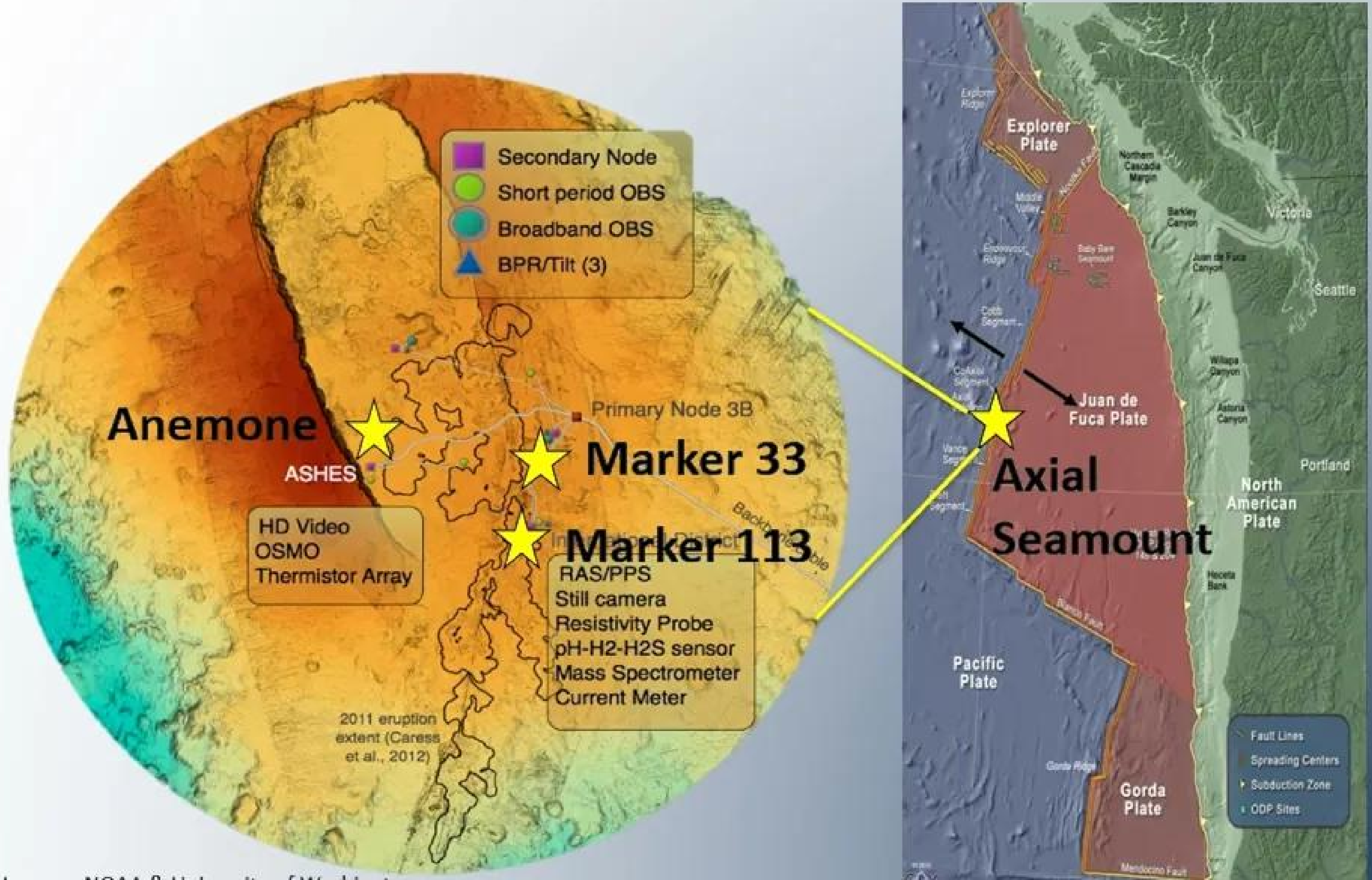
Study Site: Axial Seamount



Images: NOAA & University of Washington

1
00:00:07,349 --> 00:00:04,550
good afternoon everyone my name is

2
00:00:09,509 --> 00:00:07,359
sabrina elkasis and i am excited to talk

3
00:00:12,070 --> 00:00:09,519
to you today about my research studying

4
00:00:14,150 --> 00:00:12,080
sub-seafloor chemolithoautotrophs as

5
00:00:19,189 --> 00:00:14,160
models for understanding the potential

6
00:00:23,269 --> 00:00:20,950
there are several different ocean worlds

7
00:00:25,509 --> 00:00:23,279
in our solar system some of which are

8
00:00:27,750 --> 00:00:25,519
shown here you have probably heard of

9
00:00:30,710 --> 00:00:27,760
enceladus and

10
00:00:34,870 --> 00:00:30,720
europa which are both very heavily

11
00:00:39,990 --> 00:00:37,910
here is a profile of enceladus one of

12
00:00:42,310 --> 00:00:40,000
the main ocean worlds that i study which

13
00:00:44,389 --> 00:00:42,320

i'll use as an example

14
00:00:47,590 --> 00:00:44,399
ocean worlds and our solar system

15
00:00:49,750 --> 00:00:47,600
have thick and icy exteriors with

16
00:00:51,430 --> 00:00:49,760
liquid water below

17
00:00:53,590 --> 00:00:51,440
this means that sunlight cannot

18
00:00:56,470 --> 00:00:53,600
penetrate to the depths of the liquid

19
00:00:59,110 --> 00:00:56,480
water so survival of life here would be

20
00:01:01,430 --> 00:00:59,120
dependent entirely on chemical energy

21
00:01:06,230 --> 00:01:01,440
just like at hydrothermal vent systems

22
00:01:11,670 --> 00:01:09,350
going a bit deeper into detail enceladus

23
00:01:13,590 --> 00:01:11,680
has a chondritic core which means that

24
00:01:15,910 --> 00:01:13,600
it's undifferentiated

25
00:01:17,190 --> 00:01:15,920
it's covered in two to sixty kilometers

26
00:01:19,270 --> 00:01:17,200
of ice

27
00:01:21,670 --> 00:01:19,280
there are no plate tectonics but the

28
00:01:23,350 --> 00:01:21,680
water beneath the ice is heated by tidal

29
00:01:28,469 --> 00:01:23,360
deformation

30
00:01:31,429 --> 00:01:28,479
circulation of this water

31
00:01:34,630 --> 00:01:31,439
or flow which is key for rock water

32
00:01:37,109 --> 00:01:34,640
interactions that create energy for life

33
00:01:39,429 --> 00:01:37,119
this water and accompanying compounds

34
00:01:41,910 --> 00:01:39,439
are released as plumes in the south

35
00:01:43,670 --> 00:01:41,920
polar region of enceladus

36
00:01:45,350 --> 00:01:43,680
where the cassini probe

37
00:01:47,990 --> 00:01:45,360
detected that the plume contains

38
00:01:49,670 --> 00:01:48,000

chemicals that microbes here on earth

39
00:01:54,870 --> 00:01:49,680
use for their metabolisms at

40
00:02:01,510 --> 00:01:58,230
so a key question that we kind of were

41
00:02:03,590 --> 00:02:01,520
investigating is how is axial seamount

42
00:02:10,790 --> 00:02:03,600
our hydrothermal vent study site and

43
00:02:16,470 --> 00:02:14,070
first deep sea hydrothermal vent systems

44
00:02:17,990 --> 00:02:16,480
are where heated water flows through

45
00:02:20,390 --> 00:02:18,000
crustal rocks

46
00:02:22,630 --> 00:02:20,400
this process alters the composition of

47
00:02:24,390 --> 00:02:22,640
both the fluid and the rocks it flows

48
00:02:26,070 --> 00:02:24,400
through creating a chemical

49
00:02:28,229 --> 00:02:26,080
disequilibrium

50
00:02:30,229 --> 00:02:28,239
that provides impetus for chemical

51
00:02:32,710 --> 00:02:30,239
reactions to occur

52
00:02:35,030 --> 00:02:32,720
life at these depths without sunlight

53
00:02:36,550 --> 00:02:35,040
like ocean worlds can capitalize on

54
00:02:43,589 --> 00:02:36,560
these reactions to power their

55
00:02:48,630 --> 00:02:45,910
in our lab we specifically focus on

56
00:02:50,869 --> 00:02:48,640
sampling diffusely flowing vents

57
00:02:52,470 --> 00:02:50,879
they are a mix of vent fluids and sea

58
00:02:55,430 --> 00:02:52,480
water at

59
00:02:57,030 --> 00:02:55,440
less than 120 degrees celsius so much

60
00:02:59,910 --> 00:02:57,040
lower in temperature than the black

61
00:03:01,750 --> 00:02:59,920
smoker you can see in the picture there

62
00:03:04,710 --> 00:03:01,760
they are the largest source of new

63
00:03:08,710 --> 00:03:04,720

carbon in the vent ecosystem containing

64
00:03:11,030 --> 00:03:08,720
5 to 10 times more cells than deep water

65
00:03:12,869 --> 00:03:11,040
and holding microbial assemblages at the

66
00:03:15,270 --> 00:03:12,879
crustal interface

67
00:03:18,229 --> 00:03:15,280
thus by sampling the water from these

68
00:03:25,430 --> 00:03:18,239
vents we also get a window into life

69
00:03:31,589 --> 00:03:28,309
our study site axial seamount is a

70
00:03:35,430 --> 00:03:31,599
hydrothermal sea mount situated on top

71
00:03:37,430 --> 00:03:35,440
of the juan de fuca ridge spreading axis

72
00:03:40,390 --> 00:03:37,440
the three diffuse fence sites of

73
00:03:44,390 --> 00:03:40,400
interest within axial were anemone

74
00:03:46,789 --> 00:03:44,400
marker 33 and marker 113.

75
00:03:50,229 --> 00:03:46,799
each of these sites was sampled each

76
00:03:52,630 --> 00:03:50,239
year from 2013 to 2015.

77
00:03:55,110 --> 00:03:52,640
this gave us the opportunity to conduct

78
00:04:01,830 --> 00:03:55,120
not only spatial analyses but also

79
00:04:04,949 --> 00:04:03,910
from the different chemical measurements

80
00:04:10,789 --> 00:04:04,959
of

81
00:04:12,630 --> 00:04:10,799
see that the vents are similar in both

82
00:04:14,949 --> 00:04:12,640
temperature and ph

83
00:04:17,349 --> 00:04:14,959
the largest difference is seen with the

84
00:04:20,229 --> 00:04:17,359
hydrogen concentration which is much

85
00:04:23,270 --> 00:04:20,239
higher at anemone and below the limit of

86
00:04:25,350 --> 00:04:23,280
detection at macro 113

87
00:04:27,590 --> 00:04:25,360
we'll see later that this is because

88
00:04:29,590 --> 00:04:27,600

there are a large number of methanogens

89
00:04:32,629 --> 00:04:29,600
at marker 113

90
00:04:34,790 --> 00:04:32,639
which draws down the hydrogen level and

91
00:04:36,469 --> 00:04:34,800
increases the methane

92
00:04:37,510 --> 00:04:36,479
which you can also see in the table

93
00:04:41,030 --> 00:04:37,520
there

94
00:04:43,590 --> 00:04:41,040
the oxygen at marker 113 is half the

95
00:04:45,749 --> 00:04:43,600
concentration of the other vents

96
00:04:46,950 --> 00:04:45,759
and the lowest measured across all vents

97
00:04:48,950 --> 00:04:46,960
sampled

98
00:04:50,629 --> 00:04:48,960
i've highlighted hydrogen and methane

99
00:04:53,270 --> 00:04:50,639
again as a reminder that both of these

100
00:04:56,710 --> 00:04:53,280
compounds were detected by the cassini

101
00:04:59,430 --> 00:04:56,720
probe in the enceladus plume so

102
00:05:01,590 --> 00:04:59,440
a lot of studies now focus on studying

103
00:05:03,350 --> 00:05:01,600
methanogens which use hydrogen and

104
00:05:07,909 --> 00:05:03,360
carbon dioxide

105
00:05:12,469 --> 00:05:10,230
in this cross your study a combination

106
00:05:14,870 --> 00:05:12,479
of approaches was used to determine the

107
00:05:17,830 --> 00:05:14,880
active sub-seafloor autotrophs over

108
00:05:20,870 --> 00:05:17,840
space time and geochemical gradients and

109
00:05:23,110 --> 00:05:20,880
i am currently still analyzing that data

110
00:05:25,830 --> 00:05:23,120
metagenomics was used to understand the

111
00:05:28,189 --> 00:05:25,840
potential functions and taxonomy in the

112
00:05:30,629 --> 00:05:28,199
sampled populations

113
00:05:32,629 --> 00:05:30,639

metatranscriptomics was used to identify

114
00:05:34,230 --> 00:05:32,639
active functions within the sampled

115
00:05:36,150 --> 00:05:34,240
population

116
00:05:37,590 --> 00:05:36,160
to further tease out the autotrophic

117
00:05:40,790 --> 00:05:37,600
signal

118
00:05:43,189 --> 00:05:40,800
rna stable isotope probing was used

119
00:05:46,390 --> 00:05:43,199
in this experimental technique

120
00:05:49,230 --> 00:05:46,400
isotopic incubations label only active

121
00:05:51,590 --> 00:05:49,240
autotrophs in the sample then further

122
00:05:53,510 --> 00:05:51,600
metatranscriptomic sequencing allows us

123
00:05:56,390 --> 00:05:53,520
to determine the identity of those

124
00:05:58,870 --> 00:05:56,400
members of the microbial population

125
00:06:01,990 --> 00:05:58,880
the goal is to construct full metabolic

126
00:06:03,990 --> 00:06:02,000
and functional profiles at all sites in

127
00:06:06,309 --> 00:06:04,000
the next few slides i'll go into detail

128
00:06:10,390 --> 00:06:06,319
about how rna stable isotope probing

129
00:06:12,870 --> 00:06:10,400
works and why it is such a powerful tool

130
00:06:15,029 --> 00:06:12,880
rna stable isotope probing

131
00:06:17,189 --> 00:06:15,039
starts with an incubation of vent fluid

132
00:06:19,590 --> 00:06:17,199
which you can see in the upper right

133
00:06:22,629 --> 00:06:19,600
along with a labeled substrate in this

134
00:06:24,230 --> 00:06:22,639
case we use 12 or 13c labeled

135
00:06:26,950 --> 00:06:24,240
bicarbonate

136
00:06:28,870 --> 00:06:26,960
the controls and experiment are labeled

137
00:06:30,710 --> 00:06:28,880
at different temperatures and we use

138
00:06:33,350 --> 00:06:30,720

three different incubation temperatures

139
00:06:36,870 --> 00:06:33,360
30 55 and 80.

140
00:06:40,230 --> 00:06:36,880
then the rna is extracted quantified and

141
00:06:41,029 --> 00:06:40,240
fractionated using an ultracentrifuge

142
00:06:43,430 --> 00:06:41,039
and

143
00:06:45,430 --> 00:06:43,440
in the ultracentrifuge tube after

144
00:06:48,790 --> 00:06:45,440
spinning it for three days

145
00:06:50,790 --> 00:06:48,800
the heavier fractions are at the bottom

146
00:06:53,670 --> 00:06:50,800
which are the microbial populations that

147
00:06:55,830 --> 00:06:53,680
took up the 13c label and the lighter

148
00:06:57,589 --> 00:06:55,840
ones are at the top which are not the

149
00:07:00,070 --> 00:06:57,599
active autotrophs

150
00:07:02,150 --> 00:07:00,080
12 to 16 fractions are collected and

151
00:07:03,510 --> 00:07:02,160
then the rna is precipitated and

152
00:07:05,510 --> 00:07:03,520
quantified

153
00:07:07,270 --> 00:07:05,520
graphs like that shown on the bottom

154
00:07:08,589 --> 00:07:07,280
left are made to understand which

155
00:07:10,710 --> 00:07:08,599
fractions to take through

156
00:07:14,830 --> 00:07:10,720
metatranscriptome sequencing which we'll

157
00:07:20,469 --> 00:07:17,909
slide from the density fractionation and

158
00:07:22,870 --> 00:07:20,479
subsequent rna precipitation we create

159
00:07:26,469 --> 00:07:22,880
these graphs the green line shows the

160
00:07:29,830 --> 00:07:26,479
control with the 12c labeled bicarbonate

161
00:07:32,870 --> 00:07:29,840
and 12l means that it's light in in the

162
00:07:34,870 --> 00:07:32,880
12c labeled bicarbonate

163
00:07:38,230 --> 00:07:34,880

the orange line shows the result of the

164
00:07:41,270 --> 00:07:38,240
13c incubation and the 13h means that

165
00:07:43,029 --> 00:07:41,280
it's heavy in the 13c label

166
00:07:45,990 --> 00:07:43,039
and as you can see the peak buoyant

167
00:07:50,230 --> 00:07:46,000
density is shifted as compared to the

168
00:07:52,550 --> 00:07:50,240
control in this orange line from 1.78 to

169
00:07:53,430 --> 00:07:52,560
around 1.81

170
00:07:55,589 --> 00:07:53,440
so

171
00:07:58,550 --> 00:07:55,599
we then sequence the metatranscriptome

172
00:08:00,950 --> 00:07:58,560
of the 13c heavy fraction to identify

173
00:08:03,670 --> 00:08:00,960
the active autotrophs which are those

174
00:08:07,990 --> 00:08:03,680
which took up the labeled 13c

175
00:08:15,029 --> 00:08:11,670
so now i created these graphs

176
00:08:17,189 --> 00:08:15,039
to compare results over space time and

177
00:08:18,869 --> 00:08:17,199
different geochemical gradients

178
00:08:19,830 --> 00:08:18,879
so this one

179
00:08:21,749 --> 00:08:19,840
is

180
00:08:23,830 --> 00:08:21,759
over space

181
00:08:26,469 --> 00:08:23,840
across all three vent sites at a single

182
00:08:29,749 --> 00:08:26,479
temperature of 80 degrees c

183
00:08:32,149 --> 00:08:29,759
during the year 2013.

184
00:08:33,990 --> 00:08:32,159
marker 113

185
00:08:36,389 --> 00:08:34,000
which is in the middle is heavily

186
00:08:39,350 --> 00:08:36,399
dominated by methanocaldococcus which is

187
00:08:42,310 --> 00:08:39,360
a methanogen and which is why earlier

188
00:08:45,509 --> 00:08:42,320

when i showed the drawdown of h2 and the

189
00:08:48,870 --> 00:08:45,519
increase in methane it's due to this

190
00:08:51,350 --> 00:08:48,880
domination of this methanogen

191
00:08:52,870 --> 00:08:51,360
marker 33 has feud to none

192
00:08:55,990 --> 00:08:52,880
methanocaldococcus

193
00:08:58,470 --> 00:08:56,000
likewise thermo vibrio is present at

194
00:09:00,949 --> 00:08:58,480
marker 33 and anemone

195
00:09:04,150 --> 00:09:00,959
but does not appear at all in marker

196
00:09:09,190 --> 00:09:06,150
so next i compared

197
00:09:11,670 --> 00:09:09,200
rna sip results again over space however

198
00:09:15,509 --> 00:09:11,680
this time it was for adc so the same

199
00:09:18,150 --> 00:09:15,519
temperature as before during 2014. this

200
00:09:20,389 --> 00:09:18,160
allows us to compare across both space

201
00:09:23,670 --> 00:09:20,399
and time because we can compare it to

202
00:09:26,150 --> 00:09:23,680
the 2013 results as well

203
00:09:29,430 --> 00:09:26,160
first all of the methanocaldococcus we

204
00:09:31,190 --> 00:09:29,440
saw at marker 113 is gone again which is

205
00:09:32,870 --> 00:09:31,200
it's in the middle

206
00:09:35,190 --> 00:09:32,880
um the middle bar

207
00:09:37,990 --> 00:09:35,200
now all three event sites have a similar

208
00:09:40,790 --> 00:09:38,000
composition of d sulfurobacterium

209
00:09:43,310 --> 00:09:40,800
thermovibrio and an unclassified member

210
00:09:45,030 --> 00:09:43,320
of the family

211
00:09:47,190 --> 00:09:45,040
d-sulfurobacteriaceae

212
00:09:49,509 --> 00:09:47,200
this shows that hydrothermal vents can

213
00:09:52,230 --> 00:09:49,519

vary quite a lot in their microbial

214
00:09:53,910 --> 00:09:52,240
community composition in just one year

215
00:09:56,389 --> 00:09:53,920
this should be kept in mind when we

216
00:09:58,630 --> 00:09:56,399
capture snapshots of the geochemical

217
00:10:00,790 --> 00:09:58,640
composition of hydrothermal vents on

218
00:10:02,630 --> 00:10:00,800
other ocean worlds just because we

219
00:10:04,790 --> 00:10:02,640
measure something once doesn't mean it

220
00:10:07,910 --> 00:10:04,800
can't change drastically in a very short

221
00:10:14,069 --> 00:10:11,110
next i looked across time

222
00:10:17,430 --> 00:10:14,079
at one vent site marker 113 and at one

223
00:10:19,470 --> 00:10:17,440
temperature of 55 degrees celsius unlike

224
00:10:21,829 --> 00:10:19,480
at 80 degrees celsius where we saw

225
00:10:24,150 --> 00:10:21,839
methanocaldocus one year and did not

226
00:10:26,150 --> 00:10:24,160
seed in the next here the microbial

227
00:10:28,389 --> 00:10:26,160
community composition remains fairly

228
00:10:31,590 --> 00:10:28,399
constant over the two years with a

229
00:10:35,590 --> 00:10:31,600
slight decrease in diversity in 2014 as

230
00:10:41,590 --> 00:10:38,470
finally i looked across temperature at

231
00:10:44,150 --> 00:10:41,600
anemone event site in 2014. the

232
00:10:46,230 --> 00:10:44,160
rightmost bar represents the entire meta

233
00:10:49,590 --> 00:10:46,240
transcriptome at this site which you can

234
00:10:51,829 --> 00:10:49,600
see contains many many members however

235
00:10:53,829 --> 00:10:51,839
at each temperature we see not only a

236
00:10:56,630 --> 00:10:53,839
distillation of the members in this meta

237
00:10:59,350 --> 00:10:56,640
transcriptome but also that just a few

238
00:11:01,269 --> 00:10:59,360

families dominate at each temperature

239
00:11:03,030 --> 00:11:01,279
i did not show it by genus this time

240
00:11:05,350 --> 00:11:03,040
since the meta transcriptome becomes

241
00:11:08,550 --> 00:11:05,360
even harder to distinguish

242
00:11:11,829 --> 00:11:08,560
at 30 and 55 degrees c members of the

243
00:11:14,790 --> 00:11:11,839
family natalie aca dominate where as

244
00:11:17,750 --> 00:11:14,800
they are absent at adc

245
00:11:20,389 --> 00:11:17,760
at adc we see members of the diesel

246
00:11:24,069 --> 00:11:20,399
feral bacteriaceae and aquificacia

247
00:11:29,030 --> 00:11:26,710
the key takeaway from this talk is that

248
00:11:31,350 --> 00:11:29,040
both axial and enceladus or other ocean

249
00:11:33,350 --> 00:11:31,360
worlds have similar environments lack of

250
00:11:35,910 --> 00:11:33,360
light rock water interactions at

251
00:11:38,310 --> 00:11:35,920
hydrothermal vents chemical energy for

252
00:11:40,630 --> 00:11:38,320
life and similar temperatures with this

253
00:11:42,949 --> 00:11:40,640
study we were able to create profiles of

254
00:11:45,269 --> 00:11:42,959
active autotrophs at variable chemical

255
00:11:47,509 --> 00:11:45,279
regimes which lends us predictive power

256
00:11:49,509 --> 00:11:47,519
of what autotrophs would exist in a

257
00:11:50,870 --> 00:11:49,519
given environmental regime on other

258
00:11:53,269 --> 00:11:50,880
ocean worlds

259
00:11:55,190 --> 00:11:53,279
this will help inform efforts to

260
00:11:56,389 --> 00:11:55,200
understand and detect life on other