

What do post-shield and rejuvenated lavas tell us about the source of the Hawaiian mantle plume?

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On Hawai'i, volcanoes lie on two geographical trends (Loa and Kea). Their shield lavas define two clear geochemical trends over ~5 Myr, distinct in Pb, Nd, Sr and Hf isotopes [1,2] and in elemental concentrations [3], that reflect the sampling of different components in the deep source of the mantle plume, at the core-mantle boundary.

Hawaiian volcanoes also include post-shield and rejuvenated lavas, alkalic in composition, that occur just after the shield phase or after an eruptive hiatus of variable duration (~0.5-2 Myr), respectively. These magmas correspond to smaller degrees of partial melting and provide finer resolution of compositional variation in the plume source. We compiled all recent high-precision literature data on late-stage lavas (130 samples for Pb and 103 for Sr, Nd and Hf isotopes), and added new data for Kaula and Middle Bank volcanoes (32 samples). Except Hualalai, which is characterized by a very distinct Loa signature [4] of very low ²⁰⁶Pb/²⁰⁴Pb ratios (<18.02) and light δ⁷Li (down to 0.75 ‰), most post-shield lavas plot on the Kea side of the Pb-Pb boundary of [2]. Two groups appear: 1) post-shield lavas from the Big Island and Maui Nui (<1.7 Ma) with isotopic compositions partly overlapping those of the shield lavas from their respective volcanoes, and 2) post-shield lavas from Oahu and Kauai (>3.6 Ma) with more distinct isotopic signatures than their respective shield, and more depleted isotopic compositions (lower ²⁰⁶Pb/²⁰⁴Pb, ⁸⁷Sr/⁸⁶Sr and higher ε_{Nd}, ε_{Hf}). These latter compositions overlap with the homogeneous field defined by rejuvenated lavas, mostly from the same volcanoes, but significantly younger (<2.5 Ma). Rejuvenated lavas and >3.6 Ma post-shield lavas define mixing trends subparallel to those of the shield lavas in all binary isotope diagrams. Middle Bank post-shield lavas (6.4 Ma) are the only known exception, with Pb ratios overlapping those of Mauna Kea post-shield lavas.

Most post-shield and rejuvenated lavas on Hawai'i are devoid of the enriched signatures present on Loa trend volcanoes that have been related to sampling of the Pacific ultra-low-velocity-zone [1]. This implies either that this enriched material is not sampled by lower degrees of partial melting, or that the late-stage lavas only derive from the northeast part of the plume, which is more homogeneous and controlled by the Kea component. In contrast to shield lavas, there is also no systematic isotopic variation with time for the post-shield and rejuvenated lavas, therefore providing further insight into the source heterogeneity of the Hawaiian mantle plume.

[1] Weis et al. (2011) *Nature Geosciences* **4**, 831-838. [2] Abouchami et al (2005) *Nature* **434**, 851-856. [3] Hauri (1996) *Nature* **382**, 415-419. [4] Hanano et al. (2010) *G-cubed* doi:10.1029/2009GC002782.

Evolutionary pathways of biomineralization explored using transformed *Dictyostelium*

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The biological control mechanisms for forming functional mineralized hard materials have developed over long periods of time during evolution. In some way, evolution went hand in hand with the transition from unicellular to multicellular organisms. Our research team takes advantage of a non-mineralizing model organism with uni- and multicellular stages as part of its life cycle: The slime mold *Dictyostelium discoideum*. We recently achieved transgenic expression of a mollusc myosin chitin synthase in *Dictyostelium* and observed that this complex enzyme involved in shell biomineralization is enzymatically active in our cellular model system [1,2]. Clearly, this is only one side of the coin. There are a number of other biomineralization proteins on the other side, which interact with either chitin or mineral phases, or both. The fact that the native extracellular matrix of *Dictyostelium*, in principle, inhibits mineral precipitation can be exploited to match certain environmental conditions with heterologously expressed biomineralization genes, which then favor mineralization with increasing levels of control. Our transgenic approach might be suitable to identify key molecules in the evolutionary pathway of biomineralization inspired from contemporary organisms with some impact for today's environmental challenges such as climate change.

[1] Schönitzer V., Eichner N., Clausen-Schaumann H., Weiss I.M. (2011) *Biochemical and Biophysical Research Communications* **415**, 586-590.

[2] Kaufmann K., Weiss I.M., Eckstein V., Tanaka M. (2012) *Biochemical and Biophysical Research Communications*, in press.