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Opinion Piece

The dangers of ignoring stock complexity in fishery management: the case of the North Sea cod

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The plight of the marine fisheries is attracting increasing attention as unsustainably high exploitation levels, exacerbated by more extreme climatic conditions, are driving stocks to the point of collapse. The North Atlantic cod (*Gadus morhua*), a species which until recently formed a major component of the demersal fisheries, has undergone significant declines across its range. The North Sea stock is typical of many, with a spawning stock biomass that has remained below the *safe biological limit* since 2000 and recruitment levels near the lowest on record. Cod within the North Sea are currently managed as a single stock, and yet mounting empirical evidence supports the existence of a metapopulation of regionally variable, genetically distinct, sub-stocks. Applying the same management strategies to multiple stocks that differ in their resilience to exploitation inevitably results in the overfishing and likely collapse of the weaker components. Indeed, recent studies have identified two North Sea spawning stocks that have undergone disproportionally large collapses with very substantial reductions in egg production. Similarly affected cod stocks in the northwest Atlantic have shown little evidence of recovery, despite fishery closures. The possible implications of ignoring sub-structuring within management units for biocomplexity, local adaptation and ecosystem stability are considered.

Keywords: biocomplexity; local adaptation; extirpation; fisheries management

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The North Atlantic cod (*Gadus morhua*) has historically supported one of the largest marine fisheries, but, as with many commercially exploited species, it has undergone a significant reduction across its range in recent years, resulting in the complete closure of some of the major fishing grounds. Although there is now evidence that large, slow-growing species may undergo local extinction (extirpation) through their inclusion as by-catch (Hiddink *et al.* 2008), faster maturing species, such as cod, with large, weakly structured populations and a capacity for extensive migration, are thought to be more resilient to exploitation. Cod within the North Sea have typically been treated as a single panmictic population; however, mounting evidence from tagging surveys (Wright *et al.* 2006), molecular genetic analysis of spawning aggregations (Hutchinson *et al.* 2001) and otolith microchemistry (Gibb *et al.* 2007) supports the existence of a metapopulation of distinct spawning aggregations, with regionally varying stock dynamics (Holmes *et al.* 2008). Where equal fishing pressure is applied to stocks that differ significantly in biomass and resilience, there is the potential to bring about a collapse of the less productive populations.

Alarmingly, two recent studies indicate that several of the North Sea spawning stocks have undergone a very significant decline over the last 30 years, with a substantial reduction in egg production. Fox *et al.* (2008) undertook an ichthyoplankton survey of the North Sea in 2004, using genetic probes to assign gadoid eggs to their species of origin. The distribution of cod eggs closely matched the spawning grounds proposed in earlier studies (Daan 1978; Harding & Nichols 1987). However, the eggs were virtually undetectable on the previously productive spawning grounds off Flamborough Head, prompting Fox *et al.* (2008) to suggest that such severely depleted stocks may require 'targeted conservation measures'. Furthermore, Holmes *et al.* (2008) used cod recruitment and spawning stock biomass data from the North Sea to investigate regional trends between 1993 and 2005. They concluded that the Dogger Bank and Flamborough populations may be facing commercial extinction before the rest of the North Sea shows a similar response.

These findings corroborate the results of an earlier study by Hutchinson *et al.* (2003) in which a temporal genetic analysis of fish caught off Flamborough Head identified a significant change in the genetic composition of the population, commensurate with a gradual loss of the original population and increased influence of low numbers of incoming migrants. The study spanned the period from 1954 to 1998, but the greatest change was seen in the 17 years prior to 1998. Harding & Nichols (1987) found high densities of eggs off Flamborough Head in their 1976 survey; however, this region has supported some of the highest exploitation levels in the North Sea since the 1970s, which undoubtedly contributed to the significantly reduced densities observed by Fox *et al.* (2008). As subsequently discussed, the collapse or complete loss of such a population may have important implications for the species' genetic diversity and long-term viability, particularly where there is evidence for local adaptation. Furthermore, cod represents a key prey item and predator in the North Atlantic and, consequently, its removal is likely to have impacts across trophic levels potentially threatening ecosystem stability.

It has been argued that biocomplexity, in particular the diversity of life-history characteristics and adaptation to local variations in spawning and nursery habitat, may help fisheries to adjust to environmental change and resist the pressures of exploitation (Hilborn *et al.* 2003). Although it is difficult to determine the heritable component of biocomplexity, particularly in fishes that typically exhibit high phenotypic plasticity, it is now generally accepted that the erosion of genetic diversity is likely to be detrimental for a species' long-term viability (Hoffmann & Willi 2008). Indeed,

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evidence of decreased fitness has been detected in a variety of genetically depauperate populations, with affected traits including developmental stability (Gautschi *et al.* 2002), thermoregulation (Jones *et al.* 2004), leucocyte production (Hale & Briskie 2007), body size (Wisely *et al.* 2008), fecundity (Culver *et al.* 2008) and disease resistance (Reber *et al.* 2008 and references therein). Furthermore, the paradigm that local adaptation seldom occurs in weakly divergent, highly vagile, marine species is being challenged by mounting evidence of geographically structured variation in physiological and morphological traits (Conover *et al.* 2006). Detecting the genes that contribute to local adaptation is challenging, however, since traits are often governed by multiple genes with complex interactions and low heritability. Nevertheless, clinal variations in allelic distribution, which have been suggested to be indicative of fine-scale adaptation in the aquatic environment, have been observed in a range of functional genes including *leucine aminopeptidase* (Koehn *et al.* 1980), *glucose phosphate isomerase* (Gysels *et al.* 2004), *pantophysin* (Case *et al.* 2005; Pampoulie *et al.* 2008), immuno-related major histocompatibility complex (Dionne *et al.* 2007) and regulatory genes, which control the production of proteins at the centre of various key physiological pathways (e.g. *ependymin*, *apolipoprotein 1A*, *ferritin H1*, *beta-2 microglobulin*, *transferrin*; Larsen *et al.* 2007).

The existence of multiple spatially and temporally distributed spawning events may help to dampen annual fluctuations in recruitment. Indeed, Holmes *et al.* (2008) found a large spatial variation in recruitment trends across the North Sea, which they linked to environmental heterogeneity. Poor cod recruitment in warm years has also been linked to a match/mismatch relationship between the timing of spawning and climatically driven variations in the abundance of a copepod, *Calanus finmarchicus*, which forms a key food item for cod larvae and juveniles (Beaugrand *et al.* 2003). Such environmental fluctuations are likely to become more severe if the North Sea and surrounding waters continue to warm as predicted, highlighting the importance of maintaining multiple, spatially distributed, spawning stocks (Ottersen *et al.* (2006).

Cod occupy a key niche in the North Atlantic ecosystem, with larvae and juveniles forming an important food source for many species (Bundy & Fanning 2005; Trzcinski *et al.* 2006), while adults represent one of the main finfish predators of small fish and benthic invertebrates (Worm & Myers 2003). The removal of this predator during the collapse of the Canadian cod stocks resulted in trophic cascades, which were thought to reach down as far as the copepod and phytoplankton communities (Frank *et al.* 2005; Heithaus *et al.* 2008). Few of the Canadian cod stocks have shown signs of any recovery following closure of the fisheries, which some suggest may be due to a fishery-induced ecological regime shift (Bundy & Fanning 2005; Savenkoff *et al.* 2007).

The recent move from single-species management to ecosystem-based fisheries management reflects the recognition that a more holistic multi-species approach is required to ensure that fisheries are exploited sustainably, while conserving biodiversity and maintaining the status of the ecosystem. This is undoubtedly an important development, but priority also needs to be given to ensure that the scale at which fishery data are collected and analysed reflects the true structuring of the species (Holmes *et al.* 2008). Where data are amalgamated, as with the North Sea cod, there is a danger that more minor and yet equally important populations may undergo a collapse before their decline is detected and protective measures can be set in place. Determining the stage at which to apply such measures is predictably controversial as they have serious socio-economic implications. Furthermore, even where stocks can be suitably monitored and maintained at appropriate levels to preserve genetic diversity, the highly selective nature of most fishing techniques may inevitably lead to the evolution of less resilient populations composed of smaller, earlier maturing fish, as has been seen in cod and other species (Barot *et al.* 2004; Olsen *et al.* 2005; Jørgensen *et al.* 2008). We clearly still have a long way to go before the exploitation of wild fisheries is truly sustainable, if indeed it can be.

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