# Minor and trace element composition of iron oxides from IOCG deposits worldwide and its application to mineral exploration

EMILIE BOUTROY[1*], GEORGES BEAUDOIN[1], SARAH-JANE BARNES[2] AND LOUISE CORRIVEAU[3]

[1]Université Laval, Département de géologie et de génie géologique, emilie.boutroy.1@ulaval.ca (* presenting author)
Georges.Beaudoin@ggl.ulaval.ca
[2]Université du Québec à Chicoutimi (UQAC), Sciences de la Terre, sjbarnes@uqac.ca
[3]Geological Survey of Canada, Natural Resources Canada louise.corriveau@rncan-nrcan.gc.ca

There are significant variations in the concentration of trace elements in magnetite and hematite depending on the metallogenic environment at the time of formation of the deposit. This makes iron oxides useful as indicator minerals for mineral exploration.

Iron oxides are a major component of Iron Oxide Copper-Gold deposits (IOCG) and of Iron Oxide-Apatite deposits (IOA). Magnetite and hematite in IOCG (n= 84 samples) and IOA deposits (n= 6), representative of 8 major IOCG and IOA deposits, worldwide, representing a range of geological environments and ages of formation, were analyzed by electron microprobe analysis (EMPA). A subset of IOCG (n = 30 samples) and IOA (n= 6) was analysed by LA-ICP-MS. The IOCG deposits samples are divided based on the principal iron oxide present: (1) Hematite (n = 10), (2) Magnetite (n = 37) and (3) Hematite ± Magnetite (n =8). Similarly, IOA deposits are divided: (1) Magnetite (n = 3) and (2) Magnetite ± Hematite. In these types of deposits, iron oxides are in mineralization and in host rock alteration assemblages, and there are typically multiple generations of iron oxides. Iron oxides are studied according to their paragenetic stage: (1) ore stage and (2) hydrothermal alteration of host rocks. Hydrothermal alteration iron oxides are grouped according to the type of alteration: (1) Ca-Fe alteration (Am-Ap-Mag), (2) Na(Fe) alteration (Ab-Scp-Mag/Hem), (3) High temperature K-Fe alteration (Bt-Kfs-Mag) and (4) Low temperature K-Fe (Ser-Kfs±Chl±Cb-Hem). Preliminary results show hematite in Hematite-group IOCG deposits is depleted in Zn, Ni, Mn, V and enriched in K, Ti, Al, Si compared to magnetite in Magnetite-group IOCG deposits. In Magnetite-IOA deposits, magnetite is enriched in V, Al and Mg compared to Magnetite-Hematite-IOA deposits, which is enriched in Ca.

Compared to primary magnetite in Ni-Cu-PGE deposits, ore-stage magnetite in IOCG deposits are depleted in Ni, Cu and Cr and enriched in Ti, Al and Si.

# Functional gene pyrosequencing sheds light on the distribution and diversity of a key nitrogen cycle gene (*nirS*) in marine systems

JENNIFER L. BOWEN[*1], DAVID WEISMAN[1], AMAL JAYAKUMAR[2], MICHIE YASUDA[1] AND BESS B. WARD[2]

[1]University of Massachusetts Boston, MA, USA Department of Biology, jennifer.bowen@umb.edu (*presenting author), weisman@lydon.com, michie.yasuda@umb.edu

[2]Princeton University, Princeton, NJ, USA Department of Geosciences, ajayakum@princeton.edu, bbw@princeton.edu

## Introduction

Denitrification, a critical pathway in the nitrogen cycle that converts dissolved inorganic nitrogen to its gaseous form, plays a central role in removing nitrogen from the environment. Denitrification in estuaries, continental shelves, and oxygen minimum zones accounts for nearly 60% of the global fixed nitrogen loss [1]. There are two genes, *nirS* and *nirK* that encode functionally similar nitrite reductase enzymes that facilitate the denitrification process. The two genes do not appear to co-occur within a given microorganism but both genes are present in most environments. In the marine environment *nirS* tends to be more abundant than *nirK* [2]. Examining the structure and abundance of denitrifiers represented by the *nirS* gene in a variety of marine environments will shed new light on biogeochemical ecology of this critically important ecosystem service.

## Results and Conclusions

We used functional gene pyrosequencing to examine the abundance and diversity of denitrifying bacteria in all three major oceanic oxygen minimum zones as well as in coastal sediments from Chesapeake Bay and a New England salt marsh. To assess the role of sequencing error in inflating our diversity estimates we sequenced amplicons of four clones and show that our data analysis pipeline successfully identifies and removes the overwhelming majority of spurious sequences (Fig. 1). The data indicate an astonishing degree of diversity in the *nirS* gene, with over 3500 taxa (defined operationally as sharing 95% sequence identity), found in salt marsh sediments alone. Pyrosequencing detects distinct differences in the composition of nirS assemblages in water column and sediment environments.

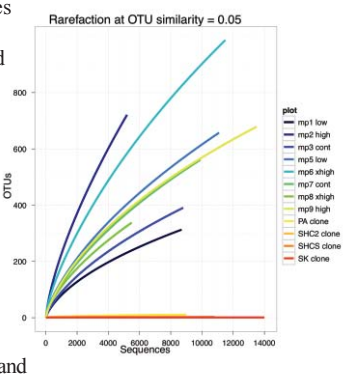


**Figure 1:** Rarefaction curves resulting from pyrosequencing of the nirS gene in salt marsh sediments and in control sequenced

[1] Seitzinger (2004) *Ecol. Appl.* **52**, 47-59. [2] Jones and Hallin (2010) *ISME J* **4**, 633-641.