Biogeochemistry of iron-rich shallow hydrothermal vent sediments revealed from functional annotation of bacteria and Zetaproteobacteria diversity

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1
00:00:07,829 --> 00:00:06,470
in our survey of the microbiome and by

2
00:00:09,750 --> 00:00:07,839
geochemistry

3
00:00:12,709 --> 00:00:09,760
of an iron-rich shallow hydrothermal

4
00:00:14,870 --> 00:00:12,719
vent in baby batangas philippines

5
00:00:16,870 --> 00:00:14,880
we used annotation and classification

6
00:00:20,550 --> 00:00:16,880
tools to probe deeper into

7
00:00:22,550 --> 00:00:20,560
cn16s rdna marker gene sequencing data

8
00:00:24,790 --> 00:00:22,560
namely functional annotation of

9
00:00:27,589 --> 00:00:24,800
prokaryotic taxa are fat protests

10
00:00:29,269 --> 00:00:27,599
and data hunter from the outputs we

11
00:00:30,150 --> 00:00:29,279
found that the predicted functional

12
00:00:32,950 --> 00:00:30,160
profile

13
00:00:33,830 --> 00:00:32,960

and microbial iron oxidizer abundances

14
00:00:35,510 --> 00:00:33,840
correlated

15
00:00:37,990 --> 00:00:35,520
with our geochemical data and

16
00:00:40,310 --> 00:00:38,000
multivariate analysis

17
00:00:41,670 --> 00:00:40,320
moreover microscope imaging of

18
00:00:43,750 --> 00:00:41,680
rust-colored mats

19
00:00:46,310 --> 00:00:43,760
showed structures resembling those

20
00:00:49,110 --> 00:00:46,320
formed by bacterial iron oxidizer

21
00:00:50,150 --> 00:00:49,120
in culture as described in literature

22
00:00:52,709 --> 00:00:50,160
supporting

23
00:00:53,510 --> 00:00:52,719
the hypothesized role of zeta protein