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Torres Strait fisheries: cross-border management and sharing of stocks

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The Torres Strait Treaty commits Australia and Papua New Guinea to cooperate in environmental protection and ecologically sustainable management of the shared stocks in Torres Strait in a way that protects the traditional way of life and livelihood of the traditional inhabitants. The Treaty also provides for freedom of movement for traditional fishing and cross-border sharing of the catch of commercial fisheries.

A cooperative approach involving Australian and PNG federal and state management agencies, community councils and commercial and traditional fishermen is the key to the successful management of the shared stocks and their environment.

Stock delineation of pilchards, *Sardinops sagax*, in Western Australia

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A large amount of work has been devoted to the determination of the stock structure of pilchards in Australia, particularly in WA. These studies have provided a plethora of data, not all of which are consistent, but a general picture has emerged whereby separation can be seen at a number of different levels.

Aspects of the population biology of the King George whiting (*Sillaginodes punctata*) in South Australia — consequences for evolutionary processes

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The fishery for the King George whiting (*Sillaginodes punctata*) in South Australia is divisible into three main regions; Gulf St Vincent, Spencer Gulf and the west coast. These are separated by York and Eyre Peninsulas. The possibility that these regions may support different stocks is considered by analysis of patterns of distribution and abundance, adult movements, the locations of spawning, and potential for larval advection.

Adult movements generally conform to a net southward trend that would account for the north/south gradient in size and age structures. However, there is virtually no inter-regional movement, which thus divides the

post-settlement populations into separate ecological units.

The few spawning locations found were restricted to southern, exposed places within each region, which corresponded to where the older, larger fish occurred. The potential for advection of larvae from these to nursery areas is accommodated by a long larval duration (80–120 days), and the prevailing water currents through the settlement season.

Each of the three regions has potential to be self-sustaining, yet the long larval durations would provide opportunity for genetic exchange between regions. These life-history and population biology data provide the context for an empirical assessment of genetic structure of populations across southern Australia (refer to abstract by Haigh, Donnellan and Fowler).

Indonesian catch off NW Australia — a discussion of surveillance data

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Where there are foreign-based fishing operations in the Australian Fishing Zone (AFZ), surveillance and enforcement data may provide a valuable insight into the amount of illegal fishing being undertaken and the possible impact on the resource.

Off north-western Australia there are a number of different Indonesian fishing operations involving so called 'traditional' sail-powered boats, motorized *perahu* and more sophisticated longline vessels. These boats fish for shark, reef fish and undertake the collection of sedentary species including trepang (*beche-de-mer*) and trochus. Indonesian boats substantially outnumber Australian boats off the north-west and exploitation levels are increasing.

Indonesians have fished off north-western Australia for centuries but, as jurisdiction was established over offshore areas and the need for resource conservation recognized, boundaries limiting or excluding Indonesians were established. Of particular interest is an area called the 1974 Memorandum of Understanding (MOU box), an area in which Australia has agreed to refrain from applying its laws with respect to traditional Indonesian fishermen. Whilst the fishing platforms may be similar the mode of fishing undertaken has evolved which, supported by surveillance data, indicates possible problems for management of the resource.

Is catadromy in barramundi obligatory?

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The "established" life history classifies barramundi (*Lates calcarifer*) as catadromous, with mature adults living and spawning in the sea and juveniles migrating upstream in their first year, remaining there for 2–3 years. Observations by researchers and fishermen suggest that this is probably not strictly the case. Juveniles are found in marine areas throughout the year and populations of barramundi flourish in areas with little permanent freshwater habitat. A recent study by Pender and Griffin investigated the habitat history of barramundi in the Mary River by examination of salt and fresh water indicator elements in scales. Chemical analysis of scales

of barramundi from salt and fresh farm ponds showed that in saltwater, strontium concentration is high and in freshwater, barium is high. Wild barramundi taken from freshwater, estuarine and marine habitats were classified by discriminant function analysis and cluster analysis on the basis of their Ba and Sr concentration as to whether they were of marine, fresh or mixed history. That analysis showed that over 90% of barramundi taken at Marsh Creek, 24 km from the freshwaters of the Mary River, had low levels of Ba and high levels of Sr, indicating that they had not had a freshwater phase. Implications of the existence of this marine "stock" of barramundi for management and allocation of the barramundi resource are discussed and further research suggested.

A preliminary analysis of stock structure in King George whiting (Perciformes: *Sillaginodes punctata*)

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We are studying the stock structure of King George whiting across its range in southern Australia using molecular genetic markers. The species is found from southern NSW through to southern WA and is the most important commercial inshore marine scalefish in South Australia. We have chosen both mitochondrial and nuclear DNA markers because preliminary allozyme studies (Dixon 1987; Donnellan unpublished data) failed to provide sufficient numbers of variable marker loci. Here, we present some preliminary results from analyses of a mitochondrial DNA marker and several microsatellites isolated to date.

A phylogenetic analysis of mitochondrial control region nucleotide sequences was used to investigate phylogeographic structure across the species range. No strong phylogeographic structure was observed at any geographic scale. We are now proceeding to examine haplotype frequencies at selected sample sites.

Analysis of allele frequencies at several microsatellite loci was carried out for some eastern Australian samples. The implications of these data will be discussed.

Do populations of the catadromous Australian bass, *Macquaria novemaculeata*, exhibit significant genetic structuring?

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Geographically separated populations of the catadromous Australian bass (*Macquaria novemaculeata*) were sampled from throughout this species' natural range and examined for genetic variability at six polymorphic nuclear (allozyme) loci and from 400 base pairs of the mitochondrial Control Region. Significant heterogeneity among bass locales were revealed by both methods, although the levels of genetic structuring present were not highly pronounced. Both allozymes and mtDNA demonstrate that *M. novemaculeata* populations are connected by moderate levels of gene flow. This is particularly apparent from DNA sequence data which demonstrate no phylogeographic structuring in mtDNA haplotypes. Gene flow in Australian bass is

expected to be restricted to adjacent or neighbouring populations as an isolation by distance pattern of population structure was evident.

Hierarchical analysis of genetic variation in the Pacific blue-eye *Pseudomugil signifer* (Pseudomugilidae) in northern Queensland, Australia

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Dendritic river systems provide a useful opportunity to study the consequences of varying levels of isolation and gene flow on population genetic structure. The Pacific blue-eye *Pseudomugil signifer* is a small freshwater fish common to coastal drainages of eastern Australia and some offshore islands. Using a hierarchical sampling design, levels of genetic divergence within and among populations from five drainages in northern Queensland were estimated by cellulose acetate electrophoresis. Analyses using F statistics revealed extensive genetic differentiation among drainages, with less within and between subcatchments within a drainage. This is concordant with the degree of physical isolation between populations and suggests that dispersal is restricted among drainages. Other results indicate that a population in the South Johnstone subcatchment may be introduced, and the relatively high degree of similarity of the Mulgrave/Russell Rivers and Barron River populations raises questions about possible historical connections between these systems.

Resource allocation between the recreational and commercial sectors of the South Australian marine scalefish fishery

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A bus-route creel survey was conducted in South Australian coastal waters to quantify the recreational boat fishery harvest of key marine species. The overall objective of the project was to compare the current resource allocation between the commercial and recreational sectors of the Marine Scalefish Fishery.

The survey covered 74 boat ramps from Victor Harbour to Ceduna from April 1994 to March 1996. The survey area was divided into two broad regions: 1) Gulf St Vincent and 2) Spencer Gulf & West Coast. Each region was surveyed for a 12-month period. In total, 631 days were sampled and 3513 interviews recorded. The results showed that nearly one million boathours (or 200 000 boatdays) were expended on recreational fishing during the survey. Just over half of this was expended in Gulf St Vincent, about 40% in Spencer Gulf and 5% in West Coast waters.

The total estimated annual harvest of the recreational fishery was 3 770 256 fish (excluding scallops, cockles, mussels and razorfish). At least 80 species of fish (including crabs and molluscs) were recorded in the recreational catch. The dominant species were King George whiting (28.2% of recorded numbers), garfish (20.14%), blue swimmer crabs (15.06%) and tommy ruff (10.55%). Together, these four species

accounted for about 75% of the observed catch.

The recreational share of nine key species ranged from 4.7% to 74.9% of the total harvest. Considerable spatial variation was evident in this share within species. Notably, the recreational share was highest in the waters near metropolitan Adelaide and a general decrease in recreational share away from the main population centres was evident.

Resource allocation and swallowtail dart (*Trachinotus botla*)

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The swallowtail dart is a surf zone carangid caught by commercial ocean beach net fishers and recreational anglers. Conflict over the allocation of swallowtail dart escalated because of the State Government Inquiry into Recreational Fishing (1992) which recommended that swallowtail dart become a "recreational only" species. Aspects of the commercial and recreational fishery are discussed. Recreational fishing lobbyists claimed that the commercial catch of swallowtail was increasing rapidly. However, a review of the available commercial catch statistics showed the commercial catch to be small and reasonably stable. The commercial catch is principally taken between May and October which is outside of the species spawning period. The size at maturity of swallowtail dart was found to be 36cm which is considerably higher than the proposed minimum legal size of 30cm. Swallowtail dart is the principal species captured by recreational club anglers fishing the surf zone; however, they are of minor importance to recreational anglers as a whole

The marine harvest refugia concept and its use as a tool for fish population enhancement

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In introducing the subject of marine harvest refugia, it might be worth considering the proposition that the only long-term solution to the problem of sustainable fisheries management may lie in the total protection from consumptive exploitation of relatively large areas of the inshore marine environment and its living resources. The establishment of such extensive "marine harvest refugia", coupled with the use where necessary of more conventional but less holistic fisheries management measures in surrounding exploited areas, should help to replenish the fishable stocks in these latter areas through protection of adult spawning stocks and of juvenile fish in their nursery habitats. Apart from providing continuous recruitment of potentially harvestable resources to these surrounding fished areas, such harvest refugia would also be available for a wide variety of other generally non-consumptive (e.g. recreational, educational, scientific and aesthetic) uses, with existing conflicts between resource production potential and these more passive uses being greatly reduced (see key papers by Davis 1981, 1989; Bohnsack 1990; Roberts and Polunin 1991; Dugan and Davis 1993).

Population structure of the southern calamary, *Sepioteuthis australis*, in southern Australia and its implications for management

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Allozyme electrophoresis was used to investigate population genetic structure within the southern calamary *Sepioteuthis australis*. Samples collected from twelve localities around southern Australia, ranging from Western Australia to New South Wales, were examined for allozyme variation at 59 enzyme loci. Thirteen polymorphic loci were detected, seven of which were sufficiently variable to be useful as routine genetic markers of population structure. There was little or no genetic differentiation across the entire range sampled at five of these seven loci. In marked contrast, the allozyme data at two loci (Pep D and FDPase) unequivocally sorted all animals into one of three genetic groups, which conformed to a spatial pattern. One group was only found near the western and eastern limits of the sampled area and another was found in between. Where these overlapped, a third hybrid-type was found. The two most likely explanations for these data are: (1) there are two very distinct stocks within *Sepioteuthis australis* which to date have produced only F1 hybrids wherever they overlap, or (2) the two loci FDPase and Pep D are tightly linked and thus are not an independent measure of population structure. Morphological, reproductive and mitochondrial DNA sequence data are currently being assessed in an effort to distinguish between these alternative explanations.

Offshore Constitutional Settlement — allocation panacea or problem?

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The Federation of Australian States under the Commonwealth in 1901 created split jurisdictions for coastal waters. The State governments took responsibility for territorial waters extending 3 nautical miles offshore and the Commonwealth from 3 nautical miles to 12 miles, then later to 200 nautical miles. Since Federation, Australia's fishing fleet has increased in size and efficiency, with consequent increased impacts on fish populations. However, fish do not recognize jurisdictional boundaries and split jurisdictions cause management problems and the possibility of overexploitation for some species. Offshore Constitutional Settlement (OCS) between the States and the Commonwealth is a mechanism that attempts to overcome split jurisdictions for fisheries management. Under OCS arrangements, jurisdictional responsibilities are usually re-defined in terms of target species, catching methods, and specified areas of waters. These arrangements do allow States to manage their principal local fisheries out to the boundary of the Australian Fishing Zone and the Commonwealth to manage widely distributed or highly migratory fisheries resources into State waters. However, fishery definitions using gear descriptions cause potential interactions. Also target species-based descriptions that form the basis of all recent OCS arrangements requires identification of bycatch species and negotiation of acceptable limits. Bycatch species and limits are scheduled in Memoranda of Understanding between the States and Commonwealth. The

application of these MOUs has resulted in taxonomic confusion, enforcement problems, high-grading and dumping for some non-selective fishing methods such as trawling.

Genetic processes in an estuarine bivalve, *Anadara trapezia* (Arcidae)

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The nature, level, and pattern of distribution of genetic variation in *Anadara trapezia* was investigated electrophoretically at both the macro-and microgeographic scales. At the macrogeographic scale, high levels of genetic heterogeneity were found among populations of *A. trapezia* along the east coast of Australia and this level of population structure was attributed to oceanic processes.

The microgeographic study revealed the existence of fine-scale spatial and temporal heterogeneity in the distribution of allozyme variation. The interpretation of these results, combined with those obtained in the previous macrogeographic analysis, leads to a complex model of population structure, namely: small effective population size and genetic neighbourhood size, but with the geographic location of a lineage shifting between generations. The proposal that patches of closely related larvae travel together in the plankton until settlement is also supported. The effects of such a pattern of population structure on the value of present models used in fisheries management, given that catchability, growth rates and age at breeding have a genetic component, are considered.

Stock identification using otolith shape analysis — (poster)

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Shape analysis of fish otoliths, as a tool for stock identification, has several advantages over traditional morphometric methods. Otolith shape is less variable than fish somatic growth (probably a factor of the otolith's dual role as an organ of equilibrium and hearing). Also, otoliths continue to grow throughout the life of the fish and are metabolically inert. Therefore, otoliths remain unaffected by short-term fluctuations in fish condition (e.g. starvation) which can confound body morphometrics.

Outline shape analysis should be used to describe otolith shape since otoliths lack homologous features used in landmark morphometrics (e.g. head length). Elliptic Fourier shape analysis is generally the most useful method to describe otolith shape and results in a series of Fourier descriptors which can be used as input data for discriminant analysis. A sample procedure to discriminate stocks of the Australian anchovy, (*Engraulis australis*), using elliptic Fourier analysis of sagittal otoliths will be described.

Utilizing microsatellite DNA technology to identify stock structure in populations of orange roughy (*Hoplostethus atlanticus*) — (poster)

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Orange roughy (*Hoplostethus atlanticus* Collett) is a deep water fish species (found at depths up to 1800m), with a long life span (up to 149 years), that only matures at about 30 years of age. This species is commercially fished in southern Australian waters; however, catch sizes have decreased considerably since the opening of the fishery in 1987. Knowledge about the stock structure and migrational routes within and between populations of this unusual fish is crucial for sustainable fishing to occur. Previous studies attempting to answer these questions have produced conflicting results. Genetic studies (mtDNA and allozymes) indicate seemingly unrealistic migration levels, whereas non-genetic studies (comparative parasitology, morphology and otolith microchemistry) suggest greater isolation between the different populations. The present study aims to determine whether a new molecular marker, microsatellite DNA, is a better tool for answering the questions about stock structure and migration of orange roughy.

Use of microsatellite loci to re-examine levels of genetic variation in cultured Atlantic salmon from Tasmania, Australia — (poster)

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Atlantic salmon (*Salmo salar* L.) were imported into Australia in the mid-1960s with an initial population established in New South Wales. Some 570 000 ova from this founding stock were then introduced to Tasmania over a three-year period in the mid-1980s to form a significant and expanding industry producing 6000 tonnes in 1994–95. The Tasmanian salmon farming industry relies on the supply of smolt from one major commercial hatchery, Salmon Enterprises of Tasmania Pty. Ltd (SALTAS).

Seven variable allozyme loci and mitochondrial DNA (mtDNA) variations in the Tasmanian broodstock were assessed in 1993, and compared with the parental River Philip population in Nova Scotia, Canada. Small but significant differences in some allozyme allele frequencies were observed. The mean heterozygosity per allozyme locus was 0.207 for the Tasmanian fish and 0.182 for the Canadian fish. Mitochondrial DNA variation was very limited but there was no evidence of a reduction in variations in the Tasmanian fish.

With the increasing use of microsatellite loci to population genetic applications, a study was undertaken to examine the extent of genetic variation in the Tasmanian broodstock with these new and potentially more powerful markets. The individuals analysed in the 1993 study were re-examined for eight polymorphic microsatellite loci. Small but significant differences in allele frequencies between the two samples of fish were found for four of the eight loci. Mean heterozygosity per microsatellite locus was more than twice that of the allozyme loci, at 0.434 (n=63) for the Tasmanian fish and 0.509 (n=63) for the Canadian fish.

The three approaches all suggest that there have been some changes in the genetic makeup of the Tasmanian fish as compared with the Canadian fish, but that diversity levels have generally been maintained. We hope to monitor levels of genetic variation every few generations to check on any longer-term changes.