

What are the concerns associated with microbiological pollution?

Microbiological pollution and its impacts is dependant on the weather (amount of rainfall), climate (temperature, intensity of light) and environmental conditions such as turbidity and amount of organic matter. Faecal indicator bacteria die off much faster in warm clear water (with increased sunlight) than in cold turbid waters which is less well penetrated by sunshine.

The release of faecal micro-organisms and pathogens into the marine environment through sewage outfall and polluted rivers is of concern from a recreational standpoint and a threat to important shellfish-growing areas. The health risk is dependent on the infectious dose and the human sensibility to micro-organisms (age- or immunity-dependent). Some pathogens are highly dangerous for humans even at low concentrations (hepatitis A virus, *E. coli* O157:H7, *V. cholerae*), while others need to be ingested in high concentrations to be harmful (*Vibrio parahaemolyticus*), or, although highly infectious, are not very dangerous (norovirus).

Risks have recently been estimated from epidemiological data and indicator concentrations in surface waters (Lopez-Pila & Szewyk, 2000). The minimum risk bathers are exposed to can be estimated from a dose response relationship for rotavirus and the ratio of faecal coliform/rotavirus in water. Because the probability to become infected by a single infectious unit is relatively high, the authors of the study considered the rotavirus model as being very sensitive to assess the illness load. Assuming that a bather ingested 100 ml water, the risk was estimated to be of 1.6:1000, if the mean value of lognormal distribution was 100 *E. coli* per 100 ml (95% percentile value: 6300 *E. coli* per 100 ml). However, based on risk assessment models, maximum risks were estimated to be 1.3 infections per 100 swimmers. The risk assessment was also applied to viral contamination of shellfish. An average virus exposure of 6 plaque forming units (PFU) per 60g of shellfish would lead to a risk estimated to be 31:1000. The rotavirus risk varied from 15:1000 to 540:1000 depending whether the shellfish was depurated or not.

Since a few years, viral zoonoses have become more evident. Unusual rotavirus strains in humans suggest that animal transmission and co-infection of environmental samples by different strains may enhance genome re-arrangements and re-assortiment. The recent diagnosis of hepatitis E virus (HEV) infections in non-travellers in developed countries raised the question of the source of infection. Molecular studies, which demonstrated similarities in the sequence of strains among animals (swine, pigs) and humans, and the detection of HEV in sewage in different countries suggest that humans may be infected through contact with effluents of animal origin. The zoonose risk can widely be extended to other micro-organisms. Thus, *E. coli* O157:H7 is a model of emerging pathogen. Intensive livestock farming and the selective pressure on micro-organisms to successfully survive in the environment have led to a horizontal transmission and accumulation of virulent factors.

Exposures of humans to pathogens in the aquatic environment for example during recreational activities may result in diseases. Susceptible populations (younger, immune deficient or older populations) may have a higher risk of contracting severe illnesses.

The World Health Organisation (WHO) is actively involved in the protection of human health providing guidelines and epidemiological reviews in this field. A link between gastroenteritidis, acute febrile respiratory illness, ear infections and generally minor self-limiting illnesses and faecal-contaminated water is clearly demonstrated. In most cases the primary disease symptoms are diarrhoea, vomiting and acute respiratory infections.



More serious or fatal diseases were less frequently reported. A few illnesses are triggered by protozoan parasites (see e.g. amoebic meningoencephalitis, septicemia, typhoid, leptospiriosis), some of which may lead to sequelae (renal disease, cardiac and nutritional disorders). Reviews covered different pathogens, especially bacteria (*Campylobacter jejuni, E. coli* O157, *Helicobacter pylori, Legionella* spp., *Mycobacter avium, Shigella* spp., *Vibrio vulnificus*), parasites (*Giardia*, Mycosporidia, *Naegeria fowleri, Schistosoma* spp.) and viruses (adenovirus, coxsackievirus, echovirus, Hepatitis A virus, Hepatitis E virus). However, only few cases have been reported in Europe, which mostly related to recreational activities in monitored areas.

The link of infectious diseases to the consumption of raw shellfish like oysters, mussels, cockles and clams has long been identified. Bacterial diseases such as cholera and typhoid fever were the first to be suspected of being linked to consumption of contaminated shellfish. Viral outbreaks associated with contaminated shellfish consumption were first suggested more than 50 years ago. Initially, the analysis of outbreaks was mainly based on epidemiological data and symptoms in patients (Richards, 1987). The development of molecular biology, and thus the ability to detect low levels of enteric viruses in shellfish, has provided more accurate assessment of shellfish as a path for disease transmission. Despite the fact that many enteric viruses can be detected in human faeces, only HAV and NoV have been clearly identified as infectious agents in consumed shellfish.

In Europe the most common illnesses associated with bivalve mollusc consumption are gastroenteritis (NoV, *Salmonella, Vibrio paraemolyticus*) and hepatitis caused by HAV. Other gastro enteric viruses, (astroviruses and parvoviruses), parasites such as *Crypstosporidium* and bacteria (*E. coli* O157:H7, *Shigella, Plesiomonas, Listeria*) have also occasionally been detected in shellfish or in shellfish related outbreaks although their true epidemiological significance is not clear.

Go to full QSR assessment report on the impacts of microbiological contamination on the marine environment of the North-East Atlantic (publication number 466/2009)