

Predicting population level risk effects of predation from the responses of individuals: A Case Study On Harbour Porpoises In Scottish Waters

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Area being submitted to: 1) General science session

Preferred presentation medium:(i) oral

Are you a student?: No

Fear of predation produces large effects on prey population dynamics through indirect risk effects that can cause even greater impacts than direct predation mortality. As yet, there is no general theoretical framework for predicting when and how these population risk effects will arise in specific prey populations, meaning there is often little consideration given to the key role predator risk effects can play in understanding conservation and wildlife management challenges. Here, we propose population predator risk effects can be predicted through an extension of individual risk trade-off theory and show for the first time that this is the case in a wild vertebrate system. This system is that of harbour porpoise - sandeels - bottlenose dolphins in Scottish waters. In this system, harbour porpoises rely heavily on the sandeels as prey, especially in spring. However, harbour porpoises are also attacked and killed by the larger bottlenose dolphin. While this is not a classic example of predation (since bottlenose dolphins do not consume the porpoises they kill), from the perspective of the harbour porpoise, it nonetheless represents an important source of mortality in eastern Scotland which does not differ from other types of predation events. In addition, bottlenose dolphin predation is absent in western Scotland, allowing comparisons to be made between high and low predation environments. Using this system, we demonstrate that the timing (in specific months of the year), occurrence (at low food availability), cause (reduction in individual energy reserves) and type (starvation mortality) of a population level predator risk effect can be successfully predicted from individual responses using a widely applicable theoretical framework (individual based risk trade-off theory). Our results suggest individually-based risk-trade-off frameworks could allow a wide range

of population level predator risk effects to be predicted from existing ecological theory, which would enable risk effects to be more routinely integrated into consideration of population processes and in applied situations such as conservation. In particular, the results of this analysis appear to predict otherwise unexpected large scale changes in the distribution of porpoises which have been recorded in the North Sea between the 1990s and the 2000s.

High-EPA oil from transgenic *Camelina sativa* as a replacement for marine fish oil in Atlantic salmon (*Salmo salar*) feeds

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Theme being submitted to: 1) General science

Preferred presentation medium: (i) oral

Are you a student?: No

The use of high levels of marine fish oil in aquafeeds is non-sustainable. However, alternative oils sourced from terrestrial plants do not contain long-chain polyunsaturated fatty acids (LC-PUFA) (Turchini et al., 2010). Consequently, feeds based on vegetable oils reduce n-3 LC-PUFA levels in farmed fish (Tocher et al., 2010). Therefore, aquaculture requires oil sources that contain high levels of n-3 LC-PUFA in order to supply the increasing demand for fish and seafood while maintaining the high nutritional quality of farmed products. One approach to the renewable supply of n-3 LC-PUFA is metabolic engineering oilseed crops with the capacity to synthesize these essential fatty acids in seeds (Sayanova and Napier, 2011). In the present study, the oilseed *Camelina sativa* was transformed with algal genes encoding the n-3 biosynthetic pathway and expression restricted to the seeds via seed-specific promoters to produce an oil containing > 20% eicosapentaenoic acid (EPA) (Ruiz-Lopez et al., 2014). This oil was investigated as a replacement for marine fish oil in feeds for post-smolt Atlantic salmon. In addition, this study with EPA-rich oil will contribute to our understanding of the biochemical and molecular mechanisms involved in the control and regulation of docosahexaenoic acid (DHA) production from EPA, and thus better inform our understanding of LC-PUFA biosynthesis.

A total of 492 post-smolt Atlantic salmon with an average body weight of 85.6 ± 0.4 g (mean \pm SD) were distributed between 9 tanks and fed one of three experimental diets in triplicate for 7-weeks. The diets contained fish oil (FO), wild-type *Camelina* oil (WCO) or EPA-*Camelina* oil (ECO) as the sole lipid sources. Growth performance, feed efficiency and fish health were determined along with nutrient and fatty acid composition. In addition, the metabolic/molecular consequences of this new ingredient were assessed by analysis of gene expression using oligonucleotide microarray.

At the end of the trial, fish from all treatments more than doubled their weight and no mortality was

recorded. Salmon fed the ECO diet showed the highest growth in terms of weight gain and SGR compared to fish fed the FO diet. Fatty acid compositions of salmon flesh reflected the respective diets with WCO-fed fish having increased levels of 18:2n-6 and 18:3n-3 and reduced EPA and DHA. Fish fed ECO had the highest level of EPA but flesh DHA was not significantly increased by the high dietary EPA. In contrast, EPA and DHA were significantly increased in liver.

The results showed that oil from transgenic *Camelina sativa* can effectively replace marine fish oil in feeds for Atlantic salmon with no negative impacts on growth or survival. The current EPA-only oil maintained EPA levels in salmon flesh similar to those in fish fed fish oil. Although there was substantial conversion of EPA to DHA in salmon liver, flesh DHA levels were not significantly increased. Therefore, transgenic oils should contain both major n-3 LC-PUFA. Furthermore, tissue transcriptomic responses were investigated to determine detailed effects on fish metabolism and health. *Camelina* oil containing approximately 20% of EPA and DHA combined has been developed and is in production for subsequent testing in salmon feeds (Ruiz-Lopez et al., 2014).

Acknowledgments

MBB and this project were partly funded by a BBSRC Industrial Partnership Award (BB/J001252/1).

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Zooplankton development: questioning the conventional view of the relationship between development and temperature

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Area being submitted to: 1) General science session;

Preferred presentation medium: (i) oral.

Are you a student?: Yes

Climate change is having, and is expected to continue to have, an ongoing influence on the biogeography of zooplankton species. Predicting the impacts of climate change at the level of individual species requires quantitative understanding of the influence of temperature on key life cycle traits, such as growth, development, egg production and mortality.

Traditionally, zooplankton population models assume that development decreases monotonically with temperature, whereas egg production rate increases monotonically. Here we synthesise existing quantitative knowledge of the life cycle of the calanoid species *Calanus finmarchicus* and *C. helgolandicus* to develop new models of growth, development and egg production rate. The principal elements of the model are ingestion and respiration rate, assimilation efficiency and the body size at which individuals become adults, and their relationship with temperature.

In contrast to the traditional view, we find that the relationship between development time and temperature is U-shaped, and that between egg production rate and temperature is dome-shaped. Our results are then put into the context of the broader knowledge of zooplankton growth and egg production and we conclude by highlighting the need for possible future experimental work.

Acknowledgements

We thank MASTS and the University of Strathclyde for funding this research.

The lipids and fatty acids of two hadal amphipods (>6000 m depth). Adaptations to life in the deep.

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Area being submitted to (delete as appropriate): 1) General science session

Preferred presentation medium (delete as appropriate): (i) oral

Are you a student? (Delete as appropriate): Yes

Lipids are vital to life, both in biological membranes and as energy (fat) reserves. High pressures and low temperatures have a solidifying effect on lipids preventing correct functioning of cellular membranes and reducing the metabolic accessibility of fat reserves. Increased unsaturation (presence of double bonds) of the fatty acids increases the pressure and lowers the temperature at which this phase transition occurs (DeLong and Yayanos, 1986).

Fatty acids are commonly employed in nutritional ecology studies as while some fatty acids can be produced de novo, others must be sourced and modified from the diet. However, the selective retention and synthesis of fatty acids may reveal more about adaptations to life in this extreme environment.

The hadal zone, deeper than 6 km, is only found in the deepest ocean trenches. Life in the hadal zone must contend with high hydrostatic pressures, low temperatures and scarce food supply. Very little is known of the ecology and physiology of deep sea organisms. Amphipods dominate the scavenging fauna at hadal depths, and are vital for the circulation and dispersal of organic material (Blankenship and Levin, 2007).

Scopelocheirus schellenbergi and *Hirondellea dubia* were caught from 6097-8148 and 7014-9281 metres depth respectively within the Kermadec Trench, South West Pacific. These species are key components of the fauna within the trench, dominating catches at these depths. Total lipid, lipid class composition and fatty acid analysis of membrane and storage lipids were investigated in relation to depth of capture.

Vertical age structuring has been observed in both species and food quality within the trench is

understood to be variable with depth (See Jamieson et al. 2009). As such the lipids and fatty acids of two hadal amphipod species were investigated over their depth ranges to provide insight into adaptations to life in the deep sea.

Acknowledgements

The authors would like to thank the crew of the RV Kaharoa, NIWA, for their assistance in the collection of the samples. The lead author would like to thank D. Pond for his invaluable assistance in both sample processing and advice thereafter.

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The future of managing our oceans: Starting at the bottom of the food-chain?

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Area being submitted to: 1) General science session

Preferred presentation medium: oral

Are you a student? No

Primary producers are important as the basis of the marine food web (a provisioning ecosystem service), and as a potential contributor to CO₂ drawdown from the atmosphere (a climate regulation service). However, primary production (PP) and derived ecosystem services are not currently considered under Marine Spatial Planning (MSP) in Scotland. This pilot study aims to start to integrate PP into the MSP process, through investigating the potential effects of a proposed marine renewable energy development in the Firth of Forth on phytoplankton in the region.

The proposed renewables developments are to be situated on 'Wee Bankie'. Banks are known to increase mixing in their locality (Moum & Nash 2000; Palmer et al. 2013), driving diapycnal nutrient fluxes (Tweddle et al. 2013), and influencing PP in the region (Davidson et al. 2013). Evidence of such mixing has been observed in the region of Wee Bankie previously (Fraser et al. 2004). This pilot study uses a selection of remotely sensed data products in order to establish what ocean surface signatures, as driven by the small bank, can be observed. For example, changes in SST as a proxy for waters subjected to mixing. By analysing spatial and temporal (e.g. seasonal and spring-neap cycles) variability in remotely sensed data, such as SST and [Chl a], we have gained an understanding of the 'background' ecosystem, before the marine renewables development is built. This allows comparison of conditions throughout the construction of the development, and the long-term influence of the development on PP. We can also model future conditions. By carrying out this analysis within the development planning stage, we have the opportunity to influence the siting and array arrangement, through a forthcoming NERC knowledge exchange programme, CORPORATES, involving the appropriate renewables companies and stakeholders, and through influencing policy and planning decisions.

Acknowledgements

This research was funded by Marine Collaboration Research Forum (MarCRF)- the collaborative forum between Marine Scotland and the University of Aberdeen.

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Polynoidae (Polychaeta) in the Southwest Indian Ocean Ridge: from the Evolutionary relationships to the Ecological adaptations

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Area being submitted to 1) General science session

Preferred presentation medium (i) oral

Are you a student? (Delete as appropriate): No

The Indian Ocean represents one of the largest gap in Deep-Sea exploration. At the end of 2011 we collected benthic samples in an unexplored area across four seamounts of the Southwest Indian Ocean Ridge (SWIOR) that extends south westwards between South Africa and Antarctica. High levels of endemism have been observed on seamounts leading to a view that the geographic distance and the unique topographic and hydrographic conditions determine faunal isolation stimulating genetic divergence. However seamounts could also represented stepping stones for fauna populations, facilitating dispersal between continental shelves and mid-ocean ridges and across large deep-sea basins.

Seven species of Polynoidae polychaete were chosen in order to analyse the phylogenetic relationships between commensal species associated with basket stars, holoturians, several deep-sea corals (scleractinians forming cold-water coral reefs and octocorals, stylasterids and antipatharians forming coral gardens) and errant species. When possible, specimens from the same species collected on different seamounts along the SWIOR were also chosen for the analysis. We used a molecular approach to generate the phylogeny of this family related to the geographical distance, the habitat requirements and the level of coral-host specificity. The results based on the analysis of multiple genes (28S, 18S, 16S and COI) showed taxonomic clustering from the genus level with higher evolutionary specificity for closer coral-host associations. Genetic sequences were also used to assess potential genetic homogeneity or endemism of the species found.

Acknowledgements

The Authors kindly thank NERC for funding this work.