

Geographical variation of $^3\text{He}/^4\text{He}$ ratios within the Canary Islands

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The Canary Islands, situated in the north Atlantic, are the subaerial expression of intra-plate 'hotspot' volcanism. The geochemical evolution and geodynamics of this voluminous and long-lived volcanic centre however has remained contentious. The lack of geophysical evidence for a coherent mantle plume beneath the archipelago has led to speculation that the islands' volcanism is the expression of some other style of mantle/lithospheric anomaly.

The present work is an extensive He and Ar isotope study across the archipelago. We aim to investigate and identify the controls of isotope variability, and relate this to the mantle origin of the Canarian volcanism.

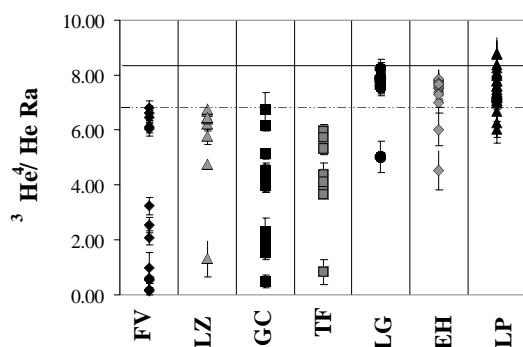


Figure 1. Inter- and Intra- Island $^3\text{He}/^4\text{He}$ Variations

Two distinct trends can be seen in Figure 1; we have estimated a maximum source $^3\text{He}/^4\text{He}$ ratio for the eastern islands (Fuerteventura [FV], Lanzarote [LZ], Gran Canaria [GC] and Tenerife [TF]) of 6.81 ± 0.08 Ra (Ra = $^3\text{He}/^4\text{He}$ normalised to air), while the western islands (La Gomera [LG], El Hierro [EH] and La Palma [LP]) have a magma source with a higher $^3\text{He}/^4\text{He}$ estimated maximum of 8.27 ± 0.46 Ra, we will detail these values in the presentation. The magma source is therefore not constant across the archipelago and causes for this will be discussed, as well as crustal level processes which may account for the intra-island variations.

The archipelago age relationship is not wholly linear from east to west. The most prominent switchback is the movement of activity from La Gomera to Tenerife. This indicates that the variation in magma source is more closely linked to the spatial geography of the islands rather than to time. Initial analyses implies that the original magma source had an approximate $^3\text{He}/^4\text{He}$ ratio of 6.81 Ra, but as the focus of activity has moved to the west this source has changed to one which has a more MORB - like signature.

Biosilicification and biodiversity in wastewater from Wairakei Power Station, New Zealand

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Introduction

The contribution of thermophilic microorganisms to the micro- and mesoscopic structure of silica sinters is established. All studied sinters from hot spring areas in the Taupo Volcanic Zone contain biomediated structural features. As part of this study, growth rates have been estimated for microstromatolite growth from various pools in the Taupo Volcanic Zone. These range from <0.001 to >0.02 mm/day. In contrast to these "slow" growth rates, biosilicification in the wastewater drains at Wairakei Power Station is remarkably fast providing an excellent laboratory to study the interaction of microbes and silica.

Biosilicification Experiments

The main drain contains the combined wastewater from geothermal bores of the Wairakei Power Station. At our experimental site, the temperature of the drain was 62°C . Standard glass microscope slides were suspended in the main drain. These were recovered over a period of 60 hours. After two hours, SEM examination showed only $0.05 \mu\text{m}$ nodules of amorphous silica. After five hours, fragments of meshwork silica had adhered to the slides. After 23 hours, the slide became coated with a fine meshwork of filaments $0.2 \mu\text{m}$ in width and of unknown length, composed of amorphous silica. Also present were larger rod-shaped organisms $\sim 0.5 \mu\text{m}$ in width and several μm in length. Further samples show that the filaments continue to thicken forming a porous mass of amorphous silica. The growth rate of the fibres is estimated to be ~ 10 mm/day.

Biodiversity Studies

Significant microbial diversity was revealed in the Wairakei drains using culture-based methods employing a range of media and temperatures (30 – 60°C). Following isolation of genomic DNA from each pure culture 16S rDNA was amplified by PCR with bacterial primers. Twenty-seven phylogenetically distinct bacterial sequence types were determined by partial ($\sim 600\text{bp}$) or near complete ($\sim 1350\text{bp}$) 16S rRNA gene sequence analysis. Isolates sharing $>97\%$ partial or near complete 16S rRNA gene sequence homologies with sequences in GenBank were affiliated with *Thermus*, *Meiothermus*, *Bacillus*, *Tepidomonas*, *Thermomonas*, *Porphyrobacter*, *Thermonema*, *Hydrogenophilus* spp. and previously uncultured bacteria.