Microbial communities in UK aquifers: current understanding and future research needs

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Abstract: The presence and activity of microorganisms in aquifers can affect, amongst other things, nutrient cycling, contaminant degradation and water flow. The introduction of a pollutant or other changes in water chemistry can alter the microbial community composition and affect aquifer functioning. To understand the microbial response to anthropogenically induced changes, a better knowledge of baseline microbial communities in uncontaminated aquifers is needed. Here, we review the information on microorganisms in UK aquifers together with examples of research from other countries on this topic, and discuss how these communities might respond to disturbance. Research into microbial communities in UK aquifers has mostly been limited to bacteria and often reveals a community dominated by Proteobacteria. The community composition is influenced by factors such as mineralogy and water chemistry, and the natural baseline community may be altered by aquifer contamination. A UK-wide survey of aquifer microbes, similar to one recently carried out in New Zealand, would provide valuable information about the current state of UK aquifer microbiology. This would lead to a greatly improved understanding of the ecosystem services provided by the microbial communities present in aquifers, allow future monitoring and assessment of the effects of pollution, and assist in groundwater resource management.

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It is well established that aquifers provide suitable environments for microbial activity (e.g. Novarino et al. 1997; West & Chilton 1997; Goldscheider et al. 2006; Pronk et al. 2009). There has been a shift from considering microorganisms only when they cause problems (such as disease outbreaks, pipeline corrosion, or blockage of water flow), to a realization that the natural ecology of groundwater is important in determining biogeochemical cycling and water quality, and may provide a means of restoring the quality of contaminated aquifers (Chapelle 1993; Humphreys 2009). The role of groundwater ecosystems in contaminated sites is generally considered in some groundwater monitoring programmes (Danielopol et al. 2004; Goldscheider et al. 2006; Danielopol & Griebler 2008), but groundwater ecosystems are generally not considered in groundwater management. This is partly because microbial processes and microbial diversity in aquifers remain poorly understood. Many questions remain about the make-up of microbial communities in groundwaters, the differences in community composition in polluted and uncontaminated aquifers, the contribution of microorganisms to contaminant attenuation, and the longer term changes that occur in microbial communities.

A first, important step towards a better understanding of the role of microorganisms in UK aquifers would be to assess current or ‘baseline’ communities in a range of geologies, along the lines of the baseline groundwater chemistry survey initiated by Edmunds et al. (2003), and similar to the UK-wide survey of soil bacteria (Griffiths et al. 2011). It is unlikely that there are truly natural microbial communities in aquifers, entirely undisturbed by anthropogenic impacts (Goldscheider et al. 2006). However, a survey of UK aquifers would provide a useful assessment of current conditions, representing a baseline for future comparisons, and would provide new understanding of the impact of pollution, climate change and human intervention on the ecosystem services that aquifers provide. Here, the term ‘uncontaminated’ aquifer is used to mean aquifers that are not affected by severe point source pollutants but may be affected by diffuse pollutants, which occur fairly ubiquitously.

Generally, a systematic approach to groundwater microbiology monitoring (except for specific pathogens) has been overlooked. The exception is a recent nationwide survey of groundwater in New Zealand, which revealed that hydrochemistry had the greatest influence on bacterial diversity of groundwater samples, with geological factors and human impact having a secondary influence (Sirisena et al. 2013).

In this paper, following an introduction to the characteristics of groundwater microbial communities, an overview of what is known about natural aquifer microbiology in the UK, supplemented with data from global studies, is presented. Finally, some microbiological issues that are current and potential future concerns for UK aquifers are discussed.

Introduction to aquifer microbial communities

The following section describes the aspects of microbiology that are specific to, or important to, aquifer environments. Many of these features are not specific to a UK setting and examples are drawn from other countries to illustrate general features or concepts. Throughout this paper, organisms are grouped on the basis of evolutionary relationships, or in terms of their functional ability. The choice depends on the usage, approach and techniques used in the study being described. For example, much DNA-based work lends itself well to a phylogenetic approach; therefore organisms are grouped according to their
Prokaryote (Archaea) Euryarchaeota
Prokaryote (Bacteria) γ-Proteobacteria
Prokaryote (Bacteria) β-Proteobacteria
Prokaryote (Bacteria) β-Proteobacteria
et al. (2009) (although no such systems have been reported in the UK). Therefore, in most aquifers the basis of the food web is mainly carbon transported into the aquifer from near-surface environments, combined with nutrient inputs from mineral weathering within the aquifer (Rogers & Bennett 2004; Uroz et al. 2009). Dissolved organic carbon is typically low in aquifers; for example, it is often less than 3 mg l⁻¹ in most UK aquifers (Goody & Hinsby 2008). Most microbially available carbon is oxidized in soil before reaching aquifers (Goldscheider et al. 2006). The low-carbon environment thus results in a low biomass and a low abundance of microorganisms, which have a patchy and uneven distribution (over space and time), determined by the local availability of nutrients (Goldscheider et al. 2006). Addition of dissolved organic carbon to groundwater has been shown to increase microbial metabolism and alter the microbial community composition (Baker et al. 2000; Findlay et al. 2003). The scarcity of carbon and other sources of chemical energy in uncontaminated aquifers makes the microbial community particularly susceptible to change following high-energy inputs from organic pollutants because indigenous microorganisms are adapted to live in low-nutrient conditions (West & Chilton 1997).

The majority of microbiological research has been focused on the bacterial community. Estimates of bacterial density range from 10⁸ to 10⁹ cells per cm⁻³ water or from 10⁴ to 10⁸ cells per cm⁻³ sediment (Pickup et al. 2001; Johnson et al. 2004; Griebler & Lueders 2009; Sorensen et al. 2013). However, the microbial community also includes archaea, fungi, other microeukaryotic organisms and viruses (see Table 1 for examples). These are less well studied but it is estimated that archaea may make up 20% of cell counts, and protozoa density may be up to 10⁶ cells per cm⁻³ (but are likely to be restricted to the upper aerobic portions of aquifers; Griebler & Lueders 2009). The pathogenic bacteria shown in Figure 1 represent the approximate size of most bacteria. Archaea are of a similar size, typically 0.1–10 µm. Protozoa and fungi range from around 1 µm to 1 mm (although multicellular fungi can grow much larger), and are therefore excluded from some areas where bacteria and archaea may be present. Each of these groups comprises both indigenous organisms and those that are introduced to the aquifer (which may be transitory or take up residence). The indigenous organisms are the residents that metabolize, grow and replicate in the low-nutrient conditions of the aquifer. The transient organisms are present only through transport from the surface layers (e.g. during periods of high water flow). This group may not be metabolically active and includes, for example, enteric organisms, which can be transported down into aquifers during the infective stage of their life cycle; or photosynthetic cyanobacteria (Sinclair & Ghirose 1989), which are unable to photosynthesize in a dark subterranean environment.

Aquifers have been assumed to have stable physico-chemical conditions, buffered by a combination of overlying soil and saturated and unsaturated sediments. However, there is growing evidence that in shallow or karst systems seasonal changes affect the composition of microbial communities (Lin et al. 2012; Zhou et al. 2012). Zhou et al. (2012), studying a Quaternary sand aquifer in

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**Table 1. Examples of different types of microorganisms present in aquifers**

<table>
<thead>
<tr>
<th>Microorganism</th>
<th>Phylum or subphylum</th>
<th>Examples of species</th>
<th>Potential role of interest in aquifers</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prokaryote (Bacteria)</td>
<td>β-Proteobacteria</td>
<td><em>Rhodothermus ferrireducens</em></td>
<td>Iron reduction</td>
</tr>
<tr>
<td>Prokaryote (Bacteria)</td>
<td>γ-Proteobacteria</td>
<td><em>Galvanella spp.</em></td>
<td>Iron oxidation and creation of iron deposits that inhibit flow</td>
</tr>
<tr>
<td>Prokaryote (Bacteria)</td>
<td>Actinobacteria</td>
<td><em>Rhodococcus spp.</em></td>
<td>Pathogenic bacteria</td>
</tr>
<tr>
<td>Prokaryote (Archaea)</td>
<td>Crenarchaeota</td>
<td><em>Nitrosopumilus maritimus</em></td>
<td>Degradation of hydrocarbons and polychlorinated biphenyls</td>
</tr>
<tr>
<td>Prokaryote (Archaea)</td>
<td>Euryarchaeota</td>
<td><em>Methanosaeta spp.</em></td>
<td>Ammonia oxidation</td>
</tr>
<tr>
<td>Eukaryotic (Protists)</td>
<td></td>
<td><em>Cercomonas spp.</em></td>
<td>Methanogenesis</td>
</tr>
<tr>
<td>Virus</td>
<td>Group IV virus (N.B. not a phylum)</td>
<td><em>Hepatitis A virus</em></td>
<td>Grazing bacterial biofilms</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Pathogenic virus</td>
</tr>
</tbody>
</table>
south Germany, noted that planktonic bacterial numbers and diversity showed significant seasonal changes in response to autumn recharge (correlated to increases in available organic carbon), although the attached bacterial community showed relatively little change. Similarly, Pronk et al. (2009) found that a core group of organisms were seasonally present in Swiss karst aquifers. This core was supplemented by seasonal changes in the communities caused by transient organisms flushed down from the upper layers during high input flow events. Therefore, any sampling strategy that aims to understand baseline microbial community characteristics in shallow or karst aquifers needs to take into account these temporal patterns.

Many studies have shown that the microbial communities attached to solid material in aquifers are different from suspended or planktonic bacteria (e.g., Holm et al. 1992; Lehman et al. 2001a,b; Griebler et al. 2002; Flynn et al. 2013). This has also been observed in a study of a contaminated sandstone aquifer in the UK (Rizoulis et al. 2013). In that study, there were marked differences between the diversity and composition of planktonic and attached bacterial communities in a phenol-contaminated sandstone aquifer. Rizoulis et al. suggested that the higher diversity in the attached biofilm samples may be because the heterogeneous biofilm structure offers ecological advantages to different types of bacteria. They also suggested that the analysis of biofilm samples captures the established and recently colonized organisms, whereas the planktonic samples capture only the transient types of bacteria. They also suggested that the analysis of biofilm samples captures the established and recently colonized organisms, whereas the planktonic samples capture only the transient types of bacteria.

Microorganisms are likely to move through both the fractures in consolidated sediment and the pore spaces in the less consolidated sediments, whereas groundwater flow and storage is within fractures in the consolidated bedrock. In karstic aquifers, organisms attach themselves to fissure walls and obtain the nutrients they need by diffusion of water from the pores. Experiments show that organisms attach themselves to fissure walls and obtain the nutrients they need by diffusion of water from the pores. The authors of the study suggested that organisms attach themselves to fissure walls and obtain the nutrients they need by diffusion of water from the pores.

Introduction to UK aquifers

The most important aquifers in the UK are the Cretaceous Chalk and the Permo-Triassic sandstones, but very little is known about the microbial communities that are present. The fractures, fissures and conduits within the Cretaceous Chalk are likely to provide a good habitat for microorganisms and often contain macro-invertebrates (Robertson et al. 2009). The well-connected network of voids provides a physical habitat and typically receives relatively frequent inputs of nutrients, carbon and oxygen to sustain these communities. Although the Chalk has a high matrix porosity, the median pore diameters of 3–4 µm and pore throats of c. 0.5 µm (Price 1987) are likely to exclude all but the smallest microorganisms from the rock matrix itself. Bacteria are found in chalk aquifers in the UK (Whitelaw & Rees 1980; Parker & James 1985; Johnson et al. 1998) and it is usually assumed that all bacteria that have been found reside in fractures. For example, Whitelaw & Rees (1980) reported nitrate-reducing and ammonia-oxidizing bacteria from throughout the unsaturated section of two English Chalk cores, but as pore size excludes bacteria from within the matrix, they suggested that organisms attach themselves to fissure walls and obtain the nutrients they need by diffusion of water from the pores. Similarly, Kimblin & Johnson (1992) were able to detect sulphate-reducing bacteria in fractured, but not in unfractured, samples of the Chalk aquifer from the Lee Valley in the London Basin, again indicating size exclusion from the matrix.

Within the Permo-Triassic sandstones, the degree of consolidation in the aquifers varies, and intergranular flow and storage occurs in the less consolidated sediments, whereas groundwater flow and storage is within fractures in the consolidated bedrock. Microorganisms are likely to move through both the fractures in consolidated sandstones and the pore spaces in the less consolidated areas. Figure 1 (modified from Bloomfield et al. 2001) shows how the sizes of different types of bacteria relate to the distribution of median pore throat sizes in unconsolidated areas of the UK Permo-Triassic sandstones. The dominant pore-throat sizes in these sandstones are 0.1–90 µm (with a range of 0.01–427 µm) (Bloomfield et al. 2001). The bacteria species described are poorly understood (Boulton et al. 2008).
A study of sediments overlaying a section of Sherwood sandstone in Yorkshire indicated that the distribution of sulphate-reducing bacteria was influenced by grain size, suggesting that physical size exclusion of bacteria occurs in fine-grained sandstone. Evidence of biological sulphate reduction ceased when the d10 value of the sand grains dropped below 1.6µm (where d10 is the estimated 10th percentile grain size based on the grain-size distribution) (Bartlett et al. 2010). However, geochemical conditions also have a strong influence on the distribution of sulphate-reducing bacteria, further restricting their distribution (Edmunds et al. 1982, 1984). A number of studies carried out on polluted sandstone aquifers have contained data from uncontaminated controls and found these uncontaminated samples to be dominated by Proteobacteria (Table 2).

There have been few microbial studies of other aquifers in the UK. However, it is likely that in many consolidated strata microbes may be largely absent from the rock matrix because pore sizes may be too small. A study of the Lincolnshire Limestone found pore sizes of 1–2µm in diameter, but pore throats were typically only 0.1–0.3 µm, suggesting that the size of the pore throats prevented the colonization of the matrix by sulphate-reducing bacteria (Bottrell et al. 2000). However, microbial communities are likely to be present in the fractures, fissures and conduits within the Lincolnshire Limestone and other carbonate aquifers, and also within fracture networks within igneous, metamorphic and sedimentary consolidated strata. It is these habitats and the high-permeability intergranular aquifers that would be most usefully studied in a future systematic survey, although it would also be useful to obtain more information to confirm the extent to which microbes are prevedented from the rock matrix by colonized strata.

It is frequently assumed that aquitard materials, such as clays and low-permeability fractured rocks, offer protection against contamination (Foster 1998; Smith 2005) by pollutants and pathogens. However, these deposits may not completely exclude microorganisms. Microbial communities have been detected within clays in non-UK settings (Lawrence et al. 2000; Takeuchi et al. 2011). On the other hand, there is evidence to suggest that biological sulphate reduction is inhibited in clays within Sherwood Sandstone (Bartlett et al. 2010). Perhaps, even if the small pore size (<1 µm) in clays restrick microorganism transport, fractures and other features may provide suitable habitats. Investigating a UK aquitard, White et al. (2008) identified that palaeo-rootholes within a Holocene lagoonal clay provided preferential pathways for pollutant flow to the underlying sand aquifer, and found evidence of pyrite frambooids indicating microbial presence and activity within the rootholes. The presence of microorganisms in clay material has potential impacts on natural attenuation and pathogen transport and implications for risk assessment models, but more research is needed on the presence and activity of microorganisms within aquitards to determine under which circumstances they provide a protective barrier and when they might provide a habitat for microorganisms.

**Microbial communities in UK aquifers**

Traditional culture-based microbiology has been supplemented by newer molecular techniques, and recent developments in techniques such as next generation DNA sequencing have made the characterization of aquifer communities on a large scale available to many laboratories (e.g. Lin et al. 2012; Pilloni et al. 2012; Gray & Engel 2013; Wilkins et al. 2013). Although there are many examples of molecular techniques applied to contaminated aquifers (e.g. Fahy et al. 2008; Aburto & Ball 2009; Rizoulis et al. 2013) these techniques have not been applied to a systematic study of the microbial composition of uncontaminated UK aquifers. Studies of contaminated UK aquifers generally focus on the impacts of remediation on water chemistry, but direct monitoring of the microorganisms involved in bioremediation is uncommon. The exception is the extensive body of literature on the occurrence of microorganisms in mine drainage waters and their use in bioremediation and bioleaching (e.g. Johnson 2012; Norris et al. 2012). Similarly, there is a body of work on in situ bioremediation, which is used to assist with the clean-up of contaminated groundwater. The principle is to use bacteria to attenuate contamination of groundwater by creating the conditions to allow microorganisms to break down specific pollutants. An example of such an approach is the use of dehalorespiring bacteria to remediate dense non-aqueous phase liquid (DNAPL) chlorinated solvents. In the UK there has been extensive work on this type of in situ bioremediation at the SABRE (Source Area in situ Bio Remediation) industrial site, where both laboratory and field studies demonstrated the effectiveness of electron donors such as linoleic acid to increase the degradation of chlorinated solvents through the activity of dehalorespiring organisms such as Dehalococcoides (Cai et al. 2012; Harkness et al. 2012; Harkness & Fisher 2013). Work carried out on acid mine drainage and in situ bioremediation may provide insights into microbial remediation processes, and a framework for investigating microbial communities in aquifers.

There are two notable features of work on the microbiology of UK aquifers. First, most molecular data from UK studies on uncontaminated aquifers come from control or reference sites in studies where the main focus is the microbiology of contaminant plumes. Second, there do not appear to be any studies of the occurrence of microorganisms other than bacteria (e.g. archaea, fungi, protozoa). The exception to this is the eukaryotic pathogen Cryptosporidium, which has been studied extensively because of the health risks associated with it (Morris et al. 2005).

Table 2 summarizes microbial studies undertaken in the UK that present data from uncontaminated sites. These studies have used community profiling techniques such as Terminal Restriction Length Polymorphism (T-RFLP) and Denaturing Gradient Gel Electrophoresis (DGGE) combined with Sanger DNA sequencing to describe microbial communities. In many cases these data are from control sites during studies of contaminated aquifers. There is one example of a UK study containing molecular analysis that does not specifically focus on contaminated aquifers (Sorenson et al. 2013). This study investigated ecosystems in the Chalk aquifer in southern England using inflatable packers to isolate single fractures at different depths in boreholes. The samples from the borehole water columns had higher bacterial cell counts than samples from the surrounding aquifer and were not biologically or chemically representative of the aquifer itself. There were also differences in both the planktonic and attached community composition in samples from different depths in the aquifer.

The uncontaminated control samples in the other studies provide information on natural bacterial communities and give an insight into how these communities might change in response to contamination. The characterization of uncontaminated aquifer samples comes largely from a series of studies on the effect of benzene pollution in a BTEX-contaminated sandstone aquifer at the Sirén RE site in the UK. At this site, the bacterial community in samples from currently uncontaminated sites, which had previously been exposed to BTEX, was more diverse than the community in contaminated samples. The communities in uncontaminated samples were dominated by β-Proteobacteria (and to a lesser extent Firmicutes) (Fahy et al. 2005; Aburto & Ball 2009). When uncontaminated samples were exposed to benzene the indigenous population shifted from one dominated by β-Proteobacteria to one dominated by Gram-positive Actinobacteria (especially Arthrobacter) (Fahy et al. 2008). The ability to degrade benzene may be linked to a shift from...
Table 2. Microbial composition of communities in uncontaminated aquifers or control sites in studies of polluted aquifers in the UK

<table>
<thead>
<tr>
<th>Aquifer type</th>
<th>Location</th>
<th>Microbiology</th>
<th>Experimental details</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sandstone</td>
<td>SIReN site, UK</td>
<td>Communities were different in contaminated and clean sites: bacterial communities from clean sites had high diversity of taxa, whereas highly contaminated sites were dominated by only a few species. (No attempt was made to identify community members)</td>
<td>T-RFLP on groundwater samples in two years (2001 and 2002)</td>
<td>Fahy et al. (2005)</td>
</tr>
<tr>
<td>Sandstone</td>
<td>SIReN site, UK</td>
<td>A shift from Proteobacteria to Actinobacteria was observed following BTEX application. Bacterial communities from clean sites are predominantly composed of Proteobacteria, particularly β-Proteobacteria. After application of BTEX a shift to a community composed mainly of Actinobacteria was observed. The community composition in the original clean mesocosms at the end of the experiment was not similar to either the starting or finishing communities of the contaminated mesocosms</td>
<td>Groundwater sampling and laboratory mesocosms T-RFLP</td>
<td>Fahy et al. (2008)</td>
</tr>
<tr>
<td>Sandstone</td>
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<td>Groundwater microcosm analysed by T-RFLP</td>
<td>Fahy et al. (2006)</td>
</tr>
<tr>
<td>Sandstone</td>
<td>SIReN site, UK</td>
<td>Degradation of benzene was faster in uncontaminated than in contaminated samples</td>
<td>Laboratory mesocosms analysed by DGGE</td>
<td>Aburto &amp; Ball (2009)</td>
</tr>
<tr>
<td>Sandstone</td>
<td>English Midlands</td>
<td>Total bacterial communities and enterobacterial community structure were variable between depths and sites, but no consistent differences were associated with phenol concentration. However, increasing phenol concentration was associated with a decrease in enzyme activity, cell counts and cultivability</td>
<td>TGGE, enzyme activity assay and ERIC-PCR on groundwater samples</td>
<td>Pickup et al. (2001)</td>
</tr>
<tr>
<td>Chalk, limestone and sandstone</td>
<td>Various sites in the UK</td>
<td>Addition of isoproturon reduced the dominance of Pseudomonas. All samples dominated by Pseudomonas (γ-Proteobacteria), with all other identifiable organisms representing &gt;10% of the community being either α-Proteobacteria or β-Proteobacteria. Addition of isoproturon reduced the dominance of Pseudomonas, but only in one instance did another genus become more dominant</td>
<td>Groundwater mesocosms analysed by FAME</td>
<td>Johnson et al. (2004)</td>
</tr>
<tr>
<td>Chalk and sandstone</td>
<td>Bridge Farm, Winchester; Gleadthorpe, Mansfield (sandstone)</td>
<td>Culturable aerobic and anaerobic bacteria had highest numbers and activities near the soil surface and in the saturated zones, although there was evidence of microbes at all points between. There was no evidence of a major role for autotrophic denitrification</td>
<td>Plate counts from core samples, ¹⁴C-labelled acetate utilization, acetylene block method</td>
<td>Kinniburgh et al. (1999)</td>
</tr>
<tr>
<td>Chalk</td>
<td>Berkshire, UK</td>
<td>Borehole samples were not representative of water from within the aquifer for planktonic or particle-attached bacteria</td>
<td>Microbial cell counts and T-RFLP on groundwater samples</td>
<td>Sorensen et al. (2013)</td>
</tr>
</tbody>
</table>

T-RFLP, Terminal Restriction Fragment Length Polymorphism; TGGE, Temperature Gradient Gel Electrophoresis, ERIC-PCR, Enterobacterial Repetitive Intergenic Consensus Polymerase Chain Reaction.
a *Rhodoferax* (β-Proteobacteria) dominated community to a *Rhodococcus* (Gram-positive Actinobacteria) and *Hydrogenophaga* (β-Proteobacteria) dominated community (Fahy et al. 2006). In this and an earlier study (Fahy et al. 2005), the effect on the microbial community structure was spatially heterogeneous, with different contaminated samples diverging in different ways when challenged with the same pollutant. The uncontaminated control (undetectable BTX since 1996, and only 0.1 mg l⁻¹ at that time) had the biggest shift in community composition and the longest lag time before degradation occurred (Fahy et al. 2006). A lag in response for previously unexposed communities appears to be typical. For example, it has also been observed in samples of the Chalk aquifer in SE England challenged with methyl tertiary butyl ether (Shah et al. 2009).

Studies from other countries confirm that a shift in species composition is a common response to pollution, and a similar shift from Proteobacteria-dominated communities to Actinobacteria has been seen in fuel-contaminated areas of aquifers (e.g. Shi et al. 1999). However, other studies report decreasing numbers of Actinobacteria and increasing γ-Proteobacteria (Hendrickx et al. 2005) and mesocosm studies report a shift in the dominating classes of Proteobacteria (from β- and γ-Proteobacteria to α-Proteobacteria) in response to fuel contamination (Shi et al. 1999). These observations are based on a limited number of studies so it is difficult to make clear predictions about the changes that are likely to be observed in other aquifers. However, the diverse findings in these studies suggest that microbial communities may have varied and site-specific responses to pollution.

More work is needed to determine how these changes affect community degradation and biogeochemical cycling, but initial results suggest that there is the capacity within uncontaminated communities to degrade pollutants after a period of adjustment (Fahy et al. 2006; Shah et al. 2009). However, there are mixed data from UK aquifers regarding the effect of previous exposure to pollutants on biodegradation. Some findings suggest no correlation (e.g. Johnson et al. 2000) whereas others identify enhanced biodegradation when there has been previous exposure to, for example, isoproturon (Johnson et al. 1998, 2000, 2004) or BTX (Fahy et al. 2006). The key factors determining whether a bacterial community can degrade pollutants appear to be the makeup of the community itself and the groundwater chemistry (Johnson et al. 2004). Johnson et al. (2004) found that the presence of isoproturon changed the community structure and degradation was accompanied by an increase in the proportion of a few dominant species, although different degrading taxa were found in different samples. This suggests that there is some flexibility in the community composition (functional redundancy) and that some functions can be carried out by different organisms. Water chemistry was demonstrated to play a role in providing the right environment for degradation (in chalk, limestone and sandstone aquifer samples), as addition of filtered groundwater from a fast degrading site was able to stimulate the degradation of isoproturon by bacterial populations from slow degrading limestone samples, and vice versa (Johnson et al. 2004).

The type of aquifer is also likely to be a key factor in the changes seen in the bacterial community in response to pollution. Johnson et al. (2004) examined the microbial response to isoproturon in different rock types and found that uncontaminated samples were all dominated by *Pseudomonas* (γ-Proteobacteria) (ranging from 93% of the isolates in sandstone to 49% and 43% in chalk and limestone). All other common organisms (making up more than 10% of the isolates) were either α- or β-Proteobacteria or unidentifiable. The addition of isoproturon reduced the proportion of *Pseudomonas* in sandstone and chalk but increased it in limestone. Only in chalk did another genus become more dominant (*Brevundimonas*, α-Proteobacteria) following addition of isoproturon. To summarize, these studies suggest that uncontaminated communities are often dominated by Proteobacteria, and pollution often results in a shift in the proportion of different proteobacterial groups as well as reduced bacterial diversity. This is a common finding across the small number of studies or even the majority of the biofilm is required to verify that a proteobacterial dominance is widespread. The Johnson et al. (2004) study is important because a range of UK aquifer rocks were investigated, although further work is required to determine whether the observed differences between these specific examples can be extrapolated to all chalk, limestone or sandstone aquifers. Overall there are relatively few studies on microbial communities, most are focused only on bacteria, and a much wider examination of all types of microbes in UK aquifers is required to understand these microbial communities.

### Global studies of uncontaminated aquifer microbiology

Table 3 shows a summary of studies from other countries that have investigated the community composition of uncontaminated aquifers (mostly using molecular methods) as well as some studies that compared uncontaminated and contaminated areas of aquifers. These studies provide a context for interpreting the UK data. As with the UK studies, communities are typically dominated by Proteobacteria (usually the β- and γ-classes; e.g. Shi et al. 1999; Detmers et al. 2004; Hendrickx et al. 2005; Boyd et al. 2007; Flynn et al. 2012). However, in one case a community equally dominated by Proteobacteria (α- and β-) and Actinobacteria was reported (Hendrickx et al. 2005). Boyd et al. (2007) found that the most abundant class of Proteobacteria was different on different types of substrate, indicating that mineralogy influences the community structure and composition. This supports the observation of Johnson et al. (2004), and suggests that the matrix mineralogy influences the microbial community composition.

Other microbial groups, such as archaea, are even less well studied than bacteria in uncontaminated aquifers. One study sequenced DNA from archaea in a single borehole in the Doñana National Park, Spain. The archaeal community at a depth of 15 m had a low diversity composed only of Group 1 Crenarchaeota, whereas the community at 80 m was composed of a diverse range of members of the Euryarchaeota (López Archilla et al. 2007). In sulphate-reducing zones, archaea can form a significant proportion (Detmers et al. 2004) or even the majority of the biofilm community (Probst et al. 2013). Flynn et al. (2013) reported that distinct differences could be detected between attached and suspended archaenal communities in the Mahomet Aquifer, Illinois, and that sulphate concentration had a role in influencing the community structure.

Eukaryotic microorganisms have also not been well studied, with the exception of some pathogens such as *Cryptosporidium* and *Giardia*. Laboratory studies indicate that organic contamination tends to increase protozoal population densities, but the relationship between pollution and diversity remains poorly understood (Novarino et al. 1997; Yagi et al. 2009). A more detailed understanding of protozoal communities in uncontaminated aquifers would be beneficial because these organisms could influence the response of aquifers to pollution events as they have been shown to influence various aspects of aquifer chemistry, water flow and bacterial communities. For example, in laboratory studies, inhibition of the growth of protozoa has been shown to have a positive effect on degradation of trichloroethene (Cunningham et al. 2009), but to have a negative effect on BTX removal (Kota et al. 1999). Protozoa also have the ability to decrease clogging in wells in some circumstances (DeLeo & Baveye 1997; Mattison et al. 2002), and affect nitrogen cycling (Strauss & Dodds 1997) and carbon cycling.
Table 3. Summary of research into community composition in uncontaminated aquifers outside the UK

<table>
<thead>
<tr>
<th>Aquifer Location</th>
<th>Aquifer Description</th>
<th>Microbiology</th>
<th>Experimental details</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Quaternary fluvioglacial and aeolian materials</td>
<td>Doñana National Park, Spain</td>
<td>Most common class of bacteria at two depths was β-Proteobacteria. Almost all of the bacteria identified in the deepest sample were from the phylum Proteobacteria; the shallowest sample contained a greater diversity of organisms. Archaeal diversity was lower in the shallow sample (only Crenarchaea compared with both Crenarchaea and Euryarchaea in the deeper sample). Sulphur-oxidizing bacteria, nitrifiers, denitrifiers and methanotrophs were all identified</td>
<td>Groundwater sample, DNA sequencing</td>
<td>López Archilla et al. (2007)</td>
</tr>
<tr>
<td>Weathered shale (unconsolidated clay-rich saprolite)</td>
<td>Oak Ridge Reservation, TN, USA</td>
<td>Type of substrate influences bacterial community structure and diversity and which class of Proteobacteria is numerically dominant</td>
<td>In situ growth on emplaced materials, T-RFLP, DNA sequencing</td>
<td>Boyd et al. (2007)</td>
</tr>
<tr>
<td>Glacial sands and gravels</td>
<td>Mohamet aquifer, IL, USA</td>
<td>Planktonic and attached bacterial communities were distinct (only 15% of species were common to both communities). There was no significant difference in the total number of species detected in each community. IRB Geothrix and Geobacter formed &gt;20% of total in most wells, but no more than 1% of planktonic bacterial community. Predominantly δ-Proteobacteria community was composed roughly of equal numbers of SRB and IRB</td>
<td>T-RFLP carried out on in situ growth on emplaced aquifer material and groundwater samples</td>
<td>Flynn et al. (2008)</td>
</tr>
<tr>
<td>Glacial sands and gravels</td>
<td>Mohamet aquifer, IL, USA</td>
<td>Investigated SRB; identified that SRB (Desulfobacter and Desulfobulbus) were nearly as abundant as IRB (Desulfuromonas, Geothrix and Geobacter)</td>
<td>In situ growth on emplaced materials, T-RFLP, DNA sequencing</td>
<td>Flynn et al. (2012)</td>
</tr>
<tr>
<td>Quaternary fluvioglacial and aeolian materials</td>
<td>Doñana National Park, Spain</td>
<td>No nitrifying activity or eukaryotes detected. Iron reducers are consistently more active than denitrifiers, sulphate reducers have more time to act</td>
<td>Groundwater sample, microscopy and BART</td>
<td>Velasco Ayuso et al. (2009)</td>
</tr>
<tr>
<td>Not described</td>
<td>Fort McCoy, Sparta, WI, USA</td>
<td>Most dominant bacterial classes were β- and γ-Proteobacteria, followed by α-Proteobacteria, SRB and high-GC Gram-positive bacteria. Contaminated samples (nitrate, toluene or BTEX) were distinct in having a greater abundance of high-GC Gram-positive bacteria relative to α-Proteobacteria. Eukaryotes or archaea were detected only in laboratory microcosms</td>
<td>Groundwater, aquifer samples and laboratory microcosms, FISH</td>
<td>Shi et al. (1999)</td>
</tr>
<tr>
<td>Tertiary marine sands</td>
<td>Garzweiler, Germany</td>
<td>FISH probes positively identified the community to be composed of 51.9% bacteria and 25.7% archaea. FISH identified Desulfomaculum as the dominant SRB not Desulfotomaculum and Desulfof批, which were the only organisms identified by culture methods</td>
<td>Groundwater samples, FISH</td>
<td>Detmers et al. (2004)</td>
</tr>
<tr>
<td>Not described</td>
<td>Northern Bohemia, Czech Republic</td>
<td>Pristine communities were dominated by β- and γ-Proteobacteria and Actinobacteria. The communities from a pristine well, placed in a BTEX-contaminated well, changed to become similar to the surrounding community, which was composed mainly of γ-Proteobacteria and had a lower number of detectable species than the pristine aquifer community</td>
<td>Fresh samples and in situ growth on emplaced materials, T-RFLP, DNA sequencing</td>
<td>Hendrickx et al. (2005)</td>
</tr>
<tr>
<td>Not described</td>
<td>Illinois, USA</td>
<td>Attached bacterial community dominated by δ-Proteobacteria; bacterial communities were dominated by other proteobacterial classes. The attached archaeal community was a distinct subset of the suspended community</td>
<td>DNA sequencing of water samples and emplaced materials</td>
<td>Flynn et al. (2013)</td>
</tr>
</tbody>
</table>

BART, biological activity reaction tests; FISH, Fluorescence In Situ Hybridization; SRB, sulphate-reducing bacteria; IRB, iron-reducing bacteria; PCR, Polymerase Chain Reaction; T-RFLP, Terminal Restriction Fragment Length Polymorphism; DGGE, Denaturing Gradient Gel Electrophoresis.
(Euringer 2008). Removal of protozoa from mesocosms increases bacterial numbers and has a strong influence on shaping bacterial community structure, suggesting that protozoa may control the size and composition of prokaryotic communities in aquifers (Nagaoasa et al. 2008; Longnecker et al. 2009). The role of protozoa in aquifer environments is particularly interesting from an ecological point of view because, in some aquifer environments, pore size and food supply preclude larger organisms and result in a truncated food web with few predators (Gibert & Deharveng 2002; Gibert et al. 2009). Therefore, microeukaryotes may be important predators or competitors for prokaryotic microorganisms (Euringer 2008). The study of microeukaryotes in aquifers might provide an opportunity to test and inform general ecological theory such as predator–prey relationships and niche differentiation in a simple natural system without the complex trophic structures that often exist in other ecosystems (Reiss et al. 2011).

Our knowledge of fungi in aquifers is also poor, but on the basis of the limited work, they appear to be found when targeted for analysis (Euringer 2008; Lategan et al. 2012; Smith et al. 2012). They are likely to be common in shallow, anaerobic, confined aquifers, probably utilizing cellulose transported from the surface as an energy source. Their impact on groundwater processes is not well understood, but one possible role could be mobilizing pollutant-degrading bacteria, with the hyphae acting as transport routes for bacteria (Kohlmeier et al. 2005).

Contemporary issues in UK aquifer microbiology

Diffuse nitrate pollution

Elevated nitrate concentrations are very common in UK groundwaters (Rivett et al. 2007), and this is likely to continue to be a problem in the future owing to a legacy of pollution from previous nitrate inputs. Under current agricultural practices and climate conditions, nitrate concentrations are generally predicted to continue rising (Stuart et al. 2007). Although nitrate concentrations may be decreasing in some areas (Environment Agency 2012; Wang et al. 2012), in many areas they are predicted to increase, especially where the unsaturated zone is thick; for example, parts of the Scottish Devonian sandstones, the Cretaceous Chalk, the Carboniferous Coal Measures, and the Yoredale and Millstone Grit of northern England (Stuart et al. 2011; Wang et al. 2012). In other aquifers, such as the Cretaceous greensands, Zechstein Group dolomites and Dinantian limestones, the peak nitrate loading may have passed (Wang et al. 2012). In other aquifers, such as the Cretaceous greensands, Zechstein Group dolomites and Dinantian limestones, the peak nitrate loading may have passed (Wang et al. 2012).

Denitrification is uncommon within the unconfined Chalk, Sherwood Sandstone and Jurassic limestone aquifers (Hiscock et al. 1991; Wilson et al. 1994; Feast et al. 1998; Rivett et al. 2007, 2008). Where it occurs it is mainly limited to saturated, oxygen-depleted areas (less than 1–2 mg L⁻¹ oxygen), particularly those with sufficient organic carbon to drive the reductive process (Rivett et al. 2008). The limited carbon supply in most aquifers means that natural processes may not be able to remediate the increasing nitrate levels typically found in the UK (Edmunds et al. 1987; Hiscock et al. 1991). Denitrifying microorganisms occur in subsurface ecosystems, but are generally restricted to anaerobic conditions (with appropriate pH, temperature, nutrients and trace minerals; Rivett et al. 2007, 2008). However, it must be remembered that within biofilms, anaerobic microorganisms may develop, which could allow anaerobic processes such as denitrification to occur even in otherwise aerobic environments (Costerton et al. 1995). In situ bioremediation strategies, such as stimulating denitrification by the injection of a carbon source (ethanol or methanol) have been proposed to assist natural attenuation, but there are unanswered questions about the biological, chemical and hydrological processes that control denitrification when using these strategies, which need to be addressed before such techniques are viable (Hiscock et al. 1991; Tompkins et al. 2001). Compared with nitrate attenuation, the pathways for ammonia removal in aquifers (biological nitrification and ion exchange) are less well studied (Buss et al. 2004). Biological removal is likely to be most significant in aerobic sections of aquifers with low cation exchange capacities (i.e. clay-poor aquifers or those with low metal oxides), and in particular at NH₄ plume margins (Buss et al. 2004). Although it is likely that most nitrification will occur in aerobic conditions, there is some evidence for the occurrence of anaerobic nitrification in UK aquifers (Buss et al. 2004; Heaton et al. 2005; Lee et al. 2006; Erguder et al. 2009).

Emerging contaminants

There is a growing awareness of the increase in new organic groundwater contaminants including nanomaterials, pharmaceuticals, personal care products, and caffeine and nicotine, which may affect groundwater quality (Lapworth et al. 2012). The full impact of these is not yet known, but because these emerging contaminants include antimicrobial or bacteriostatic compounds such as triclosan and parabens in personal care products, and benzotriazole in industrial contaminants, the impact on microbial communities and their ability to carry out ecosystem services deserves further study. These xenobiotic substances do not appear to be efficient growth substrates for microorganisms, but they can often be degraded by a process of co-metabolism where a microorganism breaks down one substrate (the pollutant) without deriving energy from it as long as another substrate is present that can be used as an energy source (Nzila 2013). This process suggests that bioremediation of these emerging pollutants may be possible and an improved knowledge of the microbial community may assist in developing new approaches to bioremediation of these emerging contaminants.

Climate change

Wilby et al. (2006) identified some ways in which climate change might affect the ecosystems of surface bodies in relation to the Water Framework Directive (WFD) (WISE 2012). A number of the effects may also be relevant for groundwater. These include altered metabolic rates of organisms, altered ecosystem productivity and biodiversity, and altered species assemblages. The effect of altered plant and animal distributions, altered fish migration and dispersal, and increased eutrophication and algal blooms at the surface could potentially have an indirect effect on groundwater, through changing nutrient inputs or cycling. There is considerable uncertainty about how climate change will affect aquifers, but it seems likely that minimum groundwater levels will decrease (Bloomfield et al. 2003), long-term pesticide accumulation will occur in Chalk aquifers (Bloomfield et al. 2006) and nitrate concentrations may increase (Stuart et al. 2011). The effects on microbial communities have not been established, but microbes may respond to different aspects of climate change such as changes in wetting and drying cycles altering nitrogen and carbon cycling (Bardgett et al. 2008; Borken & Matzner 2009). In addition, intensification of aquifer exploitation may alter the prevalence of pathogens in aquifers and lead to an increase in Cryptosporidium outbreaks (Khalidi et al. 2011). Although the extent of the effects that climate change will have on the hydrology or geochemistry of aquifers is still not clear, the direct and indirect effects of climate change on microbial communities could have an impact on water quality and health.
Table 4. Some potential pathogens that may be found in aquifers (after Environment Agency 2002; Powell et al. 2002; Pedley et al. 2006)

<table>
<thead>
<tr>
<th>Organism</th>
<th>Occurrence/host</th>
<th>Disease</th>
<th>Notes on survival</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aeromonas spp.</td>
<td>Natural inhabitants of freshwater environments</td>
<td>No clear evidence of disease, but high numbers can be an indicator of faecal contamination</td>
<td>Freshwater as habitat. Different species usually found in pristine water and sewage effluents</td>
</tr>
<tr>
<td>Campylobacter spp.</td>
<td>Found in livestock, birds, natural waters</td>
<td>Bacterial gastroenteritis</td>
<td>Survival in surface waters for days</td>
</tr>
<tr>
<td>Clostridium perfringens</td>
<td>Warm-blooded animals</td>
<td>Used as a faecal indicator, food poisoning</td>
<td>Spores are capable of surviving for longer periods than vegetative bacteria</td>
</tr>
<tr>
<td>Escherichia coli</td>
<td>Various warm-blooded animals</td>
<td>Diarrhoeal disease</td>
<td>Not stated</td>
</tr>
<tr>
<td>Legionella spp.</td>
<td>Naturally occurring in the aquatic environment</td>
<td>Legionnaires' disease, influenza-like illness</td>
<td>Grows within protozoa. Growth controlled below 20°C</td>
</tr>
<tr>
<td>Mycobacterium spp.</td>
<td>Ubiquitous; present in soil, dust, water, livestock, etc.</td>
<td>Infections of the skin and lungs</td>
<td>Persistent in the natural environment</td>
</tr>
<tr>
<td>Pseudomonas spp.</td>
<td>Widespread in the environment</td>
<td>Wide range of infections. Only some species are pathogenic, others lead to odour problems</td>
<td>Capable of growth in relatively low-nutrient environment</td>
</tr>
<tr>
<td>Salmonella spp.</td>
<td>Livestock faeces</td>
<td>Typhoid, gastroenteritis, pneumonia, reactive arthritis, meningitis</td>
<td>Survival in surface waters for hours to days</td>
</tr>
<tr>
<td>Shigella spp.</td>
<td>Human faeces</td>
<td>Bacillary dysentery (shigellosis)</td>
<td>Hours to days</td>
</tr>
<tr>
<td>Vibrio spp.</td>
<td>Brackish and saline waters and sometimes fresh water, human faeces</td>
<td>Diarrhoea, gastroenteritis, septicaemia, V. cholerae causes cholera</td>
<td>Some species will survive in freshwater</td>
</tr>
<tr>
<td>Yersinia spp.</td>
<td>Natural waters, farms, meat processing plants</td>
<td>Mild diarrhoea, infections, septicaemia, reactive arthritis</td>
<td>May be able to grow in water</td>
</tr>
<tr>
<td>Cryptosporidium parvum</td>
<td>Many warm-blooded animals including humans. Open water often contaminated</td>
<td>Diarrhoeal disease</td>
<td>Long surviving oocytes, more than several months</td>
</tr>
<tr>
<td>Giardia lamblia</td>
<td>Humans, wild and domestic animals</td>
<td>Giardiasis: diarrhoeal disease to more serious complications</td>
<td>Can remain viable for several months in cold water</td>
</tr>
<tr>
<td>Toxoplasma gondii</td>
<td>Cats, other wild animals and livestock</td>
<td>Influenza-like symptoms</td>
<td>Water-borne infections have been linked to infected wild cats</td>
</tr>
<tr>
<td>Coxsackieviruses</td>
<td>Indicator of human enteric viruses</td>
<td>Fever, pharyngitis, diarrhoea, aseptic meningitis</td>
<td>Water-borne transmission not confirmed, survive ‘longer than bacteria’</td>
</tr>
<tr>
<td>Enteric adenovirus</td>
<td>Human faeces</td>
<td>Gastroenteritis, mainly in infants; respiratory disease</td>
<td>Survive ‘longer than bacteria’</td>
</tr>
<tr>
<td>Hepatitis A Virus</td>
<td>Human faecal origin</td>
<td>Fever, nausea, liver infection</td>
<td>No water-borne outbreak confirmed in the UK; survive ‘longer than bacteria’</td>
</tr>
<tr>
<td>Norwalk-like virus</td>
<td>Strains pathogenic to humans come only from human contamination</td>
<td>Viral gastroenteritis</td>
<td>No water-borne outbreak confirmed in the UK; survive ‘longer than bacteria’</td>
</tr>
<tr>
<td>Rotavirus A and Rotavirus C</td>
<td>Human faeces</td>
<td>Gastroenteritis especially in infants; may subsequently be asymptomatic</td>
<td>Rarely water-borne; survive ‘longer than bacteria’</td>
</tr>
</tbody>
</table>

**Biofilm clogging of boreholes**

Microbial processes can alter transmission of water through accumulation of inorganic salts or organic complexes, or through gas generation, and can also cause problems through corrosion of well structures (Baveye et al. 1998; Cullimore 2000). It appears that in electron donor-limited aquifers microbial processes decrease porosity by the production of intergranular cements, whereas in electron acceptor-limited aquifers porosity is often increased by dissolution of mineral grains by microbial processes (Chapelle et al. 1997). Reduction in flow due to biofilm formation is a well-established process (e.g. Harrison et al. 2011; Wragg et al. 2012). In laboratory experiments using chalk samples, biofilm formation has been associated with bio-remedia-tion of organic contaminants (Arnon et al. 2005a,b). It has also been suggested that interventions to improve denitrification by supplementing the aquifer with a carbon source may result in clogging with biomass or microbially produced gases (e.g. CO₂ and N₂). Historically, clogging (through iron deposition) was thought to be primarily due to (electro)chemical processes because aquifers were assumed to be sterile, and bacteria found in wells were thought to result from contamination during drill-ing (Howsam 1988). The role of ‘iron’ bacteria and other bacte-ria in deposit forming as well as a host of other bacteria has now been recognized by a number of field and laboratory studies (Baveye et al. 1998). Brassington et al. (2009) suggested that iron-oxidizing bacteria (probably Gallionella and Leptothrix) can increase borehole drawdown by 20% (measured at Warrington in a Sherwood Sandstone aquifer), although reductions of up to 95% capacity have been reported for other areas of the same aquifer. Hydrogen peroxide can restore flow, probably via the biocidal effects of the hydrogen peroxide and physical scrubbing by oxygen bubbles. Although effective in reducing biofilm clogging, this approach may have other undesirable impacts on the microbial community as a whole.

A better knowledge of the microbial interactions involved in biofilm clogging is required to answer questions such as: How far beyond the well or formation screen does clogging exist? How can the pump be clogged but not the screen or vice versa? What determines which wells will clog? The answers are likely to depend upon factors such as differences in construction, design, or condition of wells (Howsam 1988); pH (Kirk et al. 2012), availability of organic matter (Cullimore 2000) water turbidity, and total nitrogen (Pavelic et al. 2007).

**Pathogens in aquifers**

Perhaps the most pressing concern about microorganisms in aquifers remains the potential impact of the transport of pathogens into drinking water. A summary of some of the microorganisms that could be present in UK aquifers along with their...
native habitats and notes on their survival in water is shown in Table 4. Waste from farm animals and human sewage treatment are the main sources of pathogen contamination. However, many pathogens have been detected in native wild animals for example, rats, mice or birds (Bouchier 1998; Simpson 2002). These may not be considered to be important reservoirs of disease, but it could be argued that the presence of pathogens in native animals and their inevitable transit into water courses means that pathogens (albeit in low numbers) could be considered to be part of the indigenous transient community in aquifers. The traditional view that aquifers provide a safe environment, free from potential pathogens, is being questioned (e.g. Pedley et al. 2006). There is evidence to indicate that facal bacteria can travel through aquifers (e.g. to depths of up to 90m in Triassic sandstone in Nottingham and Doncaster) and that both human enteric viruses (including pathogens) and facal indicator bacteria are widespread at low concentrations (Powell et al. 2002, 2003; Morris et al. 2006). As well as being widespread, viruses can be persistent: in groundwater taken from Permo-Triassic sandstone in Birmingham, some viruses were detectable by polymerase chain reaction (PCR) for over 2 years after inoculation, although their infectivity based on plaque assay lasted only for 238 days (Charles et al. 2009). In other cases, sandstone aquifers act as filters of microorganisms, and pathogens are undetectable in all but the shallower samples (Gooddy et al. 2001). Pathogen transport is a particular problem in karst aquifers with rapid flowpaths (e.g. Tranter et al. 1997). Because of their smaller pore spaces chalk aquifers can filter pathogenic organisms very effectively (Gooddy 2002; Gooddy et al. 2001), although where well-connected fissure and conduit networks are present rapid pathogen transport can occur (e.g. Dussart-Baptista et al. 2003).

Conclusions

Although there has been considerable work on certain areas of aquifer microbiology such as remediation of contaminated aquifers and pathogen transport through aquifers, our understanding of the indigenous microbial communities in UK aquifers and the contribution they make to maintaining good groundwater quality remains limited. It is clear that microbial communities play an important role in aquifer biogeochemical processes (Griebler & Lueders 2009), but globally these processes remain poorly understood. In England and Wales the Environment Agency carries out routine monitoring for nutrients and pesticides in aquifers, but there is currently no routine monitoring programme for microorganisms, except Cryptosporidium, which is routinely monitored by water companies where it has been identified as a high risk (Environment Agency 2005). There would be much to be gained from conducting a systematic nationwide survey to determine the baseline diversity that occurs at present in UK aquifers. This should allow the major drivers of microbial diversity and the factors that structure these communities to be determined, and would be of international significance because globally there have been few studies of microbial communities in aquifers not affected by serious pollution. A better understanding of the microbial diversity in aquifers and the response of microbes to pollution may also allow areas of aquifers that require greater monitoring or management input to be identified, as well as areas in which communities have greater resilience to, or protection from, detrimental anthropogenic activities. Only through an understanding of the microbiology of aquifers in their current state can we interpret the changes that result from future human impacts.

Some key areas for research include understanding the broad controls that influence microbial community structure across a range of aquifer types in the UK. This basic information should inform applied research aimed at maintaining water quality, developing strategies to improve bioremediation, monitoring pathogen transport, and preventing problems such as iron-oxidizing bacteria reducing water flow and causing biofilm clogging of boreholes. Studies of the impact of macro-invertebrates on microbial communities are also needed to improve understanding of aquifer biogeochemical processes. Additionally, there are questions about how much functional redundancy exists within microbial communities, allowing continued biogeochemical functioning following changes in community structure.

Examples of systematic surveys that have an established framework upon which future research on microbial function and local diversity can be built include the recent survey of British soil bacterial communities (Griffiths et al. 2011) and a national survey of New Zealand groundwater microbiology (Sirissen et al. 2013), the first of its kind for fractured chalk. Journal of Contaminant Hydrology, 79, 165-186. Aquifers would provide a valuable contribution to understanding the biodiversity of microorganisms and the roles they play in these environments, placing the UK at the forefront of this important area of research.

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References


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