Detection of a previously unknown deep-water source for Mt. Fuji's freshwater springs via dissolved noble gases, microbial DNA and vanadium

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For over two millennia, the freshwater springs and shallow groundwater of Mt. Fuji in Japan have been revered for their pristine quality, sparking the foundation of numerous temples and shrines, towns, and vast agriculture. Most recently, an entire microcosm of premium food industries that harness this water, such as green tea, bottled vanadium water and sake production, has emerged. Situated directly on top of a triple plate junction, Mt. Fuji is characterized by a complex layering of basaltic lava and pyroclastic mud deposits as well as the most active network of tectonic faults in all of Japan. Although the system has been studied extensively throughout the past decades, the understanding of the hydrogeological connectivity of the different aquifers is limited. Except for occurrences of minor percolation of shallow groundwaters into deeper layers [1], groundwater is thought to flow down the conically shaped mountain without a significant vertical connectivity between the different hydrogeological units [2,3]. Tagged via a novel combination of biogeochemical tracers - noble gases, vanadium and microbial DNA - we identified a previously unknown upwelling of deep groundwater into shallow groundwater and freshwater springs due its load of fluids of mantle origin (He), of its extraordinarily high concentrations of vanadium and its high abundance of extremophile microbes. This deep groundwater, which infiltrates at high altitudes and flows down to depths of more than 1 km below ground, moves up via the complex network of tectonic faults and basaltic clinkers and seems to contribute significantly to the freshwater springs and groundwater found at the southwestern foot of Mt. Fuji. Owing to this new tracer combination, the conceptual hydrogeological model of Mt. Fuji is accordingly broadened and adds another aspect to the extraordinary quality of Fuji's freshwater springs.

[1] Gmati et al., 2011, Hydrol. Res. Lett., 5, 58-63. doi:10.3178/HRL.5.58

[2] Ono et al., 2019, Hydrogeol. J., 27, 717-730. doi:10.1007/s10040-018-1889-9

[3] Segawa et al., 2015, Geomicrobiol. J., 32, 677-688. doi:10.1080/01490451.2014.991811