Examine the eDNA preference

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Extract community DNA

Feed DNA to *Haloferax volcanii* DS2 (2x)

Grow to stationary phase

Remove cells and extract remaining supernatant DNA

Sequence post feeding metagenomes

Sequence pre feeding metagenomes

Illumina MiSeq

Analysis

DNA features

1
00:00:10,940 --> 00:00:08,059
today I'm going to talk about a very

2
00:00:16,129 --> 00:00:10,950
interesting behavior of those solving

3
00:00:17,630 --> 00:00:16,139
microbes and then well before I started

4
00:00:21,019 --> 00:00:17,640
I would like to thank all my

5
00:00:23,630 --> 00:00:21,029
collaborators my lab mates or the grants

6
00:00:25,730 --> 00:00:23,640
support this project particularly AB

7
00:00:31,279 --> 00:00:25,740
grant committee to give me the chance to

8
00:00:36,049 --> 00:00:31,289
present here so this story besides the

9
00:00:40,930 --> 00:00:36,059
original of life it's more than like how

10
00:00:44,000 --> 00:00:40,940
life could adapt to beyond the earth

11
00:00:47,360 --> 00:00:44,010
particularly we already have the

12
00:00:51,490 --> 00:00:47,370
evidence that on Mars we have found the

13
00:00:54,229 --> 00:00:51,500

liquid water in the brine deposit so

14
00:00:59,950 --> 00:00:54,239
make this so loving microbes could be

15
00:01:05,479 --> 00:00:59,960
the very promising candidate to survivor

16
00:01:09,710 --> 00:01:05,489
clients are like for example Mars so on

17
00:01:14,630 --> 00:01:09,720
the earth actually we already are simple

18
00:01:18,050 --> 00:01:14,640
der study this micro communities all all

19
00:01:21,560 --> 00:01:18,060
over the world and then we call this if

20
00:01:24,770 --> 00:01:21,570
you're not familiar hello files so the

21
00:01:27,260 --> 00:01:24,780
whole group of microbes called and here

22
00:01:30,649 --> 00:01:27,270
is an example what are this kind of

23
00:01:33,370 --> 00:01:30,659
habitat looks like so this area connect

24
00:01:37,039 --> 00:01:33,380
to the sea water with relative low

25
00:01:41,240 --> 00:01:37,049
concentration of the salinity and this

26
00:01:44,420 --> 00:01:41,250
area is a red color area have a high

27
00:01:46,580 --> 00:01:44,430
salt concentration and this color is

28
00:01:51,170 --> 00:01:46,590
meaning because of those microbes living

29
00:01:54,410 --> 00:01:51,180
this region and this small area is

30
00:01:59,440 --> 00:01:54,420
artificial source and pan so evaporate

31
00:02:02,030 --> 00:01:59,450
the liquid water to extract salt so

32
00:02:04,459 --> 00:02:02,040
normally those region will have the

33
00:02:07,100 --> 00:02:04,469
concentration gradient in some of those

34
00:02:09,380 --> 00:02:07,110
pant or have a really high concentration

35
00:02:12,040 --> 00:02:09,390
you can see they already started to

36
00:02:13,880 --> 00:02:12,050
crystallize the crust all those

37
00:02:17,260 --> 00:02:13,890
concentration gradient

38
00:02:19,940 --> 00:02:17,270

the hell file communities have been fund

39
00:02:22,340 --> 00:02:19,950
so one of the challenge for those

40
00:02:27,220 --> 00:02:22,350
microbes survive in this type of

41
00:02:31,510 --> 00:02:27,230
environment is resource limitation okay

42
00:02:34,150 --> 00:02:31,520
however ah there's a one potential

43
00:02:37,370 --> 00:02:34,160
resources might be available for them

44
00:02:41,150 --> 00:02:37,380
which is the extracellular DNA molecule

45
00:02:43,970 --> 00:02:41,160
so if we think about DNA molecules we

46
00:02:47,060 --> 00:02:43,980
first will think they are genetic

47
00:02:50,920 --> 00:02:47,070
information carrier but actually as the

48
00:02:55,160 --> 00:02:50,930
large organic molecules there are also

49
00:02:59,060 --> 00:02:55,170
very nutrition to see that and then

50
00:03:02,420 --> 00:02:59,070
where it come from it could from in all

51
00:03:06,080 --> 00:03:02,430
the organisms those individual they die

52
00:03:12,050 --> 00:03:06,090
and those DNA materials or release from

53
00:03:14,660 --> 00:03:12,060
the cell so basically it exists in all

54
00:03:19,460 --> 00:03:14,670
type of ecosystem and kind of abundant

55
00:03:23,360 --> 00:03:19,470
and it has been found that some microbes

56
00:03:27,020 --> 00:03:23,370
species will take this ed na as

57
00:03:31,220 --> 00:03:27,030
nutritional supply so the question is is

58
00:03:34,940 --> 00:03:31,230
the hell file could do this so the

59
00:03:39,140 --> 00:03:34,950
answer is yes so this experiment is

60
00:03:41,569 --> 00:03:39,150
performed in dr. Parker slab showing by

61
00:03:44,870 --> 00:03:41,579
fitting this species health Eric's

62
00:03:50,229 --> 00:03:44,880
bikini I which is model species of how

63
00:03:53,300 --> 00:03:50,239

hello files so it can grow on IDI na but

64
00:03:56,180 --> 00:03:53,310
the thing is depends on where the

65
00:04:00,009 --> 00:03:56,190
stealing Eden income from its

66
00:04:03,560 --> 00:04:00,019
selectively picking for example here

67
00:04:06,830 --> 00:04:03,570
health Eric's will grow on the E DNA

68
00:04:10,930 --> 00:04:06,840
from itself but it won't grow on the DNA

69
00:04:14,360 --> 00:04:10,940
from hearing or e coli so this results

70
00:04:16,789 --> 00:04:14,370
we want to ask like okay what type of

71
00:04:19,400 --> 00:04:16,799
look II DNA they prefer what's the

72
00:04:23,270 --> 00:04:19,410
characteristic of those consumed DNA

73
00:04:26,750 --> 00:04:23,280
molecules right so talk about DNA

74
00:04:30,290 --> 00:04:26,760
molecules so here our many

75
00:04:33,230 --> 00:04:30,300
using two while you used characters to

76
00:04:36,950 --> 00:04:33,240
describe the features of DNA why is this

77
00:04:40,960 --> 00:04:36,960
GC content so DNA molecules have four

78
00:04:44,420 --> 00:04:40,970
bases a tgc so GC content basically

79
00:04:46,870 --> 00:04:44,430
calculate the percentage of GC in

80
00:04:51,080 --> 00:04:46,880
certain region could be genome

81
00:04:56,780 --> 00:04:51,090
chromosome or any region were interested

82
00:04:59,720 --> 00:04:56,790
in another thing is the DNA modification

83
00:05:03,920 --> 00:04:59,730
pattern specifically is a methylation

84
00:05:08,030 --> 00:05:03,930
pattern so here this three figures show

85
00:05:12,320 --> 00:05:08,040
three type of methylation for bacteria

86
00:05:15,020 --> 00:05:12,330
and nakia so what type of methylation

87
00:05:18,530 --> 00:05:15,030
will happen or generate here depends on

88
00:05:22,760 --> 00:05:18,540

the methylation enzymes this species

89
00:05:25,730 --> 00:05:22,770
have or carry and then different

90
00:05:28,970 --> 00:05:25,740
methylation enzyme normally have a

91
00:05:32,870 --> 00:05:28,980
specific recognition motif which is

92
00:05:35,450 --> 00:05:32,880
small DNA regions for example later

93
00:05:39,350 --> 00:05:35,460
we'll talk about the methylation enzyme

94
00:05:44,980 --> 00:05:39,360
of Health erics which using this CTA GC

95
00:05:48,530 --> 00:05:44,990
tag motif as a recognition region so to

96
00:05:52,390 --> 00:05:48,540
exam what type of a DNA they prefer to

97
00:05:55,790 --> 00:05:52,400
take we design this experiment so first

98
00:05:59,900 --> 00:05:55,800
extract the community DNA from certain

99
00:06:03,100 --> 00:05:59,910
pound and then part of it directly being

100
00:06:07,340 --> 00:06:03,110
sequenced so we obtain this pre fitting

101
00:06:10,640 --> 00:06:07,350
meta-genome dead data another part used

102
00:06:13,910 --> 00:06:10,650
as edu a source to fit the health erics

103
00:06:16,970 --> 00:06:13,920
and after feeding treatment or sequence

104
00:06:19,310 --> 00:06:16,980
the post feeling same how to obtain the

105
00:06:22,340 --> 00:06:19,320
post feeding meta-genome then we'll

106
00:06:27,200 --> 00:06:22,350
compare is pre fitting and post feeding

107
00:06:30,950 --> 00:06:27,210
sample to check like DNA features or DNA

108
00:06:34,330 --> 00:06:30,960
future changes of those groups so here

109
00:06:38,180 --> 00:06:34,340
is the summary of the results to this

110
00:06:40,150 --> 00:06:38,190
purple pink circle is the pre feeding

111
00:06:43,219 --> 00:06:40,160
sample blue

112
00:06:47,180 --> 00:06:43,229
Circle is the post feeding sample so the

113
00:06:49,490 --> 00:06:47,190

overlap area is those DNA occur in both

114
00:06:52,129 --> 00:06:49,500
samples so they're like basically

115
00:06:55,600 --> 00:06:52,139
haven't been consumed so we call the

116
00:06:58,129 --> 00:06:55,610
leftover group and then this area is

117
00:07:00,650 --> 00:06:58,139
particularly interesting is the only

118
00:07:03,520 --> 00:07:00,660
occurred in pre feeding sample but

119
00:07:06,980 --> 00:07:03,530
disappear in post feeding samples so

120
00:07:09,200 --> 00:07:06,990
potentially being consumed so we call

121
00:07:11,810 --> 00:07:09,210
the eaten group then things where we

122
00:07:14,629 --> 00:07:11,820
repeat that experiment twice so

123
00:07:16,430 --> 00:07:14,639
eventually we obtain two replicates and

124
00:07:19,640 --> 00:07:16,440
then the results are pretty consistent

125
00:07:22,610 --> 00:07:19,650
are there about eight point three eight

126
00:07:27,740 --> 00:07:22,620
point five percent of the DNA have been

127
00:07:32,180 --> 00:07:27,750
consumed then next about the GC content

128
00:07:36,050 --> 00:07:32,190
of those groups are this purple curve is

129
00:07:39,560 --> 00:07:36,060
the leftover group which is pretty

130
00:07:41,300 --> 00:07:39,570
similar to this black curve is the GC

131
00:07:44,779 --> 00:07:41,310
content distribution of the total

132
00:07:49,839 --> 00:07:44,789
community sample however the eaten group

133
00:07:53,870 --> 00:07:49,849
which is this red orange curve showing

134
00:07:55,879 --> 00:07:53,880
they have the bias towards the lower GC

135
00:07:59,629 --> 00:07:55,889
content indicate the health Eric's

136
00:08:04,010 --> 00:07:59,639
prefer to take the DNA with lower GC

137
00:08:06,950 --> 00:08:04,020
cannon and since the GC content of

138
00:08:10,939 --> 00:08:06,960

genome when we talk about that it's it

139
00:08:13,040 --> 00:08:10,949
has it's basically species-specific so

140
00:08:15,770 --> 00:08:13,050
different species normally have

141
00:08:20,029 --> 00:08:15,780
different GC content our average for

142
00:08:24,649 --> 00:08:20,039
their genome so we want you a check if

143
00:08:29,750 --> 00:08:24,659
this load GC content is contribute to by

144
00:08:32,740 --> 00:08:29,760
specific species so next we do a

145
00:08:36,640 --> 00:08:32,750
taxonomy analysis to analyze the

146
00:08:38,779 --> 00:08:36,650
composition of our sample so here is the

147
00:08:40,969 --> 00:08:38,789
compensation of the total community

148
00:08:44,029 --> 00:08:40,979
sample different color represents

149
00:08:48,230 --> 00:08:44,039
different than general settings this

150
00:08:50,510 --> 00:08:48,240
taxonomy is in genus level and then the

151
00:08:53,570 --> 00:08:50,520
leftover groups showing a very similar

152
00:08:56,690 --> 00:08:53,580
pattern to the entire community sample

153
00:09:00,710 --> 00:08:56,700
however this eatin group are

154
00:09:03,890 --> 00:09:00,720
significantly different and I check all

155
00:09:07,610 --> 00:09:03,900
the species in those general and haven't

156
00:09:10,580 --> 00:09:07,620
found no specific species abundance

157
00:09:14,600 --> 00:09:10,590
pieces in this group have low GC content

158
00:09:18,650 --> 00:09:14,610
so is this suggests this low GC content

159
00:09:21,650 --> 00:09:18,660
bias could maybe just from like some

160
00:09:26,420 --> 00:09:21,660
region of the genome or have lower GC

161
00:09:28,700 --> 00:09:26,430
content and they take that next about

162
00:09:31,580 --> 00:09:28,710
the methylation pattern so already

163
00:09:38,170 --> 00:09:31,590

mentioned hello ferrets have this

164
00:09:42,410 --> 00:09:38,180
methylation enzyme using seatac motif so

165
00:09:45,710 --> 00:09:42,420
with then if the other species in this

166
00:09:49,180 --> 00:09:45,720
eating group also share this gene then

167
00:09:53,480 --> 00:09:49,190
eventually you will generate similar

168
00:09:56,660 --> 00:09:53,490
methylation pattern so here we exam the

169
00:09:59,990 --> 00:09:56,670
presence absence status of those of this

170
00:10:03,050 --> 00:10:00,000
gene in all those species in the eating

171
00:10:06,470 --> 00:10:03,060
group and then if all the species in

172
00:10:10,220 --> 00:10:06,480
this genus have this gene we color in

173
00:10:14,210 --> 00:10:10,230
dark purple if none of the species in

174
00:10:19,220 --> 00:10:14,220
genus have this gene then we'll color in

175
00:10:23,420 --> 00:10:19,230
white so to map the status here we can

176
00:10:26,450 --> 00:10:23,430
show or we can see a lot of genus or

177
00:10:33,230 --> 00:10:26,460
species in this eating group actually

178
00:10:38,710 --> 00:10:33,240
share this methylation enzyme and we

179
00:10:42,410 --> 00:10:38,720
also connect this presence/absence

180
00:10:46,370 --> 00:10:42,420
status of this gene to this bundles

181
00:10:50,780 --> 00:10:46,380
change changes of those group so here

182
00:10:54,140 --> 00:10:50,790
this green arrow connect the genus if

183
00:10:57,830 --> 00:10:54,150
their proportion increased in Eden group

184
00:11:01,280 --> 00:10:57,840
compared to the proportion in the entire

185
00:11:04,460 --> 00:11:01,290
community sample and then the orange

186
00:11:07,280 --> 00:11:04,470
arrow connect the opposite so if this

187
00:11:09,650 --> 00:11:07,290
genus the proportion decreased

188
00:11:12,249 --> 00:11:09,660

in the Ealing group compared to the

189
00:11:15,889 --> 00:11:12,259
proportion in an entire community sample

190
00:11:19,160 --> 00:11:15,899
anyways can see there is a a very strong

191
00:11:23,120 --> 00:11:19,170
correlation pattern here is almost all

192
00:11:27,699 --> 00:11:23,130
the green error eral have a cross 12

193
00:11:31,999 --> 00:11:27,709
dark purple dot here or the orange arrow

194
00:11:34,670 --> 00:11:32,009
they have like white dot so meaning they

195
00:11:37,999 --> 00:11:34,680
don't have this gene so this results

196
00:11:40,550 --> 00:11:38,009
might suggest the sharing the similar

197
00:11:44,809 --> 00:11:40,560
methylation pattern could be a signal

198
00:11:48,889 --> 00:11:44,819
for to determine if health Eric's will

199
00:11:53,329 --> 00:11:48,899
pick this gene or not so a quick summary

200
00:11:56,600 --> 00:11:53,339
here so health Eric's makini I prefer to

201
00:12:00,110 --> 00:11:56,610
take the e DNA with lower GC content and

202
00:12:04,939 --> 00:12:00,120
similar methylation pattern and with

203
00:12:07,819 --> 00:12:04,949
this information we wonder if we put

204
00:12:09,800 --> 00:12:07,829
those species sharing this stimulant

205
00:12:13,420 --> 00:12:09,810
methylation pattern together to form a

206
00:12:16,790 --> 00:12:13,430
community and then my former our

207
00:12:20,509 --> 00:12:16,800
resource recycling system then this

208
00:12:23,720 --> 00:12:20,519
might be a really nice strategy to adapt

209
00:12:27,220 --> 00:12:23,730
the inning source limited environment

210
00:12:32,269 --> 00:12:27,230
which you know if this system can work

211
00:12:36,889 --> 00:12:32,279
then I guess hello file commit whom we

212
00:12:42,570 --> 00:12:36,899
work better okay so with that I would

213
00:12:50,260 --> 00:12:47,920

thank you sing oh yeah I was wondering

214
00:12:52,720 --> 00:12:50,270
if you looked for the that specific

215
00:12:56,130 --> 00:12:52,730
motif in the not eaten organisms as well

216
00:12:59,130 --> 00:12:56,140
and found that it wasn't present ah

217
00:13:04,990 --> 00:12:59,140
didn't do you know what I mean yeah but

218
00:13:08,560 --> 00:13:05,000
because the well if we see they actually

219
00:13:12,930 --> 00:13:08,570
are so those groups are actually pretty

220
00:13:17,530 --> 00:13:12,940
similar to the total community structure

221
00:13:22,110 --> 00:13:17,540
to the committee samples so basically we

222
00:13:25,960 --> 00:13:22,120
already check if they did if those

223
00:13:29,910 --> 00:13:25,970
groups share that gene his you know in

224
00:13:33,120 --> 00:13:29,920
the Eden group they actually have more

225
00:13:36,760 --> 00:13:33,130
general stand out compared to the

226
00:13:39,280 --> 00:13:36,770
community symbol so we did check those

227
00:13:50,740 --> 00:13:39,290
so they are already included sort of

228
00:13:54,730 --> 00:13:50,750
included in this group thank you um so I

229
00:13:57,430 --> 00:13:54,740
was wondering I is there any other kind

230
00:14:00,970 --> 00:13:57,440
of DNA that the hayloft Eric's likes to

231
00:14:04,060 --> 00:14:00,980
eat more than its own or does it it

232
00:14:06,280 --> 00:14:04,070
doesn't always go for its its own kind

233
00:14:14,380 --> 00:14:06,290
of DNA first and then things that are

234
00:14:16,300 --> 00:14:14,390
similar ah yeah all we have some before

235
00:14:21,400 --> 00:14:16,310
we do they will have some hypotheses

236
00:14:24,640 --> 00:14:21,410
like if they take DNA from you know the

237
00:14:30,340 --> 00:14:24,650
taxonomy resources saying if they're

238
00:14:32,550 --> 00:14:30,350

from like clothes related species but it

239
00:14:36,010 --> 00:14:32,560
turns out it determined by the

240
00:14:38,040 --> 00:14:36,020
methylation pattern but sharing the

241
00:14:40,930 --> 00:14:38,050
similar methylation pattern doesn't

242
00:14:49,180 --> 00:14:40,940
necessarily mean they are closed related

243
00:14:51,460 --> 00:14:49,190
species so yes so like those are species

244
00:14:53,650 --> 00:14:51,470
in those chilling those general they

245
00:14:55,750 --> 00:14:53,660
they sharing this method similar

246
00:14:58,710 --> 00:14:55,760
methylation pattern but on the phylogeny

247
00:15:01,270 --> 00:14:58,720
fellow genetic tree they are not really

248
00:15:03,870 --> 00:15:01,280
clustering together or they don't have

249
00:15:10,290 --> 00:15:03,880
those kind of pattern they just widely

250
00:15:15,850 --> 00:15:13,900
alright one last question okay so

251
00:15:18,460 --> 00:15:15,860
obviously you haven't done this here but

252
00:15:19,960 --> 00:15:18,470
has anybody looked into how much of the

253
00:15:22,380 --> 00:15:19,970
DNA that's eaten is actually

254
00:15:27,640 --> 00:15:22,390
incorporated into the bacterial

255
00:15:30,700 --> 00:15:27,650
chromosome ah you mean like map them to

256
00:15:32,860 --> 00:15:30,710
the back to that yeah like you'd have to

257
00:15:37,450 --> 00:15:32,870
do it with a monoculture and not like

258
00:15:41,770 --> 00:15:37,460
this community like you did here um you

259
00:15:46,650 --> 00:15:41,780
know because this group is now first

260
00:15:49,480 --> 00:15:46,660
it's not just from one species so well

261
00:15:52,180 --> 00:15:49,490
it definitely could try to yeah I

262
00:15:55,810 --> 00:15:52,190
haven't done that yet but I have those

263
00:15:59,880 --> 00:15:55,820

like all the DNA because this is I have

264
00:16:01,630 --> 00:15:59,890
those metagenomic samples from all those

265
00:16:04,000 --> 00:16:01,640
generals

266
00:16:06,610 --> 00:16:04,010
okay no I was just asking if anybody has

267
00:16:08,890 --> 00:16:06,620
done it with like a monoculture of one

268
00:16:12,760 --> 00:16:08,900
representative of one of these species

269
00:16:16,090 --> 00:16:12,770
that eats DNA oh yeah I haven't heard

270
00:16:20,230 --> 00:16:16,100
that because for the hell files those

271
00:16:22,630 --> 00:16:20,240
are all the all those are most most of

272
00:16:25,300 --> 00:16:22,640
them except this one thing most of them

273
00:16:28,810 --> 00:16:25,310
are archaea and i think as i know

274
00:16:31,840 --> 00:16:28,820
besides health eric's bikini I their

275
00:16:33,940 --> 00:16:31,850
only few species are successfully cut

276
00:16:36,820 --> 00:16:33,950
you know and can culturing the lab and a