



Application of DNA gene sequencing as a tracer method for deciphering the hydrogeology of the Pale di San Martino plateau in the Dolomites (Italy).

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Springs serve as the water supplies for communities in the Pale di San Martino plateau of the Dolomites in Italy. The main aquifer in the area is an 800 meter thick dolomitic fractured and karstified rock, overlain by quaternary deposits (till, landslide deposits, and alluvium). The aquiclude underlie the aquifer in the entire Pale di San Martino plateau, so the plateau results as an isolated hydrological structure from the nearest mountain groups. The aquiclude is composed of an alternation of carbonates, sandstones and clays (Werfen Formation) at different depths because of faulting. The recharge zone is a 90 km² area and the precipitation rate is about 1,800 mm. Spring flow rates are high and average 6 m³/s. The connection between springs and recharge sources has been the subject of an extensive hydrogeological study and has included tracer testing with Uranine and Tinopal CBS-X (Lucianetti et al., 2016). In the present study, indigenous bacteria were employed as a natural tracer for characterizing groundwater flow in the carbonatic and dolomitic fractured rocks. Bacteria samples were collected by filtering water from the presumed recharge areas on top of the plateau and from springs that emerge from all around the plateau at different elevations. DNA gene sequencing and biostatistical analyses were performed on thirteen samples to characterize and compare microbial diversity among the water sources and springs. Bacterial populations in groundwater systems respond to a myriad of environmental conditions which can vary along flow paths and also due to the presence of quaternary deposits that cover the hydrologic limit between the aquifer and the aquiclude. Anthropogenic activities, such as septic from the huts at high elevations in the Pale di San Martino mountains, can also have a strong impact on microbial communities. Past tracer testing and hydrologic studies provided an opportunity to test inferences on the connections between springs and water sources based on bacteria analysis and verify the usefulness of the approach.