
AbSciCon
2017
MESA, ARIZONA

1
00:00:12,250 --> 00:00:06,150
you

2
00:00:16,870 --> 00:00:14,220
[Music]

3
00:00:19,120 --> 00:00:16,880
thank you for coming everyone just a

4
00:00:23,160 --> 00:00:19,130
brief update on the title as you may

5
00:00:27,540 --> 00:00:23,170
have read so I changed the title to

6
00:00:29,859 --> 00:00:27,550
evidence for Institute iron cycling from

7
00:00:31,480 --> 00:00:29,869
focusing just on the let's autotrophs

8
00:00:34,869 --> 00:00:31,490
because I think the iron cycle in

9
00:00:39,460 --> 00:00:34,879
general makes for a more interesting

10
00:00:42,100 --> 00:00:39,470
story in my system so to get everyone

11
00:00:44,680 --> 00:00:42,110
oriented chocolate pots is in

12
00:00:47,100 --> 00:00:44,690
Yellowstone and it's in the northwest

13
00:00:51,790 --> 00:00:47,110

corner right along the given river

14
00:00:54,310 --> 00:00:51,800
denoted by the blue X and here we have a

15
00:00:59,470 --> 00:00:54,320
couple pictures of hot springs we have

16
00:01:02,619 --> 00:00:59,480
the oops there we go so we have the vent

17
00:01:05,469 --> 00:01:02,629
pool up here the flow path and then

18
00:01:07,560 --> 00:01:05,479
chocolate pots is very interesting hot

19
00:01:10,810 --> 00:01:07,570
spring because it's circum neutral pH

20
00:01:13,719 --> 00:01:10,820
mildly thermophilic and contains a high

21
00:01:17,740 --> 00:01:13,729
amount of iron and silica in the spring

22
00:01:19,420 --> 00:01:17,750
water from a biological perspective were

23
00:01:23,649 --> 00:01:19,430
interested environments like this

24
00:01:27,999 --> 00:01:23,659
because of the new and recent

25
00:01:30,730 --> 00:01:28,009
discoveries of certain neutral pH like

26
00:01:33,940 --> 00:01:30,740
environments on Mars and the evidence of

27
00:01:37,330 --> 00:01:33,950
relic hot spring-like features and if

28
00:01:40,480 --> 00:01:37,340
we're able to nail down evidence for

29
00:01:43,840 --> 00:01:40,490
internally cycling iron base metabolisms

30
00:01:46,149 --> 00:01:43,850
in environments like chocolate pots then

31
00:01:50,260 --> 00:01:46,159
this could in theory be applied to some

32
00:01:53,140 --> 00:01:50,270
of these relic features on Mars so we

33
00:01:55,060 --> 00:01:53,150
have two main hypotheses going forward

34
00:01:57,609 --> 00:01:55,070
with this study the first is that there

35
00:02:00,550 --> 00:01:57,619
are native active iron reducing

36
00:02:03,490 --> 00:02:00,560
microorganisms present in the chocolate

37
00:02:06,010 --> 00:02:03,500
pots event and also that there are lipid

38
00:02:08,919 --> 00:02:06,020

atrophic iron oxidizers which are also

39
00:02:12,009 --> 00:02:08,929
actively cycling iron and in addition as

40
00:02:15,970 --> 00:02:12,019
let the autotrophs they are fixing

41
00:02:20,050 --> 00:02:15,980
carbon debt yeah fixing co2 and able to

42
00:02:22,180 --> 00:02:20,060
supplement other sources of carbon for

43
00:02:24,730 --> 00:02:22,190
the heterotrophic community

44
00:02:27,680 --> 00:02:24,740
so backing up a little bit some of our

45
00:02:31,100 --> 00:02:27,690
initial work with materials from

46
00:02:34,449 --> 00:02:31,110
chocolate pots we ran a series of iron

47
00:02:38,510 --> 00:02:34,459
reducing enrichment culture studies and

48
00:02:41,120 --> 00:02:38,520
this is a graph showing the repeated

49
00:02:44,110 --> 00:02:41,130
transfer of these cultures for over four

50
00:02:46,850 --> 00:02:44,120
years and they've been able to sustain a

51
00:02:52,190 --> 00:02:46,860
fairly high level of iron reducing

52
00:02:54,670 --> 00:02:52,200
activity and through both 16s and meta

53
00:02:57,560 --> 00:02:54,680
genomic sequence data we've identified

54
00:03:00,979 --> 00:02:57,570
sequences that are related to known iron

55
00:03:05,380 --> 00:03:00,989
reducing taxa including a Geo vector and

56
00:03:09,050 --> 00:03:05,390
mealy factor moving one step towards

57
00:03:11,330 --> 00:03:09,060
choosing apart the infant we ran another

58
00:03:15,520 --> 00:03:11,340
series of short duration incubations

59
00:03:18,590 --> 00:03:15,530
using just the native sediments and

60
00:03:20,960 --> 00:03:18,600
amended with and without additional

61
00:03:22,729 --> 00:03:20,970
electron donor and the things I'd like

62
00:03:25,790 --> 00:03:22,739
to point out here is in this feature

63
00:03:27,500 --> 00:03:25,800

which they're the that figure which

64
00:03:30,650 --> 00:03:27,510
corresponds to material collected from

65
00:03:32,750 --> 00:03:30,660
the hot spring vent you have an almost

66
00:03:36,920 --> 00:03:32,760
equivalent level of iron reduction

67
00:03:39,170 --> 00:03:36,930
activity regardless of electron donor

68
00:03:41,870 --> 00:03:39,180
source whereas if you move a few meters

69
00:03:44,660 --> 00:03:41,880
away at site three there's still a

70
00:03:47,479 --> 00:03:44,670
measurable amount of activity of the

71
00:03:51,740 --> 00:03:47,489
organisms using their native carbon

72
00:03:54,170 --> 00:03:51,750
source but it's greatly reduced so this

73
00:03:57,819 --> 00:03:54,180
led us to the question of what is this

74
00:03:59,660 --> 00:03:57,829
internal carbon source is it coming from

75
00:04:03,289 --> 00:03:59,670
chemoautotrophs is it from the

76
00:04:05,810 --> 00:04:03,299
cyanobacterial community is it breakdown

77
00:04:08,479 --> 00:04:05,820
of plant or animal to trade detritus

78
00:04:12,020 --> 00:04:08,489
from the external environment whereas

79
00:04:15,800 --> 00:04:12,030
the carbon coming from so and we have

80
00:04:19,069 --> 00:04:15,810
16s data from this as well and several

81
00:04:21,140 --> 00:04:19,079
Oh to use related to an organism

82
00:04:24,650 --> 00:04:21,150
Ignasi bacterium while it is not

83
00:04:26,600 --> 00:04:24,660
implicated as an iron reducer it is very

84
00:04:31,320 --> 00:04:26,610
similar to this newly or a factor which

85
00:04:33,790 --> 00:04:31,330
I identified in the enrichment cultures

86
00:04:36,340 --> 00:04:33,800
taking a look now at the in Scituate

87
00:04:39,630 --> 00:04:36,350
vironment we collected a series of core

88
00:04:44,080 --> 00:04:39,640

samples moving down the flow path and

89
00:04:47,200 --> 00:04:44,090
the 16s data from these samples revealed

90
00:04:49,570 --> 00:04:47,210
sequences related to known with

91
00:04:52,690 --> 00:04:49,580
autotrophic iron oxidizers sitter

92
00:04:54,970 --> 00:04:52,700
oxidants and again this relative of a

93
00:05:00,040 --> 00:04:54,980
potential iron reducer Ignasi bacterial

94
00:05:03,670 --> 00:05:00,050
ease so magic and ohmic work flow I'll

95
00:05:06,130 --> 00:05:03,680
cover in brief you start out with a very

96
00:05:08,590 --> 00:05:06,140
complex community like chop the pots get

97
00:05:12,430 --> 00:05:08,600
all the DNA sequence it put it back

98
00:05:15,460 --> 00:05:12,440
together separate it out into bins which

99
00:05:17,950 --> 00:05:15,470
are you can think of as being different

100
00:05:19,720 --> 00:05:17,960
taxa within the community and then what

101
00:05:21,909 --> 00:05:19,730
we're really interested in is what is

102
00:05:26,290 --> 00:05:21,919
the metabolic potential of some of these

103
00:05:28,240 --> 00:05:26,300
these bins or taxa and we're taking a

104
00:05:33,010 --> 00:05:28,250
targeted meta genomic approach looking

105
00:05:35,680 --> 00:05:33,020
at which genes are appear to be involved

106
00:05:39,730 --> 00:05:35,690
in iron cycling and which ones are

107
00:05:43,240 --> 00:05:39,740
involved in carbon fixation so here we

108
00:05:47,500 --> 00:05:43,250
have the community of two metagenomes

109
00:05:49,840 --> 00:05:47,510
that I assembled from chocolate pots one

110
00:05:51,880 --> 00:05:49,850
is from water filtered from the vent

111
00:05:54,700 --> 00:05:51,890
pool and another one is a combined

112
00:05:56,560 --> 00:05:54,710
assembly from three of those sediment

113
00:06:02,230 --> 00:05:56,570

cores that I mentioned and once again

114
00:06:04,330 --> 00:06:02,240
you see bins related to this known with

115
00:06:09,640 --> 00:06:04,340
the autotroph and this possible iron

116
00:06:14,590 --> 00:06:09,650
reducer so thank you to Dave Emerson for

117
00:06:16,270 --> 00:06:14,600
the lovely introduction - I see - I will

118
00:06:18,730 --> 00:06:16,280
not be covering that in my talk because

119
00:06:20,969 --> 00:06:18,740
I found no homologues that in my system

120
00:06:23,770 --> 00:06:20,979
but I will be talking about this other

121
00:06:27,719 --> 00:06:23,780
electron or extracellular electron

122
00:06:30,940 --> 00:06:27,729
transfer system a pouring wrapped

123
00:06:33,159 --> 00:06:30,950
version where you have a pour in in

124
00:06:35,620 --> 00:06:33,169
opening in the outer membrane of the

125
00:06:37,659 --> 00:06:35,630
cell and a cytochrome which fits into

126
00:06:39,490 --> 00:06:37,669
that and is able to transfer electrons

127
00:06:41,830 --> 00:06:39,500
into or out of the cell depending on

128
00:06:43,350 --> 00:06:41,840
whether it's an iron oxidizer or I

129
00:06:47,040 --> 00:06:43,360
reducer

130
00:06:48,719 --> 00:06:47,050
and there's two homologs in particular I

131
00:06:52,740 --> 00:06:48,729
want to point out there's this MTO a

132
00:06:55,350 --> 00:06:52,750
system which is identified in said er

133
00:06:59,219 --> 00:06:55,360
oxidants and there's this geo factor

134
00:07:02,279 --> 00:06:59,229
like pouran cytochrome system and it's

135
00:07:06,779 --> 00:07:02,289
also been identified in that Ignasi

136
00:07:08,339 --> 00:07:06,789
bacterium organism these are just

137
00:07:11,100 --> 00:07:08,349
several different search tools that you

138
00:07:13,230 --> 00:07:11,110

can use hidden Markov models blastp

139
00:07:14,850 --> 00:07:13,240
homology many different ways to identify

140
00:07:15,839 --> 00:07:14,860
these genes but one of the more

141
00:07:19,860 --> 00:07:15,849
important things that we're interested

142
00:07:25,170 --> 00:07:19,870
in is the genomic context of these genes

143
00:07:28,080 --> 00:07:25,180
that genomically you need to find a pore

144
00:07:34,850 --> 00:07:28,090
in encoded next to one or several of

145
00:07:38,189 --> 00:07:34,860
these cytochromes okay we're looking for

146
00:07:40,050 --> 00:07:38,199
multiple co2 fixation pathways but for

147
00:07:43,679 --> 00:07:40,060
the sake of brevity I'm only going to

148
00:07:47,969 --> 00:07:43,689
cover Rubisco today so to quote my

149
00:07:51,749 --> 00:07:47,979
advisor if you identify a bin with an ET

150
00:07:54,119 --> 00:07:51,759
system and Rubisco that's a pretty good

151
00:07:57,379 --> 00:07:54,129
smoking gun of an organism that may be

152
00:08:01,140 --> 00:07:57,389
involved in a litter litho autotrophic

153
00:08:05,010 --> 00:08:01,150
lifestyle and we very similar search

154
00:08:09,329 --> 00:08:05,020
parameters for these genes so here I

155
00:08:13,740 --> 00:08:09,339
have a summary of all of the metagenomic

156
00:08:16,969 --> 00:08:13,750
bins from these two assemblies in red we

157
00:08:23,249 --> 00:08:16,979
have all of the bins that contained some

158
00:08:28,249 --> 00:08:23,259
model EEG system in yellow we have all

159
00:08:31,230 --> 00:08:28,259
of the bins that contained a hit for

160
00:08:34,139 --> 00:08:31,240
Rubisco and what we're mostly interested

161
00:08:36,569 --> 00:08:34,149
in is these bins that contained both

162
00:08:39,839 --> 00:08:36,579
systems and may be involved in chemo

163
00:08:41,459 --> 00:08:39,849

little otter trophy and then down here

164
00:08:44,010 --> 00:08:41,469
at the bottom are bins that were not

165
00:08:47,310 --> 00:08:44,020
involved in any of it

166
00:08:49,680 --> 00:08:47,320
so bringing this back to the two

167
00:08:52,050 --> 00:08:49,690
organisms that I've been mentioning

168
00:08:53,610 --> 00:08:52,060
throughout this talk the sitter oxidants

169
00:08:57,600 --> 00:08:53,620
and the ignominy she really is

170
00:09:00,269 --> 00:08:57,610
I just wanted to summarize the results

171
00:09:02,880 --> 00:09:00,279
in terms of those two organisms so up in

172
00:09:05,340 --> 00:09:02,890
gray we have the published genomes of

173
00:09:07,680 --> 00:09:05,350
these organisms and against utter

174
00:09:12,510 --> 00:09:07,690
oxidants containing this MTO system and

175
00:09:14,550 --> 00:09:12,520
Rubisco and the two related

176
00:09:17,190 --> 00:09:14,560
Ignasi bacterium and me leroy vector

177
00:09:20,519 --> 00:09:17,200
containing only that geo vector like TCC

178
00:09:21,360 --> 00:09:20,529
system whereas looking at the two

179
00:09:24,000 --> 00:09:21,370
metagenomes

180
00:09:27,360 --> 00:09:24,010
here we have a sitter oxidants relative

181
00:09:29,880 --> 00:09:27,370
that all of a sudden has a PCC system

182
00:09:34,769 --> 00:09:29,890
and we have these Ignasi bacterias that

183
00:09:38,100 --> 00:09:34,779
have MgO and Rubisco which is really

184
00:09:40,949 --> 00:09:38,110
interesting that sitter oxidants which

185
00:09:44,699 --> 00:09:40,959
is a known with autotrophic iron

186
00:09:46,590 --> 00:09:44,709
oxidizer contains PCC which so far has

187
00:09:48,990 --> 00:09:46,600
only been implicated in iron reduction

188
00:09:53,040 --> 00:09:49,000

so perhaps this is a relative that is

189
00:09:56,250 --> 00:09:53,050
able to carry out both iron oxidation

190
00:09:58,500 --> 00:09:56,260
and iron reduction and for the Ignasi

191
00:10:02,460 --> 00:09:58,510
bacteria Li's as I mentioned before has

192
00:10:06,389 --> 00:10:02,470
an e ET system and Rubisco so perhaps it

193
00:10:12,099 --> 00:10:06,399
is capable of carrying out a little odd

194
00:10:18,079 --> 00:10:15,710
so to wrap things up once again we have

195
00:10:21,049 --> 00:10:18,089
a highly active dissimilatory iron

196
00:10:23,599 --> 00:10:21,059
reducing community at the chocolate pots

197
00:10:25,819 --> 00:10:23,609
event and it is able to sustain itself

198
00:10:28,280 --> 00:10:25,829
using only the native carbon source

199
00:10:30,619 --> 00:10:28,290
we have metagenomic bins that are

200
00:10:33,799 --> 00:10:30,629
related to known and potential iron

201
00:10:36,289 --> 00:10:33,809
cycling microorganisms we have the

202
00:10:38,720 --> 00:10:36,299
positive identification of homologs of

203
00:10:41,629 --> 00:10:38,730
genes involved in both these eeet

204
00:10:43,970 --> 00:10:41,639
pathways and carbon fixation pathways

205
00:10:48,109 --> 00:10:43,980
and as a side note we're in the process

206
00:10:51,109 --> 00:10:48,119
of identifying lipid biomarkers from

207
00:10:54,049 --> 00:10:51,119
these materials to try and nail down a

208
00:10:57,829 --> 00:10:54,059
possible source of the carbon that's

209
00:11:01,749 --> 00:10:57,839
present in statue and one last thing I

210
00:11:05,150 --> 00:11:01,759
would like to mention so I only covered

211
00:11:06,349 --> 00:11:05,160
very briefly the model systems that

212
00:11:09,109 --> 00:11:06,359
we've been looking at but we've also

213
00:11:11,720 --> 00:11:09,119

expanded our search to look for non

214
00:11:14,769 --> 00:11:11,730
model ET systems and we're also looking

215
00:11:20,239 --> 00:11:14,779
at all of the known carbon fixation

216
00:11:22,189 --> 00:11:20,249
pathways in these systems and that I'd

217
00:11:25,099 --> 00:11:22,199
like to thank the organizers for the

218
00:11:26,659 --> 00:11:25,109
conference my funding my committee

219
00:11:29,479 --> 00:11:26,669
members who have helped with this

220
00:11:32,419 --> 00:11:29,489
project Eric and Eric and my colleagues

221
00:11:36,669 --> 00:11:32,429
back at UW Madison particularly Xiaomei

222
00:11:39,109 --> 00:11:36,679
hay who without her meta genomic

223
00:11:43,669 --> 00:11:39,119
expertise we would not have been able to

224
00:11:50,450 --> 00:11:43,679
do any of this so with that I think I

225
00:12:01,220 --> 00:11:52,460
so we definitely have time for a couple

226
00:12:03,590 --> 00:12:01,230
of questions Tim yeah yeah I really

227
00:12:06,020 --> 00:12:03,600
enjoy the Yellowstone toxemia yeah

228
00:12:09,680 --> 00:12:06,030
interesting it's a cool area

229
00:12:13,580 --> 00:12:09,690
so what non-model systems do you have in

230
00:12:17,390 --> 00:12:13,590
mind exactly as far as the Ichigo yeah

231
00:12:21,710 --> 00:12:17,400
yeah so again a lot of this credit goes

232
00:12:25,130 --> 00:12:21,720
to Xiaomei and her computer programming

233
00:12:27,950 --> 00:12:25,140
skills but we have scripts that were

234
00:12:31,700 --> 00:12:27,960
able to search our meta genomic

235
00:12:36,320 --> 00:12:31,710
sequences for the Keene binding site

236
00:12:38,480 --> 00:12:36,330
motifs and any genes that have that

237
00:12:41,960 --> 00:12:38,490
appear to be multicam cytochromes we

238
00:12:44,330 --> 00:12:41,970

then look for genes proximal to that

239
00:12:47,450 --> 00:12:44,340
that are predicted to be an outer

240
00:12:48,980 --> 00:12:47,460
membrane pore in so the ones that aren't

241
00:12:52,400 --> 00:12:48,990
homologous to any of the models but

242
00:12:55,000 --> 00:12:52,410
still seem to fit that same type of

243
00:12:59,560 --> 00:12:55,010
system with a pouran and a cytochrome

244
00:13:02,060 --> 00:12:59,570
what about the EPI or GOP ly any

245
00:13:05,660 --> 00:13:02,070
considerations about yeah so that's

246
00:13:08,110 --> 00:13:05,670
something that I've considered and we've

247
00:13:10,250 --> 00:13:08,120
discussed as a lab quite a bit but

248
00:13:13,640 --> 00:13:10,260
something that I I still need to

249
00:13:16,940 --> 00:13:13,650
investigate with these systems yeah

250
00:13:18,830 --> 00:13:16,950
thanks yeah welcome thank you so we

251
00:13:23,490 --> 00:13:18,840
still have time for another question if