
AbSciCon
2019

1
00:00:00,790 --> 00:00:07,320
[Music]

2
00:00:11,900 --> 00:00:09,100
[Applause]

3
00:00:13,270 --> 00:00:11,910
thank you everyone for coming to the

4
00:00:17,750 --> 00:00:13,280
talk and thank you to the organizers for

5
00:00:19,519 --> 00:00:17,760
give me an opportunity to speak the work

6
00:00:21,290 --> 00:00:19,529
that I'm going to be presenting is the

7
00:00:23,630 --> 00:00:21,300
result of collaboration with several

8
00:00:25,069 --> 00:00:23,640
different people all listed here and in

9
00:00:25,880 --> 00:00:25,079
particular I'd like to highlight Lucy

10
00:00:28,190 --> 00:00:25,890
Stewart

11
00:00:30,710 --> 00:00:28,200
Shrishti Kasia and big iam top Xu Alou

12
00:00:32,479 --> 00:00:30,720
who were former and current PhD students

13
00:00:35,240 --> 00:00:32,489

in my lab who did this work as well as

14
00:00:38,389 --> 00:00:35,250
some of my co p is julie huber from

15
00:00:40,730 --> 00:00:38,399
Woods Hole Oceanographic Darby Dyer from

16
00:00:41,960 --> 00:00:40,740
Mount Holyoke College and Susan Lang

17
00:00:45,080 --> 00:00:41,970
from the University of South Carolina

18
00:00:48,500 --> 00:00:45,090
the work was funded by the Gordon Betty

19
00:00:49,430 --> 00:00:48,510
Moore Foundation and by NASA and a lot

20
00:00:52,400 --> 00:00:49,440
of the work that I going to be showing

21
00:00:54,380 --> 00:00:52,410
is was published just within the last

22
00:00:56,780 --> 00:00:54,390
year and if you're interested in it

23
00:01:01,490 --> 00:00:56,790
since it's cited in the psyche on

24
00:01:05,840 --> 00:01:01,500
abstract alright so we have a rover on

25
00:01:08,420 --> 00:01:05,850
Mars and we have our Ovie's and a UVs in

26
00:01:09,560 --> 00:01:08,430
the deep ocean that are searching for

27
00:01:12,169 --> 00:01:09,570
life and trying to figure out what that

28
00:01:15,099 --> 00:01:12,179
life is doing and soon we'll have robots

29
00:01:18,859 --> 00:01:15,109
and ocean worlds in our solar system and

30
00:01:20,209 --> 00:01:18,869
it's not a big I don't need to work hard

31
00:01:21,919 --> 00:01:20,219
to convince you all that we need both

32
00:01:23,539 --> 00:01:21,929
modeling and detection in order to be

33
00:01:25,399 --> 00:01:23,549
able to determine where that life is and

34
00:01:27,050 --> 00:01:25,409
what that life is doing but what I've

35
00:01:29,480 --> 00:01:27,060
been asking myself and what I wanted to

36
00:01:31,129 --> 00:01:29,490
talk about in this presentation is how

37
00:01:32,899 --> 00:01:31,139
can we better integrate these two what

38
00:01:34,370 --> 00:01:32,909

can I do in my lab and what can we do as

39
00:01:36,440 --> 00:01:34,380
a community to try and bring these two

40
00:01:40,090 --> 00:01:36,450
things closer together

41
00:01:44,080 --> 00:01:40,100
so that's what I wanted to to talk about

42
00:01:46,730 --> 00:01:44,090
so first of all in the area of modeling

43
00:01:49,399 --> 00:01:46,740
I've been working with Lucy Stewart

44
00:01:51,849 --> 00:01:49,409
Chris augur Caroline fortunado Julie

45
00:01:54,529 --> 00:01:51,859
Huber and others to develop

46
00:01:56,599 --> 00:01:54,539
methanogenesis reactive transport model

47
00:01:59,209 --> 00:01:56,609
and the questions that we're trying to

48
00:02:01,309 --> 00:01:59,219
determine is for an individual event how

49
00:02:02,929 --> 00:02:01,319
many methanogens aren't there needed to

50
00:02:05,989 --> 00:02:02,939
be at that vente creates a the methane

51
00:02:07,639 --> 00:02:05,999
anomalies that we see what's the volume

52
00:02:09,469 --> 00:02:07,649
of rock that's occupied by these

53
00:02:12,640 --> 00:02:09,479
methanogens how deep is the biosphere

54
00:02:16,050 --> 00:02:12,650
and what's the residence time of the

55
00:02:18,190 --> 00:02:16,060
so what we've done is we've developed a

56
00:02:20,819 --> 00:02:18,200
one-dimensional pipe flow reactive

57
00:02:23,679 --> 00:02:20,829
transport model with a series of boxes

58
00:02:25,660 --> 00:02:23,689
350-degree hydrothermal fluid flowing

59
00:02:27,250 --> 00:02:25,670
through the boxes and each box you have

60
00:02:28,509 --> 00:02:27,260
a little bit of dilution of seawater and

61
00:02:30,580 --> 00:02:28,519
then once the temperature permits

62
00:02:33,160 --> 00:02:30,590
methanogens can then grow in the box

63
00:02:35,800 --> 00:02:33,170

before the fluid flows to the next one

64
00:02:37,360 --> 00:02:35,810
we also can vary the size of the box so

65
00:02:41,649 --> 00:02:37,370
that we can vary the residence time of

66
00:02:44,830 --> 00:02:41,659
the fluid through the box the the model

67
00:02:47,500 --> 00:02:44,840
is informed by chemostat work that was

68
00:02:49,990 --> 00:02:47,510
done in my lab using both a thermophilic

69
00:02:52,990 --> 00:02:50,000
and a hyperthermophilic methanogens and

70
00:02:55,800 --> 00:02:53,000
we got we determined hydrogen monoid

71
00:02:58,479 --> 00:02:55,810
kinetics for methane production and

72
00:03:00,580 --> 00:02:58,489
Arrhenius kinetics for temperature

73
00:03:03,039 --> 00:03:00,590
effects for each of these organisms to

74
00:03:06,789 --> 00:03:03,049
be able to to put plug into this model

75
00:03:08,500 --> 00:03:06,799
what we found is is that if the pipe is

76
00:03:10,270 --> 00:03:08,510
straight in other words if residence

77
00:03:13,300 --> 00:03:10,280
time remains more or less constant with

78
00:03:15,309 --> 00:03:13,310
fluid flow is that the hyperthermophilic

79
00:03:16,960 --> 00:03:15,319
methanogens dominate the system they get

80
00:03:18,490 --> 00:03:16,970
at the method the hydrogen first and

81
00:03:20,289 --> 00:03:18,500
they consume it all before the thermal

82
00:03:24,550 --> 00:03:20,299
files really have an opportunity to be

83
00:03:26,710 --> 00:03:24,560
able to use that however if the pipe is

84
00:03:29,949 --> 00:03:26,720
more flanged in residence time increases

85
00:03:31,360 --> 00:03:29,959
with flow rate or with flow then what'll

86
00:03:33,490 --> 00:03:31,370
happen is that this gives an opportunity

87
00:03:35,309 --> 00:03:33,500
for the thermal files to be able to to

88
00:03:39,610 --> 00:03:35,319

dominate the system over

89
00:03:42,659 --> 00:03:39,620
hyperthermophiles so we wanted to

90
00:03:45,219 --> 00:03:42,669
actually test this model and we went to

91
00:03:47,020 --> 00:03:45,229
axial seamount off the coast of Oregon

92
00:03:49,300 --> 00:03:47,030
and looked at two different hydrothermal

93
00:03:50,920 --> 00:03:49,310
vents and first two columns you can see

94
00:03:52,809 --> 00:03:50,930
hydrogen and methane data that was

95
00:03:55,300 --> 00:03:52,819
collected by Dave Butterfield and in

96
00:03:56,830 --> 00:03:55,310
this column here you can see a cell

97
00:03:58,509 --> 00:03:56,840
count estimates for the two different

98
00:04:02,229 --> 00:03:58,519
antigens that's based on meta genomic

99
00:04:04,059 --> 00:04:02,239
work that Julie Huber's lab did and fit

100
00:04:05,589 --> 00:04:04,069
the model to it the black line

101
00:04:07,240 --> 00:04:05,599
represents the model these circles

102
00:04:09,429 --> 00:04:07,250
represent the data that what we actually

103
00:04:12,189 --> 00:04:09,439
measured and in these figures imagine

104
00:04:14,679 --> 00:04:12,199
that the 350-degree fluid is rising up

105
00:04:16,839 --> 00:04:14,689
and is getting diluted this is magnesium

106
00:04:18,460 --> 00:04:16,849
concentration here on the side but the

107
00:04:20,469 --> 00:04:18,470
the fluid is rising up cooling and

108
00:04:21,629 --> 00:04:20,479
mixing is it as you go up towards the

109
00:04:23,360 --> 00:04:21,639
top

110
00:04:26,249 --> 00:04:23,370
and the model did a pretty good job it

111
00:04:29,070 --> 00:04:26,259
you can see hydrogen consumption here

112
00:04:31,320 --> 00:04:29,080
methane production here and in this

113
00:04:33,360 --> 00:04:31,330

particular system a marker 33 there are

114
00:04:35,670 --> 00:04:33,370
more hyperthermophilic methanogens so

115
00:04:37,740 --> 00:04:35,680
that suggests that the pipe flow at the

116
00:04:40,379 --> 00:04:37,750
particular vent is more straight that

117
00:04:43,350 --> 00:04:40,389
residence time into each box is more or

118
00:04:45,749 --> 00:04:43,360
less constant whereas at marker 113

119
00:04:47,100 --> 00:04:45,759
there are far more thermophilic

120
00:04:48,899 --> 00:04:47,110
methanogens than hyperthermophilic

121
00:04:51,510 --> 00:04:48,909
methanogens and that again suggests that

122
00:04:52,980 --> 00:04:51,520
perhaps as fluid flows the residence

123
00:04:55,649 --> 00:04:52,990
time at each temperature gets longer and

124
00:04:56,730 --> 00:04:55,659
longer some of the things we're able to

125
00:04:58,350 --> 00:04:56,740
determine from this is that there's only

126
00:05:00,540 --> 00:04:58,360
about 10 to the 11th methanogens that

127
00:05:02,249 --> 00:05:00,550
are necessary each vent to be able to

128
00:05:04,140 --> 00:05:02,259
create the methane anomaly that we saw

129
00:05:06,269 --> 00:05:04,150
that was a surprise we thought that was

130
00:05:08,399 --> 00:05:06,279
gonna be much higher than it really was

131
00:05:10,379 --> 00:05:08,409
the residence time of myth antigen

132
00:05:13,740 --> 00:05:10,389
growth temperatures was about 29 to 33

133
00:05:15,450 --> 00:05:13,750
hours only about 2 to 18 cubic meters of

134
00:05:18,629 --> 00:05:15,460
sea floor was occupied depending upon

135
00:05:20,820 --> 00:05:18,639
the porosity of the rock and the

136
00:05:25,019 --> 00:05:20,830
biosphere is we think there's only about

137
00:05:26,730 --> 00:05:25,029
2 to 30 meters deep moving forward we

138
00:05:28,769 --> 00:05:26,740

need to put more metabolic diversity

139
00:05:29,820 --> 00:05:28,779
into these types of reactive transport

140
00:05:33,089 --> 00:05:29,830
models is something that we're working

141
00:05:35,309 --> 00:05:33,099
on now and also we need to put more

142
00:05:40,529 --> 00:05:35,319
ecological theory into these into these

143
00:05:42,659 --> 00:05:40,539
models we're also in terms of the actual

144
00:05:44,550 --> 00:05:42,669
detection part of it we looked at

145
00:05:47,249 --> 00:05:44,560
methane fractionation so I work with big

146
00:05:51,300 --> 00:05:47,259
um top CEO Lou Tran new en susan lying

147
00:05:54,079 --> 00:05:51,310
and others to look at the methane carbon

148
00:05:57,329 --> 00:05:54,089
fractionation that occurs in a pure

149
00:05:58,559 --> 00:05:57,339
hyperthermophilic myth antigen and we

150
00:06:00,420 --> 00:05:58,569
varied the flux rate again in a

151
00:06:01,980 --> 00:06:00,430
chemostat to see how the organism grew

152
00:06:03,570 --> 00:06:01,990
what gene how gene expression changed

153
00:06:06,629 --> 00:06:03,580
and how carbon fractionation changed

154
00:06:08,010 --> 00:06:06,639
when hydrogen flux was high what would

155
00:06:10,019 --> 00:06:08,020
happen is the carbon would flow through

156
00:06:11,990 --> 00:06:10,029
the wood young-dal pathway and you'd see

157
00:06:14,820 --> 00:06:12,000
more methane and more energy produced

158
00:06:17,159 --> 00:06:14,830
and in that particular situation carbon

159
00:06:19,559 --> 00:06:17,169
fractionation was relatively low about

160
00:06:23,159 --> 00:06:19,569
an epsilon of about 29 part 1000

161
00:06:25,800 --> 00:06:23,169
however when hydrogen flux rate was low

162
00:06:27,360 --> 00:06:25,810
the carbon would actually flow more into

163
00:06:28,700 --> 00:06:27,370

biosynthesis so there'd be a much higher

164
00:06:31,870 --> 00:06:28,710
cell yield

165
00:06:33,950 --> 00:06:31,880
and also carbon fractionation increased

166
00:06:37,970 --> 00:06:33,960
significantly the epsilon would grow to

167
00:06:40,550 --> 00:06:37,980
about 70 to 85 per thousand and axial

168
00:06:42,200 --> 00:06:40,560
cement which I just told you about the

169
00:06:43,970 --> 00:06:42,210
carbon fractionation we think is pretty

170
00:06:45,650 --> 00:06:43,980
low so that actually fits the model that

171
00:06:47,390 --> 00:06:45,660
we think that there's probably a high

172
00:06:50,470 --> 00:06:47,400
flux of hydrogen that's beating the

173
00:06:53,750 --> 00:06:50,480
methanogens in that in that system

174
00:06:55,190 --> 00:06:53,760
moving forward we need to do more in

175
00:06:56,690 --> 00:06:55,200
terms of understanding carbon use

176
00:06:58,460 --> 00:06:56,700
efficiency for a variety of different

177
00:07:01,700 --> 00:06:58,470
organisms how that might vary with

178
00:07:03,770 --> 00:07:01,710
change in nutrient availability and also

179
00:07:05,150 --> 00:07:03,780
we need to work on a more biomarker

180
00:07:06,890 --> 00:07:05,160
information what does carbon

181
00:07:12,590 --> 00:07:06,900
fractionation look like and say lipids

182
00:07:14,240 --> 00:07:12,600
and proteins so also in the area of

183
00:07:16,040 --> 00:07:14,250
detection moving beyond with antigens

184
00:07:20,630 --> 00:07:16,050
were interested in what happens with

185
00:07:23,390 --> 00:07:20,640
minerals and could minerals provide say

186
00:07:26,000 --> 00:07:23,400
a different type of bio signature so I

187
00:07:28,490 --> 00:07:26,010
work with Shrishti Kashyap Eli Skloot

188
00:07:31,430 --> 00:07:28,500

and darvid Iyer and others to synthesize

189
00:07:33,290 --> 00:07:31,440
six different nano phase iron oxides

190
00:07:35,750 --> 00:07:33,300
that you see listed here and we worked

191
00:07:38,630 --> 00:07:35,760
with two hyperthermophilic iron reducers

192
00:07:41,270 --> 00:07:38,640
and Pyrrha dictum Delaney I and Pyrrha

193
00:07:43,240 --> 00:07:41,280
baculum Icelandic ohm that grow on iron

194
00:07:46,490 --> 00:07:43,250
oxide they reduced the iron oxides and

195
00:07:48,500 --> 00:07:46,500
what we found was that the organisms

196
00:07:51,020 --> 00:07:48,510
grow best on Farah hydrate

197
00:07:53,090 --> 00:07:51,030
they grow modestly well on the Pittock

198
00:07:55,280 --> 00:07:53,100
recite and akka gain height and they

199
00:07:59,180 --> 00:07:55,290
grow rather poorly and Meg he might Gert

200
00:08:01,610 --> 00:07:59,190
tight and hematite and that pretty much

201
00:08:03,200 --> 00:08:01,620
fits what we would expect based on the

202
00:08:05,000 --> 00:08:03,210
increasing order of crystallinity and

203
00:08:08,540 --> 00:08:05,010
the thermodynamic stability of the of

204
00:08:10,640 --> 00:08:08,550
the of the minerals themselves and I'd

205
00:08:12,260 --> 00:08:10,650
like to point out too that my PhD

206
00:08:14,030 --> 00:08:12,270
student Trish DK chef will be speaking

207
00:08:17,480 --> 00:08:14,040
in more detail about this particular

208
00:08:19,610 --> 00:08:17,490
project on on Friday and she's soon to

209
00:08:22,549 --> 00:08:19,620
be on the pH on the postdoc market so

210
00:08:27,299 --> 00:08:25,499
so what we would then wanted to do is we

211
00:08:30,479 --> 00:08:27,309
wanted to try and identify what those

212
00:08:33,779 --> 00:08:30,489
minerals are that were formed by these

213
00:08:35,189 --> 00:08:33,789

iron reducers and remember when the

214
00:08:36,990 --> 00:08:35,199
organisms are growing on Farah hydrate

215
00:08:40,139 --> 00:08:37,000
they grew best they had the highest fe2

216
00:08:42,749 --> 00:08:40,149
flux rates production rates and what we

217
00:08:46,949 --> 00:08:42,759
found was is that the we used by the way

218
00:08:48,480 --> 00:08:46,959
a combination of v nir FTIR Ramanand

219
00:08:51,420 --> 00:08:48,490
mossbauer they all pretty much gave us

220
00:08:53,939 --> 00:08:51,430
the same results but the FTIR data is

221
00:08:56,490 --> 00:08:53,949
shown here but when the organisms are

222
00:08:59,030 --> 00:08:56,500
growing on farah hydrate they produced

223
00:09:01,170 --> 00:08:59,040
magnetite was that was their end product

224
00:09:02,939 --> 00:09:01,180
however when the organisms were grown on

225
00:09:04,769 --> 00:09:02,949
the Pittock row site and acting any I

226
00:09:07,860 --> 00:09:04,779
remember this is slower growth rate

227
00:09:10,079 --> 00:09:07,870
slower fe2 production rate the mineral

228
00:09:12,929 --> 00:09:10,089
end product actually changed with

229
00:09:14,790 --> 00:09:12,939
lepetit Pro site they produced an iron

230
00:09:18,119 --> 00:09:14,800
carbonate Sidda right or a Siddha right

231
00:09:20,460 --> 00:09:18,129
like compound mineral and when they were

232
00:09:23,040 --> 00:09:20,470
growing on a Kagami night the end

233
00:09:26,309 --> 00:09:23,050
products were vivvy night which is an

234
00:09:28,319 --> 00:09:26,319
iron phosphate as well as some magnetite

235
00:09:31,139 --> 00:09:28,329
and it's a little hard to tease out in

236
00:09:32,579 --> 00:09:31,149
this picture but I certainly be happy to

237
00:09:35,179 --> 00:09:32,589
talk about in more detail if anybody's

238
00:09:38,100 --> 00:09:35,189

interested in this but we did see some

239
00:09:40,920 --> 00:09:38,110
signals that suggest that perhaps there

240
00:09:42,960 --> 00:09:40,930
is more in some cases a biogenic type of

241
00:09:46,230 --> 00:09:42,970
mineral transformation product compared

242
00:09:47,429 --> 00:09:46,240
to just a biotic li synthesized minerals

243
00:09:52,470 --> 00:09:47,439
but that's something we still are

244
00:09:54,179 --> 00:09:52,480
working on a need to tease out more so

245
00:09:55,619 --> 00:09:54,189
moving forward into the future and

246
00:09:57,449 --> 00:09:55,629
especially the area of detection and

247
00:09:59,730 --> 00:09:57,459
also in the areas of how can we couple

248
00:10:02,189 --> 00:09:59,740
modeling and detection together we are

249
00:10:04,350 --> 00:10:02,199
now in the process of taking pure thermo

250
00:10:06,569 --> 00:10:04,360
files and hyperthermophiles and getting

251
00:10:08,220 --> 00:10:06,579
spectra from them using these four

252
00:10:11,009 --> 00:10:08,230
different spectroscopy techniques this

253
00:10:13,170 --> 00:10:11,019
is FTIR here and these are all

254
00:10:15,090 --> 00:10:13,180
metabolically very different thermo

255
00:10:18,150 --> 00:10:15,100
files and hyperthermophiles and we do

256
00:10:20,910 --> 00:10:18,160
see differences especially in the near

257
00:10:22,230 --> 00:10:20,920
IR and mid IR range we we do see some

258
00:10:24,090 --> 00:10:22,240
differences between these different

259
00:10:25,710 --> 00:10:24,100
organisms so that's very tantalizing for

260
00:10:27,030 --> 00:10:25,720
us and we're hoping we can get to the

261
00:10:29,189 --> 00:10:27,040
point that we might actually be able to

262
00:10:31,799 --> 00:10:29,199
use spectroscopy in a native rock or

263
00:10:33,580 --> 00:10:31,809

even on the seafloor to be able to see

264
00:10:35,380 --> 00:10:33,590
what types of organisms are there

265
00:10:36,790 --> 00:10:35,390
that's that's still a dream so it still

266
00:10:38,440 --> 00:10:36,800
weighs off

267
00:10:41,410 --> 00:10:38,450
we're also interested in hyper spectral

268
00:10:43,330 --> 00:10:41,420
imaging this is a piece of sulphide that

269
00:10:45,280 --> 00:10:43,340
was sitting on my shelf in my office for

270
00:10:47,470 --> 00:10:45,290
ten years and we decided to put it under

271
00:10:50,230 --> 00:10:47,480
a hyper spectral image gaming camera and

272
00:10:52,870 --> 00:10:50,240
about three centimeters across this is

273
00:10:54,210 --> 00:10:52,880
just the RGB image here but what you can

274
00:10:57,000 --> 00:10:54,220
do is you can do a pixel-by-pixel

275
00:11:00,250 --> 00:10:57,010
analysis looking at the spectral

276
00:11:02,530 --> 00:11:00,260
information for each pixel and get a

277
00:11:05,770 --> 00:11:02,540
spectra for each pixel and then map out

278
00:11:07,180 --> 00:11:05,780
where you see similar spectra and this

279
00:11:09,070 --> 00:11:07,190
actually did a fairly decent job of

280
00:11:11,800 --> 00:11:09,080
mapping out where the different minerals

281
00:11:13,300 --> 00:11:11,810
were in this long term what we really

282
00:11:14,650 --> 00:11:13,310
hope you'd be able to do is to be able

283
00:11:16,720 --> 00:11:14,660
to do something like hyper spectral

284
00:11:18,520 --> 00:11:16,730
imaging and to be able to co-locate

285
00:11:20,770 --> 00:11:18,530
different mineral types and different

286
00:11:24,970 --> 00:11:20,780
microbes or Lisa some sort of a biogenic

287
00:11:27,490 --> 00:11:24,980
signal and even maybe be able to do this

288
00:11:29,440 --> 00:11:27,500

not only on fresh collected samples from

289
00:11:32,440 --> 00:11:29,450
the from hydrothermal vents onboard ship

290
00:11:38,320 --> 00:11:32,450
but maybe even one day on the seafloor

291
00:11:40,540 --> 00:11:38,330
itself so take-home message from all

292
00:11:42,130 --> 00:11:40,550
this is that we really need to improve

293
00:11:44,530 --> 00:11:42,140
the iterative process of working between

294
00:11:46,210 --> 00:11:44,540
modeling and detection and these are

295
00:11:48,340 --> 00:11:46,220
fairly obvious reasons but it's worth

296
00:11:49,870 --> 00:11:48,350
saying is in order for us to really be

297
00:11:52,570 --> 00:11:49,880
able to predict where to find life and

298
00:11:54,880 --> 00:11:52,580
what kinds of life we would find also

299
00:11:57,190 --> 00:11:54,890
determining the impact of that life and

300
00:11:59,410 --> 00:11:57,200
really to be able to ground truth the

301
00:12:02,200 --> 00:11:59,420
modeling resume results that we're

302
00:12:09,710 --> 00:12:02,210
generating so thank you very much and

303
00:12:21,330 --> 00:12:18,900
of time for questions hi Aaron Noel from

304
00:12:24,660 --> 00:12:21,340
JPL really nice talk thank you did you

305
00:12:27,360 --> 00:12:24,670
all ever do any sort of chemical

306
00:12:33,120 --> 00:12:27,370
analysis besides genomic work do you

307
00:12:35,760 --> 00:12:33,130
look for other biomarkers so we have

308
00:12:37,230 --> 00:12:35,770
done a little bit looking at the methane

309
00:12:42,450 --> 00:12:37,240
and the carbon fractionation that's

310
00:12:44,490 --> 00:12:42,460
there and we haven't done any lipid

311
00:12:46,530 --> 00:12:44,500
analysis or proteins in terms of like

312
00:12:48,360 --> 00:12:46,540
extracting that and looking directly at

313
00:12:50,250 --> 00:12:48,370

that but that's something that we hope

314
00:12:52,320 --> 00:12:50,260
to get into doing more especially if we

315
00:12:53,970 --> 00:12:52,330
can do some analysis on the carbon

316
00:12:55,620 --> 00:12:53,980
fractionation that actually occurs in

317
00:12:56,640 --> 00:12:55,630
the lipids or at the protein level so

318
00:12:58,740 --> 00:12:56,650
that's one of the areas that we're

319
00:13:10,380 --> 00:12:58,750
trying to move into in the future great

320
00:13:14,710 --> 00:13:12,640
hi John how do you know thank you for

321
00:13:16,240 --> 00:13:14,720
the talk I was wondering in your pure

322
00:13:18,580 --> 00:13:16,250
culture experiments with those mineral

323
00:13:20,260 --> 00:13:18,590
phases did you notice any variation in

324
00:13:25,270 --> 00:13:20,270
the mineral end product if you changed

325
00:13:27,390 --> 00:13:25,280
up the electron donor we haven't tried

326
00:13:31,090 --> 00:13:27,400
that but it's a great question

327
00:13:33,160 --> 00:13:31,100
especially for the pyro baculum species

328
00:13:37,630 --> 00:13:33,170
it's a facultative autotroph so we've

329
00:13:41,530 --> 00:13:37,640
grown it with organics but we'd love to

330
00:13:43,570 --> 00:13:41,540
do it autotrophic ly so who are the the

331
00:13:45,130 --> 00:13:43,580
power addicted species uses hydrogen and

332
00:13:46,990 --> 00:13:45,140
the power vacuum uses organics and we do

333
00:13:47,920 --> 00:13:47,000
see some differences there between the

334
00:13:49,750 --> 00:13:47,930
two we don't know if that's at the

335
00:13:51,720 --> 00:13:49,760
organismal level or how much of it is

336
00:13:53,650 --> 00:13:51,730
because they're using a different

337
00:13:59,050 --> 00:13:53,660
electron donor source but jill has a

338
00:14:00,700 --> 00:13:59,060

great question hi great Paul from

339
00:14:04,570 --> 00:14:00,710
Mississippi State I was curious about

340
00:14:06,400 --> 00:14:04,580
the flange Piper sister straight pipe

341
00:14:08,800 --> 00:14:06,410
was there a difference in the

342
00:14:11,500 --> 00:14:08,810
temperature in the in the straight pipe

343
00:14:13,780 --> 00:14:11,510
versus the flange pipe that could affect

344
00:14:15,580 --> 00:14:13,790
thermophiles being dominant in the

345
00:14:17,560 --> 00:14:15,590
flange five because it broadens how the

346
00:14:19,720 --> 00:14:17,570
temperature drops were able to measure

347
00:14:22,300 --> 00:14:19,730
the temperature difference well you can

348
00:14:24,010 --> 00:14:22,310
see in the modeling in some ways each

349
00:14:25,540 --> 00:14:24,020
step you might expect that there's the

350
00:14:27,850 --> 00:14:25,550
temperature inside the box is saying but

351
00:14:30,400 --> 00:14:27,860
that's really the residence time inside

352
00:14:32,440 --> 00:14:30,410
that box that really has a big impact so

353
00:14:34,060 --> 00:14:32,450
for example if hyperthermophiles spend

354
00:14:35,560 --> 00:14:34,070
very little time in their box before you

355
00:14:37,750 --> 00:14:35,570
move on to the thermal file temperatures

356
00:14:39,520 --> 00:14:37,760
then the thermal files have a chance to

357
00:14:41,620 --> 00:14:39,530
dominate the system but if

358
00:14:43,180 --> 00:14:41,630
hyperthermophiles get therefore get to

359
00:14:44,650 --> 00:14:43,190
them hydrogen first and the residence

360
00:14:47,720 --> 00:14:44,660
time is long enough then they'll

361
00:14:53,389 --> 00:14:51,169
a real quick question I was wondering

362
00:14:55,609 --> 00:14:53,399
what the flow rates you were considering

363
00:14:57,049 --> 00:14:55,619

of in terms of the residence time in

364
00:14:58,849 --> 00:14:57,059
some of your chemistry experiments and

365
00:15:01,939 --> 00:14:58,859
how that would be affected by say a

366
00:15:04,039 --> 00:15:01,949
diffusely flowing system like lost city

367
00:15:05,539 --> 00:15:04,049
for example where you have very low flow

368
00:15:09,259 --> 00:15:05,549
rates and really high thermal diffusion

369
00:15:10,999 --> 00:15:09,269
through the system so we we varied the

370
00:15:12,650 --> 00:15:11,009
the hydrogen concentration of the

371
00:15:14,479 --> 00:15:12,660
hydrogen flow rate into the reactor and

372
00:15:16,069 --> 00:15:14,489
of course as we did that that changed

373
00:15:19,549 --> 00:15:16,079
growth the temperature of the growth

374
00:15:22,669 --> 00:15:19,559
rate and we had to vary the the dilution

375
00:15:25,549 --> 00:15:22,679
rate to match that we did try a couple

376
00:15:27,109 --> 00:15:25,559
different dilution rates for our chemo

377
00:15:29,530 --> 00:15:27,119
stats at any given hydrogen

378
00:15:33,199 --> 00:15:29,540
concentration to see how much dilution

379
00:15:34,789 --> 00:15:33,209
affected the system and we found that at

380
00:15:37,340 --> 00:15:34,799
least statistically there wasn't really

381
00:15:38,599 --> 00:15:37,350
that much difference with change in

382
00:15:40,639 --> 00:15:38,609
dilution rate it really seemed to be

383
00:15:42,470 --> 00:15:40,649
primarily driven by by the hydrogen

384
00:15:44,179 --> 00:15:42,480
concentration but but that is something

385
00:15:45,889 --> 00:15:44,189
that that you have to integrate into the

386
00:15:47,869 --> 00:15:45,899
into chemostat experiment since growth

387
00:15:52,069 --> 00:15:47,879
rate varies as the as the hydrogen flux