

Original article

Spatial and temporal variability of bacterial communities in high alpine water spring sediments

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Received 20 March 2015; accepted 21 December 2015

Available online 9 January 2016

Abstract

Water springs are complex, fragile and taxa-rich environments, especially in highly dynamic ecosystems such as glacier forefields experiencing glacier retreat. Bacterial communities are important actors in alpine water body metabolism, and have shown both high seasonal and spatial variations. Seven springs from a high alpine valley (Matsch Valley, South Tyrol, Italy) were examined via a multidisciplinary approach using both hydrochemical and microbiological techniques. Amplified ribosomal intergenic spacer analysis (ARISA) and electric conductivity (EC) measurements, as well as elemental composition and water stable isotopic analyses, were performed. Our target was to elucidate whether and how bacterial community structure is influenced by water chemistry, and to determine the origin and extent of variation in space and time. There existed variations in both space and time for all variables measured. Diversity values more markedly differed at the beginning of summer and then at the end; the extent of variation in space was prevalent over the time scale. Bacterial community structural variation responded to hydrochemical parameter changes; moreover, the stability of the hydrochemical parameters played an important role in shaping distinctive bacterial communities.

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Keywords: Water springs; Bacteria; ARISA; Fingerprints; Hydrochemistry; Alps

1. Introduction

Water spring ecosystems are particularly complex and sensitive due to their being ecotones between aquatic and terrestrial ecosystems, as they share characteristics and vulnerabilities of both [1]. Furthermore, water springs are refuges for sensitive organisms or relict species [2,3]. The size and patchy distribution of water springs within catchments creates a situation of low connectivity between them. Therefore, each water spring is a partially isolated, unique ecosystem [3]. All the above mentioned features make water springs ideal “natural laboratories for ecological studies” [4]. The

hydrogeochemistry of spring water depends on three main variables: (i) the residing time of water in the aquifer; (ii) the reactivity of the rock substrate; and (iii) the pH and chemical composition of infiltrating waters [5]. Another feature that makes water spring unusual systems lies in water parameters (e.g. ionic enrichment and electric conductivity) that, in water springs, are mostly stable compared to those of surface-fed streams [6]. High mountain ecosystems, which are sensitive to natural or man-induced disturbances [7], often contain many water springs; therefore, at high altitudes, alpine water springs may experience dramatic consequences due to environmental changes.

The traditional tools used in water spring monitoring programs are based on measurement of chemical or physical parameters, whereas, when biotic components are included, studies usually focus on macrobenthos [8,9]. Studies on

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microorganisms mainly deal with photosynthetic organisms like diatoms or microalgae [10,11]. Spitale et al., in 2012 [12], carried out an extensive study on spring biota in an adjacent region. They found that a classification system based on spring biota (although prokaryotes were not included) was coherent, to a certain extent, with the traditional system based on water current velocity at the spring mouth [12,13]. Few studies focused on bacterial communities in water springs, and most were carried out in hot springs [14], mainly due to their interest for biotechnology and possible ancestral hyperthermophiles [15]. As stated by Schimel 2001, until a few years ago, ecosystem modeling rarely took into account the microbial contribution to biogeochemical cycles, since their contribution was considered constant [16]. Bacterial communities are indeed relevant heterotrophic components in alpine water bodies, especially above the tree line: Their key role in stream respiration (a decrease in dissolved oxygen over time) is well known [17,18], as their activity enriches both sediment and the water of organic matter. Bacterial communities in alpine streams have shown high seasonality [19,20] and marked spatial diversity [21].

However, since those studies were carried out on riverine and lacustrine ecosystems, very little is known about spatial and temporal variation in microbial communities in water

springs at high altitudes. Furthermore, in very few case studies was the focus on spring systems lying in oligotrophic high mountain environments such as alpine glacier catchments [3].

A rapid, inexpensive and reliable technique for detecting changes in bacterial community structure from environmental samples is amplified ribosomal intergenic spacer analysis (ARISA). This method has high resolution, since it is based on a genetic region (internal transcribed spacer or ITS), which is highly polymorphic in its length [22]. Therefore, it can provide a reliable reproducible image of variation in community structure even in very similar communities. In addition, there exist optimized protocols for data handling and parsing. The aim of the present study was to answer the following question: Does water origin and chemistry influence bacterial community structural shifts? And does bacterial community structure in water spring sediments depend on a spatial rather than on a temporal scale?

2. Materials and methods

2.1. Study site and sampling

The area of interest is located in the upper part of the Saldur Basin, corresponding to the Matsch Valley (total area 96 Km²),

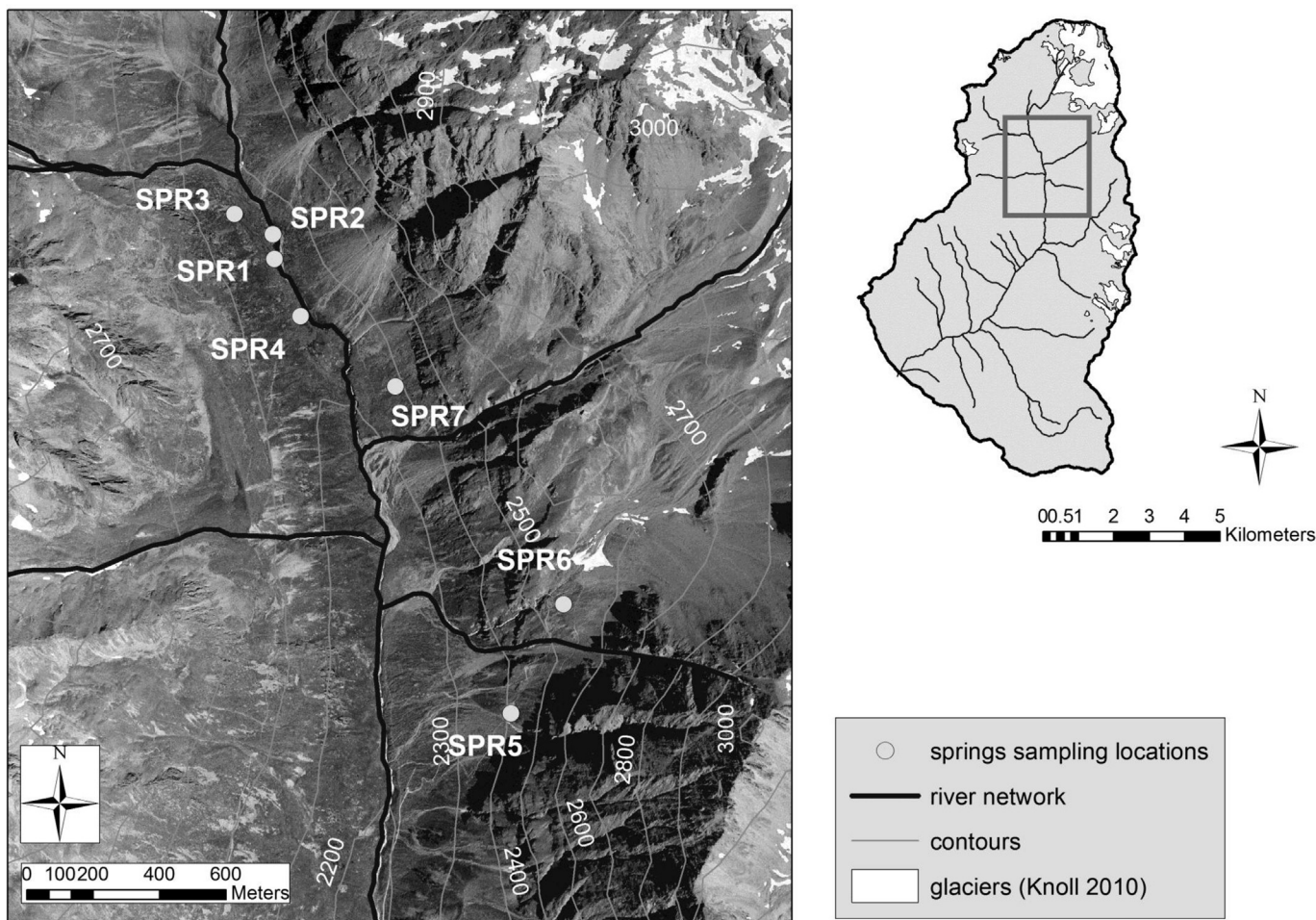


Fig. 1. Geographical locations of the water springs in the Matsch Valley.

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