Site-specific variation of biological communities along the Eastern Lau Spreading Center (ELSC)

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Understanding the distributions of animals at deep-sea hydrothermal vents has been a focus of interdisciplinary research since their discovery 30 years ago. Recent technological developments allow collection of spatially explicit imagery and *in-situ* chemical data of higher quality than previously possible, enabling detailed spatial analysis of the intact communities.

The Lau back-arc basin lies between the islands of Tonga and Fiji and is composed of a chain of disjointed hydrothermally active spreading systems, including the Eastern Lau Spreading Center (ELSC), which is bordered by the remnant Lau volcanic arc to the west and the active Tofua volcanic arc to the east. The ELSC propagates to the south, with the northernmost extent 110 km from the active Tofua arc and the southernmost extent only 40 km from the active volcanic arc. Because of variable proximity to an active volcanic arc and subduction zone, substrate type, geochemical composition, spreading rate, and crustal thickness all change along a north-south gradient on the ELSC.

During a research cruise in September 2006 to the ELSC, high-resolution, geo-referenced images were collected using the remotely operated vehicle JASON II from a total of seven diffuse flow communities in four different vent sites, two of which are basalt-hosted (Kilo Moana and Tow Cam) and the other two are andesite-hosted (ABE and Tu'i Malila). Chemical (H_2S and O_2 concentrations) and temperature data were obtained from 30 to 100 precise positions within each community using *in-situ* instruments. All data were then integrated into a geographic information system (GIS), in order to visualize the faunal distributions in relation to biological and chemical variables. De-trended correspondence analysis and canonical correspondence analysis were used to identify co-occurrence between faunal types, better define biological community types, and test the relation between the animal and chemical distribution patterns.

These tools allowed us to rapidly characterize vent community structure along the ELSC and to assess how communities differ within and between vent sites. With data collected from seven different communities, we can begin to understand how community composition changes with substrate type, recognize patterns of faunal distribution in relation to chemical and temperature gradients, elucidate biological associations, and tease apart the influence of different explanatory variables on animal distribution, such as substrate, H_2S, oxygen, and temperature.

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