

# **Bacterial diversity in tropical glacier and glacier foreland in Uganda : Glacier ecosystem influence soil formation in glacier foreland**

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Tropical region is still missing area of glacier biology, though most studies on glacier ever had been reported frequently from mid latitude to bipolar region. In tropical regions glacier retreat is more significant, especially glaciers in Rwenzori Mts. where located between Uganda and Congo was expected to disappear within a decade. Otherwise, recently novel biological aggregation, which is mainly formed by moss gemmae, was found from glacier in Rwenzori Mts. (Uetake et al. 2014). This aggregation is not simple structure only by moss gemmae, but supply habitat for many glacier microorganisms. And after retreat of glacier terminus, abundant of GMGA are left on the fresh bared rocks and became soil like structure within few years. In order to know the bacterial community structure changes after/during formation of GMGA structure and after release to glacier foreland, 16S rRNA amplicon from no GMGA covered ice surface (3 sites), GMGA (1 sites) and glacier foreland soil (6 sites) were sequenced by Miseq and sequence data set were analyzed by Qiime.

Similarity of bacterial OTU composition based on weighted Unifrac analysis shows samples are clearly divided into two sample types (glacier and soil type). Bacterial community of GMGA is closer to glacier foreland samples even on the glacier ice. This results indicate that high alpine soil in Rwenzori Mts are already formed on glacier surface. Because presence of GMGA had changed the temperature and oxygen concentration of aggregation and organic matter supply, these may be a potential reason for community changes.

Most of difference in taxonomy between glacier and soil types samples are dominance of genus Chloroflexi. Chloroflexi are most abundant in glacier foreland soil (15- 56% relative abundance: mean 34±15%) and GMGA (30% relative abundance), otherwise less in no GMGA covered ice surface (3- 6% relative abundance: mean 4±2%). Most of Chloroflexi are belong to family: Thermosporotrichaceae and Ktedonobacteraceae, otherwise closest isolate (87.4-88.4% similarity) in GenBank are isolated from thermal and aerobic environments.

## **Reference**

Uetake, J., Tanaka, S., Hara, K., Tanabe, Y., Samyn, D., Motoyama, H., Imura, S., Kohshima, S Novel Biogenic Aggregation of Moss Gemmae on a Disappearing African Glacier. PLOS ONE 9 (11): e112510. doi:10.1371/journal.pone.0112510, 2014