Microbial population changes during managed aquifer recharge (MAR)


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Managed aquifer recharge (MAR) is a technique that can be used to capture and store water in aquifers under managed conditions for later recovery and use for specific purposes [1]. There is a need to predict water quality changes during MAR, particularly when recycled water is used as the recharged water. An understanding of the interaction between the geochemistry of the aquifer and the microbial population dynamics in the groundwater is important for understanding any water quality changes. A study was undertaken to monitor the changes in the microbial population and link this to changes in the geochemistry. The results obtained showed that the recharge of recycled water to aquifers causes a change in microbial population structure which has direct links to corresponding changes in geochemistry.

There are a number of MAR methods and types of water that can be recharged. One major way MAR can be used is to assist in the recycling of water that would normally be lost or discarded to the environment. MAR has benefits for recycling water in that it can be a cheap form of storage which allows recycled water to be held prior to use. MAR can thus be used as a passive barrier in the water recycling scheme.

Additionally, MAR has been shown to be able to improve the quality of recycled water during passage through the aquifer and during storage [2], thus it may also be able to be used as a treatment barrier. However, to be able to be used as an active treatment barrier, it is important to be able to understand and manage any water quality changes that occur. Changes in the quality of the recharged water occur through a range of physical, chemical and biological processes within the aquifer. While the physical and chemical processes are generally well understood, much less is known about the biological processes. The biological processes occur through the activity of the autochthonous groundwater microorganisms. The role of these microorganisms has been shown to be important for the removal of microbial pathogens [3], trace organic compounds [4] and nutrients [3, 5]. An improved understanding of these biologically-based changes is essential for the prediction of water quality changes during MAR and to enable improved management of these schemes.

In order to gain a better understanding of autochthonous groundwater microbial populations, studies have been undertaken on the impact of changes in aquifer environments on these microbial populations. Groundwater studies have historically focused on contaminated aquifers which are segregated into discrete redox zones dominated by different physiologic microbial processes [6-9]. These and other studies have shown that numerous important geochemical processes in subsurface environments are carried out exclusively by enzyme controlled microbial processes. For example, ferric iron reduction can only occur via ferric iron-reducing bacteria [10]. Groundwater microbial populations are therefore clearly able to change the chemical nature of groundwater. Studies that have combined molecular techniques to describe microbial community structure with multivariate statistics to investigate groundwater microbial and geochemical characteristics have demonstrated an interdisciplinary approach which comprehensively explores these biogeochemical interactions [11, 12].

To further study the connections between geochemical reactions and changes in microbial populations during MAR, the bacterial population dynamics were studied in conjunction with changes in aquifer geochemistry [13,14]. This was done using multivariate statistics for two contrasting MAR techniques using secondary treated effluent at two different geographical locations (Perth, WA and Adelaide, SA). Variation in non-cultured groundwater bacterial population dynamics were studied in conjunction with changes in aquifer geochemistry. Principal component analysis (PCA) was used to investigate spatial and temporal changes in the overall 'chemical signature' of the aquifers using an array of chemical analytes which demonstrated a migrating geochemical plume.

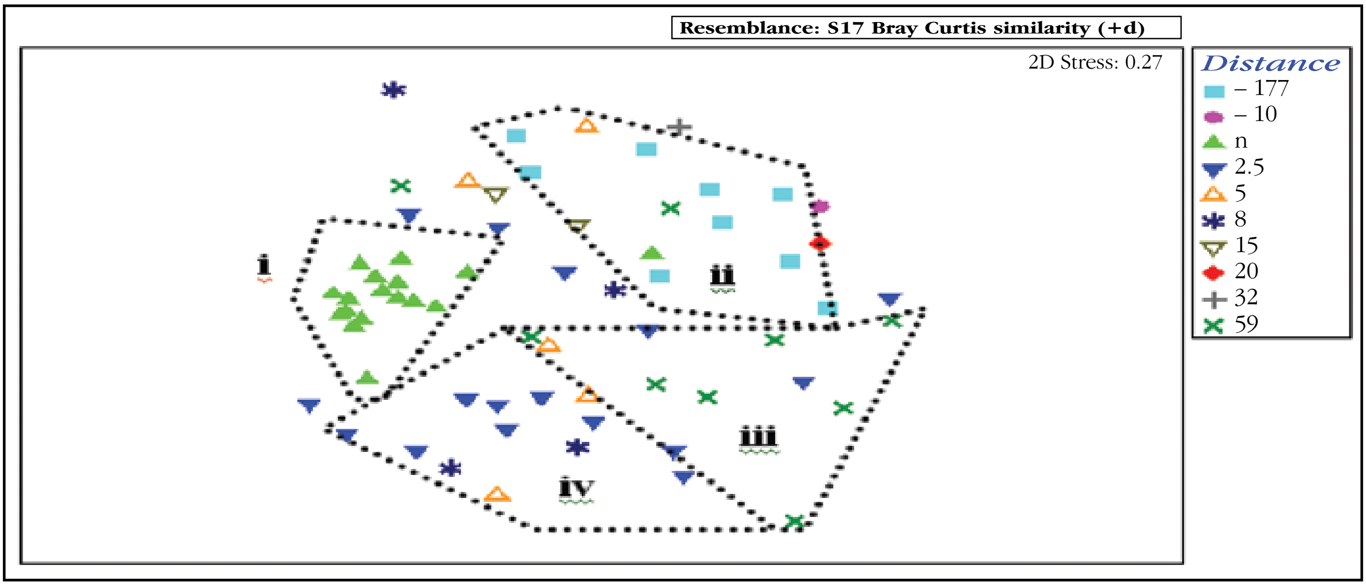

Figure 1. Example of a 2-D MDS plot for amplified microbial rDNA/DGGE banding patterns for all Perth MAR sulphate-reducing cultures demonstrating the clusters of similar population groups at different distances from the recharge site over time. Interpreted MDS clusters are i = Infiltration Galley; ii = background bore; iii = extraction bore; and iv = Monitoring bore set at 2.5 m from Infiltration Galleries

The PCA demonstrated that a migrating nutrient plume occurred in the form of a chemical gradient that varied with time. Denaturing gradient gel electrophoresis (DGGE) using DNA from cultures of groundwater bacteria and groundwater DNA extracts was used to detect spatial and temporal changes in population dynamics. Permutational multivariate analysis of variance (PERMANOVA), supported by multidimensional scaling (MDS) and principal coordinate (PCO), provided evidence of significant spatial and temporal differences in bacterial community structure. An example of these changes over time and distance can be seen in Figure 1 as the MDS plot of sulphate reducing bacteria population dynamics at one of the MAR sites studied.

Distance from the infiltration gallery (nutrient source) was able to be identified as the dominant factor that caused dissimilarities in microbial biodiversity. Distinct microbial populations developed in a distance-dependent successional manner concomitant with geochemical plume migration, suggesting that groundwater microbial populations responded to the chemical gradient. The results obtained also suggested that the groundwater bacterial populations responded to the migrating chemical gradient and to the changes in aquifer geochemistry caused by the MAR schemes. Additionally, the study showed that, at the Adelaide aquifer storage and recovery site, bacterial biodiversity was restored to background population structure when the aquifer geochemistry returned to ambient conditions during the recovery phase.

The outcomes of this study have also demonstrated that detailed microbial population changes may be able to be predicted based on observed changes in the aquifer geochemistry. Research is continuing to link the changes in microbial population dynamics and removal of nutrients, microbial pathogens and chemical contaminants.

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