



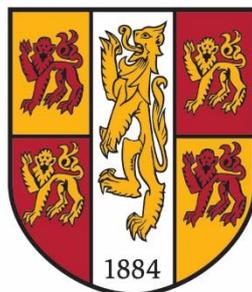
English Channel King Scallops

Research Summary

Genetic population structure (MSC Principle 1)

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Marine Stewardship Council (MSC) assessment

The MSC assessment process is divided into three key principles that underpin their mission to recognise and reward sustainable fishing practises. A fishery is assessed and given a score for a number of performance indicators under each principle.

<p>MSC Principle 1 - Resource Sustainability</p>	<p>A fishery must be conducted in a manner that does not lead to over-fishing or depletion of the exploited populations and for those populations that are depleted the fishery must be conducted in a manner that demonstrably leads to their recovery.</p>
<p>MSC Principle 2 - Ecosystem Sustainability</p>	<p>Fishing operations should allow for the maintenance of the structure, productivity, function and diversity of the ecosystem (including habitat and associated dependent and ecologically related species) on which the fishery depends.</p>
<p>MSC Principle 3 - Management Systems</p>	<p>The fishery is subject to an effective management system that respects local, national and international laws and standards and incorporates institutional and operational frameworks that require use of the resource to be responsible and sustainable.</p>

Certification requirements

Principle 1 of the MSC assessment criteria states that the unit of certification is “*The fishery or fish stock (biologically distinct unit) combined with the fishing method/gear and practice (=vessel(s) and/or individuals pursuing the fish of that stock) and management framework*”.

A biological stock can be defined as “*a group within a species population which have sufficient spatial and temporal integrity to warrant consideration as self-perpetuating units*” (Pawson 1995). For fisheries management purposes this relates to the extent to which exploitation effects of a fishery are identifiable in a species population. In order to meet the requirements of MSC Principle 1, distinct populations of the species, for which appropriate management and harvest strategy can be implemented, must be identified.

Background / data requirements

The king scallop (*Pecten maximus*) fishery in the English Channel is delineated by political and geographic boundaries. The largest management boundaries are those of ICES sub-areas VIIe and VIIe. At a national level, four Inshore Fisheries and Conservation Authorities (IFCAs) have management responsibilities for inshore waters, within 6 nautical miles of the coastline. The present management boundaries do not reflect biologically or reproductively discrete stocks. Knowledge of stock structure and connectivity is key to understanding the implications of management on adjacent stocks of the same species. Therefore, in order to

manage a fishery effectively it is necessary for management units to represent biologically distinct stocks to enable management to occur at an appropriate scale.

Action

Scallops live in aggregations, known as beds, separated by areas of unsuitable habitat. Scallop beds are connected to varying degrees via larval transport. The direction and degree of larval transport is influenced by tides, currents, and winds coupled with larval behaviour. Scallop larvae spend up to 40 days in the water column before settlement on the seabed. Larvae may be transported away from spawning grounds by currents, or retained within the vicinity of the parent population due to localised eddies and gyres (see this link for a video of scallop larval released from Lyme Bay which shows the easterly transport of larvae:

<http://global.oup.com/uk/orc/biosciences/ecology/kaiser2e/01student/videos/particle/>).

Genetic analysis can be used to understand to what extent different scallop beds are connected to each other by studying the similarity in the genetic makeup of scallops from different areas. Significant differences in the genetic signals between populations would indicate that there is little or no larval connectivity between sites occurs (one individual or less per generation). Genetic analysis of scallop tissue samples from nine sites (Figure 1) in the English Channel was undertaken. Nine previously developed microsatellites (Hold *et al.* 2013), which are a type of co-dominant DNA marker, were used to assess the genetic similarity between the nine populations and infer the degree of larval connectivity between sites.

Results

At least three management units have been identified (Figure 1). The hydrodynamics in the Baie de Seine causes localised retention of larvae and the genetic evidence indicates no transfer of larvae between the Baie de Seine and the eastern English Channel.

The samples from west Falmouth and north Cornwall were genetically similar to the Baie de Seine. This could be due to larvae travelling west from the Baie de Seine, reaching the Channel Islands and dispersing to the English coast via residual currents. There are, however other possible explanations for the similarity between these three sites:

- Random genetic mutations have occurred in all three populations, leading to the observed similarities.
- Scallops at the three sites share a parent population and significant divergence of the genetic signal has not occurred since the populations were separated (this would have occurred during the last glaciation, around 8000 years ago).

Information from fine-scale hydrodynamic modelling (work in progress, Bangor University) will provide further insight into the degree of connectivity between the sites.

The prevailing wind and currents flow from west to east up the English Channel, facilitating larval transfer from the eastern side of Falmouth Bay along the English coast to the Sussex and mid-eastern Channel populations. All the populations along this route have genetic similarities.

Within Falmouth Bay, samples from three locations showed significant genetic differentiation. This is potentially due to opposing gyres in the bay creating a physical barrier to the dispersal of larvae across the bay. One sample in Falmouth Bay had a very low effective population size (the number of breeding individuals as opposed to the total number of individuals). This may be due to a chance event of ‘sweepstake’ recruitment in one area (when all surviving individuals come from one set of parents). Other sites that indicated a low effective population size included north Cornwall and west Lyme Bay. This would suggest that specific local management of these scallop beds may be necessary.

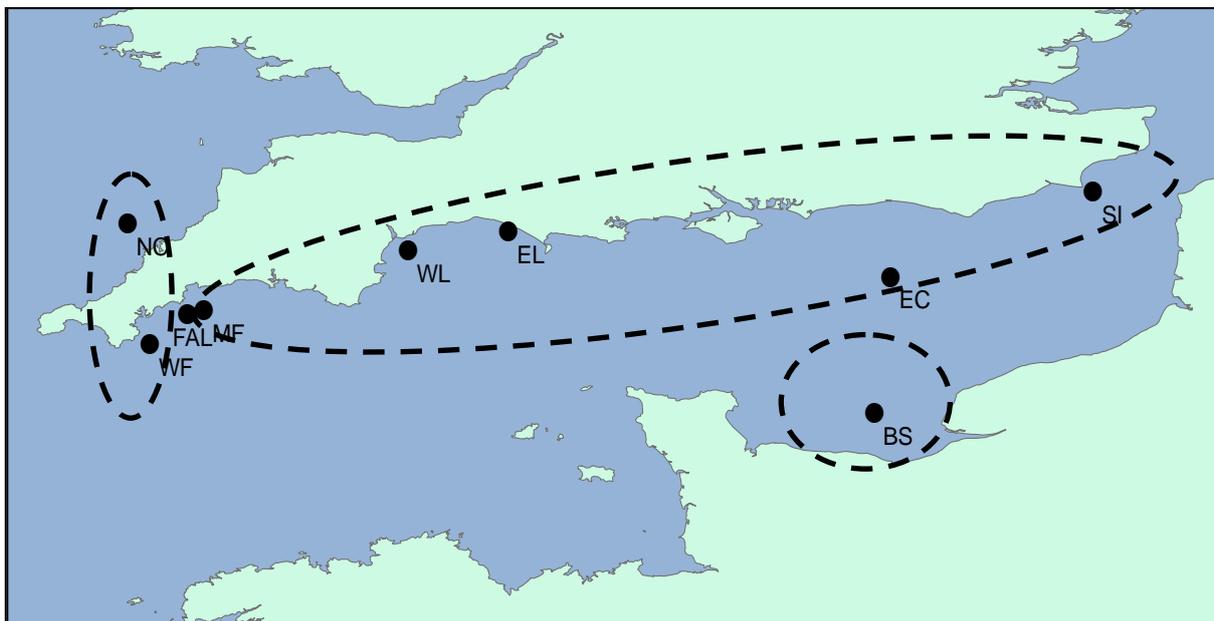


Figure 1: The location of the nine sites from which scallop tissue samples were obtained for analysis. Dashed lines indicate genetically distinct king scallop populations in the English Channel, and the largest management units that should be considered.

Management recommendations

At least three reproductively independent units have been identified and define the largest management units that should be considered. Genetic evidence indicates that the current management boundaries, dictated by east/west, or inshore/offshore divisions do not align with the biological structure of the stocks.

However, differences in spawning patterns and growth rates occur at much smaller spatial scales. Therefore, smaller management units may be appropriate. Scallops in the eastern English Channel reach 100 mm in shell length after two years of growth, but it takes scallops in the western Channel 4 or 5 years to reach that size. Spawning patterns also vary over large and small spatial scales. For example, partial spawnings occur from May to October in the

Baie de Seine (Nicolle *et al.* 2013) and in the western English Channel spawning occurs as either a single event in May or June, or several events over a protracted period (May to September) depending on the location (CEFAS 2012).

A low effective population size can lead to a risk of over-harvesting where there is no supply of larvae from other populations. A low density of adults can also prevent fertilisation occurring when larvae are released. Where larval influx is low or absent, populations are susceptible to collapse and will take longer to recover from over-harvesting. The consequences of over-harvesting are a loss of genetic diversity and inbreeding effects. Therefore, extra precautions need to be implemented to prevent this in isolated populations.

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This document is a non-technical summary of research undertaken as part of a PhD at Bangor University. The full PhD manuscript is available from Bangor University Library.

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