

## The relationship between $fO_2$ and calc-alkaline affinity of arc magmas

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Calc-alkaline differentiation, a process by which magmas become rapidly depleted in Fe early in their crystallization history, is observed exclusively in magmas in subduction zone settings and is thought to drive magmas towards the bulk composition of continental crust. Basaltic arc magmas have been proposed to achieve calc-alkaline affinity through either high magmatic  $H_2O$ , which delays the onset of plagioclase crystallization, or high magmatic  $fO_2$ , which enhances the onset of magnetite crystallization, or both. The relative importance of  $H_2O$ ,  $fO_2$ , and magmatic bulk composition in generating calc-alkaline magma series, however, is not yet clearly resolved. Here, we present new measurements of the oxidation state of Fe (expressed as  $Fe^{3+}/\Sigma Fe$  ratio) in olivine-hosted melt inclusions from basaltic arc volcanoes in the Mariana and Aleutian arcs, acquired using X-ray Absorption Near Edge Structure spectroscopy. These volcanoes span a range of calc-alkaline affinity, with THI ranging from 0.7 to 1.2 (THI = Tholeiitic Index, <1 is more calc-alkaline, >1 is more tholeiitic [1]). Measured  $Fe^{3+}/\Sigma Fe$  ratios range on average from 0.23-0.28 in the Marianas, and from 0.20-0.28 in the Aleutians, which are uniformly more oxidized than more tholeiitic basaltic glasses from the Mariana trough back-arc basin (THI=1.4;  $Fe^{3+}/\Sigma Fe=0.15-0.18$ ) or normal MORB (THI=1.6;  $Fe^{3+}/\Sigma Fe=0.16\pm 0.01$ ). Our results show a correlation between THI and  $Fe^{3+}/\Sigma Fe$  ratios at these volcanoes, such that more tholeiitic magmas contain a greater proportion of reduced Fe, and more calc-alkaline magmas a greater proportion of oxidized Fe. At the same time, the maximum dissolved  $H_2O$  contents of basaltic melt inclusions from these volcanoes also broadly correlate with THI [1], and with measured  $Fe^{3+}/\Sigma Fe$  ratios, which is consistent with prior work [2], although  $H_2O$  is not the direct cause of oxidation. These findings suggest that  $H_2O$  and  $fO_2$  may both play key roles in the development of calc-alkaline affinity in arc magmas, but their respective functions in this process may be difficult to separate in natural systems because the subducted slab delivers fluids that generate arc magmas with both elevated  $H_2O$  and  $fO_2$ .

[1] Zimmer, M.M., Plank, T., Hauri, E.H., *et al.*, 2010, *J. Pet.* **51**, 2411-2444, doi:10.1093/petrology/egq062. [2] Kelley, K.A., Cottrell, E., 2009, *Science* **325**, 605-607, doi:10.1126/science.1174156.

## Characterisation of active forest soil *Bacteria* during mineral weathering

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Acidic forest soils, while nutrient-poor, are characterised by a reservoir of inorganic nutrients trapped within the minerals contained therein. Despite the significance of such reservoirs to the long-term functioning of acidic forest ecosystems, surprisingly little is known regarding the contribution of the resident bacterial communities to the weathering of soil minerals. While the influence of mineralogy on the phylogenetic composition of mineralosphere communities in soil and other terrestrial environments <sup>[1, 2, 3]</sup> has been demonstrated, determining the activities and contributions of individual microbial taxa to weathering processes remains an ongoing challenge. Using DNA immunocapture and high-throughput sequencing, in concert with geochemistry and traditional culture-based techniques, we investigated bacterial communities on a variety of minerals during weathering in laboratory microcosms, seeded with a forest soil-derived inoculum. Our primary objectives were i) the comparison of active and inactive bacterial community fractions and ii) to determine whether mineralogy influences the phylogenetic composition of these fractions. Such analyses brings us a step closer to understanding the composition and activities of mineralosphere bacterial communities in acidic forest soils, and the likely ecological significance of particular taxa.

[1] Uroz *et al.* (2009) *Trends Microbiol.* **17**, 378-387. [2] Kelly *et al.* (2010) *Microbial Ecol.* **60**, 740-752. [3] Lepleux *et al.* (2012) *Appl. Environ. Microbiol.* **78**, 7114-7119.