

Synthesis and characterization of K-zeolites by the use of a diatomite

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Hydrothermal crystallization of K-zeolites (K-F and W-Merlinoite type) from gels obtained by the use of k-aluminate and naturally derived k-silicate is here achieved. The use of an inexpensive natural rock ("Tripoli" siliceous rock from Crotona, Italy) reduces the high costs of the usual industrial synthesis protocols and favours the exploiting of the same natural material. Chemical treatments were performed on the opaline siliceous rock, whose composition resulted in quartz, amorphous opaline silica, clay minerals and a minor amount of calcite [1], in order to obtain K-silicate. A first attack with nitric acid to eliminate the calcitic and carbonatic fraction and Fe and Mn oxides, was followed by a treatment in an alkaline bath (KOH 10%) to induce the solubilization of the siliceous fossil fraction and the production of the K₂SiO₃ solution. The second reagent, potassium aluminate, was achieved by the mixing of potash

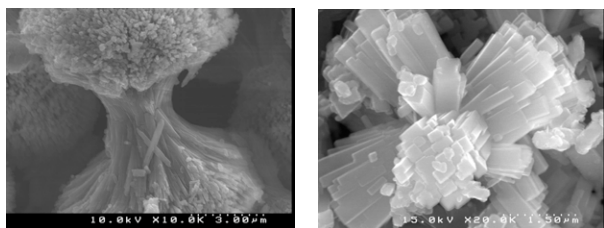


Figure 1: Left: W-Merlinoite type zeolite; right: K-F zeolite.

(20%) with Al(OH)₃ (65%). Five series of synthesis were performed inside autoclaves at a temperature of 150°C and ambient pressure by varying the ratio of the silicatic and aluminatic solutions. Infrared and X-ray spectroscopy, thermo diffraction, nuclear magnetic resonance ²⁹Si, structural refinement together with high temperature diffraction textural, chemical, and physical characterization give values comparable to those proposed by literature.

[1] Novembre *et al* (2004) *Microp. and Mesop. Mat.* **75**, 1-11.

Environmental diversity of denitrification

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The modern nitrogen cycle is a complex web of microbially mediated redox reactions found in both oxic and anoxic environments. Recently, the breadth of microbial roles in the nitrogen cycle has expanded substantially, with the discovery of both new metabolisms (ANAMMOX; anaerobic oxidation of methane coupled to denitrification), and novel organisms performing known reactions (ammonia oxidation in Archaea). Here we use metagenomics, coupled with biochemical and physiological experiments, to identify new enzyme families able to catalyze nitric oxide reduction. These results greatly expand the known diversity of organisms capable of performing denitrification, suggesting also that this metabolism is more widespread than previously recognized.

Nitric oxide reduction is catalyzed by enzymes from the heme-copper oxidoreductase (HCO) superfamily. The superfamily is extremely diverse, with members playing crucial roles in both aerobic and anaerobic respiration. It is currently divided into two reaction classes; oxygen reductases and nitric oxide reductases. The oxygen reductases are terminal enzymes in aerobic respiratory chains, and are able to conserve energy in a proton electrochemical gradient. The nitric oxide reductases (NOR) catalyze the reduction of nitric oxide to nitrous oxide ($2\text{NO} + 2\text{H}^+ + 2\text{e}^- \rightarrow \text{N}_2\text{O} + \text{H}_2\text{O}$) in microbes capable of denitrification, and are not known to conserve energy.

The HCO superfamily currently consists of three oxygen reductase families (A, B and C) and two NOR families (cNOR and qNOR). We used metagenomics and comparative genomics to discover at least seven new families capable of nitrogen cycle reactions. Five of these families (eNOR, bNOR, sNOR, gNOR, nNOR) catalyze nitric oxide reduction. The two other families are predicted to perform reactions new to the superfamily; nitric oxide dismutation ($2\text{NO} \rightarrow \text{O}_2 + \text{N}_2$) and nitrous oxide reduction ($\text{N}_2\text{O} + 2\text{H}^+ + 2\text{e}^- \rightarrow \text{N}_2 + \text{H}_2\text{O}$). All sequenced ammonia-oxidizing bacteria have the sNOR family, whereas the gNOR family is specifically found in environments where sulfide oxidation is coupled to denitrification. The eNOR and bNOR families have proton channels, which allow them to conserve energy, enabling these microbes to extract more energy from denitrification. Significantly, according to metagenomic data, the eNOR family appears to be the most common NOR found in Nature.