New Pathways for Old Metals

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1
00:00:00,820 --> 00:00:09,310
[Music]

2
00:00:14,150 --> 00:00:11,690
so I'll be taking a step back from

3
00:00:16,070 --> 00:00:14,160
multicellularity but not all the way

4
00:00:18,859 --> 00:00:16,080
back to prebiotic chemistry so right in

5
00:00:20,779 --> 00:00:18,869
the middle are all of us microbiology is

6
00:00:24,700 --> 00:00:20,789
trying to understand the diversity in

7
00:00:27,140 --> 00:00:24,710
this tiny cellular organisms and

8
00:00:28,790 --> 00:00:27,150
originally I guess I got involved in

9
00:00:30,769 --> 00:00:28,800
microbiology or interested out of

10
00:00:32,990 --> 00:00:30,779
curiosity but in the context of

11
00:00:34,729 --> 00:00:33,000
astrobiology understanding the whole

12
00:00:39,049 --> 00:00:34,739
diversity of how single cells can make a

13
00:00:41,540 --> 00:00:39,059

living is important to understand or or

14
00:00:43,310 --> 00:00:41,550
choose proper targets for exploration

15
00:00:45,380 --> 00:00:43,320
beyond ocean worlds

16
00:00:47,479 --> 00:00:45,390
I also interpret the findings from the

17
00:00:49,400 --> 00:00:47,489
data that we get back from our

18
00:00:52,910 --> 00:00:49,410
explorations and perhaps also in the

19
00:00:55,939 --> 00:00:52,920
future once we if we understand how the

20
00:00:58,220 --> 00:00:55,949
breadth of these organism on niches we

21
00:01:00,200 --> 00:00:58,230
can prevent an planet cross

22
00:01:04,460 --> 00:01:00,210
contamination by preventing organisms

23
00:01:07,510 --> 00:01:04,470
from one body going into another so in

24
00:01:09,679 --> 00:01:07,520
order to do these we need to understand

25
00:01:15,320 --> 00:01:09,689
what is what is the life on how

26
00:01:17,719 --> 00:01:15,330
microorganisms make a living essentially

27
00:01:20,210 --> 00:01:17,729
this is something that already explained

28
00:01:21,469 --> 00:01:20,220
but if you want something to if you're

29
00:01:23,420 --> 00:01:21,479
looking for something that is alive that

30
00:01:26,749 --> 00:01:23,430
grows reproduces and undergoes evolution

31
00:01:28,219 --> 00:01:26,759
that organism needs to be able to do one

32
00:01:30,770 --> 00:01:28,229
fundamental thing which is obtain energy

33
00:01:33,740 --> 00:01:30,780
and the difference with us that we

34
00:01:36,560 --> 00:01:33,750
depend on oxygen microbes prokaryotes

35
00:01:39,440 --> 00:01:36,570
can employ a wide variety of substrate

36
00:01:41,859 --> 00:01:39,450
to get energy and what that that shows

37
00:01:43,670 --> 00:01:41,869
the redox hour shows is that as long as

38
00:01:47,359 --> 00:01:43,680

microorganisms can figure out the

39
00:01:50,210 --> 00:01:47,369
biochemical strategy that allows them to

40
00:01:52,460 --> 00:01:50,220
take something to transfer electrons and

41
00:01:53,990 --> 00:01:52,470
harness the energy from the transfer of

42
00:01:55,580 --> 00:01:54,000
electrons from something that has a low

43
00:01:58,429 --> 00:01:55,590
redox potential to a higher one and

44
00:02:01,060 --> 00:01:58,439
transform that into an 18-2 ATP then

45
00:02:03,679 --> 00:02:01,070
then can they can use the energy to

46
00:02:07,750 --> 00:02:03,689
perform a wide variety of functions and

47
00:02:11,980 --> 00:02:07,760
survive and on earth we have

48
00:02:14,410 --> 00:02:11,990
huge number of Nicias tiny and big and

49
00:02:17,350 --> 00:02:14,420
all sorts of microorganisms employing

50
00:02:19,840 --> 00:02:17,360
different strategies and we had our task

51
00:02:22,270 --> 00:02:19,850
as microbiologist in a way is to

52
00:02:24,400 --> 00:02:22,280
understand each one of them and see the

53
00:02:27,520 --> 00:02:24,410
potential for each one of them even

54
00:02:29,470 --> 00:02:27,530
though if on earth they are in very

55
00:02:34,690 --> 00:02:29,480
small niches they could be predominant

56
00:02:37,420 --> 00:02:34,700
in other planets but we don't not only

57
00:02:38,950 --> 00:02:37,430
have this huge planet to explore life we

58
00:02:41,650 --> 00:02:38,960
have four other Earth's to explore

59
00:02:44,080 --> 00:02:41,660
respiratory diversity perhaps not in

60
00:02:47,650 --> 00:02:44,090
this geographical space dimension but in

61
00:02:50,830 --> 00:02:47,660
time and as Marcus already showed the

62
00:02:52,540 --> 00:02:50,840
earth our earth went through different

63
00:02:55,450 --> 00:02:52,550

transition periods over time that

64
00:02:57,850 --> 00:02:55,460
depending on on oxygen levels driven in

65
00:03:02,560 --> 00:02:57,860
turn by microorganisms and in each one

66
00:03:04,150 --> 00:03:02,570
of these scenarios the earth had

67
00:03:05,800 --> 00:03:04,160
completely different environments that

68
00:03:07,960 --> 00:03:05,810
probably select four different types of

69
00:03:09,940 --> 00:03:07,970
organisms at the beginning where there

70
00:03:11,410 --> 00:03:09,950
was no oxygen the atmospheric

71
00:03:13,530 --> 00:03:11,420
composition was also very different

72
00:03:16,420 --> 00:03:13,540
probably full of methane or hydrogen and

73
00:03:18,280 --> 00:03:16,430
so different microorganisms that perhaps

74
00:03:21,220 --> 00:03:18,290
are not very abundant now probably were

75
00:03:23,830 --> 00:03:21,230
very abundant at the beginning in the

76
00:03:27,250 --> 00:03:23,840
future so accordion worlds and also the

77
00:03:29,020 --> 00:03:27,260
oxygen that was drove different other

78
00:03:30,970 --> 00:03:29,030
electron acceptor levels such as iron

79
00:03:33,370 --> 00:03:30,980
and manganese and other substrates that

80
00:03:35,710 --> 00:03:33,380
microorganisms could incorporate for

81
00:03:38,770 --> 00:03:35,720
life and to develop different strategies

82
00:03:40,449 --> 00:03:38,780
to breed and generate energy and I am

83
00:03:45,220 --> 00:03:40,459
interested in particularly in iron and

84
00:03:48,610 --> 00:03:45,230
manganese and we know the broad trend of

85
00:03:52,000 --> 00:03:48,620
iron coming down from millimolar micro

86
00:03:54,880 --> 00:03:52,010
molar levels to nano molars in which

87
00:03:59,410 --> 00:03:54,890
nowadays iron becomes even limiting for

88
00:04:01,780 --> 00:03:59,420

life manganese is also probably

89
00:04:05,340 --> 00:04:01,790
following a similar trend and both can

90
00:04:08,860 --> 00:04:05,350
be used by bacteria to harvest energy

91
00:04:11,520 --> 00:04:08,870
and nowadays in there are very small

92
00:04:15,580 --> 00:04:11,530
pockets of the earth where these ancient

93
00:04:16,870 --> 00:04:15,590
conditions prevail and we call them some

94
00:04:18,490 --> 00:04:16,880
of them have very similar

95
00:04:21,740 --> 00:04:18,500
characteristics let's such as high iron

96
00:04:24,020 --> 00:04:21,750
no oxygen and we call these ancient of

97
00:04:26,150 --> 00:04:24,030
like the one picture that you see there

98
00:04:28,760 --> 00:04:26,160
so our strategy if you want to look at

99
00:04:31,850 --> 00:04:28,770
potential primitive mechanisms for life

100
00:04:34,490 --> 00:04:31,860
not only now but also in the past is to

101
00:04:38,120 --> 00:04:34,500
explore this ancient ocean analogues and

102
00:04:41,030 --> 00:04:38,130
search for the metabolisms that we that

103
00:04:43,730 --> 00:04:41,040
were interested in so what that's what

104
00:04:45,710 --> 00:04:43,740
we did we trying to understand the

105
00:04:47,960 --> 00:04:45,720
different forms of manganese cycling in

106
00:04:50,300 --> 00:04:47,970
the environment we took samples from

107
00:04:52,940 --> 00:04:50,310
Lake Madonna which is the original high

108
00:04:55,340 --> 00:04:52,950
iron very low carbon ancient ocean

109
00:04:56,840 --> 00:04:55,350
analog that has a manganese cycle as you

110
00:04:58,690 --> 00:04:56,850
can see there it's likely driven by

111
00:05:01,960 --> 00:04:58,700
microbes that oxidized and reduced

112
00:05:07,190 --> 00:05:01,970
manganese which ends up precipitating

113
00:05:09,560 --> 00:05:07,200

but geochemists have looked at this at

114
00:05:12,130 --> 00:05:09,570
this lake for a long time but and so

115
00:05:14,480 --> 00:05:12,140
it's very well characterized in terms of

116
00:05:18,800 --> 00:05:14,490
readouts it's we know that it's

117
00:05:21,740 --> 00:05:18,810
permanently anoxic and an iron manganese

118
00:05:23,540 --> 00:05:21,750
are our big electron donors acceptors

119
00:05:25,700 --> 00:05:23,550
but we don't know much about who is

120
00:05:28,430 --> 00:05:25,710
doing who's doing what and who is

121
00:05:30,230 --> 00:05:28,440
responsible for the manganese cycling so

122
00:05:34,010 --> 00:05:30,240
the strategy that we employed was to

123
00:05:36,580 --> 00:05:34,020
take sediments from this lake cultivated

124
00:05:39,830 --> 00:05:36,590
under three goe conditions a lot of iron

125
00:05:42,080 --> 00:05:39,840
very low oxygen with the selection

126
00:05:44,360 --> 00:05:42,090
pressure of adding only manganese as the

127
00:05:45,860 --> 00:05:44,370
electron acceptor and over time we hope

128
00:05:47,420 --> 00:05:45,870
that we would I say late organisms

129
00:05:52,060 --> 00:05:47,430
involved in manganese cycle we would

130
00:05:54,740 --> 00:05:52,070
have pure beautiful cultures cells and

131
00:05:56,540 --> 00:05:54,750
we would transfer them over time to get

132
00:05:59,420 --> 00:05:56,550
rid of all the settlements and and other

133
00:06:03,050 --> 00:05:59,430
components to obtain microbes that only

134
00:06:06,350 --> 00:06:03,060
use manganese so what what we saw after

135
00:06:12,220 --> 00:06:06,360
several transfers over around about a

136
00:06:15,710 --> 00:06:12,230
year is that I wish either this and this

137
00:06:18,020 --> 00:06:15,720
essentially shows the community

138
00:06:23,060 --> 00:06:18,030

structure who is there and what we use

139
00:06:25,340 --> 00:06:23,070
is the 16s the ribosome RNA genes as a

140
00:06:27,560 --> 00:06:25,350
phylogenetic marker to extract the whole

141
00:06:30,710 --> 00:06:27,570
the composition of the whole community

142
00:06:33,409 --> 00:06:30,720
and see who is there and the most

143
00:06:34,549 --> 00:06:33,419
important point of this figure is to

144
00:06:36,409 --> 00:06:34,559
show you that

145
00:06:39,349 --> 00:06:36,419
Murdo cyclists and we'll call the yes

146
00:06:41,809 --> 00:06:39,359
these two green and blue bars that you

147
00:06:46,759 --> 00:06:41,819
can see after a few transfers but not on

148
00:06:50,569 --> 00:06:46,769
the original inoculum were appeared and

149
00:06:54,019 --> 00:06:50,579
they are both from the same group of

150
00:06:57,859 --> 00:06:54,029
bacteria called beta Proteobacteria so

151
00:07:01,279 --> 00:06:57,869
we wanted to trying to understand why

152
00:07:03,949 --> 00:07:01,289
those were enriched in our conditions so

153
00:07:07,549 --> 00:07:03,959
we wanted to dig deeper into what were

154
00:07:09,589 --> 00:07:07,559
they doing there and and who they

155
00:07:13,699 --> 00:07:09,599
actually were so we took the whole comes

156
00:07:16,339 --> 00:07:13,709
the whole set of complete sample of DNA

157
00:07:18,079 --> 00:07:16,349
and proteins together and we did

158
00:07:20,119 --> 00:07:18,089
metagenomics and meta proteomics what

159
00:07:22,549 --> 00:07:20,129
this means is that on one hand we took

160
00:07:24,739 --> 00:07:22,559
the DNA the DNA is sequenced into very

161
00:07:26,359 --> 00:07:24,749
small small fragments are sequenced and

162
00:07:28,669 --> 00:07:26,369
then by informatica ly they're put

163
00:07:31,549 --> 00:07:28,679

together into bigger chunks eventually

164
00:07:34,339 --> 00:07:31,559
maybe making a complete genome if

165
00:07:36,409 --> 00:07:34,349
depending on the on your sample on the

166
00:07:39,669 --> 00:07:36,419
other hand we took the complete set of

167
00:07:43,429 --> 00:07:39,679
proteins also little peptides were

168
00:07:46,489 --> 00:07:43,439
passed through LC ms/ms and that pattern

169
00:07:49,369 --> 00:07:46,499
that is generated was compared back to a

170
00:07:51,949 --> 00:07:49,379
theoretical pattern from the translated

171
00:07:53,419 --> 00:07:51,959
nucleotides from the DNA and that way

172
00:07:54,919 --> 00:07:53,429
you can see which proteins are expressed

173
00:07:57,350 --> 00:07:54,929
and we did that with the help of

174
00:08:02,359 --> 00:07:57,360
brooklyn doctrine and from the

175
00:08:05,629 --> 00:08:02,369
university of washington so what we we

176
00:08:07,879 --> 00:08:05,639
saw that these declare amana that we saw

177
00:08:09,829 --> 00:08:07,889
were and reached also we could we were

178
00:08:12,649 --> 00:08:09,839
able to get the whole genome from the

179
00:08:15,889 --> 00:08:12,659
community and we compared it with known

180
00:08:19,779 --> 00:08:15,899
the terminus species we confirmed that

181
00:08:22,219 --> 00:08:19,789
this belongs to that genus and we

182
00:08:24,139 --> 00:08:22,229
compare the genomes their identity of

183
00:08:27,069 --> 00:08:24,149
the genomes to the two more to the one

184
00:08:30,709 --> 00:08:27,079
most closely related with the most

185
00:08:32,779 --> 00:08:30,719
likely closest relative and we found

186
00:08:35,540 --> 00:08:32,789
that they were 85 percent identical so

187
00:08:37,429 --> 00:08:35,550
to assign two different organisms into

188
00:08:40,489 --> 00:08:37,439

the same species you need at least 95

189
00:08:42,829 --> 00:08:40,499
percent so with 85 percent we concluded

190
00:08:47,119 --> 00:08:42,839
that this was a new genomics and genomic

191
00:08:48,079 --> 00:08:47,129
species we that was enriching our

192
00:08:51,379 --> 00:08:48,089
culture but we

193
00:08:53,809 --> 00:08:51,389
are still we weren't able to isolate it

194
00:08:55,519 --> 00:08:53,819
yet so we're calling it Candida to the

195
00:08:58,369 --> 00:08:55,529
terminus of Kolkata because it's still

196
00:09:03,590 --> 00:08:58,379
hidden in our samples it was hidden

197
00:09:05,869 --> 00:09:03,600
originally in Lake maternal and but but

198
00:09:08,509 --> 00:09:05,879
what we did but mentor proteomic reveal

199
00:09:09,769 --> 00:09:08,519
does I was that it was responsible for

200
00:09:11,509 --> 00:09:09,779
seventy-three percent of all the

201
00:09:13,790 --> 00:09:11,519
peptides that we found which means that

202
00:09:16,460 --> 00:09:13,800
even though we didn't really thought

203
00:09:17,960 --> 00:09:16,470
that this was a the most predominant or

204
00:09:20,299 --> 00:09:17,970
dominant member of the community based

205
00:09:23,299 --> 00:09:20,309
on that one genetic marker it was the

206
00:09:26,989 --> 00:09:23,309
most active and the rest of the DNA was

207
00:09:29,239 --> 00:09:26,999
probably from dead cells or or by us

208
00:09:31,280 --> 00:09:29,249
from the PCR or the method itself that

209
00:09:35,239 --> 00:09:31,290
bias is is bias depending on how many

210
00:09:36,530 --> 00:09:35,249
copies of that 16s RNA gene you have so

211
00:09:39,110 --> 00:09:36,540
then we I'm not going to go into a

212
00:09:41,929 --> 00:09:39,120
detail so don't worry but we were

213
00:09:44,030 --> 00:09:41,939

curious to see what attributes what

214
00:09:49,309 --> 00:09:44,040
forms that what lifestyle this bacteria

215
00:09:51,410 --> 00:09:49,319
has and we were here is about two things

216
00:09:55,100 --> 00:09:51,420
one their ability to transform metals

217
00:09:56,329 --> 00:09:55,110
and another thing that colder attention

218
00:09:59,119 --> 00:09:56,339
was a presence of a denitrification

219
00:10:01,489 --> 00:09:59,129
pathway that was active even though we

220
00:10:04,069 --> 00:10:01,499
had hadn't added any substrate to

221
00:10:06,799 --> 00:10:04,079
express this pathway but that's another

222
00:10:09,650 --> 00:10:06,809
story but back to the multi the multi

223
00:10:12,049 --> 00:10:09,660
humid I said these type cytochromes this

224
00:10:16,759 --> 00:10:12,059
is probably a case of structure

225
00:10:20,030 --> 00:10:16,769
determines function that just heard so

226
00:10:20,900 --> 00:10:20,040
the one thing that we rarely pay

227
00:10:23,119 --> 00:10:20,910
attention to

228
00:10:24,919 --> 00:10:23,129
besides the redox potential of different

229
00:10:26,960 --> 00:10:24,929
substrates that organisms use to make

230
00:10:29,059 --> 00:10:26,970
energy one has to consider the

231
00:10:31,819 --> 00:10:29,069
availability how the organism sees it

232
00:10:33,559 --> 00:10:31,829
and how available it is to them and even

233
00:10:35,900 --> 00:10:33,569
though manganese and iron are pretty

234
00:10:40,129 --> 00:10:35,910
good electron acceptors closer to oxygen

235
00:10:41,989 --> 00:10:40,139
than sulfate and sometimes nitrate they

236
00:10:43,579 --> 00:10:41,999
are they depend on depending on the

237
00:10:46,460 --> 00:10:43,589
redox state of the metal they're going

238
00:10:47,269 --> 00:10:46,470

to be found in solid or soluble form so

239
00:10:50,799 --> 00:10:47,279
when organisms

240
00:10:54,470 --> 00:10:50,809
reduce it or oxidize it they're going to

241
00:10:56,059 --> 00:10:54,480
either find it in a in an oxide form so

242
00:10:57,619 --> 00:10:56,069
it means that they cannot get it inside

243
00:10:58,840 --> 00:10:57,629
the cell like we do with oxygen or

244
00:11:01,000 --> 00:10:58,850
nitrate

245
00:11:02,380 --> 00:11:01,010
some other organisms or they're going to

246
00:11:03,760 --> 00:11:02,390
produce an outside which means they're

247
00:11:07,030 --> 00:11:03,770
going to that is going to precipitate

248
00:11:08,710 --> 00:11:07,040
and organisms probably do not benefit

249
00:11:12,070 --> 00:11:08,720
from precipitating things inside their

250
00:11:14,170 --> 00:11:12,080
cells so in both cases whether an

251
00:11:19,000 --> 00:11:14,180
organism's organism is oxidizing or

252
00:11:21,190 --> 00:11:19,010
reducing somehow very interestingly they

253
00:11:22,630 --> 00:11:21,200
use the same type of machinery in a way

254
00:11:24,700 --> 00:11:22,640
biochemical machinery they use this

255
00:11:25,530 --> 00:11:24,710
electron conduit that is made of

256
00:11:27,850 --> 00:11:25,540
cytochromes

257
00:11:30,160 --> 00:11:27,860
in the case of metal reducers it's

258
00:11:32,440 --> 00:11:30,170
called MTR no reduction and in the case

259
00:11:34,720 --> 00:11:32,450
of mine of metal oxidizers it's called

260
00:11:38,350 --> 00:11:34,730
MTO or Pio depending on whether the

261
00:11:40,810 --> 00:11:38,360
organism is phototrophic or not so we

262
00:11:46,510 --> 00:11:40,820
saw for the first time in this type of

263
00:11:49,420 --> 00:11:46,520

species that this organism had this gene

264
00:11:52,540 --> 00:11:49,430
this conduit that all these genes were

265
00:11:54,610 --> 00:11:52,550
together in one operon and we couldn't

266
00:11:56,110 --> 00:11:54,620
find it in any other declare Moniz as

267
00:11:57,700 --> 00:11:56,120
you can see from this graph these are

268
00:11:59,800 --> 00:11:57,710
two copies if you put them in the

269
00:12:05,410 --> 00:11:59,810
contact of a tree with closer organisms

270
00:12:07,810 --> 00:12:05,420
that also have this dis conduit which is

271
00:12:09,610 --> 00:12:07,820
important because if we had just tried

272
00:12:11,530 --> 00:12:09,620
to look at the AG on its own in the math

273
00:12:12,790 --> 00:12:11,540
the complexity of the community we

274
00:12:15,490 --> 00:12:12,800
wouldn't have known it belonged to the

275
00:12:17,350 --> 00:12:15,500
determiners with the reason we know it's

276
00:12:19,480 --> 00:12:17,360
a declare - units because we mapped it

277
00:12:23,260 --> 00:12:19,490
back to the metagenomic beam that we

278
00:12:25,710 --> 00:12:23,270
obtained and this this gene and the

279
00:12:28,300 --> 00:12:25,720
architecture of this operon is also

280
00:12:30,010 --> 00:12:28,310
present in two other beta parameters

281
00:12:33,310 --> 00:12:30,020
that are uncultured so this whole branch

282
00:12:37,660 --> 00:12:33,320
here are uncultured organisms that have

283
00:12:39,550 --> 00:12:37,670
this same operon also these this conduit

284
00:12:41,950 --> 00:12:39,560
is not present in the only other declare

285
00:12:45,370 --> 00:12:41,960
ramona's that are is unknown iron metal

286
00:12:48,910 --> 00:12:45,380
oxidizer under anoxic conditions so this

287
00:12:53,560 --> 00:12:48,920
is pretty unique and new - - these novel

288
00:12:56,410 --> 00:12:53,570

species another correlated somehow

289
00:12:59,440 --> 00:12:56,420
correlated operon that was that we saw

290
00:13:03,070 --> 00:12:59,450
is this cytochrome C rich opera as you

291
00:13:05,470 --> 00:13:03,080
probably saw from other talks the

292
00:13:06,340 --> 00:13:05,480
cytochromes are really good heme groups

293
00:13:09,610 --> 00:13:06,350
are really good at transferring

294
00:13:11,460 --> 00:13:09,620
electrons so whenever we see multi heme

295
00:13:13,890 --> 00:13:11,470
cytochromes in an organism we

296
00:13:15,090 --> 00:13:13,900
typically can very confidently say that

297
00:13:16,770 --> 00:13:15,100
they're doing some sort of election

298
00:13:19,230 --> 00:13:16,780
transfer outside of the South especially

299
00:13:22,230 --> 00:13:19,240
when there are Decca hims ten teams or

300
00:13:23,880 --> 00:13:22,240
more than ten so again we saw this under

301
00:13:26,490 --> 00:13:23,890
kitchen that was present only in these

302
00:13:28,260 --> 00:13:26,500
species this new species but not there

303
00:13:30,960 --> 00:13:28,270
well at the other determiners relatives

304
00:13:32,970 --> 00:13:30,970
again present in uncultured beta

305
00:13:34,980 --> 00:13:32,980
Protectorate rota cyclase Angelina

306
00:13:38,550 --> 00:13:34,990
Nadia's which means that they must be

307
00:13:41,100 --> 00:13:38,560
doing something that we haven't figured

308
00:13:44,460 --> 00:13:41,110
out yet many as some of these that are

309
00:13:47,880 --> 00:13:44,470
cultured and that have this operon have

310
00:13:52,740 --> 00:13:47,890
also been shown to be involved in metal

311
00:13:56,940 --> 00:13:52,750
cycling and we were also surprised to

312
00:14:00,420 --> 00:13:56,950
see this is just three examples of this

313
00:14:02,670 --> 00:14:00,430

whole genome nitrous oxide reductase is

314
00:14:04,950 --> 00:14:02,680
which means that is part of the DNA

315
00:14:07,140 --> 00:14:04,960
traffic Asian pathway it's not really

316
00:14:09,960 --> 00:14:07,150
important to the story but what is

317
00:14:13,130 --> 00:14:09,970
important is that these genome this

318
00:14:16,080 --> 00:14:13,140
strain as opposed to the other ones was

319
00:14:17,820 --> 00:14:16,090
highly enriched in sensors including in

320
00:14:19,800 --> 00:14:17,830
this nitrous oxide reductase operon

321
00:14:25,620 --> 00:14:19,810
which was pretty unique compared to the

322
00:14:27,000 --> 00:14:25,630
others which means it may use the one

323
00:14:30,210 --> 00:14:27,010
thing that I did not mention is that the

324
00:14:32,100 --> 00:14:30,220
reversibility of this conduit has been

325
00:14:34,530 --> 00:14:32,110
seen in many organisms for example metal

326
00:14:36,600 --> 00:14:34,540
reducers when you can reduce also

327
00:14:38,460 --> 00:14:36,610
electrodes if you instead of a metal you

328
00:14:40,020 --> 00:14:38,470
have an electrode but depending on the

329
00:14:45,150 --> 00:14:40,030
redox potential of the electron you can

330
00:14:46,830 --> 00:14:45,160
make the electrons go back so and many

331
00:14:48,150 --> 00:14:46,840
organisms change their metabolism

332
00:14:50,190 --> 00:14:48,160
depending on the redox potential of

333
00:14:54,090 --> 00:14:50,200
their environment so the high

334
00:14:56,400 --> 00:14:54,100
concentration of redox sensors in in

335
00:14:58,620 --> 00:14:56,410
metal reduction pathways coupled to

336
00:15:01,680 --> 00:14:58,630
nitrogen it could be an indication of

337
00:15:03,600 --> 00:15:01,690
the highly versatile flexible metabolism

338
00:15:07,860 --> 00:15:03,610

of these beta Porter bacterias in these

339
00:15:10,860 --> 00:15:07,870
unique environments so I'll just wrap it

340
00:15:14,460 --> 00:15:10,870
up by saying a couple of conclusions

341
00:15:15,690 --> 00:15:14,470
from from this short story is that doing

342
00:15:17,610 --> 00:15:15,700
this enrichment and putting the

343
00:15:19,410 --> 00:15:17,620
selection pressure allowed us to magnify

344
00:15:21,960 --> 00:15:19,420
the existence of this novel conduit

345
00:15:23,000 --> 00:15:21,970
which we will have seen by targeting the

346
00:15:28,010 --> 00:15:23,010
whole

347
00:15:30,350 --> 00:15:28,020
in situ even because the concentration

348
00:15:34,790 --> 00:15:30,360
of this population was very small the

349
00:15:36,770 --> 00:15:34,800
abundance at the same time because we

350
00:15:38,870 --> 00:15:36,780
enrich we were able to capture a genome

351
00:15:42,590 --> 00:15:38,880
by genomic meaning and that constraints

352
00:15:44,810 --> 00:15:42,600
how who we assigned this dysfunction to

353
00:15:47,980 --> 00:15:44,820
if we had just looked at a bunch of

354
00:15:51,260 --> 00:15:47,990
genes from the from the public from the

355
00:15:52,880 --> 00:15:51,270
community in situ we would have probably

356
00:15:54,920 --> 00:15:52,890
mapped it to one of different completely

357
00:15:56,330 --> 00:15:54,930
different species but now here we have

358
00:15:58,190 --> 00:15:56,340
it in the concept context of a whole

359
00:15:59,870 --> 00:15:58,200
organism and that's what we're looking

360
00:16:03,500 --> 00:15:59,880
for we're trying to understand the

361
00:16:05,300 --> 00:16:03,510
evolution of organisms big and this

362
00:16:07,370 --> 00:16:05,310
probably is the product of lateral gene

363
00:16:10,160 --> 00:16:07,380

transfer but we were able to map it

364
00:16:14,240 --> 00:16:10,170
straight on to these one species and

365
00:16:17,420 --> 00:16:14,250
also thanks to my proteomics and meta

366
00:16:19,940 --> 00:16:17,430
meta genomics we can see that this whole

367
00:16:21,410 --> 00:16:19,950
opera not just one particular gene but

368
00:16:23,150 --> 00:16:21,420
different operands we could see them

369
00:16:26,240 --> 00:16:23,160
again expressed on different samples

370
00:16:27,890 --> 00:16:26,250
from different locations so now even

371
00:16:29,870 --> 00:16:27,900
though we were not able to isolate one

372
00:16:31,670 --> 00:16:29,880
species we can collect all this

373
00:16:35,630 --> 00:16:31,680
information and perhaps that will guide

374
00:16:37,580 --> 00:16:35,640
us to further efforts in isolation or

375
00:16:40,550 --> 00:16:37,590
understanding what can they be doing as

376
00:16:42,980 --> 00:16:40,560
opposed to having one single cell in the

377
00:16:45,740 --> 00:16:42,990
lab and I'm still working on trying to

378
00:16:47,710 --> 00:16:45,750
isolate this beta protect area too

379
00:16:50,090 --> 00:16:47,720
because we do need to characterize

380
00:16:54,140 --> 00:16:50,100
biochemically everything that we see

381
00:16:56,870 --> 00:16:54,150
from our meta proteome original and I

382
00:16:58,670 --> 00:16:56,880
also would like to thank the full

383
00:17:00,320 --> 00:16:58,680
astrobiology community it's very

384
00:17:04,430 --> 00:17:00,330
inspiring to be here and listening to

385
00:17:06,380 --> 00:17:04,440
all it talks and Jen glasses lab but

386
00:17:07,670 --> 00:17:06,390
also other mentors that I've been having

387
00:17:10,819 --> 00:17:07,680
for the past two years like Chris