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Review of Stock Structure Studies of Orange Roughy (*Hoplostethus atlanticus*)

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1. Purpose

The Scientific Committee Multi-Annual Plan 2026–2028 (SC13-05) identified a priority task to investigate the stock structure of orange roughy on Westpac Bank and within the adjacent New Zealand Exclusive Economic Zone (EEZ). To date, only one peer-reviewed study has specifically examined stock structure in the eastern Tasman Sea. Smith et al. (2002) evaluated orange roughy stock structure using five complementary approaches: life-history characteristics, population length-frequency analysis, otolith shape analysis, genetic markers, and comparisons of spawning locations.

To place the findings of Smith et al. (2002) into a broader context, we undertook a comprehensive review of the available literature, including studies published since 2002, that have investigated orange roughy stock structure using a range of methodologies and analytical techniques. This review synthesizes evidence from fisheries, biological, genetic, chemical, and ecological studies to evaluate current knowledge of stock structure in orange roughy. A description of the orange roughy fisheries in the eastern Tasman Sea is also provided to support interpretation of the available stock identification evidence.

2. Background

The orange roughy (*Hoplostethus atlanticus*) is widely distributed throughout the North Atlantic and Southern Hemisphere oceans, with its greatest abundance occurring in the southwest Pacific Ocean. This deep-water, mid-slope species typically inhabits depths of 750-1250 m (Smith, 1986). Orange roughy exhibit group-synchronous ovarian development and form large spawning aggregations of mature adults during the austral winter (Robertson and Grimes, 1983). The high density of these aggregations has made the species an attractive target for deep-sea fisheries in Australia and New Zealand. However, the localized nature of spawning aggregations, coupled with intensive fishing pressure directed at reproductive adults, has led to the rapid depletion of many local populations.

A fundamental prerequisite for effective fisheries management is the identification and delineation of production units, or stocks, within a species. Inadequate understanding of stock structure may result in either overexploitation of vulnerable populations or unnecessary constraints on sustainable fisheries. For cosmopolitan deep-water species such as orange roughy, relatively high levels of genetic connectivity among geographically separated groups might be expected because of the comparatively homogeneous nature of the deep-sea environment (Tingley and Dunn, 2018). However, the occurrence of rapid and localized depletions under intensive fishing pressure suggests that demographic independence can occur at spatial scales relevant to fisheries management. Consequently, accurate characterization of population structure is essential for defining biologically meaningful stock boundaries and developing effective management strategies.

Recognizing that no single method is likely to provide conclusive evidence of stock structure, Tingley and Dunn (2018) proposed an integrated assessment framework that draws on multiple lines of evidence. These include: (i) fisheries-dependent and fisheries-independent data; (ii) morphological characteristics; (iii) life-history traits; (iv) movement and tagging information; (v) chemical and molecular markers; and (vi) habitat boundaries. By combining these complementary approaches, researchers can more effectively distinguish biologically meaningful stock units, thereby providing a stronger scientific basis for sustainable fisheries management and conservation.

3. Genetic variation

3.1. Allozyme electrophoretic methods

Allozymes are enzyme variants encoded by different alleles at the same genetic locus. Because they exhibit genetic variation among individuals and populations, they have been widely used as molecular markers to investigate evolutionary relationships, population structure, and demographic history. Ideally, molecular markers used in stock discrimination studies should be selectively neutral, with observed variation arising primarily through genetic drift rather than natural selection. Although some allozyme loci have been shown to be influenced by selection and therefore may not satisfy the assumption of neutrality, they have nevertheless proven useful for distinguishing stocks and assessing population differentiation (Tingley and Dunn, 2018).

Smith (1986) conducted the first genetic study of orange roughy using gel electrophoresis to examine variation in enzyme loci. Samples were collected from four locations around New Zealand, including two sites on the Challenger Plateau in the Tasman Sea, as well as from several locations in the North Atlantic Ocean. Analysis of seven polymorphic enzyme loci revealed little genetic differentiation among samples from the western (Challenger Plateau) and eastern (Chatham Rise, Wairarapa, and Kaikōura) regions of New Zealand, or between New Zealand and the north-eastern Atlantic population from the Rockall Trough. Smith (1986) noted that such a high degree of genetic similarity across an approximate distance of 21,000 km is unusual for a marine teleost species. He suggested that this pattern could reflect either similar selective pressures acting on geographically isolated populations or gene flow among spatially connected populations. At the time, little was known about the extent of orange roughy movements, whether through adult migration or larval dispersal. However, observations from commercial fisheries around New Zealand indicated that adults disperse from spawning aggregations, suggesting a potential mechanism for maintaining genetic connectivity across broad geographic areas.

Subsequently, Black and Dixon (1989) analysed variation at nine polymorphic enzyme loci in orange roughy samples collected from Australian and New Zealand waters. Based on observed differences in allozyme frequencies, they proposed the existence of three subpopulations: (i) New Zealand (Chatham Rise), (ii) eastern Australia and Tasmania, and (iii) South Australia.

However, this conclusion was not supported by a later and more extensive study by Elliott and Ward (1992). Using samples collected by commercial fishing vessels from six locations across southern Australia, spanning Western Australia to New South Wales, together with samples from the Chatham Rise off New Zealand, the authors examined population structure using allozyme variation at 28 loci. Orange roughy exhibited relatively high levels of genetic diversity, with average heterozygosity estimated at approximately 13% per population. Such high heterozygosity was expected to enhance the statistical power of genetic analyses aimed at detecting population subdivision. Despite the broad geographic scale of the study, encompassing approximately 3,000 km of the southern Australian coastline, no evidence of genetic differentiation was detected among Australian samples based on analyses of eleven polymorphic loci and average sample sizes of approximately 120 individuals per locality. Furthermore, allele frequencies in Australian populations were found to be very similar to those observed in the New Zealand sample from the Chatham Rise. These results suggested that, despite the occurrence of localized spawning aggregations, substantial dispersal and gene flow occurred among the Australian and New Zealand populations examined.

Elliott and Ward (1992) estimated that a minimum of approximately 200 migrants per locality per generation would be sufficient to maintain the observed levels of genetic homogeneity. They noted, however, that the actual number of migrants was likely to be considerably higher. Their findings therefore supported the hypothesis that extensive connectivity among populations may contribute to the remarkably low levels of genetic differentiation observed across much of the species' distribution.

Ward and Elliott (1993) further investigated the allozyme samples from southern Australian orange roughy populations previously analysed by Elliott and Ward (1992) to assess potential relationships between genetic variation and morphological traits. Specifically, they examined associations between single-locus and multilocus heterozygosity and fish length, a range of meristic characters, and a measure of bilateral asymmetry. The meristic traits included counts of dorsal fin spines, dorsal fin rays, anal fin spines and rays, and various categories of left and right pectoral fin rays. Asymmetry was assessed by comparing the total number of pectoral fin rays on the left and right sides of the body. Analyses revealed a significant positive correlation between multilocus heterozygosity and fish length in only one of the six southern Australian samples. However, Ward and Elliott (1993) concluded that there was little evidence for a general relationship between heterozygosity and body size in orange roughy, suggesting that the significant result observed in the Western Australian sample was likely attributable to sampling error.

Furthermore, no consistent associations were detected between either individual-locus or multilocus heterozygosity and the mean or variance of the meristic characters examined. Overall, the study found little evidence that genetic heterozygosity was related to morphological variation in orange roughy. These findings suggested that allozyme heterozygosity had limited explanatory power for variation in body size, meristic traits, or asymmetry within the populations studied, and therefore provided little support for the use of such relationships in stock discrimination.

Elliott et al. (1994) compared allozyme genetic variation in orange roughy collected from southern Australian waters with samples obtained from the North Atlantic west of Scotland, a separation of approximately 22,000 km. Individuals were screened at 11 polymorphic allozyme loci to assess the extent of genetic differentiation between these geographically distant populations. Significant heterogeneity was detected at three loci, and the overall gene-diversity statistic indicated a low but statistically significant level of genetic differentiation. In addition, Australian orange roughy exhibited lower allozyme heterozygosity than the North Atlantic sample. Although the degree of differentiation was small, the presence of significant allozyme heterogeneity suggested some historical genetic connectivity between the two regions. Based on the observed level of differentiation, Elliott et al. (1994) estimated that as few as 30 migrants per generation could be sufficient to maintain the genetic similarity observed between populations. Given the estimated orange roughy generation time of 20 to 30 years (Mace et al., 1990), even limited levels of migration could substantially reduce genetic divergence over evolutionary timescales. Direct migration of adult orange roughy across such vast distances is considered highly unlikely. Instead, Elliott et al. (1994) proposed that genetic connectivity may be maintained through a stepping-stone pattern of gene flow, whereby dispersal occurs between adjacent populations over multiple generations. Such connectivity could be facilitated by the drift of eggs and larvae in ocean currents, movements of juveniles, or shorter-distance migrations of adults between neighbouring populations. These findings highlighted the potential for low levels of gene flow to maintain genetic homogeneity across much of the species' global distribution, despite the occurrence of localized spawning aggregations and extensive geographic separation

Smith et al. (1991) reported a decline in allozyme heterozygosity on three New Zealand orange roughy fishing grounds between 1982 and 1988. The authors suggested that this reduction may have resulted from the selective removal of larger, older, and potentially more heterozygous individuals from previously unfished populations. If this hypothesis were correct, populations subjected to prolonged fishing pressure would be expected to exhibit genetic differences from more recently exploited stocks. To evaluate this possibility, Smith and Benson (1997) investigated genetic variation among orange roughy populations from both long-established and newly developed fisheries. Extensive tissue samples were collected from five locations along the east coast of New Zealand and nine locations on the Chatham Rise. Additional samples were obtained from two recently exploited fisheries: one

on the eastern Chatham Rise and another on the Louisville Ridge, located beyond New Zealand's 200-nautical-mile Exclusive Economic Zone (EEZ). Analysis of variation at eight common allozyme loci indicated that, although heterozygosity had declined relative to earlier observations, the reduction between 1982 and 1994 was not statistically significant. However, significant heterogeneity was detected at three loci when all samples were analysed collectively, suggesting that the sampled fish did not belong to a single panmictic population. No significant genetic heterogeneity was observed among samples from the east coast of New Zealand, indicating substantial genetic similarity within that region. In contrast, significant genetic differentiation was detected between the east-coast samples and the geographically closest samples from the Chatham Rise, collected at an area known as the Hole. This finding provided evidence of a genetic discontinuity between the east coast and the Chatham Rise. Furthermore, east-coast populations exhibited higher average heterozygosity than those from the Chatham Rise. Based on these results, Smith and Benson (1997) concluded that orange roughy populations east of New Zealand exhibited a pattern consistent with isolation by distance, whereby genetic differentiation increases with geographic separation as a consequence of restricted gene flow among populations. Their study provided some of the first allozyme evidence for regional population structuring in orange roughy within New Zealand waters, despite the generally low levels of genetic differentiation reported in earlier studies.

Smith et al. (1997) investigated allozyme variation in fish collected from four spawning grounds located off the east coast (Ritchie Bank, Waitaki, and Box on the eastern Chatham Rise) and the south coast (Puysegur) of New Zealand. These sites, separated by several hundred kilometres, were selected because the distances between them exceeded the likely dispersal range of larvae and each supported a significant New Zealand fishery. Of the eleven loci examined, eight were sufficiently polymorphic for analysis. Significant genetic differentiation was detected at one or more loci among all sampling locations, with the exception of Ritchie Bank and Box. The findings demonstrated that the sampled fish did not constitute a single panmictic population. Rather, the populations showed evidence of restricted gene flow among spawning sites, with migration rates estimated at approximately 13.2 migrants per generation.

3.2. Mitochondrial DNA analyses

Genetic markers derived from mitochondrial DNA (mtDNA) are commonly used to investigate maternal relationships and frequently reveal higher levels of genetic variation than allozymes. Several characteristics of the extranuclear mitochondrial genome, including its clonal inheritance, rapid evolutionary rate, and relatively conserved molecular structure, make mtDNA a powerful tool for examining fisheries stock structure and population composition. In addition, mtDNA sampling is less demanding than allozyme analysis because muscle and other tissue samples can be preserved in 95% ethanol. In

contrast, tissues collected for allozyme studies must be frozen immediately after sampling at sea and subsequently stored at −70°C in the laboratory (Smith et al., 1997; Varela et al., 2013). However, mitochondrial DNA may not be entirely evolutionarily neutral (Ballard & Kreitman, 1995).

Ovenden et al. (1989) were the first to investigate the population structure of orange roughy using mtDNA obtained from fish collected in deep-water trawl catches (680-1320 m depth) off the east and west coasts of Tasmania during 1987. The east coast population was sampled within a 36 km radius, whereas samples from the west coast were collected from areas with radii of 0.9 km and 3.4 km. Analysis of 49 individuals identified 11 mitochondrial haplotypes, with only one haplotype occurring in both east and west coast samples. Four fish from the east coast possessed four unique haplotypes, while nine fish from the west coast exhibited six additional unique haplotypes. Although the study was based on a relatively small sample size, the authors noted that theoretical studies had demonstrated that increasing sample size does not necessarily improve the accuracy of diversity estimates under certain conditions. Based on their findings, Ovenden et al. (1989) provided preliminary evidence supporting genetic subdivision within the Tasmanian orange roughy population, suggesting limited genetic exchange between populations on the eastern and western coasts of Tasmania.

The findings of Ovenden et al. (1989) were not supported by a subsequent study based on a larger and more extensive sampling programme (Smolenski et al. 1993). In that study, mitochondrial DNA (mtDNA) was extracted from ovarian tissue collected from 286 orange roughy individuals sampled from seven locations: the Great Australian Bight, South Australia (off south-eastern Kangaroo Island), the west and east coasts of Tasmania, New South Wales (NSW), New Zealand, and South Africa during 1987 to 1989. Samples were screened using 10 six-base and 3 four-base restriction enzymes. In addition, 49 individuals analysed in the earlier pilot study (Ovenden et al. 1989) were incorporated into the dataset for G-statistic (Gst) and group-variance analyses. Both analyses indicated low levels of genetic diversity. Results based on the six-base restriction enzymes provided no evidence of reproductively isolated populations within southeastern Australian waters. However, analysis of 107 fish using the three four-base restriction enzymes revealed at least partial genetic differentiation between the NSW and Tasmanian samples. This finding supported the existence of a distinct subpopulation in NSW waters, with genetically differentiated samples observed in consecutive years. The mtDNA analyses conducted with six-base restriction enzymes also detected little genetic differentiation among populations from New Zealand, southern Australia, and South Africa.

Elliott et al. (1994) examined allozyme and mitochondrial DNA (mtDNA) variation across a broader geographic range, analysing samples from five Australian locations (New South Wales, the east and west coasts of Tasmania, South Australia, and the Great Australian Bight) and comparing them with samples from the North Atlantic (ICES Fishing Area VIb). Significant heterogeneity in mtDNA haplotype frequencies was detected using χ^2 analysis;

however, this pattern was not supported by G_{st} analysis. Australian orange roughy exhibited lower allozyme heterozygosity and lower mtDNA nucleotide diversity than the North Atlantic sample. Although the observed allozyme and mtDNA heterogeneity between Australian and North Atlantic populations was statistically significant, it was limited in magnitude, suggesting either historical connectivity or low levels of gene flow between populations occupying these geographically distant regions.

Baker et al. (1995) reached similar conclusions in a study encompassing a wider sampling area in the Southwest Pacific Ocean. The study included 24 orange roughy collected from five fishing grounds in the Tasman Sea and Chatham Rise near New Zealand. For comparison, an additional four fish from the west coast of Tasmania and four from the east coast of South Africa were analysed. Mitochondrial DNA haplotypes were characterised through direct sequencing of the cytochrome *b* gene to investigate genetic relationships among regional populations. An average of 252 nucleotide base pairs was sequenced from each of 32 individuals, resulting in the identification of nine unique mtDNA haplotypes. Genetic variation in orange roughy was found to be relatively high, as indicated by both average sequence divergence and haplotype diversity. However, no significant differences in haplotype frequencies were detected among samples from New Zealand, Tasmania, and South Africa, suggesting limited genetic differentiation across these regions.

Smith et al. (1996) investigated the stock structure of orange roughy using mitochondrial DNA (mtDNA) restriction fragment-length polymorphism (RFLP) analysis. Samples were collected from four major spawning grounds: Ritchie Bank and Chatham Rise in the south-west Pacific Ocean, and Challenger Plateau and the west coast in the Tasman Sea. Additional samples were obtained from two newly discovered spawning areas, Puysegur and Waitaki, while fish from spawning grounds off Tasmania were included as outlier samples. Analysis of mtDNA variation generated by six-base restriction enzymes revealed significant genetic heterogeneity among samples from the six New Zealand spawning sites and the Tasmanian site. The southern spawning areas, Puysegur and Waitaki, were genetically similar to each other but distinct from all northern sites due to the absence of a haplotype common in northern populations. Estimates of gene flow were at least ten times higher within the northern group and within the southern group than between them. Some geographically distant spawning grounds also showed genetic similarity. For example, samples from the west coast were genetically similar to those from Ritchie Bank and Chatham Rise on the east coast. Although genetic similarity alone does not prove that fish belong to the same stock, these findings suggested that Cook Strait may not constitute a major barrier to gene flow between orange roughy populations in the Tasman Sea and the south-west Pacific Ocean.

Smith et al. (1997) re-examined the mtDNA data and found significant heterogeneity across the overall dataset, although mtDNA indicated less genetic differentiation than allozyme analyses. Only two pairwise comparisons were statistically significant: Ritchie Bank versus Waitaki, and Waitaki versus Puysegur. These results provided evidence of genetic isolation

among spawning groups and supported the existence of three genetic groupings: (1) Puysegur, (2) Waitaki, and (3) Ritchie Bank and Box. Subsequent work by Smith et al. (2002) identified additional genetic differentiation between samples collected from Challenger Plateau and Lord Howe Rise, both located west of New Zealand, providing further evidence of population structuring within the region (See Section 7).

Varela et al. (2012) examined the global population structure of orange roughy using mitochondrial DNA (mtDNA) sequence data from 546 specimens collected across 13 sampling locations in five regions: New Zealand, Australia, Namibia, Chile, and the Northeast Atlantic Ocean. New Zealand samples were obtained from Northern New Zealand (ORH1), Ritchie Bank, Chatham Rise, Puysegur, and Challenger Plateau. Additional samples from the South Pacific Regional Fisheries Management Organisation (SPRFMO) Convention Area were collected from Lord Howe Rise and Louisville Ridge. Genetic variation was assessed using sequences from the cytochrome *b* (cyt *b*) and cytochrome oxidase I (COI) genes. Analysis of pairwise Φ_{ST} values for the cyt *b* gene revealed no significant genetic differentiation among sampling sites. Similarly, pairwise Φ_{ST} comparisons based on COI sequences were generally low and non-significant, indicating a lack of genetic structure across most locations. The only evidence of weak differentiation was observed between two sites in the Northeast Atlantic. Both markers exhibited high haplotype diversity, a pattern consistent with a large historical effective population size and commonly observed in marine fish species.

Overall, analyses of mtDNA variation indicated a high degree of genetic homogeneity across the species' distribution, with no detectable genetic divergence among most sampled populations. However, the absence of differentiation in selectively neutral mtDNA markers does not necessarily imply the absence of population structure. Genetic divergence may remain undetected when effective population sizes are large or when population separation has occurred too recently for differences to accumulate. Furthermore, low levels of ongoing gene flow can maintain genetic similarity despite demographic independence. Varela et al. (2012) proposed three possible explanations for the observed genetic homogeneity: (1) panmixia, in which individuals across the species' range form a single, freely interbreeding population; (2) recent population divergence, where populations have become differentiated only recently and insufficient time has elapsed for detectable mtDNA differences to develop; and (3) limited but persistent migration, whereby a small number of migrants each generation maintain genetic connectivity among populations, even if such connectivity is insufficient to establish demographic linkage between them. These findings highlight the limitations of mtDNA markers for resolving fine-scale stock structure in orange roughy and underscore the need for complementary approaches using more informative genetic markers

3.3. Microsatellite (nuclear) DNA analyses

Nuclear DNA offers greater potential as a source of genetic markers than mitochondrial DNA (mtDNA) because of its larger size and biparental inheritance. Among available nuclear markers, microsatellites have proven considerably more effective than either allozymes or mtDNA for resolving stock structure. Microsatellite loci are highly polymorphic and have elevated mutation rates, allowing them to evolve rapidly and detect subtle patterns of population differentiation. Consequently, they can reveal fine-scale population structure that may not be detected using other genetic markers. In addition, microsatellites are typically located in non-coding regions of the genome and are therefore generally considered selectively neutral. As a result, observed genetic differences among populations are more likely to reflect restrictions to gene flow and population subdivision rather than adaptive divergence caused by natural selection within a panmictic population (Oke et al., 2002).

Oke et al. (2002) developed a suite of microsatellite markers for orange roughy and selected those exhibiting optimal levels of polymorphism for population analyses. Using six microsatellite loci from a larger set of 13 developed during the study, they analysed samples collected across a broad geographic range, including St Helens and the west coast of Tasmania, Lord Howe Island, the Western Management Zone of southern Australia, the north-west Challenger Plateau of New Zealand, Namibia, and the North Atlantic. The results revealed no significant genetic differentiation within Australian waters and no evidence of differentiation between populations from Australia and New Zealand or between Australia and the Northeast Atlantic. Furthermore, each sampling location, with one possible exception, was connected to every other location through populations with which it showed no significant genetic differentiation. These findings suggested a high degree of genetic connectivity across much of the species' distribution. Nevertheless, a weak but statistically significant pattern of isolation by distance was detected between southern Australia and the Challenger Plateau, indicating that geographic separation may have a limited influence on gene flow at large spatial scales.

White et al. (2009) further investigated orange roughy population structure using nuclear microsatellite markers. The study analysed 294 individuals collected from five regions in the Northeast and Mid-Atlantic, including Biscay, Porcupine, Hebrides, Faraday, and Sedlo Bank, together with samples from Namibia in the South Atlantic. Power analyses demonstrated that the microsatellite dataset was capable of detecting very low levels of genetic differentiation ($F_{ST} \geq 0.0025$). Despite this high statistical power and the substantial geographic distances among sampling locations, some of which exceeded 2,000 km, no evidence of population structuring was detected within the North Atlantic. However, significant genetic differentiation was observed between the pooled Northeast Atlantic samples and the Namibian sample, indicating restricted gene flow between the North and South Atlantic regions (White et al., 2009).

Carlsson et al. (2011) used eight microsatellite loci to examine population structure of orange roughy on Porcupine Bank, west of Ireland. The study analysed 388 spawning adults

and juveniles collected from seven sampling locations and specifically tested for genetic differentiation associated with local seafloor features. Although the observed differentiation was low, significant genetic differences were detected between fish inhabiting flat-bottom habitats and those associated with seamounts. These genetic results were supported by otolith chemistry analyses, which showed consistent differences in the core chemistry of fish collected from the two habitat types. Distinct chemical signatures persisted throughout the first 10 years of growth, suggesting long-term residency or site fidelity. On the basis of these findings, the authors hypothesised that seafloor topographic features such as seamounts and flats may act as discrete spawning habitats, resulting in restricted gene flow and fine-scale population structuring despite the species' apparent capacity for long-distance dispersal.

Varela, Ritchie and Smith (2013) investigated genetic diversity and population differentiation in orange roughy at a global scale using nine microsatellite loci. Samples were collected from New Zealand, Australia, Namibia, Chile, and the Northeast Atlantic Ocean. The New Zealand component included 12 sampling sites within northern New Zealand (ORH1), together with samples from Ritchie Bank, Chatham Rise, Puysegur, and Challenger Plateau. Temporal variation was also examined using samples collected from eight ORH1 sites in two different years.

Genetic diversity was consistently high across all sampling locations, with a mean expected heterozygosity (HE) of 0.86. This estimate was comparable to, although somewhat higher than, those reported by White et al. (2009) (HE = 0.72) and Carlsson et al. (2011) (HE = 0.77). In contrast, Oke et al. (2002) reported substantially lower diversity (HE = 0.40), likely reflecting the inclusion of several loci with relatively low heterozygosity that were not subsequently used by Varela et al. (2013).

Analyses revealed low but statistically significant genetic differentiation at the global scale. Differentiation was detected among Southern Hemisphere regions and between Southern Hemisphere populations and those in the Northeast Atlantic. In contrast to earlier microsatellite studies that reported little differentiation between Australia and New Zealand, Varela et al. (2013) found evidence that these regions were not genetically homogeneous. Despite these broad-scale patterns, temporal analyses of the ORH1 samples found no significant genetic differentiation between sites or years, indicating temporal stability in genetic composition and suggesting panmixia at this relatively fine spatial scale.

The absence of temporal differentiation within ORH1 contrasts with the earlier findings of Smith and Benson (1997), which suggested genetic subdivision among some New Zealand spawning aggregations. However, caution is warranted when interpreting the temporal analyses of Varela et al. (2013), as the combination of highly polymorphic microsatellite loci and sample sizes of fewer than 50 individuals at some sites may have reduced the ability to detect subtle population structure. The authors proposed that the observed

pattern of isolation by distance at the global scale may reflect a stepping-stone migration process, whereby genetic connectivity is maintained through sequential dispersal among neighbouring populations. Such a pattern is consistent with limited but ongoing adult-mediated gene flow across the species' geographic range.

Collectively, microsatellite studies have generally shown lower levels of population differentiation in orange roughy than might be expected given the species' fragmented distribution and discrete spawning aggregations. While these studies provide evidence of substantial genetic connectivity across large spatial scales, weak patterns of isolation by distance and differentiation between ocean basins suggest that gene flow is not unlimited. The results also illustrate the difficulty of detecting stock structure in long-lived marine species with large effective population sizes, where even biologically meaningful demographic separation may generate only subtle genetic signals

3.4. DNA genomics analyses

Population genomics, enabled by next-generation sequencing (NGS), allows researchers to scan entire genomes for adaptive genetic variation without prior knowledge of the selective pressures involved (Luikart et al., 2003). Compared with earlier approaches based on allozymes, short DNA sequences, or microsatellite markers, genomic methods provide substantially greater analytical power and resolution. This increased power enables the detection of very low levels of gene flow and population connectivity that were previously difficult to identify. Importantly, NGS facilitates the discovery and screening of thousands to millions of molecular markers across the genome, several orders of magnitude more than traditional methods, which typically relied on only tens of markers. Consequently, genomic approaches have greatly improved the ability to detect fine-scale population structure and quantify low levels of genetic differentiation.

Using 4,723 single nucleotide polymorphisms (SNPs) identified through NGS-based methods, Gonçalves da Silva et al. (2015) investigated genetic homogeneity and local adaptation among orange roughy stocks from five locations around Tasmania. Their analyses indicated that orange roughy from southern Australian sample sites within the Southern, Eastern, and Cascade Plateau Management Zones comprise at least several genetically connected stocks linked through drift connectivity, and potentially form a single panmictic population characterized by high levels of gene flow. Furthermore, no genetic evidence of local adaptation was detected, suggesting that none of the sampled fishing grounds could be excluded as evolutionarily compatible sources of colonizers for overfished areas examined in the study.

In a subsequent study, Gonçalves da Silva et al. (2020) applied population genomic analyses using SNP markers to investigate orange roughy population structure across the Atlantic Ocean, including two locations in the South Atlantic (off Namibia and South Africa)

and six locations in the North Atlantic (two along the Mid-Atlantic Ridge and four off the western coasts of the United Kingdom and mainland Europe). The study focused on genetic differentiation along habitat contours, with particular attention to ecological variation among putative populations and associated biogeographic patterns. Two hypotheses were tested: (i) that habitat use within a complex deep-sea environment may generate cryptic patterns of dispersal and isolation by distance (IBD), and (ii) that environmental discontinuities may promote local adaptation despite apparently high levels of gene flow.

The results demonstrated that, although orange roughy had previously been considered panmictic in the North Atlantic, neutral genetic differentiation existed among regional populations separated by distance along deep-water channels. In addition, distinct patterns of cryptic genetic structure were identified at putatively functional loci, despite evidence of substantial gene flow. These findings suggest that population structure in orange roughy is more complex than previously recognized and that fisheries currently managed as single stocks may benefit from management approaches that account for cryptic stock structure. Recognizing such hidden patterns of population differentiation could lead to more effective and sustainable fisheries management.

4. Parasitology

Parasites have long been used as biological tags for distinguishing marine fish stocks and are widely recognised as effective indicators of population structure (MacKenzie, 1983). Many parasites, particularly those in their larval stages, can persist within fish hosts for extended periods, sometimes throughout the host's lifetime. Because parasite species are not uniformly distributed across the geographic range of a host species, juvenile fish from different regions are exposed to distinct parasite communities. Consequently, the parasite assemblages present in adult fish provide a biological record of the habitats they have occupied and can be used to identify their stock or population of origin.

Lester et al. (1988) investigated whether parasite communities could be used to distinguish populations of orange roughy. The study examined 1,251 fish collected from eight locations in southern Australia and three locations in New Zealand. Fish from each sampling area were divided into three size classes, with mean lengths of approximately 28, 37, and 42 cm. Using canonical multivariate analysis, the authors analysed the abundance and occurrence of several parasite taxa, including larval nematodes (*Anisakis* spp., *Terranova* sp., and a spirurid species) and larval cestodes (*Hepatoxylon trichiuri* and *Callitetrarhynchus* sp.).

The parasite data successfully discriminated among five Australian stocks: the Great Australian Bight, South Australia/western Victoria/western and southern Tasmania, Cascade Plateau/Tasman Rise, north-eastern Tasmania, and New South Wales. Similarly, three New Zealand stocks were identified: north-eastern, south-eastern, and western New Zealand. The study found no significant differences in parasite assemblages between fish

collected during the spawning season and those sampled outside the spawning season within the same region. In Australian waters, spawning fish exhibited parasite communities similar to those of fish collected from the same locality at other times of the year. Based on these findings, the authors concluded that orange roughy exhibit limited movement among regions and are therefore largely sedentary. The distinct parasite faunas associated with different areas provided strong evidence for the existence of geographically discrete stocks.

In contrast, Gauldie and Jones (2000) questioned the usefulness of parasite load as a stock discriminator for orange roughy in New Zealand waters. The authors examined relationships between parasite load and host characteristics, including growth rate, depth of capture, sex, and date of capture. Fish were grouped according to both the New Zealand Quota Management Areas (ORH1-ORH10) and three major Regional Fisheries Areas: Ritchie Bank (ORH2), Chatham Rise (ORH4), and Challenger Plateau (ORH7). A total of 1,107 orange roughy were analysed. To avoid bias associated with simple summation of parasite numbers, parasite loads were standardised by dividing the abundance of each parasite type by its average abundance across individuals.

A total of 32 parasite species were identified. Trematodes accounted for the greatest species diversity, whereas nematodes were the most numerically abundant parasites. Significant differences in mean log-transformed parasite loads were observed among both Quota Management Areas and Regional Fisheries Areas. However, the analyses also revealed significant partial regressions between parasite load and fish length, capture depth, and month of capture. In contrast, sex, management area (or regional fishery area), and year of capture were not significant predictors of parasite load.

These results suggested that parasite load alone was not an effective stock discriminator when stock boundaries were defined according to Quota Management Areas or Regional Fisheries Areas. This conclusion contrasts with the findings of Lester et al. (1988) in Australian waters. One possible explanation for this discrepancy is the much broader parasite dataset used by Gauldie and Jones (2000), who analysed 32 parasite species compared with only seven species examined by Lester et al. (1988). The authors argued that the observed differences in parasite load between fish from the Challenger Plateau and the North Chatham Rise could be explained by factors other than stock structure. Once variation associated with fish length, depth of capture, and month of capture was accounted for, no significant differences in overall parasite load were detected between fish from the Challenger Plateau, Ritchie Bank, and other New Zealand regions.

Furthermore, the study demonstrated that parasite load in orange roughy is influenced by ontogenetic and temporal processes. These effects can obscure geographic signals and reduce the effectiveness of parasites as stock discriminators. Consequently, while parasite assemblages may provide valuable information on stock structure in some regions, their

utility as indicators of population segregation appears to vary according to ecological context and the biological characteristics of the host population.

5. Morphology

Morphological variation has been widely used to investigate both taxonomic relationships and stock structure in marine and freshwater fishes. In some cases, phenotypic studies have identified differences among populations where no corresponding genetic differentiation has been detected (Leslie & Grant, 1990). Morphometric analyses are particularly valuable because they provide quantitative measures of body shape; however, to be meaningful, morphometric data must be adjusted to remove the effects of overall body size so that comparisons reflect variation in shape rather than growth differences (Reist, 1985).

5.1. Body morphology

Elliott et al. (1995) used morphometric variation to examine the stock structure of orange roughy in southern Australian waters by comparing fish from spatially and temporally separated aggregations. Samples were collected from both spawning and non-spawning aggregations on fishing grounds located off the eastern and southern coasts of Tasmania. A total of 1,307 fish were examined, and 39 morphometric characters were measured for each individual. To remove the influence of body size on shape measurements, all morphometric variables were standardised using an allometric adjustment and subsequently analysed using both univariate and multivariate statistical methods. To minimise potential ontogenetic effects on body shape, the analyses were restricted to mature fish with standard lengths greater than 300 mm.

The study revealed significant morphological variation among orange roughy collected from geographically distinct aggregations. The results suggested the presence of at least seven morphologically distinguishable stocks within southern Australian waters. Aggregations that were widely separated in space and time exhibited the greatest degree of morphological differentiation and formed clearly distinct groups, whereas samples that were geographically or temporally closer tended to be more similar. The findings also indicated that the major spawning aggregation may comprise fish originating from different groups that arrive at the same spawning location at different stages of the spawning season. These results provide evidence of population structuring in orange roughy and suggest that movement patterns and spawning behaviour may contribute to the observed morphological differentiation among stocks.

5.2. Otolith shape

In addition to examining parasite load as a potential stock discriminator, Gauldie and Jones (2000) investigated whether otolith morphometrics could differentiate orange roughy populations from three major Regional Fisheries Areas in New Zealand. Samples for both parasite and otolith analyses were collected from the North Chatham Rise (n = 100), Challenger Plateau (n = 42), and Ritchie Bank (n = 123). Because otolith width, otolith length, and fish length were correlated, otolith width was standardised by dividing it by the product of otolith length and fish length to minimise ontogenetic effects and allow meaningful comparisons among samples. Following standardisation, the mean otolith width of fish from the North Chatham Rise was found to differ significantly from those of the Ritchie Bank and Challenger Plateau samples, whereas no significant difference was detected between the latter two regions. The authors suggested that these differences in otolith morphology could reflect underlying biological differences among populations, potentially associated with regional variation in growth rates.

Subsequently, Gauldie and Crampton (2002) examined otolith shape variation in orange roughy collected from four geographically distant regions: the North Atlantic, the waters off Namibia in the South Atlantic, the South Tasman Rise south of Tasmania, and the Chatham Rise east of New Zealand. Unlike the earlier study, which focused primarily on simple otolith dimensions, this investigation employed a more sophisticated morphometric approach. Otolith outlines were digitised from two-dimensional images and analysed using Fourier-transform decomposition, with the resulting shape variables summarised through principal component analysis (PCA). This method allowed a comprehensive assessment of overall otolith shape rather than relying on a limited set of linear measurements.

The PCA results showed substantial overlap in otolith shape among samples from all four regions. The distribution of shape variation was largely uniform, providing no clear evidence of discrete stock groupings based on otolith morphology. The authors therefore concluded that otolith shape did not support the existence of distinct orange roughy stocks among the populations examined.

The findings of Gauldie and Crampton (2002) also provided a broader context for interpreting the earlier results of Gauldie and Jones (2000). The significant differences reported between eastern and western New Zealand stocks were based primarily on the ratio of otolith width to otolith length, a relatively simple measure of shape. Because this ratio represents only one component of the more comprehensive set of shape variables analysed in the later study, the authors argued that the earlier differences may have reflected a limited aspect of otolith morphology rather than overall shape divergence. When the full range of otolith shape components was considered, no significant differences among regional samples were detected. Consequently, the study suggested that otolith morphology, when evaluated using comprehensive shape analyses, provides little support for substantial stock differentiation in orange roughy across the regions examined.

These contrasting results highlight both the potential and the limitations of otolith morphometrics in stock identification. While simple otolith measurements may reveal regional differences associated with growth or environmental conditions, more comprehensive analyses of otolith shape have not consistently demonstrated biologically meaningful stock structure. As a result, otolith morphometrics are best interpreted alongside other sources of evidence, including genetic, parasitological, and ecological data, when assessing population structure and stock boundaries in orange roughy.

6. Otolith microchemistry

Trace-element analysis of otoliths has been widely applied to fish stock discrimination and population structure studies (Thresher, 1999). Although the theoretical basis for using otolith chemistry as a stock delineation tool was established during the 1980s, the approach advanced substantially during the 1990s and 2000s through the development of increasingly sensitive analytical techniques and more sophisticated statistical methods (Campana, 1999; Thresher, 1999). Despite these advances, the utility of otolith chemistry as an indicator of population structure in marine fishes remains uncertain because of methodological limitations and unresolved questions regarding the influence of environmental factors on elemental incorporation into otoliths (Proctor & Thresher, 1998).

Edmonds et al. (1991) used inductively coupled plasma atomic emission spectrometry (ICP-AES) and inductively coupled plasma mass spectrometry (ICP-MS) to analyse trace-element concentrations in the sagittal otoliths of orange roughy collected from three regions of the south-eastern Australian fishery: waters off Adelaide (n = 28), eastern Tasmania (n = 23), and western Tasmania (n = 23). The objective was to determine whether patterns of elemental accumulation differed among capture locations, which would imply limited mixing and prolonged separation among populations. Concentrations of ten elements (Ba, Cd, Cu, K, Mg, Na, Pb, S, Sr, and Zn) were analysed using canonical variate (discriminant) analysis. The results demonstrated that elemental signatures were specific to the areas where fish were collected, with Mg, Na, and S contributing most strongly to the discrimination among regions. The first canonical variate separated the Adelaide samples from those collected around Tasmania, while the second distinguished fish from eastern and western Tasmania. These findings suggested restricted movement among the three regions and provided evidence for stock differentiation within south-eastern Australian waters.

More than a decade later, Shepard et al. (2007) investigated stable isotope composition in otoliths of pre-recruit orange roughy sampled from different habitats ("hills" and "flats") and geographic areas (northern and southern sectors) of the Porcupine Bank in the Northeast Atlantic. Age-specific profiles of carbon ($\delta^{13}C$) and oxygen ($\delta^{18}O$) isotopes were reconstructed from the otolith core to the margin, providing a record of individual life-

history patterns related to temperature, habitat depth, and metabolic activity. Stable isotope profiles were broadly consistent among individuals, suggesting strong endogenous or ontogenetic influences on isotopic variation. The data indicated that post-larval orange roughy occupy mesopelagic habitats where they forage actively in relatively warm waters before moving into colder deep-demersal environments as juveniles. As fish approached recruitment, their habitat use and metabolic characteristics increasingly resembled those of adults.

Importantly, comparisons among habitats and areas on the Porcupine Bank revealed differences in isotope profiles between fish inhabiting southern hill and flat habitats during particular life stages. These differences suggested that juvenile orange roughy from neighbouring habitats may experience distinct environmental conditions and metabolic histories. The authors concluded that habitat-associated populations may exist on the Porcupine Bank, providing evidence of fine-scale population structure within an area previously assumed to be relatively homogeneous. Such spatial structuring could have important implications for stock resilience and sustainable fisheries management.

Thresher and Proctor (2007) further explored population structure in orange roughy by examining trace-element composition in otolith primordia and ontogenetic patterns of strontium (Sr) incorporation. Fish were collected from seven locations in southern Australia, five locations around New Zealand (Lord Howe Rise, Northwest Challenger Plateau, South Challenger Plateau, Bay of Plenty, and Chatham Rise), and the North Atlantic as an outgroup. Single-point analyses of otolith primordia revealed small but statistically significant differences among sites for all measured trace elements, including Sr. Post hoc analyses identified the North Atlantic samples as a distinct outlier, differing significantly from all 11 Southwest Pacific locations for Sr, Zn, and Pb concentrations.

Within the Southwest Pacific, Sr concentrations at the otolith primordium showed highly significant geographic variation, displaying a clear latitudinal pattern across Australian, New Zealand, and Tasman Sea sampling sites. This pattern indicated the existence of spatially structured populations and suggested the operation of a common large-scale process influencing population differentiation throughout the region. The observed latitudinal gradient could reflect either a series of environmentally distinct spawning grounds supporting relatively isolated populations or dispersal from a limited number of major spawning areas across an environmental gradient. Analysis of ontogenetic variation in Sr concentrations among juveniles and young adults provided further evidence that elemental signatures were site-specific and strongly influenced by environmental conditions. Although the precise environmental drivers remain uncertain, the consistent differences observed among locations support the hypothesis that otolith chemistry reflects local environmental histories and can therefore provide valuable information about population connectivity and stock structure.

Collectively, these studies demonstrate the potential of otolith chemistry and stable isotope analyses to reveal population structure in orange roughy across a range of spatial scales. Elemental and isotopic signatures have identified regional differentiation in Australia, fine-scale habitat-related structuring in the Northeast Atlantic, and broad geographic patterns across the Southwest Pacific. While environmental influences on element incorporation remain incompletely understood, otolith-based approaches provide an important complementary line of evidence for understanding stock structure of this long-lived deep-water species.

7. Stock structure in the eastern Tasman Sea

Smith et al. (2002) investigated stock structure among four geographically proximate orange roughy fishing areas in the eastern Tasman Sea: Lord Howe Rise (LH), Northwest Challenger (NC), Southwest Challenger (SC), and Westpac Bank (WP). Five approaches were used to distinguish stocks: age and length at maturity, length-frequency analysis, otolith shape analysis, genetic analysis, and spawning period. Otolith shape analysis identified two groups, LH/NC and SC/WP. Genetic analysis detected significant heterogeneity between NC and SC at one of six nuclear DNA markers, while mitochondrial DNA markers showed no significant differences among areas. However, the significance of the nuclear marker should be interpreted cautiously because temporal heterogeneity has also been reported for this marker in east coast orange roughy populations. Life-history characteristics provided limited evidence of stock separation, although fish from LH matured at a significantly older age than those from WP, and larger fish tended to occur in northern areas. Overall, the available biological evidence supported treating LH, NC, and SC as separate stocks. In contrast, no biological differences were detected between SC and WP, which are separated by only approximately 100 km, suggesting that these fisheries exploit a single straddling stock.

Clark et al. (2016) reviewed all available evidence on orange roughy stock structure in the Tasman Sea and western Pacific Ocean within the SPRFMO Convention Area. The review incorporated information on catch distribution, spawning-ground locations, life-history characteristics, genetic studies, otolith composition and shape, morphometric characteristics, and parasite assemblages. The authors concluded that no single source of information provided a definitive description of stock structure and that different datasets often produced conflicting interpretations of stock boundaries. Nevertheless, the weight of evidence supported retaining the existing stock assessment and management units in the Tasman Sea: Lord Howe Rise, Northwest Challenger Plateau, Southwest Challenger Plateau (including Westpac Bank), West Norfolk Ridge South, and Tasman Rise. Together, these studies indicate that while some biological differentiation exists among Tasman Sea orange roughy populations, substantial uncertainty remains regarding stock boundaries,

and the current management framework continues to represent the most defensible approach based on the available evidence.

8. General remarks

Despite the application of a wide range of techniques to investigate orange roughy stock structure, there remains no clear consensus regarding the extent of connectivity among populations. In general, studies based on biological and ecological characteristics have identified diagnostically significant differences among stocks, whereas genetic studies have typically indicated high levels of gene flow and limited genetic divergence, particularly between geographically proximate populations. Overall, the available evidence suggests substantial genetic connectivity across broad spatial scales, with some indication of isolation by distance.

These apparently conflicting findings are not necessarily contradictory. Morphological differences among adult fish may arise from environmental conditions experienced during growth and development rather than from genetic differentiation. Consequently, populations with similar genetic composition may nevertheless display distinct morphological characteristics if they develop under different environmental conditions. Conversely, similarity in allele frequencies at neutral genetic loci can be maintained by relatively low levels of migration between populations. In contrast, maintaining similarity at loci subject to natural selection would require substantially higher rates of exchange among regions (Oke et al., 2002).

Given that egg and larval dispersal appears to be relatively limited, population connectivity is more likely to occur through active dispersal of juveniles, adolescents, or adults (Varela et al., 2012, 2013; Gaither et al., 2016). The life stage at which movement occurs has important implications for stock structure. Extensive adult migration would be expected to result in populations that are relatively homogeneous with respect to characteristics such as otolith chemistry and morphology. In contrast, if dispersal occurs primarily during the adolescent stage, individuals would complete most of their growth after arrival at a new location and would therefore develop characteristics reflecting local environmental conditions. Under this scenario, adult populations could be internally homogeneous while remaining morphologically distinct from populations occupying other regions.

Importantly, genetic similarity does not necessarily imply demographic connectivity. Even low levels of reproductive exchange between populations can maintain genetic homogeneity over evolutionary timescales. Elliott and Ward (1992) estimated that genetic connectivity may be sustained by the successful reproduction of relatively few migrants per generation (fewer than 200 individuals). Consequently, genetically similar populations may nonetheless function as demographically discrete stocks, a conclusion that is consistent

with many biological and demographic studies of orange roughy that have identified meaningful stock-level differences.

9. Orange roughy catch history in the Tasman Sea

Orange roughy (*Hoplostethus atlanticus*) fisheries on the Challenger Plateau developed in the early 1980s across areas both within New Zealand's Exclusive Economic Zone (EEZ), and within the SPRFMO convention area. The fishery expanded following the discovery of spawning aggregations on the southwest Challenger Plateau. Early orange roughy catch records in the high seas areas of the South Pacific included contributions from vessels from the former Soviet Union, Japan, Korea, Norway, South Africa, and China. Available summaries are reported as aggregated totals rather than consistently disaggregated by flag state (Figure 1, Figure 2, Fisheries New Zealand 2026a).

The Challenger Plateau biological stock is currently defined as comprising the southwest Challenger Plateau within New Zealand's EEZ (ORH 7A) and the adjacent Westpac Bank located in SPRFMO convention area. This stock definition has been applied in New Zealand stock assessments since 2019, with ORH 7A and Westpac Bank treated as a single biological stock and modelled within a single stock assessment (Cordue 2019; Dunn 2024).

Although represented as a single biological stock, ORH 7A and Westpac Bank are subject to different management regimes. The component of the stock within the EEZ is managed by New Zealand under the Quota Management System, while fishing on Westpac Bank in the high seas is managed through SPRFMO conservation and management measures. Total removals from the stock are constrained through the ORH 7A Total Allowable Commercial Catch (TACC), with catch taken from the Westpac Bank contributing to this overall limit (Fisheries New Zealand 2026a).

Total landings from the Challenger Plateau stock peaked at approximately 10 000–12 000 t annually during 1986–87 to 1988–89, followed by a rapid decline in catch and stock biomass. From 1990–91 onwards, catches were generally below 2100 t, and the fishery was effectively closed in 2000–01 following a reduction of the TACC to 1 t. The fishery was subsequently reopened from 2010, with catches increasing in line with higher TACCs associated with stock assessments indicating a rebuilding biomass. More recently, management actions have substantially reduced the ORH 7A TACC following the most recent stock assessment to address uncertainty in stock status and recent survey results (Fisheries New Zealand 2026a).

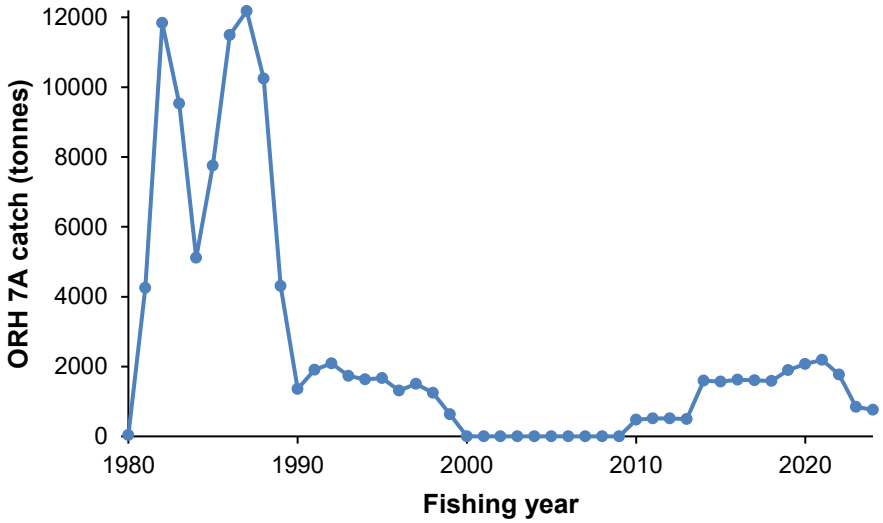

Figure 1. Reported landings in tonnes for ORH 7A from 1980/81 to 2024/25. Fishing year on x axis is first year of 1 October fishing year.

Fisheries for orange roughy also developed in adjacent areas of the Tasman Sea outside of New Zealand's EEZ (Figure 2, Figure 3). These fisheries developed progressively from the late 1980s and have been treated as separate Fisheries Management Areas in SPRFMO (Fisheries New Zealand 2026b).

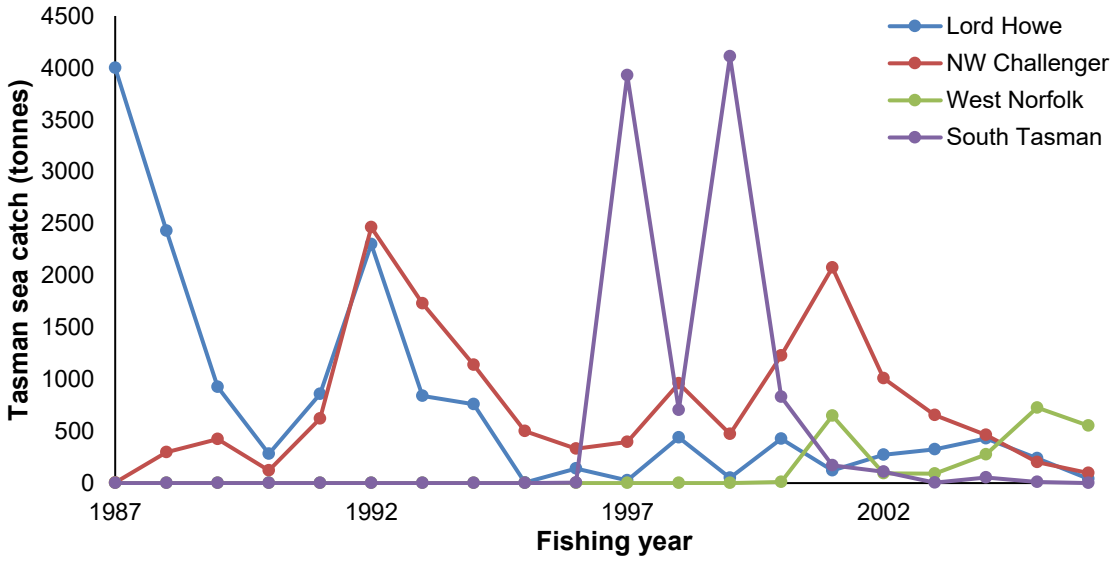

Figure 2 Estimated catches (t) of orange roughy for Tasman Sea fisheries from 1987–88 to 2006–07. (Data from New Zealand (FSU, QMS), Australia (AFMA), and various sources for other countries. Note that the fishing year for South Tasman Rise is March to February, all others are October to September). Fishing year on x axis is first year of 1 October fishing year.

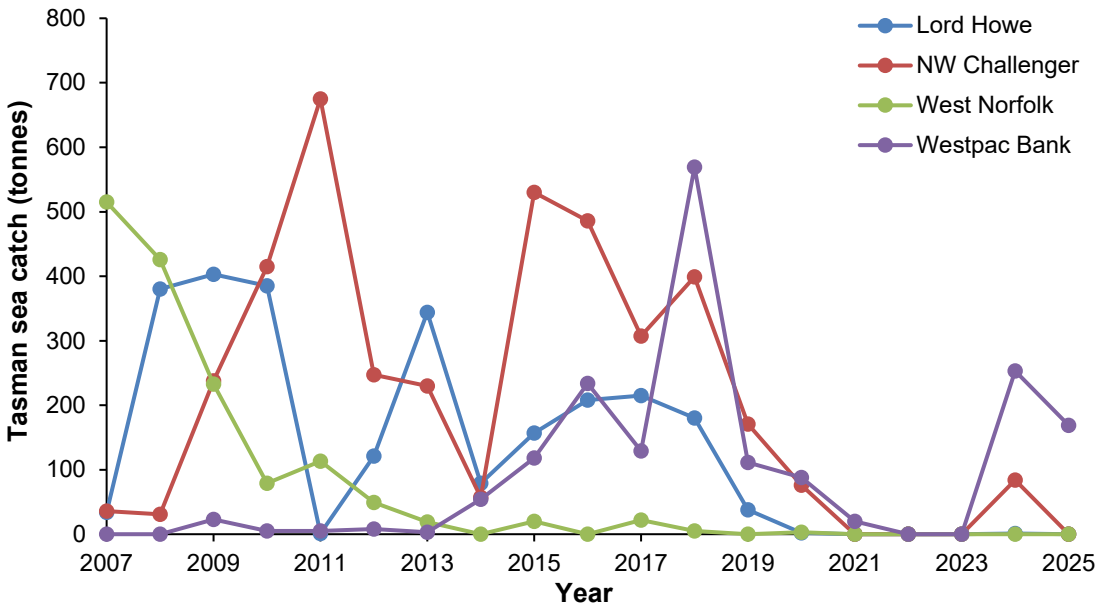

Figure 3. Annual catch for orange roughy from New Zealand vessels, by area, for the SPRFMO Area (calendar years). Westpac Bank is on the Challenger Plateau but is considered part of the straddling stock ORH 7A so landings from that area are tabulated separately. Australian catches over this period, mostly from the Tasman Sea, ranged from 0 to 148 t, mean 46 t per annum). No other nations fished in this area. NB the 'South Tasman' area has been closed to orange roughy fishing since 2007.

Historically, catches from Westpac Bank were incorporated within ORH 7A catch histories, reflecting the treatment of these areas as part of a single straddling stock (Figure 2). Since the initiation of international consultation processes in 2006 that lead to the formation of SPRFMO, Westpac Bank has been identified separately in high seas datasets (Figure 3). This reflects a change in reporting practice rather than a change in biological stock definition.

The sustainable catch limit for the Challenger Plateau stock is determined through a quantitative stock assessment undertaken by New Zealand. A corresponding catch limit for the Westpac Bank Fishery Management Area is set by the SPRFMO Commission and catch from this area is counted against the overall TACC for the stock. Historically, the Westpac Bank catch limit has been set at approximately 12.5% of the Challenger Plateau TACC, representing an estimate of the proportion of the biological stock present in the Westpac Bank area (SC7-DW07-rev1). This estimate was recognised as approximate and based on the information available at the time, with acknowledged uncertainty in both the spatial distribution of the stock and the data used to derive the estimate.

Recent stock assessment results (Dunn 2024) have increased uncertainty regarding the spatial distribution of biomass across the Challenger Plateau and Westpac Bank, and may

not provide strong support for the original basis of the 12.5% allocation. In response, recent Commission deliberations under revisions to CMM 03a have considered adjustments to this proportion (COMM13-Prop06), including an interim increase in the share of the TACC available to the Westpac Bank area (approximately 16% - CMM 03a-2026). These discussions reflect uncertainty in the underlying basis for the historical allocation as well as the need to maintain operational flexibility while constraining total removals from the stock. Recent proposals to change this allocation do not alter the overall level of catch from the biological stock, but instead redistribute catch spatially between EEZ and high seas components (COMM13-Prop06).

10. Recommendations

It is recommended that the Scientific Committee:

- **Notes:**
    - that no single method is likely to provide definitive evidence of orange roughy stock structure.
    - that despite the application of a range of techniques to investigate orange roughy stock structure, there remains no consensus regarding the level of connectivity among populations.
    - that studies based on methods other than genetics have identified diagnostically significant differences among stocks, whereas genetic studies have generally indicated high levels of gene flow and limited genetic divergence between sites, particularly among geographically proximate sites.
- **Agrees:**
    - that five techniques used by Smith et al. (2002) to determine stock structure adequately describe the stock relationships among four geographically close but spatially isolated orange roughy fisheries in the eastern Tasman Sea.
    - that none of the available literature on orange roughy population structure reviewed in this report contradicts the assumption that fish in the Westpac Bank and ORH7A management areas comprise a single biological (straddling) stock, primarily owing to their close geographic proximity.
- **Recommends:**

- that based on the best available scientific information on orange roughy stock structure, fish encountered within the ORH 7A Management Area of New Zealand's Exclusive Economic Zone (EEZ) and on the adjacent Westpac Bank within the SPRFMO Convention Area should be treated as a single biological (straddling) stock, consistent with current New Zealand stock assessments.

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