depths between 40 m and 200 m) were also excluded from the analysis.

Similar analyses were made using subsets of the suite of continental slope species. Wide-ranging and thus less informative species were excluded. With the removal of widespread species having a string range exceeding 130 units (Figure 8.2), the overall pattern was similar but the strengths of provinces were generally weaker. Two other analyses using string ranges less than 60 and 25 respectively (Figures 8.3–4), which eliminated wide-ranging to medium-ranging species, identified additional narrow units off Queensland (ca points 10–20), Tasmania (ca points 80–100), and Western Australia (ca points 170–190). These analyses were repeated using ‘informative species’ only (including those found on the shelf, see Figures 8.5–6). The pattern obtained using all informative species (Figure 8.5) was similar to that obtained in Figure 8.2. Using informative species, with ranges less than 60 string units (Figure 8.6), highlighted provincial units defined by species with relatively restricted ranges.

Fig. 8.1. All continental slope species (maximum depth >200 m)

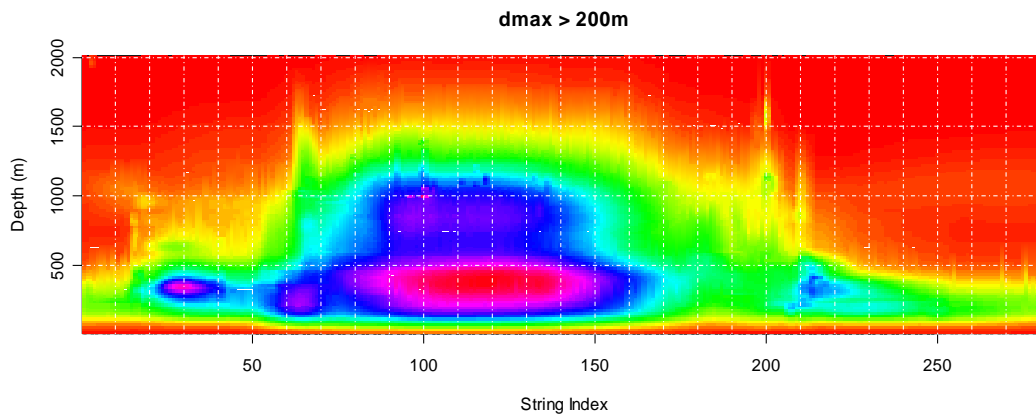


Fig. 8.2. Slope species with string ranges less than 130 units

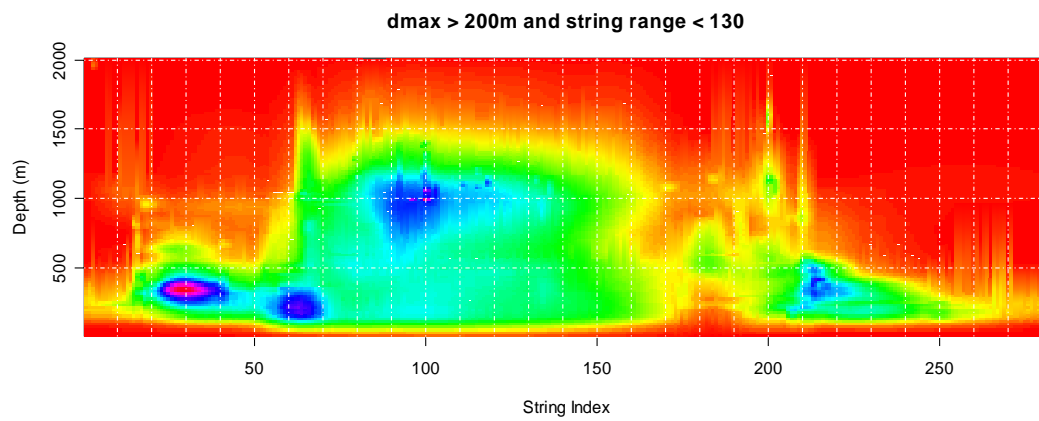


Fig. 8.3. Slope species with string ranges less than 60 units (wide-ranging species excluded)

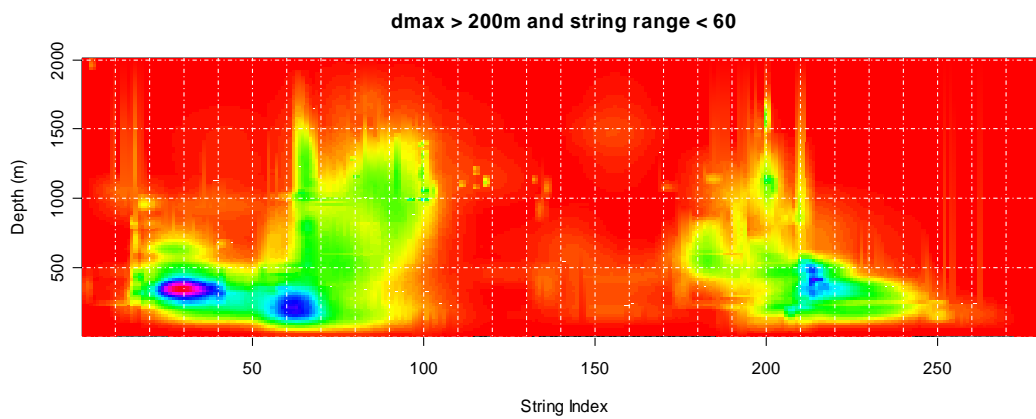


Fig. 8.4. Slope species with string ranges less than 25 units (medium-ranging species excluded)

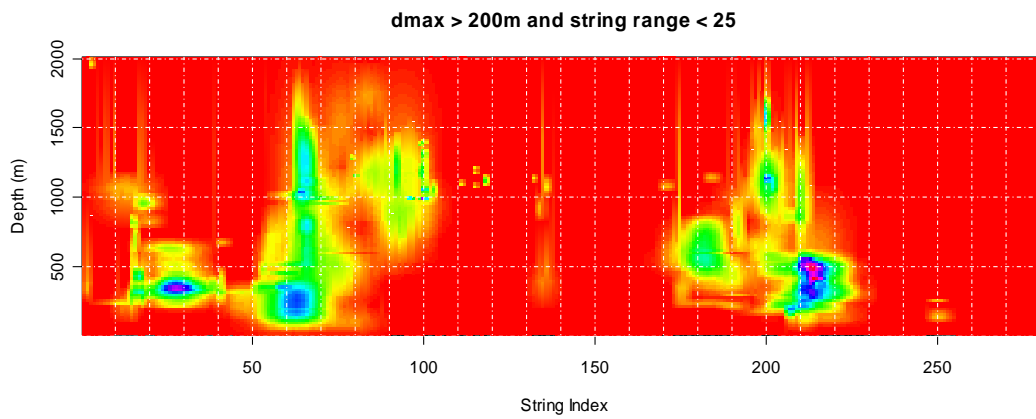


Fig. 8.5. Informative species only

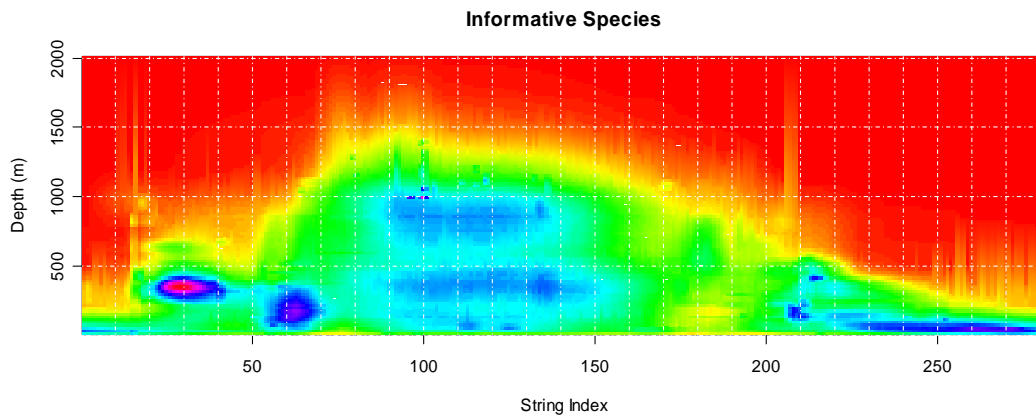


Fig. 8.6. Informative species with string ranges less than 60 units

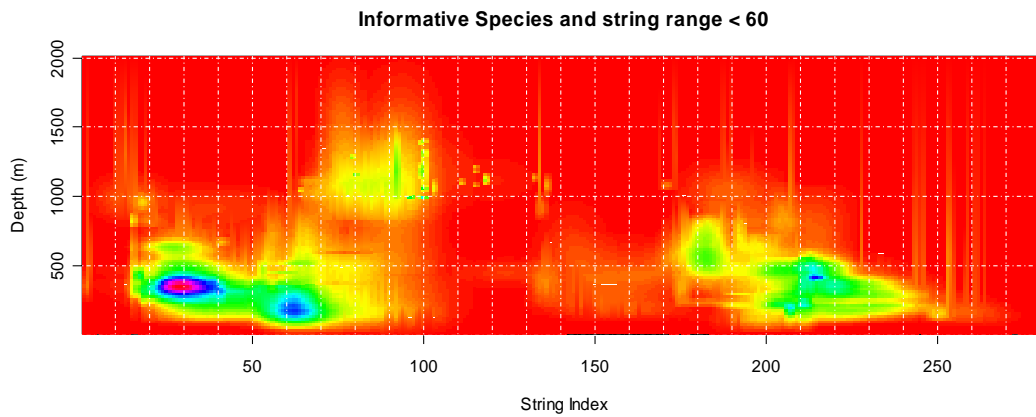


Figure 8. Two-dimensional image matrix showing variations in fish distribution by string position and depth. Differing colours reflect elevations in the Jaccard Index; purple and blue are high Jaccard values reflecting major areas of faunal change (transitions), red values reflect low levels of change. 'dmax' refers to the maximum depth of species included; 'String Index' refers to string position.

Provincial analyses

To explore further the range limits and potential province boundaries highlighted above we used a series of Jaccard and bowler-hat analyses on the complete dataset (A1, Figure 9.1), the continental slope dataset (species occurring deeper than 200 m) with no string range restrictions (A2, Figure 9.2), and variations of the A2 dataset with 130, 60 and 25 string unit range restrictions (Figures 9.3–5). High Jaccard Indices reflect zones of strong faunal change typical of biomes and a low Jaccard generally reflects greater stability typical of core provinces. High bowler-hat values reflect relative restrictedness, typical of localised endemism, and a decline in these plotted values is typical of faunal transitions.

Fig. 9.1. (Group A1 data)

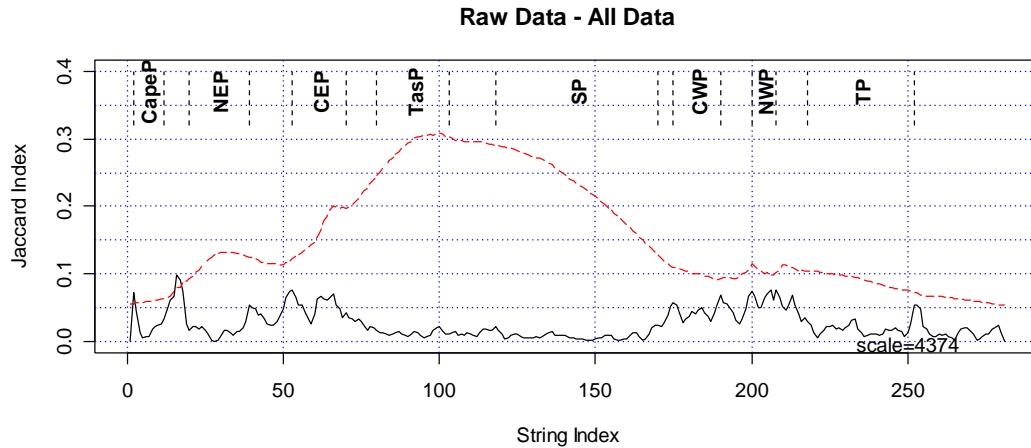


Fig. 9.2. (Group A2 data)

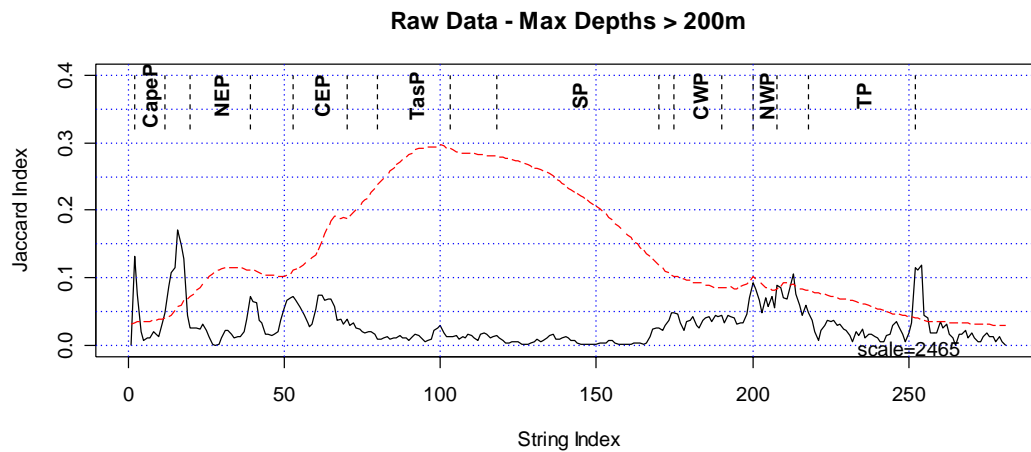


Fig. 9.3. (Group A3 data)

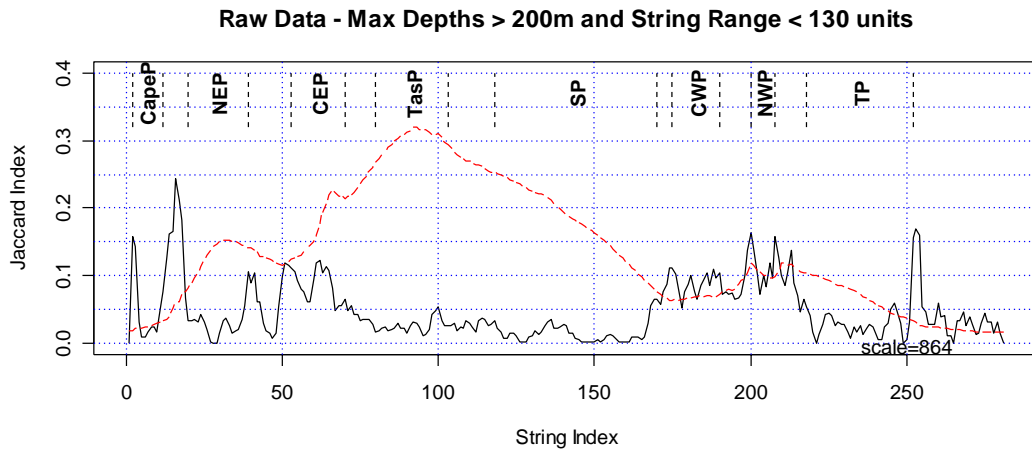


Fig. 9.4. (Group A4 data)

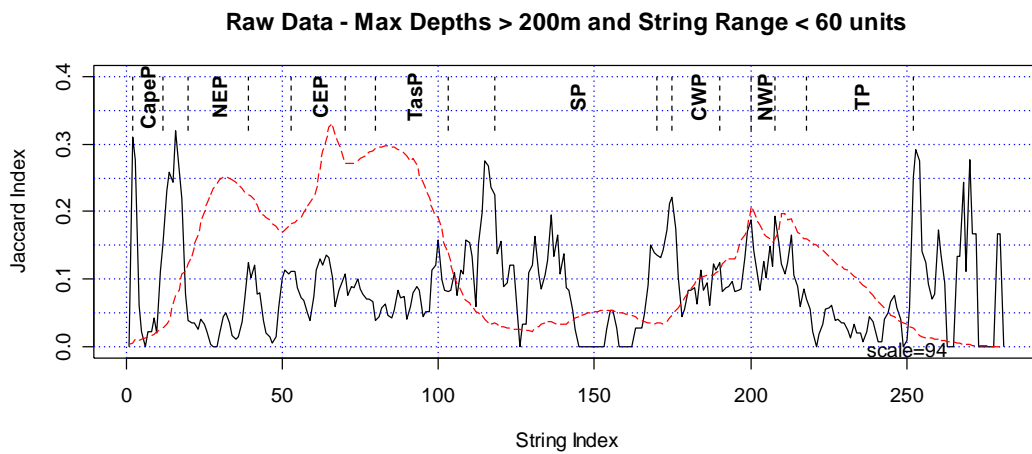


Fig. 9.5. (Group A5 data)

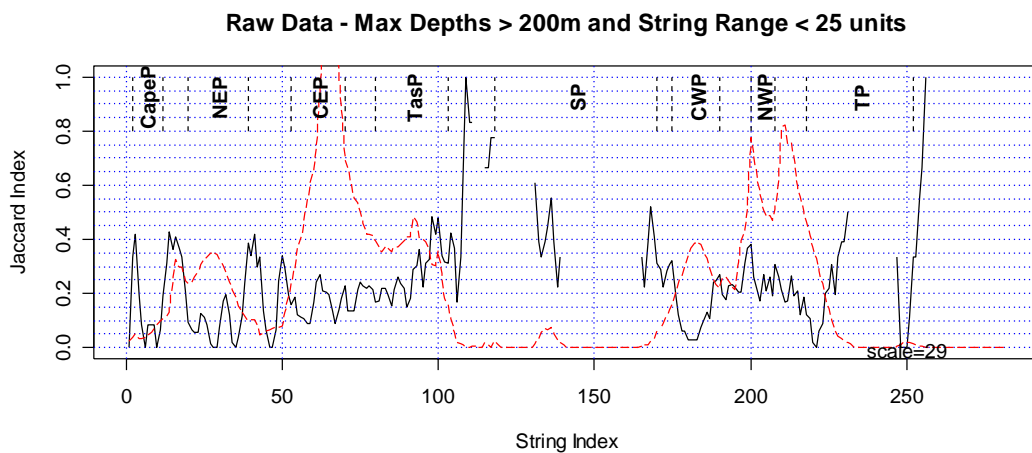


Fig. 9.6. (Group B1 data)

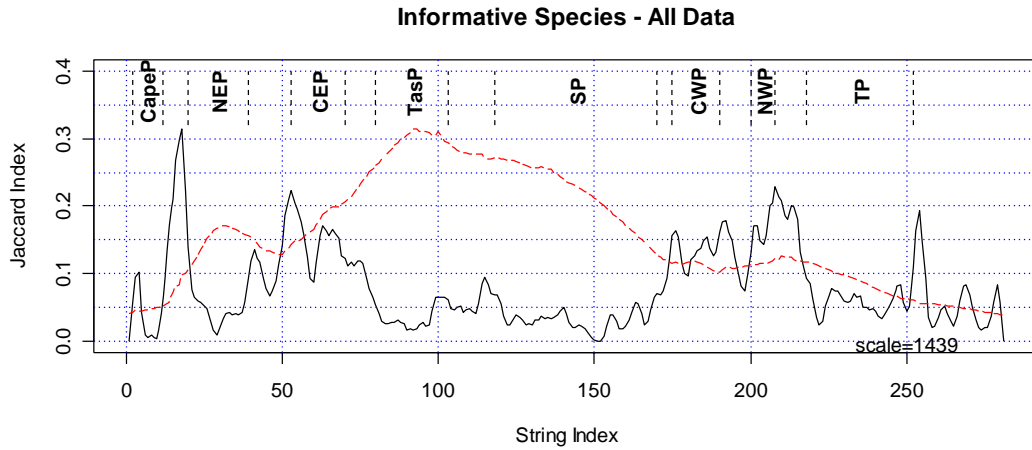


Fig. 9.7. (Group B2 data)

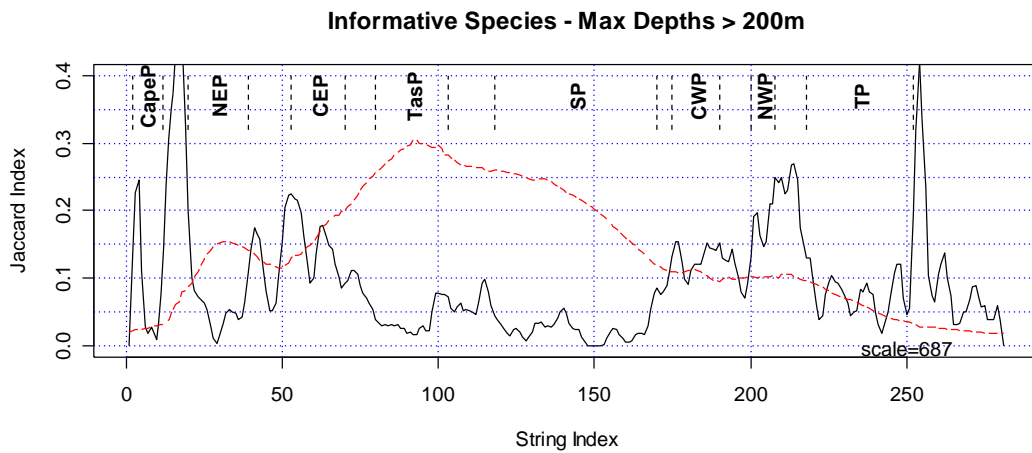


Fig. 9.8. (Group B3 data)

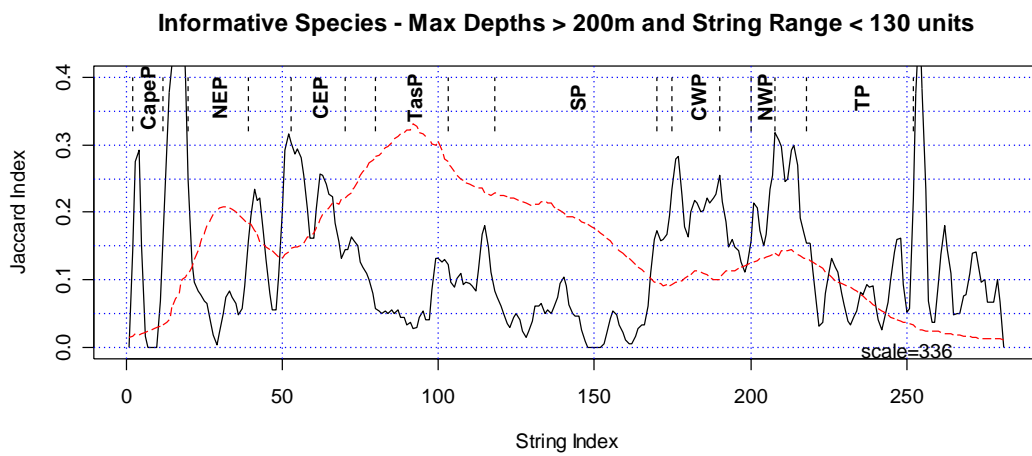


Fig. 9.9. (Group B4 data)

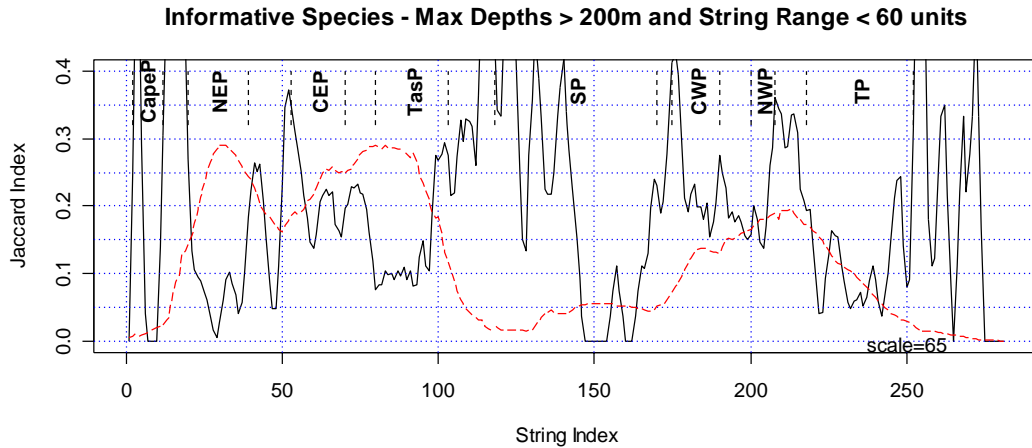


Fig. 9.10. (Group B5 data)

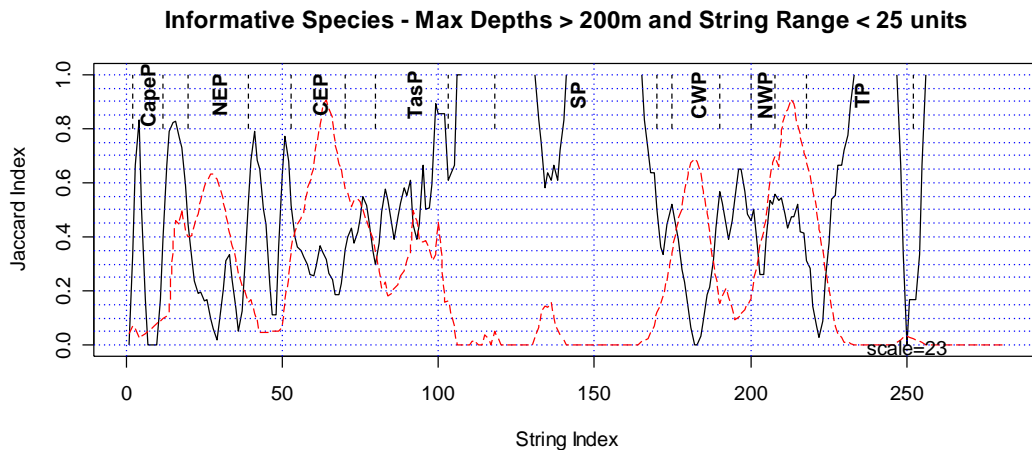


Figure 9. Jaccard Indices (black) and scaled species richness (bowler-hat normalised) values (red) at each string point, based on Group A data (9.1–5) and Group B data (9.6–10). ‘String Index’ refers to string position. Approximate province boundaries are overlaid, showing the abbreviated province names, to show how these data were used to determine provincial ranges. Multiple versions of figures such as these were used to determine provincial boundaries.

Not surprisingly, the resolution of the fine-scale faunal structure increased incrementally from analysis A1 through to A5. The least structure, useful in detecting the existence of large provinces, was evident in the ‘raw data’ (Figure 9.1), and in plots with no range restriction or a broad string restriction (Figure 9.2–3). The most detailed and potentially most useful structure for small provinces was obtained from species with string ranges of 60 or less units (Figures 9.4–5). However, the strongest faunal disjunctions (ca string points 2, 16, 115, and 252) were evident in all plots (including replicate plots not presented in this document—the strength of faunal disjunctions varies from analysis to analysis, so the composite of all plots needs to be considered when making decisions about real faunal attributes). These analyses supported the strong pattern detected in the 2-dimensional analysis (Figure 8). Analyses using string lengths of less than 25 units became fragmented in some sectors of the string through insufficient data points.

Using the entire dataset, the largest suite of species contributing to the analysis (ie, elevated bowler-hat values) comes from the southern half of Australia (ca string points 60–180, Figures 9.1–3) where most of the species are broadly distributed. This trend, strongly evident in Figure 8.1, is also reflected in the Jaccard Index plots (Figures 9.1–3). When these widespread species are removed (leaving string ranges less than 25 units, Figure 9.5), the faunal resolution across the Great Australian Bight (between string

points 110 and 170) deteriorates significantly due to the absence of narrow-ranging species. Finer scale provincial trends detected in the 2-dimensional plots (Figures 8.3–4, 6) also become evident from the plots in Figures 9.4–5.

The Group A analyses were repeated using only the informative suite of species generated by the BII analysis (Groups B1–5, Figures 9.6–10). Five plots were generated using the data subsets defined above for Group A but restricted to those species whose data confidence indices are less than or equal to 3 (ie, those species whose distributions are based on highly reliable information). In all cases, the resolutions of the Jaccard Index and the bowler-hat analyses were marginally superior compared to the group A analyses. The most useful analyses for delineating fine scale biogeographic patterns were those based on 'Max Depths >200 m and String Range <60 and 25 units' (Figures 9.4, 9.5, 9.9, 9.10), although most of these patterns were evident to some extent in all analyses. Very strong disjunctions were identified at or near string points 2, 16, 115, 174, 252, 270. However, it is likely that edge effects may be responsible for some of these high Jaccard Indices near the start and end points (0 and 281)—where the resolution of spatial patterns was marginally better using rapid assessment methodology (informative species only), rather than full datasets.

A weak or secondary provincial structure is evident from these analyses. These units are probably derived from short temporal evolutionary events or may prove to be pronounced when more data becomes available. In addition to the more widespread province defined by a suite of widely distributed temperate species around southern Australia, discussed above, there are more confined tropical provinces in the east (ca string points 10–50) and west (ca string points 175–250). These provinces are evident as low-level peaks of the bowler-hat plots at these points (Figures 9.1–2) and most apparent in Figure 9.3.

The regionalisation process provided evidence that the provincial complexity off the east and west coasts is substantially greater than off the south coast, and at smaller spatial scales. The data support the existence of eight provinces on the continental slope of Australia (Figure 10): three provinces in the east (Cape, North Eastern, and Central Eastern Provinces), three in the west (Central Western, North Western and Timor Provinces), and a small, well-defined Tasmanian Province, which is nested within a more widespread Southern Province (Table 2). The Tasmanian and Southern Provinces were probably derived from separate evolutionary events. The extent of the boundaries in the north (the Timor and the Cape Provinces) needs further evaluation to establish their association with Indonesia and PNG respectively. There are strong boundary (edge) effects at the northern limits off the eastern and the western coasts, at the start and end string points (0 and 281).

Province structure

The following string endpoints, and their approximate locations on the adjacent coast, are used to define the province boundaries (Figure 10). Candidate indicator species for these units are given below. These are typically narrow-ranging endemic species (many of them identified by the BII as informative species) that are potentially indicative of a province because their core distribution lies within that province. The candidate group also includes species that may be more widely distributed but for which the data are incomplete. Some species occurring in the tropical provinces may occur in geographic regions adjacent to Australia.

Cape Province (CP)

From Hunter Point, N of Shelburne Bay, (Qld) to Cooktown (Qld), string points 2–12 (approximately latitudes 11°25'S to 15°20'S)

Candidate indicator species: *Aulastomatomorpha phospherops*, *Bassozetus compressus*, *Etmopterus dianthus*, *Halicmetus* sp., *Monomitopus garmani*, *Notoraja laxipella*.

North Eastern Province (NEP)

From Hinchinbrook Island (Qld) to St Lawrence (Qld), string points 20–39 (approximately latitudes 18°21'S to 22°18'S)

Candidate indicator species: *Arnoglossus nigrifrons*, *Aulopus* sp., *Bembrops* sp., *Caelorinchus shcherbachevi*, *Haliutaea* spp, *Mastigopterus* sp., *Pterygotrigla robertsi*.

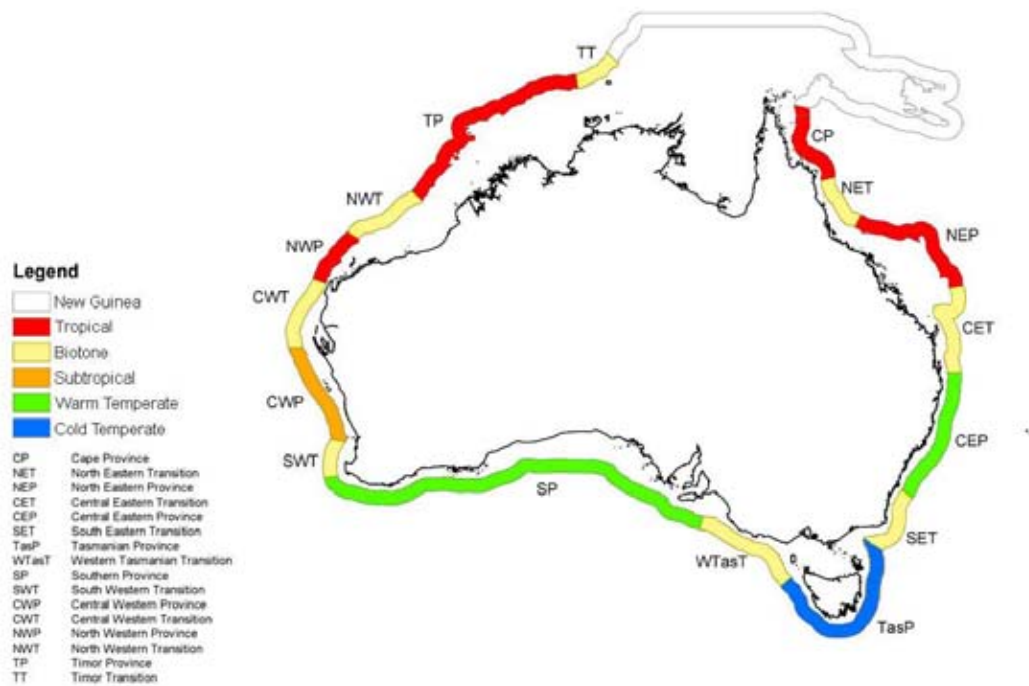


Figure 10. Bioregionalisation of Australia's demersal continental slope based on fish distribution data.

Central Eastern Province (CEP)

From Southport (Qld) to Ulladulla (NSW), string points 53–70 (approximately latitudes 27°51'S to 35°20'S)

Candidate indicator species: *Bembrops morelandi*, *Chaunax* sp., *Halieutopsis* sp., *Lepidoperca magna*, *Malthopsis* sp., *Paraliparis eastmani*, *Paraulopus okamurai*, *Duptyrus* sp. C, *Solocisquama* spp.

Tasmanian Province (TasP)

From Lakes Entrance (Vic.) to Woolnorth Point (Tas.), string points 80–103 (approximately longitudes 148°31'E to 143°50'E)

Candidate indicator species: *Cataetyx* spp, *Guttigadus* sp., *Monomitopus cf kumae*, *Paraliparis anthracinus*, *Paraliparis ater*, *Rhinochimaera africana*.

Southern Province (SP)

Kangaroo Island (SA) to Cape Leeuwin (WA), string points 118–170 (approximately longitudes 138°06'E to 114°31'E)

Candidate indicator species: *Bathyraxa* sp., *Centroberyx* sp., *Dicrolene* sp., *Notoraja* sp., *Nybelinella* sp., *Paraliparis australiensis*, *Paraliparis avellaneus*, *Pavoraja* sp.

Central Western Province (CWP)

From Perth (WA) to Shark Bay (WA), string points 175–190 (approximately latitudes 32°13'S to 26°09'S)

Candidate indicator species: *Dicrolene* sp., *Epigonus macrops*, *Monomitopus* sp., *Neomerinthe cf nielsenii*, *Parascyllium sparsimaculatum*, *Dipturus* sp.

North Western Province (NWP)

From Exmouth (WA) to Dampier (WA), string points 200–208 (approximately latitudes 21°59'S to 19°09'S)

Candidate indicator species: *Chaunax* sp., *Dibranchius* sp., *Diplacanthopoma* sp., *Hime* sp., *Leptochilichthys microlepis*, *Parapercis* cf *macrophthalmia*, *Uranoscopus* sp.

Timor Province (TP)

From Broome (WA) to Melville Island (NT), string points 218–252 (approximately latitudes 16°40'S to 9°20'S)

Candidate indicator species: *Bembrops nelsoni*, *Bythaelurus* sp., *Halicmetus* sp., *Malthopsis* spp, *Neobythites australiensis*, *Neobythites bimaculatus*, *Neobythites macrops*, *Neobythites soelae*, *Parapterygotrigla* sp., *Physiculus roseus*.

Province strengths

From the provincial strength analysis, five provinces (NEP, CEP, TasP, SP, TP, values 3.4–7.7) are considered to be strong, or well defined and three are categorised as weak (CP, CWP, NWP, values 0.9–2.2) using an index of provincial strength (Table 2).

This assessment should be treated as indicative rather than definitive. Elements of the Timor Province (highest provincial strength index) are not well known, due to limited survey data in the northern limits of the region. The province is geographically extensive (it has the second longest string range after the Southern Province) and includes 64 species (it is the second richest province after the North Western Province) that could be endemic to this region. The North Western Province, despite its low spatial coverage, has potentially as many as 76 endemic species. Conversely, the broad Southern Province, which covers most of southern Australia, has only 26 possible endemic species.

Table 2. Bioregional classification of the Australian continental slope based on the provincial structure of the demersal fish fauna, including information on the number of species in each bioregion with varying levels of range restriction. Core provincial ranges, demarcated by the endpoints of the string index, are indicated in bold text; transition zones are in plain text. Ranges correspond to string indices along the 500 m isobath. Assessments of the strengths of each province ('Strength' = string length x no. endemics/total no. string points) are indicated in bold italics; values above three are considered to be well defined or strong (see Methods section 3.7 for more information).

String index	Acronym	Name	Comments	String length	Total no. of species	No. of endemics	No. of species of depth >200 m	No. of species of depth >200 m & string <130	No. of species of depth >200 m & string <60	No. of species of depth >200 m & string <25	'Strength'
0–2	–	North-East 'edge'	Possible boundary effect – need to establish similarity to PNG to the north	2	257		84	31	6	2	
2–12	CP	Cape Province	Weak - northern extent of this province needs to be defined	10	302	24	106	46	18	6	<i>0.9</i>
12–20	NET	North Eastern Transition		8	421		219	125	95	38	
20–39	NEP	North Eastern Province	Well-defined province	19	441	70	243	134	102	32	<i>4.7</i>
39–53	CET	Central Eastern Transition		14	518		305	159	119	37	
53–70	CEP	Central Eastern Province	Well-defined province	17	639	56	445	266	146	51	<i>3.4</i>
70–80	SET	South Eastern Transition		21	536		398	234	105	37	
80–103	TasP	Tasmanian Province	Well-defined province, some overlap between broad Southern Province	23	486	52	377	219	83	31	<i>4.3</i>

String index	Acronym	Name	Comments	String length	Total no. of species	No. of endemics	No. of species of depth >200 m	No. of species of depth >200 m & string <130	No. of species of depth >200 m & string <60	No. of species of depth >200 m & string <25	'Strength'
103–118	WTasT	Western Tasmanian Transition		15	456		348	191	50	11	
118–170	SP	Southern Province	Well-defined province with its central distribution in the GAB	52	463	26	336	175	34	12	4.8
170–175	SWT	South Western Transition		5	398		283	121	26	8	
175–190	CWP	Central Western Province	Weak province	15	480	31	319	145	62	22	1.7
190–200	CWT	Central Western Transition		10	462		272	109	72	34	
200–208	NWP	North Western Province	Weak province	8	508	76	289	143	106	53	2.2
208–218	NWT	North Western Transition		10	505		283	166	137	68	
218–252	TP	Timor Province	Strong province	34	418	64	198	120	88	26	7.7
252–	TT	Timor Transition	Strong boundary effect – need to establish similarity to Timor and Indonesia	2	284		109	65	33	2	

East-west dissimilarity test

To assess the degree of overlap or segregation between species occurring in the north-east and north-west extremities of the region analysed (the EEZ), the changes in species composition between species occurring at string ranges 0–10 and 250–260 were compared (Table 3). Across both regions, a total of more than 400 species occur, and there is approximately a 50% overlap between the two regions. This implies that our dataset has not adequately resolved the continuity and disjunction of species at the endpoints of the range.

Table 3. Species dissimilarity test between north-east and north-west extremities of the analysis region based on the Jaccard Index.

Region	Number of species
West (string 250–260)	322
East (string 0–10)	309
Both West and East	219
Total	412 (Jaccard Index = 0.47)

Biomic analyses

The Jaccard and bowler-hat analyses of depth distribution data support the existence of multiple biomes within the provinces (Figure 11). A series of 2-dimensional analyses, on data from each province independently using differing string length and depth interval constraints (Table 4), produced patterns indicating the presence of three biomes on the continental slope: an upper slope biome, a mid-upper slope biome and a mid-slope biome. There is an additional, ill-defined biome on the outer continental shelf.

Table 4. Biomic structure on the outer continental shelf and slope in each province. Each biome is defined by its primary upper depth limit (in metres), 'modal' depth, and lower depth limit. Analyses are based, where possible, on information using 20 units either side of the mid-point of each of the provinces. For the transition region between provinces, a linear connection can be used for each of the biomes. Estimates of depth ranges for the 'Outer Shelf' are preliminary because of potential edge effects associated with the exclusion of species occurring in depths less than 40 m. Hence, no modal depth was provided. The '?' refers to a second weak disjunction at the mid-range of this biome. See main text for description of analyses.

Province	Outer Shelf	Upper Slope	Mid-Upper Slope	Mid-Slope
Entire Route	75–200	300–440–520	650–700–750	860–1020–1140
Cape	125–220	200–340–470	590–660–780	890–960–1130
North Eastern	125–225	250–330–475	600–660–760	890–960–1130
Central Eastern	80–220	280–425–490	610–?–830	910–960–1080
Tasmanian	90–220	310–425–520	650–700–775	880–980–1100
Southern	80–220	310–440–520	650–700–750	860–1040–1140
Central Western	145–230	300–400–510	650–700–800	890–960–1075
North Western	150–225	300–380–530	650–700–780	900–960–1100
Timor	140–220	225–340–500		750–825–1000
Average depth intervals	112–220	275–504	631–778	870–1099
Standardised depth intervals	110–220	275–500	630–775	870–1100
No. of spp in core + transition zone	106	187	30	100

The most biogeographically structured plot was obtained for species whose depth ranges varied by less than 250 m. The presence of three bands, indicating biomes, is evident in the plot of the entire string route data (Figure 11.1) with bands at depths of 300–520 m (median 440 m), 650–750 m (700 m) and 860–1140 m (1020 m). Depth limits of biomes (as bands) were determined using peaks and troughs in the Jaccard Index, as in the provincial analyses. These bands were found in most of the provinces (Figures 11.1–8) and varied only marginally in their median depths and limits (Table 4). In the Timor Province (Figure 11.9), with little survey information available at different depths, maximum depth range interval needed to be increased to 400 m so that enough species were obtained for the analyses. In this case, only upper and mid-slope biomes were identified.

Biomic structure

The features of these biomes and their standardised intervals are provided below:

Outer Shelf biome (110–220 m depth)

Biomic structure nearest the inshore is not clear, due to edge effects, but evidence exists of a unit on the outer continental shelf. This outer shelf assemblage (characterised by a fully inclusive suite of 106 species) varies in median position from 138–195 m (mean 167 m), with limits averaging 112–220 m.

Indicator species: *Asymbolus parvus*, *Raja* sp., *Physiculus nigrescens*, *Aulotrachichthys novaezelandicus*, *Ocosia* cf *zaspilota*, *Bovitrigla leptacanthus*, *Satyrichthys rieffeli*, *Malakichthys levis*, *Parasclopsis tanyactis*, *Parapercis binivirgata*, *Eubalichthys quadrispinis*.

Upper Slope biome (275–500 m depth)

The first continental slope unit, the upper slope biome (characterised by 187 species), varies in median position from 330–440 m (mean 391 m), with limits averaging 275–504 m (Table 4). This assemblage seems to be distributed at slightly shallower depths in the eastern provinces than elsewhere in Australia. It is well defined using both the Jaccard Index and some bowler-hat analyses (Figures 11.2 and 11.3).

Indicator species: *Iago garricki*, *Squalus* sp., *Raja* sp., *Chlorophthalmus* cf *acutifrons*, *Malthopsis provocator*, *Neobythites longipes*, *Caelorinchus amydrozosterus*, *Antigonia* cf *malayana*, *Plectrogenium nanum*, *Pterygotrigla* sp., *Bembrops philippinus*, *Foetorepus apricus*.

Mid–Upper Slope biome (630–775 m depth)

A mid-upper slope assemblage (characterised by 30 species), varying in median position from 660–700 m (mean 689 m), is evident in all provinces apart from the Timor Province (see above). Its development is varied and contains substructure (two assemblages) in the Central Eastern Province. Its average limits range from 631–778 m, and once again it tends to be slightly shallower in the eastern provinces.

Indicator species: *Etmopterus dislineatus*, *Notoraja* spp., *Chaunax* sp., *Solocisquama* sp., *Lamprogrammus niger*, *Kuronezumia pallida*, *Nezumia merretti*, *Caelorinchus smithi*, *Caelorinchus spathulata*.

Mid-Slope biome (870–1100 m depth)

A mid-slope assemblage (characterised by 100 species) varies in median position from 960–1040 m (mean 979 m), except in the Timor Province (825 m) where mid-slope data are less complete. Its average limits vary from 870–1099 m.

Indicator species: *Bathyyroconger vicinus*, *Bathysaurus ferox*, *Antimora rostrata*, *Bathygadus cottoides*, *Kuronezumia leonis*, *Nezumia kapala*, *Trachonurus gagates*, *Nezumia coheni*, *Sphegmacrurus richardi*, *Macrurocyttus acanthopodus*.

Lower Slope biome (ca 1500+ m depth)

Assemblages beyond mid-slope depths could be evaluated due to a serious lack of data in most provinces. Evidence from the SEMR study (CSIRO 2001) suggests that a biome with an upper limit of about 1600 m occurs off south-eastern Australia.

Fig. 11.1

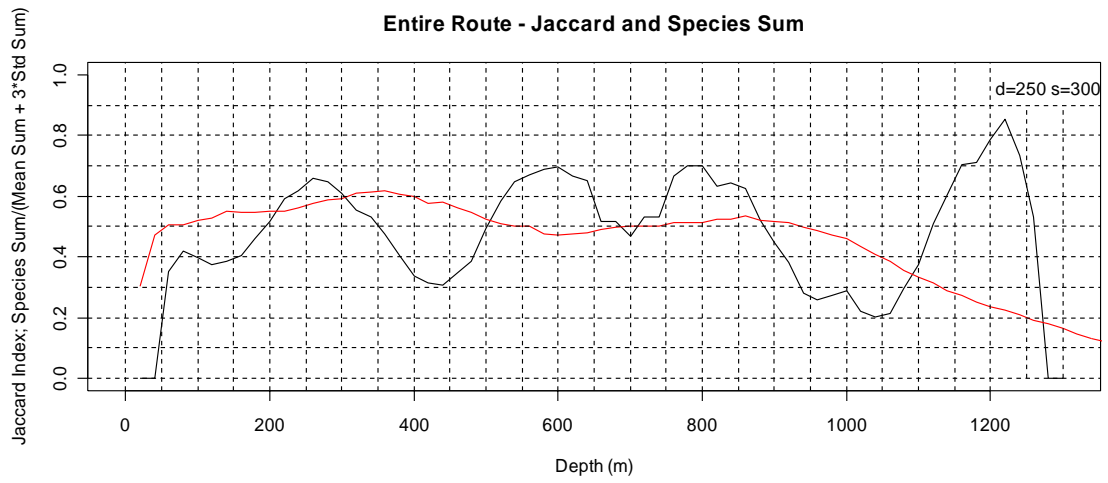


Fig. 11.2

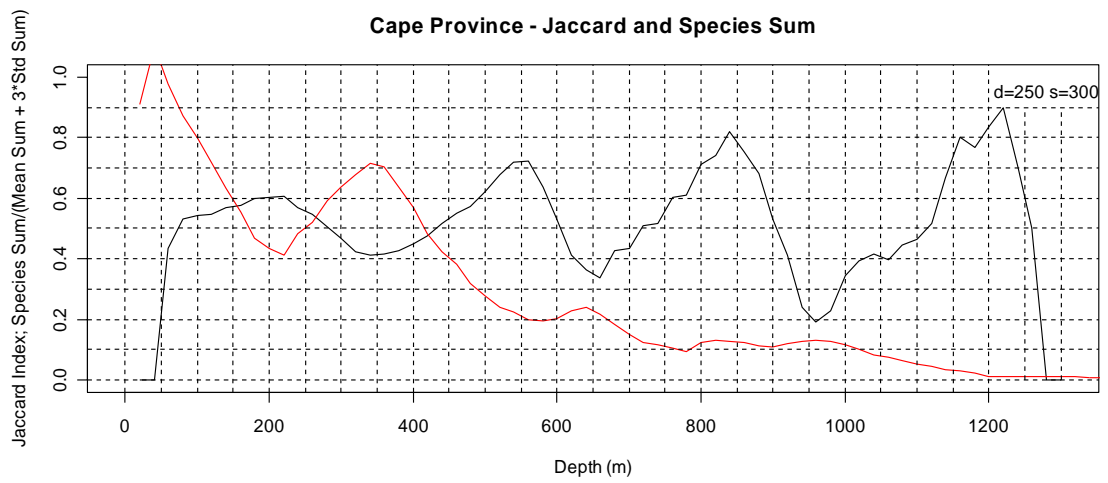


Fig. 11.3

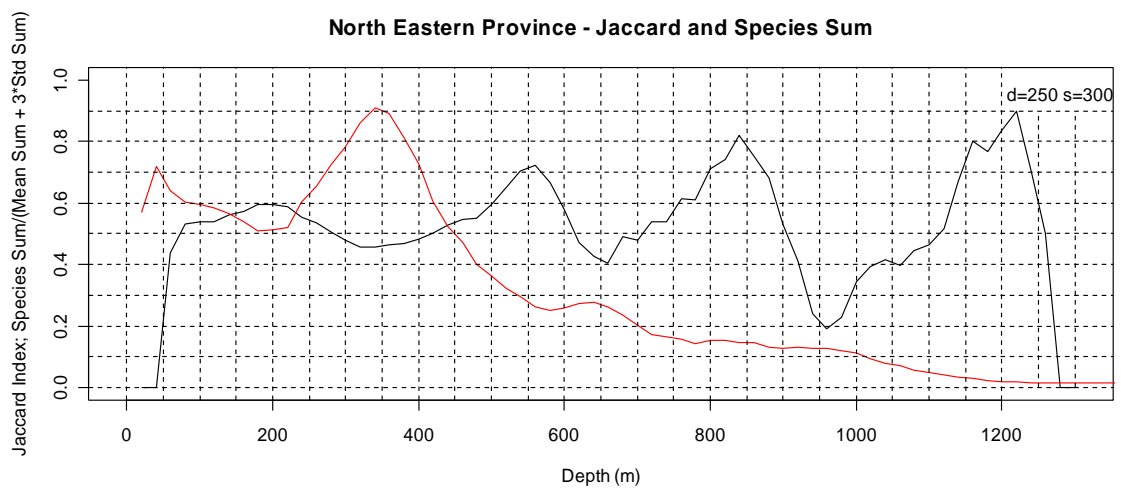


Fig. 11.4

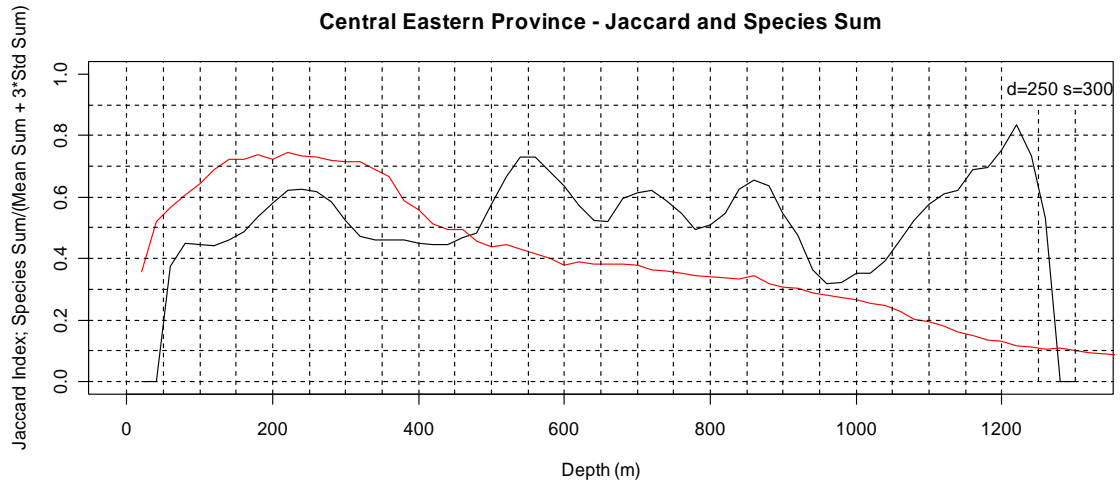


Fig. 11.5

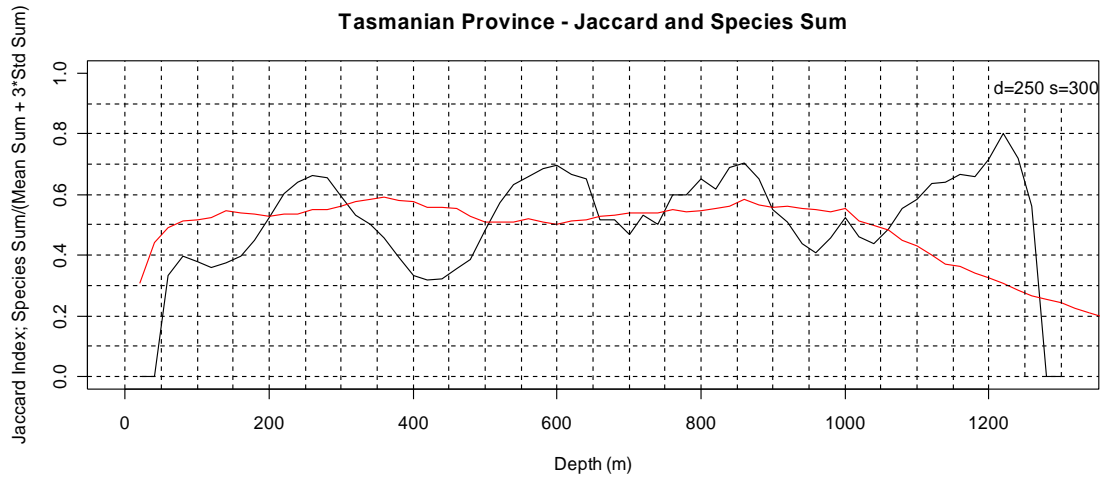


Fig. 11.6

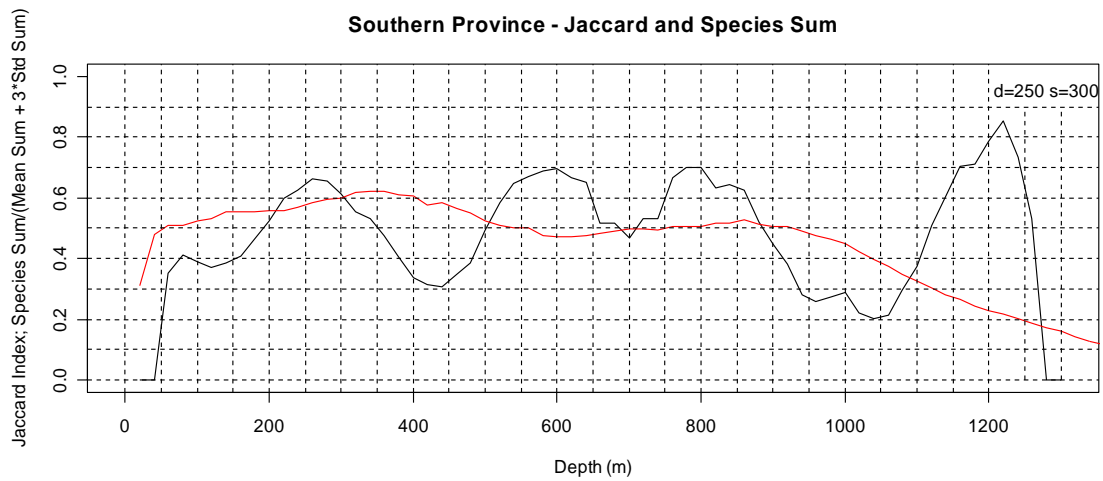


Fig. 11.7

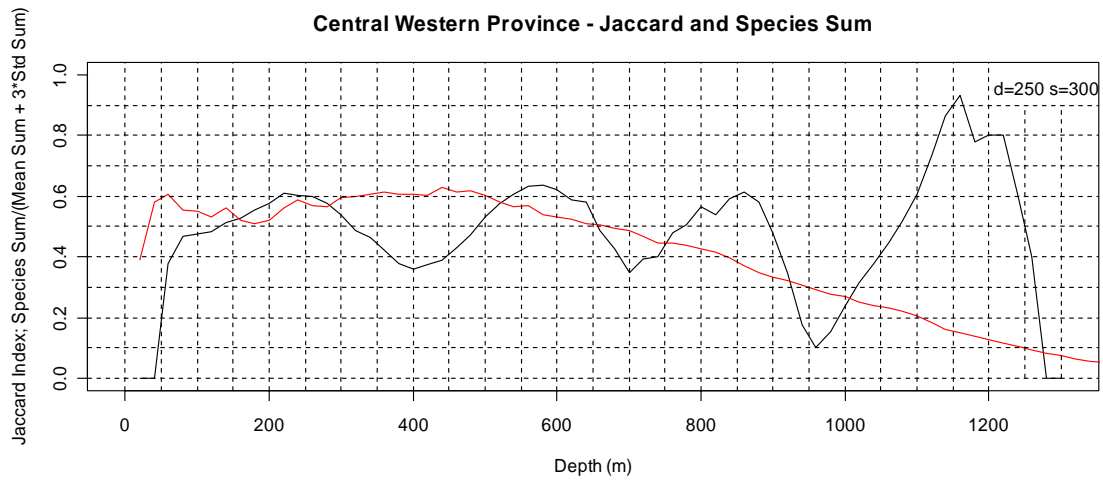


Fig. 11.8

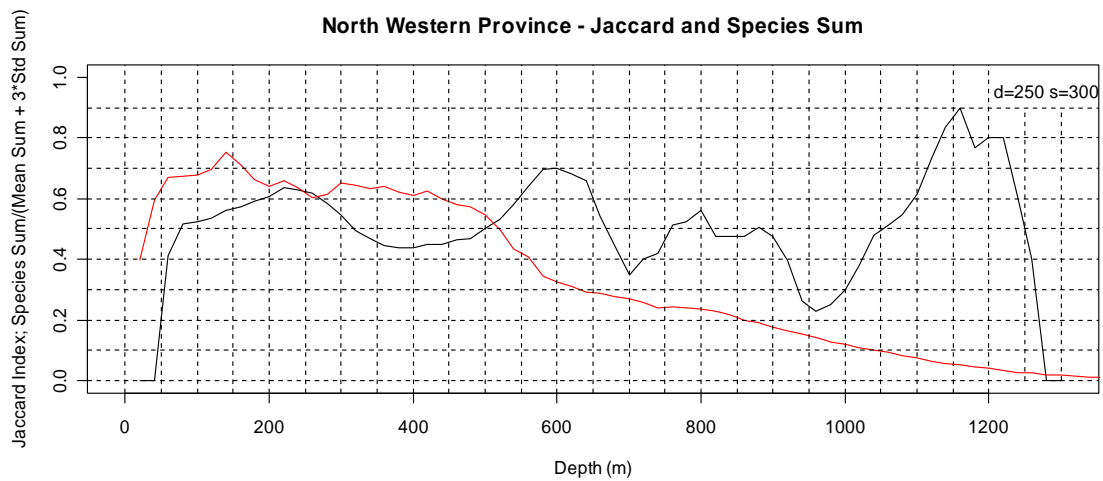


Fig. 11.9

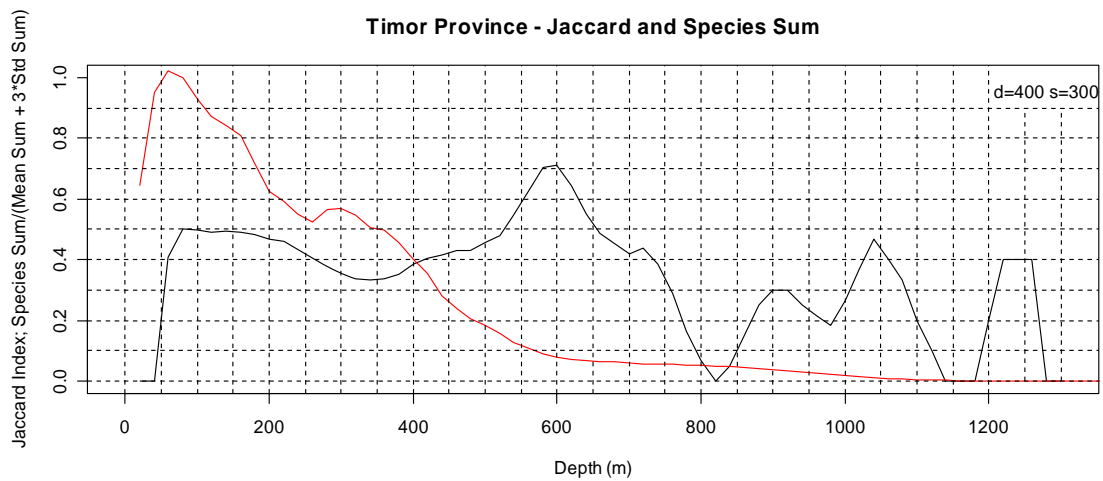


Figure 11. Jaccard Indices (in black) and weighted normalised (bowler-hat) values (in red) by depth for the entire string length, provided separately at each province.

Analysis of species richness in relation to depth revealed a general trend of species numbers declining with increasing depth. Five hundred or so species were recorded from the continental shelf, while fewer than 20 species occurred at 2000 m (Figure 12). This decrease in species number may be due to reduced sampling effort in greater depths, but is likely to reflect a true decrease in biodiversity. Depth is commonly recognised as an important variable influencing the structure of fish communities (Francis et al. 2002), and reduced species abundance with increasing depth has been documented (Powell et al. 2003).

The biomic scheme discussed above (Table 4), which provided evidence of four distinct biotic zones, was mapped on a plot of species richness against depth (Figure 12). Similar patterns between richness and biomic structure were observed on the outer shelf, the mid-slope and the upper slope, but a mid-upper slope biome was less evident. The distribution of depth range data for the entire string route shows a general trend for shelf species to occur within relatively narrow depth ranges, whereas the depth ranges of a slope species widen with depth. This result conforms with similar studies which suggest that some species range more widely with increasing depth (eg, Powell et al. 2003), perhaps reflecting a decrease in trophic resources with increasing depth, as reported by Stefanescu et al. (1993).

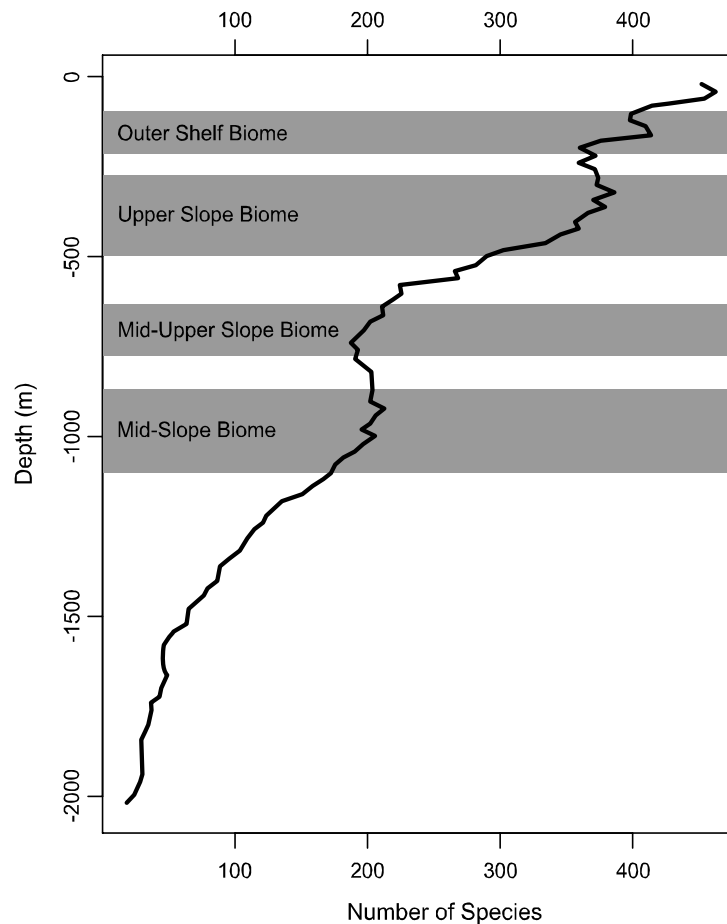


Figure 12. Decay in species richness with depth and associated biomic structure. Grey areas refer to biomes with clear transitional depths between the biomes.

5. Conclusion

This study is the first comprehensive biogeographic appraisal of Australia's deepwater demersal fishes. The raw data generated by this project appear to demonstrate a biogeographic structure that draws some parallels to patterns displayed in the coastal biota.

Determining the biogeographic structure of this very large geographic region has been a daunting exercise in such a short time frame. It has involved considerable baseline research to improve data quality, and developing special imaging tools and new analytical techniques to visualise faunal patterns.

Provinces

Evidence of strong patterns in the distribution of the deepwater fish fauna was discovered, with some parallels to the patterns inshore (IMCRA 1996), as well as some marked differences. Notably, the offshore fauna is less complex in temperate regions, but more complex off both the tropical Indian and Pacific Ocean coasts. A well-defined province off Tasmania coincides with a more pronounced, cool temperate inshore province (the Maugean Province). Similarly, a deepwater province off New South Wales coincides with an eastern warm temperate inshore province (the Peronian Province). The offshore provincial structure is less complex in the Great Australian Bight, with evidence for only a single province across this region (although there are separate inshore provinces in the south-west and in the South Australian gulfs). A subtropical province off Western Australia weakly coincides with an equivalent inshore province. However, off both the tropical north-east and north-west coasts, the respective inshore provinces (the Damperian and Solanderian Provinces) are each replaced by two distinct provinces offshore (Figure 10).

Biomes

The existence of multiple biomes on the Australian continental slope was already evident from the few studies that have examined community structure in deepwater demersal fishes (Last & Harris 1981, Williams, et al. 2001, CSIRO 2001). Each of these studies identified a biome (indicated by unique assemblages of fish species) near the continental shelf break (ca 200 m), as well as biomes at greater depths. Analysis of our data supports the presence of stratified partitioning of provincial faunas by depth, first flagged in the SEMR regionalisation (CSIRO 2001). Three well-defined biomes were found: an upper slope biome, a mid-upper slope biome and a mid-slope biome, as well as an ill-defined biome on the outer continental shelf.

In the present study, a well-developed, biomic assemblage of fishes was identified just below the shelf break in each offshore province. The depth intervals of this upper slope biome varied only slightly, being slightly shallower in the east than in other areas of the region. In the earlier SEMR study, the upper slope biome of the Tasmanian Province was considered to occur between depths of 325 and 575 m, compared to 310–520 m in the present study.

In the SEMR study, a mid-slope biome was identified between depths of 850–1125 m. The present study found a strong mid-slope band in all provinces in similar depths (off Tasmania, between depths of 880–1100 m). In the present study, an additional, less obvious biome was identified on the mid-upper slope in 590–830 m, with a median depth across all provinces of 689 m. Off Tasmania, the mid-upper slope biome varied from depths of 650 to 775 m. This biome was evident in all provinces, except the Timor Province.

Faunal assemblages beyond the mid-slope cannot be evaluated due to a lack of data.

However, given the consistency of structure along Australia's continental slope, a biome beyond the mid-slope detected in the SEMR study (CSIRO 2001) probably persists across the whole Australian region. This study found a biomic transition zone on the outer continental slope, between depths of 1125 m and about 1600 m. Hence there is probably a lower slope biome from depths of 1600 m to at least the bottom of the slope (ca 2000 m). For management purposes, a lower slope biome should be recognised. Studies in other regions (eg, Powell et al. 2003) have reported decreasing heterogeneity in the fish fauna beyond the continental slope (ie, deeper than 2000 m). In the absence of good biological information, geological surrogates could be used to define the biogeographic structure beyond the slope (ie, on the continental rise and the abyss).

Biomic patterns on the continental shelf were less clear, possibly due to edge effects caused by the exclusion of data from the coastal zone fauna. Nevertheless, weak evidence of faunal structure needing further investigation was found on the outer continental shelf. Studies off north-western Australia (Lyne 2003) found at least three, depth-partitioned faunal assemblages (biomes) on the continental shelf. It will be important to convert string datasets from the past IMCRA regionalisation (1996), based on coastal fishes, to an equivalent format used in the offshore regionalisations so that these patterns can be investigated properly across the EEZ.

An improved demersal fish database (OZFISHCAM)

The data validation component of the study involved a team of State and Australian government scientists, as well as international scientists. This team effort produced reliable results that would have been impossible to achieve otherwise. Baseline data on Australian deepwater fishes has been greatly enhanced, and will provide an important framework for both research at the species and community levels, which is needed by conservation and fisheries managers. The enhancement of the CAAB faunal database, which includes depth and geographic distributional profiles of deepwater fish species, will ultimately be useful to many user groups.

Australian demersal slope fishes are generally poorly studied compared to the inshore fauna. Prior to this study, most specimens recorded on research voyages or deposited in collections were given a 'cataloguing identification' that was often unreliable. As a result, many taxa were lumped under a single species name, often sharing the name of similar animals occurring overseas. Validating specimen data for Australia's demersal slope fishes necessitated an unprecedented level of taxonomic examination of the local fauna, which resulted in the discovery of many new species. The taxonomic validation process also provided a dataset of relatively high quality for the biogeographic analyses.

This study highlights the importance and value of research collections—resolving taxonomic problems requires the examination of multiple specimens from a wide geographic coverage. Access to multiple collections was essential for specialists to accurately classify the species for data analysis. The resultant increase in the number of validated species, combined with the general narrowing of species ranges, increased the resolution of the analysis beyond the level expected. Additionally, the identification of a number of species with extremely narrow ranges, often in areas that have been well sampled, raises concerns for their conservation, and has implications for marine management. The combined use of non-validated historical datasets and poor species identifications could have resulted in the identification of erroneous bioregions that were not reflective of the true biogeographic structure on the Australian continental slope and outer shelf.

A gap analysis based on historical data demonstrated a lack of information from the extreme north-west and north-east sectors of the AMJ. A plot of the number of species at each depth interval along the coastline confirmed this gap in the data, but also provided evidence of a

strong discontinuity between the faunas of these sectors. The analysis also provided a means of prioritising the national survey effort to obtain better data coverage. A strategic plan to survey the least well-covered areas of the AMJ is needed. It should be thought through carefully to maximise the gains, perhaps using the highly successful NORFANZ survey as a model. This survey covered a wide geographic area and managed to obtain good biological, bathymetric and physical data in a relatively short time frame. A comparison of the fishes sampled in the NORFANZ survey indicated that they are quite different to those of eastern Australia (almost half of one biogeographically informative group—sharks and rays—were not found in eastern Australian provinces). The NORFANZ data are still to be fully analysed, but preliminary assessments indicate that the Tasman seamounts (including Norfolk and Lord Howe Islands) should be managed as separate regional units.

The data used in this project is far superior to anything previously available. Without the thorough efforts of the research team, the analyses could not have been attempted with confidence. However, there are some limitations in these analyses. As survey gaps are filled, our knowledge of the fauna will steadily improve and this could affect how we perceive the extent of the provinces defined in this study. The gaps identified in this project are real, and a strategic plan is needed to ensure that a better coverage of the region is obtained. This is particularly important in a large region such as Australia, which is one of the most complex and diverse of all major global marine regions. The major areas requiring attention are the relatively accessible continental shelf off south-west Australia, and the continental slopes off north-east and north-west Australia. More remote and difficult-to-survey areas include the ocean depths below the mid-continental slope, as well as some offshore islands, eg, Christmas and Cocos (Keeling) Islands.

New research tools

This project was largely driven by the aim of producing the first national biogeographic framework for Australia's deepwater biota. It was ground breaking in several other ways as well. The development of new research tools is an important outcome of this project. Incorporating the point data from all major Australian fish collections into an online species database (OZFISHCAM), with a point data mapping facility, was a significant achievement, and a first for a major marine faunal group in Australia. Access to this OZFISHCAM facility enabled participants to 'ground truth' species identifications as recorded in voyage data, and enabled them to target the examination of extra-limital specimens (those collected beyond the accepted distribution for a given species) on museum visits. Although the database is presently restricted for use by project participants, it provides a useful case study to contribute to the development of the Online Zoological Collections of Australian Museums (OZCAM) project. OZCAM aims to connect museum faunal databases throughout Australia, but should not be confused with the database and data point mapping facility developed here. The point data mapping facility can be considered a *prima facie* study for OZCAM, demonstrating the strengths and weaknesses of this type of approach. However, the level of information included in this database is far more comprehensive than that available to OZCAM due to the negotiation of unrestricted access to fish collection data, and the inclusion of commercial-in-confidence data and sensitive unpublished information.

The research tools developed in this project could be customised to produce an interrogative database that would enable the user to produce sub-lists of the fish fauna at any geographic location in the Australian EEZ, and between any depth intervals. This facility would enable managers and researchers to almost instantaneously determine the fish composition within any marine bioregion (even at geomorphological scales). This database could be linked to images of the species, and eventually to other taxonomic and biological data, to provide a unique means of characterising and accessing our marine biodiversity. This prototype of baseline biodiversity data could be expanded to include invertebrates and marine plants.

The analytical methods used in the project are useful in visualising and defining patterns and structure in the demersal fish distribution data. The team searched unsuccessfully for other, more objective methods of analysing the data. However, no perfect spatial analytical method could be found and research is continuing to find alternatives. New methods may need to be derived, such as modifying methods (eg, cladistics) used in classical taxonomy. These new methods could provide an interpretation of the possible evolutionary history of the provinces and their component species. Although biogeographic interpretations have been undertaken for many groups of plants and animals in our region, the patterns have never been integrated to produce a holistic scheme.

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Acronyms and abbreviations

AMJ	Australian Marine Jurisdiction
AMS	Australian Museum, Sydney
BII	Biogeographic Information Index
BWG	Bioregionalisation Working Group
CAAB	Codes for Australian Aquatic Biota
CapeP	Cape Province
CEP	Central Eastern Province
CET	Central Eastern Transition
CMR	CSIRO Marine Research
CP	Cape Province
CSIRO	Commonwealth Scientific and Industrial Research Organisation
CWP	Central Western Province
CWT	Central Western Transition
EEZ	Exclusive Economic Zone
IMCRA	Interim Marine and Coastal Regionalisation for Australia
MAGNT	Museum and Art Gallery of the Northern Territory
MPA	Marine Protected Area
MYA	Million Years Ago
NEP	North Eastern Province
NET	North Eastern Transition
NORFANZ	Joint Australia and New Zealand survey of seamounts of the Tasman Sea
NMV	Museum Victoria, Melbourne
NSW	New South Wales
NWP	North Western Province
NWT	North Western Transition
OTU	Operational Taxonomic Unit
OZCAM	Online Zoological Collections of Australian Museums
OZFISHCAM	Online Zoological Fish Collections of Australian Museums
QM	Queensland Museum
SAM	South Australian Museum
SEMR	South-east Marine Region
SET	South Eastern Transition
SP	Southern Province
SWT	South Western Transition
TasP	Tasmanian Province
TP	Timor Province
TT	Timor Transition
WAM	Western Australian Museum
WTasT	Western Tasmanian Transition

Glossary (definitions sourced from dictionaries unless stated otherwise)

Biome

Major regional ecological communities of plants and animals extending over large natural areas (Abercrombie et al. 1951). In the sea these equate to units such as coastal, demersal shelf and slope, abyssal, neritic, epipelagic, mesopelagic and bathypelagic.

Biomic

In reference to biomes.

Bioregion

Assemblages of flora, fauna and the supporting geophysical environment contained within distinct but dynamic spatial boundaries (Welsh 1994). Biogeographic regions vary in size, with larger regions found where areas have more subdued environmental gradients. These are defined and delineated at the meso-scale.

Biotones

Zones of transition between core provinces. The biotones are not simply ‘fuzzy’ boundaries but represent unique transition zones between the core provinces. An important implication is that management-related boundaries are best placed within the biotones in order that conservation measures fully protect the core provinces.

Candidate indicator species

Species that typify a province as their core distribution lies within a province. They may or may not be endemic to the province. For instance, an indicator species may be a species whose Australian distribution only occurs in that province, but it may also occur in south-east Asia.

Continental rise

The sloping part of the ocean floor at depths of about 2000–4000 m, between the continental rise and the abyssal plain.

Continental shelf

The shelf-like part of the ocean floor beside continents and extending from the coast to a depth of about 200 m; the lower limit of the continental shelf is called the shelf break.

Continental slope

The sloping, often steep, part of the ocean floor bordering the continental shelf and extending to a depth of about 2000 m; divided into the upper slope (200–700 m), mid-slope (700–1400 m) and lower slope (1400–2000 m).

Demersal

Occurring or living on or near the bottom of an aquatic environment.

Ecosystem

All of the organisms in a given area in interaction with their non-living environment and each other. In practice, ecosystems are mapped and described using biophysical data.

Ecotone

A transition zone between two or more diverse communities, which usually contains members of those communities.

Exclusive Economic Zone (EEZ)

An area beyond and adjacent to the territorial sea, subject to the specific legal regime of

Australia, under which the rights and jurisdiction of Australia and the rights and freedoms of other States are governed by the relevant provisions of the United Nations Convention on the Law of the Sea. Australia's EEZ was proclaimed in August 1994, and extends 200 n miles from the coast and includes ocean around island territories.

Inshore

The near coastal waters extending from the coastline and estuaries out to 3 n miles, which is the boundary of the State and Territory waters.

Marine Protected Area

Any area of estuarine, intertidal or sub-tidal terrain, together with its overlaying water and associated flora, fauna, historical and cultural features, which has been reserved by law or other effective means to protect part or all of the enclosed environment (Kelleher & Kenchington 1992).

Meso-scale region

Large scale spatial unit (ie, in terms of 100s or 1000s of km in length)

Offshore

The area of the Exclusive Economic Zone extending from the border of the 3 n mile State and Territory waters to the limit of Australia's international marine boundary.

Province

A large-scale biogeographic unit derived from evolutionary processes in which suites of endemics co-exist.

Provincial

With reference to a province.

String

Artificial line derived for this project and drawn adjacent to the Australian coast to produce a 1-dimensional expression of a species distributions from a 2-dimensional range polygon. The deepwater string is comprised of 281 more or less equally spaced points (the string index) and the distributions of species are plotted to these points.

String data

Distributional data ordinated to a string(s).

String index

Refers to the entire series of 281 points of the deepwater string, which runs adjacent to the entire Australian coastline.

String position

Refers specifically to one or more points on the string index, which represent(s) a certain geographic location; for example, string position 177 is adjacent to Perth (WA).

String unit

Distance between two neighbouring points on the string.

Zootone

A transition zone between two or more biogeographic provinces, which usually contains members of each of those provinces.

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Appendix 1. Core project personnel

Core personnel who contributed to the project (and areas of expertise).

CSIRO Marine Research

Peter Last (Fish systematics, biogeography and ecology; report author)

Vincent Lyne (Visualisation, data analysis, biological oceanography; report author)

Gordon Yearsley (Fish systematics, biogeography and ecology; report author)

Daniel Gledhill (Fish systematics, biogeography and ecology; report author)

Spikey Riddoch (Fish collection technician and taxonomy)

Alastair Graham (Fish collection management and taxonomy)

Tony Rees (Data manipulation, and database enhancement and management; report author)

Alan Williams (Fish systematics, biogeography and ecology)

William White (Fish systematics, biogeography and ecology; report author)

Roger Scott (Visualisation, data analysis)

Bill Venables (Visualisation, data analysis)

Museum Victoria

Martin Gomon (Fish systematics, biogeography and ecology; report author)

Dianne Bray (Fish systematics and collection management)

Australian Museum

Mark McGrouther (Fish systematics, collection management and data enhancement)

Queensland Museum

Jeff Johnson (Fish systematics and collection management)

New South Wales Fisheries Research Institute

Ken Graham (Fisheries biology, taxonomy and ecology)

Museum and Art Gallery of the Northern Territory

Barry Russell (Fish systematics, biogeography and ecology)

California Academy of Sciences

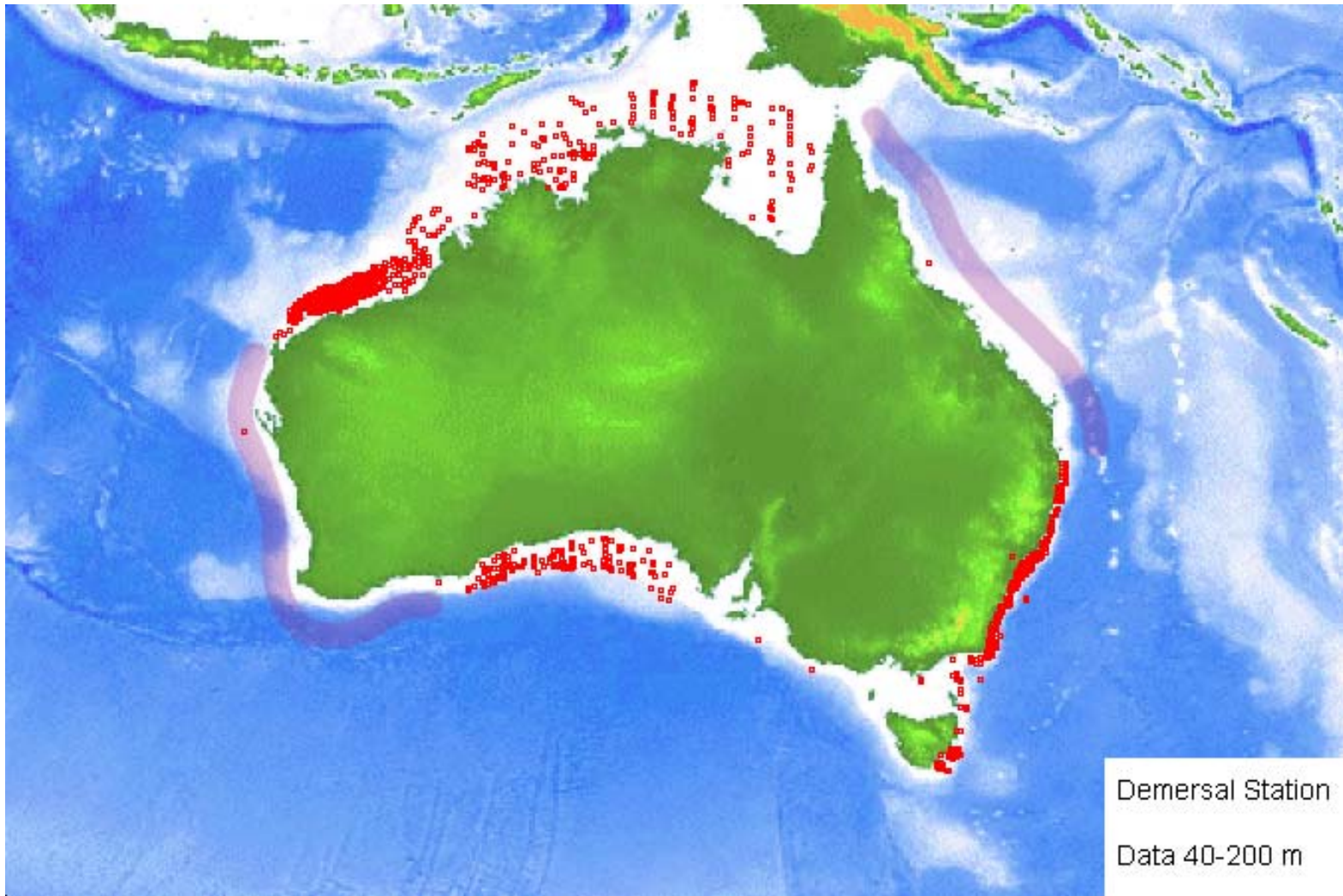
Tomio Iwamoto (Fish systematics, biogeography and ecology)

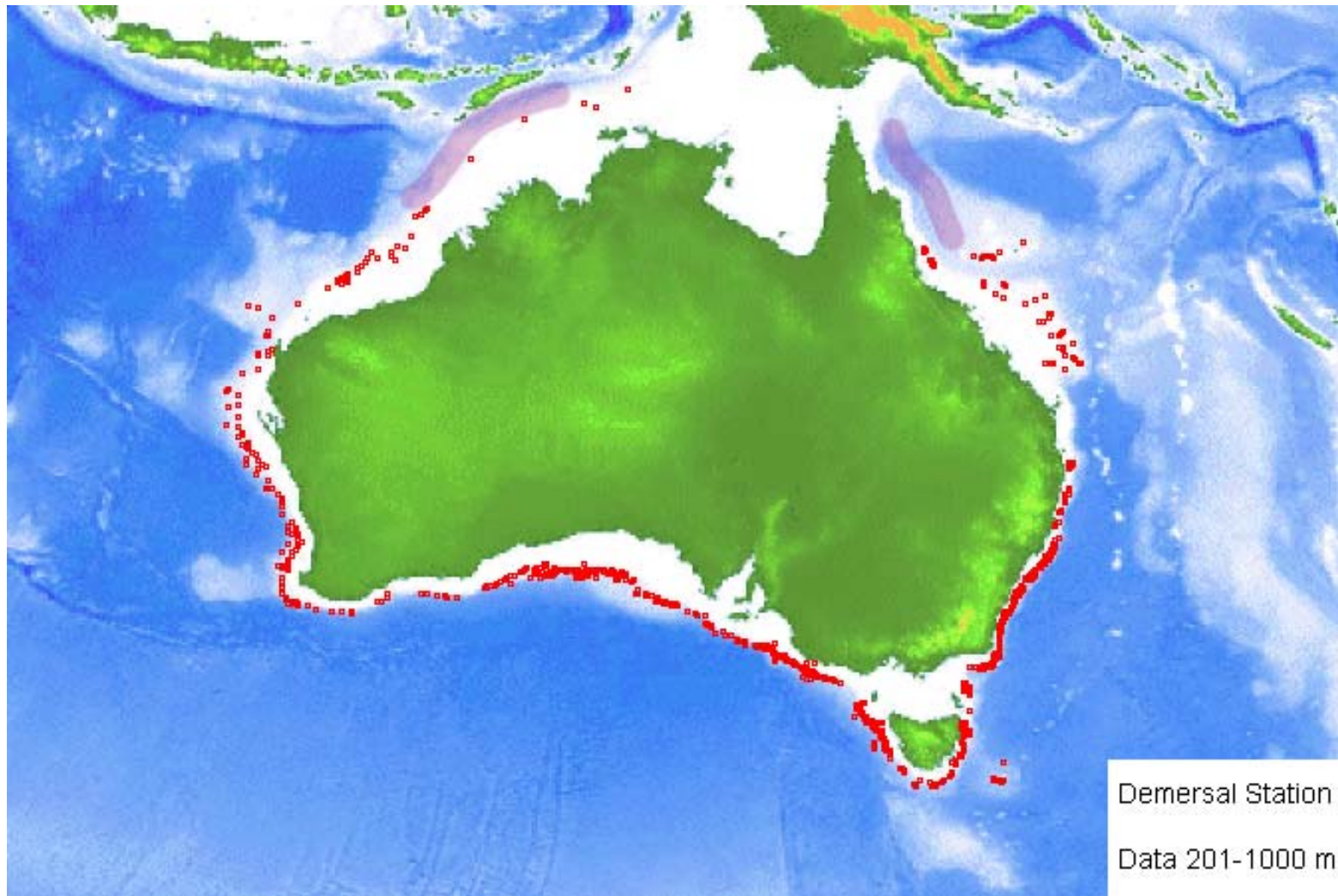
Hokkaido University

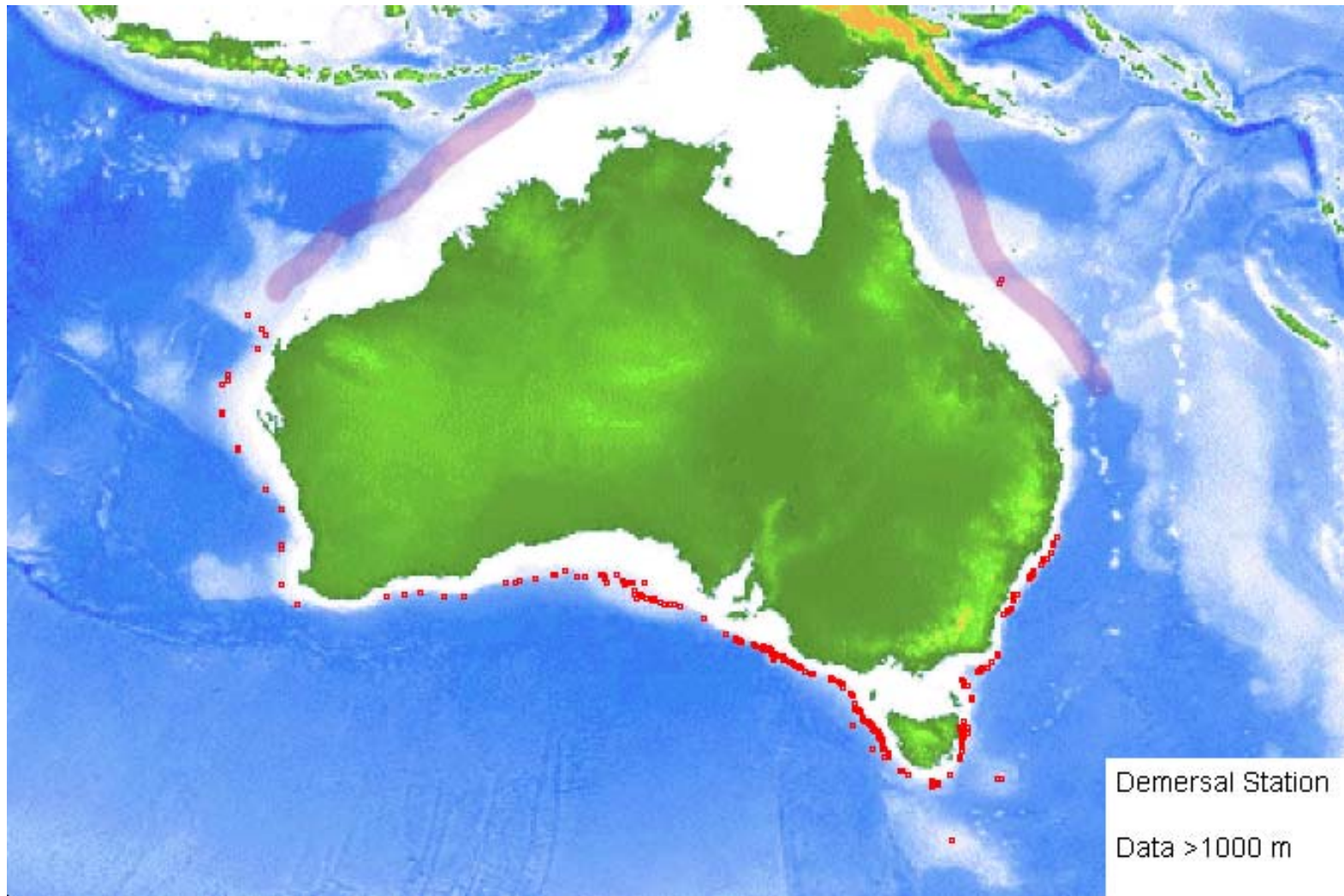
Kunio Amaoka (Fish systematics, biogeography and ecology)

Appendix 2. Provisional data distribution for demersal stations deeper than 40 m

Provisional data distribution for demersal stations deeper than 40 m (from both CSIRO voyages and external agencies) mapped to the resolution of 0.1 degrees to illustrate spatial coverage by depth. (A) 40–200 m depth; (B) 201–1000 m depth; (C) >1000 m depth. Survey gaps or areas of inadequate sampling are demarcated by pink overlays.







Appendix 3. Sample page of the provisional Species Database

Sample page of the provisional Species Database established soon after commencement of the project. Each row represents a species and is colour coded: white—species considered to occur demersally on the continental slope as well as uncategorised species; blue—demersal estuarine and coastal, green—demersal continental shelf. Pelagic and freshwater species were also colour coded but are not represented on this sample page. Geographic coordinates were determined from earlier bioregionalisations.

SPCODE	FAMILY	SCIENTIFIC_NAME	AUTHORITY	Long 1	Lat 1	Long 2	Lat 2	Min Dept	Max Depth	Habitat
37 287059	Scorpaenidae	<i>Ocosia</i> sp. [Last]		112.91	-27.94	153.61	-8.42	3	100	
37 287016	Scorpaenidae	<i>Paracentropogon longispinus</i>	(Cuvier, 1829)	114.91	-21.67	144.30	-8.42	30	200	
37 287060	Scorpaenidae	<i>Paracentropogon vespa</i>	Ogilby, 1910							
37 287061	Scorpaenidae	<i>Parascorpaena aurita</i>	Rüppell, 1838							
37 287096	Scorpaenidae	<i>Parascorpaena mcadamsi</i>	(Fowler, 1938)							
37 287062	Scorpaenidae	<i>Parascorpaena mossambica</i>	(Peters, 1855)							
37 287071	Scorpaenidae	<i>Parascorpaena picta</i>	(Kuhl & van Hasselt, 1829)	112.91	-26.74	153.44	-8.42	3	30	
37 287063	Scorpaenidae	<i>Pteroidichthys godfreyi</i>	(Whitley, 1954)	113.93	-22.52	149.75	-8.42			
37 287064	Scorpaenidae	<i>Pterois antennata</i>	(Bloch, 1787)	112.91	-33.85	153.70	-8.42	3	50	
37 287104	Scorpaenidae	<i>Pterois lunulata</i>	Temminck & Schlegel, 1842							
37 287027	Scorpaenidae	<i>Pterois mombasae</i>	(Smith, 1957)	114.57	-21.54	130.67	-9.50	30	200	
37 287097	Scorpaenidae	<i>Pterois radiata</i>	Cuvier, 1829							
37 287012	Scorpaenidae	<i>Pterois russelli</i>	Bennett, 1831	113.84	-22.52	149.75	-8.42	3	200	
37 287040	Scorpaenidae	<i>Pterois volitans</i>	(Linnaeus, 1758)	112.91	-36.26	159.35	-8.42	0	200	
37 287065	Scorpaenidae	<i>Rhinopias aphanes</i>	Eschmeyer, 1973	149.69	-37.58	153.82	-27.15	3	100	
37 287036	Scorpaenidae	<i>Richardsonichthys leucogaster</i>	(Richardson, 1848)	113.71	-22.52	144.83	-8.45	3	200	
37 287066	Scorpaenidae	<i>Scorpaena cardinalis</i>	Richardson, 1842							
37 287098	Scorpaenidae	<i>Scorpaena cookii</i>	Günther, 1875							
37 287067	Scorpaenidae	<i>Scorpaena grandisquamis</i>	Ogilby, 1910	148.42	-23.52	152.11	-20.12	3	30	
37 287068	Scorpaenidae	<i>Scorpaena izensis</i>	Jordan & Starks, 1904	114.73	-21.35	130.43	-9.50	30	200	
37 287069	Scorpaenidae	<i>Scorpaena maculipinnis</i>	(Smith, 1957)							
37 287070	Scorpaenidae	<i>Scorpaena moultoni</i>	Whitley, 1961							
37 287041	Scorpaenidae	<i>Scorpaena neglecta</i>	Temminck & Schlegel, 1844	114.73	-21.33	130.66	-9.50	30	200	
37 287008	Scorpaenidae	<i>Scorpaena papillosa</i>	(Bloch & Schneider, 1801)	114.43	-44.08	151.68	-31.97	3	130	
37 287092	Scorpaenidae	<i>Scorpaena</i> sp. [Last]								
37 287044	Scorpaenidae	<i>Scorpaena</i> sp. cf <i>oglinus</i>	(Smith, 1946)	118.88	-19.21	122.65	-13.62			
37 287072	Scorpaenidae	<i>Scorpaena sumptuosa</i>	Castelnau, 1875	112.61	-35.41	135.10	-24.16	3	100	

Appendix 4. Biogeographic Information Index (BII)

The following definition of the Biogeographic Information Index (BII), and discussion relating to the scoring of genera, is taken from IMCRA (1996).

Biogeographic Information Index (BII):

$$BII = C (2A + B) / \log (n + 1)$$

where *BII = Biogeographic Information Index*
 A = biogeographic potential
 B = information content qualifier
 C = value within each ecosystem
 n = number of species in the genus

The biogeographic potential (A) incorporates both the species richness of the genus and the extent of the species' distribution (eg, very restricted within Australia, subregional endemics, about half the Australian coastline, through to international species). Endemics are considered to be more informative than widely distributed species in delineating intraregional biogeographic patterns. Similarly, highly restricted endemics are likely to be more useful than those that occur more widely through the region so the range extents were considered when formulating the criteria (see below). The information qualifier (B) serves to include an index of the reliability of the distributional information for the species within the genus. Collective relevance of the species to the continental slope is modified according to the variable 'C' – zero values of C result in zero BII values eliminating the genus from the candidate groups for the continental slope. The presence of the variable \log_n enabled the size of the group concerned to be factored in or out. Consequently, genera with low BII scores are considered to be more informative than those with high values.

The biogeographical potential (A) of genera were assessed according to the following eight criteria:

1. *High richness (10 or more species in the genus) and almost all members with very restricted distributions*
2. *Low/medium richness (9 or fewer species in the genus) and almost all members with very restricted distributions*
3. *High richness and mostly subregional species (diversity high to low) but not applying to 1 or 2*
4. *Low/medium richness and mostly subregional species (diversity high to low) but not applying to 1 or 2*
5. *Mixed genus, including endemics and international species, but a few species have very restricted Australian distributions*
6. *Mainly broadly distributed Australian endemics*

7. *Broad mix of international and Australian subregional endemics*

8. *Almost all species with international distributions*

The information qualifier (B) takes into account the quality of distributional information available for each genus. Distributions were scored according to the following weightings:

1. *Well defined for most species in the genus (ie, easily determined or has been studied extensively)*
2. *Reasonably well known for most of the species in the genus (ie, good baseline data exists but only general studies available)*
5. *An even mixture of both well defined and poorly known species within the genus*
9. *Poorly defined*
0. *Unknown*

The relative value (C) of each genus was weighted according to the following criteria:

1. *High potential value (ie, most species occurring on the continental slope)*
Medium value (ie, half or so of species occurring on the continental slope)
2. *Low potential value (ie, few species occurring on the continental slope)*
5. *Genus unlikely to occur on the continental slope.*

Appendix 5. Biogeographic Information Index (BII) scores for the most informative genera

Biogeographic Information Index (BII) scores for the most informative 91 genera (ie, those with a BII of less than 30). Species in bold were added to the list based on recalculated BII's at the end of the project.

Genus	Number of species*	BII score	Family	Family common name
<i>Dipturus</i>	23	4.35	Rajidae	skates
<i>Urolophus</i>	16	4.88	Urolophidae	stingarees
<i>Pavoraja</i>	8	5.24	Rajidae	skates
<i>Cephaloscyllium</i>	7	6.64	Scyliorhinidae	catsharks
<i>Etmopterus</i>	11	7.41	Squalidae	dogfishes
<i>Paraliparis</i>	28	7.52	Liparidae	snailfishes
<i>Asymbolus</i>	8	7.86	Scyliorhinidae	catsharks
<i>Scorpaena</i>	24	8.58	Scorpaenidae	scorpionfishes
<i>Trygonoptera</i>	6	8.87	Urolophidae	stingarees
<i>Squalus</i>	9	9.00	Squalidae	dogfishes
<i>Lepidotrigla</i>	19	9.22	Triglidae	searobins
<i>Antigonia</i>	13	9.60	Caproidae	deepsea boarfishes
<i>Squatina</i>	4	9.64	Squatinae	angel sharks
<i>Caelorinchus</i>	35	9.97	Macrouridae	whiptails
<i>Thamnaconus</i>	6	11.57	Monacanthidae	leatherjackets
<i>Pristiophorus</i>	5	11.57	Pristiophoridae	sawsharks
<i>Narcine</i>	5	11.57	Narcinidae	numbfishes
<i>Coryphaenoides</i>	10	12.00	Macrouridae	whiptails
<i>Centroprorus</i>	7	12.85	Squalidae	dogfishes
<i>Chimaera</i>	5	12.85	Chimaeridae	shortnose chimaeras
<i>Euclichthys</i>	4	12.88	Euclichthyidae	Eucla cods
<i>Neosebastes</i>	7	13.29	Neosebastidae	gurnard perches
<i>Notoraja</i>	6	14.31	Rajidae	skates
<i>Hydrolagus</i>	6	14.31	Chimaeridae	shortnose chimaeras
<i>Halieutaea</i>	14	14.31	Ogcocephalidae	deepwater batfishes
<i>Paraulopus</i>	7	14.40	Paraulopidae	cucumberfishes
<i>"Foetorepus"</i>	13	14.81	Callionymidae	stinkfishes
<i>Physiculus</i>	9	15.42	Moridae	morid cods
<i>Apristurus</i>	8	15.72	Scyliorhinidae	catsharks
<i>Arnoglossus</i>	14	16.16	Bothidae	lefteye flounders
<i>Malthopsis</i>	13	16.58	Ogcocephalidae	deepwater batfishes
<i>Galeus</i>	3	16.61	Scyliorhinidae	catsharks
<i>Dicrolene</i>	7	16.61	Ophidiidae	cusk eels
<i>Rexea</i>	4	17.17	Gempylidae	gemfishes
<i>Pseudorhombus</i>	14	17.28	Paralichthyidae	sand flounders
<i>"Callionymus"</i>	28	17.29	Callionymidae	stinkfishes
<i>Parapercis</i>	31	17.62	Pinguipedidae	grubfishes

<i>Nezumia</i>	9	17.72	Macrouridae	whiptails
<i>Eubalichthys</i>	6	17.75	Monacanthidae	leatherjackets
<i>Cataetyx</i>	6	17.75	Bythitidae	live-bearing cuskis
<i>Setarches</i>	10	18.24	Setarchidae	deepwater scorpionfishes
<i>Hoplostethus</i>	8	18.27	Trachichthyidae	roughies
<i>Monomitopus</i>	8	19.91	Ophidiidae	cusk eels
<i>Dasyatis</i>	9	19.93	Dasyatidae	stingrays
<i>Chaunax</i>	9	19.93	Chaunacidae	coffinfishes
<i>Uranoscopus</i>	9	19.93	Uranoscopidae	stargazers
<i>Ventrifossa</i>	6	20.56	Macrouridae	whiptails
<i>Scolecenchelys</i>	11	20.85	Ophichthidae	snake eels
<i>Dibranchius</i>	6	20.96	Ogcocephalidae	deepwater batfishes
<i>Neomerinthe</i>	4	20.96	Scorpaenidae	scorpionfishes
<i>Chlorophthalmus</i>	6	21.30	Chlorophthalmidae	greeneyes
<i>Lepidoperca</i>	7	21.30	Serranidae	rockcods
<i>Engyprosoon</i>	6	21.30	Bothidae	lefteye flounders
<i>Anoplocapros</i>	4	21.46	Ostraciidae	boxfishes
<i>Pterygotrigla</i>	11	21.46	Triglidae	searobins
<i>Neoplatycephalus</i>	3	22.42	Platycephalidae	flatheads
<i>Mustelus</i>	3	22.42	Triakidae	hound sharks
<i>Halieutopsis</i>	6	22.48	Ogcocephalidae	deepwater batfishes
<i>Epigonus</i>	6	23.13	Apogonidae	cardinal fishes
<i>Parascyllium</i>	5	23.13	Parascylliidae	collared carpetsharks
<i>Satyrichthys</i>	10	23.13	Peristediidae	armoured gurnards
<i>Psenopsis</i>	5	23.13	Centrolophidae	trevallas
<i>Centroberyx</i>	5	23.61	Berycidae	redfishes
<i>Helicolenus</i>	4	23.61	Sebastidae	ocean perches
<i>Champsodon</i>	9	24.00	Champsodontidae	gapers
<i>Bembrops</i>	9	24.00	Percophidae	duckbills
<i>Hoplichthys</i>	6	24.42	Hoplichthyidae	ghost flatheads
<i>Kathetostoma</i>	3	24.91	Uranoscopidae	stargazers
<i>Aulopus</i>	3	24.91	Aulopidae	threadsails
<i>Saurida</i>	11	25.02	Bathysauridae	deepsea lizardfishes
<i>Halaelurus</i>	2	25.15	Scyliorhinidae	catsharks
<i>Parapterygotrigla</i>	4	25.15	Triglidae	searobins
<i>Malakichthys</i>	5	25.15	Percichthyidae	temperate basses
<i>Macroramphosus</i>	4	25.75	Macroramphosidae	bellowsfishes
<i>Centroscymnus</i>	4	25.75	Squalidae	dogfishes
<i>Lepidion</i>	4	26.58	Moridae	morid cods
<i>Solegnathus</i>	6	26.99	Syngnathidae	pipefishes
<i>Branchiostegus</i>	7	28.40	Malacanthidae	tilefishes
<i>Priacanthus</i>	6	28.40	Priacanthidae	bigeyes
<i>Epinephelus</i>	46	28.71	Serranidae	rockcods
<i>Heterodontus</i>	3	29.90	Heterodontidae	horn sharks
<i>Rhizoprionodon</i>	3	29.90	Carcharhinidae	whaler sharks

<i>Benthodesmus</i>	4	29.90	Trichiuridae	cutlassfishes
<i>Notopogon</i>	3	29.90	Macroramphosidae	bellowsfishes
<i>Neobythites</i>	11	29.90	Ophidiidae	cusk eels
<i>Sirembo</i>	9	29.90	Ophidiidae	cusk eels
<i>Poecilopsetta</i>	5	29.90	Pleuronectidae	righteye flounders
<i>Synaphobranchus</i>	3	29.90	Synaphobranchidae	basketwork eels
<i>Trachonurus</i>	4	29.90	Macrouridae	whiptails
<i>Bembras</i>	3	29.90	Platycephalidae	flatheads
<i>Pristipomoides</i>	8	29.90	Lutjanidae	tropical snappers

*Where an original genus was split due to nomenclatural issues, this column occasionally includes representatives of closely related genera

Appendix 6. Standardised online data entry form

Standardised data entry form, which was available online to taxonomic specialists locally and overseas. This form was designed to consistently capture and score biogeographic data.

EDIT distribution data - *Foetorepus phasis* (37 427002)

Authorised editor for this taxon: Gordon Yearsley (others can insert comments via the ****Messages**** field only)

Bioreg 2 data last updated: 02-FEB-2004 by Gordon Yearsley

Change History:

... 09-01-2004: Bioreg 2 string = 65-121, overall depth range: 126-437m, core depth range: 170-330m (Gordon Yearsley)

... 02-02-2004: Bioreg 2 string = 65-121, overall depth range: 126-437m, core depth range: 170-330m (Gordon Yearsley)

... 11-02-2004: Bioreg 2 string(s) adjusted based on amended algorithm, from previously entered coords (Tony Rees)

Click [here](#) to show "multiple maps" page for this species (including most recently entered modelled data)

Note, details can be saved incrementally, ie, fields completed as data available. Use "String completeness" and "Depth completeness" fields to indicate current state of data entry completion or verification.

Bioreg 1 overall string (converted to new, slope-based values): 67-80, 83-92, 104-104
Bioreg SE overall string: 66-184

Bioreg 2 String Segments (max. 3 can be entered). NB strings go **clockwise** around Australia starting off at Cape York (zero) and running through to 281.

NEW: Enter strings with lower (start) point preceding higher (end) point in each case, unless the string passes through zero: in this instance, make sure the "crosses zero" box is checked.

[STRING POINTS REFERENCE MAP](#)

Need lat/long for a placename? Enter (minimum 3) characters into the box below and press "search" to interrogate the **Gazetteer of Australia 2001 via the *Geoscience Australia* website

State: Any/All ACT NSW QLD SA
 TAS VIC WA

Search for:

If you prefer to enter values in lat/longs, the equivalent string start or end points will be calculated automatically for you (leave picklist value/s as "no start [or end] point selected").

Use the "Based On..." field to record the source of the string point wherever appropriate (e.g. specimen ref., literature record, etc.).

A: NORMAL distribution (segments 1-3)

Segment 1 start - EITHER enter a start lat/long, or select a string position from the list:

♣ Latitude (deg, min S): Longitude (deg, min E):
 ♣ (or) Start string point:

♣ Based on:

details:

Segment 1 end - EITHER enter an end lat/long, or select a string position from the list:

♣ Latitude (deg, min S): Longitude (deg, min E):
 ♣ (or) End string point:

 Crosses zero?

♣ Based on:

details:

Segment 2 start - EITHER enter a start lat/long, or select a string position from the list:

♣ Latitude (deg, min S): Longitude (deg, min E):
 ♣ (or) Start string point:

♣ Based on:

details:

Segment 2 end - EITHER enter an end lat/long, or select a string position from the list:

♣ Latitude (deg, min S): Longitude (deg, min E):
 ♣ (or) End string point:

 Crosses zero?

♣ Based on:

details:

NOTE: additional "normal" segment 3 can be entered at the end of the form if needed.

<p>String start confidence:</p> <p><input type="radio"/> not yet entered</p> <p><input type="radio"/> 1: excellent</p> <p><input type="radio"/> 2: good</p> <p><input type="radio"/> 3: satisfactory</p> <p><input type="radio"/> 4: poor</p> <p><input type="radio"/> 5: doubtful</p>	<p>String end confidence:</p> <p><input type="radio"/> not yet entered</p> <p><input type="radio"/> 1: excellent</p> <p><input type="radio"/> 2: good</p> <p><input type="radio"/> 3: satisfactory</p> <p><input type="radio"/> 4: poor</p> <p><input type="radio"/> 5: doubtful</p>
---	---

String Completeness:

Bioreg 1 depth range entered: 100-437 m
Bioreg SE "overall" depth range entered: 124-639 m
New (Bioreg 2) OVERALL depth range in metres

min: confidence:
max: confidence:

New (Bioreg 2) CORE depth range in metres - if known

min: confidence:
max: confidence:

Depth Completeness:

Biome/s occupied

Comma separated list, example: C, SH, SL
NB - use the following abbreviations:

- | | |
|---|---|
| <ul style="list-style-type: none">• PS - Pelagic, Shelf (0-200m)• PE - Pelagic, Epipelagic (0-200m, oceanic)• PM - Pelagic, Mesopelagic (200-1000m, oceanic)• PB - Pelagic, Bathypelagic (1000-2000m, oceanic)• PA - Pelagic, Abyssopelagic (2000m+, oceanic) | <ul style="list-style-type: none">• F - Freshwater• E - Estuarine• C - Coastal (0-40m)• SH - Shelf Demersal (40-200m)• SL - Slope Demersal (200-2000m)• A - Abyssal (2000m+) |
|---|---|

Taxon Distribution Notes (if relevant - for display on public "Taxon Report" page)

Admin Comments (for record owner use)

1/2/04
SA or Vic endpoint still uncertain. Need to check SA for specimens and N
11/12/03 Depth data based on CSIRO specimen (min) and AMS specimen

Messages (Non-record owners may use this field to send a comment to the record owner)

your CAAB username

password:

Save Entered Data

Segment 3 start - EITHER enter a start lat/long, or select a string position from the list:

Latitude (deg, min S): Longitude (deg, min E):

(or) Start string point:

No start point selected

Based on: No method selected

details:

Segment 3 end - EITHER enter an end lat/long, or select a string position from the list:

Latitude (deg, min S): Longitude (deg, min E):

(or) End string point:

No end point selected

Crosses zero?

Based on: No method selected

details:

Segment 4 start - EITHER enter a start lat/long, or select a string position from the list:

Latitude (deg, min S): Longitude (deg, min E):

(or) Start string point:

No start point selected

Based on: No method selected

details:

Segment 4 end - EITHER enter an end lat/long, or select a string position from the list:

Latitude (deg, min S): Longitude (deg, min E):

(or) End string point:

No end point selected

Crosses zero?

Based on: No method selected

details:

C: EXTRA-LIMITAL distribution (segment 5)

Segment 5 start - EITHER enter a start lat/long, or select a string position from the list:

Latitude (deg, min S): Longitude (deg, min E):

(or) Start string point:

No start point selected

Based on: No method selected

details:

Segment 5 end - EITHER enter an end lat/long, or select a string position from the list:

Latitude (deg, min S): Longitude (deg, min E):

(or) End string point:

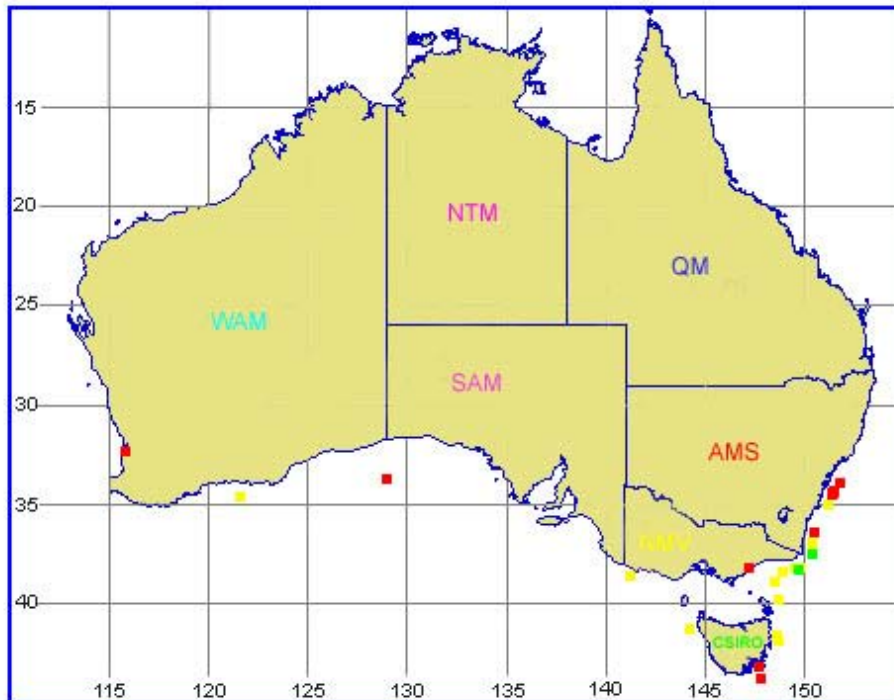
No end point selected

Crosses zero?

Based on: No method selected

Appendix 7. Point data mapping facility

Point data mapping facility incorporating records for all registered specimens in major Australian fish collections. Two screens are shown. The first shows capture locations for the species queried, with colour coding to depict the collection at which the specimens are registered. Selecting a dot (ie, a specimen capture locality), reveals a pop-up screen (example shown, lower image), containing a summary of the specimen collection data.



Total holdings of *Foetorepus phasis* from all collections = 29 lots

NB: Some records, eg LHI, Coral Sea and a few from overseas will not show on map.

A screenshot of a web browser window. The address bar shows the URL: http://data.austmus.gov.au/cgi_bin/texhtml.exe?form=fishes. The browser interface includes a menu bar (File, Edit, View, Favorites, Tools, Help), a toolbar with navigation buttons (Back, Forward, Home, Search, Favorites, Go, Links), and a main content area. The content area displays the following specimen data:

Taxon: **Foetorepus phasis**
Museum: **NMV**
Size range: **-73mm**
Coll. date: **1988 Aug 17**
Cap. depth: **510-521m**
[View the data search page](#)

The browser's status bar at the bottom shows the Internet Explorer logo and the text "Internet".

Appendix 8. Typical CMR data warehouse map

Typical map displaying records as held in CMR's data warehouse for the queried species.

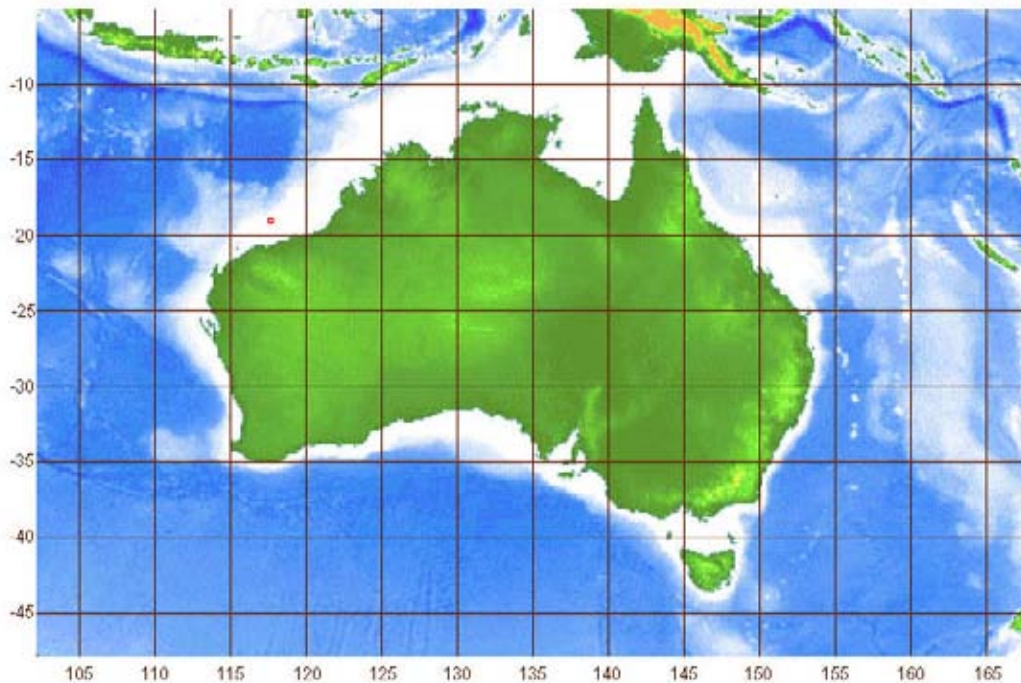
(8a) Displayed records (in this example, just one) summarise cruise stations at which that species was recorded. Different maps can be selected to show parts of the Australian coastline at higher resolution. **(8b)** Selecting a dot (ie, a station at which the species was recorded) links to a screen summarising CMR catch data holdings (eg, vessel and lat/long), and including a hotlink to more information such as the metadata.

App 8a

Dataset extent map

Current CMR Data Warehouse records - *Foetorepus phasis* (37 427002)

[c-squares Home page](#)

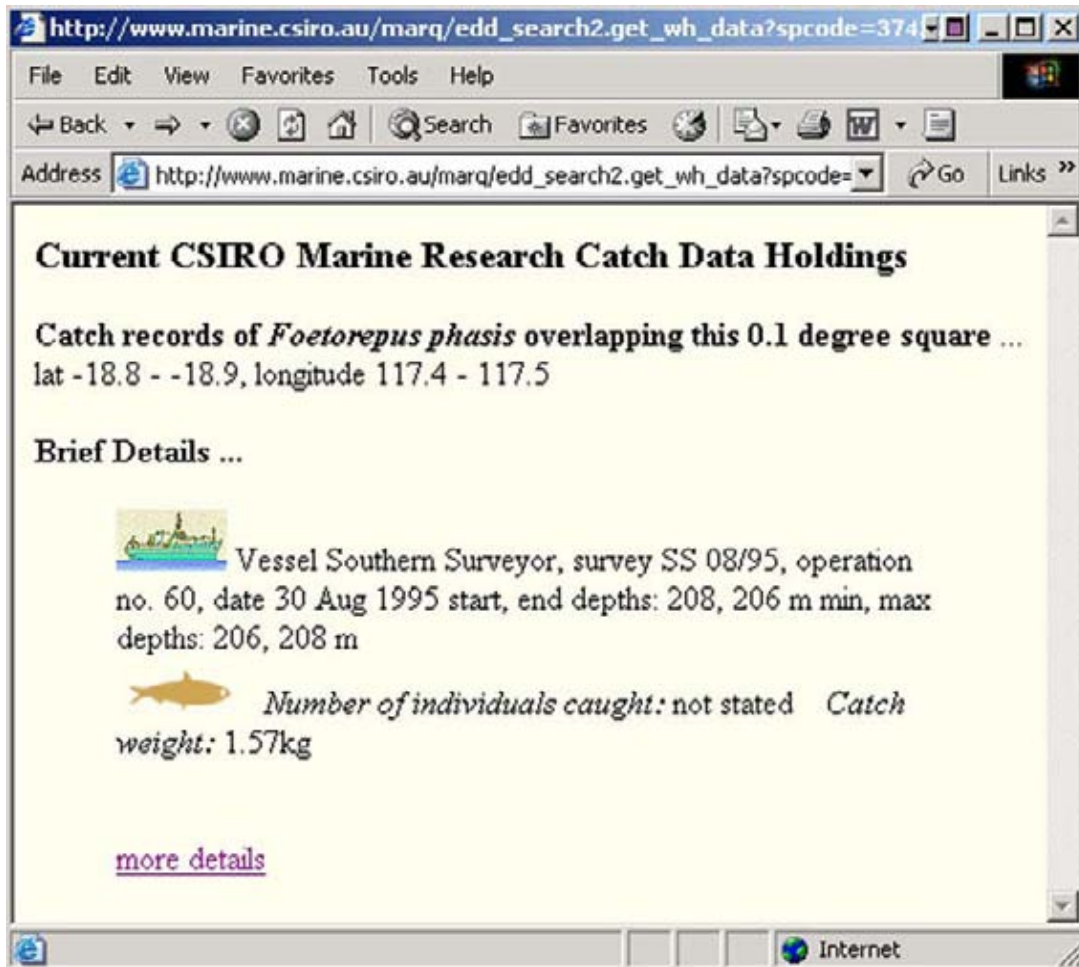


Please note, current CMR Data Warehouse holdings include only a subset of total CMR catch data and may also contain erroneous data awaiting verification. This map is indicative only and should not be used as an authoritative record of the actual distribution of this taxon.

This is an active map, click on any highlighted square to query the source data. (HINT: It may be helpful to zoom to a smaller region, and/or press 'Enlarge', before doing so).

Dataset extent map produced by CMR [c-squares mapper](#)

App 8b





The screenshot shows a web browser window with the address bar containing the URL: http://www.marine.csiro.au/marq/edd_search2.get_wh_data?sPCODE=374. The browser's menu bar includes File, Edit, View, Favorites, Tools, and Help. The address bar also features a search icon, a home icon, and a go button. The main content area displays the following information:

Current CSIRO Marine Research Catch Data Holdings

Catch records of *Foetorepus phasis* overlapping this 0.1 degree square ...
lat -18.8 - -18.9, longitude 117.4 - 117.5

Brief Details ...

 Vessel Southern Surveyor, survey SS 08/95, operation no. 60, date 30 Aug 1995 start, end depths: 208, 206 m min, max depths: 206, 208 m

 *Number of individuals caught:* not stated *Catch weight:* 1.57kg

[more details](#)

The browser's status bar at the bottom shows the Internet icon and the text "Internet".

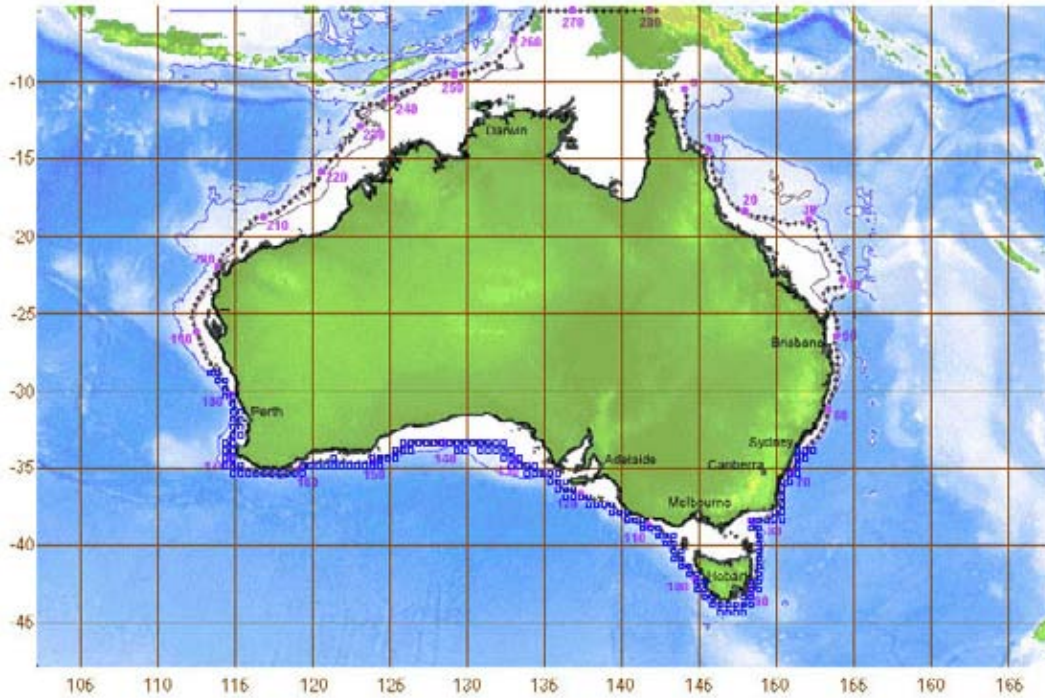
Appendix 9. Online map showing historical modelled distribution

Online map showing historical modelled distribution for a particular species. These data relate to the earlier shelf bioregionalisation study (IMCRA 1996) and the restricted slope study (SEMR, CSIRO 2001). Both these earlier studies only provided provisional data for slope species in a national context.

Dataset extent map

Bioreg 1/SE modelled distribution - *Foctoropus phasis* (37 427002)

[c-squares Home page](#)



Start/stop points: 066-184 (Bioreg SE)

Depth range: 124 m (Bioreg SE data) - 639 m (Bioreg SE data)

Please note, current modelled distribution is for test purposes only and may contain erroneous or incomplete values. This map should not be used as an authoritative record of the actual distribution of this taxon.

Dataset extent map produced by CMR [c-squares mapper](#)

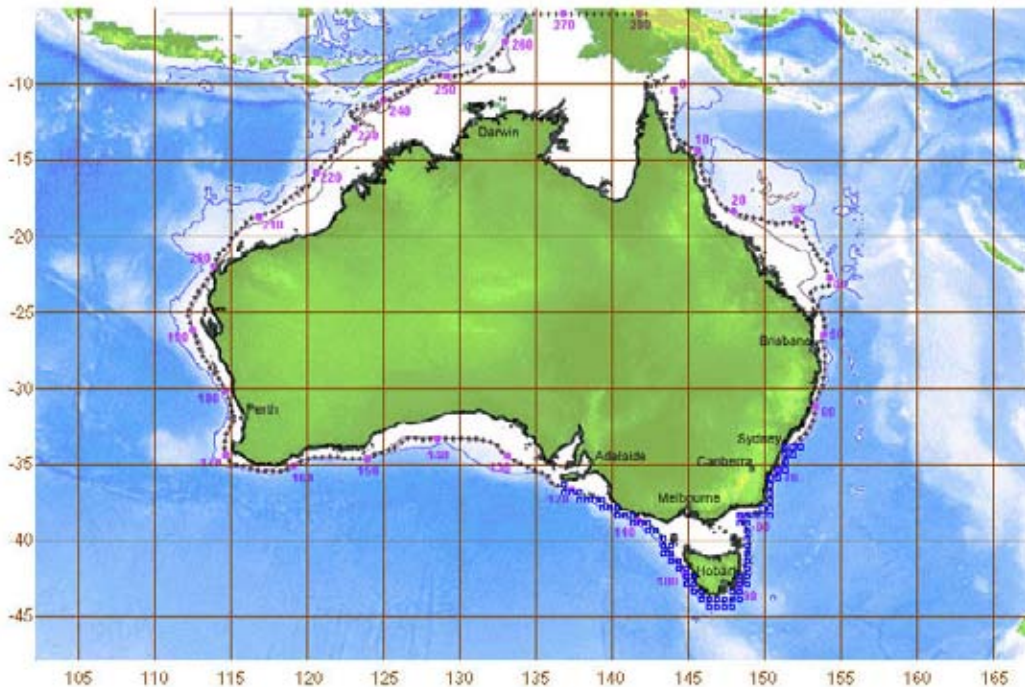
Appendix 10. Online map showing latest modelled distribution

Online map showing latest modelled distribution. At the start of this project, this online map displayed historical data from previous studies (see Appendix 9). As new BIOREG 2 data were entered, the map was updated in real time to display current modelled distribution. The map below shows the final modelled distribution for the same species as displayed in Appendix 9.

Dataset extent map

Latest modelled distribution - *Foetorepus phasis* (37 127002)

[c-squares Home page](#)



Start/stop points: 066-121 (Bioreg 2 (normal))

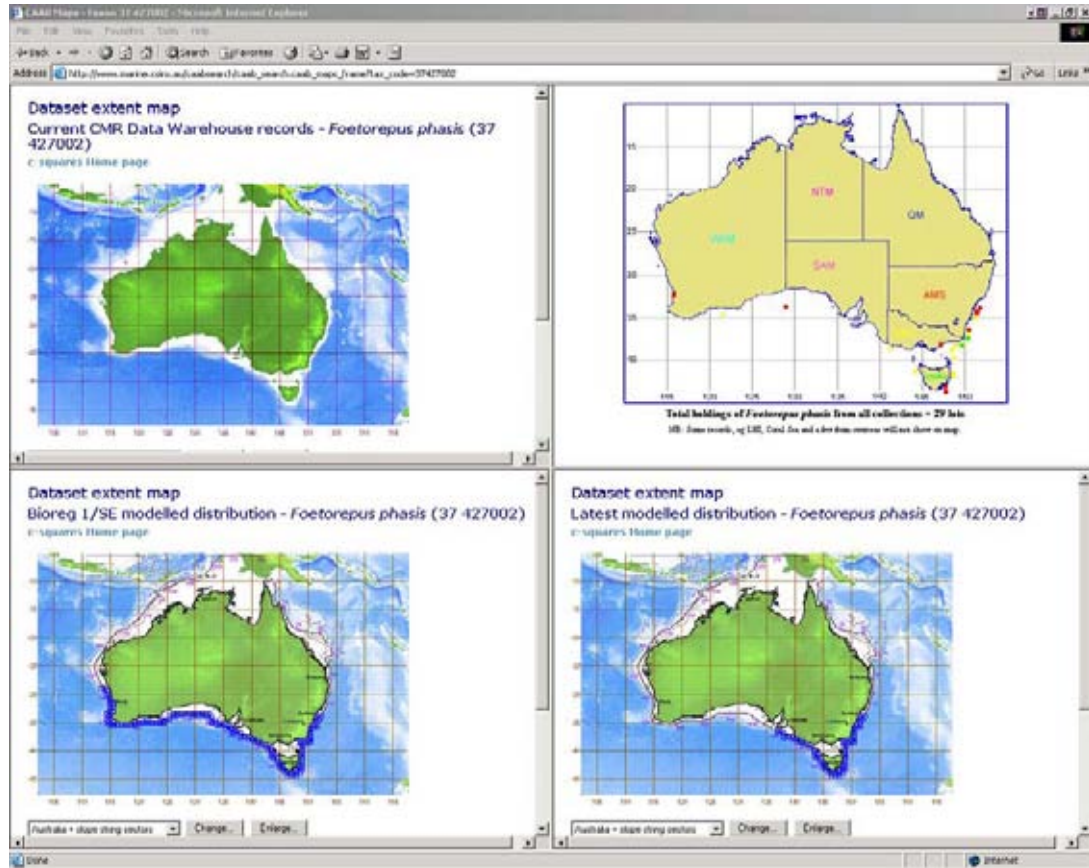
Depth range: 126 m (Bioreg 2 data) - 437 m (Bioreg 2 data)

Please note, current modelled distribution is for test purposes only and may contain erroneous or incomplete values. This map should not be used as an authoritative record of the actual distribution of this taxon.

Dataset extent map produced by CMR [c-squares mapper](#)

Appendix 11. Screen image of the 'multiple maps' display

Full screen image of the 'multiple maps' display. This web page allowed taxonomic specialists to easily compare the four maps discussed in Appendices 7–10.



Appendix 12. Taxonomic specialists who participated in the Hobart workshop

Taxonomic specialists who participated in the Hobart workshop, held at CSIRO Marine Research from October 28 to November 11, 2002.

CSIRO Marine Research

Peter Last

Gordon Yearsley

Tony Rees

Alan Williams

Daniel Gledhill

Alastair Graham

Spikey Riddoch

Museum Victoria

Martin Gomon

Dianne Bray

Australian Museum

Mark McGrouther

New South Wales Fisheries Research Institute

Ken Graham

Queensland Museum

Jeff Johnson

Museum and Art Gallery of the Northern Territory

Barry Russell

Appendix 13. Most informative genera that increased in number of species

Most informative genera (ie, those with a Biogeographic Information Index (BII) of less than 30) that increased in number of species based on expert examinations. Species in bold were added to the list based on recalculated BII's at the end of the project.

Genus	Initial # of species	Final # of species*	% change in species number
<i>Scorpaena</i>	12	24	100.0
<i>Antigonia</i>	5	13	160.0
<i>Caelorinchus</i>	15	35	133.3
<i>Thamnaconus</i>	5	6	20.0
<i>Coryphaenoides</i>	9	10	11.1
<i>Centrophorus</i>	5	7	40.0
<i>Euclichthys</i>	1	4	300.0
<i>Notoraja</i>	4	6	50.0
<i>Hydrolagus</i>	4	6	50.0
<i>Haliutaea</i>	4	14	250.0
<i>Paraulopus</i>	2	7	250.0
" <i>Foetorepus</i> "	12	13	8.3
<i>Physiculus</i>	5	9	80.0
<i>Arnoglossus</i>	12	14	16.7
<i>Malthopsis</i>	2	13	550.0
<i>Dicrolene</i>	2	7	250.0
<i>Pseudorhombus</i>	10	14	40.0
" <i>Callionymus</i> "	19	28	47.4
<i>Parapercis</i>	22	31	40.9
<i>Nezumia</i>	7	9	28.6
<i>Cataetyx</i>	2	6	200.0
<i>Setarches</i>	2	10	400.0
<i>Hoplostethus</i>	7	8	14.3
<i>Monomitopus</i>	3	8	166.7
<i>Dasyatis</i>	7	9	28.6
<i>Chaunax</i>	3	9	200.0
<i>Ventrifossa</i>	5	6	20.0
<i>Dibranchius</i>	2	6	200.0
<i>Neomerinthe</i>	2	4	100.0
<i>Lepidoperca</i>	6	7	16.7
<i>Pterygotrigla</i>	4	11	175.0
<i>Haliutopsis</i>	2	6	200.0
<i>Epigonus</i>	5	6	20.0
<i>Satyrichthys</i>	5	10	100.0
<i>Psenopsis</i>	3	5	66.7
<i>Centroberyx</i>	4	5	25.0
<i>Helicolenus</i>	2	4	100.0

<i>Bembrops</i>	3	9	200.0
<i>Hoplichthys</i>	5	6	20.0
<i>Parapterygotrigla</i>	2	4	100.0
<i>Malakichthys</i>	2	5	150.0
<i>Lepidion</i>	3	4	33.3
<i>Solegnathus</i>	5	6	20.0
<i>Branchiostegus</i>	6	7	16.7
<i>Benthodesmus</i>	3	4	33.3
<i>Neobythites</i>	3	11	266.7
<i>Sirembo</i>	3	9	200.0
<i>Poecilopsetta</i>	3	5	66.7
<i>Trachonurus</i>	3	4	33.3
<i>Bembras</i>	1	3	200.0
<i>Pristipomoides</i>	7	8	14.3

*Where an original genus was split due to nomenclatural issues, this column occasionally includes representatives of closely related genera

Appendix 14. Summary of NORFANZ voyage

Summary of NORFANZ voyage taken from 'Voyage Report of a Biodiversity Survey of Seamounts and Slopes of the Norfolk Ridge and Lord Howe Rise (NORFANZ), May-June 2003' by Clark, M, Roberts, C, Williams, A, & Last, P.

NORFANZ VOYAGE SUMMARY (May–June, 2003)

(Extracted from Voyage Report)

A survey of the biodiversity of fishes and benthic invertebrates was carried out on the Lord Howe Rise and Norfolk Ridge in May-June 2003. The “NORFANZ” programme has principal objectives to survey, sample and document the biodiversity from seamounts and slopes on the Norfolk Ridge and Lord Howe Rise, to support biosystematics research projects, to assess the faunal uniqueness and conservation value, and to relate observed distribution patterns with measured biological and physical parameters.

An international team of scientists was involved in the 4-week long survey on the NIWA research vessel *Tangaroa*. Fourteen seamount and slope sites were sampled, 10 on the Norfolk ridge, and 4 on the Lord Howe Rise. A total of 168 stations were completed consisting of 144 trawl-sled-dredge shots, 15 casts to measure oceanographic conditions, and 9 camera drops to photograph fauna on the seafloor. Trawl depths ranged from less than 100 m to over 2000 m. A mixture of gear was used, including bottom trawls, a midwater trawl, beam trawl, epibenthic sleds, rock and pipe dredges.

Over 500 fish species, and 1300 macro-invertebrate species, were provisionally identified on board. This is regarded as a minimum estimate of biodiversity, as sampling intensity on individual seamounts was not sufficient to measure the complete faunal composition. About 20% of the fish species are likely to be either new records for the region, or new to science. It may take researchers around the world several years to examine fully the material, especially the invertebrates, and describe the unknown species.

There were a number of special features of the survey that contributed to its success. There was a very high level of collaboration and cooperation between the New Zealand and Australian funding agencies, and all the scientific institutes and museums. The team of international scientists covered a wide range of skills and experience, and this enabled a lot to be achieved during the survey. The variety of gear types deployed during the survey were able to sample different components of the fauna, and will contribute to a better understanding of the structure of the benthic community. The multibeam system used by *Tangaroa* enabled bathymetry and bottom type to be rapidly assessed, and was a valuable aid to planning the trawling. Photographs were taken of every species caught, and used as a reference guide throughout the survey to ensure accuracy and consistency of identifications. Overall, there were very strong and productive synergies developed between scientists from various disciplines, and this was coupled with the experience of the officers and crew, to produce an excellent survey result.

Appendix 15. Preliminary list of Australian fish genera on the continental shelf and slope

Preliminary list of Australian fish genera occurring on the continental shelf and slope as recorded in the generic database, with contributors and external specialists assigned. Genera highlighted in pink are unlikely to occur on the slope. Preliminary, literature-based depth ranges of members of each genus demarcated by upper and lower limits in either 'coast', 'shelf' or 'slope' columns; 'X' designates likely presence.

Family	Genus	No. species	Depth Distribution				Custodian	Project Collaborators	Potential External Collaborators
			Coast	Shelf	Slope	Pelagic			
Myxinidae	<i>Eptatretus</i>	2		X	X		Gledhill	Mok	
Hexanchidae	<i>Heptranchias</i>	1		100	400		Gledhill	Last	Compagno
	<i>Hexanchus</i>	2		100	1200		Gledhill	Last	Compagno
	<i>Notorynchus</i>	1	3	136			Gledhill	Last	Compagno
Chlamydoselachidae	<i>Chlamydoselachus</i>	1		120	1280		Gledhill	Last	Compagno
Heterodontidae	<i>Heterodontus</i>	3	3	X	275		Gledhill	Last	Compagno
Odontaspidae	<i>Carcharias</i>	1	3	190			Gledhill	Last	Compagno
	<i>Odontaspis</i>	1		X	420		Gledhill	Last	Compagno
Mitsukurinidae	<i>Mitsukurina</i>	1		X	1200		Gledhill	Last	Compagno
Parascyllidae	<i>Parascyllium</i>	5	3	X	435		Last		Compagno
Scyliorhinidae	<i>Apristurus</i>	8			590-1500		Last		Compagno
	<i>Asymbolus</i>	8	X	40	400		Last		Compagno
	<i>Atelomycterus</i>	2	27	122			Last		Compagno
	<i>Aulohaelurus</i>	1	X	X			Last		Compagno
	<i>Cephaloscyllium</i>	7	X	X	700		Last		Compagno
	<i>Galeus</i>	3		150	640		Last		Compagno
	<i>Halaaelurus</i>	2		110	900		Last		Compagno
	<i>Parmaturus</i>	1			590		Last		Compagno
Pseudotriakidae	<i>Pseudotriakis</i>	1					Gledhill	Last	Compagno
Triakidae	<i>Furgaleus</i>	1	X	X	220		Gledhill	Last	Compagno
	<i>Galeorhinus</i>	1	X	X	550		Gledhill	Last	Compagno
	<i>Hemitriakis</i>	2		145	400		Gledhill	Last	Compagno
	<i>Hypogaleus</i>	1		40	X	230	Gledhill	Last	Compagno
	<i>Iago</i>	1			250-475		Gledhill	Last	Compagno
	<i>Mustelus</i>	3	3	X	400		Last		Compagno
Carcharhinidae	<i>Rhizoprionodon</i>	3		X	200		Gledhill	Last	Compagno
	<i>Scoliodon</i>	1					Gledhill	Last	Compagno

Family	Genus	Sp	Distribution				Custodian	Project Collaborators	Potential External Collaborators
			Coast	Shelf	Slope	Pelagic			
Squalidae	<i>Triaenodon</i>	1	8	X	300		Gledhill	Last	Compagno
	<i>Centrophorus</i>	5		100	2400		Last		Compagno
	<i>Centroscyllium</i>	1			730-1200		Last		Compagno
	<i>Centroscymnus</i>	4			240-1550		Last		Compagno
	<i>Cirrhigaleus</i>	1		146	640		Gledhill	Last	Compagno
	<i>Dalatias</i>	1		40	1800		Gledhill	Last	Compagno
	<i>Deania</i>	2		70	1450		Gledhill	Last	Compagno
	<i>Etmopterus</i>	11			250-1380		Last		Compagno
	<i>Euprotomicrus</i>	1				X	Gledhill	Last	Compagno
	<i>Isistius</i>	1				X	Gledhill	Last	Compagno
	<i>Scymnodalatias</i>	1				X	Gledhill	Last	Compagno
	<i>Somniosus</i>	1				X	Gledhill	Last	Compagno
	<i>Squaliolus</i>	1				X	Gledhill	Last	Compagno
	<i>Squalus</i>	9	X	X	600		Last		Compagno
	<i>Zameus</i>	1			550-2000		Last		Compagno
Oxynotidae	<i>Oxynotus</i>	1	45	X	650		Gledhill	Last	Compagno
Echinorhinidae	<i>Echinorhinus</i>	2		11	900		Gledhill	Last	Compagno
Pristiophoridae	<i>Pristiophorus</i>	5		40	630		Yearsley	Last	Compagno
Squatinae	<i>Squatina</i>	5		X	315		Last	Yearsley	Compagno
Torpedinidae	<i>Torpedo</i>	2			400-750		Yearsley	Last	Compagno
Hypnidae	<i>Hypnos</i>	1	2	X	220		Yearsley	Last	Compagno
Narcinidae	<i>Narcine</i>	5	10	X	640		Yearsley	Last	Compagno
Rajidae	<i>Bathyraja</i>	1			2300		Last		Compagno
	<i>Irolita</i>	2		50-200			Gledhill	Last	Compagno
	<i>Notoraja</i>	4			400-1120		Last		Compagno
	<i>Pavoraja</i>	8	30	X	1200		Last		Compagno
	<i>Raja</i>	23	3	X	1500		Last	Yearsley	Compagno
Anacanthobatidae	<i>Anacanthobatis</i>	2			420-1120		Last		Compagno
Dasyatididae	<i>Dasyatis</i>	7	12	X	360	X	Last	Yearsley	Compagno
	<i>Taeniura</i>	2			X		Last	Yearsley	Compagno
Hexatrygonidae	<i>Hexatrygon</i>	1			900-1120		Last	Yearsley	Compagno
Urolophidae	<i>Plesiobatis</i>	1			350-680		Last	Yearsley	Compagno

Family	Genus	Sp	Distribution				Custodian	Project	Potential External
			Coast	Shelf	Slope	Pelagic			
	<i>Trygonoptera</i>	6	2	200			Yearsley	Last	Compagno
	<i>Urolophus</i>	16	2	X	420		Yearsley	Last	Compagno
Chimaeridae	<i>Chimaera</i>	5			300-1300		Last		Didier
	<i>Hydrolagus</i>	4		120	1400		Last		Didier
Rhinochimaeridae	<i>Harriotta</i>	2			350-1700		Last		Didier
	<i>Rhinochimaera</i>	2			760-1200		Last		Didier
Muraenesocidae	<i>Oxyconger</i>	1		X	X		Yearsley	Last/Gledhill	
Nettastomatidae	<i>Hoplunnis</i>	1			312		Yearsley	DG / PL / JJ / SR	
	<i>Nettastoma</i>	2			500-940		Yearsley	DG / PL / JJ / SR	
	<i>Nettenchelys</i>	1					Yearsley	DG / PL / JJ / SR	
	<i>Saurenchelys</i>	2			X		Yearsley	DG / PL / JJ / SR	
	<i>Venefica</i>	1			1254		Yearsley	DG / PL / JJ / SR	
Congridae	<i>Ariosoma</i>	3	X	X			Yearsley	DG / PL / JJ / SR	
	<i>Bassanago</i>	2			870		Yearsley	DG / PL / JJ / SR	Smith
	<i>Bathycongrus</i>	2					Yearsley	DG / PL / JJ / SR	Smith
	<i>Bathyuroconger</i>	1			854-1139		Yearsley	DG / PL / JJ / SR	Smith
	<i>Blachea</i>	1			300-312		Yearsley	DG / PL / JJ / SR	Smith
	<i>Conger</i>	3	X	X			Yearsley	DG / PL / JJ / SR	
	<i>Diploconger</i>	1		X			Yearsley	DG / PL / JJ / SR	
	<i>Gavialiceps</i>	1					Yearsley	DG / PL / JJ / SR	Smith
	<i>Gnathophis</i>	3		X	X		Yearsley	DG / PL / JJ / SR	Smith
	<i>Heteroconger</i>	1	X				Yearsley	DG / PL / JJ / SR	
	<i>Lumiconger</i>	1		X			Yearsley	DG / PL / JJ / SR	
	<i>Macrocephenchelys</i>	1					Yearsley	DG / PL / JJ / SR	Smith
	<i>Parabathymyrus</i>	1					Yearsley	DG / PL / JJ / SR	Smith
	<i>Poeciloconger</i>	1					Yearsley	DG / PL / JJ / SR	Smith
	<i>Rhynchoconger</i>	1		X	X		Yearsley	DG / PL / JJ / SR	Smith
	<i>Scalanago</i>	1		X			Yearsley	DG / PL / JJ / SR	
	<i>Uroconger</i>	1		X			Yearsley	DG / PL / JJ / SR	Smith
Colocongridae	<i>Coloconger</i>	1			?-892		Yearsley	DG / PL / JJ / SR	Smith
Ophichthidae	<i>Scolenchelys</i>	11	X	X	X		Yearsley	DG / PL / JJ / SR	McCosker
Synaphobranchidae	<i>Diastranchus</i>	1			X		Riddoch		Smith

Family	Genus	Sp	Distribution				Custodian	Project Collaborators	Potential External Collaborators
			Coast	Shelf	Slope	Pelagic			
Halosauridae	<i>Histiobranchus</i>	2			X		Riddoch	Smith	
	<i>Ilyophis</i>	1			X		Riddoch	Smith	
	<i>Simenchelys</i>	1			X		Riddoch	Smith	
	<i>Synaphobranchus</i>	3			X		Riddoch	Smith	
	<i>Aldrovandia</i>	1			X		Last	Riddoch	
	<i>Halosauropsis</i>	1			X		Last	Riddoch	
	<i>Halosaurus</i>	2			X		Last	Riddoch	
Lipogenyidae	<i>Lipogenys</i>	1			X		Last	Riddoch	
Notacanthidae	<i>Notacanthus</i>	2			X		Last	Riddoch	
Argentinidae	<i>Argentina</i>	1		X			Yearsley	Williams	
	<i>Glossanodon</i>	1			X		Yearsley	Williams	
	<i>Microstoma</i>	1				X	Yearsley	Williams	
	<i>Nansenia</i>	1			X		Yearsley	Williams	
Bathylagidae	<i>Bathylagichthys</i>	2				X	Yearsley	Williams	
	<i>Bathylagoides</i>	1				X	Yearsley	Williams	
	<i>Bathylagus</i>	1				X	Yearsley	Williams	
	<i>Lipolagus</i>	1				X	Yearsley	Williams	
	<i>Melanolagus</i>	1				X	Yearsley	Williams	
Alepocephalidae	<i>Alepocephalus</i>	3			X		Williams	Yearsley	
	<i>Asquamiceps</i>	1			X		Williams	Yearsley	
	<i>Bajacalifornia</i>	1			880		Williams	Yearsley	
	<i>Bathytroctes</i>	1			913-1139		Williams	Yearsley	
	<i>Conocara</i>	1			913-1139		Williams	Yearsley	
	<i>Ericara</i>	1			X		Williams	Yearsley	
	<i>Herwigia</i>	1			X		Williams	Yearsley	
	<i>Leptoderma</i>	3			913-1280		Williams	Yearsley	
	<i>Narctetes</i>	1			913-1258		Williams	Yearsley	
		<i>Photostylus</i>	1				X	Williams	Yearsley
	<i>Rouleina</i>	2			X		Williams	Yearsley	
	<i>Talismania</i>	3			X		Williams	Yearsley	
	<i>Xenodermichthys</i>	1				X	Williams	Yearsley	
Leptoichthyidae	<i>Leptoichthys</i>	1			1139-1158		Williams	Yearsley	

Family	Genus	Sp	Distribution				Custodian	Project Collaborators	Potential External Collaborators
			Coast	Shelf	Slope	Pelagic			
Platyroctidae	<i>Holtbyrnia</i>	1				X	Gomon		
	<i>Maulisia</i>	2				X	Gomon		
	<i>Perspasia</i>	1				X	Gomon		
	<i>Platyroctes</i>	1				X	Gomon		
Aulopodidae	<i>Aulopus</i>	3	X	X	210		Yearsley		
Synodontidae	<i>Bathysaurus</i>	1			945-1104		Russell	Last	
	<i>Saurida</i>	11	X	X	320		Russell	Last	
Chlorophthalmidae	<i>Bathysauropsis</i>	1			X		Gomon	Sato	
	<i>Chlorophthalmus</i>	6			X		Gomon	Sato	
Paraulopidae	<i>Paraulopus</i>	?		X	X		Gomon	Sato	
Neoscopelidae	<i>Neoscopelus</i>	3				X	Gomon		
Bathypteroidae	<i>Bathypterois</i>	3			X		Gomon		
Ipnopidae	<i>Ipnops</i>	1			X		Gomon		
Ateleopodidae	<i>Atelopus</i>	1			457-684		Yearsley		
Lophidae	<i>Lophiodes</i>	3		180	780		Last	Caruso	
	<i>Lophiomus</i>	1		70	612		Last	Caruso	
	<i>Sladenia</i>	1			1150		Last	Caruso	
Antennariidae	<i>Allenichthys</i>	1		X	X		Last	Pietsch	
Chaunacidae	<i>Bathychaunax</i>	1			890-1500		Last	Caruso	
	<i>Chaunax</i>	3		X	1060		Last	Caruso	
Ogcocephalidae	<i>Coelophrys</i>	1			1000-1140		Last		
	<i>Dibranchus</i>	2			300		Last		
	<i>Halleutaea</i>	4		X	435-1115		Last		
	<i>Halleutopsis</i>	2			940		Last		
	<i>Malthopsis</i>	2			X		Last		
Moridae	<i>Antimora</i>	1			350-3000		Gomon	Last	Paulin
	<i>Austrophycis</i>	2			X		Gomon	Last	Paulin
	<i>Eeyorius</i>	1	X				Gomon	Last	Paulin
	<i>Euclichthys</i>	1			306-571		Gomon	Last	Paulin
	<i>Gadella</i>	1					Gomon	Last	Paulin
	<i>Halargyreus</i>	1			700-1400		Gomon	Last	Paulin
	<i>Laemonema</i>	2			980		Gomon	Last	Paulin

Family	Genus	Sp	Distribution				Custodian	Project	Potential External
			Coast	Shelf	Slope	Pelagic			
	<i>Lepidion</i>	3			785-945		Gomon	Last	Paulin
	<i>Lotella</i>	3	X				Gomon	Last	Paulin
	<i>Mora</i>	1			500-990		Gomon	Last	Paulin
	<i>Physiculus</i>	5		X	500		Gomon	Last	Paulin
	<i>Pseudophycis</i>	3	X	X	X		Gomon	Last	Paulin
	<i>Tripterophycis</i>	1		X	770		Gomon	Last	Paulin
Phycidae	<i>Gaidropsarus</i>	1		X	X		Gomon	Last	Paulin
Bregmacerotidae	<i>Bregmaceros</i>	6				X	Gomon	Last	Gill?
	<i>Micromesistius</i>	1		70	800	X	Gomon	Last	
Merlucciidae	<i>Lyconus</i>	1			X		Yearsley		Iwamoto
	<i>Macruronus</i>	1			450-825		Yearsley		Iwamoto
	<i>Merluccius</i>	4		60	800		Yearsley		Iwamoto
Aphyonidae	<i>Aphyonus</i>	1			X		Last	Gomon	Nielson
	<i>Barathronus</i>	1			X		Last	Gomon	Nielson
Bythitidae	<i>Beaglichthys</i>	1					Last	Gomon	Nielson
	<i>Brosmolus</i>	1					Last	Gomon	Nielson
	<i>Brosmophyciops</i>	1	X				Last	Gomon	Nielson
	<i>Cataetyx</i>	2			X		Last	Gomon	Nielson
	<i>Dermatopsis</i>	2	X				Last	Gomon	Nielson
	<i>Diancistrus</i>	1	X				Last	Gomon	Nielson
	<i>Dinematichthys</i>	3	X				Last	Gomon	Nielson
	<i>Diplacanthopoma</i>	1		X	868		Last	Gomon	Nielson
	<i>Dipulus</i>	1	X				Last	Gomon	Nielson
	<i>Melodichthys</i>	1					Last	Gomon	Nielson
	<i>Monothrix</i>	2	X				Last	Gomon	Nielson
	<i>Ogilbia</i>	1	X				Last	Gomon	Nielson
Ophidiidae	<i>Saccogaster</i>	1		X	X		Last	Gomon	Nielson
	<i>Bassozetus</i>	1			1460-1500		Last	Gomon	Nielson
	<i>Brotula</i>	1		X			Last	Gomon	Nielson
	<i>Brotulotaenia</i>	2				X	Last	Gomon	Nielson
	<i>Dannevigia</i>	1			200-390		Last	Gomon	Nielson
	<i>Dicrolene</i>	2			435-1160		Last	Gomon	Nielson

Family	Genus	Sp	Distribution				Custodian	Project Collaborators	Potential External Collaborators
			Coast	Shelf	Slope	Pelagic			
	<i>Epetriodus</i>	1			714-892		Last	Gomon	Nielson
	<i>Eretmichthys</i>	1			1460-1500		Last	Gomon	Nielson
	<i>Genypterus</i>	2	X	X	1000		Last	Gomon	Nielson
	<i>Glyptophtidium</i>	2			480		Last	Gomon	Nielson
	<i>Homostolus</i>	1			610		Last	Gomon	Nielson
	<i>Hoplobrotula</i>	1			320-440		Last	Gomon	Nielson
	<i>Hypopleuron</i>	1			X		Last	Gomon	Nielson
	<i>Lamprogrammus</i>	1				X	Last	Gomon	Nielson
	<i>Monomitopus</i>	3			870-1260		Last	Gomon	Nielson
	<i>Neobythites</i>	3			X		Last	Gomon	Nielson
	<i>Ophidion</i>	1			X		Last	Gomon	Nielson
	<i>Porogadus</i>	1			1100		Last	Gomon	Nielson
	<i>Pycnocraspedum</i>	1			X		Last	Gomon	Nielson
	<i>Sirembo</i>	3		X	X		Last	Gomon	Nielson
	<i>Spottobrotula</i>	1		X	X		Last	Gomon	Nielson
	<i>Xyelacyba</i>	1			1160		Last	Gomon	Nielson
Parabrotulidae	<i>Parabrotula</i>	1				X	Last	Gomon	Nielson
Carapidae	<i>Carapus</i>	3	X	X			Riddoch	Gomon	Olney/Markle
	<i>Echiodon</i>	2	X	X	X		Gomon	Riddoch	Olney/Markle
	<i>Encheliophis</i>	5	X	X			Gomon	Riddoch	Olney/Markle
	<i>Euryleuron</i>	1	X	X	X		Gomon	Riddoch	Olney/Markle
	<i>Onuxodon</i>	3	X				Gomon	Riddoch	Olney/Markle
	<i>Pyramodon</i>	3		X	510		Gomon	Riddoch	Olney/Markle
Zoarcidae	<i>Melanostigma</i>	1				X	Gomon		Anderson
Macrouridae	<i>Asthenomacrus</i>	1			X		Williams	Graham	Iwamoto
	<i>Bathygadus</i>	1			X		Williams	Graham	Iwamoto
	<i>Caelorinchus</i>	15		X	X		Williams	Graham	Iwamoto
	<i>Cetonurichthys</i>	1			X		Williams	Graham	Iwamoto
	<i>Cetonurus</i>	1			X		Williams	Graham	Iwamoto
	<i>Coryphaenoides</i>	9			X		Williams	Graham	Iwamoto
	<i>Cyanomacrus</i>	1			X		Williams	Graham	Iwamoto
	<i>Gadomus</i>	2			X		Williams	Graham	Iwamoto

Family	Genus	Sp	Distribution				Custodian	Project	Potential External
			Coast	Shelf	Slope	Pelagic			
	<i>Haplomacrourus</i>	1			X		Williams	Graham	Iwamoto
	<i>Hymenocephalus</i>	4			X		Williams	Graham	Iwamoto
	<i>Hyomacrourus</i>	1			X		Williams	Graham	Iwamoto
	<i>Idiolorhynchus</i>	1			X		Williams	Graham	Iwamoto
	<i>Kuronezumia</i>	2			X		Williams	Graham	Iwamoto
	<i>Lepidorhynchus</i>	1			X		Williams	Graham	Iwamoto
	<i>Lucigadus</i>	1			X		Williams	Graham	Iwamoto
	<i>Macrouroides</i>	1			X		Williams	Graham	Iwamoto
	<i>Macrourus</i>	1			X		Williams	Graham	Iwamoto
	<i>Malacocephalus</i>	1			X		Williams	Graham	Iwamoto
	<i>Mataeocephalus</i>	1			X		Williams	Graham	Iwamoto
	<i>Mesobius</i>	2			X		Williams	Graham	Iwamoto
	<i>Nezumia</i>	7			X		Williams	Graham	Iwamoto
	<i>Odontomacrus</i>	1			X		Williams	Graham	Iwamoto
	<i>Pseudonezumia</i>	1			X		Williams	Graham	Iwamoto
	<i>Sphagemacrus</i>	1			X		Williams	Graham	Iwamoto
	<i>Squalogadus</i>	1			X		Williams	Graham	Iwamoto
	<i>Trachonurus</i>	3			X		Williams	Graham	Iwamoto
	<i>Trachyrinchus</i>	1			X		Williams	Graham	Iwamoto
	<i>Ventrifossa</i>	5			X		Williams	Graham	Iwamoto
Polymixiidae	<i>Polymixia</i>	2				300-510	Gomon	Johnson	
Trachichthyidae	<i>Aulotrachichthys</i>	2	X	X	X		Gomon		
	<i>Gephyroberyx</i>	1				275-490	Gomon		
	<i>Hoplostethus</i>	7				320-870	Gomon		
	<i>Optivus</i>	3	X	X			Gomon		
	<i>Paratrachichthys</i>	1	X	X			Gomon		
	<i>Sorosichthys</i>	1	X	X			Gomon		
	<i>Trachichthys</i>	1	X	X			Gomon		
Berycidae	<i>Beryx</i>	2				200-670	Yearsley		
	<i>Centroberyx</i>	4		X		380	Yearsley		
Holocentridae	<i>Ostichthys</i>	2		X		225	Johnson		
	<i>Pristilepis</i>	1		X		X	Johnson		

Family	Genus	Sp	Distribution			Custodian	Project Collaborators	Potential External Collaborators
			Coast	Shelf	Slope			
Parazenidae	<i>Parazen</i>	1			300-480	Bray		
	<i>Macrurocyttus</i>	1				Bray		
Zeniontidae	<i>Zenion</i>	2		X	735	Bray		
Zeidae	<i>Cyttomimus</i>	1			X	Bray		
	<i>Cyttopsis</i>	2		X	615	Bray		
	<i>Cyttus</i>	3	X	X	1000	Bray		
	<i>Zenopsis</i>	2		X	X	Bray		
	<i>Zeus</i>	1	X	X	230	Bray		
Oreosomatidae	<i>Allocyttus</i>	2			X	Yearsley		McDowall
	<i>Neocyttus</i>	2			X	Yearsley		McDowall
	<i>Oreosoma</i>	1			X	Yearsley		McDowall
	<i>Pseudocyttus</i>	1			X	Yearsley		McDowall
Caproidae	<i>Antigonia</i>	5		X	435	Yearsley		Santini/Tyler
Veliferidae	<i>Metavelifer</i>	a		X	X	Yearsley		
	<i>Velifer</i>	2		X	210	Yearsley		
Macroramphosidae	<i>Centriscoops</i>	2		X	675	Gomon		Duhmel
	<i>Macroramphosus</i>	4		X	300	Gomon		Duhmel
	<i>Notopogon</i>	3		X	710	Gomon		Duhmel
Syngnathidae	<i>Solegnathus</i>	5		X	X	Last		Kuiter
Scorpaenidae	<i>Ablabys</i>	1	X			Last	MG / GY / JJ	
	<i>Apistops</i>	1	X			Last	MG / GY / JJ	
	<i>Apistus</i>	1				Last	MG / GY / JJ	
	<i>Brachypterioides</i>	1				Last	MG / GY / JJ	
	<i>Centropogon</i>	2	X			Last	MG / GY / JJ	
	<i>Cheroscorpaena</i>	1	X			Last	MG / GY / JJ	
	<i>Cottapistus</i>	3	X			Last	MG / GY / JJ	
	<i>Dampierosa</i>	1	X			Last	MG / GY / JJ	
	<i>Dendrochirus</i>	3	X			Last	MG / GY / JJ	
	<i>Ectreposebastes</i>	1			X	Last	MG / GY / JJ	Eschmeyer
	<i>Erosa</i>	1	X			Last	MG / GY / JJ	
	<i>Glyptauchen</i>	2	X			Last	MG / GY / JJ	
	<i>Gymnapistes</i>	1	X			Last	MG / GY / JJ	

Family	Genus	Sp	Distribution				Custodian	Project	Potential External
			Coast	Shelf	Slope	Pelagic			
	<i>Helicolenus</i>	2	X	X	770		Last	MG / GY / JJ	Eschmeyer
	<i>Hypodytes</i>	1	X				Last	MG / GY / JJ	
	<i>Inimicus</i>	3	X				Last	MG / GY / JJ	
	<i>Lioscorpius</i>	1		X			Last	MG / GY / JJ	
	<i>Maxilllicosta</i>	3	X				Last	MG / GY / JJ	
	<i>Minous</i>	3	X	X			Last	MG / GY / JJ	
	<i>Neocentropogon</i>	2		X			Last	MG / GY / JJ	
	<i>Neomerinthe</i>	2		X	440		Last	MG / GY / JJ	Eschmeyer
	<i>Neosebastes</i>	7	X	X	225		Last	MG / GY / JJ	Eschmeyer
	<i>Notesthes</i>	1	X				Last	MG / GY / JJ	
	<i>Ocosia</i>	1					Last	MG / GY / JJ	
	<i>Paracentropogon</i>	2	X	X			Last	MG / GY / JJ	
	<i>Parascorpaena</i>	3					Last	MG / GY / JJ	
	<i>Pteroidichthys</i>	1	X				Last	MG / GY / JJ	
	<i>Pterois</i>	5	X	X			Last	MG / GY / JJ	
	<i>Rhinopias</i>	1	X				Last	MG / GY / JJ	
	<i>Richardsonichthys</i>	1	X				Last	MG / GY / JJ	
	<i>Scorpaena</i>	12	X	X			Last	MG / GY / JJ	
	<i>Scorpaenodes</i>	10	X	X			Last	MG / GY / JJ	
	<i>Scorpaenopsis</i>	8	X	X			Last	MG / GY / JJ	
	<i>Sebastapistes</i>	3					Last	MG / GY / JJ	
	<i>Setarches</i>	2		X	650		Last	MG / GY / JJ	Eschmeyer
	<i>Synanceia</i>	2	X				Last	MG / GY / JJ	
	<i>Taenianotus</i>	1					Last	MG / GY / JJ	
	<i>Tetraroge</i>	1					Last	MG / GY / JJ	
	<i>Trachyscorpia</i>	2			880		Last	MG / GY / JJ	Eschmeyer
Triglidae	<i>Chelidonichthys</i>	2	X	X			Last	Gomon	
	<i>Gargariscus</i>	1		X	X		Last	Gomon	Richards
	<i>Heminodus</i>	1			300-500		Last	Gomon	Richards
	<i>Lepidotrigla</i>	19	X	X	350		Gomon		Richards
	<i>Parapterygotrigla</i>	2		X	300		Last	Gomon	Richards
	<i>Peristedion</i>	1		X	470		Last	Gomon	Richards

Family	Genus	Sp	Distribution				Custodian	Project	Potential External
			Coast	Shelf	Slope	Pelagic			
Platycephalidae	<i>Pterygotrigla</i>	4	X	X	400		Last	Gomon	Richards
	<i>Satyrichthys</i>	5		X	715		Last	Gomon	Richards
	<i>Bembras</i>	1		X	300		Gomon		Richards
	<i>Cociella</i>	1					Gomon		
	<i>Cymbacephalus</i>	1	X	X			Gomon		Knapp
	<i>Elates</i>	1		X	220		Gomon		Knapp
	<i>Inegocia</i>	2		X			Gomon		Knapp
	<i>Leviprora</i>	1	X				Gomon		Knapp
	<i>Neoplatycephalus</i>	3		X	440		Gomon		Knapp
	<i>Onigocia</i>	3	X	X			Gomon		Knapp
	<i>Papilloculiceps</i>	2					Gomon		Knapp
	<i>Platycephalus</i>	11	X	X			Gomon		Knapp
	<i>Ratabulus</i>	1		X	210		Gomon		Knapp
	<i>Rogadius</i>	3	X	X			Gomon		Knapp
<i>Sorsogona</i>	1	X	X			Gomon		Knapp	
<i>Suggrundus</i>	6	X	X			Gomon		Knapp	
<i>Thysanophrys</i>	6	X	X			Gomon		Knapp	
Hoplichthyidae	<i>Hoplichthys</i>	5		X	1060		Gomon	McGrouther	
Cottidae	<i>Antipodocottus</i>	2			X		Yearsley		Nelson
Ereuniidae	<i>Ereunias</i>	1			565-760		Williams	Last	Awami
Psychrolutidae	<i>Ebinania</i>	1			X		Yearsley	Riddoch	Nelson
	<i>Psychrolutes</i>	3			435-945		Yearsley	Riddoch	Nelson
Cyclopteridae	<i>Paraliparis</i>	1			1030		Yearsley	Riddoch	Stein
Dactylopteridae	<i>Dactyloptena</i>	4	X	X	250		Last		Eschmeyer
Acropomatidae	<i>Acropoma</i>	1		X	320		Yearsley	Last	Matsuura
	<i>Apogonops</i>	1		X	510		Yearsley	Last	Matsuura
	<i>Doederleinia</i>	1		X	400		Yearsley	Last	Matsuura
	<i>Lateolabrax</i>	1	X				Yearsley	Last	Matsuura
	<i>Malakichthys</i>	2			480		Yearsley	Last	Matsuura
	<i>Polyprion</i>	2	X	X	350	X	Yearsley	Last	Matsuura
	<i>Sphyraenops</i>	1				X	Yearsley	Last	Matsuura
	<i>Synagrops</i>	3		X	715		Yearsley	Last	Matsuura

Family	Genus	Sp	Distribution				Custodian	Project Collaborators	Potential External Collaborators
			Coast	Shelf	Slope	Pelagic			
Serranidae	<i>Acanthistius</i>	5	X				Gomon	Johnson	Randall
	<i>Aethaloperca</i>	1	X				Gomon	Johnson	Randall
	<i>Anthias</i>	4	X	X			Gomon	Johnson	Randall
	<i>Anyperodon</i>	1	X				Gomon	Johnson	Randall
	<i>Caesioperca</i>	2	X	X			Gomon	Johnson	Randall
	<i>Caesiocorpis</i>	1	X				Gomon	Johnson	Randall
	<i>Callanthias</i>	2	X	X	270		Gomon	Johnson	Anderson
	<i>Caprodon</i>	2	X	X	375		Gomon	Johnson	Roberts
	<i>Centrogenys</i>	1	X				Gomon	Johnson	Randall
	<i>Cephalopholis</i>	11	X	X			Gomon	Johnson	Randall
	<i>Chelidoperca</i>	4		X			Gomon	Last / Johnson	Randall
	<i>Cromileptes</i>	1	X				Gomon	Johnson	Randall
	<i>Epinephelides</i>	1	X				Gomon	Johnson	Randall
	<i>Epinephelus</i>	46	X	X	330		Gomon	Johnson	Heemstra?
	<i>Gracila</i>	1	X				Gomon	Johnson	Randall
	<i>Hypoplectrodes</i>	6	X				Gomon	Johnson	Randall
	<i>Lepidoperca</i>	6		X	225		Gomon	Johnson	Roberts
	<i>Liopropoma</i>	3	X	X	510		Gomon	Johnson	Randall
	<i>Luzonichthys</i>	1	X				Gomon	Johnson	Randall
	<i>Ostracoberyx</i>	2					Gomon	Johnson	Randall
	<i>Othos</i>	1	X				Gomon	Johnson	Randall
	<i>Plectranthias</i>	11	X	X	320		Gomon	Johnson	Roberts
	<i>Plectropomus</i>	5	X	X			Gomon	Johnson	Randall
	<i>Pseudanthias</i>	19	X				Gomon	Johnson	Randall
	<i>Rainfordia</i>	1	X				Gomon	Johnson	Randall
	<i>Saloptia</i>	1					Gomon	Johnson	Randall
	<i>Sayonara</i>	1			156-164		Gomon	Johnson	Randall
	<i>Selenanthias</i>	1			200-204		Gomon	Johnson	
	<i>Serranocirrhitus</i>	1	X				Gomon	Johnson	Randall
	<i>Trachypoma</i>	1	X				Gomon	Johnson	Randall
	<i>Triso</i>	1		X	240		Gomon	Johnson	
	<i>Variola</i>	2	X	X			Gomon	Johnson	Randall

Family	Genus	Sp	Distribution				Custodian	Project Collaborators	Potential External Collaborators
			Coast	Shelf	Slope	Pelagic			
Banjosidae	<i>Banjos</i>	1		130	215		Yearsley	Last	
Priacanthidae	<i>Cookeolus</i>	1		X	300		Yearsley	Last	
	<i>Heteropriacanthus</i>	1		X			Yearsley	Last	
	<i>Priacanthus</i>	6		X	320		Yearsley	Last	
	<i>Pristigenys</i>	1		X	250		Yearsley	Last	
Apogonidae	<i>Epigonus</i>	5			600-980		Gledhill	Last	
Malacanthidae	<i>Branchiostegus</i>	6		X	230		Gledhill	Last	
Emmelichthyidae	<i>Emmelichthys</i>	2	X	X	400		Gledhill		
	<i>Plagiogeneion</i>	2		X	550		Gledhill		
Lutjanidae	<i>Etelis</i>	2		100	350		Russell		Allen
	<i>Lipocheilus</i>	1		X	250		Russell		Allen
	<i>Paracaesio</i>	2	X	X	320		Russell		Allen
	<i>Pinjalo</i>	1		X			Russell		Allen
	<i>Pristipomoides</i>	7		50	350		Russell		Allen
Nemipteridae	<i>Nemipterus</i>	13	3	X	300		Russell		
	<i>Parascloopsis</i>	3	4	X	350		Russell		
Haemulidae	<i>Hapalogenys</i>	1		X	250		Russell		
Lethrinidae	<i>Wattsia</i>	1		100	300		Russell		
Sparidae	<i>Dentex</i>	1	30	X	346		Russell		
Pempheridae	<i>Parapriacanthus</i>	2	X	X	550		Russell		
Chaetodontidae	<i>Chaetodon</i>	34	X	X	250		Russell		Burgess
Pentacerotidae	<i>Evistias</i>	1	15	180			Last	Gledhill	
	<i>Histiopterus</i>	1		X	421		Last	Gledhill	
	<i>Parazanclistius</i>	1	10	200			Last	Gledhill	
	<i>Paristiopterus</i>	2	30	X	260		Last	Gledhill	
	<i>Pentaceroopsis</i>	1	X	X	260		Last	Gledhill	
	<i>Pentaceros</i>	1	37	X	700		Last	Gledhill	
	<i>Pseudopentaceros</i>	1			350-600		Last	Gledhill	
	<i>Zanclistius</i>	1	26	X	540		Last	Gledhill	
Oplegnathidae	<i>Oplegnathus</i>	1		X	380		Last	Gledhill	
Cheilodactylidae	<i>Nemadactylus</i>	3	X	X	400		Last	Gledhill	
Latrididae	<i>Latris</i>	1	X	X	300		Last	Gledhill	Roberts

Family	Genus	Sp	Distribution				Custodian	Project	Potential External
			Coast	Shelf	Slope	Pelagic			
Cepolidae	<i>Cepola</i>	1	X	X	300		Last	Gledhill	
Labridae	<i>Bodianus</i>	14	X	X	220		Gomon		
Pinguipedidae	<i>Parapercis</i>	22	X	X	390		Johnson	Last	
Percophidae	<i>Acanthapritis</i>	2			X		Gomon	Bray	Nelson
	<i>Bembrops</i>	3		X	320		Gomon	Bray	Nelson
	<i>Chrionema</i>	2		X			Gomon	Bray	Nelson
	<i>Enigmapercis</i>	2	X	60			Gomon	Bray	Nelson
	<i>Pteropsaron</i>	1					Gomon	Bray	Nelson
Uranoscopidae	<i>Squamicroedia</i>	1	X				Gomon	Bray	Nelson
	<i>Ichthyoscopus</i>	6	1	130			Gomon		Kishimoto
	<i>Kathetostoma</i>	3	1	X	700		Gomon		Kishimoto
	<i>Pleuroscopus</i>	1			435-900		Gomon		Kishimoto
	<i>Uranoscopus</i>	9	X	X	400		Gomon		Kishimoto
	<i>Xenocephalus</i>	3	10	X	460		Gomon		Kishimoto
Champsodontidae	<i>Champsodon</i>	9		55	612		Gomon		
Callionymidae	<i>Callionymus</i>	19	X	X	X		Yearsley	Johnson	Fricke
	<i>Centrodraco</i>	1			350		Yearsley	Johnson	Fricke
	<i>Dactylopus</i>	1	X	X			Yearsley	Johnson	Fricke
	<i>Diplogrammus</i>	2	X				Yearsley	Johnson	Fricke
	<i>Repomucenus</i>	1	X	X			Yearsley	Johnson	Fricke
	<i>Synchiropus</i>	12	X	X	490		Yearsley	Johnson	Fricke
Scombrobracidae	<i>Scombrobrax</i>	1			854-1293		Yearsley		
Gempylidae	<i>Diplospinus</i>	1				X	Gledhill		Parin
	<i>Gempylus</i>	1				X	Gledhill		Parin
	<i>Lepidocybium</i>	1		X	X		Gledhill		Parin
	<i>Nealotus</i>	1				X	Gledhill		Parin
	<i>Neopinnula</i>	1			200-570		Gledhill		Parin
	<i>Nesiarchus</i>	1			200-1200		Gledhill		Parin
	<i>Paradiplospinus</i>	1			X	X	Gledhill		Parin
	<i>Promethichthys</i>	1		100	750		Gledhill		Parin
	<i>Rexea</i>	4		X	600		Gledhill		Parin / Paxton
	<i>Rexichthys</i>	1			270-470		Gledhill		Parin

Family	Genus	Sp	Distribution				Custodian	Project Collaborators	Potential External Collaborators
			Coast	Shelf	Slope	Pelagic			
	<i>Ruvettus</i>	1		100	470		Gledhill	Parin	
	<i>Thyrsites</i>	1	X	X			Gledhill	Parin	
	<i>Thyrsitoides</i>	1		X	470		Gledhill	Parin	
	<i>Tongaichthys</i>	1			300		Gledhill	Parin	
Trichiuridae	<i>Aphanopus</i>	3			400-1600		Gledhill	Parin	
	<i>Assurger</i>	1		150	400		Gledhill	Parin	
	<i>Benthodesmus</i>	3			200-960		Gledhill	Parin	
	<i>Lepidopus</i>	1		100	600		Gledhill	Parin	
	<i>Lepturacanthus</i>	1	X	100			Gledhill	Parin	
	<i>Tentoriceps</i>	1	30	110			Gledhill	Parin	
	<i>Trichiurus</i>	2		X	350		Gledhill	Parin	
Centrolophidae	<i>Centrolophus</i>	1			X		Last	McDowall	
	<i>Hyperoglyphe</i>	1			380		Last	McDowall	
	<i>Icichthys</i>	1			X		Last	McDowall	
	<i>Psenopsis</i>	3		X	868		Last	McDowall	
	<i>Schedophilus</i>	3		X	X		Last	McDowall	
	<i>Seriolella</i>	3	X	X	X		Last	McDowall	
	<i>Tubbia</i>	1			X		Last	McDowall	
Nomeidae	<i>Nomeus</i>	1			X	X	Last	McDowall	
Ariommatidae	<i>Ariomma</i>	2		X	318		Last	McDowall	
Psettodidae	<i>Psettodes</i>	1		X			Last	Gledhill	
Citharidae	<i>Brachypleura</i>	1		X			Last	Gledhill	
	<i>Citharoides</i>	3		X	435		Last	Gledhill	
	<i>Lepidoblepharon</i>	1			X		Last	Gledhill	
Bothidae	<i>Arnoglossus</i>	12	X	X	X		Last	Gledhill	
	<i>Asterorhombus</i>	2		X	X		Last	Gledhill	
	<i>Bothus</i>	3	X	X			Last	Gledhill	
	<i>Chascanopsetta</i>	1			467		Last	Gledhill	
	<i>Crossorhombus</i>	2		X	X		Last	Gledhill	
	<i>Engyprosopon</i>	6		X	X		Last	Gledhill	
	<i>Grammatobothus</i>	2		X			Last	Gledhill	
	<i>Kamoharia</i>	1		X	X		Last	Gledhill	

Family	Genus	Sp	Distribution				Custodian	Project	Potential External
			Coast	Shelf	Slope	Pelagic			
	<i>Laeops</i>	2		X	X		Last	Gledhill	Hensley
	<i>Lophonectes</i>	1		X	240		Last	Gledhill	Hensley
	<i>Mancopsetta</i>	1			800-1400		Last	Gledhill	Hensley
	<i>Parabothus</i>	1			X		Last	Gledhill	Hensley
	<i>Psettina</i>	3		X	X		Last	Gledhill	Hensley
	<i>Taeniopsetta</i>	1			300		Last	Gledhill	Hensley
Paralichthyidae	<i>Pseudorhombus</i>	10	1	X	300		Last	Gledhill	Munroe
Pleuronectidae	<i>Azygopus</i>	1		150	900		Last	Gledhill	Munroe
	<i>Nematops</i>	2			250-600		Last	Gledhill	Munroe
	<i>Poecilopsetta</i>	3		X	320		Last	Gledhill	Munroe
Samaridae	<i>Samariscus</i>	3	X	X	X		Last	Gledhill	Munroe
Soleidae	<i>Synaptura</i>	3	X	X	X		Last	Gledhill	Munroe
Cynoglossidae	<i>Cynoglossus</i>	9	X	X			Last	Gledhill	Munroe
	<i>Paraplagusia</i>	5	X	X			Last	Gledhill	Munroe
	<i>Symphurus</i>	3		X	X		Last	Gledhill	Munroe
Triacanthidae	<i>Pseudotriacanthus</i>	1		X			Gomon		Santini/Matsuura
	<i>Triacanthus</i>	2		X			Gomon		Santini/Matsuura
	<i>Tripodichthys</i>	3		X			Gomon		Santini/Matsuura
	<i>Trixiphichthys</i>	1		X			Gomon		Santini/Matsuura
Triacanthodidae	<i>Bathypylax</i>	2			X		Gomon		Santini/Matsuura / Paxton
	<i>Halimochirurgus</i>	2		81	447		Gomon		Santini/Matsuura / Paxton
	<i>Macrorhamphosodes</i>	2		80	550		Gomon		Santini/Matsuura / Paxton
	<i>Paratriacanthodes</i>	2			390-550		Gomon		Santini/Matsuura / Paxton
	<i>Triacanthodes</i>	1		190	275		Gomon		Santini/Matsuura / Paxton
	<i>Tydemania</i>	1			420-555		Gomon		Santini/Matsuura / Paxton
Monacanthidae	<i>Eubalichthys</i>	6	X	X	270		Last		Hutchins
	<i>Nelusetta</i>	1	X	X	360		Last		Hutchins
	<i>Thamnaconus</i>	5	X	X	250		Last		Hutchins
Ostraciidae	<i>Anoplocapros</i>	4	10	X	300		Graham	Johnson	
	<i>Kentrocapros</i>	1		X	X		Graham	Johnson	
Tetraodontidae	<i>Omegophora</i>	2	X	X	255		Graham	Johnson	Matsuura
	<i>Torquigener</i>	13	X	X	X		Graham	Johnson	Matsuura

Family	Genus	Sp	Distribution				Custodian	Project Collaborators	Potential External Collaborators
			<i>Coast</i>	<i>Shelf</i>	<i>Slope</i>	<i>Pelagic</i>			
Triodontidae	<i>Triodon</i>	1	30	X	228		Graham Johnson		
Diodontidae	<i>Allomycterus</i>	1	5	X	320		Graham Johnson	Leis	

