U-Pb dating of zircon, Rb-Sr and Sm-Nd isotopic analysis of layered intrusion Kivakka (N. Karelia)

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Results of Rb-Sr and Sm-Nd isotopic analysis of the 38 samples of Kivakka layered basic-ultrabasic pluton and country rocks and *in situ* U-Pb dating analysis of 13 zircon grains from two zones of norites, gabbro-norites and subzone of interstratification of bronsitites and norites are presented. Kivakka cone shaped body consists of four main zones: (topdown) gabbros, gabbro-norites, norites and olivinites. Country rocks are migmatized biotitic and amphibolic gneisses, granite-gneisses and granite-diorite-gneisses of upper Archean.

U-Pb isotopic analysis were done using LA-ICP-MS. Zircon grains an age of 2443 ± 5 Ma (MSWD = 0.006). Obtained age are in good agreement with data of many layered intrusions of the eastern Baltic Shield [1] and age of one zircon fraction from gabbro-norites of Kivakka intrusion (2445±2 Ma) [2]. Initial Nd and Sr isotopic rations were calculated using obtained U-Pb age. We have found clear inverse correlation between initial Nd isotopic composition and Nd content in the Kivakka layered rock suite. Variations of Nd initial isotopic ratios could be interpreted as a result of parent basic melt interaction with country acid rocks in the magma chamber during crystallization. Many similar layered intrusions at the North Karelia have Nd isotopic composition shifted toward crustal significances. Thus, it is possible that discovered interaction between basic melt and country rocks accompanied formation other layered intrusions in Karelia too.

1. Amelin Y.V., Semenov V.S. 1996. CMP. 124: 255-272.

2. Barkov A.Y. et. al. 1991. Abstract of the conference Isotopic geological techniques. 21-23 (on Russian).

Expression of *Shewanella* sp. str ANA-3 metal reduction genes in response to iron(III) and arsenate

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The expression of genes associated with metal reduction have the potential of serving as indicators of biological activity linked to geochemical conditions. In arsenic contaminated sediments arsenate is often associated with iron (III) hydroxides and can be released or sequestered through microbial iron (III) dissimilatory reduction or arsenate respiration. Shewanella sp. str. ANA-3 utilizes an arsenate respiratory reductase (encoded by the arrA/B genes) to reduce arsenate to arsenite coupled to oxidation of an electron donor. Additionally, ANA-3 has a cluster of metal reducing genes (mtrCABDEF/omcA) that encodes *c*-type decaheme cytochromes and non-cytochromes, some of which are involved in reduction of soluble and insoluble metal oxides such as iron and manganese hydroxides. Previous studies have primarly focused on the expression of the mtrCAB/omcA cluster in the presence of iron and manganese oxides but questions remain about the function of the MtrDEF proteins and whether the mtr/omc cluster also responds to other metals and metalloids. The goal of our study was to investigate the expression of the mtr/omc gene cluster in the presence of arsenate, soluble and insoluble iron (III). ANA-3 cells were grown aerobically or anaerobically with arsenate, iron (III)citrate, iron (III)oxide, iron (III)oxide-arsenate, RNA extracted and quantitative RT-PCR (qRT-PCR) used to monitor the exrepssion of the mtr/omc cluster. Our results showed that the mtrCAB/omcA genes were expressed highest with arsenate compared to cells grown with iron (III)-citrate. Expression of mtrCB was highest compared to mtrA/omcA in samples grown with iron (III)oxide. The mtrc/omc cluster was not expressed in samples grown under oxygen conditions. In contrast, little to no expression of the mtrDEF genes was detected in samples grown anaerobically with iron (III) citrate, iron (III) oxide or arsenate conditions. These results show that the mtrCAB/omcA genes are expressed in the presence of arsenic and iron and imply that their expression is repressed in the presence of oxygen. More work is needed to determine if changes in varying iron-arsenic concentrations, redox states and mineral phases leads to changes in the expression of the mtr/omc and arrA genes.