Chapter 1

General introduction

Estuaries, although limited in surface area when compared to South Africa's marine environment, represent one of the most valuable habitats along the coast. Usually calm, sheltered and shallow, estuaries are highly productive systems (Correll, 1978). It is a specialised environment that serves as an important nursery area for juvenile fish (Blaber, 1974b) and a rich feeding ground for the adults of certain species (Tilney & Hecht, 1993). Dusky kob, *Argyrosomus japonicus* (Temminck & Schlegel, 1843) and spotted grunter, *Pomadasys commersonnii* (Lacepède, 1801) are two of South Africa's most targeted angling species, and both are dependent on estuaries for their survival.

Two oceans flank South Africa's coastline, the warm Indian Ocean and the cool Atlantic Ocean (Fig. 1.1). The warm Agulhas Current in the southwestern Indian Ocean flows along the eastern and southeastern coast of Africa, before meandering offshore in the vicinity of the Agulhas Bank (Branch *et al.*, 1994). The cool Benguela Current in the southeastern Atlantic Ocean flows northwards along the west coast of South Africa and Namibia, this marine environment influences physico-chemical conditions in the entire coastal zone, including the adjacent estuaries (Schumann, 2000). Depending on their distribution along the coast, South African estuaries can be divided into three groups: subtropical, warm-temperate and cool temperate (Fig. 1.1). The Agulhas current interacts with 117 subtropical and 123 warm-temperate estuaries, while the Benguela interacts with 10 cool-temperate estuaries (Whitfield, 1998).

There are few sheltered shores along South Africa's approximately 3100 km coastline, most of which is almost constantly subjected to turbulent wave action. Estuaries, on the other hand, offer sheltered environments but have varying turbidities, temperature and salinity fluctuations (Whitfield, 1998). Day (1980) defined an estuary in a South African context as follows: "An estuary is a partially enclosed coastal body of water, which is either permanently or periodically open to the sea, and within which there is a measurable variation of salinity due to the mixture of sea water with fresh water derived from land drainage". Estuaries act as nursery areas for juvenile fishes and feeding grounds for adults of certain species and therefore play an important role in the life histories, maintenance of diversity and productivity of coastal fish communities (Blaber, 1981; Braird *et al.*, 1996; Whitfield, 1998). However, estuaries represent a highly specialised habitat and less than 10% of the approximately 1500 fish species along the South African coast makes use of this environment. Estuarine dependent fishes are defined as those taxa whose southern African populations would be adversely affected by the loss of estuaries from the subcontinent (Whitfield, 1994). Based on the level of dependence on estuaries, fish species can be divided into five categories (Table 1).

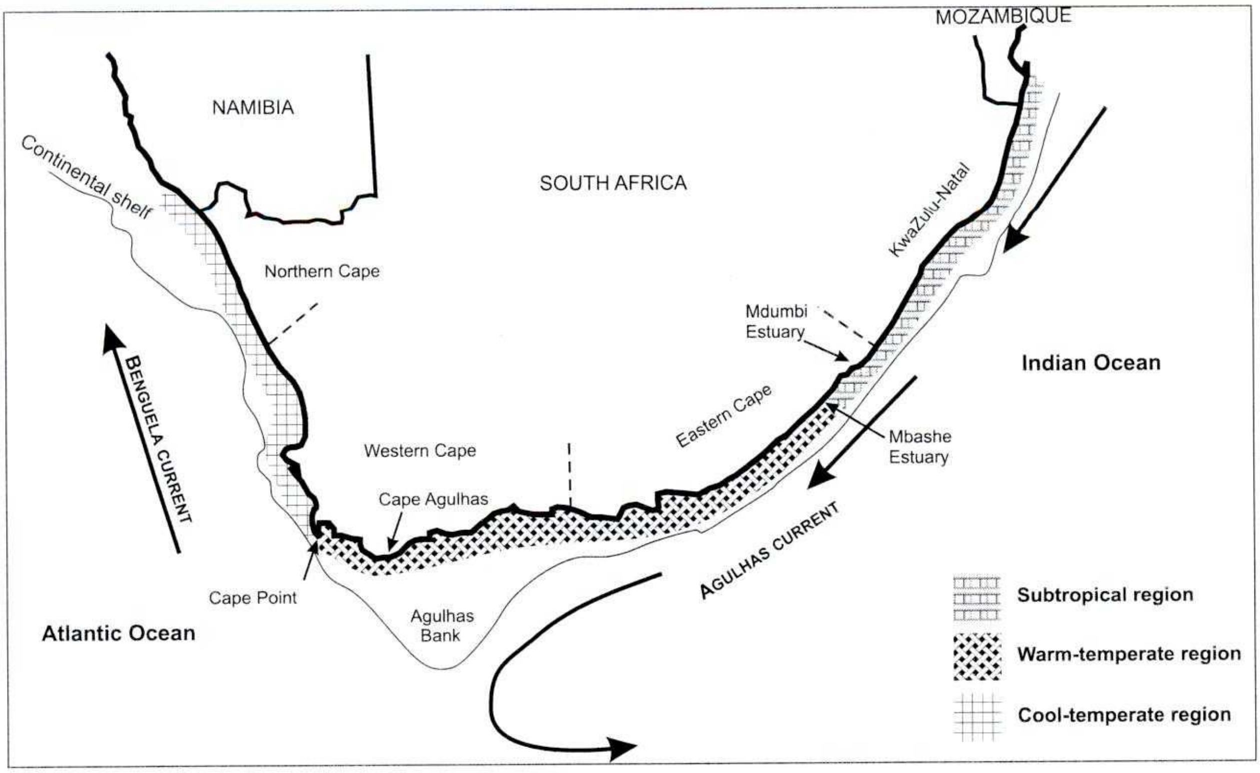

Fig. 1.1 Map of the southern African coastline. Arrows indicate major ocean currents that influence the adjacent estuarine environment. Cape Point and the Mbashe Estuary were regarded as the boundaries of the warm-temperate estuarine region (Maree *et al.*, 2000) although more recent research (Harrison, 2002) have placed these boundaries at Cape Agulhas and the Mdumbi Estuary respectively.

Larval and juvenile fish enter the estuaries mainly from late winter to early summer, and grow rapidly in these systems due to elevated temperatures, abundant food supplies and protection from predators (Blaber, 1974a). Fish generally migrate back to sea before they become sexually mature, while adult fish numbers can increase seasonally as they enter estuaries to feed (Wallace *et al.*, 1984).

Two of South Africa's fish species for which the estuarine environment is a vital habitat are *A. japonicus* and *P. commersonnii*. Whitfield (1998) lists *A. japonicus* and *P. commersonnii* as species that are dependent on estuaries and both species have been placed in category IIa. Apart from dependence at the juvenile stage, both *P. commersonnii* and *A. japonicus* adults also frequently enter estuaries to feed.

Table 1.1: The five major categories of fish utilizing southern African estuaries (Table 11 from Whitfield, 1998)

Category	Description
I	Estuarine species that breed in southern African estuaries. Further subdivided into:
Ia	Resident species which have not been recorded spawning in the marine environment.
Ib	Resident species which also have marine or freshwater breeding populations.
II	Euryhaline marine species which usually breed at sea with the juveniles showing varying degrees of dependence on southern African estuaries. Further subdivided into:
IIa	Juveniles dependent on estuaries as nursery areas.
IIb	Juveniles occur mainly in estuaries, but are also found at sea.
IIc	Juveniles occur in estuaries, but are usually more abundant at sea.
III	Marine species which occur in estuaries in small numbers, but are not dependent on these systems.
IV	Euryhaline freshwater species, whose penetration into estuaries is determined primarily by salinity tolerance. Includes some species which may breed in both freshwater and estuarine systems.
V	Obligate catadromous species which use estuaries as transit routes between marine and freshwater environments.

Estuarine dependent fish taxa include some of South Africa's most important angling species, both for recreational anglers and as a food source for subsistence fishermen and to a lesser extent the commercial fishery. Dusky kob comprises approximately 18% of the catch composition by weight in estuaries and spotted grunter 20%. Only the mugilid, *Liza richardsonii,* is a more important fishery target (32%) but utilization of this species is mainly on the west coast where large numbers are netted (Lamberth & Turpie, 2003).

Argyrosomus japonicus

Argyrosomus japonicus (Fig. 1.2) is distributed from the Cape of Good Hope to southern Mozambique, although only abundant from Cape Agulhas to northern KwaZulu-Natal. Although most abundant in the warm-temperate and subtropical waters of south-east Africa, they also occur along Australia's southern seaboard and from Hong Kong northwards along the Chinese coast to southern Korea and Japan. It also occurs off Oman, Pakistan and India in the northern Indian Ocean. In South African waters, *A. japonicus* is a continental coastal species that can be found in estuaries, the surf and nearshore zone with a maximum recorded depth of 100 meters (Griffiths, 1996b; Griffiths & Heemstra, 1995; Heemstra & Heemstra, 2004). They utilise estuaries throughout their range, especially the larger systems such as Lake St Lucia (Whitfield, 1994). In estuaries they prefer turbid water where they hunt by combining olfactory and lateral line senses and are therefore well equipped to forage in these waters (Van der Elst, 1988).

Spawning takes place at night in the nearshore marine environment (Griffiths, 1996b) and usually coincides with the summer rainfall season along the East Coast. Elevated river flow into the coastal zone increases water turbidities and boosts planktonic productivity (Heydorn *et al.*, 1978) upon which *A. japonicus* larvae depend for food. Recruitment of the postflexion larvae and 0+juveniles into estuaries occur mostly at 20–30 mm total length (TL), which corresponds to an age of approximately one month (Griffiths, 1996b). According to Whitfield (1994) the olfactory cues from estuaries in the adjacent marine environment are probably the most important factor influencing the recruitment of estuarine dependent species such as *A. japonicus*.

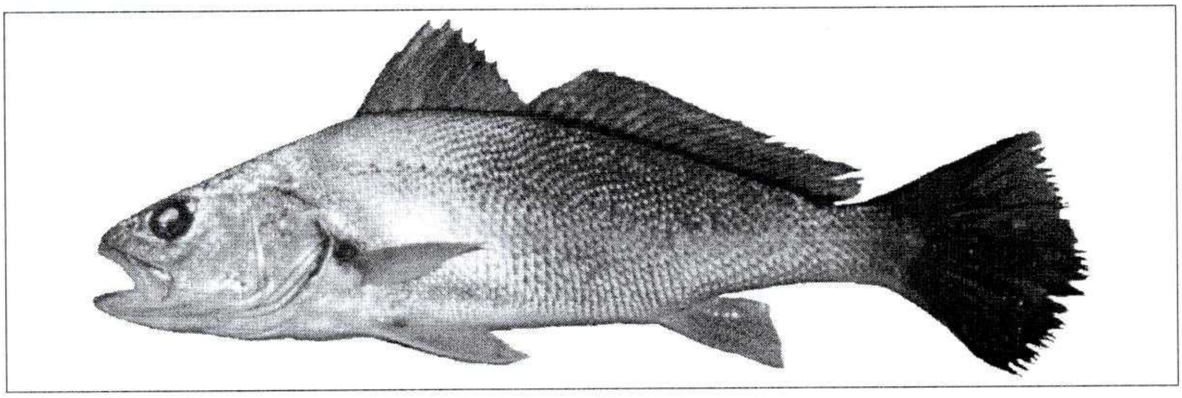

Fig. 1.2 Juvenile *Argyrosomus japonicus* (128 mm standard length).

Recruitment of *A. japonicus* into estuaries occurs mainly between October and February (Wallace & van der Elst, 1975). Early juveniles, 20–30 mm TL, appear to remain in the upper reaches of estuaries where they concentrate in the more turbid, oligohaline areas (<5% salinity). At approximately 15 cm TL they move into the middle and lower reaches, with some entering the adjacent marine surf zone (Griffiths, 1996b). Juveniles grow rapidly and can attain 35 cm TL in the first year. Individuals older than a year still tolerate a wide range of salinities (3–66‰) but subadults cannot survive prolonged exposure to very low salinities (<3%), especially in combination with low temperatures (Blaber & Whitfield, 1976). Juveniles (<50 mm TL) prey mainly on calanoid copepods and mysids (Griffiths, 1996b). Larger juveniles (>17 cm TL) feed mainly on fish, shrimps and penaeid prawns, with small fish species such as *Gilchristella aestuaria* dominating the diet of these size classes. Subadult *A. japonicus* also target these prey species, as well as the juveniles of marine migrant species (Griffiths, 1997a, b; Whitfield, 1998).

Tagging data show that juvenile *A. japonicus* do not travel far and are likely to remain close to their natal estuaries, forming localised populations until they reach sexual maturity (Bullen & Mann, 2004a; Griffiths, 1996b). Fifty percent of females reaches sexual maturity at 100 cm TL and males at 95 cm TL. These sizes translate to six years of age in females and five years in males, while all males are mature at the of age seven years and females at the age of eight years (Griffiths & Hecht, 1995). Most *A. japonicus* caught inshore (estuaries and surf zone) are less than seven years old, whereas those from the offshore linefishery are generally older than six years. Although an age of 42 years has been recorded, individuals older than 27 years are rare. Adult *A. japonicus* with a body mass in excess of 45 kg are often caught, with some individuals attaining 75 kg (Griffiths & Heemstra, 1995).

The increase of mature individuals ready to breed, which are caught by lineboats in KwaZulu-Natal between August and November, suggests that adult fish from the southeastern and southern Cape migrate there to spawn. Spawning also occurs in the Cape region, where spawning as far west as Cape Infanta has been recorded from October to January. This indicates that breeding might commence in KwaZulu-Natal and continues as a portion of the spawning population returns to southern waters. A general absence of individuals with spent gonads in KwaZulu-Natal and their presence in southeastern and southern Cape waters also implies a return migration once spawning is completed (Griffiths, 1996b; Griffiths & Heemstra, 1995).

Because of its life history characteristics, age at sexual maturity, and having evolved with relatively low rates of natural mortality, *A. japonicus* is unlikely to be able to sustain high levels of exploitation. Estuarine and shore anglers have been targeting this species for more than four decades and it is estimated that the species' biomass is between 1.0 and 4.5% of its pristine levels (Griffiths, 1997d; Lamberth & Turpie, 2003). There are at least three phases where they are particularly vulnerable to human activities. Recreational and commercial lineboat fishermen target the dense spawning aggregations off the KwaZulu-Natal coast. Recreational anglers target juveniles that inhabit the surf zone and estuaries. Although early juveniles are not exploited directly, these size classes are estuarine dependent and most of South Africa's estuaries have already been degraded in various degrees, mostly by impacts in the catchments (Griffiths, 1996b).

Pomadasys commersonnii

Pomadasys commersonnii (Fig. 1.3) is a western Indian Ocean coastal species, that occurs from India to South Africa (Heemstra & Heemstra, 2004). It has an estuarine distribution in South African waters from the southern Cape eastwards up the coast into southern Mozambique, while their marine distribution can occasionally reach False Bay during the summer (Whitfield, 1998). *Pomadasys commersonnii* is mainly found in shallow water with depths of less than 30 meters (Smith & McKay, 1986).

Spawning occurs at sea in the shallow inshore zone from August to December, although ripe and running specimens have occasionally been found in estuaries (Wallace, 1975b). Larval development occurs in the marine environment. Juveniles are recruited into estuarine nursery areas at approximately 20–30 mm TL, and they are most abundant in the upper reaches, even entering fresh water (Wallace & van der Elst, 1975; Whitfield, 1998). Size classes between 4 and 16 cm TL predominate in estuaries but post-spawning individuals also enter estuaries to feed. Juveniles return to the sea after one year (approximately 15 cm TL) where they stay until maturity (Wallace, 1975a). Males are mature by 30 cm and females by 36 cm standard length (SL), about three years of age. Tagging data suggest that adults are fairly resident and tend to congregate in the vicinity of estuary mouths (Bullen & Mann, 2004b; Fennessy & Radebe, 2000). Currently *P. commersonnii* is maximally or optimally exploited, with the spawner biomass estimated at 40% of pristine levels (Lamberth & Turpie, 2003).

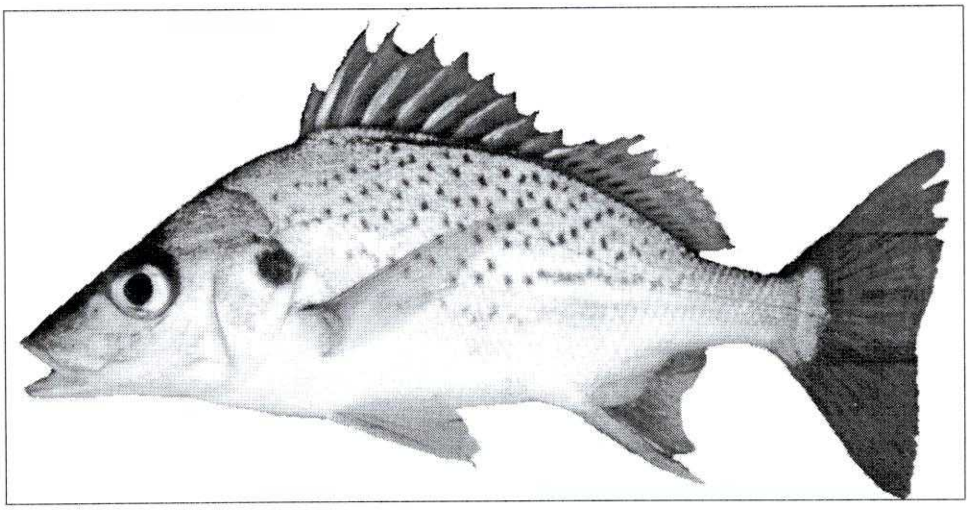

Fig. 1.3 Juvenile *Pomadasys commersonnii* (123 mm standard length).

Pomadasys commersonnii can survive in salinities from 0–90‰, but mass mortalities have been recorded when low salinities (<4%) coincide with water temperatures below 13°C (Blaber & Whitfield, 1976). Sampling and experiments have shown that *P. commersonnii* is indifferent to water turbidity (Cyrus & Blaber, 1987). Early juveniles in estuaries feed mainly on pelagic copepods and mysids (Wooldridge & Bailey, 1982), while subadults and adults prey predominantly on benthic anomurans and bivalves (Hecht & van der Lingen, 1992). Although *P. commersonnii* feeds during daylight hours they are mainly crepuscular and nocturnal (Marais, 1984). The maximum recorded size is 87 cm TL, approximately 15 years old (Whitfield, 1998).

Species importance

Both *A. japonicus* and *P. commersonnii* are preferred target species of shore and estuarine anglers. Estuaries are favoured by recreational anglers and subsistence fishermen due to the high abundance of fish and the accessibility and protected waters of these systems (Baird *et al.*, 1996). In the warm-temperate and subtropical estuaries, *A. japonicus* and *P. commersonnii* are the two most important angling species. On the Cape south coast *P. commersonnii* makes up 45% of catches and *A. japonicus* 6% of catch weight. Catches on the Cape east coast are dominated by *A. japonicus* (48%) and *P. commersonnii* (31%), whereas in KwaZulu-Natal *A. japonicus* constitutes 35% and *P. commersonnii* 11% of catch weight. Altogether this amounts to an annual ±377 tons of *A. japonicus* and ±416 tons of *P. commersonnii* of a total ±2100 tons of fish caught in estuaries. Recreational angling in estuaries is worth nearly R429 million per annum. Furthermore, it is estimated that the contribution of estuarine dependent fish species to inshore fisheries is worth R519 million per annum. In total, the value of estuarine and estuarine dependent fisheries in 1997 was estimated to be ±R952 million with a projected value of about R1.162 billion in 2000 (Lamberth & Turpie, 2003).

From the above, it is clear that the economic value of *A. japonicus* and *P. commersonnii* cannot be underestimated, even at the individual estuary level. In order to sustain this source of income, healthy fish populations are of utmost importance. The increase in fishing pressures to unsustainable levels has caused severe depletion of fish stocks in South African and global waters. In the 1950s fishing efforts intensified and over exploitation of marine resources commenced. Since the late 1980s, world fish landings have started to decline and future prospects are uncertain unless drastic measures are put in place to reduce the rates of exploitation (Pauly *et al.*, 2003; Pauly & Watson, 2003). Overfishing not only depletes fish populations but also has the effect of altering the entire marine ecosystem (Jackson *et al.*, 2001). To maintain a profitable fishery, information on the species' population history and composition is needed to formulate effective recovery and management strategies. Fish is the last major food source on this planet that is harvested from natural populations (Ryman *et al.*, 1995). The fishing industry is worth over a billion Rand to South Africa each year (Lamberth & Turpie, 2003), yet little detailed information is available about the population sizes, structures and dynamics of most of our fish species (Mann, 2000); information that is of utmost importance for the sustainable utilisation of these resources.

Stock determination

The oceans cover more than 70% of the earth's surface and most of them are interlinked. When compared to continental land masses there are few natural barriers in the oceans, with many marine species having a high dispersal potential, resulting in widespread areas that are genetically connected (Avise, 1998; Palumbi, 1994; Waples, 1998). Several studies have shown that marine species, especially those along continental margins typically show high levels of gene flow. This might be due to dispersal of pelagic larvae, through migrating adults or large effective population sizes. Consequently this translates into low levels of population genetic differentiation (Carvalho & Hauser, 1998; Exadactylos *et al.*, 1998; Gold *et al.*, 1999; Hilbish, 1996; Waples, 1998; Ward, 2000; Ward *et al.*, 1994). However, increasingly studies are showing that a lack of barriers and high dispersal potential do not necessarily translate into high gene flow or low levels of population differentiation (Avise, 1998; Hilbish, 1996; Hutchinson *et al.*, 2001; Lundy *et al.*, 2000; Luttikhuizen *et al.*, 2003; Smith *et al.*, 2002; Stephenson, 1999; Waples, 1998). Behavioural philopatry during some stage in the life cycle of a species might be responsible for low gene flow and differences in population characterisitics (Avise, 1998; Carvalho & Hauser, 1998).

Most organisms show some form of discontinuous aggregation of individuals in space and/or time. Each aggregation has a specific character or genetic make-up that is influenced by gene flow from other aggregations, genetic drift and natural selection. In exploited marine species these aggregations are referred to as "stocks" (Shaklee & Bentzen, 1998). Correct identification of stocks are important for the proper management of exploited species and the preservation of their genetic diversity (Booke, 1999). Various definitions of a stock exist, including that of Ihssen, *et al.* (1981): "a stock is an intraspecific group of randomly mating individuals with temporal and spatial integrity". Most fisheries consist of more than one fishing ground and the question then arises: do these different fishing grounds exploit one or more stocks of the same species? The high diversity that exists at population and species levels, and the risk due to overexploitation, drives the quest to describe and monitor fish population structure (Carvalho & Hauser, 1998). The answer is of critical importance to management because, for each stock, a separate assessment of sustainable fishing should be determined (Ward, 2000). It is the genetic variation that exists at not only the species level but within and among populations that is essential in the management programme of species. Genetic variation is what allows species to keep on adapting to changing environments and to respond to pressures (O'Connell & Wright, 1997).

Considering the above, it is surprising how few fishery assessments implement stock identification requirements. For effective management and stock rebuilding programmes it is not only stock structure that is important, but also the distribution of fishing effort and mortality among stocks. Correct stock identification and estimation of exchange between them is a major challenge for scientists and managers. It assists in the recognition and protection of spawning and nursery areas, the development of an optimal harvesting and monitoring strategy, and in catch allocations between competing fisheries (Begg *et al.*, 1999).

Determining stock structure is a critical biological and management issue. Various environmental factors, biological information, phenotypic and genotypic variation have been studied in order to infer stock structure (Begg *et al.*, 1999; Waldman, 1999). Phenotypic characters usually reflect short-term environmentally induced differences, such as prolonged separation of postlarval fish in different environments, thus providing an indirect measure of genetic isolation (Begg *et al.*, 1999; Waples, 1998). Results obtained from phenotypic markers should only be interpreted with the understanding of their inheritance (Booke, 1999). Information obtained from mark/recapture surveys on later life stages (juveniles and adults) and collection of early life stages (eggs and larvae) from different regions gives some indication of movement. How far and in which direction larvae actually disperse cannot, however, be accurately mapped (Thresher, 1999). The overall recapture rate for the South African Sedgewick's/ORI/WWF Tagging Programme is 5.2% (Bullen & Mann, 2004b). In addition, movement or migration does not necessarily translate into gene flow (Ferris & Berg, 1987; Waples, 1998). However, baseline information provided by life history parameters usually assists in the initial recognition and delineation of geographically isolated stocks (Begg *et al.*, 1999).

Genetic variation on the other hand reflects evolutionary differences between stocks (Begg *et al.*, 1999; Begg & Waldman, 1999). Failure to detect differences indicates that (a) it might be one stock, (b) that the specific marker could not resolve the question, (c) recent separation has occurred or (d) that the sampling was inadequate. Even low amounts of gene flow can result in genetic homogeneity among samples, yet the actual amount of gene flow is important in assessing stock models. In large populations neutral markers will diverge relatively slowly through genetic drift and it may take millions of generations before they reach equilibrium and only then will the marker fully reflect the reproductive isolation among existing populations (Carvalho & Hauser, 1998; Dizon *et al.*, 1992; Waldman, 1999; Ward, 2000). Although very little gene flow is necessary to obscure any evidence of separate stock structure, limited gene flow cannot be relied on for the rebuilding of a depleted stock (Waples, 1998). Failure in recognising stock structures can lead to depletion of spawning components that result in a loss of genetic diversity and unknown ecological consequences (Begg *et al.*, 1999).In species that are not amenable to direct study, gene frequencies can be used to draw inferences about species biology (Beaumont & Nichols, 1996).

Genetics is a valuable tool in stock identification, it is however not without problems and limitations (Ward, 2000). Specific genetic markers, protein or DNA, all have shortcomings and limitations. For a marker to be useful, its functional behaviour needs to be understood and monitored (Booke, 1999). Genetic data, combined with information on aspects of species biology, biogeography, behaviour, migration, reproduction and oceanographic data will contribute to the best possible management plan. Genetic data can provide a direct basis for stock structuring and for the interpretation of other observed patterns, e.g. phenotypic patterns (Ihssen *et al.*, 1981). Although a multi-disciplinary approach is likely to be very costly for most species, the integration of all available information before decision-making is of the utmost importance for an optimal management strategy (Waldman, 1999).

It is difficult to determine stock structure in species with a high gene flow (= low F_{ST} values). Mean F_{ST} for marine species are estimated at 0.062, while 60% of marine species have a F_{ST} value of less than 0.03 (Ward *et al.*, 1994). Estuarine species especially those that spawn within estuaries generally show lower levels of gene flow (= higher F_{ST} values) because of retention mechanisms (Bilton *et al.*, 2002; Chenoweth & Hughes, 2003; Chenoweth *et al.*, 1998; Stefanni & Thorley, 2003). Estuarine dependant marine species breeds at sea and particularly those that undergo spawning migrations shows gene flow comparable to that found in typical marine species. Low levels of F_{ST} observed in marine species reflect the high dispersal capabilities and lack of barriers. The low levels of differentiation observed in many marine species necessitate the use of large sample sizes, as well as multiple markers to discriminate the genetic signal from genetic noise. The estimation of population genetic parameters can be affected by the noise. The common principle in all stock identification studies is that the signal from the among-stock variation must exceed the noise of within-stock variation. Apart from large sample sizes, temporally separated samples should also be analysed, since patterns of genetic relatedness or differentiation that is consistent over time are unlikely to be due to sampling problems (Gold *et al.*, 1999; Waldman, 1999; Waples, 1998; Ward, 2000). Taking all the problems that might arise into consideration, it is important that one understands the ecology and life history of the species under investigation. This will help facilitate effective strategies to minimize sampling errors and to adjust for possible bias that might occur (Waples, 1998).

Genetic markers

Stock identification based on genetic methods allows for indirect testing of reproductive isolation and gene flow between stocks (Shaklee & Bentzen, 1998). The initial method employed to determine genetic differences was based on indirect expression of DNA loci, in the form of blood group and protein variation. This method was followed with the advent of allozyme analysis (protein electrophoresis) in the 1970s, and allozymes have become the primary marker that most studies have relied upon. Allozymes is a cost-effective application that is easy to apply and large sample sizes can be analysed (Begg & Waldman, 1999; Carvalho & Hauser, 1998; Park & Moran, 1994; Shaklee & Bentzen, 1998; Ward, 2000). Allozymes have been used for 30 years, and is far from obsolete and can still yield valuable information. The speed and simplicity of allozyme analysis is one of its major advantages. Disadvantages are that it requires fresh or frozen material, most species show low levels of variability at allozyme loci and some allozyme loci may be under selection. Methods were then developed that more directly examined DNA variability and initially employed the use of restriction enzymes. However the development of polymerase chain reaction (PCR) technologies and DNA sequencing provided the best method to determine genetic differences (Carvalho & Hauser, 1998; Ward, 2000). The most rapidly expanding marker used in population and fisheries biology studies is microsatellites. Microsatellites are co-dominant nuclear markers that are inherited in a Mendelian way and is ideal for fine scale stock structure investigations (Carvalho & Hauser, 1998; DeWoody & Avise, 2000; O'Connell & Wright, 1997; Shaklee & Bentzen, 1998; Ward, 2000).

The advantage of PCR-based genetic markers over protein electrophoresis is the ease of sample collecting and storage. Non-lethal sampling can be done since only a small piece of material is required, eggs and larvae can be used and archived material such as scales and otoliths can be analysed (Hutchinson *et al.*, 1999; Ward, 2000). Analysing archive material such as scales have been used with success to determine the loss in genetic diversity that coincided with a decline in population size (Hauser *et al.*, 2002). Access to several markers, ranging from low to high variability, and the use of non-coding regions make the data less liable to the influence of natural selection and more likely to reflect stochastic processes. The limitation of the method is that it is more expensive and that it takes more time to develop (Ward, 2000).

Initially most studies were limited to mitochondrial DNA (mtDNA), a small (±16 000 base pairs in length) circular molecule in the cytoplasm. In most organisms, including most fish, it is maternally inherited and thus haploid. Therefore, studying mtDNA allows one to characterise maternal lineages within and among species. The mtDNA contains 13 protein-coding genes, two ribosomal-coding genes, 22 genes that code for transfer RNAs and one non-coding segment, the control region. Furthermore the mitochondrial genome does not undergo recombination and the genes have different mutation rates (Avise, 1998; Faith & Pollock, 2003; Ferris & Berg, 1987; Meyer, 1993; Moritz *et al.*, 1987; Park & Moran, 1994). However, it must be noted that several studies have indicated that recombination in the mtDNA genome do occur in animals including vertebrates such as humans and fish (Awadalla *et al.*, 1999; Hoarau *et al.*, 2002; Ladoukakis & Zouros, 2001; Lunt & Hyman, 1997; Rokas *et al.*, 2003)

The section with the highest substitution rate in vertebrates (two to five times higher than mitochondrial protein coding genes) is the control region, making it useful for population studies. The length of this segment in fish varies from 800–1500 base pairs (bp), mostly due to tandem repeat sequences and large insertions, but it also contains conserved sequence blocks similar to those found in mammals. The hypervariable region I (5' end) has considerable size variation among species due to the presence of tandem repeat sequences. It also shows high levels of nucleotide substitution, which is most useful in intraspecific studies. The hypervariable region II (3' end) in some species have long repetitive sequences making it less suitable for population studies (Lee *et al.*, 1995).

Due to the haploid nature and absence of recombination in mtDNA, the signal obtained from genetic drift is stronger than for nuclear loci. If there is equilibrium between drift and migrations, and drift and mutation, together with equal dispersal of males and females between stocks, mtDNA effective population size is expected to be one quarter that of nuclear genes. This means that genetic drift and loss of genetic variation within reproductively isolated stocks occurs at a faster rate in mtDNA than in nuclear genes. Thus, on average, mtDNA variation is expected to be greater between stocks and less within stocks. In most species, mtDNA has a higher mutation rate than single copy nuclear DNA, providing high-resolution analyses of recent evolutionary events (Birky *et al.*, 1989; Ferris & Berg, 1987; Meyer, 1993; Shaklee & Bentzen, 1998; Waples, 1998; Wilson *et al.*, 1985).

In order to fully understand the dynamic processes that shape species and their populations, more than one type of molecular marker needs to be investigated. Only then can the genetic data in combination with biological and life history data lead to an optimal management strategy for the sustainable utilisation of the species.

Thesis preview

The following chapters deal with the intraspecific variation of *Argyrosomus japonicus* (chapter 2) and *Pomadasys commersonnii* (chapter 3) based on analysis of their mtDNA control region sequences.

The overall aim of the study was to determine the genetic diversity and population structure of the species based on the genetic marker, and to link the genetic data with existing survey and other ecological and life history data.

Chapter 4 gives an integrated summary for the two species.