

# Human Health

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## KEY HEADLINES

- Toxin producing phytoplankton, pathogenic vibrios (bacteria commonly found in low salinity water) and noroviruses all have the potential to impact human health.
- The relationship between climate change and toxin producing phytoplankton is complex. Considerable unknowns remain about how climate change will impact this part of the plankton community and confidence in predicting these impacts in UK waters remains low.
- A recent study in Scotland has shown short term weather events as well as wind mediated transport of offshore phytoplankton populations can influence the toxicity of coastal shellfish. This highlights the requirement for long term data sets to identify the impacts of climate change from shorter term seasonal and interannual variability.
- Emerging evidence from peer-reviewed scientific studies has suggested that increasing seawater temperatures and extreme weather events such as heatwaves and extreme precipitation, drive the abundance of pathogenic vibrios in the environment. A recent spate of reported infections in Northern Europe underlines these observations. Climate warming in the region may therefore increase human infections.

## 1. INTRODUCTION

The marine ecosystem plays an important role in the UK and Irish rural economies through aquaculture and tourism. Three groups of organisms which have the potential to negatively impact human health via these industries are phytoplankton, pathogenic bacteria and noroviruses.

Marine phytoplankton are single-celled algae that inhabit the water column. A small subset of species within this group can produce toxins that can accumulate in the flesh of shellfish and can pose a risk to human health if consumed. Human health is protected from this threat by EU directive 91/492/EEC and subsequent amendments. These are enforced by the Food Standards Agency UK and Food Standards Scotland. Blooms of toxin producing algae are known as 'harmful algal blooms' or HABs. The main organisms of concern in UK waters are the dinoflagellate *Alexandrium* (associated with the production of toxins responsible for paralytic shellfish poisoning (PSP)), *Dinophysis* (toxins associated with diarrhetic shellfish poisoning (DSP)) and the diatom *Pseudo-nitzschia* (toxins associated with amnesic shellfish poisoning (ASP)). The dinoflagellates *Azadinium* (azaspiracid toxins –

AZA), *Protoceratium reticulatum*, *Lingulodinium polyedrum* and *Gonyaulax spinifera* (yessotoxins - YTX) are less of an issue in UK waters although AZA can cause problems for the Irish shellfish industry. Phytoplankton exhibit considerable intra and interannual variability. Multi-decadal datasets are needed to identify impacts of climate change over inherent variability. Data from the continuous plankton recorder (CPR) collected over the last five decades have shown that the phytoplankton community in the North Sea and north east Atlantic has been impacted by climate change over a multi-decadal scale. Changes in the dominance of the two phytoplankton groups, diatoms and dinoflagellates resulting from increasing temperature in the 1980s (Edwards *et al.*, 2002) and increases in wind intensity in the 1990s (Alvarez-Fernandez *et al.*, 2012; Beaugrand *et al.*, 2014) have been observed. Specific studies on HAB genera identified in CPR samples have shown shifts in their distribution in the North Sea since the 1960s (Edwards *et al.*, 2006). Increasing sea surface temperatures and wind intensity are thought to be the driver behind an increase in the abundance of the diatom *Pseudo-nitzschia* in the NE Atlantic in the mid 1990s (Hinder *et al.*, 2012).

One group of environmental bacteria, pathogenic vibrios, are an increasingly important cause of disease around the world. These bacteria can cause a range of infections in humans, such as gastroenteritis, wound infections and sepsis (blood poisoning). Transmission is mostly driven by the consumption of contaminated seafood and/or exposure to seawater, often recreationally through swimming. The species *Vibrio vulnificus*, *V. parahaemolyticus* and *V. cholerae* represent the species most often implicated in human diseases. These bacteria grow in warm, low salinity waters and their abundance in the natural environment mirrors ambient environmental temperatures. Of concern is that the rapid warming of coastal environments such as recently experienced in Northern Europe (see e.g. Lima & Wetthey, 2012; Mackenzie & Schiedek, 2007) may increase the geographical spread of these pathogens as well as clinical risk in this region. It is likely that climate change is playing a significant role in mediating the spread of these important infectious disease agents, with wide ranging impacts. Climate warming increases the geographical range over which these bacteria can flourish.

Human noroviruses (NoV) are the most common cause of epidemic infectious intestinal disease (IID) and a major cause of foodborne and waterborne illness worldwide. In the UK, approximately 17 million cases of illness and one million general practice consultations due to IID occur annually (Tam *et al.*, 2012). Norovirus are highly contagious, rapidly and prolifically shed by symptomatic and asymptomatic individuals, very stable in the environment outside the human host and resistant to many forms of disinfection (Campos and Lees, 2014). Norovirus transmission occurs through person-to-person contact via the faecal-oral route or exposure to contaminated surfaces; or foodborne or contamination from food handlers or further upstream in the food production system through contamination with human sewage. This is particularly relevant to bivalve shellfish in the marine environment. The epidemic patterns of NoV are mainly driven by host, viral and climatic factors (Lopman *et al.*, 2009). Increases in NoV abundance in the marine environment are usually associated with low water temperatures (Campos *et al.*, 2017). During periods of heavy rainfall, wastewater treatment plants may be overwhelmed and sewage overflows or bypasses into local waterways may occur. These events can mobilise NoV in the environment (Campos *et al.*, 2016) and have been linked to elevated numbers of people requiring treatment for IID (Jagai *et al.*, 2015). The understanding of the role of environmental transmission on disease incidence and how best to target control measures for NoV remains poor (Lopman *et al.*, 2012).

## 2. TOPIC UPDATE

The complexity of how climate change impacts the marine environment is increasingly acknowledged. Previous MCCIP report cards have shown a regional aspect to warming of the waters in the UK e.g. with water temperatures increasing more in the Southern North Sea than in the North (Dye *et al.*, 2013b). Variation in ocean circulation as well as freshwater inflows can also have a regional influence on the physical properties of water around the UK coast (Dye *et al.*, 2013a). Separation of climate change impacts from short term fluctuations such as weather events and long term multidecadal cycles such as the North Atlantic Oscillation (NAO) and the Atlantic Multidecadal Oscillation (AMO) is difficult and must be considered when examining the impacts of climate change on biota. This is why long term multi-decadal time series of data are required for the impacts of climate change to be identified.

## 2.1 HABs

The potential impacts of increasing temperatures, changing weather patterns, ocean acidification and increased flood risk on HABs in UK waters have already been detailed in previous report cards (Bresnan *et al.*, 2010; 2013). A thorough review of this topic (Wells *et al.*, 2015) consolidates the view that the impacts of climate change on HABs remains complex (Hallegraeff, 2010). Wells *et al.*, (2015) details the 'unknowns' that exist behind the assumptions of how climate will impact HABs and recommends a standardised approach to future research studies and monitoring to address this issue.

Within the UK the relationship between climate change and HAB events has not been directly investigated since the last report card however the aquaculture industry continues to be impacted by algal toxins. Effort has focused on a number of laboratory and modelling studies which have increased our knowledge about the relationship between environmental drivers and HABs.

**PSP:** Closures of shellfish harvesting areas along the south coast of England since 2013 have been of a short duration. In Scotland closures have been enforced in the Clyde, west coast, Western Isles, and Shetland. Laboratory experiments using the PSP toxin producing *Alexandrium catenella* (previously named *Alexandrium tamarensis* Group I) and the non-toxin producing *Alexandrium tamarensis* (previously named *Alexandrium tamarensis* Group III) (John *et al.*, 2014; Fraga *et al.*, 2015) isolated from Scottish waters reveal that toxin production in *A. catenella* is maximal at 12°C. When both species are grown in co-culture, growth rate and yield are greater in *A. tamarensis* suggesting a potential competitive impact in areas where both species occur (Eckford-Soper *et al.*, 2016).

**DSP:** During 2013 a number of people were intoxicated with DSP as a result of eating *Mytilus edulis* from the Shetland islands. This intoxication event was associated with an exceptionally rapid increase in *Dinophysis* cell densities which exceeded any growth rate published in the scientific literature (Whyte *et al.*, 2014). Analysis of wind patterns suggests that advection of *Dinophysis* cells from offshore areas played a role in this event (Whyte *et al.*, 2014). Prolonged closures of shellfish harvesting areas resulting from high concentrations of DSP toxins continue to be enforced in Loch Fyne in Scotland. These prolonged closures are also thought to be influenced by wind patterns (Morris *et al.*, 2010).

**AZA:** Concentrations of azaspiracid above the closure limit of 160 mg KG<sup>-1</sup> were recorded for the first time in shellfish from the south coast of England in 2015. As a result of its small size, *Azadinium* is difficult to monitor using routine light microscopy techniques. Investigations into the ecology of this genus in UK waters are at a very early stage and how it responds to the impacts of climate change are unknown.

**ASP:** The frequency of closures of shellfish harvesting areas due to elevated concentrations of domoic acid (DA) were low, however the first closures of *Mytilus edulis* harvesting areas were enforced along the south coast of England in 2014 and in Belfast Lough, Northern Ireland in 2015. Laboratory studies on a strain of *P. australis* (a confirmed DA producer in UK waters) isolated from the English channel revealed its optimum growth rate to occur between 13.5 and 18.5°C and that DA was produced during both exponential and stationary growth phases (Thorel *et al.*, 2014).

A regional study of marine mammals revealed ASP and PSP toxins to be found in urine and faeces of harbour seals (*Phoca vitulina*) round the Scottish coast (Jensen *et al.*, 2015). The impact of long term exposure of marine mammals to algal toxins in UK waters is currently being investigated. Other recent studies have found several species of marine mammals

in Alaska exposed to algal toxins (Lefebvre *et al.*, 2016) with the potential for this exposure to increase as environmental conditions in the Arctic change.

A study into new and emerging algal toxins (e.g. brevetoxin, pinnatoxin, cyclic imines) was performed. Methodologies to monitor these new toxins were developed but to date these toxins have not been detected in UK waters (Turner *et al.*, 2015a; Davidson *et al.*, 2015).

The capacity to model the risk of HAB events has increased since the last report card. A system of HAB warning alerts has been developed, modelling cell counts and weather data to predict risk from HABs in the south west coast of Ireland and the Shetland Islands. These alerts provide useful warnings to shellfish farmers about the pending risk from harmful algal blooms (Cusack *et al.*, 2016; Dabrowski *et al.*, 2016). A model has also been used to track the transport of the fish killing dinoflagellate *Karenia mikimotoi* from offshore areas around the Scottish coast (Gillibrand *et al.*, 2016).

Several key datasets relating to pathogenic vibrios have emerged since the 2013 MCCIP report that provide new information in this emerging area.

## 2.2 Vibrios

### Survey data (2012-2014):

Cefas has carried out *ad hoc* monitoring of two sites along the south coast of the UK to determine the prevalence of pathogenic bacteria in bivalve shellfish product. This study represents the first attempt to establish an understanding of the prevalence of these bacteria in this region. On numerous occasions (particularly during summer months), potentially pathogenic strains were directly isolated. In particular, *V. parahaemolyticus*, a bacterium that can cause gastroenteritis through the consumption of shellfish produce, was isolated on almost all sampling occasions, directly from shellfish matrices. Interestingly, of the 85 recovered strains, 35 contain either the virulence marker *trh* (n=31) and/or *tdh* (n=4). These are genes normally associated with human clinical infections. These toxigenic strains make up ~41% of total isolated, much higher than previously thought. The actual virulence potential of these strains is unknown, and a lack of reported shellfish-associated infections should be noted.

A molecular analysis of CPR samples for the presence of *Vibrio* has revealed a positive relationship with northern hemisphere temperature as well as the AMO (Vezzulli *et al.*, 2016).

## 2.3 Tetrodotoxin

A recent study by Cefas (Turner *et al.*, 2015b) identified the potent toxin agent tetrodotoxin in UK bivalve shellfish species in sampled shellfish. Tetrodotoxin (TTX) is the causative toxin responsible for pufferfish/fugu poisoning, a fatal marine poisoning normally associated with fish originating in tropical regions. The toxin and its structural analogues are thought to originate from a variety of marine bacteria, including *Vibrio* spp. (Pratheepa *et al.*, 2013). *Vibrio* strains identified from these same shellfish matrices were analysed using a range of chemical techniques and TTX was also identified in bacterial cell cultures providing additional compelling evidence for the production of TTX by *Vibrio* spp. It should be noted that while the human health risk determined from the samples analysed in this study has been shown to be low, the potential for health impacts remains, particularly if the levels of TTX were to increase in areas associated with shellfish harvesting. It is important to note that while bacterial pathogens may be eliminated in shellfish products following effective cooking, TTXs are heat stable and will thus not be destroyed in the food preparation process (Turner *et al.*, 2015b).

## 2.4 Increase in reported *Vibrio* wound cases in NW Europe (2014)

A recent study led by Cefas underlined the potential role of climate change in mediating the risk of waterborne infectious disease in NW Europe (Baker-Austin *et al.*, 2016). This study outlined the emergence of *Vibrio*-associated wound infections in the region, particularly during heatwave events, where two major factors appeared to drive infections. These are a) the proliferation of *Vibrio* bacteria in low salinity water during sustained period of warm weather and, b) the concomitant increase in human exposure (e.g. recreational swimming) in both space and time during these events. More recently, a significant increase in reported infections in NW Europe emerged in 2014 following the most intense heatwave experienced in the region (July-August 2014). This incident is noteworthy as the number of infections reported in this region was significantly higher than any other reporting year (an almost 100% increase on the 'worst' year on record, 2006) with 89 cases reported in Finland and Sweden and at least one identified fatality. Many of these cases were reported at high latitudes (~65N) in sub-arctic regions, highlighting the increasing geographical spread of these bacteria in the environment, potentially driven by warming. Using recent climate data, the scale and extent of this heatwave is unprecedented, with surface seawater temperatures along coastal areas of Northern Sweden and Finland exceeding all previous records. This heatwave follows several recent similar episodes (e.g. 1994, 1997, 2003, 2006 and 2010) which suggests that significant heatwave events may become common under a warming climate system (Baker-Austin *et al.*, 2016). These findings have consequences for the UK because under a warming climate system we may observe a potential increase in clinical risk, particularly in low salinity areas around the UK coast. Indeed, given climate projection data for NW Europe suggests significant warming, these are clearly public health threats that may become more pertinent in the future.

No changes in confidence relating to pathogenic vibrios since the 2013 report, however increasing data as well as anecdotal case studies such as those presented here indicate some well-defined risks have emerged.

## 2.5 Norovirus

### Surveillance of norovirus and identification of environmental risk factors

Cefas has conducted investigations into the relationships between catchment hydrometric, climatic, physical and demographic factors, and levels of NoV in shellfish from 31 sampling sites on the coast of England and Wales. The study found significantly higher quantities of the virus in shellfish from colder waters (<5°C) than in warmer waters (>10°C) (Campos *et al.*, 2017). Norovirus levels were also positively associated with the number and frequency of sewage discharges, volumes of sewage discharged to the study sites and river flows. Levels of NoV in shellfish were positively associated with the number of storm overflow events. Rainfall patterns directly influence flow rates in sewerage networks, particularly in combined sewerage systems. However, one study reported that changes in rainfall patterns have not been linked to anthropogenic climate change and the impact of climate change on river flows has not yet been detected (Watts *et al.*, 2015). Further studies are needed to assess human health impacts associated with projected increases in water temperature, which in theory would be linked with lower virus contamination levels and improvements to sewerage infrastructure associated with growing human population density and activity on the UK coast.

Cefas has also undertaken detailed characterisations of NoV contamination in untreated sewage and treated effluents



subject to primary, secondary and tertiary treatments, and investigated the fate and behaviour of NoV in nearshore waters at two sites. NoV concentrations in storm tank discharges were similar to those observed in untreated effluent, indicating that storm water constitutes a major polluting source of NoV to the environment (Campos *et al.*, 2016). This is relevant because many sewer systems in the UK carry combined flows of household and industrial wastewater together with surface water runoff in a single pipe system for treatment at the sewage treatment works. Therefore, where storm overflows (SOs) cannot be eliminated, the frequencies, volumes and pollutant loads of spills should be controlled to reduce human exposure to NoV and prevent new cases of human infection.

### 3. HOW OUR UNDERSTANDING HAS DEVELOPED OVER THE PAST DECADE?

#### 3.1 HABs:

There has been a substantial amount of work performed in UK waters over the last decade which has greatly improved our understanding of HAB diversity and dynamics (Edwards *et al.*, 2006; Fehling *et al.*, 2006; Collins *et al.*, 2009; Davidson *et al.*, 2009; Hall and Frame 2010; Brown *et al.*, 2011; Fehling *et al.*, 2012; Gowen *et al.*, 2012; Hinder *et al.*, 2012; Turner *et al.*, 2014; Whyte *et al.*, 2014; Bresnan *et al.*, 2015; Davidson *et al.*, 2015; Jensen *et al.*, 2015; Turner *et al.*, 2015a; Gillibrand *et al.*, 2016).

There is a strong regional distribution in HAB genera and events in UK waters (Bresnan *et al.*, 2013). Studies performed in the last decade reveal the *Alexandrium* population in Scotland to be diverse with *Alexandrium catenella*, *A. tamarense*, *A. minutum*, *A. tamutum* and *A. ostenfeldii* identified (Collins *et al.*, 2009; Brown *et al.*, 2011; Touzet *et al.*, 2010; Davidson *et al.*, 2015). In Scotland, the main PSP producer has been confirmed as *A. catenella* (Higman *et al.*, 2001; Collins *et al.*, 2009) while in England *A. minutum* is the causative organism (Percy, 2006). This regional difference is reflected in the different PSP toxin profiles recorded in UK shellfish (Turner *et al.*, 2014). Laboratory studies on Scottish isolates of *A. catenella* and *A. tamarense* suggest that *A. tamarense* had a stronger growth rate and higher biomass than *A. catenella* when grown in co-culture (Eckford-Soper *et al.*, 2016).

The inherent variability in HAB dynamics in UK waters meant that in previous report cards, low confidence was given in predicting the potential impacts from climate change (Bresnan *et al.*, 2010; 2013). The arrivals of new HAB species from other geographic regions (e.g. *Gymnodinium catenatum* from the Iberian peninsula) have not been reported over the last decade. A detailed study was performed to establish the methodology to address new and emerging HAB toxins (e.g. brevetoxins, pinnatoxins, cyclic imines) however none were recorded in UK shellfish (Turner *et al.*, 2015a; Davidson *et al.*, 2015). Closures of shellfish harvesting areas as a result of concentrations of AZA and YTX above the closure limit have been enforced in UK waters in low numbers. A link with climate has not yet been investigated.

Previous report cards suggested with low confidence that increased stratification from warming temperatures or increased nutrients could increase the incidence of HABs. Modelling studies on the fish killing dinoflagellate *Karenia mikimotoi* suggest stratification may not be the only driver of these blooms and that transport in the coastal current as well as seeding from offshore blooms influence the incidence of these blooms in coastal areas (Davidson *et al.*, 2009; Gillibrand *et al.*, 2016).

The importance of the influence of weather on HAB events was confirmed in 2013 when *Dinophysis* was the cause

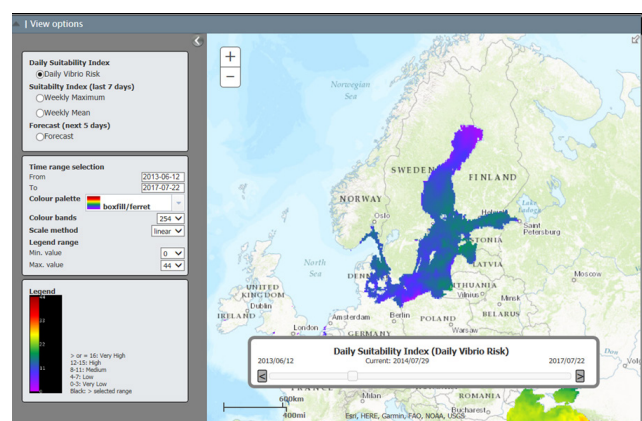
of a DSP intoxication event after consumption of *Mytilus edulis* from Shetland. A change in wind direction transported a population of *Dinophysis* inshore resulting in a sudden increase in DSP toxins in *M. edulis* (Whyte *et al.*, 2014). Wind driven advection is also suggested to have influenced prolonged DSP events in Loch Fyne (Morris *et al.*, 2010) and has been identified as a driver of phytoplankton community shifts in multi-decadal studies from the CPR (Alvarez-Fernandez *et al.*, 2012; Hinder *et al.*, 2012; Beaugrand *et al.*, 2014).

In addition to shellfish, algal toxins (DA and saxitoxin (PSP)) has been recorded in the urine and faeces of harbour seals from Scottish waters in the last decade (Hall and Frame 2010; Jensen *et al.*, 2015). The impact of long term exposure of marine mammals to algal toxins in UK waters is currently being investigated. Recent studies have shown algal toxins to be present in marine mammals as far north as Northern Alaska (Lefebvre *et al.*, 2016).

#### 3.2 Vibrios

The understanding of *Vibrio* dynamics has changed significantly in the last decade due to several inter-relating factors. A greater understanding of the physio-chemical parameters that govern and/or restrict bacteria such as vibrios in the marine environment has also been greatly extended in the last decade. An excellent example is the apparent low incidence of vibrios in the Mediterranean Sea, where large numbers of cases would be expected based on population density, exposure (e.g. recreationally and seafood consumption related) and temperature. By developing risk models based on microbiological growth data obtain in different temperature and salinity profiles it was determined that the most probable reason low numbers of reported cases (and in particular *Vibrio vulnificus*, the most serious *Vibrio* pathogen) are observed is that the Mediterranean is too saline an environment to support populations of these pathogens. This contrasts with the Baltic Sea, which provides far more favourable conditions for these pathogens where outbreaks can occur during heatwaves (Baker-Austin *et al.*, 2016b).

Methods for the isolation, testing and characterisation of strains have developed over the last decade allowing fundamental questions such as the clonal relationship of bacteria involved in a given outbreak to be addressed. Techniques such as next generation sequencing based



**Figure 1:** *Vibrio* risk analysis during a significant heatwave event, July 2014, Northern Europe. The *Vibrio* risk portal identified a sustained and anomalous body of warm water during the summer of 2014 that occurred during a significant heatwave event during July and August 2014. A noticeable increase in reported *Vibrio* infections (almost 100 cases) were reported during this episode (Baker-Austin *et al.* 2016a).

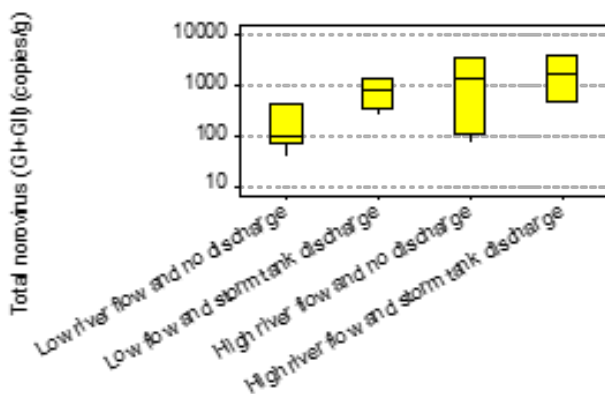
Techniques such as next generation sequencing based methods, facilitate the examination of strains from geographically diverse outbreaks to potentially determine routes of transmission, rates of evolutionary change and glean clearer insights into the evolution of virulence potential (Baker-Austin *et al.*, 2016b).

The utilisation of remote sensing data, coupled to standard epidemiological and microbiological studies, alongside climate and climate projection data has been instrumental in building a clearer insight into these disease risks over the last decade. This simple yet data-rich approach has been successfully applied to identify discernible environmental signatures prior to *Vibrio* outbreaks. For example, during heatwave events, the use of satellite imagery to identify areas undergoing intense warming has been coupled to case report information to help further enhance future predictive capabilities (Baker-Austin *et al.*, 2013). During the 2006 European heatwave, an increase in reported *Vibrio* infections was identified. This integration of approached has only recently been instigated but has vastly improved our understanding of the types of environmental conditions that prevail during outbreak situations, and may be usefully applied for proactive risk management purposes (Figure 1). This approach has now been implemented into a free to use web tool, see the online: <https://e3geoportal.ecdc.europa.eu/SitePages/Vibrio%20Map%20Viewer.aspx>.

### 3.3 Norovirus

Better characterisation exists of the causes of periods of high NoV risk for downstream bathing and shellfish harvesting areas. These include intermittent spills from sewerage systems, episodes of reduced retention and treatment at wastewater treatment works, periods of increased flushing of urban diffuse pollution loadings and re-entrainment of deposited and mainly particulate-associated loadings in rivers during high flow conditions (Kay, 2013). Heavy rainfall and flooding have been identified as the most common events preceding cases of waterborne disease (Cann *et al.*, 2013).

Projected increased winter river flows and periods of high rainfall throughout UK catchments are likely to increase the NoV load to nearshore environments (Campos *et al.*, 2014). In one UK estuary, Campos *et al.*, (2015) found that levels of NoV in shellfish during high-flows and storm overflow discharges were 10 times higher than those during low-flow conditions (Figure 2). In the USA, new probability-based models based on water depth and temperature, wind, rainfall and salinity have been developed to predict oyster NoV



**Figure 2.** Levels of norovirus in shellfish sampled at a UK estuary during four environmental conditions.

outbreaks making it possible to prevent, or at least reduce, human exposure to NoV (Wang and Deng, 2016). Similar models could be developed in the UK and at least one project is currently exploring the use of models that link this type of information with Earth Observation data for near real-time prediction of *E. coli* in shellfish harvesting areas (Schmidt *et al.*, 2017).

Improvements in the predictive capability of global and regional climate models (GCMs/RCMs) provide better insights into areas currently undergoing change and areas where potential risks may greatly increase or emerge in the future. This type of information is extremely important for risk managers, clinicians and public health bodies as a proactive means of ameliorating and managing changing risk, particularly in regions where these types of pathogens may emerge in the short to medium term. These future projections are allowing regions to be identified where it is possible to provide detailed advice for risk assessment purposes. This detailed information was not available ten years ago.

## 4. KNOWLEDGE GAPS AND KEY CHALLENGES

The complexities of climate change on HABs has been comprehensively reviewed in the peer-reviewed literature (Hallegraeff 2010, Wells *et al.*, 2015) as well as previous report cards (Bresnan *et al.*, 2010; 2013). One major challenge is the routine identification of shellfish toxin producing cells to species level which often requires electron microscopy or molecular based methodology. The role of offshore advections has begun to be addressed (Whyte *et al.*, 2014; Gillibrand *et al.*, 2016), however many knowledge gaps remain e.g. impacts of ocean acidification (OA) on UK HAB species, impacts of grazing and the interaction between HABs and other marine trophic levels. There are no changes of confidence since the last report card (Bresnan *et al.*, 2013).

A number of critical data gaps for Vibrios exist. Systems of epidemiology and surveillance for a number of waterborne infectious diseases are poor in Europe and the UK, and a large number of cases are likely to be under-reported or missed using current systems. A second knowledge gap is the apparent inconsistency between the isolation of potentially pathogenic strains and incidence of reported cases. Again, this may be related to deficiencies in the current systems of epidemiology. An important challenge is to link detailed epidemiological data to identify likely routes of exposure, risk characteristics (e.g. individuals at particular risk of infections) as well as possible mechanisms to disrupt disease transmission. There is also a requirement for data about warming trends and the emergence of different toxin groups (e.g. TTX) in the UK as well as how oceanic currents drive the movement of these pathogens in the environment. The provision of baseline survey work on shellfish species would provide critical information regarding the temporal and spatial prevalence of these new toxins.

## 5. EMERGING ISSUES (CURRENT AND FUTURE)

The environmental parameters with the potential to impact HABs have been thoroughly reviewed in previous report cards (Bresnan *et al.*, 2010; 2013). Impacts of OA on the marine ecosystem are gaining more attention, particularly with multifactorial experiments. The role of offshore processes needs to be studied further as do the interactions between HABs and the total phytoplankton and zooplankton communities. The impact of low level exposure of top predators to HAB toxins through the consumption of fish and shellfish vectors requires further investigation. These algal toxins can co-occur and information about impacts on other mammalian species may be important for assessing risk to humans.

The recent detection of TTX in bivalve shellfish, potentially

linked to vibrios in shellfish matrices is of interest and requires further characterisation, particularly in the context of a warming marine environment in the UK.

Further research is required to understand the effect of extreme weather events on the fate and behaviour of NoV and the consequential human health risks in the UK. Many climate models available for UK estuaries have insufficient resolution and spatial coverage and this constrains the development of whole catchment models to support risk prediction and pollution remediation strategies for human pathogens (Robins *et al.*, 2016).

Disease surveillance for NoV remains a key challenge even in the developed world. It is compromised by the large range of disease symptoms and severity, the lack of disease reporting, and the diverse exposure pathways. Detailed molecular epidemiology linked to environmental monitoring is required to associate virus strains with pollution sources and pathways to exposure and disease (Bridge *et al.*, 2010).

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