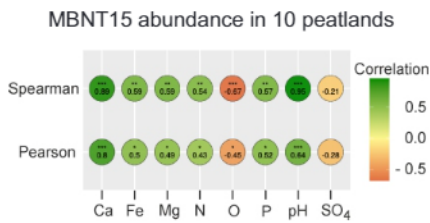
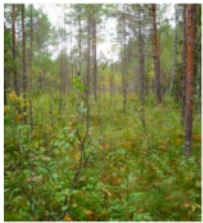
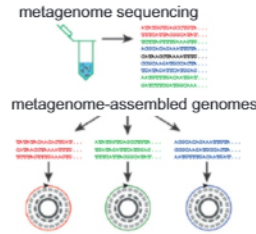


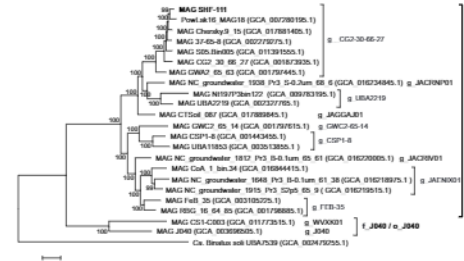
Genome analysis of the candidate phylum MBNT15 bacterium from a boreal peatland predicted its respiratory versatility and dissimilatory iron metabolism



Positive correlation with pH, total nitrogen, pH, Fe, Ca, Mg, and P

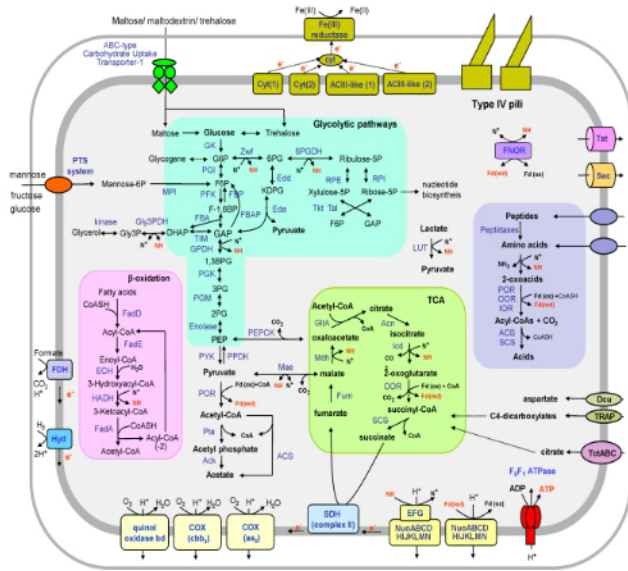


Complete 2,677,482 bp long genome of MBNT15 bacterium SHF-111

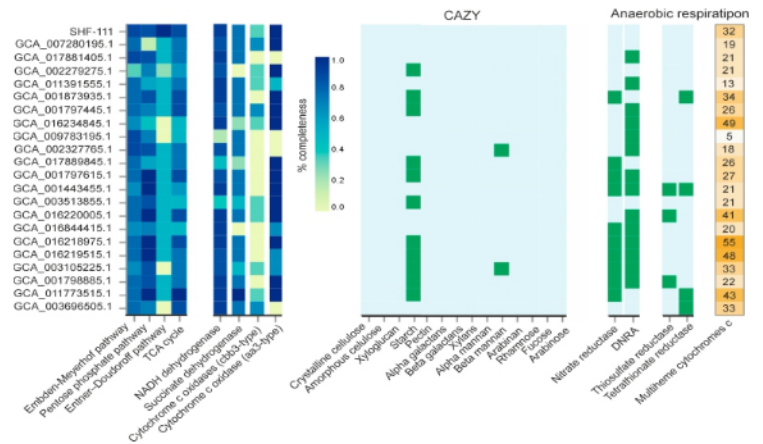


Genome-based phylogeny of the candidate phylum MBNT15

Main metabolic pathways of the SHF-111 bacterium



Comparative analysis of the main metabolic pathways along MBNT15: aerobic respiration and dissimilatory iron reduction



Candidatus *Deferrimicrobium borealis* SHF-111
Candidatus *Deferrimicrobiota* phyl. nov.