

Environmental protection design of Chinese highway tunnel

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The environmental protection design of highway tunnel mainly includes 3 aspects: environmental protection design for tunnel portal, water-proof and drainage environment protection design, environmental protection landscape and illumination design in tunnel.

The principle of environmental protection design for tunnel portal is 'natural, concise, harmonious with environment, not exaggerating deliberately and protecting original natural landscape of tunnel'. The content of environmental protection design for tunnel portal is the selection of tunnel portal placement and type. The selection of tunnel portal placement should be a placement that protects the natural status of mountain massif to a largest degree. The selection of tunnel portal placement should avoid high side slope and is good for being compatible with environment. Bamboo-truncating and end wall portal types are recommended because of convenient in construction, handsome appearance, reasonable strength distribution and good seismic behavior.

The principle of water-proof and drainage environment protection design is 'prevention first, blocking and intercepting coordination, and supported by clearing'. The main method to deal with this problem of adopting combined lining to prevent water, improving the anti-permeability of concrete, dealing with the deformation joint and construction joint and so on.

The purpose of environmental protection landscape and illumination design in tunnel is to improve the driving environment and the comfort index. The main methods are: to increase light illumination in tunnel, to arrange artificial green landscape in tunnel, to plant green plants at the tunnel portal and so on.

[1] CUI GUANG-YAO (2010) *Geochimica et Cosmochimica Acta*, **74**(12) Supplement **1**, A199. [2] Xu WL, Zhang JQ(2010) *Geochimica et Cosmochimica Acta*, **74**(12) Supplement **1**, A1162.

Elucidating the functions of the active microbial community of Iron Snow in an acidic lake

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Lignite mine lakes are characterized by low pH, low nutrient status, and high concentrations of Fe (II) and sulfate. In lignite mine lake 77, located in Brandenburg, Germany, microbial oxidation of Fe (II) at redoxclines with opposing Fe (II) and oxygen gradients leads to the formation of iron-rich macroscopic aggregates (Iron Snow, IS). The IS provides an important input for the reduction of Fe (III) in the anoxic hypolimnion which shows different pH values ranging from 3.3 - 4 to 3.4 - 5.9 in the center basin (CB) or north basin (NB), respectively. Thus, the diversity and function of the IS microbial communities responsible for Fe-cycling may be dissimilar. This study aimed to i) characterize microbial communities from CB and NB and ii) explore active Fe-cycling microorganisms through RNA- and proteomic-based methods. Fe (III) mineral schwertmannite was the dominating iron oxide in CB and NB samples using SEM, EDX and Raman spectroscopy. Metaproteomics analyses was performed using detergent-based cellular lysis for total protein extraction followed by LC-MS/MS interrogation. Spectral matches were accomplished using an artificial metagenome, (assembled using 175 genomes of sequenced reference isolates) and yielded a total of 390 different proteins representing 43 microorganisms in NB samples, and 105 proteins tracing back to 27 genus from CB samples. Proteins of *Chlorobium*, *Acidiphilium*, *Acidovarax*, *Azoarcus*, *Burkholderia* and *Geobacter* species were detected in both NB and CB samples. *Acidithiobacillus* related proteins were only determined in NB while those related to *Ferroplasma* and *Sulfolobus* were discovered in CB primarily. Detections of cytochrome c class I of *Acidiphilium* JF5 in both NB and CB indicated its active role in Fe (III) reduction among the lake. Carboxysome proteins were found in *Acidimicrobium ferrooxidans* and *Acidithiobacillus* species, suggesting their capacity of CO₂-fixation coupled to Fe (II) oxidation in the upper oxic water epilimnion in Lake 77. 16S rRNA gene libraries and q-PCR for functional proteins will further provide insights into the ecophysiology of the Fe-cycling microorganisms in acidic environments.