

## U-bearing hematite: A tool for dating Iron Oxide Copper Gold systems?

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Hematite, the most abundant mineral in Iron Oxide Copper Gold (IOCG) deposits in the Gawler Craton of South Australia, may incorporate significant amounts of U, W, Mo and radiogenic Pb. These elements are concentrated in hematite grains which display either oscillatory and/or sectorial compositional zoning, or are porous. The presence of U and Pb raises the potential for novel geochronology applications aimed at constraining the timing of mineralization.

Meaningful preliminary age data were obtained for U-bearing hematite by LA-ICP-MS techniques on zoned grains. In the absence of suitable, matrix-matched standards, GJ-1 zircon was used as the primary standard. <sup>207</sup>Pb/<sup>206</sup>Pb ages obtained on the zoned hematite (1590±7, 1583±3 Ma; Fig. 1) are statistically indistinguishable from ages for emplacement of the Gawler Range Volcanics and associated Hiltaba Intrusive Suite, and consistent with a major ore-forming event in the region at ~1.59 Ga.

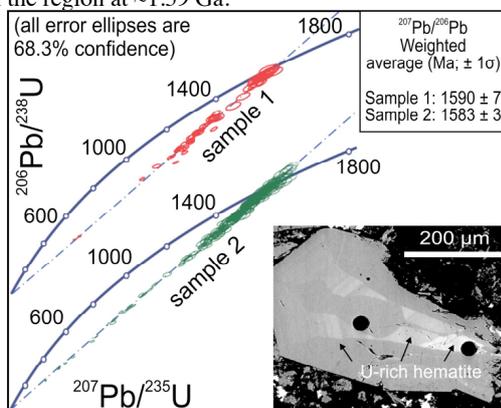


Fig. 1 U/Pb Concordia plots for dated U-hematite. All lower intercepts are at zero. BSE image shows typical zoning in dated grains.

Provided that matrix-associated mass fractionation can be constrained, and suitable standards are fabricated, the ability to date an abundant refractory mineral like hematite could represent a valuable tool for dating IOCG deposits and, potentially, other iron-bearing ores.

## Subseafloor biosphere of the Canterbury basin

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The subseafloor microbiota is diverse and complex, hosting metabolically active communities down to depths of more than 1000 meters below the seafloor (mbsf), as revealed by molecular and metagenomic studies. It harbors representatives from the three domains of life, i.e., numerous endemic and/or as yet uncultured *Archaea* and *Bacteria*, in addition to bacterial endospores, protists and fungi belonging to *Eukarya*. Although background molecular data on bacterial and archaeal lineages inhabiting subsurface sediment above 1000 mbsf exists, most deep-subsurface microorganisms detected so far were refractory to cultivation. Deeply buried microorganisms form an almost untapped diversity, as sub-sea-floor prokaryotic culturability in most studies is less than 0.1% of all microscopically detected cells. So far, active prokaryotes have been discovered down to 1626 mbsf, and microeukaryotes down to 113 mbsf, but the lower limit of the deep subsurface biosphere remains elusive.

Here we report on the microbial prokaryotic and eukaryotic communities of a core of nearly 2 km collected in the Canterbury basin during IODP Expedition 317. A very stringent high-throughput 454-pyrosequencing approach targeting the 16S/18S rRNA genes for *Bacteria*, *Archaea* and *Eukarya*, along with real-time PCR analysis (genetic markers and functional genes), cell counts and cultures, were performed to assess microbial abundance, diversity and activity at different depths. Our results suggest that a diversity of microorganisms exists down to 1922 mbsf in the seafloor of the Canterbury basin and that this diversity is to a certain extent alive.