Microbial modelling in coastal environments and early warning systems: useful tools to limit shellfish microbial contamination


To reduce human health risks and significant revenue losses due to the closure of shellfish-farming areas, it is necessary to maintain good water quality and food safety in marine environments. The major pathways introducing enteric bacteria and/or viruses into coastal areas are via urban and agricultural effluents. These microorganisms, and others naturally residing in marine waters such as

Vibrio spp., may subsequently contaminate filter-feeding shellfish (Lee and Younger 2002; see Potasman et al. 2002 and Butt et al. 2004 for reviews on potential pathogenic microorganisms in shellfish). Shellfish are often consumed raw or undercooked and thus have been implicated in some foodborne diseases (Lipp and Rose 1997; Feldhusen et al. 2000; Yam et al. 2000). By implementing shellfish farming regulations, the incidence of enteric shellfish-borne diseases, especially Salmonella spp. outbreaks, has been considerably reduced worldwide (Richards 2003). However, enteric viruses are still detected in shellfish (Le Guyader et al. 1998; 2000) and have been implicated in shellfish-borne outbreaks after oyster consumption, in some cases with the shellfish meeting European Union (EU) bacteriological standards (Gill et al. 1983; Richards 1985; Dowell et al. 1995; Otsu 1999; Le Guyader et al. 2006). This suggests that, if conventional depuration can remove faecal indicators and bacterial pathogens such as Escherichia coli or Salmonella spp. (Marino et al. 2003), it is less effective for eliminating faecal viruses from shellfish (Lee and Younger 2002; Loisy et al. 2005a). Thus, growing shellfish in an environment free from microbial contamination seems to be a more suitable solution than depurating potentially contaminated filter feeders. The use of tools such as statistical or hydrodynamic models applied to faecal microorganisms and early warning systems for shellfish production sites, could predict microbial contamination in shellfish-harvesting areas (Grange 1999; Tattersall et al. 2003; Martinez-Urtaza et al. 2004; Pommepuy et al. 2006).

16.1 MODELLING ENTERIC MICROORGANISMS IN COASTAL ENVIRONMENTS

When entering a coastal environment, faecal microorganisms, free and bound, undergo different processes: (i) physical dilution induced by currents and mixing, (ii) physico-chemical conditions: sunlight irradiation, salinity, temperature, pH and nutrient availability, which can result in bacterial stress or viral degradation (Trousselier et al. 1998; Rozen and Belkin 2001), and (iii) biotic effects, including competition with other microorganisms and grazing (Barcina et al. 1991; Rozen and Belkin 2001).

In order to evaluate and/or to predict the impact of such microbial contamination in bathing or shellfish-harvesting areas, modelling tools have been developed. They are mainly dedicated to faecal microbial indicators such as faecal coliforms (FC) (Roberts and Williams 1992; Ribeiro and Araujo 2002), E. coli (Tattersall et al. 2003; Armisen et al. 2006), enterococci (Bell et al. 1992) or F-RNA-specific bacteriophages and astrovirus (Riou et al. 2007).
The models are classified in two main categories: statistical or process-based dynamic models.

**16.1.1 Statistical models**

The main objectives of this type of model are: (i) to describe the microbial contamination that results from sewage inputs or non-point sources in a specific site, according to relevant environmental conditions, and (ii) to predict water quality. These models are based on linear or logistic regression analyses that link environmental parameters such as rainfall, wind or sunlight to faecal contamination, mostly to faecal coliforms or *E. coli* (EPA 1999; Crowther et al. 2001; Martinez-Urtaza et al. 2004). Their development requires large monitoring data sets of both (i) rainfall in the upstream watershed (one or more rainfall stations; rainfall characteristics: amount, duration, lag time) or other relevant environmental parameters, and (ii) faecal microorganisms occurrence at the representative monitoring station (bathing or shellfish-farming area). Then, predictive tools are built and the results obtained by rainfall based alert curve models (such as the quantity of rain during the past 24 hours, EPA 1999) or by real-time monitoring of different hydrometeorological variables (Olyphant 2005) that define the conditions of closure of shellfish-farming or bathing areas (Wither et al. 2005). These models could also provide cost-effective management tools for the exploratory investigation of any monitoring point that is failing to meet water quality standards. Their application to the data collected on the Fylde coast (United Kingdom) have shown significant positive and negative relations between microbial concentrations and rainfall, the tide height at the time of sampling, onshore winds and sunlight, respectively (Crowther et al. 2001). Furthermore, general linear modelling was performed to relate *E. coli* shellfish contamination to environmental factors in shellfish-farming areas in the United Kingdom (Lee and Morgan 2003). Regression analysis models were also used for other bacteria, including *Salmonella* spp. (Martinez-Urtaza et al. 2004) and *Aeromonas* spp. (Maalej et al. 2003) or viruses – norovirus, hepatitis A virus, human adenovirus and enterovirus (Hernroth et al. 2002; Formiga-Cruz et al. 2003) in coastal waters or shellfish.

Another modelling approach is the use of artificial neural network (ANN) models. Among the different ANN architectures, the multi-layer perceptron architecture is commonly used for prediction (Gamal El-Din and Smith 2002). According to Brion et al. (2005), ANN models predict the presence and absence of norovirus and other viruses in shellfish with better precision than logistic regression models. Artificial neural networks were coupled with hydrodynamic models in order to model the faecal coliform contamination of an estuarine
system (Scarlatos 2001; Lin et al. 2008). They assisted in identifying correlations between FC and various parameters involved such as pH, temperature and turbidity (Scarlatos 2001) and in providing rapid predictions of the FC concentrations in coastal waters (Lin et al. 2008). Although a regression tree (Gray and McDonell 1997) has already been used in wildlife modelling (such as distribution of *Frankia* spp. strains and symbiotic bacteria, Oakley et al. 2004 or Marbled Murrelets, a seabird in coastal British Columbia, Canada, Yen et al. 2004), this tool has not often been used to predict microbial contamination in coastal environment. However, an extension of tree regression, named “Random forests”, was used to study relationships of the concentrations of *E. coli* and enterococci in bathing waters to numerous potential explanatory variables including weather, hydrological conditions and contaminant sources (Parkhurst et al. 2005).

### 16.1.2 Process-based dynamic models

Considering the limits of statistical models (including no distinction between inputs, no consideration of advection, transport, or microbial decay rate and no provision of spatial and temporal distribution), other models describing the processes were developed. For the development of a shellfish and/or water quality model, different sub models are needed: (i) a hydrodynamic model which provides knowledge of current and mixing coefficients, (ii) a dispersion model which integrates transport and diffusion of bacteria/viruses, and (iii) a biological model (microbial decay) which describes the decay of bacteria/viruses depending on environmental conditions (light, temperature and sediment).

#### 16.1.2.1. Hydrodynamic models

In the past, the description of hydrodynamic conditions was based on physical modelling (such as tank-based simulations). Problems of scaling and cost lead engineers to use numerical models which are cheaper and potentially more efficient for water quality applications. Numerical models are useful tools to assess different discharge strategies or best location of outfall, effects of load reduction or impact of local construction.

A range of models with differing levels of sophistication were developed and adapted for a wide variety of hydrodynamics. The choice of a model depends on local hydrological features, which is a function of local dynamic processes. These models are based either on open sources (Falconer and Lin 1997; Fiandrino et al. 2003; Pommepuy et al. 2004) or on commercial packages (Roberts 1999; Kashefipour et al. 2002; Servais et al. 2007) which include user-friendly interfaces.
Usually, a distinction is made between near and far field (Monteiro et al. 1992; Roberts and William 1992). In the former, the mixing is due to the turbulence induced by the discharge itself (near the diffuser) and leads to a local dilution factor of 100-fold or more. Beyond the near field, the far field is the area where dispersion is due to coastal currents and mixing under the influence of physical processes such as tides, wind-induced circulation, waves or, in addition, it can be density driven. Near field models are usually termed pseudo-empirical models, based on extensive experimental studies often on multiport diffusers (Monteiro et al. 1992; Roberts 1999). The linkage of near field and far field solutions is particularly important in modelling deep discharges (Monteiro et al. 1992).

Hydrodynamic models aim to resolve fluid dynamical equations (known as Navier Stockes equations) under various levels of simplification. When the dispersion away from the outfall is mainly longitudinal, as in a well mixed estuary (Yang et al. 2002) or in an elongated lagoon (Steets and Holden 2003), a one dimensional model is suitable. These models are based on vertical and lateral integration of the complete set of equations. When a spatial description is needed, for example in open coastal ocean, 2D models are used if the water property can be considered as well mixed. This includes generally shallow water areas where tidal or wind induced currents generate high turbulence and vertical homogeneity (Pommepuy and Salomon 1991; Kashefipour et al. 2002; Pommepuy et al. 2004). In case of thermal and/or haline vertical stratification, complete 3D models are needed. This is usually the case of estuaries where high river discharges occur and when the surrounding area is under fresh water influence (Falconer and Lin 1997) or in calm areas where temporary stratification can occur, for example, in a lagoon (Friandrino et al. 2003).

Numerical models, however, have to be used carefully because they have uncertainties linked to the model itself and to the site specific application. Models have to include high level turbulence closure in complex hydrodynamic environment, realistic open boundary conditions and meteorological forcing. In situ measurements are generally needed to validate hydrodynamic model simulations. Simulation of currents and mixing in shellfish-farming areas to estimate contamination requires a knowledge of bathymetry adapted to the high spatial resolution needed for local application (typical mesh size in the order of 100 m) and this constraint usually requires new empirical bathymetric data acquisition (Kashefipour et al. 2002).

16.1.2.2 Dispersion models

Microbial dispersion is due to transport (or advection) by currents and diffusion by turbulence. Two approaches are used for dispersion models, the Eulerian
and/or Lagrangian approaches (Monteiro et al. 1992; Tattersall et al. 2003). The first one consists of the calculation of a concentration at nodes of a fixed grid by solving the continuity equation. These models need to incorporate a high level advection scheme to avoid numerical diffusion (Monteiro et al. 1992). The Lagrangian approach involves tracking virtual particles which are hypothesised to carry a part of the discharge. Advection of each particle is calculated by temporal integration of the local current estimated by interpolation of current components calculated according to a fixed grid. The diffusion process is simulated at a step in which each particle is submitted to a random displacement determined by the diffusion coefficient (Roberts 1999b). This approach was used, for example, to simulate particle movements from any location of the model during a mean tide within the French coastal areas in Normandy (Riou et al. 2007). The Lagrangian approach is potentially very efficient but becomes unfeasible for long-term modelling due to the considerable amount of particles to track. Hybrid approaches have been proposed (Monteiro et al. 1992) and they usually promote the use of the Lagrangian model for near field and of the Eulerian model for far field or for low contamination and spatial gradient applications.

16.1.2.3. Parameters specific to a microbial application

Microbial applications aim at describing the fate of bacteria and/or viruses in coastal waters and their concentration in shellfish due to local or diffuse microbial input. In addition to the physical dispersion model described previously, they gather a decay model in seawater and a shellfish concentration model and eventually a transport of bound organisms model.

For an application of hydrodynamic models to microorganisms, the faecal input location and their fluxes have to be specified (Pommepuy et al. 2006). The main faecal sources are: (i) domestic fluxes originating from a sewage treatment plant (for example, $10^{12}$–$10^{13}$ FC/s from raw sewage discharge from San Francisco, USA population 1 million inhabitants, Robert and Williams 1992; and $1.6 \times 10^8$ FC/s from a town of 30,000 inhabitants; Salomon and Pommepuy 1990), (ii) non point source from rivers (river fluxes from $9 \times 10^6$ to $5 \times 10^{10}$ FC/s; Baudart et al. 2000) or from runoff from pastured land (Crowther et al. 2002; 2003; Kay et al. 2007), and (iii) boats (Sobsey et al. 2003). Currently, many studies are published for FC, but very few data are available for viruses and/or pathogenic bacteria. However, with the recent development of molecular techniques like real-time polymerase chain reaction (PCR) or Reverse Transcription-PCR (RT-PCR), quantitative inputs have been obtained for non culturable viruses or viable but non culturable pathogenic bacteria (Schoeyerer...
et al. 2001; Gilbride et al. 2006). Using real-time RT-PCR, a mean astrovirus concentration of $1 \times 10^4$ astrovirus genomes for 100 ml of raw sewage had been recorded at the outlet of a biological sewage treatment plant. This corresponded to an average flux of $3 \times 10^7$ astrovirus genomes/s (for a city of 120 000 inhabitants; Le Cann et al. 2003).

Microbial decay in the coastal environment

As faecal microorganisms are non-conservative elements, their fate in the coastal environment is dependent on their decay rate in that environment. Their fate depends on the bacterium itself (species, strain and physiological status), on physical and chemical characteristics encountered in the environment (temperature, salinity, organic matter content, oxygenation, pH), on atmospheric conditions (mainly sunlight irradiation) and on biotic factors (predation and competition; Chamberlin and Mitchell 1978; Martin et al. 1998; Troussellier et al. 1998; Rozen and Belkin 2001). Environmental conditions before exposure to seawater are also important, and pre-adaptation to some of the marine deleterious effects were shown to be beneficial (Dupray and Derrien 1995; Munro et al. 1995; Gourmelon et al. 1997). As for viruses, which generally act as inert particles, their survival is longer than that of bacteria and depends mainly on environmental parameters such as temperature, salinity, predation and sunlight irradiation (Bosch 1995; Wait and Sobsey 2001).

Numerous experiments have been conducted in order to determine microbial (especially faecal bacterial indicators) decay rates in coastal environments. This decay rate is often expressed as $T_{90}$: the time for bacterial or viral concentration to decrease by one log unit. The major factor affecting bacterial decline in the sea was shown to be sunlight irradiation (Sinton et al. 1994; Rozen and Belkin 2001). Diurnal variations were recorded (Bellair et al. 1977; Chamberlin and Mitchel 1978). The role of turbidity on light penetration was also observed and thus its impact on $T_{90}$ was demonstrated (Pompey et al. 1992; Alkan et al. 1995; Kay et al. 2005). A relationship between $T_{90}$ and daily light intensity, suspended solid concentration and depth has been obtained from experimental data for *E. coli* (Guillaud et al. 1997). Nevertheless, results obtained from *in vitro* or *in situ* experiments are generally variable and difficult to compare because of the great variability existing among the protocols that are used. So, for a study in a defined area, it is advisable to measure microbial survival and environmental parameters such as sunlight *in situ* rather than to rely on literature data only.

In the process-based dynamic models, different microbial decay models are used. The prediction of faecal contamination is generally based on faecal coliform or *E. coli* counts only. The decay model generally uses the first order
kinetic model, proposed by Chick (1908), which integrates a term summarizing all biological aspects of microorganisms (Crane and Moore 1986; Kashefipour et al. 2002). This model achieves a reasonable level of accuracy (Salomon and Pompépuy 1990; Pompépuy et al. 2006), when using the following equation:

\[ \frac{N_t}{N_0} = 10^{-kt} \]

where \( N_t \): number of bacteria (or viruses) at time \( t \), \( N_0 \): number of bacteria (or viruses) at time \( 0 \), \( t \): time in days, and \( k \): first order or die-off rate constant, generally estimated by \( T_{90} \) (\( k = \frac{2.303}{T_{90}} \)).

More complex models derived from Chick’s laws were proposed to express results obtained with bacterial populations composed of distinct subgroups and to describe non-constant decrease rates or to integrate the effects of parameters such as temperature, sunlight, or salinity (Crane and Moore 1986). A comparison of different log-linear and non-linear models (Gonzalez 1995) revealed that non-linear models adequately describe bacterial survival in the aquatic environment.

For microbial modelling in coastal environments, microbial decay is simulated with varying levels of refinement. Most existing process-based models assume a constant value for \( T_{90} \) (for example, 8, 16 and 24 h respectively, in Monteiro et al. 1992; Garcia-Barcina et al. 2002; and Pompépuy et al. 2004). However, variable \( T_{90} \) values, obtained according to different parameters such as sunlight intensity (Fiandrino et al. 2003); to diurnal variations (Roberts et al. 1999b; Kashefipour et al. 2002); surface/underlying water (Roberts and Williams 1992); season (Bell et al. 1992); or to wet and dry weather (Kashefipour et al. 2002) were also used. In a modelling study of nearshore coastal waters (United Kingdom), three different procedures for estimating the decay rate coefficients of faecal coliform according to solar radiation were tested (Kashefipour et al. 2006). A time-dependant decay rate for faecal coliforms considering the effects of light, salinity and temperature has been introduced into a 3D model (Hogdins et al. 1998). In another model, the decay rate depended on bacterial adaptative responses to the marine environment and on the effect of stress on bacterial physiology (Martin et al. 1998; Troussellier et al. 1998).

As opposed to faecal bacterial indicators, the potential survival of bacterial or viral pathogen in coastal environments has not been widely investigated. Some \( T_{90} \) values, mainly obtained from \textit{in situ} experiments were reviewed in Pompépuy et al. (2006). It should be highlighted that viruses are much more persistent in coastal environments than bacteria. Therefore, a \( T_{90} \) value of 30 days has been reported in a norovirus modelling study in a French shellfish-farming area (Pompépuy et al. 2004).
Microbial contamination in shellfish

To model faecal microbial contamination of shellfish, the relationship between bacterial and/or viral concentrations in the harvesting water and in shellfish flesh has to be specified. Indeed, shellfish filter their food as particles in suspension from surrounding waters and subsequently concentrate and retain potential pathogenic microorganisms present in those waters.

The bioaccumulation and elimination kinetics of enteric bacteria and viruses by bivalve molluscs were found to vary with shellfish species, their physiological status, the types of microorganism and environmental conditions such as temperature and season (Prieur et al. 1990; Burkhardt et al. 1992; Lees et al. 1995; Burkhardt and Calci 2000). In some studies, the concentration of faecal microorganisms in water and in shellfish was determined simultaneously and expressed per 100 ml of water and per 100 g of shellfish flesh and intra-valvular liquid, respectively (Burkhardt and Calci 2000; Shieh et al. 2003). For faecal coliform or *E. coli*, the concentration factor between water and shellfish could vary from 1- to about 100-fold greater concentrations in the shellfish (Prieur et al. 1990; Burkhardt and Calci 2000; Shieh et al. 2003) and even more for viruses and phages. For example, in a study including 18 pairing of water/shellfish batches (Gulf of Mexico), the accumulation rate varied from 2 to 146 and 0.2 to 222 for *E. coli* and male-specific coliphages respectively (Shieh et al. 2003). From data collected in the United Kingdom, Lees et al. (1995) established a relation between geometric means (GMs) of *E. coli* in shellfish and the corresponding GMs in seawater. For the pooled data set, a seawater GM of 100 will give a bioconcentration factor of 5.9 for mussels, and of 2.6 to 6.9 for oysters (Lees et al. 1995; European Commission 1996).

Among studies modelling microbial contamination in shellfish in the coastal environment, microbial concentration values in water (predicted at the shellfish sampling sites) were converted to values in shellfish flesh using a constant factor (Pommepuy et al. 2004; Riou et al. 2007) or using the European Commission (1996) relationships in the study of Tattershall et al. (2003). A more complex approach (taking shellfish grazing, filtration rate of oyster and retention efficiency of faecal coliform by oyster into account) was developed by Fiandrino et al. (2003).

Microorganisms bound to sediment particles

Enteric bacteria or viruses could be free organisms, possibly associated with dissolved material or bound to organic or inorganic particles, particularly small ones (Gerba 1984; Rao et al. 1986; Prieur et al. 1990; Auer and Niehaus 1993; Baudart et al. 2000). In the study of Auer and Niehaus (1993), 90.5% of faecal
coli coms were found to be associated with particles from 0.45–10 μm. These bound organisms can sediment and possibly be resuspended along with their associated sediment particles during tidal variations, waves, storms, heavy rains, and/or dredging operations (Grimes 1980; Pettibone et al. 1996; Coelho et al. 1999). Superficial bed sediments often exhibit a higher microbial contamination than the particles entrained in overlying waters (Martines-Mazanares et al. 1992; Irvine and Pettibone 1993; Craig et al. 2002) and of bottom sediments (Ferguson et al. 1996). This is due in part to the greater bacterial or viral survival within these surface sediments (Le Guyader et al. 1991; Chung and Sobsey 1993; Davies et al. 1995).

Adsorption to particles, sedimentation of bound faecal microorganisms and resuspension as sediment particles may be important factors affecting bacterial concentrations in water and thus, in shellfish. However, they are not currently specified in modelling systems (Boehm et al. 2003). In fact, considering that microorganisms associated with particles and sediment greatly complicate microbial modelling in natural waters, there is a need for the application of a sediment transport model to account for resuspension of faecal microorganisms associated to sediment particles under the action of turbulence and waves. Moreover, many uncertainties still exist concerning microbial contamination of sediment, including the effects of bound microorganisms and their behaviour in coastal environments. At present, the models which aim to describe the effect of sediment transport and in particular, the resuspension of bound faecal microorganisms are not numerous (Steets and Holden 2003; Harris et al. 2004; Sanders et al. 2005).

16.1.2.4. Model use

Most applications of process-based dynamic models focus on faecal coliforms or E. coli in coastal water (Head et al. 1992; Falconer and Lin 1997; Roberts 1999; Kashefiopour et al. 2002; Servais et al. 2007). They more rarely address shellfish harvesting areas (Pommeypuy and Salomon 1991; Fiandrino et al. 2003; Tattersall et al. 2003; Riou et al. 2007). Two examples of microbial modelling in French shellfish-farming areas are presented below.

Faecal coliform contamination of shellfish in a Mediterranean lagoon with large-scale shellfish farming was modelled during flow events (Fiandrino et al. 2003). Simulations were based on bacterial transport and survival and coupled models were forced by the input of bacterial loads from the two main rivers (Vène and Pallas). Different flow types (reference, sudden and constant) were considered and subsequent spatial and temporal bacterial contamination of lagoon surface water and shellfish were estimated. Most of the time, the gradual changes of faecal
coliform abundances in the lagoon were due to biological rather than physical processes. In fact, the ratio of biological decay to physical dilution was found to be of 1 to 50 in a lagoon and of less than 0.002 in an estuary (Salomon and Pommepuy 1990). This indicates that, when the flushing time is very long, biological effects dominate processes determining faecal indicator concentrations. In contrast, in estuaries and coastal areas under the influence of strong tidal currents, physical mechanisms dominate faecal indicator fate and transport because of the high dispersion characteristics produced.

Bacterial contamination of shellfish depends on the receiving area. In the case of the Pallas River area, a simulated sudden input of bacteria led to a short-term (about one day) contamination of shellfish. A constant input of the same amount of bacteria induced a lower level but significant contamination, which was maintained during the entire simulation period (10 days). By contrast, bacterial inputs from the Vène River, led to shellfish contamination only when they were delivered through a flood event. Management of river flow, such as by installation of retention basins on watersheds to regulate the river’s hydraulic characteristics might be a way to limit the impact of bacterial contamination of shellfish.

In another study, viral and bacterial contamination in a shellfish-harvesting area was modelled with the aim of simulating the effect of domestic discharges on water quality (Pommepuy et al. 2004). The model comprised water concentrations corresponding to 20 days of domestic discharges in the sea during a viral epidemic in the population. The $T_{90}$ values used for *E. coli* and norovirus were 1 and 30 days, respectively. Based on the faecal flux measured from the wastewater treatment plant, average microbial flux was estimated at $3.4 \times 10^9$ *E. coli* per second. Viral input was estimated at $10^6$ viruses/s based upon the incidence and excretion rate in the population (3%, 60 000 inhabitants). Results from the model calculations were found to be similar to *E. coli* concentrations observed in shellfish. According to this model, physical dilution was sufficient to dilute viral input and limit contamination. Despite the very long viral $T_{90}$ assumed, the calculated viral flux was not sufficient to pollute the area. These calculations were in good agreement with actual viral shellfish contamination data (based on RT-PCR analyses).

### 16.2 EARLY WARNING SYSTEMS FOR SHELLFISH PRODUCTION SITES

At present, it is not possible to measure bacterial and/or viral concentrations in water or shellfish flesh and to obtain an immediate quantitative result to evaluate
and prevent human health risk. To provide this information, environmental parameters which are proven to be correlated with coliform contamination could be considered. Thus, alternative parameters – salinity or turbidity variations – are used to predict microbial contamination because real-time sensors for these physicochemical parameters are available (Grange 1999; Butler et al. 2001; Olyphant 2005; Le Saux et al. 2006; Pommepuy et al. 2008; Haramoto et al. 2007).

Early warning systems, based on modelling, whether statistical or deterministic, were developed or are under development: they aim at obtaining real-time data for risk management. However, few reports were published on these early warning systems. They are used for notification of events, monitoring harvesting closures and for calculation of re-opening time and date for shellfish growing areas. These predictive systems are based on (i) simple relationships between the observed rainfall and faecal microorganism concentrations (Grange 1999) or on (ii) complex models of the dominant mixing and transport processes (EPA 1999; Grange 1999).

The early warning system, proposed by Le Saux et al. (2006), is based on real-time observation from control points. The information is immediately sent to a computer which synthesizes the information, if the parameter exceeds defined values, the system moves into an alarm mode (Figure 16.1). Different parameters could be recorded (rainfall, salinity, sewage network key-points, disease epidemics in the contributing community etc) and gathered in a database. Particular events which could cause a deterioration in water quality could thus, be detected and shellfish producers immediately informed (such as an alarm from point 2).

In Europe, an early warning system for shellfish-farming areas is under development (Le Saux et al. 2006). The main goal of developing such a system is to predict a potential viral contamination in shellfish taking the following key parameters into account – salinity variations near shellfish at the producing areas; weather conditions in the watershed; and viral disease outbreaks in the local population. Validation of the above parameters is necessary for such systems, involving a comparison of water quality conditions at different sites which could serve as the basis for any water quality advisory notification.

In New Zealand, harvest criteria based on rainfall, river discharge level or salinity as a proxy for faecal coliform contamination have been developed by NIWA in collaboration with the marine farming industry and health authorities (Grange 1999). Data, collected by a series of tipping bucket rain gauges, water level recorders or salinity measuring buoys, are stored at remote stations and downloaded via telemetry or cell phone and compared to pre-determined criteria. The information is automatically faxed to shellfish harvesters and
regulatory authorities, who can also access the data via remote fax machine, often connected to cell phones on vessels (Grange 1999). It is noteworthy that these early warning systems are site-specific as some relevant criteria could be different from one area to another. Such autonomous monitoring networks have also proposed to protect against toxic algal blooms in a fish farm located in a south-eastern Tasmania estuary (Butler et al. 2001).

Other parameters, such as real-time data acquired from sewage network key-points and/or disease outbreak monitoring, also provide useful data to be considered in early warning systems. For example, epidemics are recorded in the human population by European Networks (for example in France, sentiweb: www.b3jussieu.fr). These networks could provide information on the occurrence of gastroenteritis in a specific part of the country and, consequently, warn of a possible input of viral pathogen in coastal environment. In the case of sewage, expert systems for monitoring wastewater treatment plants are already available (Punal et al. 2002). They could be associated with neural networks to predict wastewater input from sewage treatment plants or agricultural activities. The hydraulic loads and wastewater flow which would reach the river and ultimately the coast can be calculated (Crowther et al. 2002; Gamal El-Din and Smith 2002).
16.3 CONCLUSIONS

A broad variety of statistical or process-based models is now available to predict microbial contamination in the coastal environment. The models require information on environmental parameters which can determine microbial contamination at a specific site. They also provide potential for examination of various scenarios by considering, separately or together, different parameters or events that would degrade water quality and thus, contaminate shellfish. Furthermore, a recent study indicates that when combined to epidemiological models, process-based models could predict coastal health risk (Harris et al. 2004).

While uncertainties are addressed within process-based models (Harris et al. 2004), the most important ones are due to microbial data. In fact, very little precise empirical information exists on microbial behaviour in the environment and when available, they mostly concern faecal indicators and rarely pathogenic bacteria or viruses. Information is sparse on microbial inputs and their decay rates in environmental water, particularly for microorganisms bound to sediment particles, or in shellfish. Collecting this information is necessary to explain shellfish contamination and thus manage the risks.

To improve microbial modelling, different actions have to be developed. First of all, more sensitive, reproducible and standardized methods have to be developed to evaluate microbial concentrations in shellfish, waters and other compartments involved in water degradation – in sewage, catchment systems and sediment. Quantitative molecular methods such as real-time PCR or RT-PCR are now available. If applied to the environment, these methods would give more precise information on the level of non culturable viruses and of viable and culturable or viable but non culturable bacteria in impacted areas (Loisy et al. 2005b; Wade et al. 2006).

Moreover, technological progress leads us to reconsider research on pathogenic microorganism survival in situ and shellfish contamination/decontamination dynamics in the environment and/or during depuration processes. Investigations to improve the knowledge-base of the area would also be of greatest importance to validate coastal models and identify, for example, the role of diffuse sources from animal origins which could carry human pathogenic bacteria or viruses. The development and application of microbial source tracking methods in order to identify sources of faecal pollution could also provide useful additional data (Blanch et al. 2004; Gourmelon et al. 2007; Santo Domingo and Sadowsky 2007; Santo Domingo et al. 2007; Stoeckel and Harwood 2007).

Early warning systems have already been described and first applications presented (Grange 1999; Pommepuy et al. 2008). They are predictive tools based on the observation of the most relevant environmental parameters
involved in water degradation, such as salinity variations, sewage or river discharge (EPA 1999; Punal et al. 2002). However, further information derived from data recorded by epidemiological survey networks should be included in these systems, together with data on emerging pathogens or presence of related outbreaks in the coastal population leading to more accurate risk assessment and management (Le Saux et al. 2006).

In a near future, direct and real-time data on pathogen observations in the environment provided by biosensors, DNA chips (Rose and Grimes 2001; Picup et al. 2003; Lee et al. 2006; Lazcka et al. 2007) or rapid techniques (enzymatic analyses, for example) could be integrated into early warning systems. This would provide an additional safeguard for an efficient consumer protection.

16.4 REFERENCES


Microbial modelling and early warning systems


